

		GTG GA GGTTCTTTTT		
		AC A		
GAM1759	KIAA1877	3' CTTATTCTTCTGCCATGAGT 66748	CCA__	
		ACTC AGAAGAATAAG		
		TGAG TCTTCTTATTC		
		TACCG		
GAM1759	KIAA1906	3' CTTATTCTTCTTGACTTTTGG 73571	CTCC_	
		CCA CAAGAAGAATAAG		
		GGT GTTCTTCTTATTC		
		TTTCA		
GAM1759	OSBPL11	3' CTTAATTTCCCAAGAGTGGTG 43206	CCAA AA	
		CACCACTC GAAG TAAG		
		GTGGTGAG CTTT ATTC		
		AACC A_		
GAM1759	YME1L1	3' TCATTCTTGATGTGGTGTA 58438	TCC _	
		TACACCAC CAAGAA GA		
		ATGTGGTG GTTCTT CT		
		TA_ A		
GAM1759	ZNF262	3' CTTATTTTGTGTTGGGAGT 18723	A	
		ACTCCCAAG AGAATAAG		
		TGAGGGTTT TTTTATTC		
		G		
GAM1759	LOC91960	3' TGTGGCTTGGAACGTGGTGTA 68294	TC_ AAGA	
		TACACCAC CCAAG ATA		
		ATGTGGTG GGTTT TGT		
		CAA GG__		
GAM1760	CYP4A11	3' AACTCCTGCCTGCCCTCCA 7584	AA _	
		TGGA GCAGGTAG AGTT		
		ACCT CGTCCGTC TCAA		
		CC C		
GAM1760	EHD2	3' AAGCCAAGGCTTCTTCCCA 28207	A C AGAG	
		TGG AAG AGGT TTGGCTT		
		ACC TTC TTCG AACCGAA		
		C _ G__		
GAM1760	GALE	3' AAAGCAGCAGCTGCCTGCTCTC 63858	A AGTTG	
	CA	TGGA AGCAGGTAG GCTTT		
		ACCT TCGTCCGTC CGAAA		
		C GACGA		
GAM1760	LCP1	3' AAAGCCAACATGTGGCTCCTCC 11280	A_ AGGTAGA	
		GGA AGC GTTGGCTTT		

CCT TCG CAACCGAAA
 CC GTGTA__
 GAM1760 BTBD3 3' AAAGCCAAACTCTTCTCTCCA 31024 AA C T _
 TGGAGAGGAGAGTTGGCTTT
 ||||| ||||| |||||
 ACCTCTCTCTCAA CCGAAA
 _ _ _ A
 GAM1760 FLJ20694 3' AAAGCCAAACTGACCATCTGCT 35966 AG__ _
 TTCCA TGGAAAGCAGGT AGTTGGCTTT
 ||||| ||||| |||||
 ACCTTTCGTCTA TCAA CCGAAA
 CCAG A
 GAM1760 HSPC157 5' GTCCTACTACCTGCTTTCCA 27191 _ TT
 TGGAAAGCAGGTAGAGGGC
 ||||| ||||| |||||
 ACCTTTCGTCCATCTCCTG
 A _
 GAM1760 KIAA1522 3' CCACCCTCCTGCCTTCCA 65604 A T A T
 TGGAGCAGGAGGTGG
 ||||| ||||| |||||
 ACCTTCGTCC TC CA CC
 C _ C _
 GAM1760 PP1628 5' AAGCCAGCCCCTCCTCCCA 48069 AA C TAGA
 TGGAGGAGG GTTGGCTT
 ||||| ||||| |||||
 ACC TC TCC CGACCGAA
 C_ C C__
 GAM1760 TIX1 3' AGTTGGCTTTAAACCACCTGCT 62405 A T_____ TTGG
 TCCCA TGG AAGCAGG AGAG CT
 ||||| ||||| |||||
 ACC TTCGTCC TTTC GA
 C ACCAAA__ GGTT
 GAM1760 LOC118987 3' CCAACCCAAGGATCTGCTTTC 74393 AGA__
 GAAAGCAGGT GTTGG
 ||||| ||||| |||||
 CTTTCGTCTA CAACC
 GGAACC
 GAM1760 LOC132617 3' AAAGCCAACTCTACAATGCTCA 76405 A G_
 AAGCA GTAGAGTTGGCTTT
 ||||| ||||| |||||
 A TCGT CATCTCAACCGAAA
 C AA
 GAM1760 LOC152503 3' CCACTTTCCTGCTTTCCA 86976 T T
 TGGAAAGCAGGAGAGTGG
 ||||| ||||| |||||
 ACCTTTCGTCC TTTCA CC
 _ _
 GAM1761 COL18A1 3' AACTCAGCACAAGGCCATCT 56158 CA AC _ C
 AGAGC TGTGTTGGGT
 ||||| ||||| |||||

TCT CG ACACGAC C CA
 AC GA T A
 GAM1761 HOXB9 3' TGCAAAGCCAGTGCTGTCT 44000 T G_
 AGACAGCACTG GTT GCG
 ||||| ||| |||
 TCTGTCGTGAC CGA CGT
 _ AA
 GAM1761 RAB11A 3' GTTAAACAGTGCTGCCT 17415 A G
 AG CAGCACTGT TTGGC
 || ||||| |||||
 TC GTCGTGACA AATTG
 C _
 GAM1761 STXBP1 3' CTGTACGCGAGCTCGGCGC 13475 A T G
 GC CTG GTT GCGTACAG
 || ||| |||||
 CG GGC CGA CGCATGTC
 C T G
 GAM1761 TARBP2 3' TACCTCTGACACAGACTGCCT 16074 A CA TG C_
 AG CAG CTGTGT G GTA
 || ||| ||||| | |||
 TC GTC GACACA C CAT
 C A_ GT TC
 GAM1761 TARBP2 3' TACCTCTGACACAGACTGCCT 16075 A CA TG C_
 AG CAG CTGTGT G GTA
 || ||| ||||| | |||
 TC GTC GACACA C CAT
 C A_ GT TC
 GAM1761 ZNF236 3' ACGCCACAGTCAGCGTCT 24734 A _ GTT
 AGAC GC ACTGT GCGGT
 |||| || ||||| |||||
 TCTG CG TGACA CCGCA
 _ AC _
 GAM1761 ASB16 3' TGTACTCCACGTGCTGTC 55990 TGTGT C
 GACAGCAC TGG GTACA
 ||||| ||| |||||
 CTGTCGTG ACC CATGT
 C_ T
 GAM1761 BRAG 3' CTGTGCCACTCAATGCCATC 30099 CA C T T GT
 GA GCA TG GT GGC ACAG
 || ||| || ||| |||||
 CT CGT AC CA CCG TGTC
 AC A T _ _
 GAM1761 CGRP-RCP 5' CTGTACGCCAACACGGTGCTGT 27890
 C GACAGCACTGTGTTGGCGTACAG
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 CTGTCGTGGCACAACCGCATGTC
 GAM1761 CL25084 3' ACAAACACTGTGCTGTCT 32285 T GGC
 AGACAGCAC GTGTT GT
 ||||| ||||| ||

TCTGTCGTG CACAA CA
 T AA_
 GAM1761 DLAD 5' CTGCAGAGTAACAACACAGCCT 41409 C CA ___ GTA_
 ATCT AGA AG CTGTGTTG GC CAG
 ||| || ||||| || |||
 TCT TC GACACAAC TG GTC
 A C_ AA AGAC
 GAM1761 FLJ00024 5' CGCGTGACGCAGTGCTGTCT 64494 _
 AGACAGCACTGTGTTG GCG
 ||||| ||||| |||
 TCTGTCGTGACGCAGT CGC
 G
 GAM1761 FLJ13204 3' ACATGGCACAGTTCTGCCT 45755 A C GC
 AG CAG ACTGTGTTG GT
 || ||| ||||| ||
 TC GTC TGACACGGT CA
 C T A_
 GAM1761 FLJ22242 3' CCAAACACAGTGCCTTCT 47555 CA _
 AGA GCACTGTGTT GG
 ||| ||||| ||
 TCT CGTGACACAA CC
 TC A
 GAM1761 GABARAPL3 5' CGCACACTTGACCAGTGCTGT 51781 T ____ _
 T GACAGCACTG GT TG GCG
 ||||| || |||
 TTGTCGTGAC CA AC CGC
 _ GGTTC A
 GAM1761 GT650 3' CTGCATAACAACACAGTGC 54551 GC A
 GCACTGTGTTG GT CAG
 ||||| || |||
 CGTGACACAAC TA GTC
 AA C
 GAM1761 HSA277841 3' CTGTTGTGCACACAGTGC 38267 TG T
 GCACTGTGT GCG ACAG
 ||||| || |||
 CGTGACACA TGT TGTC
 CG _
 GAM1761 KIAA0397 3' CTGCACCCAGCACAGCCTGC 62349 _ C A
 GCA CTGTGTTGG GT CAG
 ||| ||||| || |||
 CGT GACACGACC CA GTC
 CC _ C
 GAM1761 KIAA1862 3' TGCACAGCCTCGGTGCTG 69515 T_ _
 CAGCACTG GTTG GCG
 ||||| || |||
 GTCGTGGC CGAC CGT
 TC A
 GAM1761 NIR3 3' GCACCACACAGTGCTCCCT 66827 AC T C
 AG AGCACTGTGT GG GT
 || ||||| || ||

TC TCGTGACACA CC CG
 CC _ A
 GAM1761 SEC8 3' CCACACACAGTGATGCCT 41735 A G _
 AG CA CACTGTGT TGG
 || || ||||| ||
 TC GT GTGACACA ACC
 C A C
 GAM1761 LOC120939 3' CGCAGCACAGTGCTAATCT 76760 C_ G
 AGA AGCACTGTGTTG CG
 ||| ||||| ||
 TCT TCGTGACACGAC GC
 AA _
 GAM1761 LOC126248 3' CTGGACTCAGCACAGTGC 74932 C A
 GCACTGTGTTGG GT CAG
 ||||| || ||
 CGTGACACGACT CA GTC
 _ G
 GAM1761 LOC153505 3' CTGTACGCGTCCATCGCTGTCT 81705 ACT TTG
 AGACAGC GTG GCGTACAG
 ||||| || |||||
 TCTGTCTG TAC CGCATGTC
 C_ CTG
 GAM1761 LOC160646 5' CTGTACGCCAAGGAACTGGTC 83110 _ CA GTG
 GAC AG CT TTGGCGTACAG
 ||| || |||||
 CTG TC GG AACCGCATGTC
 G AA _
 GAM1761 LOC200107 3' CTGCACGTTGGCCAGTCCTGTC 89985 C T TG A
 T
 AGACAG ACTG GT GCGT CAG
 ||||| ||| || ||| ||
 TCTGTC TGAC CG TGCA GTC
 C _ GT C
 GAM1761 LOC203378 3' TGTACAGTCATGCTGTCT 92310 CTGTGT _
 AGACAGCA TGGC GTACA
 ||||| || |||||
 TCTGTCTG ACTG CATGT
 _ A
 GAM1761 LOC219690 5' TGACGCCAGCCACCGTGT 94669 T _ A
 GCAC GTG TTGGCGT CA
 |||| || ||||| ||
 TGTG CAC GACCGCA GT
 C C C
 GAM1761 LOC54518 3' TACACATTCTGTCACTGCTGTT 39300 TGT_ GC
 GACAGCACTG TG GTA
 ||||| || ||
 TTGTCGTGAC AC CAT
 TGTCTT A_
 GAM1761 LOC91300 5' TACACCCCGCGAGTGCTTC 96240 C _ TT C
 GA AGCACT GTG GG GTA
 || ||||| || |||

CT TCGTGA CGC CC CAT
 _ G C_ A
 GAM1761 LOC91300 5' TACACCCCGCGAGTGCTTC 96241 C _ TT C
 GA AGCACT GTG GG GTA
 || ||||| ||| || |||
 CT TCGTGA CGC CC CAT
 _ G C_ A
 GAM1761 LOC92249 5' TACAAACCAACACAGCATCATC 69111 CAGCA C__
 T AGA CTGTGTTGG GTA
 ||| ||||| |||
 TCT GACACAACC CAT
 ACTAC AAA
 GAM1762 ANKTM1 3' CCACCCTTCTTGCTGTCC 24697 CC A
 GGACAGCGAGG AGG TGG
 ||||| ||| |||
 CCTGTCGTTCT TCC ACC
 _ C
 GAM1762 ATP1A2 3' TCCATTTCCCACTTCCAC 7370 C CGA CCA
 GTGGA AG GG GGATGGA
 ||||| || || |||||
 CACCT TC CC TTTACCT
 _ AC_ _
 GAM1762 B3GAT1 3' CCACGGCCCCACTGTCCAC 38451 CGA AGGA
 GTGGACAG GGCC TGG
 ||||| ||| |||
 CACCTGTC CCGG ACC
 ACC C__
 GAM1762 B3GAT1 3' CCACGGCCCCACTGTCCAC 55051 CGA AGGA
 GTGGACAG GGCC TGG
 ||||| ||| |||
 CACCTGTC CCGG ACC
 ACC C__
 GAM1762 COL1A1 3' CTCCATCCCAACCTGGCTCCC 5395 AC G CCA
 GG AGC AGG GGATGGAG
 || ||| ||| |||||
 CC TCG TCC CCTACCTC
 C_ G AAC
 GAM1762 DAAM2 3' CTCCATCCTGTCTACTAATCCA 93901 CAGCG C
 C GTGGA AGGC AGGATGGAG
 |||| ||| |||||
 CACCT TCTG TCCTACCTC
 AATCA _
 GAM1762 EGFR 3' CTCCATCCCAACAGCCATGCCC 19085 ACA A CA__
 GC GTGG GCG GGC GGATGGAG
 ||| ||| ||| |||||
 CGCC CGT CCG CCTACCTC
 _ A ACAAC
 GAM1762 ELAVL3 3' CCACCCAGGCTGGGCTGTTCA 9224 GA A_ A
 C GTGGACAGC GGCC GG TGG
 ||||| ||| ||| |||

			CACTTGTCG TCGG CC ACC		
			GG AC C		
GAM1762	ELAVL3	3'	CCATCCTCCTGCCCCAC	9225	ACA G CC
			GTGG GC AGG AGGATGG		
			CACC CG TCC TCCTACC		
			CC_ _ _		
GAM1762	EN1	3'	CCACCGCCTCGCTGCC	9247	A CA A
			GG CAGCGAGGC GG TGG		
			CC GTCGCTCCG CC ACC		
			_ _ _		
GAM1762	KLHL1	5'	CCCCGGGCCCCGCTGTCC	40870	A A AT
			GGACAGCG GGCC GG GG		
			CCTGTCGC CCGG CC CC		
			C G _		
GAM1762	LGI1	3'	TCCATCCTTAAGTGTCCA	18735	CGAGGCC
			TGGACAG AGGATGGA		
			ACCTGTC TCCTACCT		
			AAT_		
GAM1762	LOXL1	5'	TCCTGAGAGCCTCTGTCCAC	60822	C _
			GTGGACAG GAGGC CAGGA		
			CACCTGTC CTCCG GTCCT		
			T AGA		
GAM1762	MUC5B	3'	CTCCATCCCCATGCTCTGTCCA	67398	CGA CA_
	C		GTGGACAG GGC GGATGGAG		
			CACCTGTC TCG CCTACCTC		
			_ TACC		
GAM1762	NXF5	3'	TCCATCCCAGTGTCCAC	53090	G GAGGCCA
			GTGGACA C GGATGGA		
			CACCTGT G CCTACCT		
			_ AC_		
GAM1762	NXF5	3'	TCCATCCCAGTGTCCAC	53690	G GAGGCCA
			GTGGACA C GGATGGA		
			CACCTGT G CCTACCT		
			_ AC_		
GAM1762	NXF5	3'	TCCATCCCAGTGTCCAC	53693	G GAGGCCA
			GTGGACA C GGATGGA		
			CACCTGT G CCTACCT		
			_ AC_		
GAM1762	NXF5	3'	TCCATCCCAGTGTCCAC	53695	G GAGGCCA
			GTGGACA C GGATGGA		

			CACCTGT G	CCTACCT	
			AC		
GAM1762	NXF5	3'	TCCATCCCAGTGTCCAC	53697	G GAGGCCA
			GTGGACA C	GGATGGA	
			CACCTGT G	CCTACCT	
			AC		
GAM1762	PDE4A	3'	CCATCCTGGCCGCACCCC	21679	ACA GA
			GG GC GGCCAGGATGG		
			CC CG CCGGTCCTACC		
			CCA		
GAM1762	PTPN1	3'	CTCCACCTCCACCCACTGTCCG	12577	CGA CC_ A
	C		GTGGACAG GG AGG TGGAG		
			CGCCTGTC CC TCC ACCTC		
			AC_ ACC _		
GAM1762	SARDH	3'	CCATCCCATGCTGTCCAT	24017	A CCAG
			GTGGACAGCG GG GATGG		
			TACCTGTCGT CC CTACC		
			A		
GAM1762	SF3B3	3'	CCACCACCATCACTGCCAC	25783	A C _ CCA A
			GTGG CAG GA GG GG TGG		
			CACC GTC CT CC CC ACC		
			_ A A A _		
GAM1762	SLC20A2	3'	TCCATCCCACACTGTTCAC	23120	CGAGGCCA
			GTGGACAG GGATGGA		
			CACTTGTC CCTACCT		
			ACAC		
GAM1762	SLC9A3R2	3'	CCATCCTGCCCTGCCAC	62099	A CGA C
			GTGG CAG GGC AGGATGG		
			CACC GTC CCG TCCTACC		
			C C_ _		
GAM1762	SOST	3'	CCCCTTGACCTCGCTGCCCAT	48223	A C_ AT
			GTGG CAGCGAGG CAGG GG		
			TACC GTCGCTCC GTTC CC		
			C AC C_		
GAM1762	SOX13	3'	CTCCATCCTCAAAGCCCCAC	20279	ACA GAGGCC
			GTGG GC AGGATGGAG		
			CACC CG TCCTACCTC		
			CC_ AAAC_		
GAM1762	SURF5	3'	CCGCAGGCCTCCTGTCCAC	23124	C AGGA
			GTGGACAG GAGGCC TGG		

CACCTGTC CTCCGG GCC
_ AC_
GAM1762 SYNGR1 3' CCATCCTGGGCCCCAC 17498 ACAGCGA _
GTGG GGCC AGGATGG
|||| ||| |||||
CACC CCGG TCCTACC
C_ G
GAM1762 WNT5A 5' CCCCGGGGCCTCGCCCCCAC 14119 ACA A_ AT
GTGG GCGAGGCC GG GG
|||| ||||| || ||
CACC CGCTCCGG CC CC
CCC GG _
GAM1762 ARTN 5' CCCAGCCCTCGCTGCCAC 55113 A _ CA
GTGG CAGCGAGG C GG
|||| ||||| | ||
CACC GTCGCTCC G CC
_ C AC
GAM1762 ATPW 5' CTCCATCCCGGCCCCAGCCCA 32258 ACA GA_ A
TGG GC GGCC GGATGGAG
||| || ||| |||||
ACC CG CCGG CCTACCTC
_ ACC C
GAM1762 C22orf4 3' CCGCAGCTGGCCTCACTGTCC 61270 C GA_
GGACAG GAGGCCAG TGG
||||| ||||| |||
CCTGTC CTCCGGTC GCC
A GAC
GAM1762 C5orf4 3' CCATCCTGGCCTCCTCTC 33426 C C
GA AG GAGGCCAGGATGG
|| || |||||
CT TC CTCCGGTCCTACC
C _
GAM1762 C5orf4 3' CCATCCTGGCCTCCTCTC 51488 C C
GA AG GAGGCCAGGATGG
|| || |||||
CT TC CTCCGGTCCTACC
C _
GAM1762 C8orf14 5' TTTCATTAGCCTGGCTGTCCAC 55083 G CAG
GTGGACAGC AGGC GATGGAG
||||| ||| |||||
CACCTGTCG TCCG TTACTTT
G A_
GAM1762 DKFZp547H236 5' CCTGGCCTCCTGCCCCAC 79245 A C
GTGG CAG GAGGCCAGG
|||| ||| |||||
CACC GTC CTCCGGTCC
C _
GAM1762 FLJ10292 3' TCCATCCCCACTATCTAC 36434 C CGA CCA
GTGGA AG GG GGATGGA
||||| || || |||||

			CATCT TC CC CCTACCT		
			A A__ __		
GAM1762	FLJ21977	3'	TCCATCCTAGCCCCAC 50875	ACAGCGA	C
			GTGG GGC AGGATGGA		
			CACC CCG TCCTACCT		
			C__ A		
GAM1762	FLJ22471	3'	CCACCCGCGCTGTCCAT 47859	A CCA	A
			GTGGACAGCG GG GG TGG		
			TACCTGTGCGC CC CC ACC		
			G __ _		
GAM1762	JAM1	3'	CTCCATCTACCACCATCCAC 34225	CAGCGA	CCA
			GTGGA GG GGATGGAG		
			CACCT CC TCTACCTC		
			ACCA__ A__		
GAM1762	JAM1	3'	CTCCATCTACCACCATCCAC 58514	CAGCGA	CCA
			GTGGA GG GGATGGAG		
			CACCT CC TCTACCTC		
			ACCA__ A__		
GAM1762	JAM1	3'	CTCCATCTACCACCATCCAC 58542	CAGCGA	CCA
			GTGGA GG GGATGGAG		
			CACCT CC TCTACCTC		
			ACCA__ A__		
GAM1762	JAM1	3'	CTCCATCTACCACCATCCAC 58570	CAGCGA	CCA
			GTGGA GG GGATGGAG		
			CACCT CC TCTACCTC		
			ACCA__ A__		
GAM1762	KIAA0523	5'	CCTGGCCTCACTCCCAC 68356	AC	C
			GTGG AG GAGGCCAGG		
			CACC TC CTCCGGTCC		
			C_ A		
GAM1762	KIAA0544	3'	CCACGGCCTCGCCACCAC 71459	ACA	AGGA
			GTGG GCGAGGCC TGG		
			CACC CGCTCCGG ACC		
			AC_ C__		
GAM1762	KIAA1029	3'	CTCCATCCCAGTTCAGACTGTC 24426	CGA_	CA
	CA		TGGACAG GGC GGATGGAG		
			ACCTGTC TTG CCTACCTC		
			AGAC AC		
GAM1762	KIAA1199	3'	CCACCCTAGCCCTTGCTGCCAC 72929	A	_ C A
			GTGG CAGCGAGG C AGG TGG		

			CACC GTCGTTCC G TCC ACC		
			— C A C		
GAM1762	KIAA1453	3'	CCACCCCACATTGCTGTCCA 47660	GGCCA A	
			TGGACAGCGA GG TGG		
			ACCTGTCGTT CC ACC		
			ACAC_ C		
GAM1762	MAP	3'	CCACCCCCGCATGCGTCTGTCC 43366	_ AG_ CA A	
	AC		GTGGACAG CG GC GG TGG		
			CACCTGTC GC CG CC ACC		
			T GTA CC C		
GAM1762	MGC23244	3'	CCATCCTGAGACCCCGTCC 58829	AGC A C__	
			GGAC G GG CAGGATGG		
			CCTG C CC GTCCTACC		
			__ C AGA		
GAM1762	MGC3036	3'	CAGGTGGCCTCGCTGCC 43981	A GGA	
			GG CAGCGAGGCCA TG		
			CC GTCGCTCCGGT AC		
			— GG_		
GAM1762	moblak	3'	CTCCACCCTCACTCCATCCAC 56397	CAGC GCC A	
			GTGGA GAG AGG TGGAG		
			CACCT CTC TCC ACCTC		
			AC__ AC_ C		
GAM1762	NUDE1	5'	CCGCGTTGGCCTCGCCGCC 35053	ACA GA	
			GG GCGAGGCCAG TGG		
			CC CGCTCCGGTT GCC		
			GC_ GC		
GAM1762	PTPRN2	3'	TCCATCCCGCCCTTCCCAC 56446	AC CGA CA	
			GTGG AG GGC GGATGGA		
			CACC TC CCG CCTACCT		
			CT __ C_		
GAM1762	PTPRN2	3'	TCCATCCCGCCCTTCCCAC 56447	AC CGA CA	
			GTGG AG GGC GGATGGA		
			CACC TC CCG CCTACCT		
			CT __ C_		
GAM1762	SCYA22	3'	CTCCATCCCTGTGGCTGTC 92590	GAG CA	
			GACAGC GC GGATGGAG		
			CTGTCG TG CCTACCTC		
			G_ TC		
GAM1762	UBP1	3'	CTCCATCTCTGACCACCCCCAC 27991	ACAGCGA C _	
			GTGG GG CAG GATGGAG		

CACC CC GTC CTACCTC
 CCCA__ A T
 GAM1762 LOC115129 3' CCAGTTCCCTCCATCCAC 73613 CAGC CCA __
 GTGGA GAGG GGA TGG
 |||| ||| ||| |||
 CACCT CTCC CCT ACC
 AC__ __ TG
 GAM1762 LOC116113 3' CTCCACCCCTCCTCCATCCAC 93836 CAGC CCA A
 GTGGA GAGG GG TGGAG
 |||| ||| || |||||
 CACCT CTCC CC ACCTC
 AC__ TC_ C
 GAM1762 LOC148760 3' CTCCATCCCAACCCCTGCACCA 85363 ACA A CCA_
 C GTGG GCG GG GGATGGAG
 ||| ||| || |||||
 CACC CGT CC CCTACCTC
 A__ C CAAC
 GAM1762 LOC150848 5' CCATTCCCCTTCCAC 86318 C CGA CCA
 GTGGA AG GG GGATGG
 |||| || || |||||
 CACCT TC CC CTTACC
 _ A__ __
 GAM1762 LOC152897 5' CCATCCTGGCTGCTGATCCA 81604 _ GA
 TGGA CAGC GGCCAGGATGG
 ||| ||| |||||
 ACCT GTCG TCGGTCCTACC
 A __
 GAM1762 LOC153577 5' CTCCATCTGTTCTCCACCTAC 87237 AC C__ GC G
 CCAC GTGG AG GAG CAG ATGGAG
 ||| || ||| |||||
 CACC TC CTC GTC TACCTC
 CA CACC TT _
 GAM1762 LOC157349 3' CCATCCCGTTCTGTCC 82331 CGA CA
 GGACAG GGC GGATGG
 |||| ||| |||||
 CCTGTC TTG CCTACC
 __ C_
 GAM1762 LOC197342 3' CTCCAGCCTGGCCTCACTGTCC 89363 C A
 GGACAG GAGGCCAGG TGGAG
 |||| ||||| |||||
 CCTGTC CTCCGGTCC ACCTC
 A G
 GAM1762 LOC221466 3' CTCCACCCAGCCTCTGTTCCC 95313 AC _ CA A
 CAT GTGG AGC GAGGC GG TGGAG
 ||| ||| |||| || |||||
 TACC TTG CTCCG CC ACCTC
 CC T AC C
 GAM1762 LOC221543 5' CTTGCGTAACCTCACTGTCTAC 95376 C CCAGGA
 GTGGACAG GAGG TGGAG
 ||||| ||| |||||

		CATCTGTC CTCC GCTTC	
		A AATG__	
GAM1762	LOC256866 5'	CTTGGCCTCACCGTCTAC 98013	AGC
		GTGGAC GAGGCCAGG	
		CATCTG CTCCGGTTC	
		CCA	
GAM1762	LOC257490 5'	CCACCCCAGGTGTCCTGTCCAT 99559	C G A_ A
		GTGGACAG GA GCC GG TGG	
		TACCTGTC CT TGG CC ACC	
		_ G AC C	
GAM1762	LOC257596 5'	CTTCGGTAACCTCACTGTCTAC 99779	C CCAGGA
		GTGGACAG GAGG TGGAG	
		CATCTGTC CTCC GCTTC	
		A AATG__	
GAM1762	LOC58512 3'	CTCCATCCTCAGCCCTCTGCCC 65283	A CGA C_
	AC	GTGG CAG GGC AGGATGGAG	
		CACC GTC CCG TCCTACCTC	
		C TC_ AC	
GAM1762	LOC90522 3'	CTCCATCCCATGTCCCGCCCA 63854	ACA A CA_
		TGG GCG GGC GGATGGAG	
		ACC CGC CTG CCTACCTC	
		___ C TAC	
GAM1762	LOC90784 5'	CTCCACCCCACTTCCGTCCA 64695	AGC CCA A
		TGGAC GAGG GG TGGAG	
		ACCTG CTTC CC ACCTC	
		C_ AC_ C	
GAM1762	LOC92979 3'	CATTGTCTGGCCTCACTGCCCA 57252	A C _
	C	GTGG CAG GAGGCCAG GATG	
		CACC GTC CTCCGGTC TTAC	
		C A TG	
GAM1763	AXL 3'	CTCTAGATTCCATTGGTCCAA 41884	AT GC C
		TTG ACT TGGAATC AGAG	
		AAC TGG ACCTTAG TCTC	
		C_ TT A	
GAM1763	COL4A3 3'	CTCTGGAAGAGCAGTATCAGCA 49384	GGAA
		TGTTGATACTGCT TCCAGAG	
		ACGACTATGACGA AGGTCTC	
		GA__	
GAM1763	COL4A3 3'	CTCTGGAAGAGCAGTATCAGCA 49385	GGAA
		TGTTGATACTGCT TCCAGAG	

		ACGACTATGACGA AGGTCTC		
		GA__		
GAM1763 COL4A3	3'	CTCTGGAAGAGCAGTATCAGCA 49386	GGAA	
		TGTTGATACTGCT TCCAGAG		
		ACGACTATGACGA AGGTCTC		
		GA__		
GAM1763 HD	3'	CTCTGAGACAGCAGTATCACA 10914 T	GAA _	
		TGT GATACTGCTG TC CAGAG		
		ACA CTATGACGAC AG GTCTC		
		_ _ _ A		
GAM1763 NPEPPS	3'	CTCTTCACAACAGTATCAACA 63784	C _ ATCC	
		TGTTGATACTG TG GA AGAG		
		ACAACTATGAC AC CT TCTC		
		A A _ _		
GAM1763 PCDHGA1	3'	CTCCAGATTCCAGCCATAAAC 38838	GATACT	CA
		GTT GCTGGAATC GAG		
		CAA CGACCTTAG CTC		
		ATAC_ AC		
GAM1763 PCDHGA10	3'	CTCCAGATTCCAGCCATAAAC 50313	GATACT	CA
		GTT GCTGGAATC GAG		
		CAA CGACCTTAG CTC		
		ATAC_ AC		
GAM1763 PCDHGA11	3'	CTCCAGATTCCAGCCATAAAC 38845	GATACT	CA
		GTT GCTGGAATC GAG		
		CAA CGACCTTAG CTC		
		ATAC_ AC		
GAM1763 PCDHGA12	3'	CTCCAGATTCCAGCCATAAAC 50320	GATACT	CA
		GTT GCTGGAATC GAG		
		CAA CGACCTTAG CTC		
		ATAC_ AC		
GAM1763 PCDHGA2	3'	CTCCAGATTCCAGCCATAAAC 38852	GATACT	CA
		GTT GCTGGAATC GAG		
		CAA CGACCTTAG CTC		
		ATAC_ AC		
GAM1763 PCDHGA3	3'	CTCCAGATTCCAGCCATAAAC 50096	GATACT	CA
		GTT GCTGGAATC GAG		
		CAA CGACCTTAG CTC		
		ATAC_ AC		
GAM1763 PCDHGA4	3'	CTCCAGATTCCAGCCATAAAC 38860	GATACT	CA
		GTT GCTGGAATC GAG		

			CAA	CGACCTTAG	CTC		
			ATAC__	AC			
GAM1763	PCDHGA5	3'	CTCCAGATTCCAGCCATAAAC	50294	GATACT	CA	
			GTT	GCTGGAATC	GAG		
			CAA	CGACCTTAG	CTC		
			ATAC__	AC			
GAM1763	PCDHGA6	3'	CTCCAGATTCCAGCCATAAAC	50296	GATACT	CA	
			GTT	GCTGGAATC	GAG		
			CAA	CGACCTTAG	CTC		
			ATAC__	AC			
GAM1763	PCDHGA7	3'	CTCCAGATTCCAGCCATAAAC	50301	GATACT	CA	
			GTT	GCTGGAATC	GAG		
			CAA	CGACCTTAG	CTC		
			ATAC__	AC			
GAM1763	PCDHGA8	3'	CTCCAGATTCCAGCCATAAAC	26602	GATACT	CA	
			GTT	GCTGGAATC	GAG		
			CAA	CGACCTTAG	CTC		
			ATAC__	AC			
GAM1763	PCDHGA9	3'	CTCCAGATTCCAGCCATAAAC	50308	GATACT	CA	
			GTT	GCTGGAATC	GAG		
			CAA	CGACCTTAG	CTC		
			ATAC__	AC			
GAM1763	PCDHGB1	3'	CTCCAGATTCCAGCCATAAAC	38877	GATACT	CA	
			GTT	GCTGGAATC	GAG		
			CAA	CGACCTTAG	CTC		
			ATAC__	AC			
GAM1763	PCDHGB2	3'	CTCCAGATTCCAGCCATAAAC	50326	GATACT	CA	
			GTT	GCTGGAATC	GAG		
			CAA	CGACCTTAG	CTC		
			ATAC__	AC			
GAM1763	PCDHGB3	3'	CTCCAGATTCCAGCCATAAAC	38885	GATACT	CA	
			GTT	GCTGGAATC	GAG		
			CAA	CGACCTTAG	CTC		
			ATAC__	AC			
GAM1763	PCDHGB4	3'	CTCCAGATTCCAGCCATAAAC	50331	GATACT	CA	
			GTT	GCTGGAATC	GAG		
			CAA	CGACCTTAG	CTC		
			ATAC__	AC			
GAM1763	PCDHGB5	3'	CTCCAGATTCCAGCCATAAAC	38892	GATACT	CA	
			GTT	GCTGGAATC	GAG		

		CAA CGACCTTAG CTC			
		ATAC__ AC			
GAM1763	PCDHGB6	3' CTCCAGATTCCAGCCATAAAC 50336	GATACT	CA	
		GTT GCTGGAATC GAG			
		CAA CGACCTTAG CTC			
		ATAC__ AC			
GAM1763	PCDHGB7	3' CTCCAGATTCCAGCCATAAAC 38901	GATACT	CA	
		GTT GCTGGAATC GAG			
		CAA CGACCTTAG CTC			
		ATAC__ AC			
GAM1763	PCDHGC3	3' CTCCAGATTCCAGCCATAAAC 51530	GATACT	CA	
		GTT GCTGGAATC GAG			
		CAA CGACCTTAG CTC			
		ATAC__ AC			
GAM1763	PCDHGC4	3' CTCCAGATTCCAGCCATAAAC 38907	GATACT	CA	
		GTT GCTGGAATC GAG			
		CAA CGACCTTAG CTC			
		ATAC__ AC			
GAM1763	PCDHGC5	3' CTCCAGATTCCAGCCATAAAC 51557	GATACT	CA	
		GTT GCTGGAATC GAG			
		CAA CGACCTTAG CTC			
		ATAC__ AC			
GAM1763	SPON1	3' CTCTAGATTCCAGAGTCACCA 63118	T ACTG	C	
		TG TGAT CTGGAATC AGAG			
		AC ACTG GACCTTAG TCTC			
		C A__ A			
GAM1763	DOCK3	3' CTGATCAGCCAGTATCAACA 67093	_ AATC		
		TGTTGATACTG CTGG CAG			
		ACAACTATGAC GACT GTC			
		C A__			
GAM1763	KIAA1384	3' CTCTGGAATGAACAGTATCACA 65179	T CTGGAA		
		TGT GATACTG TCCAGAG			
		ACA CTATGAC AGGTCTC			
		_ AAGTA_			
GAM1763	PDE8B	3' TCTAGACTGGTATCAGCA 68204	G__		
		TGTTGATACT CTGGA			
		ACGACTATGG GATCT			
		TCA			
GAM1763	THG-1	5' CTCTGGAGTTCAGCAGCAACA 48913	ATA A		
		TGTTG CTGCTGGA TCCAGAG			

		ACAAC GACGACTT AGGTCTC		
		— G		
GAM1763	LOC138311 3'	CTCTGGATTCCAGCACACAGA 76721	GATAC	
	CA	TGTT TGCTGGAATCCAGAG		
		ACAG ACGACCTTAGGTCTC		
		ACACC		
GAM1763	LOC147645 3'	GGACTCCAGTATCACA 79070	T ACT A	
		TGT GAT GCTGGA TCC		
		ACA CTA TGACCT AGG		
		— — C		
GAM1763	LOC148894 3'	ATTTCAGCAGCACCAACA 85416	ATA	
		TGTTG CTGCTGGAAT		
		ACAAC GACGACTTTA		
		CAC		
GAM1763	LOC151518 3'	ATTCCAGCAGTCCAACA 86621	AT	
		TGTTG ACTGCTGGAAT		
		ACAAC TGACGACCTTA		
		C_		
GAM1763	LOC256714 3'	CTCTGTTGGAAAGCAGTATCAA 98044	GGAATC	
		TTGATACTGCT CAGAG		
		AACTATGACGA GTCTC		
		AAGGTT		
GAM1763	LOC51162 5'	CTGGGCTCCAGCAGCATCAGCA 33050	A AT	
		TGTTGAT CTGCTGGA CCAG		
		ACGACTA GACGACCT GGTC		
		C CG		
GAM1763	LOC92078 3'	TCTGGAAATCAGTATCACA 68613	T CTGGAA	
		TGT GATACTG TCCAGA		
		ACA CTATGAC AGGTCT		
		— TAA —		
GAM1764	ABP1 5'	GCAGAGCGAACTGGGAGCAGAG 63799	CCGC C	
		CTCTGTTCTT CGCTC GC		
		GAGACGAGGG GCGAG CG		
		TCAA A		
GAM1764	AHCY 3'	GGCAACTGAGAAAGAACAGAG 7304	— — — —	
		CTCTGTTCTT C C GCC		
		GAGACAAGAA G G CGG		
		A A TCAA		
GAM1764	BSN 3'	GGCAGAGGCAAGAGCAGAG 14387	CC G _	
		CTCTGTTCTT GCC CT CC		

		GAGACGAGAA CGG GA GG	
		___ A C	
GAM1764 CSE1L	5'	GCGGAGCGGCGGCAGGAGC 62513	—
		GTTCTT CCGCCGCTCCGC	
		CGAGGA GGCGGCGAGGCG	
		C	
GAM1764 EHD4	3'	AGTGGCAAAAAATAGAG 58362	C CC
		CTCTGTT TT GCCGCT	
		GAGATAA AA CGGTGA	
		A AA	
GAM1764 EIF2C1	3'	AGCCCAGCTGAAGAACAGA 25181	C C__
		TCTGTTCTTC GC GCT	
		AGACAAGAAG CG CGA	
		T ACC	
GAM1764 JUND	3'	GAGAGAAGAACAGAGT 19298	CGCCG
		ACTCTGTTCTTC CTC	
		TGAGACAAGAAG GAG	
		A___	
GAM1764 KCNK4	3'	GCAGAGCAGCAGAGCAGG 33985	TCC C C
		TCTGTTCT GC GCTC GC	
		GGACGAGA CG CGAG CG	
		___ A A	
GAM1764 MYO1D	3'	GCGGAACAGCCCATCCAGCAGA 72249	CTTCC_ CGC
GT		ACTCTGTT GC TCCGC	
		TGAGACGA CG AGGCG	
		CCTACC ACA	
GAM1764 NUP62	3'	GGCAAAGCAGCACAGTGTGAAT 33786	TTCC___ C CC
AGA		TCTGTT GC GCT GCC	
		AGATAAG CG CGA CGG	
		TGTGACA A AA	
GAM1764 RABIF	3'	GGCATGTGCAGAAAAACAGAGT 12728	C C C TCC
		ACTCTGTT TTC GC GC GCC	
		TGAGACAA AAG CG TG CGG	
		A A _ TA_	
GAM1764 RAX	3'	GCAGGGGAGGCGGAAAAATAGA 26466	C G _
GT		ACTCTGTT TTCCGCC CTCC GC	
		TGAGATAA AAGGCGG GGGG CG	
		A A A	
GAM1764 RBM10	3'	GGCAGGGAAGGACAGAGT 20247	—
		ACTCTGTTCTTCC GCC	

			TGAGACAGGAAGG CGG		
			GA		
GAM1764	RGS16	3'	GGCAGGGCCCAGGAGAACAAAG 12869	C	T GCC C
	T		ACT TGTTCT CC GCTC GCC		
			TGA ACAAGA GG CGGG CGG		
			A _ ACC A		
GAM1764	ROM1	3'	GGAACAGCAAAGAACAGAGT 6165	CC	CGC
			ACTCTGTTCTT GC TCC		
			TGAGACAAGAA CG AGG		
			A_ ACA		
GAM1764	SLC21A2	3'	GCAAAGCAAGTGATGAAGCAGA 20084	_ TTC	C_ CC
	GT		ACTCTGTT C CGC GCT GC		
			TGAGACGA G GTG CGA CG		
			A TA_ AA AA		
GAM1764	SMARCA5	5'	AGCCCCGCGGAAGAGCAGA 14588	C_	
			TCTGTTCTTCCGC GCT		
			AGACGAGAAGGCG CGA		
			CCC		
GAM1764	SYNGR1	3'	GGCAGAGCGGCAAGGACAGGG 17507	CC	C
			CTCTGTTCTT GCCGCTC GCC		
			GGGACAGGAA CGGCGAG CGG		
			_ A		
GAM1764	TRAM	5'	AGCAGCTGGGAAGAGCAGA 27451	_	C
			TCTGTTCTTCC GC GCT		
			AGACGAGAAGG CG CGA		
			GT A		
GAM1764	VAT1	3'	AGCAGGGAAGTACAGAGT 22088	T	GCC
			ACTCTGT CTTCC GCT		
			TGAGACA GAAGG CGA		
			T GA_		
GAM1764	CBX1	3'	AGCAATGGAAAAGAACAGA 23308	_	CC
			TCTGTTCT TCCG GCT		
			AGACAAGA AGGT CGA		
			AA AA		
GAM1764	CDC14A	5'	GGCGGAGCAGCAGCTGCAGCAG 14786	_	TCTTCC C
			CT CTGT GC GCTCCGCC		
			GA GACG CG CGAGGCGG		
			C TCGA_ A		
GAM1764	CDC14A	5'	GGCGGAGCAGCAGCTGCAGCAG 53964	_	TCTTCC C
			CT CTGT GC GCTCCGCC		

		GA GACG CG CGAGGCGG	
		C TCGA__ A	
GAM1764 CDC14A	5'	GGCGGAGCAGCAGCTGCAGCAG 53966	_ TCTTCC C
		CT CTGT GC GCTCCGCC	
		GA GACG CG CGAGGCGG	
		C TCGA__ A	
GAM1764 DKFZp547I224	5'	GATGGGGAAAAAACAGAG 39956	C_ G C
		CTCTGTT TTCC CCG TC	
		GAGACAA AAGG GGT AG	
		AA _ _	
GAM1764 ECE2	3'	GCAGGGAAAAGGAAGAACAGAG 28732	GCCG C
T		ACTCTGTTCTTCC CTC GC	
		TGAGACAAGAAGG GGG CG	
		AAAA A	
GAM1764 FLJ10648	3'	CGAAGCAAACCAAGAACAGAG 36890	CCGCC C
		CTCTGTTCTT GCT CG	
		GAGACAAGAA CGA GC	
		CCAAA A	
GAM1764 GRIN3A	3'	GCGGAGCAAGTGCCAAGCAGA 56783	CTTC C_
		TCTGTT CGC GCTCCGC	
		AGACGA GTG CGAGGCG	
		ACC_ AA	
GAM1764 INE1	3'	GCAGGTGTTAGACGAAAGAACA 14757	C CC_ T _
GA		TCTGTTCTT CG GC CC GC	
		AGACAAGAA GC TG GG CG	
		A AGAT T A	
GAM1764 KIAA0410	3'	GCAGAGCTTAAGAATAGA 29426	CCGCC C
		TCTGTTCTT GCTC GC	
		AGATAAGAA CGAG CG	
		TT__ A	
GAM1764 KIAA0872	3'	AGCGCGGAAGACAGAGT 30739	T C
		ACTCTGT CTTCCGC GCT	
		TGAGACA GAAGGCG CGA	
		_ _	
GAM1764 KIAA0964	5'	GCGGAACGGCAGAGCGGG 30448	TCC C
		TCTGTTCT GCCG TCCGC	
		GGGCGAGA CGGC AGGCG	
		_ A	
GAM1764 KIAA1218	5'	AGCAGCACAAAAGAAACAGAGT 95958	_ CC_ C
		ACTCTGTT CTT GC GCT	

			TGAGACAA GAA CG CGA		
			A AACA A		
GAM1764 KIAA1285	3'	AGCAAGGAGAACAGAGT	91978	T GCC	
		ACTCTGTTCT CC GCT			
		TGAGACAAGA GG CGA			
		_ AA_			
GAM1764 KIAA1322	3'	GGCAGCCGAGAAGAACAGA	73112	_ CC _	
		TCTGTTCTTC CG GCT CC			
		AGACAAGAAG GC CGA GG			
		A _ C			
GAM1764 KIAA1391	3'	AGTGGAGAAAAACAGAGT	67851	C CG	
		ACTCTGTT TTC CCGCT			
		TGAGACAA AAG GGTGA			
		A A_			
GAM1764 MGC13251	3'	AGCAGCCATAGAAAGGACAGA	52134	_ C_ C	
		TCTGTTCTT C GC GCT			
		AGACAGGAA G CG CGA			
		A ATAC A			
GAM1764 MYH7B	3'	GGCGGAGCAGCAGGCCAACA	71058	CTT _ C	
		TGTT CC GC GCTCCGCC			
		ACAA GG CG CGAGGCGG			
		CC_ A A			
GAM1764 NCOA2	3'	GGCAAGGAGAAGAGCAAAGT	22572	C CG GCT	
		ACT TGTTCTTC CC CC			
		TGA ACGAGAAG GG GG			
		A A_ AAC			
GAM1764 PTRF	3'	GGCAGTGGGGAAGACAGAG	64242	T G _	
		CTCTGT CTTCC CCGCT CC			
		GAGACA GAAGG GGTGA GG			
		_ _ C			
GAM1764 RHOBTB2	3'	AGCAGGAGGAAAAGCAGAGT	61593	C G _	
		ACTCTGTT TTCC CC GCT			
		TGAGACGA AAGG GG CGA			
		A A A			
GAM1764 TAGAP	3'	AGACTGCAAGGAACAGAGT	55099	CC CG_	
		ACTCTGTTCTT GC CT			
		TGAGACAAGGA CG GA			
		A_ TCA			
GAM1764 VELI1	3'	AGTGTAAGAAGAATAAAGT	17417	C CGC	
		ACT TGTTCTTC CGCT			

	TGA ATAAGAAG GTGA		
	A AAT		
GAM1764 LOC145783 5'	GCGGAGCGACGGAGACACAG 77949	TC	C
	CTGT TTCCG CGCTCCGC		
	GACA GAGGC GCGAGGCG		
	CA A		
GAM1764 LOC150157 3'	AGCAAATGAAAAGAACAGA 86020	__	CC_
	TCTGTTCT TCCG GCT		
	AGACAAGA AGGT CGA		
	AA AAA		
GAM1764 LOC151516 5'	GGCGGAGCTTCCAGAACAAAG 81068	C	TCCGCC
	CT TGTTCT GCTCCGCC		
	GA ACAAGA CGAGGCGG		
	A CCTT__		
GAM1764 LOC153769 3'	GGCGGAGCAGCATGAGAAAGA 81807	G	CC C
	TCT TTCTT GC GCTCCGCC		
	AGA AAGAG CG CGAGGCGG		
	_ TA A		
GAM1764 LOC161734 3'	GATGGGGAAAAAACAGAG 88467	C_	G C
	CTCTGTT TTCC CCG TC		
	GAGACAA AAGG GGT AG		
	AA _ _		
GAM1764 LOC167026 5'	GGCGGAGCGGCGGGCGGA 88620	TCTT	
	TCTGT CCGCCGCTCCGCC		
	AGGCG GGCGGCGAGGCGG		

GAM1764 LOC196890 3'	AGCAAATGAAAAGAACAGA 91222	__	CC_
	TCTGTTCT TCCG GCT		
	AGACAAGA AGGT CGA		
	AA AAA		
GAM1764 LOC200731 5'	AGCACTGAAGAACAGAGT 91688	CGCC	
	ACTCTGTTCTTC GCT		
	TGAGACAAGAAG CGA		
	TCA_		
GAM1764 LOC221504 5'	CGGAGCGGCGGGGCAGGAG 94020	GTTC	
	CTCT TTCCGCCGCTCCG		
	GAGG GGGGCGGCGAGGC		
	AC_		
GAM1764 LOC221663 5'	GCAAAGCCCAGAACAGAGT 95462	TCCGCC	CC
	ACTCTGTTCT GCT GC		

TGAGACAAGA CGA CG
 CC___ AA
 GAM1764 LOC256310 3' GGCAGAGCAGCGGGAGCAGGAG 98102 GTT C C
 CTCT CTTCCGC GCTC GCC
 ||| ||||| ||| |||
 GAGG GAGGGCG CGAG CGG
 AC_ A A
 GAM1764 LOC51762 3' GGCCTAGCAAAAGAACAGA 33708 CCGCC CC
 TCTGTTCTT GCT GCC
 ||||| ||| |||
 AGACAAGAA CGA CGG
 AA___ TC
 GAM1764 LOC91266 5' GGCTGAGGAAAAACAGAGT 66024 ___ C
 ACTCTGT TCTTC GCC
 ||||| |||| |||
 TGAGACA AGGAG CGG
 AAA T
 GAM1765 HADHB 5' CTCGCGGACGTCAGCCAAGATT 5738 __ A A
 CCA TGGAATCTTG C GGC TCC CGAG
 ||||| ||| ||| |||
 ACCTTAGAAC G CTG AGG GCTC
 C A C C
 GAM1765 BHLHB2 5' CTCAAAGCCGAAGATTCCA 14763 G ATCCAC
 TGGAATCTT CGGC GAG
 ||||| ||| |||
 ACCTTAGAA GCCG CTC
 _ AAA___
 GAM1765 CPSF1 3' CGTGGATGCCGTCACCACCA 65160 AATCTT
 TGG GCGGCATCCACG
 ||| |||||
 ACC TGCCGTAGGTGC
 ACCAC_
 GAM1765 DKFZP434K0427 3' TCTCACAGATGTGCTGTATCC 50500 ATCT CCAC___
 GGA TGCGGCAT GAGA
 ||| ||||| |||
 CCT ATGTCGTG CTCT
 ___ TAGACA
 GAM1765 FLJ14166 3' TCTCGTTCCGGAAGATTCCA 44992 G CATCCA
 TGGAATCTT CGG CGAGA
 ||||| ||| |||||
 ACCTTAGAA GCC GCTCT
 G TTG___
 GAM1765 FLJ20618 3' TCTCACAAGGCTGCACCAGATT 35888 ___ ATCCAC
 CCA TGGAATCT TGCGGC GAGA
 ||||| ||||| |||
 ACCTTAGA ACGTCG CTCT
 CC GAACA_
 GAM1765 LOC125988 5' TCTCAGAGCCGCAAGACACCA 74900 AA A CAC
 TGG TCTTGCGGC TC GAGA
 ||| ||||| || |||

ACC AGAACGCCG AG CTCT
 AC _ A_
 GAM1765 LOC148697 3' TCTCGTGGACACCCACATCTCA 79681 GA CT C CA
 TG AT TG GG TCCACGAGA
 || || || || |||||
 AC TA AC CC AGGTGCTCT
 TC C_ _ AC
 GAM1765 LOC195977 3' GGATGCCGCCCAAGATTCC 88933 _
 GGAATCTT GCGGCATCC
 ||||| |||||
 CCTTAGAA CGCCGTAGG
 CC
 GAM1766 BBS4 3' ATTTGCCCAAAGGGAATCCAGA 53447 G_ G_ A
 ACA TGTCTGGA CT TTGG CAAAT
 ||||| || ||| ||||
 ACAAGACCT GG AACC GTTTA
 AA GA C
 GAM1766 CENTD2 3' CCAACAACTCCAGAACA 31539 C_
 TGTCTGAG TGTTGG
 ||||| ||||
 ACAAGACCTC ACAACC
 AA
 GAM1766 HAMP 3' TCCTGCTGCCCCAGAACA 41289 A T T
 TGTCTGG GC GT GGA
 ||||| || |||
 ACAAGACC CG CG CCT
 C T T
 GAM1766 ITGA11 3' TCTGCCGGCCCCCAGGACA 25213 A_ TT
 TGTCTGG GCTG GGA
 ||||| ||| ||
 ACAGGACC CGGC TCT
 CC CG
 GAM1766 KITLG 3' ATTTGCATGGCTCCAGAA 8023 TGGA
 TTCTGGAGCTGT CAAAT
 ||||| ||||
 AAGACCTCGGTA GTTTA
 C_
 GAM1766 MAPK4 5' CCTGGGCAGCTCCAGATCA 12300 T _
 TG TCTGGAGCTGTT GG
 || ||||| ||
 AC AGACCTCGACGG CC
 T GT
 GAM1766 MGAT2 3' ATTTGTCCAAACAGGACA 11557 GAGCTG
 TGTCTG TTGGACAAAT
 |||| |||||
 ACAGGAC AACCTGTTTA
 A_
 GAM1766 PSPHL 5' TTGTCATACAGCTCCAAACA 94499 C TG
 TGTT TGGAGCTGT GACAA
 ||| ||||| ||||

ACAA ACCTCGACA CTGTT
 _ TA
 GAM1766 TTC3 3' TATTTGTCCAACAACTGTCAGA 13885 _ C
 ATA TGTTCCTGG AG TGTTGGACAAATA
 ||||| || |||||
 ATAAGACT TC ACAACCTGTTTAT
 G A
 GAM1766 FLJ14213 3' TGATAACAGCTCCAGAA 46218 GA
 TTCTGGAGCTGTTG CA
 ||||| ||
 AAGACCTCGACAAT GT
 A_
 GAM1766 H2BFQ 3' TTTAAGAGAACTCCAGGACA 60079 _ G
 TGTTCTGGAG CT TTGGA
 ||||| || ||||
 ACAGGACCTC GA AATTT
 AA G
 GAM1766 LRG 3' TCCATCCATGCTTCCTAGAACA 54825 _ _ _ T_
 TGTTCT GGA GC TG TGA
 ||||| || || ||||
 ACAAGA CCT CG AC ACCT
 T T T CT
 GAM1766 NMT2 3' ATTTGTCCATGTAACAGAACA 17852 GA TGT
 TGTTCTG GC TGGACAAAT
 ||||| || |||||
 ACAAGAC TG ACCTGTTTA
 AA T__
 GAM1766 NYD-SP21 3' TATTTGTCCAATCTAGATTCAG 51863 G _
 AACA TGTTCTGGA CT GTTGGACAAATA
 ||||| || |||||
 ACAAGACTT GA TAACCTGTTTAT
 A TC
 GAM1766 PSPH 3' TTGTCGTACAGCTCCAAACA 17143 C TG
 TGTT TGGAGCTGT GACAA
 ||| ||||| ||||
 ACAA ACCTCGACA CTGTT
 _ TG
 GAM1766 LOC122258 3' CCACCAGCCTCCGGAACA 59820 _ T
 TGTTCTGGAG CTG TGG
 ||||| || ||||
 ACAAGGCCTC GAC ACC
 C C
 GAM1766 LOC151826 3' ATTTGTCCAACCTAGCACA 81176 T AGCT
 TGT CTGG GTTGGACAAAT
 ||| ||| |||||
 ACA GATC CAACCTGTTTA
 C ____
 GAM1766 LOC169611 3' TCCAGTGGCAGCTCCAGAA 83663 ____
 TTCTGGAGCTGT TGA
 ||||| ||||

AAGACCTCGACG ACCT
 GTG
 GAM1766 LOC196746 3' TCAGAGCAGCTCCAAGACA 88903 TC G_
 TGT TGGAGCTGTT GA
 ||| ||||| ||
 ACA ACCTCGACGA CT
 GA GA
 GAM1766 LOC204119 5' TGCCACAACCTCAGAACA 92343 G C T A
 TGTTCTG AG TGT GG CA
 ||||| || || ||
 ACAAGAC TC ACA CC GT
 _ A _ _
 GAM1766 LOC253142 5' TTGCTAGGATGCCCCAGAATA 99230 A TG_ A
 TGTTCTGG GC TTGG CAA
 ||||| || ||| ||
 ATAAGACC CG GATC GTT
 C TAG _
 GAM1767 ADAT1 3' CCAGCAAAGAATGAAGGC 24914 _ C
 GTC CATTCTTTGC GG
 ||| ||||| ||
 CGG GTAAGAAACG CC
 AA A
 GAM1767 M17S2 5' CCGGTAGCGGACGGTCCTT 20910 ATTCT
 AAGGACCGTCC TTGCCGG
 ||||| |||||
 TTCCTGGCAGG GATGGCC
 C____
 GAM1767 ST14 5' CCGGCAGGGACGACGCCT 42042 AC CAT
 AGG CGTC TCTTTGCCGG
 || ||| |||||
 TCC GCAG AGGGACGGCC
 _ C_
 GAM1767 HTGN29 5' GCCAACTGTGTGGCGGTCC 39885 _ TC T
 GGACCGTC CAT TT GC
 ||||| || ||
 CCTGGCGG GTG AA CG
 T TC C
 GAM1767 PMAIP1 3' GCAAGAATGGAAGACCCTT 41211 ACCG T
 AAGG TCCATTCTT GC
 ||| ||||| ||
 TTCC AGGTAAGAA CG
 CAGA _
 GAM1767 LOC144278 3' GCCAGCAAAGACTGCTCGATGG 77274 _ T C
 TCCT AGGACCGTC CA TCTTTGC GGC
 ||||| || ||||| ||
 TCCTGGTAG GT AGAAACG CCG
 CTC C A
 GAM1767 LOC147976 3' CCGGTGAATGAAGACCCT 79287 ACC CA _ TG
 AGG GTC TTC TT CCGG
 || ||| || |||

		TCC CAG AAG AA GGCC	
		___ _ T GT	
GAM1767	LOC254263 5'	GCCGGCAGCGGACGCGCC 96367	AC ATTCT
		GG CGTCC TTGCCGGC	
		CC GCAGG GACGGCCG	
		GC C___	
GAM1768	HAL 5'	GCCACTCCTGCATAAAGCTC 10903	TGAAAA
		GAGCTTTATGC GGTGGC	
		CTCGAAATACG TCACCG	
		TCC___	
GAM1768	HMG2 3'	GGCCACCTTGGCACAAAAGC 19809	A C AA
		GCTTT TG TG AAGGTGGCC	
		CGAAA AC AC TTCCACCGG	
		_ _ GG	
GAM1768	NMI 5'	GGCCACCTCCTCAGGAAG 17436	ATG AA
		CTTT CTGA AGGTGGCC	
		GAAG GACT TCCACCGG	
		___ CC	
GAM1768	PACE 3'	GGCCACCTCTCCAAGGGCTT 11944	A CT AAA
		GAGCTTT TG GA GGTGGCC	
		TTCGGGA AC CT CCACCGG	
		_ CT ___	
GAM1768	PYCR1 3'	CCACCTTCTCTAGAGCTC 70639	TGCT A_
		GAGCTTTA GA AAGGTGG	
		CTCGAGAT CT TTCCACC	
		___ CC	
GAM1768	SDC1 3'	GGCCACCTCCCCAGCATTCCAG 12991	TT_ AAA
	C	GCT ATGCTG AGGTGGCC	
		CGA TACGAC TCCACCGG	
		CCT CCC	
GAM1768	FLJ11560 5'	GCCCAGGCCAGCATAAAG 48008	AAAA ___
		CTTTATGCTG GGT GGC	
		GAAATACGAC CCG CCG	
		___ GAC	
GAM1768	KIAA0446 5'	CCACCTTTTGAAGAGCTC 69446	ATGCTG
		GAGCTTT AAAAGGTGG	
		CTCGAGA TTTTCCACC	
		AG___	
GAM1768	KIAA0971 3'	GTTGTTCTCAGCATAAAGT 30677	AAA TG
		GCTTTATGCTGA GG GC	

		TGAAATACGACT TT TG	
		C__ GT	
GAM1768 KIAA1393	3'	GGCCACCTTGGCACAAAAGC 72574	A C AA
		GCTTT TG TG AAGGTGGCC	
		CGAAA AC AC TTCCACCGG	
		_ _ GG	
GAM1768 KIAA1656	3'	GGCCACCTCCTCCTAGAAGCC 66377	A ATGCT AA
		G GCTTT GA AGGTGGCC	
		C CGAAG CT TCCACCGG	
		_ ATC__ CC	
GAM1768 KIAA1884	3'	GCCACCTTCATCTACCAAGGCT 73728	ATGCT A_
	C	GAGCTTT GA AAGGTGGC	
		CTCGGAA CT TTCCACCG	
		CCAT_ AC	
GAM1768 PP3501	3'	GGCCACCGTTGACAGCATAAAG 41683	AAAA_
		CTTTATGCTG GGTGGCC	
		GAAATACGAC CCACCGG	
		AGTTG	
GAM1768 SDCCAG3	3'	GGTGTTCTCAGCATGAAGCTC 22803	AAA TG
		GAGCTTTATGCTGA GG GCC	
		CTCGAAGTACGACT CT TGG	
		__ TG	
GAM1768 SP140	3'	GGCCACCTCCATGCAGAAGC 24327	A TGAAA
		GCTTT TGC AGGTGGCC	
		CGAAG ACG TCCACCGG	
		_ TACC_	
GAM1768 LOC148760	3'	GGCCACCTTCTCCAACAAGCTC 85364	TA CT A
		GAGCTT TG GA AAGGTGGCC	
		CTCGAA AC CT TTCCACCGG	
		CA __ C	
GAM1768 LOC150170	5'	ACCTGTTTCACATAAAGC 80414	C _
		GCTTTATG TGAAA AGGT	
		CGAAATAC ACTTT TCCA	
		_ G	
GAM1768 LOC150175	5'	ACCTGTTTCACATAAAGC 80453	C _
		GCTTTATG TGAAA AGGT	
		CGAAATAC ACTTT TCCA	
		_ G	
GAM1768 LOC150215	5'	ACCTGTTTCACATAAAGC 80456	C _
		GCTTTATG TGAAA AGGT	

CGAAATAC ACTTT TCCA
 _ G
 GAM1768 LOC150218 5' ACCTGTTTCACATAAAGC 80525 C _
 GCTTTATG TGAAA AGGT
 ||||| |||| ||||
 CGAAATAC ACTTT TCCA
 _ G
 GAM1768 LOC152065 3' GGCCACCTTCTCCTTGGCAGGC 86737 TTA _ A
 TC GAGCT TGCT GA AAGGTGGCC
 |||| ||| || |||||
 CTCGG ACGG CT TTCCACCGG
 _ TTC C
 GAM1768 LOC152267 3' GGCCACCTTGGCACAAAAGC 61036 A C AA
 GCTTT TG TG AAGGTGGCC
 |||| || || |||||
 CGAAA AC AC TTCCACCGG
 _ _ GG
 GAM1768 LOC158292 5' CCTCTGGACCCAGCATAAGGCT 88046 AAAA_ T
 C GAGCTTTATGCTG GG GG
 ||||| || ||
 CTCGGAATACGAC TC CC
 CCAGG T
 GAM1768 LOC219997 3' GCCACCTCTTCAGCCTC 93256 CTTTAT A
 GAG GCTGAA AGGTGGC
 || |||| |||||
 CTC CGACTT TCCACCG
 _ C
 GAM1768 LOC256269 3' GGCCACCTTGGCACAAAAGC 96608 A C AA
 GCTTT TG TG AAGGTGGCC
 |||| || || |||||
 CGAAA AC AC TTCCACCGG
 _ _ GG
 GAM1768 LOC91963 5' GGCCACCTCCTCTGAGAAGC 68321 ATGCT AA
 GCTTT GA AGGTGGCC
 |||| || |||||
 CGAAG CT TCCACCGG
 AGT_ CC
 GAM1769 CCND2 3' TCCCCAGCAAATCATCGGGCCA 10056 CCACA _ A
 TGGCCTGATGAT GC GG GA
 ||||| || || ||
 ACCGGGCTACTA CG CC CT
 AA_ A C
 GAM1769 GCN5L2 5' CTCCGCTGCGGGGGAGGCC 60529 GATGA A
 GGCCT TCC CAGCGGAG
 |||| || |||||
 CCGGA GGG GTCGCCTC
 GG_ C
 GAM1769 GJA5 3' CTGACCAGATCATCAGCCA 19164 C CACAG
 TGGC TGATGATC CGG
 |||| ||||| ||

		ACCG ACTACTAG GTC		
		— ACCA_		
GAM1769	HIVEP3	3' TCCCCGCTGTGGTTGGCAGCCA 44702	C ATGAT	A
		TGGC TG CCACAGCGG GA		
		ACCG AC GGTGTCGCC CT		
		_ GGTT_ C		
GAM1769	HOXD1	5' CCGCCGGTATATTAGGCCA 44696	AT ACA	
		TGGCCTGATG CC GCGG		
		ACCGGATTAT GG CGCC		
		AT C_		
GAM1769	SUFU	3' CCTTGTGACCCATCAGGCCA 32934	ATC C	
		TGGCCTGATG CACAG GG		
		ACCGGACTAC GTGTT CC		
		CCA _		
GAM1769	ARHGEF15	3' CTGTGGACCACAGGCCA 30953	A A	
		TGGCCTG TG TCCACAG		
		ACCGGAC AC AGGTGTC		
		_ C		
GAM1769	DKFZP586J1624	3' CTCCGCCAGTCACCATCAGGC 32043	ATCCACA_	
	CA	TGGCCTGATG GCGGAG		
		ACCGGACTAC CGCCTC		
		CACTGACC		
GAM1769	KIAA1671	3' CTTTGCTTATGAATCATCAGAC 66282	C C C_	
	C	GG CTGATGAT CA AGCGGAG		
		CC GACTACTA GT TCGTTTC		
		A A AT		
GAM1769	MGC18079	3' CCGCGGACCTCAGGCCA 59033	TGA ACA	
		TGGCCTGA TCC GCGG		
		ACCGGACT AGG CGCC		
		CC_ _		
GAM1769	LOC115110	3' TGCAGACATCAGGCCA 72186	A CACA	
		TGGCCTGATG TC GCG		
		ACCGGACTAC AG CGT		
		_ A_		
GAM1769	LOC159110	5' TCTCCGCTGCCCCGGTCAACCA 82995	CCTGA CA_	
		TGG TGATC CAGCGGAGA		
		ACC ACTGG GTCGCCTCT		
		A_ CCCC		
GAM1769	LOC159116	5' TCTCCGCTGCCCCGGTCAACCA 82978	CCTGA CA_	
		TGG TGATC CAGCGGAGA		

		ACC ACTGG GTCGCCTCT		
		A_____CCCC		
GAM1769	LOC165476 5'	CTCCGCTGCCTGCTCAGCCA	88550	C TGATCCA
		TGGC TGA CAGCGGAG		
		ACCG ACT GTCGCCTC		
		_ CGTCC_		
GAM1769	LOC200032 5'	CTGACCAGATCATCAGCCA	85475	C CACAG
		TGGC TGATGATC CGG		
		ACCG ACTACTAG GTC		
		_ ACCA_		
GAM1769	LOC219654 5'	CTCCGCTGCGGAGGGGGGCC	92932	GATGA A
		GGCCT TCC CAGCGGAG		
		CCGGG AGG GTCGCCTC		
		GGG_ C		
GAM1769	LOC255862 3'	TCAAATGTAGACTATCAGGCCA	96115	A C GCG
		TGGCCTGATG TC ACA GA		
		ACCGGACTAT AG TGT CT		
		C A AAA		
GAM1770	FBXL7 3'	ATCATCAAATTACATGTGT	25487	CCTCT
		ACACATGTAA GTGAT		
		TGTGTACATT TACTA		
		AAAC_		
GAM1770	LIF 3'	AATCACAGAGCCTTTGCGTG	11300	C_
		CATGTAA CTCTGTGATT		
		GTGCGTT GAGACACTAA		
		TCC		
GAM1770	MAPK4 3'	GGAGACCACATGTGTGCA	12302	AAC
		TGCACACATGT CTCT		
		ACGTGTGTACA GAGG		
		CCA		
GAM1770	OPHN1 3'	AGTTTTAGGGTACATGTGCACA	11905	CA A T T
		TG CACATGTA CC CTG GATT		
		AC GTGTACAT GG GAT TTGA		
		AC _ _ T		
GAM1770	SCAMP1 3'	AATCACAGAAATGATATTCTGC	18012	CAC AACC
	A	TGCA ATGT TCTGTGATT		
		ACGT TATA AGACACTAA		
		CT_ GTAA		
GAM1770	AD024 3'	AGTTTTAGGGTACATGTGCACA	40709	CA A T T
		TG CACATGTA CC CTG GATT		

			AC GTGTACAT GG GAT TTGA		
			AC _ _ T		
GAM1770	C1orf9	3'	AATCACAGCCTGCATACATATG 33157	CAC	ACCT__
	CA		TGCA ATGTA CTGTGATT		
			ACGT TACAT GACACTAA		
			A__ ACGTCC		
GAM1770	caspr5	3'	AGAGACACATGTGTGCA 56252	AAC	
			TGCACACATGT CTCT		
			ACGTGTGTACA GAGA		
			CA_		
GAM1770	FLJ20625	3'	AATCACAGAGAAAAATGTG 35896	GTAAC	
			CACAT CTCTGTGATT		
			GTGTA GAGACACTAA		
			AAAA_		
GAM1770	FLJ22639	3'	ACAGATTACATGTGTTCA 45995	C	CC
			TG ACACATGTAA TCTGT		
			AC TGTGTACATT AGACA		
			T _		
GAM1770	HSPC125	3'	AATCACAGAAATTCCTATGTG 27175	TAACC__	
	T		ACACATG TCTGTGATT		
			TGTGTAT AGACACTAA		
			CCTTTAA		
GAM1770	KIAA1975	5'	TCTAGGGTACATGTGCACA 74432	CA	A T T
			TG CACATGTA CC CTG GA		
			AC GTGTACAT GG GAT CT		
			AC _ _ _		
GAM1770	LOC121601	3'	CACAGTGCATGTTGCA 74559	C	ACCT
			TGCA ACATGTA CTGTG		
			ACGT TGTACGT GACAC		
			_ _ _		
GAM1770	LOC146901	3'	GCTGAGATTACAGGTGTGCA 84905	A	C T
			TGCACAC TGTA CTC GT		
			ACGTGTG ACATT GAG CG		
			G A T		
GAM1770	LOC148760	3'	ATAGCACATGTGTGCA 85361	AACCT	
			TGCACACATGT CTGT		
			ACGTGTGTACA GATA		
			C__		
GAM1770	LOC152078	3'	CACAGAGGCCCTGTTATGTGGC 81286	A	TAA__
	A		TGC CACATG CCTCTGTG		

ACG GTGTAT GGAGACAC
 _ TGTCCC
 GAM1770 LOC158377 3' ATCACAGAACTGCAGCA 88129 ACACA ACC
 TGC TGTA TCTGTGAT
 ||| ||| |||||
 ACG ACGT AGACACTA
 _ CA_

GAM1770 LOC200014 3' AATTGCAGTCACGTGTATGCA 89909 C AACCT TG
 TGCA ACATGT CTG ATT
 ||| ||||| ||| |||
 ACGT TGTGCA GAC TAA
 A CT_ GT

GAM1770 LOC220824 3' ACAGATTACATGTGTTCA 92478 C CC
 TG ACACATGTAA TCTGT
 || ||||| |||||
 AC TGTGTACATT AGACA
 T _

GAM1770 LOC221692 3' GGTGAAGCTTCATGTGTGCA 93855 _
 TGCACACATG TAACC
 ||||| |||||
 ACGTGTGTAC GTTGG
 TTCGAA

GAM1770 LOC222550 3' AATCAGGCAGCTATATATGTGC 96017 C ACCT _
 A TGCACA ATGTA CTGT GATT
 ||||| ||||| ||| |||
 ACGTGT TATAT GACG CTAA
 A C_ GA

GAM1770 LOC57086 3' TCTAGGGTACATGTGCACA 40129 CA A T T
 TG CACATGTA CC CTG GA
 || ||||| || ||| ||
 AC GTGTACAT GG GAT CT
 AC _ _ _

GAM1770 LOC90317 3' AATCACAGAAGTGTAATACGTG 62925 A _ C
 TGGCA TGC CACATGTA AC TCTGTGATT
 ||| ||||| || |||||
 ACG GTGTGCAT TG AGACACTAA
 _ AATG A

GAM1771 IRS1 3' CCATAGATGGTTCTCAATTGTA 19874 C TGAAC
 TACA ATTGAGAACC ATGG
 ||| ||||| ||| |||
 ATGT TAACTCTTGG TACC
 _ TAGA_

GAM1771 SERPINF1 3' CCTGTAAGGTTTCAATG 12038 A GA T
 CATTGAGA CCT ACA GG
 ||||| ||| ||| ||
 GTAAC TTT GGA TGT CC
 _ A_ _

GAM1771 HSA243396 3' CCATGTTCAAGCAATGTCAATG 37844 GAAC_
 CATTGA CTGAACATGG
 ||||| |||||

			GTAAC				
			GTAAC				
GAM1771	KIAA1387	3'	CAGGAATTTTCAATATGTA	71444	C	___	
			TACA ATTGAGAA CCTG				
			ATGT TAACTTTT GGAC				
			A AA				
GAM1771	MGC16063	3'	TTCAAATTCCAATGTGTA	54930	A	CC	
			TACACATTG GAA TGAA				
			ATGTGTAAC CTT ACTT				
			_ AA				
GAM1771	SMCR8	3'	CCATGCTCAGGTTTGACTATGT	59253	TGA_	A	
			ACAT GAACCTGA CATGG				
			TGTA TTTGGACT GTACC				
			TCAG C				
GAM1771	UPLC1	3'	CCATGCTAGGCCCAATGT	35227	AGAA	AA	
			ACATTG CCTG CATGG				
			TGTAAC GGAT GTACC				
			CCC_ C_				
GAM1771	ZNF334	3'	CCATAAGTCAACCCTCAATGT	36637	AACC	AC_	
			ACATTGAG TGA ATGG				
			TGTAAGTC ACT TACC				
			CCA_ GAA				
GAM1771	LOC145082	3'	TATGGAATGCCCTTAATGTGTA	84196		AACCTGAA	
			TACACATTGAG CATG				
			ATGTGTAATTC GTAT				
			CCGTAAG_				
GAM1771	LOC157723	3'	CCAAGTAAGTTCTCAAATGT	82465	_	GA A	
			ACATT GAGAACCT AC TGG				
			TGTAA CTCTTGGA TG ACC				
			A A_ A				
GAM1771	LOC219988	5'	CCATGTTCGGCCCAATG	93262	AGAAC		
			CATTG CTGAACATGG				
			GTAAC GGCTTGTACC				
			CCCC_				
GAM1772	ANKTM1	3'	TTCCATCTAGTACGGGGC	24704	_	TC	
			GCCCTGTG TGG TGGAA				
			CGGGGCAT ATC ACCTT				
			G T_				
GAM1772	APBA2	3'	TTCCAGACTCTAGGGT	19743	TGT		
			GCCCTG GGTCTGGAA				

			TGGGAT TCAGACCTT		
			C__		
GAM1772	AQP6	5'	TTCAAGGCCACAGGGC 55020	GT	G
			GCCCTGT GGTCT GAA		
			CGGGACA CCGGA CTT		
			__ A		
GAM1772	C5R1	3'	TTCCAGACCAGGCTGGC 9978	CT	G
			GCC GT TGGTCTGGAA		
			CGG CG ACCAGACCTT		
			T_ G		
GAM1772	CD22	3'	CCAGACACCGCCACATGGC 10100	C	_ _
			GCC TGTG TGG TCTGG		
			CGG ACAC GCC AGACC		
			T C AC		
GAM1772	CD59	3'	TTCCAGATAGCAGGGC 7032	GTG	
			GCCCTGT GTCTGGAA		
			CGGGACG TAGACCTT		
			A__		
GAM1772	CHRM1	5'	CCGCTGCCAGCACAGGGC 96431	_	C_
			GCCCTGTG TGGT TGG		
			CGGGACAC ACCG GCC		
			G TC		
GAM1772	CYLN2	3'	TTCACACACACACAGAGG 14095	_	_ C
			CC CTGTGTG GT TGGA		
			GG GACACAC CA ACTT		
			A A C		
GAM1772	DGCR2	3'	TTCCAGACCAGCGGGGC 18910	G	
			GCCCTGT TGGTCTGGAA		
			CGGGGCG ACCAGACCTT		
			-		
GAM1772	DGKQ	3'	TCCACGTCACACAGTGGC 9046	_	TC
			GCC CTGTGTGG TGGA		
			CGG GACACACT ACCT		
			T GC		
GAM1772	DHFR	3'	TTCCAGACCAGCCTGGC 7661	CT	G
			GCC GT TGGTCTGGAA		
			CGG CG ACCAGACCTT		
			TC _		
GAM1772	DIA1	3'	CCACATCGCACACGGGGC 24648	_	C
			GCCCTGTGTG GT TGG		

			CGGGGCACAC TA ACC		
			GC C		
GAM1772 DPYSL3	3'	CCAGATACTCATGGGC	9123	_ T _	
		GCCC TG GTG GTCTGG			
		CGGG AC CAC TAGACC			
		T T A			
GAM1772 FGFR2	3'	TTCCAGACCAGCCTGGC	43657	CT G	
		GCC GT TGGTCTGGAA			
		CGG CG ACCAGACCTT			
		TC _			
GAM1772 FGFR2	3'	TTCCAGACCAGCCTGGC	43670	CT G	
		GCC GT TGGTCTGGAA			
		CGG CG ACCAGACCTT			
		TC _			
GAM1772 FGFRL1	3'	TTCCAGACACACGTGC	41912	CC G	
		GC TGTGTG TCTGGAA			
		CG GCACAC AGACCTT			
		T_ _			
GAM1772 FLRT2	5'	TTCCAGACCAGCCCGGGC	26006	T_ G	
		GCCC GT TGGTCTGGAA			
		CGGG CG ACCAGACCTT			
		CC _			
GAM1772 GALNT3	3'	TTCCAGACCAGCCTGGGC	16829	T_ G	
		GCCC GT TGGTCTGGAA			
		CGGG CG ACCAGACCTT			
		TC _			
GAM1772 HTR4	3'	TTCCATGGAAGACACAGGGT	7887	GG _	
		GCCCTGTGT TCT GGAA			
		TGGGACACA AGG CCTT			
		GA TA			
GAM1772 KIR2DL5	3'	TTCCAGACATACAAGAGG	40452	G_ _	
		CCT TGTG GTCTGGAA			
		GGA ACAT CAGACCTT			
		GA A			
GAM1772 MADH6	5'	TTCCAGACACATTTAGGG	19979	T _	
		CCCTG GTG GTCTGGAA			
		GGGAT TAC CAGACCTT			
		T A			
GAM1772 MSF	5'	CCAGCCAGCGCGCAGGGC	89465	_ T	
		GCCCTGTGT GG CTGG			

			CGGGACGCG CC GACC	
			CGA _	
GAM1772	MSR1	3'	TTCCAGATTACAAAGGC 57797	CTG
			GCC TGTGGTCTGGAA	
			CGG ACATTAGACCTT	
			AA_	
GAM1772	MSR1	3'	TTCCAGATTACAAAGGC 57798	CTG
			GCC TGTGGTCTGGAA	
			CGG ACATTAGACCTT	
			AA_	
GAM1772	NCALD	5'	TTCCAGGGGCTGCAGAGC 50194	C _ GG
			GC CTGT GT TCTGGAA	
			CG GACG CG GGACCTT	
			A T G_	
GAM1772	NRL	3'	TCCAGACCTGCACAGGGT 21628	_
			GCCCTGTGT GGTCTGGA	
			TGGGACACG CCAGACCT	
			T	
GAM1772	OGG1	5'	TCCAGGCGACTAGAAGGC 34161	_ T G
			GCC CTG GT GTCTGGA	
			CGG GAT CA CGGACCT	
			AA _ G	
GAM1772	OGG1	5'	TCCAGGCGACTAGAAGGC 34166	_ T G
			GCC CTG GT GTCTGGA	
			CGG GAT CA CGGACCT	
			AA _ G	
GAM1772	OGG1	5'	TCCAGGCGACTAGAAGGC 11892	_ T G
			GCC CTG GT GTCTGGA	
			CGG GAT CA CGGACCT	
			AA _ G	
GAM1772	OPA3	3'	TTCCAGACCAGCCTGGC 47851	CT G
			GCC GT TGGTCTGGAA	
			CGG CG ACCAGACCTT	
			TC _	
GAM1772	PLXNA1	3'	TTCCAGACGGACCGGGC 72776	T G G
			GCCC GT TG TCTGGAA	
			CGGG CA GC AGACCTT	
			C G _	
GAM1772	PTK7	3'	TTCTGGGCACACAGGGT 12553	G TG
			GCCCTGTGTG TC GAA	

			TGGGACACAC GG CTT		
			_ GT		
GAM1772	PTPN14	5'	TTCCAGAGGGCCCACTGGGC 19429	T	___
			GCCC GTGTGGT CTGGAA		
			CGGG CACACCG GACCTT		
			T GGA		
GAM1772	SAA4	3'	CCAGACAGGGACACAGGGT 22513	G	___
			GCCCTGTGT GTCTGG		
			TGGGACACA CAGACC		
			GGGA		
GAM1772	SCA7	3'	TTCCAGAGAACACAGGGC 6193	GG	
			GCCCTGTGT TCTGGAA		
			CGGGACACA AGACCTT		
			AG		
GAM1772	SCNN1G	3'	CCAGACGTGTGCACAGGG 8299		___
			CCCTGTGTG GTCTGG		
			GGGACACGT CAGACC		
			GTG		
GAM1772	SMARCC1	3'	TTCCATCTATCACAGGGT 13255	_ TC	
			GCCCTGTG TGG TGGAA		
			TGGGACAC ATC ACCTT		
			T T_		
GAM1772	SMS	5'	CCAGGCATGGCACAGGGC 17185	G	___
			GCCCTGTGT GTCTGG		
			CGGGACACG CGGACC		
			GTA		
GAM1772	SPON1	3'	TTCCAGAGTCACCAATGGC 63127	C_ T _	
			GCC TG GTGG TCTGGAA		
			CGG AC CACT AGACCTT		
			TA _ G		
GAM1772	SSR2	3'	TTCCAGACTCCAAAGGGT 13418	G TG	
			GCCCT TG GTCTGGAA		
			TGGGA AC CAGACCTT		
			A CT		
GAM1772	TACC1	3'	CCAGTCCAGATACAGGGC 21868	___ T	
			GCCCTGTG TGG CTGG		
			CGGGACAT ACC GACC		
			AG T		
GAM1772	TLR4	3'	TTCCAGAAACATATGGGC 57504	_ GG	
			GCCC TGTGT TCTGGAA		

			CGGG ATACA AGACCTT		
			T A_		
GAM1772	TLR4	3'	TTCCAGAAACATATGGGC	57505	_ GG
			GCCC TGTGT TCTGGAA		
			CGGG ATACA AGACCTT		
			T A_		
GAM1772	TLR4	3'	TTCCAGAAACATATGGGC	13778	_ GG
			GCCC TGTGT TCTGGAA		
			CGGG ATACA AGACCTT		
			T A_		
GAM1772	TLX1	3'	CCAGAGCCACACATGGGC	19815	_ _
			GCCC TGTGTGG TCTGG		
			CGGG ACACACC AGACC		
			T G		
GAM1772	TMOD	3'	TTCCAGATCAACATGGC	13812	C G
			GCC TGT TGGTCTGGAA		
			CGG ACA ACTAGACCTT		
			T _		
GAM1772	TNFRSF1B	3'	TTCTTGGCATCACAGGGC	8406	TG T_
			GCCCTGTG GTC GGAA		
			CGGGACAC CGG CCTT		
			TA TT		
GAM1772	7h3	3'	TTCCAGCATGGACACAGGG	53438	G_ _
			CCCTGTGT GT CTGGAA		
			GGGACACA TA GACCTT		
			GG C		
GAM1772	AP4M1	5'	TTCCGGGGGCCGCAGGGC	17550	GT _
			GCCCTGT GGTCT GGAA		
			CGGGACG CCGGG CCTT		
			_ G		
GAM1772	ARAP3	5'	TTCCAGATCGCAGGC	42790	CTG
			GCC TGTGGTCTGGAA		
			CGG ACGCTAGACCTT		
			_		
GAM1772	ARHGEF15	3'	TTCCAGATGAGCCAGTGC	30956	C T G_
			GC CTG GT GTCTGGAA		
			CG GAC CG TAGACCTT		
			T _ AG		
GAM1772	BANP	5'	TCCAGCTACCTCACGGGGC	66806	T _
			GCCCTGTG GGT CTGGA		

				CGGGGCAC CCA GACCT			
				T TC			
GAM1772	C11orf11	3'	CCAGACCTGCAGCACAAAGTGC	94875	C	_	_____
			GC CT GTGT GGTCTGG				
			CG GA CACG CCAGACC				
			T A ACGT				
GAM1772	C20orf28	3'	TTCCAGACTTCACCAGGC	31849	CT	T	
			GCC GTG GGTCTGGAA				
			CGG CAC TCAGACCTT				
			AC T				
GAM1772	C21orf69	3'	TTCCAGATCTCCAGGGC	55237	TGT		
			GCCCTG GGTCTGGAA				
			CGGGAC CTAGACCTT				
			CT_				
GAM1772	C6.1A	3'	TTCCAGACCAGCCTGGGC	44539	T_	G	
			GCCC GT TGGTCTGGAA				
			CGGG CG ACCAGACCTT				
			TC _				
GAM1772	C7orf10	3'	TCCAGATTTCTTACATGGC	45639	C	T_	
			GCC TGTG GGTCTGGA				
			CGG ACAT TTAGACCT				
			T TCT				
GAM1772	DDX34	3'	TCCGGCGGCTCACAGGGC	28680	T	_	
			GCCCTGTG GGT CTGGA				
			CGGGACAC TCG GGCCT				
			_ GC				
GAM1772	DKFZp547E052	3'	TTCCAGATGCATAAGGC	51093	C	G	
			GCC TGTGTG TCTGGAA				
			CGG ATACGT AGACCTT				
			A _				
GAM1772	DKFZp547O146	3'	TTCCGTAGGAACAAGGGC	39968	G	GG	_____
			GCCCT TGT TCT GGAA				
			CGGGA ACA GGA CCTT				
			_ A_ TG				
GAM1772	DKFZP564M182	3'	TTCCAAAGACCACAAGGG	78651	G		_____
			CCCT TGTGGTCT GGAA				
			GGGA ACACCAGA CCTT				
			_ AA				
GAM1772	DOCK3	3'	TTCCAGATGATGCGGGC	67102	T	G	
			GCCC GTGT GTCTGGAA				

		CGGG CGTA TAGACCTT	
		— G	
GAM1772	EDG1	5' TTCCTGGGGACACAGGGT 60055	GG T
		GCCCTGTGT TC GGAA	
		TGGGACACA GG CCTT	
		GG T	
GAM1772	FLJ10040	5' TCCAGACAGGTTGCCAGGGC 36221	T ____
		GCCCTG GTG GTCTGGA	
		CGGGAC CGT CAGACCT	
		— TGGA	
GAM1772	FLJ10665	3' TTCCAGACCAGCCTGGGC 36921	T_ G
		GCCC GT TGGTCTGGAA	
		CGGG CG ACCAGACCTT	
		TC _	
GAM1772	FLJ11126	3' CCAGGTGTCACACGGGGC 37649	__
		GCCCTGTGTGG TCTGG	
		CGGGGCACACT GGACC	
		GT	
GAM1772	FLJ11850	3' TTCCAGAGTCATAGGGC 43025	TGG
		GCCCTGTG TCTGGAA	
		CGGGATAC AGACCTT	
		TG_	
GAM1772	FLJ14675	3' TTCCAGAAAGTCACACAG 52591	__
		CTGTGTGG TCTGGAA	
		GACACACT AGACCTT	
		GAA	
GAM1772	FLJ14957	3' TTCCACATCTACAGGGT 52828	T C
		GCCCTGTG GGT TGGAA	
		TGGGACAT CTA ACCTT	
		— C	
GAM1772	FLJ20170	5' TCCAGTCAGCCACAGGGT 35167	__ T
		GCCCTGTG TGG CTGGA	
		TGGGACAC ACT GACCT	
		CG _	
GAM1772	FLJ20211	3' TTCCAGACCAGCCTGGC 35270	CT G
		GCC GT TGGTCTGGAA	
		CGG CG ACCAGACCTT	
		TC _	
GAM1772	FLJ22167	5' TTGCAAACCCACAGGGC 44882	T C G
		GCCCTGTG GGT TG AA	

CGGGACAC CCA AC TT
 _ A G
 GAM1772 FLJ22378 3' TCCAGGTGGACACACGGGC 47601 _ GG_
 GCCC TGTGT TCTGGA
 |||| |||| ||||
 CGGG ACACA GGACCT
 C GGT
 GAM1772 FLJ31455 3' TTCCAGACCAGCCTGGC 59296 CT G
 GCC GT TGGTCTGGAA
 ||| || |||||
 CGG CG ACCAGACCTT
 TC _
 GAM1772 FLJ31762 5' CCAGACACGCGCACGGGC 58760 _ _
 GCCC TGTGTG GTCTGG
 |||| |||| ||||
 CGGG ACGCGC CAGACC
 C A
 GAM1772 FLJ31762 3' TTCCAGACCTCAGGGC 58768 TGT
 GCCCTG GGTCTGGAA
 |||| |||||
 CGGGAC CCAGACCTT
 T__
 GAM1772 FLJ32954 5' TTCCACCTCTACAGGGC 59190 T TC
 GCCCTGTG GG TGGAA
 ||||| || ||||
 CGGGACAT TC ACCTT
 C C_
 GAM1772 GT650 3' TCCAGACACCATACAAAGG 54553 C_ _
 CC TGTGTGG TCTGGA
 || ||||| ||||
 GG ACATACC AGACCT
 AA AC
 GAM1772 H2AFY 5' TTCCAGACTTCGGGGT 18089 TGT
 GCCCTG GGTCTGGAA
 |||| |||||
 TGGGGC TCAGACCTT
 T__
 GAM1772 HABP4 3' TTCCAGCTGGGCCAAGGG 71085 _ G T
 CCCT GT TGG CTGGAA
 |||| || |||||
 GGGA CG GTC GACCTT
 AC G _
 GAM1772 HUMAGCGB 5' TTCCAGAACCTGGACATGGC 26137 C G _ _
 GCC TGT T GGT CTGGAA
 ||| ||| || |||||
 CGG ACA G CCA GACCTT
 T G T A
 GAM1772 KIAA0014 3' TTCCAGCCCTACAGGGC 28546 T T
 GCCCTGTG GG CTGGAA
 ||||| || |||||

CGGGACAT CC GACCTT
C _
GAM1772 KIAA0186 3' TTCCAGACCAGCCCGGGC 41129 T_ G
GCCC GT TGGTCTGGAA
|||| || |||||
CGGG CG ACCAGACCTT
CC _
GAM1772 KIAA0450 3' TCCGTGGGCCACGAGGGC 28371 G _
GCCCT TGTGGTCT GGA
|||| ||||| ||
CGGGA GCACCGGG CCT
_ TG
GAM1772 KIAA1272 3' TTCCAGAAATACAGGGT 70735 GG
GCCCTGTGT TCTGGAA
||||| |||||
TGGGACATA AGACCTT
A_
GAM1772 KIAA1327 5' TTCCAGAAGCTCACCAGG 72728 T _
CCTG GTGG TCTGGAA
|||| ||| |||||
GGAC CACT AGACCTT
_ CGA
GAM1772 KIAA1608 3' TTCCAGACTGGGCAGAGG 46106 _ G
CC CTGT TGGTCTGGAA
|| ||| |||||
GG GACG GTCAGACCTT
A G
GAM1772 KIAA1679 3' TCCTACTGTACACAGGGT 70715 _ CT
GCCCTGTGT GGT GGA
||||| ||| ||
TGGGACACA TCA CCT
TG T_
GAM1772 LIG-1 5' TTCCAGGCGCAGCGGC 64615 _ GTG
GCC CTGT GTCTGGAA
||| ||| |||||
CGG GACG CGGACCTT
C _
GAM1772 MGC10960 3' TTCCAGCCACACAGGGC 51983 T
GCCCTGTGTGG CTGGAA
||||||| |||||
CGGGACACACC GACCTT
_
GAM1772 MGC11271 3' TTCCATGGACAACACAAAGG 44494 C_ G _
CC TGTGT GTCT GGAA
|| |||| ||| |||
GG ACACA CAGG CCTT
AA A TA
GAM1772 MGC2474 3' CCAGACCTCCATACAGGG 43952 _
CCCTGTGT GGTCTGG
||||| |||||

GGGACATA CCAGACC
CCT

GAM1772 MGC26641 3' TTCCAGACCAGCCTGGT 59327 CT G
GCC GT TGGTCTGGAA
||| || |||||
TGG CG ACCAGACCTT
TC _

GAM1772 MGC3101 3' TTCCAGTCACACAGAGC 44107 C T
GC CTGTGTGG CTGGAA
|| ||||| |||||
CG GACACACT GACCTT
A _

GAM1772 OCT11 3' TTCCAGAGTTCCCACATGGGC 27596 T ____
GCCC GTGTGG TCTGGAA
||| ||||| |||||
CGGG TACACC AGACCTT
_ CTTG

GAM1772 OS4 3' TTCCAGACCAGCATCCAG 20399 _ _
CTG TG TGGTCTGGAA
||| || |||||
GAC AC ACCAGACCTT
CT G

GAM1772 PF1 5' TCCAGACGAATGCCAGCGC 96835 C _ G_
GC CTG TGT GTCTGGA
|| ||| ||| |||||
CG GAC GTA CAGACCT
C C AG

GAM1772 POR1 3' TTCCTGGCCACAGGGC 25731 GT T
GCCCTGT GGTC GGAA
||||| ||| |||
CGGGACA CCGG CCTT
_ T

GAM1772 PRAC 3' TTCCAGACCAGCCTGGGC 51504 T_ G
GCCC GT TGGTCTGGAA
||| || |||||
CGGG CG ACCAGACCTT
TC _

GAM1772 PRO2289 3' CCAGGAGTGCACATGGGC 38411 _ G_
GCCC TGTGTG TCTGG
||| ||||| |||
CGGG ACACGT GGACC
T GA

GAM1772 SARM 3' CCAGAGGCCATACAGAGC 31280 C _
GC CTGTGTGGT CTGG
|| ||||| |||
CG GACATACCG GACC
A GA

GAM1772 TOSO 5' TTCCAGATTGTGAAGGGT 19569 G TG
GCCCT TG GTCTGGAA
||||| || |||||

	TGGGA GT TAGACCTT	
	A GT	
GAM1772 UBE3B	3' CCAGACTGTCAGCACAGGG 77441	_____
	CCCTGTGT GGTCTGG	
	GGGACACG TCAGACC	
	ACTG	
GAM1772 LOC118471	3' TTCCAGACCAGCCTGGGC 74355	T_ G
	GCCC GT TGGTCTGGAA	
	CGGG CG ACCAGACCTT	
	TC _	
GAM1772 LOC118851	5' TCCAACACTTAACACAGGGC 76018	_ C_
	GCCCTGTGT GGT TGGA	
	CGGGACACA TCA ACCT	
	AT CA	
GAM1772 LOC121504	3' TTCCAAACCAAACTGGGT 74556	T G_ C
	GCCC GT TGGT TGGAA	
	TGGG CA ACCA ACCTT	
	T AA A	
GAM1772 LOC123242	5' TCCACCGCAGCACAGGGC 76120	G C_
	GCCCTGTGT GT TGGA	
	CGGGACACG CG ACCT	
	A CC	
GAM1772 LOC128553	5' TTCCAGACATCAGAGGGC 75263	G TG
	GCCCT TG GTCTGGAA	
	CGGGA AC CAGACCTT	
	G TA	
GAM1772 LOC129228	5' TTCCAGACAGACAGGC 76321	C G G
	GCC TGT TG TCTGGAA	
	CGG ACA AC AGACCTT	
	_ G _	
GAM1772 LOC129881	5' TTCCAGATCTAGGAGC 75411	_ TGT
	GC CCTG GGTCTGGAA	
	CG GGAT CTAGACCTT	
	A _	
GAM1772 LOC130536	5' TCCAAGAGCAGCTCAGGGC 76247	T_ G _
	GCCCTG G TG TCT GGA	
	CGGGAC C AC AGA CCT	
	T G G A	
GAM1772 LOC132625	3' TTCCAGACCAGCCTGGGC 76447	T_ G
	GCCC GT TGGTCTGGAA	

CGGG CG ACCAGACCTT
 TC _
 GAM1772 LOC132954 5' TTCCAGCCTGGAGAAGGC 75584 _ G T T
 GCC CT TG GG CTGGAA
 ||| ||| || |||||
 CGG GA GT CC GACCTT
 AA G _ _
 GAM1772 LOC134121 3' TTCCAAACCTAGAGGAGT 75640 _ G T C
 GC CCT TG GGT TGGAA
 || ||| || ||| |||||
 TG GGA AT CCA ACCTT
 A G _ A
 GAM1772 LOC135818 3' TTCCAGACCAGCCTGGGT 75755 T_ G
 GCCC GT TGGTCTGGAA
 |||| || |||||
 TGGG CG ACCAGACCTT
 TC _
 GAM1772 LOC135932 5' TTCCTTGCTACACAGAGC 76701 C CT
 GC CTGTGTGGT GGAA
 || ||||| |||
 CG GACACATCG CCTT
 A TT
 GAM1772 LOC137964 3' TTCCAGACTCCAGGGC 75804 TGT
 GCCCTG GGTCTGGAA
 ||||| |||||
 CGGGAC TCAGACCTT
 C_
 GAM1772 LOC137964 3' TTCCTACCTCACAGGGC 75805 T CT
 GCCCTGTG GGT GGAA
 ||||| ||| |||
 CGGGACAC CCA CCTT
 T T_
 GAM1772 LOC142964 3' TCCAGACCACAGGACTGC 76970 _ GT
 GC CCTGT GGTCTGGA
 || |||| |||||
 CG GGACA CCAGACCT
 TCA _
 GAM1772 LOC144100 3' TCCAAGGAGGGCACGGGGC 77185 GG _
 GCCCTGTGT TCT GGA
 ||||| ||| |||
 CGGGGCACG AGG CCT
 GG AA
 GAM1772 LOC145601 3' TCTGTGGGCAGCACAGGGC 84356 G _
 GCCCTGTGT GTCT GGA
 ||||| ||| |||
 CGGGACACG CGGG TCT
 A TG
 GAM1772 LOC145946 3' TCCAGAGCTCCTATAGGGC 84561 T _
 GCCCTGTG GG TCTGGA
 ||||| || |||||

	CGGGATAT CC AGACCT		
	_ TCG		
GAM1772 LOC146184 5'	TTCCAGACTGTGTGGGT 84597	T TG	
	GCCC G TGGTCTGGAA		
	TGGG T GTCAGACCTT		
	_ GT		
GAM1772 LOC147165 5'	TTCCAGACCATTCAGGC 85089	C T_	
	GCC TG GTGGTCTGGAA		
	CGG AC TACCAGACCTT		
	_ CT		
GAM1772 LOC148697 3'	TTCACAGACACAGGC 79682	GTG _	
	GCCCTGT GTCTG GAA		
	CGGGACA CAGAC CTT		
	_____ A		
GAM1772 LOC150271 5'	TCCAGACTGGTGACACAGGC 86147	_____	
	GCCCTGTGT GGTCTGGA		
	TGGGACACA TCAGACCT		
	GTGG		
GAM1772 LOC150481 3'	TTCCAGGAGCTCTAGGC 80719	T_ GG	
	GCCCTG GT TCTGGAA		
	CGGGAT CG GGACCTT		
	CT A_		
GAM1772 LOC151720 5'	TTCCAGACGCTCCCAGGC 81160	T__ G	
	CCCTG GTG TCTGGAA		
	GGGAC CGC AGACCTT		
	CCT _		
GAM1772 LOC152860 3'	TTCCAGCTTACATGGC 81584	CT T	
	GCC GTGTGG CTGGAA		
	CGG TACATT GACCTT		
	_ C		
GAM1772 LOC154760 5'	TTCTTGCTACACAGAGC 87457	C CT	
	GC CTGTGTGGT GGAA		
	CG GACACATCG CCTT		
	A TT		
GAM1772 LOC158117 3'	TTCTGACATCACAGGC 82615	TG T	
	GCCCTGTG GTC GGAA		
	CGGGACAC CAG TCTT		
	TA _		
GAM1772 LOC158450 5'	TTCTGGGGACCCAGGC 82817	TGT _	
	GCCCTG GGTCT GGAA		

	CGGGAC CCAGG TCTT	
	___ GG	
GAM1772 LOC158504 5'	TTCTGGGGACCCAGGGC 82831	TGT ___
	GCCCTG GGTCT GGAA	
	CGGGAC CCAGG TCTT	
	___ GG	
GAM1772 LOC163882 3'	TTCCAGACACAGACATGC 83044	CC G _
	GC TGT TG GTCTGGAA	
	CG ACA AC CAGACCTT	
	T_ G A	
GAM1772 LOC166106 5'	TTCCAGGTGGTCAAGGGC 88608	G _ GG
	GCCCT TG T TCTGGAA	
	CGGGA AC G GGACCTT	
	_ T GT	
GAM1772 LOC197358 5'	TCCATTGGACCACAAGGG 89446	G ___
	CCCT TGTGGTCT GGA	
	GGGA ACACCAGG CCT	
	_ TTA	
GAM1772 LOC199923 3'	TTCCAGACCAGCCTGGGC 89880	T_ G
	GCCC GT TGGTCTGGAA	
	CGGG CG ACCAGACCTT	
	TC _	
GAM1772 LOC201252 3'	TCCAGAAATCTGCACAGGGT 89554	TG ___
	GCCCTGTG G TCTGGA	
	TGGGACAC C AGACCT	
	GT TAA	
GAM1772 LOC201799 3'	TTCCAGACCAGAGAGGT 90494	_ GTG
	GCC CT TGGTCTGGAA	
	TGG GA ACCAGACCTT	
	A G_	
GAM1772 LOC202020 3'	TTCCAGACCAGCCTGGC 90606	CT G
	GCC GT TGGTCTGGAA	
	CGG CG ACCAGACCTT	
	TC _	
GAM1772 LOC203275 3'	TTCTGACATCACAGGGC 90859	TG T
	GCCCTGTG GTC GGAA	
	CGGGACAC CAG TCTT	
	TA _	
GAM1772 LOC203696 5'	TTCAGGAACATCACAGGGC 92336	_ G_
	GCCCTGTG TG TCTGGA	

	CGGGACAC AC GGA	CTT	
	T AA		
GAM1772 LOC219347 5'	TTCCGTGGAGACACAGGG	94582	GG _
	CCCTGTGT TC TGGAA		
	GGGACACA GG GCCTT		
	GA T		
GAM1772 LOC219722 5'	TCCAGAGCTAGCACAGGG	94686	_ _
	CCCTGTG TGG TCTGGA		
	GGGACAC ATC AGACCT		
	G G		
GAM1772 LOC221543 3'	TTCCAGACCAGCCTGGC	95391	CT G
	GCC GT TGGTCTGGAA		
	CGG CG ACCAGACCTT		
	TC _		
GAM1772 LOC221749 3'	TTCCAGGTGCCACAGGC	93653	CTG _
	GCC TGTGGT CTGGAA		
	CGG ACACCG GACCTT		
	_ TG		
GAM1772 LOC253001 5'	TCCACCGCAGCACAGGGC	97998	G C_
	GCCCTGTGT GT TGGA		
	CGGGACACG CG ACCT		
	A CC		
GAM1772 LOC253897 3'	TTCCAGACTCCAGGGC	97817	TGT
	GCCCTG GGTCTGGAA		
	CGGGAC TCAGACCTT		
	C_		
GAM1772 LOC253897 3'	TTCTACCTCACAGGGC	97818	T CT
	GCCCTGTG GGT GGAA		
	CGGGACAC CCA CCTT		
	T T_		
GAM1772 LOC254351 3'	TTCCAGACCGCCTGGGC	96697	TGT
	GCCC GTGGTCTGGAA		
	CGGG CGCCAGACCTT		
	TC_		
GAM1772 LOC255042 3'	TTCCAGAGCAAGCAGGGC	97063	G G
	GCCCTGT TG TCTGGAA		
	CGGGACG AC AGACCTT		
	A G		
GAM1772 LOC255070 3'	CCAGCGAGCCCACGGGGC	98707	T _
	GCCCTGTG GGT CTGG		

CGGGGCAC CCG GACC
 _ AGC
 GAM1772 LOC257095 5' TTCCAGTCCGTCCACATGGC 98725 C _ T
 GCC TGTG TGG CTGGAA
 ||| ||| ||| |||||
 CGG ACAC GCC GACCTT
 T CT T
 GAM1772 LOC257596 3' TTCCAGACCAGCCTGGC 99794 CT G
 GCC GT TGGTCTGGAA
 ||| || ||||| |||||
 CGG CG ACCAGACCTT
 TC _
 GAM1772 LOC84661 5' TTCCAGACCCCATGTAGGC 51794 CT_ T
 GCC GTG GGTCTGGAA
 ||| ||| ||||| |||||
 CGG TAC CCAGACCTT
 ATG C
 GAM1772 LOC91373 3' TTCCAGATTTAGAGGC 66421 _ TGT
 GCC CTG GGTCTGGAA
 ||| ||| ||||| |||||
 CGG GAT TTAGACCTT
 A _
 GAM1772 LOC91875 3' TTCCAGCTCTCTACAGGGC 68035 T T_
 GCCCTGTG GG CTGGAA
 ||||| || |||||
 CGGGACAT TC GACCTT
 C TC
 GAM1772 LOC92609 3' TTCCAGACCAAGACTTGGGC 73212 T_ G_
 GCCC GT TGGTCTGGAA
 |||| || ||||| |||||
 CGGG CA ACCAGACCTT
 TT GA
 GAM1772 LOC93349 3' TTCCAGAACCACAGGGC 57279 TGG
 GCCCTGTG TCTGGAA
 ||||| |||||
 CGGGACAC AGACCTT
 CA_
 GAM1772 LOC93512 5' TTCCAGACCATTCCAGGC 72880 C T_
 GCC TG GTGGTCTGGAA
 ||| || ||||| |||||
 CGG AC TACCAGACCTT
 _ CT
 GAM1773 LMNB1 3' CTCTGGATGATGGATTCCA 19932 TC CT
 TGA TTA GTCCAGAG
 |||| ||| |||||
 ACCT GGT TAGGTCTC
 TA AG
 GAM1773 C3orf1 3' AGTGCTCTGAACTTGAACTC 63105 TC ACT C
 GA TT GT CAGAGCACT
 || || || ||||| |||||

		CT AA CA GTCTCGTGA		
		CA GTT A		
GAM1773	RNF34	3' GTGGGGACAGAAAGATCCAT 47817	A	AGA
		ATGGATCTT CTGTCC GC		
		TACCTAGAA GACAGG TG		
		A GG_		
GAM1773	SMUG1	3' AGTGCCCTAGACAGTAACTTCT 27467	TC	C A
	A	TGGA TTA CTGTGTC AG GCACT		
		ATCT AATGACAG TC CGTGA		
		TC A C		
GAM1773	SPRY4	3' GTGCTCTCTAAGAGTCCA 49029 _	CTGTCC	
		TGGA TCTTA AGAGCAC		
		ACCT AGAAT TCTCGTG		
		G C_____		
GAM1773	LOC145622	3' AGTGCTCTGGAGTTTGGACCC 77802	A	TACTG
		GG TCT TCCAGAGCACT		
		CC AGG AGGTCTCGTGA		
		C TTTG_		
GAM1773	LOC145676	5' AGTGCTCTGAAGGTGTAAGCCA 77842	ATCT	GTC
	T	ATGG TACT CAGAGCACT		
		TACC GTGG GTCTCGTGA		
		GAAT AA_		
GAM1773	LOC152283	5' AGTGCTCTGAGTCAGAGACCG 86864	A	TA TC_
		TGG TCT CTG CAGAGCACT		
		GCC AGA GAC GTCTCGTGA		
		_ _ TGA		
GAM1773	LOC89231	3' CTGCTGAACAGCAAGGTCCA 94297	A	C _
		TGGATCTT CTGT CAG AG		
		ACCTGGAA GACA GTC TC		
		C A G		
GAM1774	ATP8A2	3' TCTGGTTGCCAAACCAGAT 95159	CAGA	GT
		GTCTGGTT GG GCCAGA		
		TAGACCAA CC TGGTCT		
		A__ GT		
GAM1774	BHLHB3	3' TCTGGAGACCAAACCAGAT 48491	CAGA	GTG
		GTCTGGTT GG CCAGA		
		TAGACCAA CC GGTCT		
		A__ AGA		
GAM1774	CYP27B1	5' GCACCCTGAACCAGAC 7604	GA	
		GTCTGGTTCA GGGTGC		

CAGACCAAGT CCCACG

GAM1774 DGCR2	3'	CTGGCACCCCTTTTGCCTGAC	18900	T TC
		GTC GGT AGAGGGTGCCAG		
		CAG CCG TTTCCCACGGTC		
		T T_		
GAM1774 EGFL4	3'	CTGGCACCCCTGCTGCTGAC	62464	T T_ A
		GTC GGT CAG GGGTGCCAG		
		CAG TCG GTC CCCACGGTC		
		_ TC _		
GAM1774 EPHB2	3'	TCTGGGAGCCTAAACCAGGC	16702	CAGA G_
		GTCTGGTT GGGT CCAGA		
		CGGACCAA TCCG GGTCT		
		A_ AG		
GAM1774 GPX1	5'	CTGGGCCAGACCAGAC	6967	CAGAG G
		GTCTGGTT GGT CCAG		
		CAGACCAG CCG GGTC		
		A_ _		
GAM1774 NFE2	5'	TCCGGGAACCTGGACCAGAC	21603	GAG G_ A
		GTCTGGTTCA GGT CC GA		
		CAGACCAGGT CCA GG CT		
		_ AG C		
GAM1774 POLL	3'	TCCGGCACCCCTCTGGGGTAGG	26092	G A
		TCTG TTCAGAGGGTGCC GA		
		GGAT GGGTCTCCCACGG CT		
		G C		
GAM1774 RGS3	3'	TCTGGCACCCCTGGGTGGA	35532	G TT A
		TCT G CAG GGGTGCCAGA		
		AGG T GTC CCCACGGTCT		
		_ GG C		
GAM1774 RGS3	3'	TCTGGCACCCCTGGGTGGA	41194	G TT A
		TCT G CAG GGGTGCCAGA		
		AGG T GTC CCCACGGTCT		
		_ GG C		
GAM1774 RGS3	3'	TCTGGCACCCCTGGGTGGA	56318	G TT A
		TCT G CAG GGGTGCCAGA		
		AGG T GTC CCCACGGTCT		
		_ GG C		
GAM1774 RGS3	3'	TCTGGCACCCCTGGGTGGA	57056	G TT A
		TCT G CAG GGGTGCCAGA		

		AGG T GTC CCCACGGTCT	
		_GG C	
GAM1774 RGS3	3'	TCTGGCACCCCCTGGGTGGA 58453	G TT A
		TCT G CAG GGGTGCCAGA	
		AGG T GTC CCCACGGTCT	
		_GG C	
GAM1774 RGS3	3'	TCTGGCACCCCCTGGGTGGA 58454	G TT A
		TCT G CAG GGGTGCCAGA	
		AGG T GTC CCCACGGTCT	
		_GG C	
GAM1774 RNF28	3'	TCCAGCAGACACTGAACCAGA 51852	AGGG CA
		TCTGGTTCAG TGC GA	
		AGACCAAGTC ACG CT	
		ACAG AC	
GAM1774 SH3BP2	3'	CTAGGGCTGAACCAGGC 13064	AGGGTG _
		GTCTGGTTCAG CC AG	
		CGGACCAAGTC GG TC	
		G_____ A	
GAM1774 SIGLECL1	5'	CTGGCACCTCCAACCCGAC 54862	T CA G
		GTC GGTT GAGG TGCCAG	
		CAG CCAA CTCC ACGGTC	
		C C_ _	
GAM1774 SLC1A5	3'	GCACCCTCCAGGACAGGA 20068	G A_
		TCT GTTC GAGGGTGC	
		AGG CAGG CTCCCACG	
		A AC	
GAM1774 SLC1A5	3'	GCACCCTCCAGGACAGGA 79238	G A_
		TCT GTTC GAGGGTGC	
		AGG CAGG CTCCCACG	
		A AC	
GAM1774 SMARCD2	3'	CTAGCCTTTCTAAACCA 13261	C T C
		TGGTT AGAGGG GC AG	
		ACCAA TCTTTC CG TC	
		A _ A	
GAM1774 STC1	3'	CTGGCTGTCCAACCAGAC 13461	CAGA GT_
		GTCTGGTT GG GCCAG	
		CAGACCAA CC CGGTC	
		_____ TGT	
GAM1774 TCAP	3'	GCACCCTCTGTTAGTGC 14789	_ TT
		GT CTGG CAGAGGGTGC	

CG GATT GTCTCCCACG
T _

GAM1774 TMPRSS3 3' TCTAGGGACCAGAACCAAAC 51524 C AGAG G _
GT TGGTTC GGT CC AGA
|| ||||| ||| ||||
CA ACCAAG CCA GG TCT
A A_ G A

GAM1774 TMPRSS3 3' TCTAGGGACCAGAACCAAAC 51551 C AGAG G _
GT TGGTTC GGT CC AGA
|| ||||| ||| ||||
CA ACCAAG CCA GG TCT
A A_ G A

GAM1774 TMPRSS3 3' TCTAGGGACCAGAACCAAAC 44035 C AGAG G _
GT TGGTTC GGT CC AGA
|| ||||| ||| ||||
CA ACCAAG CCA GG TCT
A A_ G A

GAM1774 ARHGDIG 3' GCACCCCCCGTGAGTGACCAGA 8622 _ GA_
C GTCTGGT TCA GGGTGC
||||| ||| |||||
CAGACCA AGT CCCACG
GTG GCCC

GAM1774 BPNT1 3' CTGGCCTAAACCAGAT 65382 C AGGGT
GTCTGGTT AG GCCAG
||||| || |||||
TAGACCAA TC CGGTC
A _

GAM1774 C11orf11 3' TCTGGCACCCCCTGCTCCAG 94883 TT A
CTGG CAG GGGTGCCAGA
||| ||| |||||
GACC GTC CCCACGGTCT
TC C

GAM1774 CGI-96 3' CTGTTTCAGAACCCAGAC 32293 A GGTGC
GTCTGGTTC GAG CAG
||||| ||| |||
CAGACCAAG CTT GTC
A _

GAM1774 COLEC10 3' CTGGCCCCAAAGCCAGAC 22238 CAGAG T
GTCTGGTT GG GCCAG
||||| || |||||
CAGACCGA CC CGGTC
AA_ _

GAM1774 FLJ00024 5' CTGCTCCCCCAAACCAGAC 64495 CAGA T C
GTCTGGTT GGG GC AG
||||| ||| |||
CAGACCAA CCC CG TC
ACC_ T _

GAM1774 FLJ10232 3' CTGGCAGGAGCCAGAC 36378 AGAGGG
GTCTGGTTC TGCCAG
||||| |||||

CAGACCGAG ACGGTC
 G_____
 GAM1774 FLJ11000 3' CTGGACCTGAAGCCAGAC 37526 CAGA G
 GTCTGGTT GGGT CCAG
 ||||| ||| |||
 CAGACCGA TCCA GGTC
 AG__ _
 GAM1774 FLJ12876 3' TCTGACAATGTGACCAGAC 43101 T GAGGG C
 GTCTGGT CA TG CAGA
 ||||| || || |||
 CAGACCA GT AC GTCT
 _ GTA__ A
 GAM1774 FLJ12891 3' GCCTTTCTGGACCAAAC 46927 C T
 GT TGGTTCAGAGGG GC
 || ||||| |||
 CA ACCAGGTCTTTC CG
 A _
 GAM1774 FLJ13096 3' TCTTATATCCTCTATACCAAAC 47176 C TC CC
 GT TGGT AGAGGGTG AGA
 || ||| ||||| |||
 CA ACCA TCTCCTAT TCT
 A TA AT
 GAM1774 FLJ21195 3' CTGTGCCCCCTAAACCAGGC 42704 C A T _
 GTCTGGTT AG GGG GC CAG
 ||||| || ||| |||
 CGGACCAA TC CCC CG GTC
 A _ _ T
 GAM1774 FLJ31300 3' TCTGGCACCCCTTCCCCA 58935 TTC A
 TGG AG GGGTGCCAGA
 ||| || ||||| |||
 ACC TC CCCACGGTCT
 CCT _
 GAM1774 GCAT 3' TCTGAGCCCTGAACCA 60633 GA GC
 TGGTTCA GGGT CAGA
 ||||| ||| |||
 ACCAAGT CCCG GTCT
 _ A_
 GAM1774 HEI10 5' TCCAGCACCCCTGTGTGCCAG 41298 T G CA
 CTGGT CA AGGGTGC GA
 ||||| || ||||| |||
 GACCG GT TCCCACG CT
 T G AC
 GAM1774 HSPC251 3' TCCAGCAGACCACTGAACCAGA 33665 A G_ CA
 C GTCTGGTTCAG GG TGC GA
 ||||| || ||| |||
 CAGACCAAGTC CC ACG CT
 A AG AC
 GAM1774 KIAA1872 3' CTGGGCCAACCAGAC 63608 CAGAG G
 GTCTGGTT GGT CCAG
 ||||| ||| |||

CAGACCAA CCG GGTC

GAM1774 MGC10992 3' CTGACGCTGAACCAGA 53770 GAGG C
TCTGGTTCA GTG CAG
||||||| ||| |||
AGACCAAGT CGC GTC

_____ A
GAM1774 MGC3222 3' CTGGCACCCGCCGAC 44544 T TCAGA
GTC GGT GGGTGCCAG
||| ||| |||||
CAG CCG CCCACGGTC

C _____
GAM1774 MGC4342 3' CTGGTGCCCTGCACCAGAC 44515 T GA TG
GTCTGGT CA GGG CCAG
||||| || ||| |||
CAGACCA GT CCC GGTC
C _ GT

GAM1774 MGC4415 3' CTGGCACCCCTCTCCCTGCC 49761 TC__
GGT AGAGGGTGCCAG
||| |||||
CCG TCTCCCACGGTC
TCCC

GAM1774 MMP24 3' GGCACCCTCTGTGGGA 22921 G TT
TCT G CAGAGGGTGCC
||| | |||||
AGG T GTCTCCCACGG
G _

GAM1774 MMP24 3' TCTGGCACCCAGCTGCCAG 22922 TCAGA
CTGGT GGGTGCCAGA
||||| |||||
GACCG CCCACGGTCT
TCGA_

GAM1774 MOV10 3' CTGACCCTGAACCAGA 40934 GA GC
TCTGGTTCA GGGT CAG
||||||| ||| |||
AGACCAAGT CCCA GTC

_____ _
GAM1774 NAG73 5' CTAGCACCCCTCTGTGGTAG 51791 GTT C
CTG CAGAGGGTGC AG
||| ||||| |||
GAT GTCTCCCACG TC
GGT A

GAM1774 NR2F1 3' CTGGTTCCAAACCAGAT 97642 CAGA T
GTCTGGTT GGG GCCAG
||||||| ||| |||||
TAGACCAA CCT TGGTC

A _ _
GAM1774 OBTP 5' TCTGTATTGTCAAACCAGAC 34670 CA G C
GTCTGGTT GA GGTGC AGA
||||||| || ||||| |||

		CAGACCAA CT TTATG TCT	
		A_ G _	
GAM1774	P114-RHO-GEF 3'	CTGGCACCTCCTGAGCC 31670	_
		GGTTCAG AGGGTGCCAG	
		CCGAGTC TCCCACGGTC	
		C	
GAM1774	PIP5K1C 3'	TCTGGCGCCTCCAATCCAGAC 71311	TTCA G
		GTCTGG GAGG TGCCAGA	
		CAGACC CTCC GCGGTCT	
		TAAC _	
GAM1774	SEC15B 3'	CTGATACCAAAGCCAGAC 67265	CAGAG C
		GTCTGGTT GGTG CAG	
		CAGACCGA CCAT GTC	
		AA_ A	
GAM1774	TMLHE 3'	CTGGCACCTGGCTACCAGA 37047	TCAG
		TCTGGT AGGGTGCCAG	
		AGACCA TCCCACGGTC	
		TCGG	
GAM1774	TRIM26 3'	CTGGCATTTTAAACAGAC 14349	GTTCAG
		GTCTG AGGGTGCCAG	
		CAGAC TTTTACGGTC	
		AAA_	
GAM1774	TXNL2 3'	CACCTTTCTGAATCAGAC 22577	_
		GTCTGGTTCAGAG GGTG	
		CAGACTAAGTCTT CCAC	
		T	
GAM1774	LOC115399 3'	CTCGGCCCCGAACCAGGC 73812	AGA T _
		GTCTGGTTC GGG GCC AG	
		CGGACCAAG CCC CGG TC	
		_ _ C	
GAM1774	LOC124044 3'	CTGACCTCAAACCAGAT 76532	CA GTGC
		GTCTGGTT GAGG CAG	
		TAGACCAA CTCC GTC	
		A_ A_	
GAM1774	LOC130120 5'	CAGTCTTTGCTGACCAGAC 75416	_ G
		GTCTGGTT CAGAGG TG	
		CAGACCAG GTTTCT AC	
		TC G	
GAM1774	LOC144473 3'	TCTGCAGTCTGAACCTAAC 83997	CT GGG C
		GT GGTTCAGA TGC AGA	

	CA CCAAGTCT ACG TCT		
	AT G__ _		
GAM1774 LOC146713 3'	CTGACATTAGAACTAGAC 84728	AGAG	C
	GTCTGGTTC GGTG CAG		
	CAGATCAAG TTAC GTC		
	A__ A		
GAM1774 LOC149332 5'	CTGTAAGTCTGAACCAAGC 85548	TC	GGG C
	G TGGTTCAGA TGC AG		
	C ACCAAGTCT ATG TC		
	GA GA_ _		
GAM1774 LOC150960 3'	CATCTTTCTGAACCAAAC 80870	C	_
	GT TGGTTCAGAG GGTG		
	CA ACCAAGTCTT CTAC		
	A T		
GAM1774 LOC151171 5'	CTGGCACCCAACACCCAGAC 80947	TTCAGA	
	GTCTGG GGGTGCCAG		
	CAGACC CCCACGGTC		
	CACAA_		
GAM1774 LOC152274 5'	CCTGAAGTCTGAACCAGGC 81337		_____
	GTCTGGTTCAGA GGG		
	CGGACCAAGTCT TCC		
	GAAG		
GAM1774 LOC158125 3'	CTGGTCCCCAAAACCAGAC 82618	CAGA	TG
	GTCTGGTT GGG CCAG		
	CAGACCAA CCC GGTC		
	AA__ CT		
GAM1774 LOC158219 5'	CTGGCACCCCTTCTCCAG 82690	TTCA	
	CTGG GAGGGTGCCAG		
	GACC TTCCCACGGTC		
	TCC_		
GAM1774 LOC158563 3'	CTAGGCATAGCCTGAACCAGA 82845	AGG	_
	TCTGGTTCAG GTGCC AG		
	AGACCAAGTC TACGG TC		
	CGA A		
GAM1774 LOC197136 3'	CTGACCTCAAACCAGAT 91287	CA	GTGC
	GTCTGGTT GAGG CAG		
	TAGACCAA CTCC GTC		
	A_ A__		
GAM1774 LOC200779 3'	CTGCCTTTCTGAACCAAAC 90290	C	T C
	GT TGGTTCAGAGGG GC AG		

		CA ACCAAGTCTTTC CG TC		
		A _ _		
GAM1774	LOC256073 5'	CTGTCTCCCTGACCAGAC 98486	CAG	TGC
		GTCTGGTT AGGG CAG		
		CAGACCAG TCCC GTC		
		_ TCT		
GAM1774	LOC257494 3'	CTGGCATTTTAAACAGAC 99634	GTT	CAG
		GTCTG AGGGTGCCAG		
		CAGAC TTTTACGGTC		
		AAA_		
GAM1774	LOC90019 3'	TCCAGCTCATGTCTGAACCAGA 57536	AG_	T CA
		TCTGGTTCAG GG GC GA		
		AGACCAAGTC CT CG CT		
		GTA _ AC		
GAM1774	LOC90288 3'	TCTAGCACCTTCCCAAAC 62801	C	TTCA C
		GT TGG GAGGGTGC AGA		
		CA ACC TTCCCACG TCT		
		A C_ A		
GAM1774	LOC92231 3'	CTGGCCTGAGCCAGAC 69090	AGGGT	
		GTCTGGTTCAG GCCAG		
		CAGACCGAGTC CGGTC		
		_		
GAM1775	EHF 3'	TCCAAAACCCAAGGTTGGCT 25127	AT	_ C
		AGT GCCT GGGT TTGGA		
		TCG TGA CCCA AACCT		
		GT A A		
GAM1775	EPHA2 3'	CCATCGGCCAAGAATACTTGAA 16675	GC	G T_
	G	CTTCAAGTAT CT GGTC TGG		
		GAAGTTCATA GA CCGG ACC		
		A_ A CT		
GAM1775	ITGA5 3'	CCCAGAGACATACTTGAAG 61933	C_	
		CTTCAAGTATG CTGGG		
		GAAGTTCATAC GACCC		
		AGA		
GAM1775	TREM2 3'	TCCAAGACTGTCATATT 39098	CCTG	
		AAGTATG GGTCTTGGA		
		TTTATAC TCAGAACCT		
		TG_		
GAM1775	UQCRB 3'	CCAACATAGGCATACTTAAG 21939	C	GGTC
		CTT AAGTATGCCTG TTGG		

GAA TTCATACGGAT AACC
 _ AC_
 GAM1775 ATP10D 3' CAGAGACCACTTGAAG 73526 ATGCCTG _
 CTTCAAGT GGTCT TG
 ||||| |||||
 GAAGTTCA CCAGA AC
 _____ G
 GAM1775 B3GNT7 3' CCCTTCCAGGCAACCTGAA 71678 A A TCTT
 TTCA GT TGCCTGGG GG
 ||| || ||||| ||
 AAGT CA ACGGACCT CC
 C _ TC_
 GAM1775 DKFZp547I224 3' TCCAAAATTGACCACATACTTG 39963 CCTG ____
 GA TTCAAGTATG GGTC TTGGA
 ||||| ||| |||||
 AGGTTTCATAC CCAG AACCT
 A_ TTAA
 GAM1775 FLJ22341 3' CCAAGCTCAGGCACACCCAAG 45114 CAA A T
 CTT GT TGCCTGGG CTTGG
 ||| || ||||| |||||
 GAA CA ACGGACTC GAACC
 CC_ C _
 GAM1775 KIAA0779 3' CCGAACAGCATACTTGAAG 86908 C GGTC
 CTTCAAGTATGC TG TTGG
 ||||| || |||||
 GAAGTTCATACG AC AGCC
 _ A_
 GAM1775 LOC144233 3' CCAAGGCACATAATTGAA 77246 G CCTGG
 TTCAA TATG GTCTTGG
 |||| ||| |||||
 AAGTT ATAC CGGAACC
 A A_
 GAM1775 LOC147341 3' ACCCAGGCATAACTGAAG 85116 AG
 CTTCA TATGCCTGGGT
 |||| |||||
 GAAGT ATACGGACCCA
 CA
 GAM1775 LOC221088 5' TCCAAGGTGCTGGCCACTCGAA 94888 A AT TGGG
 G CTTC AGT GCC TCTTGGA
 |||| ||| ||| |||||
 GAAG TCA CGG GGAACCT
 C C_ TCGT
 GAM1776 DMD 3' ACTTTCCACTGACAACGAA 5461 G CAA A
 TT GTT CGG TGGAAAGT
 || ||| ||| |||||
 AA CAA GTC ACCTTTCA
 G CA_ _
 GAM1776 DMD 3' ACTTTCCACTGACAACGAA 15678 G CAA A
 TT GTT CGG TGGAAAGT
 || ||| ||| |||||

		AA CAA GTC ACCTTTCA		
		G CA_ _		
GAM1776 DMD	3'	ACTTTCCACTGACAACGAA 15681	G	CAA A
		TT GTT CGG TGGAAAGT		
		AA CAA GTC ACCTTTCA		
		G CA_ _		
GAM1776 DMD	3'	ACTTTCCACTGACAACGAA 15684	G	CAA A
		TT GTT CGG TGGAAAGT		
		AA CAA GTC ACCTTTCA		
		G CA_ _		
GAM1776 DMD	3'	ACTTTCCACTGACAACGAA 15688	G	CAA A
		TT GTT CGG TGGAAAGT		
		AA CAA GTC ACCTTTCA		
		G CA_ _		
GAM1776 DMD	3'	ACTTTCCACTGACAACGAA 15693	G	CAA A
		TT GTT CGG TGGAAAGT		
		AA CAA GTC ACCTTTCA		
		G CA_ _		
GAM1776 DMD	3'	ACTTTCCACTGACAACGAA 15696	G	CAA A
		TT GTT CGG TGGAAAGT		
		AA CAA GTC ACCTTTCA		
		G CA_ _		
GAM1776 DMD	3'	ACTTTCCACTGACAACGAA 15701	G	CAA A
		TT GTT CGG TGGAAAGT		
		AA CAA GTC ACCTTTCA		
		G CA_ _		
GAM1776 DMD	3'	ACTTTCCACTGACAACGAA 15705	G	CAA A
		TT GTT CGG TGGAAAGT		
		AA CAA GTC ACCTTTCA		
		G CA_ _		
GAM1776 DMD	3'	ACTTTCCACTGACAACGAA 15708	G	CAA A
		TT GTT CGG TGGAAAGT		
		AA CAA GTC ACCTTTCA		
		G CA_ _		
GAM1776 DMD	3'	ACTTTCCACTGACAACGAA 15711	G	CAA A
		TT GTT CGG TGGAAAGT		
		AA CAA GTC ACCTTTCA		
		G CA_ _		
GAM1776 DMD	3'	ACTTTCCACTGACAACGAA 15715	G	CAA A
		TT GTT CGG TGGAAAGT		

		AA CAA GTC ACCTTTCA		
		G CA_ _		
GAM1776 DMD	3'	ACTTTCCACTGACAACGAA 15720	G CAA A	
		TT GTT CGG TGGAAAGT		
		AA CAA GTC ACCTTTCA		
		G CA_ _		
GAM1776 AKAP6	3'	TGACTTTCAGGTTTGTGAAC 16254	G_	
		GTTCAACGGAT GAAAGTCA		
		CAAGTTGTTTG CTTTCAGT		
		GA		
GAM1776 FLJ10803	3'	GTGACTTTCAGTTAAAGCCAA 37205	CAACG G	
		TTGGTT GAT GAAAGTCAC		
		AACCGA TTG CTTTCAGTG		
		AA_ _ A		
GAM1776 KIAA0882	3'	TGACCATCTTTCCATCAAATCA 83537	CAACG	_____
A		TTGGTT GATGGAAA GTCA		
		AACTAA CTACCTTT CAGT		
		A_ _ CTAC		
GAM1776 MSTP028	3'	TGACCCCTGTCGTTGAAC 50068	AT AAA	
		GTTCAACGG GG GTCA		
		CAAGTTGCT CC CAGT		
		GT C_ _		
GAM1777 GPD1	3'	TCATGCCACCACATTTG 60398	C C	
		TAAATG GGTGGCAT GA		
		GTTTAC CCACCGTA CT		
		A _		
GAM1777 IL5RA	5'	TCGCATGGCCACCGCATTT 6906	AT_	
		AAATGCGGTGGC CGA		
		TTTACGCCACCG GCT		
		GTAC		
GAM1777 MYO1C	3'	TGCCGATGCCAAATATTTG 61873	CGG A	
		TAAATG TGGCATCG CA		
		GTTTAT ACCGTAGC GT		
		AA_ C		
GAM1777 C6orf37	3'	TGTCACACTGCATTTA 68097	GCATC	
		TAAATGCGGTG GACA		
		ATTTACGTCAC CTGT		
		A_ _		
GAM1777 DNAJC6	3'	TTGCAGAACCACCGCATT 29498	CA GA	
		AATGCGGTGG TC CAA		

	TTACGCCACC AG GTT	
	A_ AC	
GAM1777 FLJ11210 3'	GTCGATGTGCATGCTTTTA 60319	T GTG
	TAAA GCG GCATCGAC	
	ATTT CGT TGTAGCTG	
	T ACG	
GAM1777 FLJ12476 3'	TCGATCTTCTGCATTTA 43270	T C
	TAAATGCGG GG ATCGA	
	ATTTACGTC TC TAGCT	
	T _	
GAM1777 KIAA1034 3'	TCGATGGCATCCGCATTTG 63134	_ G
	TAAATGCGG TG CATCGA	
	GTTTACGCC AC GTAGCT	
	T G	
GAM1777 KIAA1987 3'	TCATGTAAGTGCATTTA 89391	G C
	TAAATGCGGT GCAT GA	
	ATTTACGTCA TGTA CT	
	A _	
GAM1777 MGC16063 3'	TGTCCTGGCCACTGCATT 54929	ATC
	AATGCGGTGGC GACA	
	TTACGTCACCG CTGT	
	GTC	
GAM1777 LOC147949 3'	TGTCAGATGTCCACATTGCA 79279	_ _ _
	TGCG GTGG CATC GACA	
	ACGT CACC GTAG CTGT	
	TA T A	
GAM1777 LOC150577 3'	GTCCTCACCGCATTTG 86258	CATC
	TAAATGCGGTGG GAC	
	GTTTACGCCACT CTG	
	C_	
GAM1777 LOC158219 3'	TGTGTGTCACCACATT 82694	C CG
	AAATG GGTGGCAT ACA	
	TTTAC CCACTGTG TGT	
	A _	
GAM1777 LOC202020 3'	TGTCTCACCACATTTA 90605	C CATC
	TAAATG GGTGG GACA	
	ATTTAC CCACT CTGT	
	A _	
GAM1777 LOC90826 5'	TGTCGATGCAGGTTTATTTG 64788	CGGTG
	TAAATG GCATCGACA	

			GTTTAT CGTAGCTGT		
			TTGGA		
GAM1777	LOC93587	3'	TTGTCTTTACCTGCATTTA 73042	_	CATC
			TAAATGC GGTGG GACAA		
			ATTTACG CCATT CTGTT		
			T T__		
GAM1778	ELF3	3'	TGACCTTGACCTTGACCAA 16685	T	GAT AAA
			TTGGT CAAGG GG GTCA		
			AACCA GTTCC TC CAGT		
			_ AGT _		
GAM1778	JAK2	3'	TGACCTTCATTCTGAGACCAA 18318	CAA	AA
			TTGGTT GGGATGGA GTCA		
			AACCAG TCTTACTT CAGT		
			AG_ C_		
GAM1778	SLC10A2	5'	ACTCTCTGTCTTGACCAA 6590	CAA	A
			TTGGTT GGGATGGA AGT		
			AACCAG TTCTGTCT TCA		
			_ C		
GAM1778	FLJ10803	3'	GTGACTTTCAGTTAAAGCCAA 37205	CAAGG	G
			TTGGTT GAT GAAAGTCAC		
			AACCGA TTG CTTTCAGTG		
			AA_ A		
GAM1778	KIAA1958	5'	GTGACTTTGAACCCCAAACC 82788	CAA	ATGG
			GGTT GGG AAAGTCAC		
			CCAA CCC TTTCAGTG		
			A_ CAAG		
GAM1778	MARCKS	3'	ACTTTCACCCCTGCCCA 11411	TTCA	A
			TGG AGGG TGGAAAGT		
			ACC TCCC ACCTTTCA		
			CG_ _		
GAM1778	TUB	5'	GTGGGACCATCCCTTAAACC 13898	C	AAAG
			GGTT AAGGGATGG TCAC		
			CCAA TTCCCTACC GGTG		
			A AG_		
GAM1778	LOC80298	3'	ACTTTTACCTTGAACCA 48062	GATG	
			TGGTTCAAGG GAAAGT		
			ACCAAGTTCC TTTTCA		
			A_		
GAM1779	ABCE1	5'	GGGGATCGTTTTCTCCAGA 60261	C	CTG
			TCTGGAGAAA TG CCTC		

			AGACCTCTTT GC GGGG		
			T TA_		
GAM1779 AKAP13	3'	TGAGGCAGCTGCCTCCTGA	59238	T	AAACT
		TC GGAG GCTGCCTCA			
		AG CCTC CGACGGAGT			
		T CGT_			
GAM1779 AKAP13	3'	TGAGGCAGCTGCCTCCTGA	23090	T	AAACT
		TC GGAG GCTGCCTCA			
		AG CCTC CGACGGAGT			
		T CGT_			
GAM1779 AKAP13	3'	TGAGGCAGCTGCCTCCTGA	24220	T	AAACT
		TC GGAG GCTGCCTCA			
		AG CCTC CGACGGAGT			
		T CGT_			
GAM1779 ALOX12B	5'	GGGCAGCAGCTTTTCCAGA	8537		A
		TCTGGAGAA CTGCTGCCT			
		AGACCTTTT GACGACGGG			
		C			
GAM1779 BCL7A	3'	GAGGCGGCGTTACCTCCAGA	40984		A_ T
		TCTGGAG AAC GCTGCCTC			
		AGACCTC TTG CGGCGGAG			
		CA _			
GAM1779 CEACAM1	3'	GAGGCTTTCTCCAGG	9930		CTGCT
		TCTGGAGAAA GCCTC			
		GGACCTCTTT CGGAG			

GAM1779 CLDN3	3'	TGGGGCAGCTTCCCCAG	8961	A	ACT
		CTGG GAA GCTGCCTCA			
		GACC CTT CGACGGGGT			
		C _			
GAM1779 COL10A1	5'	AGGCACCATCTCCAGG	6682		AAC C
		TCTGGAGA TG TGCCT			
		GGACCTCT AC ACGGA			
		_ C			
GAM1779 CUTL1	3'	GAGCCCCAGTCTCTTCAGA	10348		A CT C
		TCTGGAGA ACTG GC TC			
		AGACTTCT TGAC CG AG			
		C CC _			
GAM1779 CYBB	3'	GAGAGTGTTTCTCCA	76846	T	GC
		TGGAGAAAC GCT CTC			

ACCTCTTTG TGA GAG

GAM1779 DNASE1	5'	GAAGTGCTTCTTCAGA	19072	ACT T C
		TCTGGAGAA GC GC TC		
		AGACTTCTT CG TG AG		
		_____ A		
GAM1779 DXYS155E	3'	GAGGATGGCTCTCCAGA	18688	AACT _
		TCTGGAGA GCTG CCTC		
		AGACCTCT CGGT GGAG		
		_____ A		
GAM1779 EFNA1	3'	TGGGGCAGCACTCCCCAGA	16666	A AAC
		TCTGG GA TGCTGCCTCA		
		AGACC CT ACGACGGGGT		
		C C__		
GAM1779 EGR1	3'	TGAGCTTCGGTTCTCCAGA	10493	A CT C
		TCTGGAGAA CTG GC TCA		
		AGACCTCTT GGC CG AGT		
		_____ TT _		
GAM1779 FLT1	3'	TGAGGAGAGTTTTCTCCA	10664	_ G G
		TGGAGAAA CT CT CCTCA		
		ACCTCTTT GA GA GGAGT		
		T _ _		
GAM1779 FRK	5'	AGCCGGTAAGTCTCTCCAGG	10715	A _ C
		TCTGGAGA ACT GCTG CT		
		GGACCTCT TGA TGGC GA		
		C A C		
GAM1779 GAB2	3'	GAGGCAGCATCTCCAGA	55405	AAC
		TCTGGAGA TGCTGCCTC		
		AGACCTCT ACGACGGAG		

GAM1779 GAB2	3'	GAGGCAGCATCTCCAGA	25458	AAC
		TCTGGAGA TGCTGCCTC		
		AGACCTCT ACGACGGAG		

GAM1779 GP9	3'	TGAGGCAGGTCCCCAGA	5725	A AACTG
		TCTGG GA CTGCCTCA		
		AGACC CT GACGGAGT		
		C G__		
GAM1779 GPC6	5'	AGGCAGCAGCCTTCCCAG	20329	A A_
		CTGG GAA CTGCTGCCT		

GACC CTT GACGACGGA
 _ CC
 GAM1779 GUCA2B 3' TGAGGCAGCCCAGCTCCTGA 24020 T AACT
 TC GGAG GCTGCCTCA
 || ||| |||||
 AG CCTC CGACGGAGT
 T GACC_
 GAM1779 GUCY1A3 5' GAGTCAGTTTTCCAGA 64226 AACT C
 TCTGGAGA GCTG CTC
 ||||| ||| ||
 AGACCTTT TGAC GAG
 _ T
 GAM1779 IL8RA 3' TGAGGCAGGCACTGCCA 7153 _ AAAC _
 TGG AG TGC TGCCTCA
 ||| || ||| |||||
 ACC TC ACG ACGGAGT
 G _ G
 GAM1779 MADH6 5' AGGCAGGGCTTTCCAGA 19972 AA TG
 TCTGGAGA C CTGCCT
 ||||| | |||||
 AGACCTTT G GACGGA
 CG _
 GAM1779 MGAM 3' GGGGCAGTTTCTCCAGG 72812 G
 TCTGGAGAAACTGCT CC
 ||||| ||||| ||
 GGACCTCTTTGACGG GG
 _
 GAM1779 MYO7A 3' GAGGCAGCAGTGGGTTTCAGG 6032 GAA
 TCTGGA ACTGCTGCCTC
 ||||| |||||
 GGA CTT TGACGACGGAG
 GGG
 GAM1779 NEUROD2 3' AGGAGTGCTTCTCCAGG 21592 ACT G
 TCTGGAGAA GCT CCT
 ||||| ||| ||
 GGACCTCTT TGA GGA
 CG_ _
 GAM1779 NPY2R 3' TGAACAGAAATTTCTCCAGG 8067 CTG CC
 TCTGGAGAAA CTG TCA
 ||||| ||| ||
 GGACCTCTTT GAC AGT
 AAA A_
 GAM1779 OXTR 3' TGAATAGACATTTCTCCA 8083 C _ CC
 TGGAGAAA TG CTG TCA
 ||||| || ||| ||
 ACCTCTTT AC GAT AGT
 _ A A_
 GAM1779 PARK2 3' GAGGAGCCTTTCCAGA 17078 AACT G
 TCTGGAGA GCT CCTC
 ||||| ||| |||

			AGACCTTT CGA GGAG		
			C___ _		
GAM1779	PARK2	3'	GAGGAGCCTTTCCAGA 26542	AACT	G
			TCTGGAGA GCT CCTC		
			AGACCTTT CGA GGAG		
			C___ _		
GAM1779	PARK2	3'	GAGGAGCCTTTCCAGA 26546	AACT	G
			TCTGGAGA GCT CCTC		
			AGACCTTT CGA GGAG		
			C___ _		
GAM1779	PMCHL1	3'	GAGGTGTTCTCCAGA 49917	ACTGC	
			TCTGGAGAA TGCCTC		
			AGACCTCTT GTGGAG		

GAM1779	PPP2R4	3'	TGAGGCATGTCTTTCCAGA 61184	A TGC	
			TCTGGAGA AC TGCCTCA		
			AGACCTTT TG ACGGAGT		
			C T__		
GAM1779	PRX	3'	GAGGCAGCCCTTCCAGA 40896	AAACT	
			TCTGGAG GCTGCCTC		
			AGACCTT CGACGGAG		
			CC___		
GAM1779	REV3L	5'	TGAGGAAGATTTCTCTCA 12825	_ CTG	G
			TG GAGAAA CT CCTCA		
			AC CTCTTT GA GGAGT		
			T A__ A		
GAM1779	RXRA	3'	TGAGGCAGCAGCCTTC 12925	AAA	
			GGAG CTGCTGCCTCA		
			CTTC GACGACGGAGT		
			C__		
GAM1779	SIRPB2	3'	GAGAAGCTTCTCTAGA 55858	ACT	GC
			TCTGGAGAA GCT CTC		
			AGATCTCTT CGA GAG		
			__ A_		
GAM1779	SIRPB2	3'	GAGAAGCTTCTCTAGA 38272	ACT	GC
			TCTGGAGAA GCT CTC		
			AGATCTCTT CGA GAG		
			__ A_		
GAM1779	SURF5	3'	TGAGGCAGCATTTCCTCCA 23130	A C	
			TGGAG AA TGCTGCCTCA		

		ACCTC TT ACGACGGAGT	
		C T	
GAM1779 TAF1C	5'	GAGGCCCATTTTCCAGA 20265	AC CT
		TCTGGAGAA TG GCCTC	
		AGACCTTTT AC CGGAG	
		__ C_	
GAM1779 VANG2	3'	TGAGACATCGGACTCTCCGGA 72095	AA C C
		TCTGGAGA CTG TG CTCA	
		AGGCCTCT GGC AC GAGT	
		CA T A	
GAM1779 WARS	3'	GAGGCAGCAGCCCTCGAGG 67865	G AAA
		TCT GAG CTGCTGCCTC	
		GGA CTC GACGACGGAG	
		G CC_	
GAM1779 ZNF45	5'	GA CTTGGCACTTCTCCAGA 14250	AC CC
		TCTGGAGAA TGCTG TC	
		AGACCTCTT ACGGT AG	
		C_ TC	
GAM1779 ARHF	3'	GGGACAGTTTCTCAGA 39272	G CTG
		TCTG AGAACTG CCT	
		AGAC TCTTTGAC GGG	
		_ A_	
GAM1779 BLR1	3'	TGAGGCAGGGAAGTCCCCAGG 9940	A AA_ G
		TCTGG GA CT CTGCCTCA	
		GGACC CT GG GACGGAGT	
		C GAA _	
GAM1779 BLR1	3'	TGAGGCAGGGAAGTCCCCAGG 53119	A AA_ G
		TCTGG GA CT CTGCCTCA	
		GGACC CT GG GACGGAGT	
		C GAA _	
GAM1779 C20orf150	3'	TGAAGCCGAGCTCCTCCAGA 66017	AAACT __ C
		TCTGGAG GCT GC TCA	
		AGACCTC CGA CG AGT	
		CT__ GC A	
GAM1779 C20orf4	3'	GGGCAGCAATCTCTCCAGG 31948	AAC
		TCTGGAGA TGCTGCCT	
		GGACCTCT ACGACGGG	
		CTA	
GAM1779 C20orf7	3'	TGAATATGCACCTTCTCCAGA 44383	AC TGCC
		TCTGGAGAA TGC TCA	

			AGACCTCTT ACG AGT		
			CC TATA		
GAM1779	C6orf26	3'	AGAAAGCAGCTTTCTCCA 48268	_	GC
			TGGAGAAA CTGCT CT		
			ACCTCTTT GACGA GA		
			C AA		
GAM1779	CASKIN1	3'	TGAGGCGGATTTCCCCAGA 40784	A	CTG
			TCTGG GAAA CTGCCTCA		
			AGACC CTTT GGCGGAGT		
			C A__		
GAM1779	CCR8	3'	TGAGGCAGATGCCTCTAGA 19041	AA	ACTG
			TCTGGAG CTGCCTCA		
			AGATCTC GACGGAGT		
			CGTA__		
GAM1779	CPGL2	5'	GAAGCCGCTTTGTTCTCCAGA 74884	ACT_	T C
			TCTGGAGAA GC GC TC		
			AGACCTCTT CG CG AG		
			GTTT C A		
GAM1779	CSRP2BP	5'	TGAAGCAGCAGTGGGACCAG 70657	AGAA	C
			CTGG ACTGCTGC TCA		
			GACC TGACGACG AGT		
			AGGG A		
GAM1779	DGKD	3'	TGAAACAACACTTTCTCCAG 60113	C C	CC
			CTGGAGAAA TG TG TCA		
			GACCTCTTT AC AC AGT		
			C A AA		
GAM1779	DKFZP434A043	3'	TGAGGTAGTAATTTCTCAGA 31823	GA	C
			TCTG GAAA TGCTGCCTCA		
			AGAC CTTT ATGATGGAGT		
			TC A		
GAM1779	DKFZP434P0111	3'	TGAGGGTGTCTTTCCAGA 67963	A T	TG
			TCTGGAGA AC GC CCTCA		
			AGACCTTT TG TG GGAGT		
			C _ _		
GAM1779	DKFZP586M1120	3'	TGAGGCAGCAGCTCCCAG 49287	A	AA
			CTGG GA CTGCTGCCTCA		
			GACC CT GACGACGGAGT		
			_ C_		
GAM1779	ERG-1	3'	TGAGACATGTTTCTCCAGG 42102	TGC	C
			TCTGGAGAAAC TG CTCA		

		GGACCTCTTTG AC GAGT	
		T__ A	
GAM1779 FASTK	3'	TGAGGCAGAAGCTCCAGG 47690	AAACTG
		TCTGGAG CTGCCTCA	
		GGACCTC GACGGAGT	
		GAA__	
GAM1779 FLJ14855	5'	GGTCCCAGTTTTCCAGA 53766	A CT_
		TCTGGAGAA CTG GCC	
		AGACCTTTT GAC TGG	
		_ CCT	
GAM1779 FLJ20249	3'	TGAGGAGTCCCTCCCAGA 80223	A AACT G
		TCTGG GA GCT CCTCA	
		AGACC CT TGA GGAGT	
		_ CCC_ _	
GAM1779 FLJ20730	3'	TGAAGAAGCAGTTTCTCAGA 36053	G GCC
		TCTG AGAAACTGCT TCA	
		AGAC TCTTTGACGA AGT	
		_ AGA	
GAM1779 FLJ21007	5'	TGAAGCTTGCACAAGCTCTCCA 48648	AAC__ T_ C
	GA	TCTGGAGA TGC GC TCA	
		AGACCTCT ACG CG AGT	
		CGAAC TT A	
GAM1779 FLJ22938	5'	GAGGAGTTTTTCCAGA 45486	GCTG
		TCTGGAGAACT CCTC	
		AGACCTTTTTGA GGAG	

GAM1779 GPT2	3'	TGAGGCAGCAGCCTCTA 56772	AAA
		TGGAG CTGCTGCCTCA	
		ATCTC GACGACGGAGT	
		C__	
GAM1779 KIAA0515	5'	GAGGAGCTTCTCCAG 64550	ACT G
		CTGGAGAA GCT CCTC	
		GACCTCTT CGA GGAG	

GAM1779 KIAA0542	3'	GGGGCAGCTCCTCCAGG 66665	AAACT
		TCTGGAG GCTGCCTC	
		GGACCTC CGACGGGG	
		CT__	
GAM1779 KIAA0561	3'	GAGGGAGCTTTCCAGA 66479	AACT G
		TCTGGAGA GCT CCTC	

AGACCTTT CGA GGAG
 _____ G
 GAM1779 KIAA0652 3' TGAGGCAGCAATCTTTGG 29125 TG AAC
 C GAGA TGCTGCCTCA
 | ||| |||||
 G TTCT ACGACGGAGT
 GT A__
 GAM1779 KIAA1026 3' GAGACGGCTTTTTCCA 71738 CT C
 TGGAGAAA GCTG CTC
 ||||| ||| ||
 ACCTTTTT CGGC GAG
 _____ A
 GAM1779 KIAA1030 3' GAGGCAGCTGAGCCGAGA 94981 _ AGAA
 TCT GG ACTGCTGCCTC
 ||| || |||||
 AGA CC TGACGACGGAG
 G GAG_
 GAM1779 KIAA1086 3' TGAGGCAGGGGGTCCCCA 71291 A AA G
 TGG GA CT CTGCCTCA
 ||| || |||||
 ACC CT GG GACGGAGT
 C GG _
 GAM1779 KIAA1277 3' GAGGCAGGTTCTCAGA 65077 G ACTG
 TCTG AGAA CTGCCTC
 ||| ||| |||||
 AGAC TCTT GACGGAG
 _ G__
 GAM1779 KIAA1322 3' TGAGATAGTTTTTCCAGA 73118 CTGC
 TCTGGAGAACTG CTCA
 ||||| |||
 AGACCTTTTTGAT GAGT
 A__
 GAM1779 KIAA1634 3' GCATCAGTCTCTTCTCCAGA 64124 _ C
 TCTGGAGAA ACTG TGC
 ||||| ||| ||
 AGACCTCTT TGAC ACG
 CTC T
 GAM1779 KIAA1638 3' TGAAACAACGGTGACCTCTCCA 47824 A__ C CC
 GG TCTGGAGA ACTG TG TCA
 ||||| ||| |||
 GGACCTCT TGGC AC AGT
 CCAG A AA
 GAM1779 KIAA1742 3' AGGTATTTCTCCAGA 78137 CTGC
 TCTGGAGAAA TGCCT
 ||||| |||
 AGACCTCTTT ATGGA

 GAM1779 KIAA1771 5' GGGTTACCAGACCTCTCCAGA 79866 AA_ CT_
 TCTGGAGA CTG GCCT
 ||||| ||| |||

		AGACCTCT GAC TGGG		
		CCA CAT		
GAM1779 KIAA1831	5'	GGAGCAGTCTCTCCGGA	64525	A G
		TCTGGAGA ACTGCT CC		
		AGGCCTCT TGACGA GG		
		C _		
GAM1779 KIAA1894	3'	GAGGCAACCTTTGCCTTCTTCA	74285	ACT _____
	GA	TCTGGAGAA GC TGCCTC		
		AGACTTCTT CG ACGGAG		
		C__ TTTCCA		
GAM1779 KIAA1937	3'	GAGGCAGTGTCCCCCAGG	74071	AGAA T
		TCTGG AC GCTGCCTC		
		GGACC TG TGACGGAG		
		CCC_ _		
GAM1779 KIAA1985	3'	TGAAAAGCACTTTCTCCA	45018	C GCC
		TGGAGAAA TGCT TCA		
		ACCTCTTT ACGA AGT		
		C AA_		
GAM1779 LCHN	3'	TGAGATGCTTTCTCCAGA	87480	CT TGC
		TCTGGAGAAA GC CTCA		
		AGACCTCTTT CG GAGT		
		_ TA_		
GAM1779 MGC13007	3'	CAGTTCAGTTATCTCCAGA	51277	_ _
		TCTGGAGA AACTG CTG		
		AGACCTCT TTGAC GAC		
		A TT		
GAM1779 MGC16385	5'	TGAAGCAGCAGCTGGGCTAGG	59543	AGAAA C
		TCTGG CTGCTGC TCA		
		GGATC GACGACG AGT		
		GGGTC A		
GAM1779 MGC26914	3'	TGAATAGACATTTCTCCA	59332	C _ CC
		TGGAGAAA TG CTG TCA		
		ACCTCTTT AC GAT AGT		
		_ A A_		
GAM1779 MRPL20	3'	AGGCATTTTTTCCAGA	36199	CTGC
		TCTGGAGAAA TGCCT		
		AGACCTTTTT ACGGA		
		T__		
GAM1779 NCX	5'	GAGGCCACTCTCCGGA	32944	AAC CT
		TCTGGAGA TG GCCTC		

		AGGCCTCT AC CGGAG		
		C__ _		
GAM1779	PPP1R13B	3' TGAGGCCCTTTCTCCAG 31660		CTGCT
		CTGGAGAAA GCCTCA		
		GACCTCTTT CGGAGT		
		CC__		
GAM1779	PSKH1	3' AGGCTCCAGCCTCTCCAGA 68791		AA CT
		TCTGGAGA CTG GCCT		
		AGACCTCT GAC CGGA		
		CC CT		
GAM1779	PTPLA	3' AGGTGCTTTTTTCCAGA 27266		CT T
		TCTGGAGAAA GC GCCT		
		AGACCTTTTT CG TGGA		
		— —		
GAM1779	SEMA4G	5' GGGCAGCTGTCTCCAGA 96330		AACT
		TCTGGAGA GCTGCCT		
		AGACCTCT CGACGGG		
		GT__		
GAM1779	SPAF	3' TGAAGCGATTTCTTTTTCCAGA 83521		CTGC_ C
		TCTGGAGAAA TGC TCA		
		AGACCTTTTT GCG AGT		
		CTTTA A		
GAM1779	SUN1	3' TGAGTTTCCCAGTTTCTACAGA 47926	G	CTGC_
		TCTG AGAAACTG CTCA		
		AGAC TCTTTGAC GAGT		
		A CCTTT		
GAM1779	TSPAN-2	3' GGGTCAGTTTCTCAGA 20375	G	CT
		TCTG AGAAACTG GCCT		
		AGAC TCTTTGAC TGGG		
		— —		
GAM1779	USP24	3' TGAAAATGCTGTGTTCTCCAGA 92795		_ T TGCC
		TCTGGAGAA AC GC TCA		
		AGACCTCTT TG CG AGT		
		G T TAAA		
GAM1779	LOC123096	3' TGAGGCAGACACTCCAG 74654		AAAC _
		CTGGAG TG CTGCCTCA		
		GACCTC AC GACGGAGT		
		___ A		
GAM1779	LOC129831	5' TGAGACAGCAGCGGTGGCAGA 75398		GAGAA _
		TCTG ACTGCTGC CTCA		

	AGAC TGGCGACG GAGT	
	GG____ ACA	
GAM1779 LOC134637 3'	TGAGAACACCTTCTCCAGG 75693	AC CTGC
	TCTGGAGAA TG CTCA	
	GGACCTCTT AC GAGT	
	CC AA__	
GAM1779 LOC146420 3'	TGAACTTCCAGATTCTCCAGA 84653	A CTGCC
	TCTGGAGAA CTG TCA	
	AGACCTCTT GAC AGT	
	A CTTCA	
GAM1779 LOC147711 5'	TGAGCAGGCAAGTCTCTTCAGA 79117	A _ GC
	TCTGGAGA ACT GCT CTCA	
	AGACTTCT TGA CGG GAGT	
	C A AC	
GAM1779 LOC148753 3'	TGAGACTCCATTTTCTCCAGG 85373	C CTGC
	TCTGGAGAAA TG CTCA	
	GGACCTCTTT AC GAGT	
	T CTCA	
GAM1779 LOC150290 3'	TGAGGCAGATGGTGCCCAGA 80592	AGAA _
	TCTGG ACTG CTGCCTCA	
	AGACC TGGT GACGGAGT	
	CG__ A	
GAM1779 LOC153218 5'	TGAAATAGAACTTTTCCAGA 81658	ACTG CC
	TCTGGAGAA CTG TCA	
	AGACCTTTT GAT AGT	
	CAA_ AA	
GAM1779 LOC153769 3'	AGGCAGCATTTCAGA 81805	AAAC
	TCTGGAG TGCTGCCT	
	AGACTTT ACGACGGA	

GAM1779 LOC157570 5'	TGAGGCTTTTTCTTCAGA 82397	CTGCT
	TCTGGAGAAA GCCTCA	
	AGACTTCTTT CGGAGT	
	TT__	
GAM1779 LOC197259 5'	TGAGGCAGTGGCCTCCGGA 89304	AAA TG
	TCTGGAG C CTGCCTCA	
	AGGCCTC G GACGGAGT	
	C__ GT	
GAM1779 LOC199923 3'	TGAGTTAGCCAGTTTCTTCAGA 89879	_ C
	TCTGGAGAAACTG CTG CTCA	

	AGACTTCTTTGAC GAT GAGT	
	C T	
GAM1779 LOC200940 3'	TGAGGCAGGCGGATCTCCTGA 90398	T AA _
	TC GGAGA CTGC TGCCTCA	
	AG CCTCT GGCG ACGGAGT	
	T A_ G	
GAM1779 LOC201685 3'	AGGAGCTATTTTCCAGA 91834	ACT G
	TCTGGAGAA GCT CCT	
	AGACCTTTT CGA GGA	
	AT_ _	
GAM1779 LOC205327 3'	AGTCAATGTTTCTCCAGA 91067	TGC C
	TCTGGAGAAAC TG CT	
	AGACCTCTTTG AC GA	
	TA_ T	
GAM1779 LOC221288 3'	TGAAGCAGCAGTATCTAGA 95264	GAA C
	TCTGGA ACTGCTGC TCA	
	AGATCT TGACGACG AGT	
	A_ A	
GAM1779 LOC222057 3'	AGGTCAGCCTCTCCAGG 94345	AACT _
	TCTGGAGA GCTG CCT	
	GGACCTCT CGAC GGA	
	C_ T	
GAM1779 LOC222057 3'	GAGTCAGCCTCTCCAGG 94354	AACT C
	TCTGGAGA GCTG CTC	
	GGACCTCT CGAC GAG	
	C_ T	
GAM1779 LOC253254 5'	TGAGAAGAACTTCTTCAGA 98908	ACTG GC
	TCTGGAGAA CT CTCA	
	AGACTTCTT GA GAGT	
	CAA_ A_	
GAM1779 LOC254672 3'	GAGGTGTTCTCCAGA 96295	ACTGC
	TCTGGAGAA TGCCTC	
	AGACCTCTT GTGGAG	

GAM1779 LOC255975 3'	GAGTCAGCCTCTCCAGG 97582	AACT C
	TCTGGAGA GCTG CTC	
	GGACCTCT CGAC GAG	
	C_ T	
GAM1779 LOC256789 3'	TGAGGCTGTACTCTCTAGA 99312	AAC T
	TCTGGAGA TGC GCCTCA	

		AGATCTCT ATG CGGAGT		
		C_ T		
GAM1779	LOC257336 5'	GGGCCCTAGTCCTCCAGA 97900	AA	CT
		TCTGGAG ACTG GCCT		
		AGACCTC TGAT CGGG		
		C_ CC		
GAM1779	LOC257449 3'	AGGTATTTCTCCAGA 63373	CTGC	
		TCTGGAGAAA TGCCT		
		AGACCTCTTT ATGGA		
GAM1779	LOC91923 5'	AGAGTTCCAGTTTCTCCA 68169	CT	_
		TGGAGAACTG GC CT		
		ACCTCTTTGAC TG GA		
		CT A		
GAM1779	LOC92876 5'	AGAGTTCCAGTTTCTCCA 71346	CT	_
		TGGAGAACTG GC CT		
		ACCTCTTTGAC TG GA		
		CT A		
GAM1779	LOC93496 3'	TGAAACAGACTTACACTTCTTC 72863	ACTG_	CC
	AGA	TCTGGAGAA CTG TCA		
		AGACTTCTT GAC AGT		
		CACATTCA AA		
GAM1780	AKAP1 3'	ACTATGGGTTCTCTTCGCAAA 14472	A	CTT C
		TTTGT GA GGAACCCA AGT		
		AAACG CT TCTTGGGT TCA		
		_ TC_ A		
GAM1780	AKAP1 3'	ACTATGGGTTCTCTTCGCAAA 58373	A	CTT C
		TTTGT GA GGAACCCA AGT		
		AAACG CT TCTTGGGT TCA		
		_ TC_ A		
GAM1780	EGF 3'	ACTATAGGTTTTGGTTCCACAA 10488	A	C TG CAC
		TTGT GA T GAACC AGT		
		AACA CT G TTTGG TCA		
		C T GT ATA		
GAM1780	EZH1 3'	GACTGTGGGTTCCAAATTAC 10551	AC	
		GTAG TTGGAACCCACAGTC		
		CATT AACCTTGGGTGTCAG		
		A_		
GAM1780	STAC 3'	GACTGTGGAGTAATAGCCACAA 13427	AGA	TGGA _
	A	TTTGT CT AC CCACAGTC		

AAACA GA TG GGTGTCAG
 CC_ TAA_ A
 GAM1780 CCR1 3' GACTGTGGGCTCCATTC 8927 CT A
 GA TGGA CCCACAGTC
 || ||| |||||
 CT ACCT GGTGTCAG
 T_ C
 GAM1780 FLJ10483 3' GACTGTGGAAGAGATTACAAA 36652 A GGAAC
 TTTGTAG CTT CCACAGTC
 ||||| || |||||
 AAACATT GAG GGTGTCAG
 A AA____
 GAM1780 KIAA1871 3' ACTGTAAGAGTCTACAAA 61890 GGAACCC
 TTTGTAGACTT ACAGT
 ||||| || |||||
 AAACATCTGAG TGTCA
 AA_____
 GAM1780 LOC150821 3' GGGTTCCACATCCACAAA 60944 A CT
 TTTGT GA TGGAACCC
 ||||| || |||||
 AAACA CT ACCTTGGG
 C AC
 GAM1780 LOC151057 3' ACTGTGGGTACACCTATAAA 86379 ACT GA
 TTTGTAG TG ACCCACAGT
 ||||| || |||||
 AAATATC AC TGGGTGTCA
 C_ A_
 GAM1780 LOC157507 5' ACTGTAAAAGTCTGCAA 82377 GGAACCC
 TTTGTAGACTT ACAGT
 ||||| || |||||
 AAACGTCTGAA TGTCA
 AA_____
 GAM1780 LOC203339 5' GGATTCCCAGTCTACAAA 92214 T C
 TTTGTAGACT GGAA CC
 ||||| || |||||
 AAACATCTGA CCTT GG
 C A
 GAM1780 LOC51030 3' ACTGTAAATTAACCAATCTAC 32695 C AACCC____
 AAA TTTGTAGA TTGG ACAGT
 ||||| || |||||
 AAACATCT AACC TGTCA
 _ AAATTAAA
 GAM1780 LOC90906 3' GACTGTGGATCCCAAACCTTTGC 64951 C_ AAC
 A TGTAGA TTGG CCACAGTC
 ||||| || |||||
 ACGTTT AACC GGTGTCAG
 CA CTA
 GAM1781 ELF3 3' TGACCTTGACCTTGACCAA 16685 T GAT AAA
 TTGGT CAAGG GG GTCA
 ||||| || |||||

			AACCA GTTCC TC CAGT		
			AGT		
GAM1781	JAK2	3'	TGACCTTCATTCTGAGACCAA 18318	CAA	AA
			TTGGTT GGGATGGA GTCA		
			AACCAG TCTTACTT CAGT		
			AG_ C_		
GAM1781	SLC10A2	5'	ACTCTCTGTCTTGACCAA 6590	CAA	A
			TTGGTT GGGATGGA AGT		
			AACCAG TTCTGTCT TCA		
			C		
GAM1781	FLJ10803	3'	GTGACTTTCAGTTAAAGCCAA 37205	CAAGG	G
			TTGGTT GAT GAAAGTCAC		
			AACCGA TTG CTTTCAGTG		
			AA_ A		
GAM1781	KIAA1958	5'	GTGACTTTGAACCCCAAACC 82788	CAA	ATGG
			GGTT GGG AAAGTCAC		
			CCAA CCC TTTCAGTG		
			A_ CAAG		
GAM1781	MARCKS	3'	ACTTTCCACCCTGCCCA 11411	TTCA	A
			TGG AGGG TGGAAAGT		
			ACC TCCC ACCTTTCA		
			CG_ _		
GAM1781	TUB	5'	GTGGGACCATCCCTTAAACC 13898	C	AAAG
			GGTT AAGGGATGG TCAC		
			CCAA TTCCCTACC GGTG		
			A AG_		
GAM1781	LOC80298	3'	ACTTTTACCTTGAACCA 48062	GATG	
			TGGTTCAAGG GAAAGT		
			ACCAAGTTCC TTTCA		
			A_		
GAM1782	ABCB8	3'	CCGGCTGCCTCCCTCCCA 24203	_	
			TGGGAGGG GGCAGCTGG		
			ACCCTCCC CCGTCGGCC		
			T		
GAM1782	ABP1	3'	CAGCCCCCAGTTCCTCCCCCA 63797	A C	_
			TGGG GGGGG AGCT GGGCTG		
			ACCC CCTCC TTGA CCCGAC		
			_ _ CC		
GAM1782	ACTN1	5'	CAGCCCAGCCCTACTCCCTCCC 8469	CA_	
			GGGAGGGGG GCTGGGCTG		

			CCCTCCCTC CGACCCGAC		
			ATCC		
GAM1782	ADRBK1	3'	TCAGGGGCTGCCCGCTCCCA 9669	G	GGG
			TGGGAG GGGCAGCT CTGA		
			ACCCTC CCGTCGG GACT		
			G G__		
GAM1782	ALDOA	3'	CAGGCCCTGCCCCCTCCCA 5263	CT	G
			TGGGAGGGGGCAG GG CTG		
			ACCCTCCCCCGTC CC GAC		
			__ G		
GAM1782	AMH	3'	CAGCTCGCGCCCCTTCCCA 6651	A	T
			TGGGAGGGGGC GC GGGCTG		
			ACCCTTCCCCG CG CTCGAC		
			__ _		
GAM1782	AR	5'	TCAGCCAACCCCCCTCACCA 5277	__	CAGCTG
			TGG GAGGGGG GGCTGA		
			ACC CTCCCC CCGACT		
			A CAA__		
GAM1782	ARF1	3'	CAGCCCAGCTGTTCCCT 71195	A	
			GG GGGGGCAGCTGGGCTG		
			TC CCCTTGTCGACCCGAC		
			__		
GAM1782	ARHG	3'	CAACCCAGTGCCCCCTCCCA 77086	G	C
			TGGGAGGGGGCA CTGGG TG		
			ACCCTCCCCCGT GACCC AC		
			__ A		
GAM1782	ASGR2	5'	CAGCCCAGCTCCAGCTCC 56043	GG	C
			GGAG GG AGCTGGGCTG		
			CCTC CC TCGACCCGAC		
			GA _		
GAM1782	ASGR2	5'	CAGCCCAGCTCCAGCTCC 56044	GG	C
			GGAG GG AGCTGGGCTG		
			CCTC CC TCGACCCGAC		
			GA _		
GAM1782	ASGR2	5'	CAGCCCAGCTCCAGCTCC 56045	GG	C
			GGAG GG AGCTGGGCTG		
			CCTC CC TCGACCCGAC		
			GA _		
GAM1782	C18orf2	3'	CATCCCGCCCCACCCCCCA 49460	A	_ AGCT C
			TGGG GG GGGC GGG TG		

			ACCC CC CCCG CCC AC		
			C A ____ T		
GAM1782	CACNB1	3'	CAGCAACCCTGCCCCCTCCCA 7405	AG	CTGG
			TGGG GGGGCAG GCTG		
			ACCC CCCCGTC CGAC		
			CT CCAA		
GAM1782	CACNG3	5'	CCAGCCGGCCCCCGCCCCA 22564	A_	A_
			TGGG GGGGGC GCTGG		
			ACCC CCCCCG CGACC		
			CG GC		
GAM1782	CAMLG	5'	CCACTGCCACCCCTCCCA 9996	__	C
			TGGGAGGGG GCAG TGG		
			ACCCTCCCC CGTC ACC		
			AC _		
GAM1782	CAV1	5'	CAGCCACCGCCCCCTCC 10022	CA	TG_
			GGAGGGGG GC GGCTG		
			CCTCCCC CG CCGAC		
			_ CCA		
GAM1782	CBFA2T3	3'	TCAGACGTGCTCCCTCCCA 19019		GC GG
			TGGGAGGGGGCA TG CTGA		
			ACCCTCCCTCGT GC GACT		
			_ A_		
GAM1782	CD74	3'	TCAGCCCCAGCCCTCCCC 16381	AG	AGCT
			GGG GGGGC GGGCTGA		
			CCC CCCC CG CCCGACT		
			CT ACC_		
GAM1782	CKM	5'	CAGCCCAGCCAGGTCTCCT 10198	A__	
			AGGGGGC GCTGGGCTG		
			TCCTCTG CGACCCGAC		
			GAC		
GAM1782	CNP	3'	CAGCCCAGCTGCTCTGCCCA 53616	AG	
			TGGG GGGGCAGCTGGGCTG		
			ACCC TCTCGTCGACCCGAC		
			G_		
GAM1782	COL1A1	3'	CAACCTGGCTCCCTCCCA 5391	GGC	TG C
			TGGGAGGG AGC GG TG		
			ACCCTCCC TCG CC AC		
			_ GT A		
GAM1782	EGFL4	5'	TCAGACCTGCCCCCTCCCA 62474		CTGGG
			TGGGAGGGGGCAG CTGA		

		ACCCTCCCCCGTC GACT	
		CA__	
GAM1782	EPHA8	3' CAGCCCTGCCCCCCTCCC 40429	CA T
		GGGAGGGGG GC GGGCTG	
		CCCTCCCCC CG CCGAC	
		C_ T	
GAM1782	EVX1	5' CAGCAGCTCCGCGCCCTCCCA 10545	G _ GG
		TGGGAGGG GC AGCT GCTG	
		ACCCTCCC CG TCGA CGAC	
		G CC _	
GAM1782	FGFR1	3' CAGCCACTTCATCCCCTCCCA 7017	CAGCTG
		TGGGAGGGGG GGCTG	
		ACCCTCCCCT CCGAC	
		ACTTCA	
GAM1782	FGFR1	3' CAGCCACTTCATCCCCTCCCA 7018	CAGCTG
		TGGGAGGGGG GGCTG	
		ACCCTCCCCT CCGAC	
		ACTTCA	
GAM1782	FOSB	3' AGACCCTGCCCCCTGCCA 23054	G GCT _
		TGG AGGGGGCA GGG CT	
		ACC TCCCCGT CCC GA	
		G _ A	
GAM1782	FOSB	3' TCTAGCCACTCCCTCCCA 23058	CA
		TGGGAGGGGG GCTGGG	
		ACCCTCCCTC CGATCT	
		AC	
GAM1782	FOXD2	5' TCAGTCCCCCGCCCCCTCCC 16793	AGCT
		GGGAGGGGGC GGGCTGA	
		CCCTCCCCCG CCTGACT	
		CCC_	
GAM1782	GPRK6	3' CAGCCCTGGCCCTTCCCA 10865	G GCT
		TGGGAGGGG CA GGGCTG	
		ACCCTTCCC GT CCGAC	
		G _	
GAM1782	GRLF1	3' TCAGCTGCGCCCCCTCCCA 79262	CA TG
		TGGGAGGGGG GC GGCTGA	
		ACCCTCCCC CG TCGACT	
		CG _	
GAM1782	HOXC6	3' TCAGCTCTGGACCCCTCCC 16911	CAGCT
		GGGAGGGGG GGGCTGA	

		CCCTCCCCC CTCGACT	
		AGGT_	
GAM1782 HR	5'	CAGCTCTGGCACTGCCCCCTCC 37907	___ TG _
	CA	TGGGAGGGGGCA GC G GCTG	
		ACCCTCCCCCGT CG C CGAC	
		CA GT T	
GAM1782 IMMP2L	5'	CCAACAACGCGCCCTCTCCCA 51705	A _____
		TGGGAGGGGGC GC TGG	
		ACCCTCTCCCG CG ACC	
		_ CAACA	
GAM1782 IMPDH1	3'	CAGCCTGGCCCCACCCCA 7950	AG CA TG
		TGGG GGGG GC GGCTG	
		ACCC CCCC CG CCGAC	
		CA _ GT	
GAM1782 INHBC	3'	CCTGGCTACCCCTTCCA 19859	C TG
		TGGGAGGGGG AGC GG	
		ACCTTCCCCC TCG CC	
		A GT	
GAM1782 ITGA3	3'	CAGCCCCAGCCCCTTCC 11029	AGCT
		GGAGGGGGC GGGCTG	
		CCTTCCCCG CCGAC	
		AC__	
GAM1782 MAFF	3'	CCCACTGCCCCTCCCA 25577	AG C _
		TGGG GGGGCAG TG GG	
		ACCC CCGGTC AC CC	
		CT _ A	
GAM1782 MSI1	3'	CCTAGGACCGCCCCCTCCC 11698	AG__
		GGGAGGGGGC CTGGG	
		CCCTCCCCCG GATCC	
		CCAG	
GAM1782 MYL1	5'	TCAACCCAACCACCTCTT 55323	CAGC__ C
	CCA	TGGGAGGGGG TGGG TGA	
		ACCTTCTCCT ACCC ACT	
		ACCACCA A	
GAM1782 NFIA	5'	CCGCAGCCGCCCCCTCCC 70884	A _
		GGGAGGGGGC GCTG GG	
		CCCTCCCCCG CGAC CC	
		C G	
GAM1782 NTF5	5'	CAGGTGGTTGCCCCCTCCC 21630	GGG
		GGGAGGGGGCAGCT CTG	

	CCCTCCCCCGTTGG GAC	
	TG_	
GAM1782 PACSIN1	3' CAGCCCAGCCCTGTTTCCCCTC 93877	— —
	GAGGGG GCA GCTGGGCTG	
	CTCCCC TGT CGACCCGAC	
	TT CC	
GAM1782 PCDH11X	5' TCAACCCCTCTCCTCTCCCA 28016	C CT C
	TGGGAGGGGG AG GGG TGA	
	ACCCTCTCCT TC CCC ACT	
	C _ A	
GAM1782 PCDH11Y	5' TCAACCCCTCTCCTCTCCCA 53168	C CT C
	TGGGAGGGGG AG GGG TGA	
	ACCCTCTCCT TC CCC ACT	
	C _ A	
GAM1782 PIK3R2	5' CAACCCAGCGGACCCTCCCA 18509	GGCA C
	TGGGAGGG GCTGGG TG	
	ACCCTCCC CGACCC AC	
	AGG_ A	
GAM1782 PIK4CB	3' CCAGCTCTACCCCTCCCA 12129	GC_
	TGGGAGGGG AGCTGG	
	ACCCTCCCC TCGACC	
	ATC	
GAM1782 PIK4CB	3' CCAGGGACCTACCCCTCCCA 12130	GC ____
	TGGGAGGGG AG CTGG	
	ACCCTCCCC TC GACC	
	A_ CAGG	
GAM1782 PK428	5' TCAGGGACCTCGCCCCCTCCC 14603	AGCT G_
	GGGAGGGGGC GG CTGA	
	CCCTCCCCG CC GACT	
	CT_ AGG	
GAM1782 PKP2	3' CAGCCCAGCCTTGCCCACC 17106	_ _
	GG GGGCA GCTGGGCTG	
	CC CCCGT CGACCCGAC	
	A TC	
GAM1782 PLA2G4C	5' CAGCCCGCGACCTCCTCCCA 73806	CA T
	TGGGAGGGGG GC GGGCTG	
	ACCCTCCTCC CG CCCGAC	
	AG _	
GAM1782 PNU TL1	3' TCAGCACCACCCCTCCCA 12193	CAGC _
	TGGGAGGGGG TGG GCTGA	

		ACCCTCCCC ACC CGACT	
		_____ A	
GAM1782 PNUTL2	3'	CCATGCCGGCCCCCTCCCA 55371	G A_ _
		TGGGAGGGG C GC TGG	
		ACCCTCCCC G CG ACC	
		_ GC T	
GAM1782 PNUTL2	3'	CCATGCCGGCCCCCTCCCA 55372	G A_ _
		TGGGAGGGG C GC TGG	
		ACCCTCCCC G CG ACC	
		_ GC T	
GAM1782 PNUTL2	3'	CCATGCCGGCCCCCTCCCA 55373	G A_ _
		TGGGAGGGG C GC TGG	
		ACCCTCCCC G CG ACC	
		_ GC T	
GAM1782 POU2F2	3'	CAGCCATGCCTCCCCTCCCA 12212	CA TG
		TGGGAGGGGG GC GGCTG	
		ACCCTCCCCT CG CCGAC	
		C_ TA	
GAM1782 PPGB	3'	CCAGGACTGCCCCCTTCCCA 6125	_ _
		TGGGA GGGGGCAG CTGG	
		ACCCT CCCCCGTC GACC	
		T AG	
GAM1782 PPP2R4	3'	CCAGCAGTGGCCCCTCCC 61179	G _
		GGGAGGGG CA GCTGG	
		CCCTCCCC GT CGACC	
		G GA	
GAM1782 PRCC	3'	CAGCCCAGCTGGCCTGGCCC 21063	AG G
		GGG GGG CAGCTGGGCTG	
		CCC TCC GTCGACCCGAC	
		GG G	
GAM1782 PTPRN	3'	CAGCCTCCTCCCACCACCTCC 12624	_ CAGCT_
CA		TGGGAGGG GG GGGCTG	
		ACCCTCCC CC TCCGAC	
		A ACCCTCC	
GAM1782 RANBP3	3'	CAGCCCTCTGCCCTGCCCA 24630	A CT
		TGGG GGGGGCAG GGGCTG	
		ACCC TCCCCGTC CCCGAC	
		G T_	
GAM1782 RFX1	3'	CTTGCCCGCCCCCTCCCA 12849	_ A TG
		TGGGAGGGGG C GC GG	

		ACCCTCCCC G CG TC	
		C C GT	
GAM1782 RGR	3'	TCATCCCTCACCCCCTCCCA 12861	CAGCT C
		TGGGAGGGGG GGG TGA	
		ACCCTCCCC CCC ACT	
		ACT__ T	
GAM1782 RXRA	3'	CCAGCTGGGCCCCTCCCA 12916	G_
		TGGGAGGGGG CAGCTGG	
		ACCCTCCCC GTCGACC	
		GG	
GAM1782 RXRB	3'	CAGCTTCCCGCCGCCCCCCCCCA 42029	A A T _
		TGGG GGGGGC GC GG GCTG	
		ACCC CCCCCG CG CC CGAC	
		_ C C TT	
GAM1782 RYR1	5'	CAGCCCGCAGCCCCCTCCC 6771	A T
		GGGAGGGGGC GC GGGCTG	
		CCCTCCCCCG CG CCCGAC	
		A _	
GAM1782 SLC7A6	3'	CAGGAATTTGCTGCCCCCACC 15638	GA TGGG_
A		TGG GGGGGCAGC CTG	
		ACC CCCCCGTCG GAC	
		AC TTTAAG	
GAM1782 SNCB	3'	CAGTGTTGCCTCCTCCCA 13285	TGG
		TGGGAGGGGGCAGC GCTG	
		ACCCTCCTCCGTTG TGAC	

GAM1782 SNL	3'	TCTCCCAGCCACCTCCTCCCA 13292	CA CT
		TGGGAGGGGG GCTGGG GA	
		ACCCTCCTCC CGACCC CT	
		AC T_	
GAM1782 SOX12	3'	CAGCAGCCAGCCCCCTCC 23681	A_ GG
		GGAGGGGGC GCT GCTG	
		CCTCCCCCG CGA CGAC	
		AC _	
GAM1782 SYNGR1	3'	TCAGCCCAGAAGCCCTTCC 17512	G AG
		GGAGGGG C CTGGGCTGA	
		CCTTCCC G GACCCGACT	
		_AA	
GAM1782 TAGLN	3'	CAGCCCAGCCTGCCCCCT 60376	_
		AGGGGGCAG CTGGGCTG	

		TCCCCCGTC GACCCGAC	
		C	
GAM1782 TCF7	3'	CCAGTGTGCACCCCTCCC 13616	--
		GGGAGGGG GCA GCTGG	
		CCCTCCCC CGT TGACC	
		A G	
GAM1782 TFEB	3'	CCAGGGGACACCTCCCTCCCA 93750	___ AG
		TGGGAGGGG GC CTGG	
		ACCCTCCCT CG GACC	
		CCA GG	
GAM1782 THRA	5'	CACTCCCTGGCCCCTCCCA 13753	G CT GC
		TGGGAGGGG CAG GG TG	
		ACCCTCCCC GTC CC AC	
		G ___ TC	
GAM1782 TMEPAI	3'	CCAGCTGCTACCCCCTCCC 39826	___
		GGGAGGGG GCAGCTGG	
		CCCTCCCC CGTCGACC	
		CAT	
GAM1782 WARS	3'	TCAGCCCATGCCCCCTCCCA 67867	GC
		TGGGAGGGGGCA TGGGCTGA	
		ACCCTCCCCCGT ACCCGACT	

GAM1782 WWP2	3'	CCGAGGCCGCCCCTCCCA 61726	G A G_
		TGGGAGGGG C GCT GG	
		ACCCTCCCC G CGG CC	
		_C AG	
GAM1782 20D7-FC4	3'	TCAGCCCCAACCCCCTCCC 61570	CAGCT
		GGGAGGGG GGGCTGA	
		CCCTCCCC CCCGACT	
		AAC_	
GAM1782 ANKRD2	3'	CAGCCCAGCCAGCTACCC 72587	_ A_
		GGG GGC GCTGGGCTG	
		CCC TCG CGACCCGAC	
		A AC	
GAM1782 Apg4B	3'	CCGTGCTGCCTCCCCCA 26181	A _
		TGGG GGGGGCAGC TGG	
		ACCC CCTCCGTCG GCC	
		C T	
GAM1782 ARTN	5'	CCAGCATCTACCCCCTCCCA 15611	CA_
		TGGGAGGGG GCTGG	

		ACCCTCCCC CGACC		
		CATCTA		
GAM1782	BA108L7.2 3'	CCACTGCACCCCCTCCCA 49068	___	C
		TGGGAGGGG GCAG TGG		
		ACCCTCCCC CGTC ACC		
		CA _		
GAM1782	BICD2 3'	CCGTGTTGCCCCCTCCCA 70908	_	
		TGGGAGGGGGGCAGC TGG		
		ACCCTCCCCCGTTG GCC		
		T		
GAM1782	C14orf4 3'	CAACCCAACTCGACCCTCCC 67897	GGC C	C
		GGGAGGG AG TGGG TG		
		CCCTCCC TC ACCC AC		
		AGC A A		
GAM1782	C5orf6 3'	TCAGCCCCACCCCTCCC 33957	CAGCT	
		GGGAGGGGG GGGCTGA		
		CCCTCCCC CCGACT		
		AC___		
GAM1782	CBX6 3'	CCAAAGATGCCCCCTCCCA 27408	GC___	
		TGGGAGGGGGCA TGG		
		ACCCTCCCCCGT ACC		
		AGAA		
GAM1782	CNNM2 3'	CAGCCCCTGCTCCTCCTCCCA 34939	C T_	
		TGGGAGGGGG AGC GGGCTG		
		ACCCTCCTCC TCG CCGAC		
		_ TC		
GAM1782	CSR1 3'	TCAGGCACCACCCCTCC 33186	CAGC _ _	
		GGAGGGGG TGG GC TGA		
		CCTCCCC ACC CG ACT		
		___ A G		
GAM1782	DGKZ 3'	CAGCCCCCGCTCCTGCCCCACC 14676	AG	CT___
	CCA	TGGG GGGGCAG GGGCTG		
		ACCC CCCCGTC CCGAC		
		CA CTCGCC		
GAM1782	DJ37E16.5 3'	CCTTGCAACCCCTCCCA 40094	CA T	
		TGGGAGGGGG GC GGG		
		ACCCTCCCC CG TCC		
		AA T		
GAM1782	DKFZP434J193 3'	TCAACCCCAGGCCACCCCA 71563	A G AG	C_
		TGGG GG GGC CTGGG TGA		

	ACCC CC CCG GACCC ACT		
	_ A _ CA		
GAM1782 DKFZP434J193 3'	TCAGCTGAATCCCCTCCCA 71564	___	
	TGGGAGGGGG CAGCTGG		
	ACCCTCCCCT GTCGACT		
	AA		
GAM1782 DKFZP434N1817 3'	CAGCCCAGCCCTGCCTCCC 68719	G CA	
	GGGAGG GG GCTGGGCTG		
	CCCTCC TC CGACCCGAC		
	G C_		
GAM1782 DKFZp434P2235 3'	CATGCCCAGCCCCTCCCA 51045	GGCA _	
	TGGGAGGG GCTGGGC TG		
	ACCCTCCC CGACCCG AC		
	_____ T		
GAM1782 DKFZp547J036 3'	TCAGCCCAGCCAGGCCCCCTCC 51123	A__	
C	GGGAGGGGGC GCTGGGCTGA		
	CCCTCCCCCG CGACCCGACT		
	GAC		
GAM1782 DKFZp547O146 3'	CAGCCCAGCCCCGCCCTCCC 39965	_ CA	
	GGGAGGG GG GCTGGGCTG		
	CCCTCCC CC CGACCCGAC		
	G C_		
GAM1782 DKFZP586G1122 3'	TCAACCCTGAACCCCTCCCA 61940	GCAGCT C	
	TGGGAGGGG GGG TGA		
	ACCCTCCCC CCC ACT		
	AAGT__ A		
GAM1782 DKFZP586M1019 3'	CAGCCCTTCGAGCCCCCTCCC 32171	AGCT_	
	GGGAGGGGGC GGGCTG		
	CCCTCCCCCG CCGAC		
	AGCTT		
GAM1782 DNAJC5 3'	CCAGTCTCCCCCTCCCA 62133	C _	
	TGGGAGGGGG AG CTGG		
	ACCCTCCCC TC GACC		
	C T		
GAM1782 FBXO2 5'	CCGTAGCCGCCTCCTCCCA 25141	A _	
	TGGGAGGGGGC GCTG GG		
	ACCCTCCTCCG CGAT CC		
	C G		
GAM1782 FLJ00007 3'	CCTTGGGCTGCCCTCCCCCA 71776	A _	
	TGGG GGGGGCAGCT GGG		

	ACCC CTCCCGTCGG TCC	
	C GT	
GAM1782 FLJ00024	3' TCAGGGGCGCCCCTCCCA 64505	_ AG
	TGGGAGGGG GC CTGG	
	ACCCTCCCC CG GACT	
	G GG	
GAM1782 FLJ10535	3' TCAACCCATTTCCCTCCC 36757	CAGC C
	GGGAGGGGG TGGG TGA	
	CCCTCCCTT ACCC ACT	
	T__ A	
GAM1782 FLJ10759	3' CAGCCCAGCCCTGACCTC 37120	_ CA
	GAGG GGG GCTGGGCTG	
	CTCC TCC CGACCCGAC	
	AG _	
GAM1782 FLJ12387	3' CCTTATGCACTGCCCTCCCA 43375	_____ GCT
	TGGGAGGGG GCA GGG	
	ACCCTCCCC CGT TCC	
	GTCA AT_	
GAM1782 FLJ12681	3' CATCCCACCCTCCTCCCA 43183	CAGC C
	TGGGAGGGGG TGGG TG	
	ACCCTCCTCC ACCC AC	
	C__ T	
GAM1782 FLJ12783	3' CCAGGATTGCCCCTCTCCCA 49484	AG__
	TGGGAGGGGGC CTGG	
	ACCCTCTCCCG GACC	
	CTTAG	
GAM1782 FLJ12788	3' CAACCAGCCCCTCTCCCA 42844	CA GC
	TGGGAGGGGG GCTGG TG	
	ACCCTCTCCC CGACC AC	
	_ A_	
GAM1782 FLJ12875	3' CCTTGTGTTACCCCCTCCCA 44916	CA__ T
	TGGGAGGGGG GC GGG	
	ACCCTCCCC TG TCC	
	ATTG T	
GAM1782 FLJ13153	5' CAGCCCAGCCCCTGCTCCC 45922	G CA
	GGGAG GGG GCTGGGCTG	
	CCCTC TCC CGACCCGAC	
	G C_	
GAM1782 FLJ14126	3' CAGCCCCCTCTCCTCCCA 46274	CAGCT
	TGGGAGGGGG GGGCTG	

ACCCTCCTCT CCGAC
 CC____
 GAM1782 FLJ14327 3' CAGCCCTTTCTCTGCCCCAC 46676 A CT____
 CCA TGGG GGGGGCAG GGGCTG
 ||| ||||| |||||
 ACCC CCCCCGTC CCGAC
 A TCCTTT
 GAM1782 FLJ14800 3' TCAACCCCTGGCCCCCTCCC 52689 AGCT C
 GGGAGGGGGC GGG TGA
 ||||| ||| |||
 CCCTCCCCCG CCC ACT
 GTC_ A
 GAM1782 FLJ14810 3' CAACCCATCCCCCACCCA 52696 A CAGC C
 TGGG GGGGG TGGG TG
 ||| |||| ||| ||
 ACCC CCCCC ACCC AC
 A T____ A
 GAM1782 FLJ20320 5' CCTACACTGCCTCCTCCCA 35421 C_
 TGGGAGGGGGCAG TGGG
 ||||| ||||| |||
 ACCCTCCTCCGTC ATCC
 AC
 GAM1782 FLJ20542 3' CACCTCTGCCCTCTCCCA 50743 CT C
 TGGGAGGGGGCAG GGG TG
 ||||| ||||| ||| ||
 ACCCTCTCCCGTC TCC AC
 — —
 GAM1782 FLJ20850 3' CAGCCCAGCCCTAACTGCCA 36174 G GG CA
 TGG AG GG GCTGGGCTG
 ||| || ||||| |||||
 ACC TC TC CGACCCGAC
 G AA C_
 GAM1782 FLJ23058 5' TCAGCCCAGCTGGGTTCC 45528 GGGG
 GGAG CAGCTGGGCTGA
 ||| ||||| |||||
 CCTT GTCGACCCGACT
 GG_
 GAM1782 FLJ23604 3' CAGCCCATGCACCCCTCCC 47546 _ GC
 GGGAGGGG GCA TGGGCTG
 ||||| ||| |||||
 CCCTCCCC CGT ACCCGAC
 A _
 GAM1782 FLJ32332 3' CAGCCCGTGGCCCTCCCA 58942 GGCA T
 TGGGAGGG GC GGGCTG
 ||||| || |||||
 ACCCTCCC TG CCGAC
 GG_ _
 GAM1782 GMEB2 3' CTGAGCCGGCCCCCTCCCA 25661 G A_ G
 TGGGAGGGG C GCT GG
 ||||| ||| ||| ||

		ACCCTCCCC G CGA TC	
		_ GC G	
GAM1782 HA-1	3'	CAGCGGGCGCCTCCTCCCA 66154	A GG
		TGGGAGGGGGC GCT GCTG	
		ACCCTCCTCCG CGG CGAC	
		_ G_	
GAM1782 HTCD37	3'	CAGCAGAGCACTCCCTCCCA 68297	CA GG
		TGGGAGGGGG GCT GCTG	
		ACCCTCCCTC CGA CGAC	
		A_ GA	
GAM1782 KDELRI	5'	CAGCCCAGCTACCCGTTT 23296	G C
		GAG GGG AGCTGGGCTG	
		CTT CCC TCGACCCGAC	
		G A	
GAM1782 KIAA0275	3'	CAGCCCAGCCCTGACCCCT 29323	G _
		AGGGG CA GCTGGGCTG	
		TCCCC GT CGACCCGAC	
		A CC	
GAM1782 KIAA0285	3'	TCAACCCTCACCTCCTCCCA 29689	CAGCT C
		TGGGAGGGGG GGG TGA	
		ACCCTCCTCC CCC ACT	
		CACT_ A	
GAM1782 KIAA0321	5'	CAGCCACACCACCCTCTCCCA 63046	CAGCTG
		TGGGAGGGGG GGCTG	
		ACCCTCTCCC CCGAC	
		ACCACA	
GAM1782 KIAA0397	3'	CAGCCCAGCCCTGCCCCC 62342	_
		GGGGGCA GCTGGGCTG	
		CCCCCGT CGACCCGAC	
		CC	
GAM1782 KIAA0542	3'	TCAGCCAGCAGCCCCCTCCC 66668	A G
		GGGAGGGGGC GCTGG CTGA	
		CCCTCCCCCG CGACC GACT	
		A _	
GAM1782 KIAA0792	3'	CAGCCCAGCAGTCCCTCC 28763	G A
		GGAGGGG C GCTGGGCTG	
		CCTCCCT G CGACCCGAC	
		_ A	
GAM1782 KIAA1023	3'	CAGCCCAGCCTGTTCTCTCCCA 34675	_
		TGGGAGGGGGCAG CTGGGCTG	

	ACCCTCTCTTGTC GACCCGAC	
	C	
GAM1782 KIAA1029	5' CCAGCTGACCACCCCTCCCA 24424	__
	TGGGAGGGG G CAGCTGG	
	ACCCTCCCC C GTCGACC	
	AC A	
GAM1782 KIAA1100	3' TCAGCCTGGTCCCACCCCCA 30443	A _ CA TG
	TGGG GG GGG GC GGCTGA	
	ACCC CC CCC TG CCGACT	
	_ A _ GT	
GAM1782 KIAA1130	3' CACGCCACCCCTCCCA 63078	CAGC _
	TGGGAGGGGG TGGGC TG	
	ACCCTCCCCC ACCCG AC	
	_____ C	
GAM1782 KIAA1317	5' TCAACCCAACCTCCTCTCA 87214	CAGC C
	TGGGAGGGGG TGGG TGA	
	ACTCTCCTCC ACCC ACT	
	A _ A	
GAM1782 KIAA1514	3' CAGCCAGCTGCCCCCTTCCA 39325	G
	TGGGAGGGGGCAGCTGG CTG	
	ACCTTCCCCCGTCGACC GAC	

GAM1782 KIAA1554	3' CAACCCTGACCTTCCCCCTCCC 96852	C CT__ C
A	TGGGAGGGGG AG GGG TG	
	ACCCTCCCC TC CCC AC	
	T CAGT A	
GAM1782 KIAA1582	5' CAACCCAGCTGCCTGGCCT 65984	AGG C
	GGG GGGCAGCTGGG TG	
	TCC TCGTCGACCC AC	
	GG_ A	
GAM1782 KIAA1762	3' CAGCAGAGTCCTGCCTCCTCCC 64528	_ GG
A	TGGGAGGGGGCAG CT GCTG	
	ACCCTCCTCCGTC GA CGAC	
	CT GA	
GAM1782 KIAA1831	3' CCATTGCTCCACGCCCTCCCA 64522	_____ C
	TGGGAGGG GGCAG TGG	
	ACCCTCCC TCGTT ACC	
	GCACC _	
GAM1782 KIAA1879	5' CCATGCTGGCCACCCCTCC 73934	_____ _
	GGAGGGGG CAGC TGG	

	CCTCCCCC	GTCG ACC	
	ACCG	T	
GAM1782 KIAA1893	3'	CAGCCCCATCCCCTCTCCCA	73587 CAGCT
		TGGGAGGGGG	GGGCTG
		ACCCTCTCCC	CCCGAC
		CTAC_	
GAM1782 KIAA1957	3'	CCGGGACGCCCCCTCCCA	76214 AG G
		TGGGAGGGGGC	CT GG
		ACCCTCCCCCG	GG CC
		CA G	
GAM1782 MGC1127	3'	CACCCCACACCCCTCCCA	54331 GCAGC C
		TGGGAGGGG	TGGG TG
		ACCCTCCCC	ACCC AC
		AC_	C
GAM1782 MGC13057	5'	CAGCAAGCCCCCTCCCA	51283 CA GG
		TGGGAGGGGG	GCT GCTG
		ACCCTCCCC	CGA CGAC
		_	A_
GAM1782 MGC14436	5'	TCAGCCGAAAGCCCCCGCCCA	52930 A CA G_
		TGGG GGGGG	GCT GGCTGA
		ACCC CCCCC	CGA CCGACT
		G	_ AAG
GAM1782 MGC14832	3'	CAGCCACCTCATACCCCTTCC	51339 CAGCTG_
CA		TGGGAGGGGG	GGCTG
		ACCCTTCCCC	CCGAC
		CATACTCCA	
GAM1782 MGC15416	3'	TCAGCCCGACTGCCCTCCTCCC	51406 _ C
A		TGGGAGG GGGCAG	TGGGCTGA
		ACCCTCC CCGTC	GCCCGACT
		T	A
GAM1782 MGC15476	3'	CCAGCTATGGCCCCCTCTCA	59607 _
		TGGGAGGGGGC	AGCTGG
		ACTCTCCCCCG	TCGACC
		GTA	
GAM1782 MGC3035	5'	CAGCCCCCTCCCCTTCC	44394 C CT
		GGAGGGGG	AG GGGCTG
		CCTTCCCC	TC CCCGAC
		_	C_
GAM1782 MGC4707	3'	TCAGCCCAGCCAGTGGCCCC	44364 G _
		GGGG CA	GCTGGGCTGA

		CCCC GT CGACCCGACT G GAC	
GAM1782 MIL1	3'	CCAGTGGCACCCCTCCCA 31725 TGGGAGGGGG GCTGG ACCCTCCCC TGACC ACGG	CA__
GAM1782 NFAT5	5'	CAGCCTCCCCCCTCCCA 57761 TGGGAGGGGG GGGCTG ACCCTCCCC TCCGAC CC__	CAGCT
GAM1782 NKD1	3'	TCAACTCTGCCCCACCCCA 53588 TGGG GGGGCAG GG TGA ACCC CCCCCTC TC ACT CA _ A_	AG CT GC
GAM1782 NKD1	3'	TCAGCCCACACCCTTCCCA 53589 TGGGAGGGG TGGGCTGA ACCCTTCCC ACCCGACT AC__	GCAGC
GAM1782 OAZ2	5'	CCTGCGCCGCTCCTCCCA 11875 TGGGAGGGGGC GC TGGG ACCCTCCTCCG CG GTCC C C	A _
GAM1782 PF1	5'	TCAGGAGCGCCCCCTCCC 96834 GGGAGGGGGC GCT CTGA CCCTCCCCCG CGA GACT _ G_	A GGG
GAM1782 PIP5K1C	3'	TCAGGCTCCCCGCCCTCC 71308 GGAGGGGGC GG CTGA CCTCCCCCG TC GACT CCCC G	AGCT G
GAM1782 PLAGL2	3'	CAGCAATGAGCTGTCCCCCTCC 70954 TGGGAGGGGG CAGCT GCTG ACCCTCCCC GTCGA CGAC T GTAA	_ GG__
GAM1782 PPY2	3'	CAGCCCAGCTCTCCCCTCC 41173 GGAGGGGG AGCTGGGCTG CCTCCCCT TCGACCCGAC C	C
GAM1782 QKI	5'	CAGCCCAGAGAGACCCCCCG 66042 TGGG GGG CTGGGCTG 	A GGCAG

GCCC CCC GACCCGAC
 _ AGAGA
 GAM1782 RPH3A 3' TCAGCCCACCTCCCTCACCA 30937 _ CAGC
 TGG GAGGGGG TGGGCTGA
 ||| ||||| |||||
 ACC CTCCCTC ACCCGACT
 A C__
 GAM1782 SCGF 5' CCAGAGGCCACCCCTCCCA 12944 _ AG
 TGGGAGGGG GC CTGG
 ||||| || |||
 ACCCTCCCC CG GACC
 AC GA
 GAM1782 SEC14L1 3' CATCCCCTGCCCCCTCCCA 13005 CT C
 TGGGAGGGGGCAG GGG TG
 ||||| ||| ||
 ACCCTCCCCCGTC CCC AC
 _ T
 GAM1782 SFXN5 3' AGGCTGCCTGCCCCATCCCA 58645 G CT G
 TGGGA GGGGCAG GG CT
 |||| ||||| |||
 ACCCT CCCCCTC TC GA
 A CG G
 GAM1782 SLC26A10 5' CCAGATTGCCCCCTCTCA 56840 _
 TGGGAGGGGGCAG CTGG
 ||||| |||||
 ACTCTCCCCCGTT GACC
 A
 GAM1782 SOX17 5' TCATTCCCCACCCCTCCC 42631 CAGC C__
 GGGAGGGGG TGGG TGA
 ||||| ||| |||
 CCCTCCCCC ACCC ACT
 _ CTT
 GAM1782 STMN3 3' CAGCCCCAACACCCCTTCCCA 32463 GCAGCT
 TGGGAGGGG GGGCTG
 ||||| |||||
 ACCCTTCCC CCGAC
 ACAAC_
 GAM1782 TACTILE 3' TCAGCCCAGACTCCTGCCA 20593 G GCAG
 TGG AGGGG CTGGGCTGA
 ||| |||| |||||
 ACC TCCTC GACCCGACT
 G A__
 GAM1782 TLN1 3' CCAAGTGCCTGCCCCCTCCCA 21901 AG _
 TGGG GGGGCAG C TGG
 ||| ||||| | |||
 ACCC CCCCCTC G ACC
 CT C TGA
 GAM1782 TOMM34 3' CAGCCCAGCTAGCTGATC 23314 GGG _
 GA GGC AGCTGGGCTG
 || ||| ||||| |||||

			CT TCG TCGACCCGAC		
			AG_ A		
GAM1782	WFDC2	3'	CAGCCCACCTGCCCTCCCC 55778	A	C
			GGG GGGGGCAG TGGGCTG		
			CCC CTCCCGTC ACCCGAC		
			_ C		
GAM1782	WFDC2	3'	CAGCCCACCTGCCCTCCCC 55779	A	C
			GGG GGGGGCAG TGGGCTG		
			CCC CTCCCGTC ACCCGAC		
			_ C		
GAM1782	YARS	3'	CAGCCCAGCATCTTCCCCCC 14853	A	CA
			GGG GGGGG GCTGGGCTG		
			CCC CCTTC CGACCCGAC		
			C TA		
GAM1782	LOC112476	3'	CCTGGCCGCCTCCTCCCA 59785	A	TG
			TGGGAGGGGGC GC GG		
			ACCCTCCTCCG CG CC		
			C GT		
GAM1782	LOC113730	5'	CAGCCCAGACCCTCCCCCA 73499	A	CAG
			TGGG GGGGG CTGGGCTG		
			ACCC CCTCC GACCCGAC		
			_ CA_		
GAM1782	LOC115110	5'	CAGCCCAGCCCCGGTTCCTCCC 72173	_____	CA
			GGGAGG GGG GCTGGGCTG		
			CCCTCC CCC CGACCCGAC		
			TTGG _		
GAM1782	LOC116150	3'	TCAGCCCAGCTACTTCCC 57425	GGGC	
			GGGAGG AGCTGGGCTGA		
			CCCTTC TCGACCCGACT		
			A_		
GAM1782	LOC123775	3'	TCATTTCCACCCACCCCCCA 76143	A _	CAGC C_
			TGGG GG GGG TGGG TGA		
			ACCC CC CCC ACCC ACT		
			C A _ TTT		
GAM1782	LOC124930	3'	CACCCCCACCCCTTCCCA 74822	CAGCT	C
			TGGGAGGGGG GGG TG		
			ACCCTTCCCC CCC AC		
			AC_ C		
GAM1782	LOC130497	3'	GCGGGGCAGCCCCCTCCCA 75452	A	GG
			TGGGAGGGGGC GCT GC		

	ACCCTCCCCCG CGG CG	
	A GG	
GAM1782 LOC134187 5'	CCACTTCTGCCCCCTTCCA 76464	C__
	TGGGAGGGGGCAG TGG	
	ACCTTCCCCCGTC ACC	
	TTC	
GAM1782 LOC138389 5'	CAGCCCAGGCACCCTCC 76728	G AG
	GGAGGG GC CTGGGCTG	
	CCTCCC CG GACCCGAC	
	A _	
GAM1782 LOC143677 3'	CACTTGCGCGCCCCTCCCA 83893	A TG C
	TGGGAGGGGGC GC GG TG	
	ACCCTCCCCCG CG TC AC	
	_ GT _	
GAM1782 LOC143915 5'	CCATTATCTGCCCCCTCCCA 83904	C__
	TGGGAGGGGGCAG TGG	
	ACCCTCCCCCGTC ACC	
	TATT	
GAM1782 LOC144262 5'	CCAAGTGTAGCCCCTCCCA 77259	_ GC
	TGGGAGGGG GCA TGG	
	ACCCTCCCC TGT ACC	
	GA GA	
GAM1782 LOC144402 5'	CCAAGGCGCCTCCTCCCA 77323	A _
	TGGGAGGGGGC GCT GG	
	ACCCTCCTCCG CGG CC	
	_ AA	
GAM1782 LOC145678 3'	CCAGGGTGACCCCTCCCA 84432	G G _
	TGGGAGGGG CA C TGG	
	ACCCTCCCC GT G ACC	
	A G G	
GAM1782 LOC145757 3'	CAGCCCAGGCACCTCCTCCCA 77919	CAG
	TGGGAGGGGG CTGGGCTG	
	ACCCTCCTCC GACCCGAC	
	ACG	
GAM1782 LOC145989 3'	CCCAGCCACCTCCTCCCA 60289	CA
	TGGGAGGGGG GCTGGG	
	ACCCTCCTCC CGACCC	
	AC	
GAM1782 LOC146562 3'	CAGCCCCCAGGCCCTCTCCCA 58251	AGCT
	TGGGAGGGGGC GGGCTG	

	ACCCTCTCCCG CCCGAC		
	GACC		
GAM1782 LOC146782 3'	CATGCCCAGCCCCTCCCA 76804	GGCA	_
	TGGGAGGG GCTGGGC TG		
	ACCCTCCC CGACCCG AC		
	_____ T		
GAM1782 LOC147136 5'	CAGCAAGCTGCCCCCTCC 78858	GG	
	GGAGGGGGCAGCT GCTG		
	CCTCCCCCGTCGA CGAC		
	A_		
GAM1782 LOC148181 5'	CAGCCCAGCTCATGCCTCCC 79430	GGGC	
	GGGAGG AGCTGGGCTG		
	CCCTCC TCGACCCGAC		
	GTAC		
GAM1782 LOC148250 5'	TCAGAGCATGCCCCCTCCCA 79495	_ GGG	
	TGGGAGGGGGCA GCT CTGA		
	ACCCTCCCCCGT CGA GACT		
	A _____		
GAM1782 LOC148697 3'	CAACCCAGCTGCCTTACCT 79675	AG	C
	GGG GGGGCAGCTGGG TG		
	TCC TTCCGTCGACCC AC		
	A_ A		
GAM1782 LOC149134 5'	TCACATGACTGTCCCCTCCCA 85521	CT GGC	
	TGGGAGGGGGCAG G TGA		
	ACCCTCCCCTGTC T ACT		
	AG AC_		
GAM1782 LOC150368 3'	CCTGACTGCCCCCTCCCA 80514	CT	
	TGGGAGGGGGCAG GGG		
	ACCCTCCCCCGTC TCC		
	AG		
GAM1782 LOC150886 3'	TCAGCCCAACACGCTCCCCTCC 86333	_ AGC_	
CA	TGGGAGGGG GC TGGGCTGA		
	ACCCTCCCC CG ACCCGACT		
	T CACA		
GAM1782 LOC151470 3'	CCATCTTACCCCCTCCCA 81055	C C_	
	TGGGAGGGGG AG TGG		
	ACCCTCCCC TC ACC		
	A TCT		
GAM1782 LOC154222 5'	TCAGCGTCACCTCCTCCCA 87393	CA TGG	
	TGGGAGGGGG GC GCTGA		

	ACCCTCCTCC TG CGACT	
	AC ____	
GAM1782 LOC154990 5'	CAGCCCAGCTCATGCCTCCC 82147	GGGC
	GGGAGG AGCTGGGCTG	
	CCCTCC TCGACCCGAC	
	GTAC	
GAM1782 LOC155179 3'	CAGCCCAGCCTGTTCTCTCCCA 82223	_
	TGGGAGGGGGCAG CTGGGCTG	
	ACCCTCTCTTGTC GACCCGAC	
	C	
GAM1782 LOC157349 5'	CCAGCGGGCACCACCCTCCCA 82330	_ CA__
	TGGGAGGG GG GCTGG	
	ACCCTCCC CC CGACC	
	A ACGGG	
GAM1782 LOC163682 3'	CAGCCCTTCCCACCCCA 88398	A _ CAGCT
	TGGG GG GGG GGGCTG	
	ACCC CC CCC CCGAC	
	_ A TT__	
GAM1782 LOC163682 3'	CAGCCTACCCACCCCTCC 88399	CAGC _
	GGAGGGGG TG GGCTG	
	CCTCCCC AC CCGAC	
	ACCC T	
GAM1782 LOC170393 3'	CAGCCCCTGCTTGGCCCTCCC 83733	G _ T_
A	TGGGAGGGG CA GC GGGCTG	
	ACCCTCCCC GT CG CCGAC	
	G T TC	
GAM1782 LOC196337 5'	TCAGCCCAGCTATGGCCC 89026	__
	GGGC AGCTGGGCTGA	
	CCCG TCGACCCGACT	
	GTA	
GAM1782 LOC200301 5'	TCAGAAATGCCCCCTCCCA 90153	GCTGGG
	TGGGAGGGGGCA CTGA	
	ACCCTCCCCCGT GACT	
	AAA__	
GAM1782 LOC205095 3'	CCAGTGCACCCCGTCCCA 92381	_ _ G
	TGGGA GGGG GCA CTGG	
	ACCCT CCCC CGT GACC	
	G A _	
GAM1782 LOC219562 3'	CATGCCCAGCCCCTCCCA 92448	GGCA _
	TGGGAGGG GCTGGGC TG	

	ACCCTCCC	CGACCCG AC	
	_____	T	
GAM1782 LOC220018 5'	TCAACCCAAGGGACCCCTCCC	95030	GCAGC C
	GGGAGGGG	TGGG TGA	
	CCCTCCCC	ACCC ACT	
	AGGGA	A	
GAM1782 LOC220739 3'	TCAGCCCAGCTCTGCCTCGCA	94528	G G C
	TG GAGG GG	AGCTGGGCTGA	
	AC CTCC TC	TCGACCCGACT	
	G G	_	
GAM1782 LOC221486 3'	TCAGCCCAGCACCTGCTCCCA	92659	G CA
	TGGGAG GGG	GCTGGGCTGA	
	ACCCTC TCC	CGACCCGACT	
	G A	_	
GAM1782 LOC254295 5'	TCAGCCCAGCTGCTTGGCCT	97897	AGG
	GGG	GGGCAGCTGGGCTGA	
	TCC TTCGT	CGACCCGACT	
	GG	_	
GAM1782 LOC255612 5'	CAGCCCCTGTCCCCCCCCA	99365	A CT
	TGGG GGGGGCAG	GGGCTG	
	ACCC CCCCTGTC	CCCGAC	
	C	_____	
GAM1782 LOC255975 3'	CAGCCCAGCTCATGCCTCCC	97572	GGGC
	GGGAGG	AGCTGGGCTG	
	CCCTCC	TCGACCCGAC	
	GTAC		
GAM1782 LOC256867 5'	CACGTCTGCCCCCGCCA	96511	GA GCT _
	TGG GGGGGCA	GGGC TG	
	ACC CCCCCGT	CCTG AC	
	GC	_____ C	
GAM1782 LOC257016 3'	TCAGCCCAGCCCACCCTC	96753	_ CA
	GAGGG GG	GCTGGGCTGA	
	CTCCC CC	CGACCCGACT	
	A	_____	
GAM1782 LOC257181 3'	CATGCCCAGCCCCTCCCA	96229	GGCA _
	TGGGAGGG	GCTGGGC TG	
	ACCCTCCC	CGACCCG AC	
	_____	T	
GAM1782 LOC257457 5'	CCAAGCCTGCCCCCTTCCA	63315	_ _
	TGGGAGGGGGCAG	CT GG	

	ACCTTCCCCCGTC GA CC	
	C A	
GAM1782 LOC51107 5'	CAGCTGGCGCGCCCTCCCA 32607	_ A TG G
	TGGGAGGGG GC GC G CTG	
	ACCCTCCCC CG CG C GAC	
	G _ GT _	
GAM1782 LOC51308 3'	CAGCAGTCGCCTCCTCCCA 33960	A GG
	TGGGAGGGGGC GCT GCTG	
	ACCCTCCTCCG TGA CGAC	
	C _	
GAM1782 LOC51713 3'	CCGGGCGCGGCCCTCCCA 33228	A_ G
	TGGGAGGGGGC GCT GG	
	ACCCTCCCCCG CGG CC	
	GCG G	
GAM1782 LOC91252 3'	CCAGAGCTGCCCACCTCCCA 65937	_ G_
	TGGGAGG GGGCAGCT GG	
	ACCCTCC CCCGTCA CC	
	A GA	
GAM1782 LOC91300 5'	CAGCCCCTGCTCAGCCCCTCCC 96233	_____ CT
A	TGGGAGGGG GCAG GGGCTG	
	ACCCTCCCC CGTC CCCGAC	
	GACT _	
GAM1782 LOC91300 5'	CAGCCCCTGCTCAGCCCCTCCC 96234	_____ CT
A	TGGGAGGGG GCAG GGGCTG	
	ACCCTCCCC CGTC CCCGAC	
	GACT _	
GAM1782 LOC91409 3'	TCAGCCCAGCCCTAACCTC 66574	GGCA_
	GAGGG GCTGGGCTGA	
	CTCCC CGACCCGACT	
	AATCC	
GAM1782 LOC92223 5'	CAACCCGCCGCTGCCCCCTCCC 69044	_ C
	GGGAGGGGGCAGC TGGG TG	
	CCCTCCCCCGTCG GCCC AC	
	CC A	
GAM1783 GADD45B 3'	CACGAGGACCATCGGGG 32246	C ACTG
	TCCCCGATGG CC CGTG	
	GGGGGCTACC GG GCAC	
	A A_	
GAM1783 ITGA3 3'	CACGCAGTGC GGATCCGGGA 11028	C GG _
	TCCC GAT CC CACTGCGTG	

AGGG CTA GG GTGACGCAC
 C _ C
 GAM1783 LEP 3' TCACACAGTGGGTGGTGG 5869 G G C
 CC AT GCCCACTG GTGA
 || || ||||| ||||
 GG TG TGGGTGAC CACT
 _ G A
 GAM1783 LOXL2 5' ACTGCGTGATCCAGCCATCGGA 11350 C C_____ TGC
 GA TC CCGATGGC CAC GT
 || ||||| || ||
 AG GGCTACCG GTG CA
 A ACCT__A CGT
 GAM1783 SFRS7 3' TCACGCAGCAGGAGCAGGGGA 60151 GATGG CA
 TCCCC CC CTGCGTGA
 |||| || |||||
 AGGGG GG GACGCACT
 ACGA_ AC
 GAM1783 SIRT7 3' ACTGCGTGACCTGGCCATCGAG 33735 C _____ TGC
 GA TCC CGATGGCC CAC GT
 || ||||| || ||
 AGG GCTACCGG GTG CA
 A TCC__A CGT
 GAM1783 TBL1X 3' ACGCGTGACCCAGCCATCGGGG 20127 C_____ TGC
 A TCCCCGATGGC CAC GT
 ||||| || ||
 AGGGGCTACCG GTG CA
 ACCC__A CGT
 GAM1783 CTRP5 5' CGAAGGAGGCCATCGGGGA 32230 CA G
 TCCCCGATGGCC CT CG
 ||||| || ||
 AGGGGCTACCGG GA GC
 AG A
 GAM1783 CXYorf1 5' GGTGCAGGCCATTGGAGA 82918 C _
 TC CCGATGGCC CACT
 || ||||| ||||
 AG GGTTACCGG GTGG
 A AC
 GAM1783 DKFZP434J1813 5' CGCGGCTGGGCCGTCGGAGA 62437 C _
 TC CCGATGGCCCA CTGCG
 || ||||| ||||
 AG GGCTGCCGGGT GGCGC
 A C
 GAM1783 DKFZP727M111 5' ACGCGTGACCAGGACCATCGGG 32050 _ _____ TGC
 CCCGATGG CC CAC GT
 ||||| || || ||
 GGGCTACC GG GTG CA
 A ACC__A CGT
 GAM1783 FLJ11506 3' TGTATGGGCCATGGAGA 45437 C G C
 TC CC ATGGCCCA TGCG
 || || ||||| ||||

AG GG TACCGGGT ATGT
 A _ _
 GAM1783 FLJ22169 5' CATGTATGCTCATCGGGGA 44230 _ CCAC
 TCCCCGATG GC TGC GTG
 ||||| || |||||
 AGGGGCTAC CG ATGTAC
 T T__
 GAM1783 FLJ23598 3' CACACAAGCACTTCATCGGGGG 96504 CCCAC_ C
 TCCCCGATGG TG GTG
 ||||| || |||
 GGGGGCTACT AC CAC
 TCACGA A
 GAM1783 FOXP1 3' CACGCAGCAGTATTGGGGG 52043 G CCA
 TCCCCGATG C CTGCGTG
 ||||| | |||||
 GGGGGTTAT G GACGCAC
 _ AC_
 GAM1783 HSBP1 5' CAAGCTGGGCATCGGGGA 9519 G CT G
 TCCCCGATG CCA GC TG
 ||||| ||| |||
 AGGGGCTAC GGGT CG AC
 _ _ A
 GAM1783 HSH2 3' TCAGAGCAAGGCCCTCAGGGA 52743 C T CAC G_
 TCCC GA GGCC TGC TGA
 ||| || ||| ||| |||
 AGGG CT CCGG ACG ACT
 A C A__ AG
 GAM1783 KIAA1904 3' CGGGGCAAGCCGTCGGGGA 73865 CCA G
 TCCCCGATGGC CT CG
 ||||| ||| |||
 AGGGGCTGCCG GG GC
 AAC G
 GAM1783 SIAT4A 5' CACACAGCCGTGTCTGGGA 13134 C _ CCAC C
 TCCC GAT GGC TG GTG
 ||| ||| ||| ||| |||
 AGGG CTG CCG AC CAC
 T TG _ A
 GAM1783 STC2 3' CACACAGTGGGTGCTGGG 14933 ATG C
 CCCG GCCCACTG GTG
 ||| ||||| |||
 GGGT TGGGTGAC CAC
 CG_ A
 GAM1783 ZDHHC3 3' ACGCGTGATATTGACCATCGGG 33926 CC_____ TGC
 GA TCCCCGATGG CAC GT
 ||||| ||| |||
 AGGGGCTACC GTG CA
 AGTTAT__A CGT
 GAM1783 LOC149837 5' CAGAGGGGGCCATCAGGGA 85890 C A_
 TCCC GATGGCCC CTG
 ||| ||||| |||

AGGG CTACCGGG GAC
 A GA
 GAM1783 LOC152313 5' CACACTGGGCCATGAGGGA 86845 CG CTGC
 TCCC ATGGCCCA GTG
 ||| ||||| ||
 AGGG TACCGGGT CAC
 AG CA__
 GAM1783 LOC166983 5' TGGAGCAGGCCATCGGGGA 88619 CA G
 TCCCCGATGGCC CT CG
 ||||| || ||
 AGGGGCTACCGG GA GT
 AC G
 GAM1783 LOC196500 3' ACGCGTGATCAAGGCCATCGGG 89079 TGC
 CCCGATGGCC CAC GT
 ||||| || ||
 GGGCTACCGG GTG CA
 AACT__A CGT
 GAM1783 LOC199958 3' TCACGTAGGGAGCCCCAGG 91493 GAT _ A
 CC GGC CC CTGCGTGA
 || ||| || |||||
 GG CCG GG GATGCACT
 ACC A _
 GAM1783 LOC200093 5' GGTGCAGGCCATTGGAGA 63775 C _
 TC CCGATGGCC CACT
 || ||||| |||
 AG GGTTACCGG GTGG
 A AC
 GAM1783 LOC90342 5' CACGCAGTGGACAGTAAGGG 63009 GA__ GC
 CCC TG CCACTGCGTG
 ||| || |||||
 GGG AC GGTGACGCAC
 AATG A_
 GAM1783 LOC91040 5' GGTGCAGGCCATTGGAGA 65349 C _
 TC CCGATGGCC CACT
 || ||||| |||
 AG GGTTACCGG GTGG
 A AC
 GAM1783 LOC91828 5' CGGGGTGGGCCTTCGGGGA 67858 T G
 TCCCCGA GGCCCACT CG
 ||||| ||||| ||
 AGGGGCT CCGGGTGG GC
 T G
 GAM1784 IRS1 3' CCATAGATGGTTCTCAATTGTA 19874 C TGAAC
 TACA ATTGAGAACC ATGG
 ||| ||||| |||
 ATGT TAACTCTTGG TACC
 _ TAGA_
 GAM1784 SERPINF1 3' CCTGTAAGGTTTCAATG 12038 A GA T
 CATTGAGA CCT ACA GG
 ||||| ||| ||| ||

		GTAAC TTT GGA TGT CC		
		— A —		
GAM1784	HSA243396	3' CCATGTT CAGCAATGTCAATG 37844	GAAC_	
		CATTGA CTGAACATGG		
		GTAAC T GACTTGTACC		
		GTAAC		
GAM1784	KIAA1387	3' CAGGAATTTTCAATATGTA 71444	C	—
		TACA ATTGAGAA CCTG		
		ATGT TAACTTTT GGAC		
		A AA		
GAM1784	MGC16063	3' TTCAAATTC CAATGTGTA 54930	A	CC
		TACACATTG GAA TGAA		
		ATGTGTAAC CTT ACTT		
		— AA		
GAM1784	SMCR8	3' CCATGCTCAGGTTTGACTATGT 59253	TGA_	A
		ACAT GAACCTGA CATGG		
		TGTA TTTGGACT GTACC		
		TCAG C		
GAM1784	UPLC1	3' CCATGCTAGGCCCAATGT 35227	AGAA	AA
		ACATTG CCTG CATGG		
		TGTAAC GGAT GTACC		
		CCC_ C_		
GAM1784	ZNF334	3' CCATAAGTCAACCCTCAATGT 36637	AACC	AC_
		ACATTGAG TGA ATGG		
		TGTAAC TC ACT TACC		
		CCA_ GAA		
GAM1784	LOC145082	3' TATGGAATGCCCTTAATGTGTA 84196		AACCTGAA
		TACACATTGAG CATG		
		ATGTGTAATTC GTAT		
		CCGTAAG_		
GAM1784	LOC157723	3' CCAAGTAAGTTCTCAAATGT 82465	—	GA A
		ACATT GAGAACCT AC TGG		
		TGTAA CTCTTGGA TG ACC		
		A A_ A		
GAM1784	LOC219988	5' CCATGTT CGGCCCAATG 93262	AGAAC	
		CATTG CTGAACATGG		
		GTAAC GGCTTGTACC		
		CCCC_		
GAM1785	ATP6V0C	3' CCCCAGTAGTTGGTCTTGTA 88658	CTG	_ A
		TACAAGATCA ACT CTG GG		

		ATGTTCTGGT TGA GAC CC	
		___ T C	
GAM1785 DLX4	3'	GTCCCCAGAACCCCTTGGTCTTG 57114	CTGAC A
		CAAGATCA TCTG GGAC	
		GTTCTGGT AGAC CCTG	
		TCCCA C	
GAM1785 MNT	3'	TCCTCAGAGGCTGAGCCTGTA 40089	AGA CTGA
		TACA TCA CTCTGAGGA	
		ATGT AGT GAGACTCCT	
		CCG CG__	
GAM1785 TCF2	3'	GTCCCCAGAACCCAGCTGCAGAT 6617	AGAT _ AC A
G		CA CA CTG TCTG GGAC	
		GT GT GAC AGAC CCTG	
		AGAC C CA C	
GAM1785 VNN1	3'	TCCTCAGAGCAATTCTCTGTA 17423	_ TCAC A
		TACA AGA TG CTCTGAGGA	
		ATGT TCT AC GAGACTCCT	
		C TA__ _	
GAM1785 BMF	5'	CCTCAGAGTCAAACCTTTGTG 54280	ATCAC
		TACAAG TGA CTCTGAGG	
		GTGTTT ACTGAGACTCC	
		CAA__	
GAM1785 DDX33	3'	GTCCTCAGTGCGTGACCCTGT 39786	AGA T ACT
		ACA TCAC G CTGAGGAC	
		TGT AGTG C GACTCCTG	
		CCC _GT_	
GAM1785 FLJ20364	3'	CCTCAGAGCCATGTATTTG 35528	AT C A
		CAAG CA TG CTCTGAGG	
		GTTT GT AC GAGACTCC	
		AT _ C	
GAM1785 HMGN4	3'	TCCTTTCCCCAGTGATTTGTA 22034	A ACTCT
		TACA GATCACTG GAGGA	
		ATGT TTAGTGAC TTCCT	
		_ CCCT_	
GAM1785 KIAA0449	3'	TCCCCAGCACTCATGATCTTG 34639	C CT_ A
		CAAGATCA TGA CTG GGA	
		GTTCTAGT ACT GAC CCT	
		_ CAC C	
GAM1785 KIAA1061	3'	GTCCTCAGAGTGCAATTCCTG 71723	A TCAC _
		CA GA TG ACTCTGAGGAC	

		GT CT AC TGAGACTCCTG	
		C TT__ G	
GAM1785 KIAA1535	3'	GTCCTCAGCTCAAGAATCCTGT 80214	A CAC CT
	A	TACA GAT TGA CTGAGGAC	
		ATGT CTA ACT GACTCCTG	
		C AGA C_	
GAM1785 LCHN	3'	TCCTCAGAGTATGTCTTG 87478	CACTG
		CAAGAT ACTCTGAGGA	
		GTTCTG TGAGACTCCT	
		TA__	
GAM1785 MAGEH1	3'	TCATAATCTATGATCTTGTA 26772	CT CTC
		TACAAGATCA GA TGA	
		ATGTTCTAGT CT ACT	
		AT AAT	
GAM1785 LOC154789	5'	TCCTCAGAGCTCTCCTGTG 82034	A TCACT _
		TACA GA GA CTCTGAGGA	
		GTGT CT CT GAGACTCCT	
		C ____ C	
GAM1785 LOC197201	3'	TCCTCAGAAGGTATTTGTA 89289	ATC GAC
		TACAAG ACT TCTGAGGA	
		ATGTTT TGG AGACTCCT	
		A__ A__	
GAM1785 LOC255193	3'	CCTCAGAGTCAGGCCTGTA 97103	AGATCA
		TACA CTGACTCTGAGG	
		ATGT GACTGAGACTCC	
		CCG__	
GAM1785 LOC96597	5'	TCCCCAGAATTCTCTTGT 67468	TCACT C_ A
		ACAAGA GA TCTG GGA	
		TGTTCT CT AGAC CCT	
		____ TA C	
GAM1786 DLG5	5'	CAGCAGCAGCAGGTGTTGA 83811	CG TCGGAA
		TCAACACC GCT GCTG	
		AGTTGTGG CGA CGAC	
		A_ CGA__	
GAM1786 KCNK7	5'	CCAGCCCCTCCCAGGTGCCTGA 20345	A_ C CTTC AA
		TCA CACC GG GG GCTGG	
		AGT GTGG CC CC CGACC	
		CC A CT__ C_	
GAM1786 KCNK7	5'	CCAGCCCCTCCCAGGTGCCTGA 54055	A_ C CTTC AA
		TCA CACC GG GG GCTGG	

		AGT GTGG CC CC CGACC		
		CC A CT__ C_		
GAM1786 KCNK7	5'	CCAGCCCCTCCCAGGTGCCTGA 54062	A_	C CTTC AA
		TCA CACC GG GG GCTGG		
		AGT GTGG CC CC CGACC		
		CC A CT__ C_		
GAM1786 KCNK7	5'	CCAGCCCCTCCCAGGTGCCTGA 54232	A_	C CTTC AA
		TCA CACC GG GG GCTGG		
		AGT GTGG CC CC CGACC		
		CC A CT__ C_		
GAM1786 TNFRSF6B	5'	CCAGCCAGTGCCGGGTGCTGG 33596	A	TTCGGAA
		TCA CACCCGGC GCTGG		
		GGT GTGGGCCG CGACC		
		C TGAC__		
GAM1786 CARD9	3'	CCAGCCGGACTGCCGGGCATTG 42546	CA	__ GAA
G		TCAA CCCGGC TTCG GCTGG		
		GGTT GGGCCG AGGC CGACC		
		AC TC __		
GAM1786 CARD9	3'	CCAGCCGGACTGCCGGGCATTG 54474	CA	__ GAA
G		TCAA CCCGGC TTCG GCTGG		
		GGTT GGGCCG AGGC CGACC		
		AC TC __		
GAM1786 FLJ21438	3'	CTGGCTGGGCGCGGCACTGA 62192	ACA	CGGA TG
		TCA CCCGGCTT AGC G		
		AGT GGGCCGGG TCG C		
		CAC __ GT		
GAM1786 KIAA1560	3'	CCAGCTTCTGGCTCAAGAGTTG 64849	ACCC_	TT
A		TCAAC GGC CGGAAGCTGG		
		AGTTG TCG GTCTTCGACC		
		AGAAC __		
GAM1786 MAPK11	3'	CCAGGGAAGCCTGGGTGT 58100	_	GGAAG
		ACACCC GGCTTC CTGG		
		TGTGGG CCGAAG GACC		
		T G__		
GAM1786 MAPK11	3'	CCAGGGAAGCCTGGGTGT 12313	_	GGAAG
		ACACCC GGCTTC CTGG		
		TGTGGG CCGAAG GACC		
		T G__		
GAM1786 LOC130497	3'	CCAGCCAAGAGCCGGGCGTT 75446	A	CGGAA
		AAC CCCGGCTT GCTGG		

			TTG GGGCCGAG CGACC		
			C AAC__		
GAM1786	LOC203052	3'	CCAGCTCTGTGCCGGGTG 92076	TT	A
			CACCCGGC CGGA GCTGG		
			GTGGGCCG GTCT CGACC		
			T_ _		
GAM1786	LOC256905	5'	CCAGGGATAGCCGGGTATTGA 98659	C	TCGGAAG
			TCAA ACCCGGCT CTGG		
			AGTT TGGGCCGA GACC		
			A TAGG__		
GAM1786	LOC91409	3'	CAGCTTCCAATATGTTGA 66570	CCC	CTTC
			TCAACA GG GGAAGCTG		
			AGTTGT TC CCTTCGAC		
			A_ A__		
GAM1787	ADCY2	3'	CTGGGAGAACTAACAGAGGAGA 65649	GCC_	T
			TCTCCTT AGTT CTCCCAG		
			AGAGGAG TCAA GAGGGTC		
			ACAA _		
GAM1787	ARF4L	5'	GGGAAAGGCTCGAGGAGA 70390	CC	C
			TCTCCTTG AGTTT TCCC		
			AGAGGAGC TCGGA AGGG		
			_ A		
GAM1787	ARNT2	3'	TGCTGGGAAAATGGGCAAGCAG 30092	C	A C
	A		TCT CTTGCC GTTT TCCCAGCA		
			AGA GAACGG TAAA AGGGTCGT		
			C G _		
GAM1787	AXIN2	5'	TGCTGAGAGGAACTGGAAGAAG 17391	C G	C
	A		TCT CTT CCAGTTTCTC CAGCA		
			AGA GAA GGTCAAGGAG GTCGT		
			A _ A		
GAM1787	CDK5R2	3'	GCCAGGAGAACTGCAG 15449	C	CA
			TTGC AGTTTCTCC GC		
			GACG TCAAAGAGG CG		
			_ AC		
GAM1787	CHRM1	3'	GCTGGGAGAAAAGCCAGATGA 96434	TC T	CAG
			TC CT GC TTTCTCCCAGC		
			AG GA CG AAAGAGGGTCG		
			TA C A__		
GAM1787	CPT1A	3'	CTGGAGCTGCTGGGAAGGA 10290	G TT	C
			TCCTT CCAGT CTCC AG		

		AGGAA GGTCG GAGG TC	
		G TC _	
GAM1787 CRP	3'	TGCTGGGAAACGGTCCAAAAGA 72084	CCTT_ A TC
		TCT GCC GTT TCCCAGCA	
		AGA TGG CAA AGGGTCGT	
		AAACC _ _	
GAM1787 CSPG4	3'	GCTAAGAGGGCAAGGAGA 10325	AGTTT CC
		TCTCCTTGCC CTC AGC	
		AGAGGAACGG GAG TCG	
		_ _ _ AA	
GAM1787 DLG5	5'	TGCTGGGAGAGCCAACAAGGAG 83825	CCA T
G		TCTCCTTG GTT CTCCCAGCA	
		GGAGGAAC CGA GAGGGTCGT	
		AAC _	
GAM1787 DLX4	5'	GCCGGAGGCTTGAAAAGAGA 57112	CTTG TT CA
		TCTC CCAG TCTCC GC	
		AGAG GGTT GGAGG CG	
		AAAA C_ C_	
GAM1787 EDN1	3'	TGCTGGTTCTGACTGGCAAAG 10480	_ TCTC_
GA		TCCTT GCCAGTT CCAGCA	
		AGGAA CGGTCAG GGTCGT	
		A TCCTT	
GAM1787 EPHB2	3'	GCTGAAAATGACAGGGAGA 16699	C G TCCC
		TCTCCTTG CA TTTC AGC	
		AGAGGGAC GT AAAG TCG	
		A A _	
GAM1787 FS	5'	GCCGGGCCCGGCAGCAAGGAG 42081	CA TCT A
		CTCCTTGC GTT CCC GC	
		GAGGAACG CGG GGG CG	
		A_ CC_ C	
GAM1787 GTF2I	3'	TGCTGGGAAATGACAGGGA 53383	C GTTTC
		TCCTTG CA TCCCAGCA	
		AGGGAC GT AGGGTCGT	
		A AA_	
GAM1787 GTF2I	3'	TGCTGGGAAATGACAGGGA 53385	C GTTTC
		TCCTTG CA TCCCAGCA	
		AGGGAC GT AGGGTCGT	
		A AA_	
GAM1787 HAS3	3'	TGCCAGGAGGAACAAAGAGA 19233	C GCCA CA
		TCTC TT GTTTCTCC GCA	

			AGAG AA CAAGGAGG CGT		
			A ____ AC		
GAM1787 MBNL	5'	GCCAGGAAATCAAGGAGG	41068	CCA	CCCA
		TCTCCTTG GTTTCT GC			
		GGAGGAAC TAAAGG CG			
		____ AC__			
GAM1787 MEST	5'	GCTGACGCCTGGCAGGGAGA	70460	TTTCTCC	
		TCTCCTTGCCAG CAGC			
		AGAGGGACGGTC GTCG			
		CGCA____			
GAM1787 NRCAM	3'	GCTGGGAAAAGAAGGA	18455	GCCAG C	
		TCCTT TTT TCCCAGC			
		AGGAA GAA AGGGTCG			
		____ A			
GAM1787 PCDHA1	3'	TGCCAAGACTTCTGCTGGCAAG	38786	T	TTC__ CCA
GGA		TC CCTTGCCAGT TC GCA			
		AG GGAACGGTCG AG CGT			
		____ TCTTC AAC			
GAM1787 PCDHA1	3'	TGCCAAGACTTCTGCTGGCAAG	49416	T	TTC__ CCA
GGA		TC CCTTGCCAGT TC GCA			
		AG GGAACGGTCG AG CGT			
		____ TCTTC AAC			
GAM1787 PCDHA10	3'	TGCCAAGACTTCTGCTGGCAAG	38792	T	TTC__ CCA
GGA		TC CCTTGCCAGT TC GCA			
		AG GGAACGGTCG AG CGT			
		____ TCTTC AAC			
GAM1787 PCDHA10	3'	TGCCAAGACTTCTGCTGGCAAG	49857	T	TTC__ CCA
GGA		TC CCTTGCCAGT TC GCA			
		AG GGAACGGTCG AG CGT			
		____ TCTTC AAC			
GAM1787 PCDHA11	3'	TGCCAAGACTTCTGCTGGCAAG	38794	T	TTC__ CCA
GGA		TC CCTTGCCAGT TC GCA			
		AG GGAACGGTCG AG CGT			
		____ TCTTC AAC			
GAM1787 PCDHA12	3'	TGCCAAGACTTCTGCTGGCAAG	38800	T	TTC__ CCA
GGA		TC CCTTGCCAGT TC GCA			
		AG GGAACGGTCG AG CGT			
		____ TCTTC AAC			
GAM1787 PCDHA13	3'	TGCCAAGACTTCTGCTGGCAAG	38801	T	TTC__ CCA
GGA		TC CCTTGCCAGT TC GCA			

			AG GGAACGGTCG	AG	CGT		
			—	TCTTC	AAC		
GAM1787	PCDHA2	3'	TGCCAAGACTTCTGCTGGCAAG	38807	T	TTC__	CCA
	GGA		TC CCTTGCCAGT	TC	GCA		
			AG GGAACGGTCG	AG	CGT		
			—	TCTTC	AAC		
GAM1787	PCDHA3	3'	TGCCAAGACTTCTGCTGGCAAG	38809	T	TTC__	CCA
	GGA		TC CCTTGCCAGT	TC	GCA		
			AG GGAACGGTCG	AG	CGT		
			—	TCTTC	AAC		
GAM1787	PCDHA4	3'	TGCCAAGACTTCTGCTGGCAAG	38815	T	TTC__	CCA
	GGA		TC CCTTGCCAGT	TC	GCA		
			AG GGAACGGTCG	AG	CGT		
			—	TCTTC	AAC		
GAM1787	PCDHA5	3'	TGCCAAGACTTCTGCTGGCAAG	38817	T	TTC__	CCA
	GGA		TC CCTTGCCAGT	TC	GCA		
			AG GGAACGGTCG	AG	CGT		
			—	TCTTC	AAC		
GAM1787	PCDHA6	3'	TGCCAAGACTTCTGCTGGCAAG	38823	T	TTC__	CCA
	GGA		TC CCTTGCCAGT	TC	GCA		
			AG GGAACGGTCG	AG	CGT		
			—	TCTTC	AAC		
GAM1787	PCDHA6	3'	TGCCAAGACTTCTGCTGGCAAG	49821	T	TTC__	CCA
	GGA		TC CCTTGCCAGT	TC	GCA		
			AG GGAACGGTCG	AG	CGT		
			—	TCTTC	AAC		
GAM1787	PCDHA7	3'	TGCCAAGACTTCTGCTGGCAAG	38825	T	TTC__	CCA
	GGA		TC CCTTGCCAGT	TC	GCA		
			AG GGAACGGTCG	AG	CGT		
			—	TCTTC	AAC		
GAM1787	PCDHA8	3'	TGCCAAGACTTCTGCTGGCAAG	38831	T	TTC__	CCA
	GGA		TC CCTTGCCAGT	TC	GCA		
			AG GGAACGGTCG	AG	CGT		
			—	TCTTC	AAC		
GAM1787	PCDHA9	3'	TGCCAAGACTTCTGCTGGCAAG	49854	T	TTC__	CCA
	GGA		TC CCTTGCCAGT	TC	GCA		
			AG GGAACGGTCG	AG	CGT		
			—	TCTTC	AAC		
GAM1787	PCDHAC1	3'	TGCCAAGACTTCTGCTGGCAAG	38782	T	TTC__	CCA
	GGA		TC CCTTGCCAGT	TC	GCA		

AG GGAACGGTCG AG CGT
 _ TCTTC AAC
 GAM1787 PCDHAC2 3' TGCCAAGACTTCTGCTGGCAAG 38785 T TTC__ CCA
 GGA TC CCTTGCCAGT TC GCA
 || ||||| || |||
 AG GGAACGGTCG AG CGT
 _ TCTTC AAC
 GAM1787 PEA15 3' GCTGGAAGAAGGAAGAAG 15011 C G AGT C
 CT CTT CC TTCT CCAGC
 || ||| || |||||
 GA GAA GG AAGA GGTCG
 A _ _ A
 GAM1787 PKHD1 3' GCTGGGACAACATAAGAAGA 57715 C GCC TC
 TCT CTT AGTT TCCCAGC
 ||| ||| |||||
 AGA GAA TCAA AGGGTCG
 A _ _ C_
 GAM1787 PLCB2 3' CTGGGACATTTAGCAAGGAGG 17112 C TTTC
 TCTCCTTGC AG TCCCAG
 ||||| || |||||
 GGAGGAACG TT AGGGTC
 A TAC_
 GAM1787 PRX 3' GCTAAAATGGGCAAGGG 40897 A CTCCC
 TCCTTGCC GTTT AGC
 ||||| ||| |||
 GGGAACGG TAAA TCG
 G A____
 GAM1787 TACC1 3' CTGAGAAGAGGAGTGCAAGGAG 21871 CAG _ C
 A TCTCCTTGC TTTCT C CAG
 ||||| ||||| |||
 AGAGGAACG GGAGA G GTC
 TGA A A
 GAM1787 VCX 5' CTGGGAGAAGGAAGTGAGA 69701 _ G AGT
 TCTC CTT CC TTCTCCCAG
 ||| ||| || |||||
 AGAG GAA GG AAGAGGGTC
 T _ _
 GAM1787 ABHD2 5' GCTCTAAACTGGCAGGAGA 23795 T CTCCC
 TCTCCT GCCAGTTT AGC
 ||||| ||||| |||
 AGAGGA CGGTCAAA TCG
 _ TC____
 GAM1787 AIF1 5' TGCTGAAGGCCAGCAGGAAGA 17929 C CAGTT CC
 TCT CTTGC TCT CAGCA
 ||| |||| ||| |||||
 AGA GGACG GGA GTCGT
 A ACCC_ A_
 GAM1787 C1orf34 3' GCCGACCTGCTCAGCAAGGAGA 61312 C_ TTC CCA
 TCTCCTTGC AGT TC GC
 ||||| ||| || ||

AGAGGAACG TCG AG CG
 AC TCC C__
 GAM1787 CENTG3 3' TGCTGAGAGGACGAAGCCAAGG 50048 CCA _ _
 A TCCTTG GTTTC TCC CAGCA
 ||||| ||||| || |||||
 AGGAAC CGAAG AGG GTCGT
 _ C AGA
 GAM1787 dJ383J4.3 3' TGCTGAAAGAGACTGCAGGAGA 67499 T C CC
 TCTCCT GC AGTTTCT CAGCA
 ||||| || ||||| |||||
 AGAGGA CG TCAGAGA GTCGT
 _ _ AA
 GAM1787 DKFZP434B168 5' GGAAGAAAAACCAGCAAGAAGG 31870 C CAG__ C
 TCT CTTGC TTTCT CC
 || ||||| ||||| ||
 GGA GAACG AAAGA GG
 A ACCAA A
 GAM1787 DKFZP434F0318 3' CTGGGAGAAAAAAGAGAGGA 48753 GCCAG
 TCCTT TTTCTCCCAG
 ||||| |||||
 AGGAG AAAGAGGGTC
 AGAAA
 GAM1787 DKFZP564K0822 3' GCTGGGAAAAGACAGGAGA 95698 TGCCA C_
 TCTCCT GTTT TCCCAGC
 ||||| ||| |||||
 AGAGGA CAGA AGGGTCG
 _ AA
 GAM1787 DKFZP586M1120 3' CTGGGAAACCCAAAGGAGA 49280 GCCA TC
 TCTCCTT GTT TCCCAG
 ||||| ||| |||||
 AGAGGAA CAA AGGGTC
 ACC_ _
 GAM1787 EPB41L1 3' GAACTGGCCCAGCTAAGGAGA 71108 _
 TCTCCTT GCCAGTTT
 ||||| |||||
 AGAGGAA CGGTCAAG
 TCGACC
 GAM1787 FLJ10901 3' GCTGGAAAAAAGTGTTCATAG 37368 CT C__ CTC
 AGG TCTC TG CAGTTT CCAGC
 |||| || ||||| |||||
 GGAG AC GTCAAA GGTCG
 AT TTT AAA
 GAM1787 FLJ12568 3' TGCTGGAAGAACTAGTGAAGA 47143 C TG C C
 GA TCTC T C AGTTTCT CCAGCA
 |||| | ||||| |||||
 AGAG A G TCAAAGA GGTCGT
 A GT A A
 GAM1787 FLJ13441 3' TGCTGGGAGCTACAGCAAG 43920 CA TT
 CTTGC GT CTCCCAGCA
 |||| || |||||

	GAACG CA GAGGGTCGT	
	A_ TC	
GAM1787 FLJ20424 3'	GGAAAATCTAGCAAGGAGA 35617	C T C
	TCTCCTTGC AG TT TCC	
	AGAGGAACG TC AA AGG	
	A T A	
GAM1787 FLJ31762 3'	TGCCAAAAACCAGCACAAGGAG 58767	__ CA CTCCCA
A	TCTCCT TGC GTTT GCA	
	AGAGGA ACG CAAA CGT	
	AC AC AAC__	
GAM1787 GPS2 5'	GCCGGAAGCTGCGAGGAGA 16889	C CCCA
	TCTCCTTGC AGTTTCT GC	
	AGAGGAGCG TCGAAGG CG	
	_ C__	
GAM1787 KIAA0286 3'	TGCTGGBAATAAACAAAGCAG 68862	CA_ C_
	TTGC GTTT TCCCAGCA	
	GACG CAAA AGGGTCGT	
	AAA TA	
GAM1787 KIAA0603 3'	TGCTGGGTATAGGCAAGGA 29837	AGTTTCT
	TCCTTGCC CCCAGCA	
	AGGAACGG GGGTCGT	
	ATAT__	
GAM1787 KIAA0987 3'	GAGAAGGTGGTGCAGGAGA 25508	_ G
	TCTCCT TGCCA TTTCTC	
	AGAGGA GTGGT GAAGAG	
	C G	
GAM1787 KIAA1189 3'	CTGGGAGGGGCTAGAAGA 72507	C TGCC TT
	TCT CT AGT CTCCCAG	
	AGA GA TCG GAGGGTC	
	A ____ GG	
GAM1787 KIAA1609 5'	GGAAGCCCGGCAGGGAGA 74708	A_
	TCTCCTTGCC GTTTCT	
	AGAGGGACGG CGAAGG	
	CC	
GAM1787 KIAA1737 3'	CTGAGTGGCAGGGAGA 67940	G TTCTCC
	TCTCCTTGCCA T CAG	
	AGAGGGACGGT A GTC	
	G _____	
GAM1787 MGC14436 5'	GCCGGGAGAGACAGGA 52928	TGCCA A
	TCCT GTTTCTCCC GC	

			AGGA CAGAGAGGG CG		
			_____ C		
GAM1787	MGC2941	3'	GCCAGAAATGCAAGGA 44415	CA	CCCA
			TCCTTGC GTTTCT GC		
			AGGAACG TAAAGA CG		
			_____ C_____		
GAM1787	MRPS27	3'	CTGGGAGAAACCAAGGCTGA 31328	T_	CCA
			TC CCTTG GTTTCTCCCAG		
			AG GGAAC CAAAGAGGGTC		
			TC _____		
GAM1787	MRPS27	3'	CTGGGAGAAATTCAGGA 31329	TGCC	
			TCCT AGTTTCTCCCAG		
			AGGA TTAAAGAGGGTC		
			C_____		
GAM1787	MUC17	3'	TGCTGGGAGATTCTCAAATAGA 95928	CC	CC TT
			TCT TTG AG TCTCCCAGCA		
			AGA AAC TC AGAGGGTCGT		
			TA _ TT		
GAM1787	PIGPC1	3'	TGCTGAGATGGACTCCAGAAGA 42351	C	GCC_ TC C
	AGA		TCT CTT AGTT TC CAGCA		
			AGA GAA TCAG AG GTCGT		
			A GACC GT A		
GAM1787	RP4-622L5	3'	TGCTGGGGTCTGGCATAGA 39431	CT	TTTC
			TC TGCCAG TCCCAGCA		
			AG ACGGTC GGGGTCGT		
			AT T_____		
GAM1787	STX3A	3'	CTGGGAGAATAAAATGAGA 16068	C	GCCAGT
			TCTC TT TTCTCCCAG		
			AGAG AA AAGAGGGTC		
			T AAT_____		
GAM1787	TRPV5	5'	GCCAGTGTCTGCAAGGAGA 39524	C	TTT CCCA
			TCTCCTTGC AG CT GC		
			AGAGGAACG TC GA CG		
			_ TGT C_____		
GAM1787	TRPV6	5'	TGCTGGGAGACTCCCAAGGA 38464	CC	TT
			TCCTTG AG TCTCCCAGCA		
			AGGAAC TC AGAGGGTCGT		
			CC _____		
GAM1787	TUSP	5'	TGGTTCTGAAACAACAAGGAGA 40035	CCA	TC_____
			TCTCCTTG GTTTC CCA		

AGAGGAAC CAAAG GGT
 AA_ TCTT
 GAM1787 LOC115286 3' TGCTAAGATACCGGCATGGAGA 73766 T A T CCC
 TCTCC TGCC GT TCT AGCA
 |||| |||| || ||||
 AGAGG ACGG CA AGA TCGT
 T C T A__
 GAM1787 LOC145761 5' TGCCAAAAAGAGGCCCTGGCAG 84485 T TT CCA__
 GAGA TCTCCT GCCAG TCTC GCA
 |||| |||| |||| ||||
 AGAGGA CGGTC GGAG CGT
 _ CC AAAAAC
 GAM1787 LOC146445 3' TGCTAGGAAAACTGGTGA 84685 TG C C
 T CCAGTTT TCC AGCA
 | |||| || ||||
 A GGTC AAA AGG TCGT
 GT A A
 GAM1787 LOC149721 3' TGCTGGGGACAGCAAG 80321 CA TCT
 CTTGC GTT CCCAGCA
 |||| || |||| ||||
 GAACG CAG GGGTCGT
 A_ __
 GAM1787 LOC151963 3' TTGAGAAAACTGGCAGGAAGA 81220 C C C
 TCT CTTGCCAGTTT TC CAG
 || |||| |||| || ||||
 AGA GGACGGTCAAA AG GTT
 A A A
 GAM1787 LOC153514 5' TGCCAGGAAATTGCCAAG 81713 C C CCA
 CTTG CAGTTTCT GCA
 |||| |||| || ||||
 GAAC GTTAAAGG CGT
 C AC__
 GAM1787 LOC153733 5' GCTGGGAACACAAGGAGA 81801 CCA TTC
 TCTCCTTG GT TCCCAGC
 |||| || || |||| ||||
 AGAGGAAC CA AGGGTCG
 A_ __
 GAM1787 LOC154789 5' TGCTCTCAACTAGCAGAGAGA 82035 C C TCTCCC
 TCTC TTGC AGTT AGCA
 |||| |||| |||| ||||
 AGAG GACG TCAA TCGT
 A A CTC__
 GAM1787 LOC222193 3' TGCTGAAAAGTGGGAAGGAGA 95845 G G CTCC
 TCTCCTT CCA TTT CAGCA
 |||| || || |||| ||||
 AGAGGAA GGT AAA GTCGT
 G G A__
 GAM1787 LOC245771 5' GCTGGAAAAAAGTGTTCATAG 94482 CT C__ CTC
 AGG TCTC TG CAGTTT CCAGC
 |||| || |||| |||| ||||

GGAG AC GTCAAA GGTCG
AT TTT AAA
GAM1787 LOC253482 3' TGCTAAGCTTTTGGCAAGAGA 97870 C TTT CCC
TCTC TTGCCAG CT AGCA
||||| || ||||
AGAG AACGGTT GA TCGT
_ TTC A_
GAM1787 LOC255565 3' TGCCAGAAGTTGGGCAGAGAGA 96805 C AG_ CCCA
TCTC TTGCC TTTCT GCA
||||| |||| ||
AGAG GACGG GAAGA CGT
A GTT C_
GAM1787 LOC90010 3' TGCCAGAAGTTGGGCAGAGAGA 61724 C AG_ CCCA
TCTC TTGCC TTTCT GCA
||||| |||| ||
AGAG GACGG GAAGA CGT
A GTT C_
GAM1788 SCAMP1 3' GCTAAATAAATATTCTCC 54500 T C
GGA AATATT ATTTAGC
||| ||||| |||||
CCT TTATAA TAAATCG
C A
GAM1788 SCAMP1 3' GCTAAATAAATATTCTCC 54501 T C
GGA AATATT ATTTAGC
||| ||||| |||||
CCT TTATAA TAAATCG
C A
GAM1788 NX-17 3' TGAATATCAGCCCCTAATA 40706 ATA_
TATTAGGG ATATTCA
||||| |||||
ATAATCCC TATAAGT
CGAC
GAM1788 LOC161589 3' GCTAAATGAATATTATCCCTAA 83159
TA TATTAGGGATAATATTCATTTAGC
|||||
ATAATCCCTATTATAAGTAAATCG
GAM1789 ACP 3' GATTAGAAAAATACTGGATA 67387 CTCCG
TATCCAGTAT TGATT
||||| ||||
ATAGGTCATA ATTAG
AAAAG
GAM1789 CYP51 3' AGGTAATTGGCAGATTCT 7609 T _ GT
AG ATCT CC GATTACCT
|| ||| || |||||
TC TAGA GG TTAATGGA
T C _
GAM1789 DCN 3' TAAAAGCTAGATACTGGA 10389 CC GA
TCCAGTATCT GT TTA
||||| || |||

		AGGTCATAGA CG AAT	
		T_ AA	
GAM1789 DCN	3'	TAAAAGCTAGATACTGGA 56869	CC GA
		TCCAGTATCT GT TTA	
		AGGTCATAGA CG AAT	
		T_ AA	
GAM1789 SMT3H1	3'	AGTTGAAGGGAAAATACTGGA 60627	___ CG
		TCCAGTA TCTC TGATT	
		AGGTCAT AGGG GTTGA	
		AAA AA	
GAM1789 KIAA0429	3'	AGGTAATCACAATAGATA 29241	CC_
		TATCT GTGATTACCT	
		ATAGA CACTAATGGA	
		TAA	
GAM1789 KIAA0993	3'	GTAAATTGAAGATACTGG 64821	C TGA
		CCAGTATCT CG TTAC	
		GGTCATAGA GT AATG	
		A TA_	
GAM1789 KIAA1432	5'	GATGAGGAAAATACTGGAT 67304	C_ GTG
		ATCCAGTAT TCC ATT	
		TAGGTCATA AGG TAG	
		AA AG_	
GAM1789 KIAA1600	3'	AGGCATTAAGAGATATTAGATA 71939	C CG TA
		TATC AGTATCTC TGAT CCT	
		ATAG TTATAGAG ATTA GGA	
		A A_ C_	
GAM1789 LOC145009	3'	AGGTAATTGGCAGATTCT 60967	T _ GT
		AG ATCT CC GATTACCT	
		TC TAGA GG TTAATGGA	
		T C _	
GAM1789 LOC150481	3'	AGGTGGTCAAGAGACACTGGA 80693	A CG
		TCCAGT TCTC TGATTACCT	
		AGGTCA AGAG ACTGGTGGGA	
		C A_	
GAM1789 LOC158191	3'	AGGTGGTCAAGAGACACTGGA 82664	A CG
		TCCAGT TCTC TGATTACCT	
		AGGTCA AGAG ACTGGTGGGA	
		C A_	
GAM1789 LOC196319	3'	AGGCTTATGAAGATGCTGGA 91189	C TTA
		TCCAGTATCT CGTGA CCT	

		AGGTCGTAGA GTATT GGA		
		A C__		
GAM1789	LOC90141	3' AGGTAATTCCAAAATACTGG 62298	CTCCGT	
		CCAGTAT GATTACCT		
		GGTCATA TTAATGGA		
		AAACC_		
GAM1789	LOC90786	5' AGGTGGGGACCAGGGATACT 64726	C_ GA	
		AGTATCTC GT TTACCT		
		TCATAGGG CA GGTGGA		
		AC GG		
GAM1789	LOC91549	3' AGGTTTAGGAGGAGATACTAAG 67023	C_ GTGATT	
	ATA	TATC AGTATCTCC ACCT		
		ATAG TCATAGAGG TGGA		
		AA AGGATT		
GAM1790	CCR9	3' CTGACCACACCCACAAGGC 49123	__ AC	
		GTC GTGG GTGGTCAG		
		CGG CACC CACCAGTC		
		AA CA		
GAM1790	COL1A1	3' TGACCAACCGAACATGACCAAA 5397	GA __	
		TTTGGTCGTG CG TGGTCA		
		AAACCAGTAC GC ACCAGT		
		AA CA		
GAM1790	SLC20A2	5' TGA CTGAACACAACCAAA 23122	C GACG	
		TTTGGT GTG TGGTCA		
		AAACCA CAC GTCAGT		
		A AA__		
GAM1790	UBE2L3	3' TGGCTGCTCCAAAACCAAA 13967	CG C TG	
		TTTGGT TGGAG GTCA		
		AAACCA ACCT C CGGT		
		AA _GT		
GAM1790	FLJ14640	5' GCTGAGGCCTCGACCAAA 52549	T ACGTGG	
		TTTGGTCG GG TCAGC		
		AAACCAGC CC AGTCG		
		T GG__		
GAM1790	KIAA1596	3' TGGCTGTGTCCCAACCAAA 71481	CGT TG	
		TTTGGT GGACG GTCA		
		AAACCA CCTGT CGGT		
		ACC GT		
GAM1790	KIAA1854	3' GCTGACACCCACGTCCAAA 72210	T AC G	
		TTTGG CGTGG GTG TCAGC		

AAACC GCACC CAC AGTCG
 T _ _
 GAM1790 PDZD2 5' GAGCCATGGACGTCCACAACCA 81724 C T_____ TCAG
 AG TTTGGT GTGGACG GG C
 ||||| ||||| || |
 GAACCA CACCTGC CC G
 A AGGT__A GAC
 GAM1790 TTYH2 3' GCTGGGATTCCCGACCAAA 51978 T CGTGG
 TTTGGTCG GGA TCAGC
 ||||| || |||||
 AAACCAGC CCT GGTCG
 _ TAG_
 GAM1790 LOC204084 3' GGCCACCTCCACGACCAA 90999 C
 TTGGTCGTGGA GTGGTC
 ||||| |||||
 AACCAGCACCT CACCGG
 C
 GAM1790 LOC91759 5' GGCTGACCAAGCGCCAAA 67694 T GGACG
 TTTGG CGT TGGTCAGCC
 ||||| || |||||
 AAACC GCG ACCAGTCGG
 _ A_
 GAM1791 ILF1 3' GCCGCCCTCACAGGACCCAC 16921 CAC AGC
 GTG TTTG GAGGGCGGC
 || ||||| |||||
 CAC GGAC CTCCCGCCG
 CCA A_
 GAM1791 PSA 5' CCGCCCTCGCCGCGGCAC 41260 ACTT A
 GTGC TG GCGAGGGCGG
 |||| || |||||
 CACG GC CGCTCCCGCC
 CC__ _
 GAM1791 PSA 5' CCGCCCTCGCCGCGGCAC 55222 ACTT A
 GTGC TG GCGAGGGCGG
 |||| || |||||
 CACG GC CGCTCCCGCC
 CC__ _
 GAM1791 CHODL 5' GCCGCCCTCGCTCCACGCA 46885 ACTTT
 TGC GAGCGAGGGCGGC
 || |||||
 ACG CTCGCTCCCGCCG
 CAC_
 GAM1791 DKFZP564I1171 5' GCCGCCCTCGTGCCACGCAC 72047 ACTT A_
 GTGC TG GCGAGGGCGGC
 |||| || |||||
 CACG AC TGCTCCCGCCG
 C__ CG
 GAM1791 KIAA0420 3' CCACCTGCTCTCAAAAGCACTA 64084 AC CGA C
 TAGTGC TTTGAG GGG GG
 ||||| ||||| || ||

		ATCACG AAACTC TCC CC	
		A_ TCG A	
GAM1791	LOC149050 5'	CCGCCCTCGCTGCCGCAC 61060	ACTTTG
		GTGC AGCGAGGGCGG	
		CACG TCGTCCCGCC	
		CCG__	
GAM1791	LOC150244 5'	GCCGCCCTCGCCCTGCAC 80551	CTTTGA
		GTGCA GCGAGGGCGGC	
		CACGT CGTCCCGCCG	
		CC__	
GAM1791	LOC152106 5'	GCCGCCCTCAACCGACGCAT 70597	ACT AGC
		GTGC TTG GAGGGCGGC	
		TACG AGC CTCCCGCCG	
		C__ CAA	
GAM1791	LOC153474 5'	GCCGCCCTCGTGCCACGCAC 81704	ACTT A_
		GTGC TG GCGAGGGCGGC	
		CACG AC TGCTCCCGCCG	
		C__ CG	
GAM1791	LOC257354 3'	CCACCTGCTCTCAAAAGCACTA 96786	AC CGA C
		TAGTGC TTTGAG GGG GG	
		ATCACG AAACTC TCC CC	
		A_ TCG A	
GAM1792	BACE 3'	ACCTAAAATTAAGAAGTACAAT 58077	AGAA C
	A	TATTGTATTT GGTTT AGGT	
		ATAACATGAA TTAAA TCCA	
		GAA_ A	
GAM1792	BACE 3'	ACCTAAAATTAAGAAGTACAAT 25026	AGAA C
	A	TATTGTATTT GGTTT AGGT	
		ATAACATGAA TTAAA TCCA	
		GAA_ A	
GAM1792	PRKCSH 3'	ACCTGTGACCTCAATACAATA 12292	TA A T
		TATTGTATT GA GGTT CAGGT	
		ATAACATAA CT CCAG GTCCA	
		_ _ T	
GAM1792	SIGLEC6 3'	AGACCCTCCAAATACAGTA 60603	A A
		TATTGTATTT GA GGTTT	
		ATGACATAAA CT CCAGA	
		C C	
GAM1792	TERF1 3'	ACCTGATGCCTAAATACAA 34386	AGA T
		TTGTATTT AGGT TCAGGT	

			AACATAAA TCCG AGTCCA		
			____ T		
GAM1792	FLJ20079	3'	ACCTACAGGTTCTGAATACAA 34966		GGTTTC
			TTGTATTTAGAA AGGT		
			AACATAAGTCTT TCCA		
			GGACA_		
GAM1792	KIAA1077	3'	CCTTACCCTAAACACAGTA 73286	A	AA TTC
			TATTGT TTTAG GGT AGG		
			ATGACA AAATC CCA TCC		
			C _ T_		
GAM1792	MISS	3'	ACTTTCCCCTTCTAAATAAATA 58638	G	TTTC
			TATT TATTTAGAAGG AGGT		
			ATAA ATAAATCTTCC TTCA		
			_ CCT_		
GAM1792	STK38L	3'	ACCAGCCACTTCTGAATACAAT 69685		GTTTCA
	A		TATTGTATTTAGAAG GGT		
			ATAACATAAGTCTTC CCA		
			ACCGA_		
GAM1792	LOC153894	3'	ACTTTCCCCTTCTAAATAAATA 81875	G	TTTC
			TATT TATTTAGAAGG AGGT		
			ATAA ATAAATCTTCC TTCA		
			_ CCT_		
GAM1793	IL1RAPL2	5'	CAGCTCTCCCCAAAGTCCACAG 34274	A	ACTC
	A		TCTGTGGAC TTG GGAGCTG		
			AGACACCTG AAC TCTCGAC		
			A CCC_		
GAM1793	TM4SF4	5'	CTCCAAGGACACAGTTCACAGA 17256	AT	A_ C
			TCTGTGGAC TG CT GGAG		
			AGACACTTG AC GA CCTC		
			AC AG A		
GAM1793	FLJ31547	5'	CAGCCGCGGTCAATGTTACACAG 59488		TC A_
	A		TCTGTGGACATTGAC GG GCTG		
			AGACACTTGTAAGTCC CC CGAC		
			_ GC		
GAM1793	MGC11271	3'	AGCCCCCATGTCCGCAGA 44492	T	ACTC A
			TCTGTGGACAT G GG GCT		
			AGACGCCTGTA C CC CGA		
			_ C_ _		
GAM1793	LOC118611	5'	CAGCGGAGTCAACATTCACAGA 75993	CA	GGA
			TCTGTGGA TTGACTC GCTG		

	AGACACTT AACTGAG CGAC	
	AC G__	
GAM1793 LOC129892 5'	CAGCTCCAATTTGTCTACAGA 75412	TTGACTC
	TCTGTGGACA GGAGCTG	
	AGACATCTGT CCTCGAC	
	TTAA__	
GAM1793 LOC150271 5'	GGGTAACCAAGGTCCACAGA 86145	A __
	TCTGTGGAC TTG ACTC	
	AGACACCTG AAC TGGG	
	G CAA	
GAM1793 LOC221583 3'	CAGTGAATCAAGTGCCACAGA 93758	A _ C GGA
	TCTGTGG CATT GA TC GCTG	
	AGACACC GTGA CT AG TGAC	
	C A A __	
GAM1794 PROK1 3'	CACCAACCTGCTGGCTTTAGAA 51567	TCAC G AGC
	TTCT GG CAGCA TGGTG	
	AAGA TC GTCGT ACCAC	
	TT__ G CCA	
GAM1794 HSA404617 5'	CACCAGCTCGCCCTTCTGAGAA 73089	CAC_ AGCA
	TTCTT GGGC AGCTGGTG	
	AAGAG CCCG TCGACCAC	
	TCTT C__	
GAM1794 KIAA0431 3'	CACCAGCTTGGGCAACATAAGA 31546	CACGG AG
A	TTCTT GC CAAGCTGGTG	
	AAGAA CG GTTCGACCAC	
	TACAA G_	
GAM1794 PAK6 5'	ACCAGCCTGCAGTGGAGAA 39806	GG CAA
	TTCTTCAC GCAG GCTGGT	
	AAGAGGTG CGTC CGACCA	
	A_ __	
GAM1794 LOC90670 3'	TTTGCTGCCCTGAAGAA 64486	C
	TTCTTCA GGGCAGCAAG	
	AAGAAGT CCCGTCGTTT	
	—	
GAM1795 CEACAM6 3'	CAACTCTTGGTATTACCC 11755	CC A
	GGG ATACCAAGGG TG	
	CCC TATGGTTCTC AC	
	AT A	
GAM1795 FXYD7 3'	CAGCATCCCCGTGTATGGCCC 42096	CAA AT
	GGGCCATAC GGG GTGCTG	

			CCCGGTATG CCC TACGAC		
			TG_ C_		
GAM1795	GCK	3'	TCAGCACACCCCAAGGGACAAC 54297	CCATA AA A	
	CC		GGG CC GGG TGTGCTGA		
			CCC GG CCC ACACGACT		
			AACAG AA C		
GAM1795	GCK	3'	TCAGCACACCCCAAGGGACAAC 54298	CCATA AA A	
	CC		GGG CC GGG TGTGCTGA		
			CCC GG CCC ACACGACT		
			AACAG AA C		
GAM1795	GCK	3'	TCAGCACACCCCAAGGGACAAC 5684	CCATA AA A	
	CC		GGG CC GGG TGTGCTGA		
			CCC GG CCC ACACGACT		
			AACAG AA C		
GAM1795	MUCDHL	5'	AGCCCCTTGTTGACCC 35275	C T ATGT	
			GGG CA ACCAAGGG GCT		
			CCC GT TGGTCCC CGA		
			A _ _		
GAM1795	MUCDHL	5'	AGCCCCTTGTTGACCC 41914	C T ATGT	
			GGG CA ACCAAGGG GCT		
			CCC GT TGGTCCC CGA		
			A _ _		
GAM1795	PRX	3'	CAGCACATCCCCCGCCTGGTCC 40890	TACCAA	
			GGGCCA GGGATGTGCTG		
			CCTGGT CCCTACACGAC		
			CCGCC_		
GAM1795	TEM8	3'	TCAGCACATCAGTCATATGCCC 50828	C CCAAGG	
			GGGC ATA GATGTGCTGA		
			CCCG TAT CTACACGACT		
			_ ACTGA_		
GAM1795	DKFZp586H0623	3'	CATGTCCCCTTGGCAGGCCC 34497	ATA _	
			GGGCC CCAAGGG ATGTG		
			CCCGG GGTCCC TGTAC		
			AC_ C		
GAM1795	FLJ12517	3'	CAGCATTTTTTCAGTTGGCCC 43716	T CA T	
			GGGCCA AC AGGGA GTGCTG		
			CCCGGT TG TTTT TACGAC		
			_ AC _		
GAM1795	FLJ12529	3'	CAGCACGTTTCTCATATAGCCC 46083	C CCA GG	
			GGGC ATA AG ATGTGCTG		

	CCCG TAT TC TGCACGAC		
	A AC_ TT		
GAM1795 FLJ12577	3' CAGCTCCTCAGCATGGCCT 48885	ACCAA	TGT
	GGGCCAT GGA GCTG		
	TCCGGTA TCCT CGAC		
	CGAC_ _		
GAM1795 FLJ20128	3' CAGCTTCCCTTGGTCAGCCC 35081	CAT	TGT
	GGGC ACCAAGGGA GCTG		
	CCCG TGGTTCCCT CGAC		
	AC_ T_		
GAM1795 FLJ22686	3' TCAGCACAGCCCAGCCGGCCC 46955	ATACCAA	A
	GGGCC GGG TGTGCTGA		
	CCCGG CCC ACACGACT		
	CCGA_ G		
GAM1795 HEMK	3' TCAGCCTCTCCTCACTATGGCC 32962	CCAA	TGT
C	GGGCCATA GGA GCTGA		
	CCCGGTAT TCCT CGACT		
	CAC_ CTC		
GAM1795 KIAA0152	3' TCAACACATCCCTTCAGTGA 28981	C ACC	C
C	GGG CAT AAGGGATGTG TGA		
	CTC GTG TTCCCTACAC ACT		
	A AC_ A		
GAM1795 KRTAP4-2	3' CAGCATTCTTGATATGATCC 53519	GC C	GAT
	GG CATA CAAGG GTGCTG		
	CC GTAT GTTCT TACGAC		
	TA A _		
GAM1795 POFUT1	3' TCAAGGTGTCCCCCAATGTGGC 70982	CCAA	TG GC
CC	GGGCCATA GGA T TGA		
	CCCGGTGT CCCT G ACT		
	AACC GT GA		
GAM1795 SEC61A1	3' CAGGCTCCTCCATATGGCCC 26228	CCAA	T G
	GGGCCATA GGA GT CTG		
	CCCGGTAT TCCT CG GAC		
	ACC_ _ _		
GAM1795 LOC146350	5' TCAGTACATCCCTGGCACAGTC 84649	CATA	A
C	GGGC CCA GGGATGTGCTGA		
	CCTG GGT CCCTACATGACT		
	ACAC _		
GAM1795 LOC146506	3' CACAGCCCCCAGTATGGCC 78491	CAA	A
	GGCCATAC GGG TGTG		

CCGGTATG CCC ACAC
 ACC G
 GAM1795 LOC150197 3' CAGCACAGTGCAGTGTGGCCC 80418 CAAGGGA
 GGGCCATAC TGTGCTG
 ||||| |||||
 CCCGGTGTG ACACGAC
 ACGTG__
 GAM1795 LOC158147 3' TCAGTCCCCCTCAGCATGGGCC 70079 G ACCA ATGT
 GG CCAT AGGG GCTGA
 || ||| ||| |||||
 CC GGTA TCCC TGA CT
 G CGAC CC__
 GAM1795 LOC170370 5' CAGCTGGAGGCCTTCAGTACAG 83725 CA CA ATGT__
 CCC GGGC TAC AGGG GCTG
 ||| ||| ||| |||
 CCCG ATG TTCC CGAC
 AC AC GGAGGT
 GAM1795 LOC221935 3' TCAGCGTTGCTGAGTATGGCCC 94207 CA G GT
 GGGCCATAC AG GAT GCTGA
 ||||| || ||| |||||
 CCCGGTATG TC TTG CGACT
 AG G __
 GAM1795 LOC222484 3' CACATGAATCCCTTGGCATGAC 96000 C A __ C
 C GG CAT CCAAGGGAT GTG TG
 || ||| ||||| ||| ||
 CC GTA GGTTCCTA TAC AC
 A C AG _
 GAM1796 ENO1 3' ACACAGACCCCTCCCCTCGTGT 9277
 CA TGACACGAGGGGAGGGGTCTGTGT
 |||||
 ACTGTGCTCCCCTCCCCAGACACA
 GAM1796 ESR1 3' ACACAGACCCCTTTGCATTC 5507 GG__
 GAG GAGGGGTCTGTGT
 ||| |||||
 CTT TTCCCAGACACA
 ACGT
 GAM1796 STAT6 3' ACTCCATCCCCCGTATCA 13446 C A _
 TGA ACG GGGGA GGGGT
 ||| ||| ||||| |||||
 ACT TGC CCCCT CCTCA
 A C A
 GAM1796 KIAA1259 5' ACACAGACCCCTTTAGATGCT 50796 _ CGA A
 CA TGA CA GGGG GGGGTCTGTGT
 ||| || ||| |||||
 ACT GT TTTC CCCCAGACACA
 C AGA _
 GAM1796 KIAA1297 5' CACAGACCTGCTCGGTCA 72630 A GGGAG
 TGAC CGAG GGGTCTGTG
 ||| ||| |||||

			ACTG GCTC	TCCAGACAC		
			_ G____			
GAM1796	LOC150157	5'	ACAGTCCTCCCCCTGCATCA	86017	CA G	A T
			TGA C AGGGG GGGG CTGT			
			ACT G TCCCC CTCC GACA			
			AC _ _ T			
GAM1796	LOC151808	5'	ACACAGACCCCGTTGCTC	86684	G A	
			GAG GG GGGGTCTGTGT			
			CTC TT CCCCAGACACA			
			G G			
GAM1796	LOC196890	5'	ACAGTCCTCCCCCTGCATCA	91220	CA G	A T
			TGA C AGGGG GGGG CTGT			
			ACT G TCCCC CTCC GACA			
			AC _ _ T			
GAM1796	LOC256072	3'	ACACAGACCCCTCCCCTCGTGT	96156		
	CA		TGACACGAGGGGAGGGGTCTGTGT			
			ACTGTGCTCCCCTCCCAGACACA			
GAM1797	AHCY	3'	TCTGCGTTTCACCCTCCA	7305	AA	_
			TGGA GTGAGGCG AGA			
			ACCT CACTTTGC TCT			
			CC G			
GAM1797	BCL2L2	3'	CTCACTGCTGCACTTTCCA	15757	A	____
			TGGAAAGTG GGC GAG			
			ACCTTTCAC TCG CTC			
			G TCA			
GAM1797	EXT1	5'	TCCCGGGGCTCATTTTCCA	5523	G_	A
			TGGAAAGTGAG CG GA			
			ACCTTTTACTC GC CT			
			GGG C			
GAM1797	ICAM5	5'	CTCGCCTCCTGTGCTTTCC	60566	_____	
			GGAAAGT GAGGCGAG			
			CCTTTCG CTCCGCTC			
			TGTC			
GAM1797	OCA2	3'	TCTTGTAATCACTTTTCA	60826	G_	
			TGGAAAGTGA GCGAGA			
			ACTTTTCACT TGTCT			
			AA			
GAM1797	C6orf37	5'	TCTCGCTTGCGCTTTCCA	68096	_____	
			TGGAAAGTG AGGCGAGA			

	ACCTTTCGC TTCGCTCT		
	G		
GAM1797 DKFZP564D166	3' TCTCAATCGCACTTTTCA	48019	A C_
	TGGAAAGTG GG GAGA		
	ACTTTTCAC CT CTCT		
	G AA		
GAM1797 FLJ20419	3' ATCCCGCCTCACTTCGTCTCTA	35604	_____ A ____
	TGGA AAGTGAGGCG GA T		
	ATCT TCACTCCGC CT A		
	CTGC C ____		
GAM1797 LSM4	3' TCTCAGGGCAGCATTTTCCA	25567	AG ____
	TGGAAAGTG GC GAGA		
	ACCTTTTAC CG CTCT		
	GA GGA		
GAM1797 MGC4796	3' TCTCACCTTCCTGCTTTTCA	62169	_____ C_
	TGGAAAGT GAGG GAGA		
	ACTTTTCG TTCC CTCT		
	TCC CA		
GAM1797 NDP52	3' TCTGGTTAGCACTTTTCTA	20679	A_ G
	TGGAAAGTG GGC AGA		
	ATCTTTCAC TTG TCT		
	GA G		
GAM1797 NDP52	3' TCTTGCTGTAACCTTTCCA	20680	GA_
	TGGAAAGT GGCGAGA		
	ACCTTTCA TCGTTCT		
	ATG		
GAM1797 SEMA5A	5' TCTCCTTGGAACCTTTCCA	15600	___ C
	TGGAAAGTG AGG GAGA		
	ACCTTTCAC TTC CTCT		
	GG _		
GAM1797 TLE4	3' TCTTAACCTCACTTCCCA	68516	A C_
	TGG AAGTGAGG GAGA		
	ACC TCACTCC TTCT		
	C AA		
GAM1797 LOC116028	3' TCTCATGTTGCATTTTCCA	74098	AG ____
	TGGAAAGTG GC GAGA		
	ACCTTTTAC TG CTCT		
	GT TA		
GAM1797 LOC221968	3' TCTCTGACCAGCTTTTCCA	94154	GA __
	TGGAAAGT GG C GAGA		

	ACCTTTTCG CC G CTCT	
	A_ A T	
GAM1797 LOC254742 3'	TCTCTGTAGTACTTTTCA 97479	AG _
	TGGAAAGTG GC GAGA	
	ACTTTTCAT TG CTCT	
	GA T	
GAM1798 PPP1R8 3'	ACTCTAAGGCATTACTTTTAA 12228	_ TT
	TTAAAAGTAA GCCTTA GT	
	AATTTTCATT CGGAAT CA	
	A CT	
GAM1798 PPP1R8 3'	ACTCTAAGGCATTACTTTTAA 26918	_ TT
	TTAAAAGTAA GCCTTA GT	
	AATTTTCATT CGGAAT CA	
	A CT	
GAM1798 PPP1R8 3'	ACTCTAAGGCATTACTTTTAA 57507	_ TT
	TTAAAAGTAA GCCTTA GT	
	AATTTTCATT CGGAAT CA	
	A CT	
GAM1798 SERPINB13 3'	ATAACTGGCTTATTTTAA 25697	TTA
	TTAAAAGTAAGCC TTGT	
	AATTTTATTTCGG AATA	
	TC_	
GAM1798 ATP6V1D 3'	ACAAAAAGGCTTACTTTTGA 32589	A
	TTAAAAGTAAGCCTT TTGT	
	AGTTTTCATTTCGGAA AACA	
	A	
GAM1798 C11orf15 3'	TGTAACAATAAAAAATAATTTTT 40597	AAGCC
GA	TTAAAAGT TTATTGTTACA	
	AGTTTTTA AATAACAATGT	
	ATAAA	
GAM1798 C6orf33 3'	ACAATAGAAGCTGACTTTTAA 56707	A C_
	TTAAAAGT AGC TTATTGT	
	AATTTTCA TCG GATAACA	
	G AA	
GAM1798 MBLL39 3'	AAGGATAAAGTTTACTTTTAA 59255	C G
	TTAAAAGTAAGC TTATT TT	
	AATTTTCATTTG AATAG AA	
	A G	
GAM1798 MBLL39 3'	AAGGATAAAGTTTACTTTTAA 20446	C G
	TTAAAAGTAAGC TTATT TT	

		AATTTTCATTTG AATAG AA		
		A G		
GAM1798	MGC15705	3' TGTAATAAAGGTTACCTTTAA 52247	A A	AT
		TTAAA GT AGCCTT TGTTACA		
		AATTT CA TTGGAA ATAATGT		
		C C _		
GAM1798	LOC145630	5' TAAGAATAAGGCCTACTTT 77797	A	G
		AAAGTA GCCTTATT TTA		
		TTTCAT CGGAATAA AAT		
		C G		
GAM1798	LOC149722	5' TGTAACAATAAGAATTGC 85758	GC	
		GTAA CTTATTGTTACA		
		CGTT GAATAACAATGT		
		AA		
GAM1798	LOC220477	5' ACTTGAAGGCATCACTTTTAA 76502	AA_	ATT
		TTAAAAGT GCCTT GT		
		AATTTTCA CGGAA CA		
		CTA GTT		
GAM1798	LOC255055	3' ACAATGAGCTTAATTTTAA 96518	G	C
		TTAAAA TAAGC TTATTGT		
		AATTTT ATTCG AGTAACA		
		A _		
GAM1799	ALDH3A2	5' CAGCCCGCTGCCAGAGCCGGGG 69796	ATG_	A
	A	TCCCTGGCTT AGC GGCTG		
		AGGGGCCGAG TCG CCGAC		
		ACCG C		
GAM1799	CAPNS1	3' CAGCCTGCCAGGCCAGG 10013	TA	A
		CCTGGCT TG GCAGGCTG		
		GGACCGG AC CGTCCGAC		
		_ _		
GAM1799	CASP10	3' CAGCCTGCTTTCACACTAAGGA 53245	C	CTTAT
		TCC TGG GAGCAGGCTG		
		AGG ATC TTCGTCCGAC		
		A ACACT		
GAM1799	DLEC1	3' TGGCCCCACAAGCCAGG 24723	A	AGCA
		CCTGGCTT TG GGCTG		
		GGACCGAA AC CCGGT		
		C C_		
GAM1799	DLEC1	3' TGGCCCCACAAGCCAGG 24724	A	AGCA
		CCTGGCTT TG GGCTG		

GGACCGAA AC CCGGT
C C___
GAM1799 DYT1 3' CAGCCCACTCATCGCAGGG 5477 G TT CA
CCCTG C ATGAG GGCTG
||||| | ||||| |||||
GGGAC G TACTC CCGAC
C AC
GAM1799 LPIN1 5' CAGCCTGCTGAGAACTAG 67985 C ATG
CTGG TT AGCAGGCTG
|||| | |||||
GATC AA TCGTCCGAC
_GAG
GAM1799 RCV1 5' CAGCCTGCGGCCAGGGG 12801 TATGA
TCCCTGGCT GCAGGCTG
||||||| |||||
GGGGACCGG CGTCCGAC

GAM1799 TNXB 5' CTCAGCCTTGGGCCAAGCCTGG 51634 CT TA A ___
A TCC GGCT TG GC AGGCTGAG
||| ||| || || |||||
AGG CCGA AC CG TCCGACTC
T_ _ _ GGT
GAM1799 C20orf150 3' CAGCCTGCCCTCAAGCCAAGGA 66009 C ATGA
TCC TGGCTT GCAGGCTG
||| ||||| |||||
AGG ACCGAA CGTCCGAC
A CTCC
GAM1799 C20orf39 5' CAGCCTGCCGGCCAGGCGA 46571 _ TAT A
TC CCTGGCT G GCAGGCTG
|| ||||| | |||||
AG GGACCGG C CGTCCGAC
C _ _ _
GAM1799 CBX6 3' CAGCCTGCCTGAAGCAAAGGA 27407 CTG ATGA
TCC GCTT GCAGGCTG
||| ||| |||||
AGG CGAA CGTCCGAC
AAA GTC_
GAM1799 CD84 3' CTCAGCCTGTAAGCAAAGCAGG 81570 G A A___
CCTG CTT TG GCAGGCTGAG
|||| ||| || |||||
GGAC GAA AC TGTCCGACTC
_ _ GAA
GAM1799 CYP2D6 3' CAGCCTGCTCCTAGCCCAGAGG 5451 _ C T
CC CTGG TTA GAGCAGGCTG
|| ||| ||| |||||
GG GACC GAT CTCGTCCGAC
A C C
GAM1799 DKFZP586J0619 3' CTCAGCCTGCCCAGCAGGGA 82317 G TAT A
TCCCTG CT G GCAGGCTGAG
||||| || | |||||

AGGGAC GA C CGTCCGACTC
 — — C
 GAM1799 FKHL18 3' CAGCCCTGGTGAGCCAAGGA 80370 C G CA
 TCC TGGCTTAT AG GGCTG
 ||| ||||| || |||||
 AGG ACCGAGTG TC CCGAC
 A G —
 GAM1799 FLJ14800 3' CAACCTGCTCAGGCACCACAGA 52684 CC CTTA C
 TC TGG TGAGCAGG TG
 || ||| ||||| ||
 AG ACC ACTCGTCC AC
 AC ACGG A
 GAM1799 FLJ14957 3' CTCAGCCCACTCATACCTAGAG 52816 C CT CA
 A TC CTGG TATGAG GGCTGAG
 || ||| ||||| |||||
 AG GATC ATACTC CCGACTC
 A C_ AC
 GAM1799 KIAA1023 3' CAGGCTCAGAAGCCAGGGA 34677 A AGG
 TCCCTGGCTT TGAGC CTG
 ||||| ||||| |||
 AGGGACCGAA ACTCG GAC
 G —
 GAM1799 KIAA1655 5' CTCAGCCCACTCCCAAACCAG 67183 C AT CA
 CTGG TT GAG GGCTGAG
 |||| || ||| |||||
 GACC AA CTC CCGACTC
 A CC AC
 GAM1799 MGC35521 3' CTCAGGTGTCTAGTAAGCCAG 59666 GA GG
 CTGGCTTAT GCA CTGAG
 ||||| ||| |||||
 GACCGAATG TGT GACTC
 AC G_
 GAM1799 MGC5508 3' CAGCCTGCCTCACCAGGGA 44264 CTTA _
 TCCCTGG TGAG CAGGCTG
 ||||| ||| |||||
 AGGGACC ACTC GTCCGAC
 — C
 GAM1799 PADI1 3' CAGCCTGCACTGAGTCA 62700 TGA
 TGGCTTA GCAGGCTG
 ||||| |||||
 ACTGAGT CGTCCGAC
 CA_
 GAM1799 RIN3 5' CTCAGCCTGCCTCCCAAGGGA 46162 _ CTTAT _
 TCCCT GG GAG CAGGCTGAG
 |||| || ||| |||||
 AGGGA CC CTC GTCCGACTC
 A C_ C
 GAM1799 SOX17 3' CAGCCTGCAGGCCAG 42630 ATGA
 CTGGCTT GCAGGCTG
 ||||| |||||

GACCGGA CGTCCGAC

GAM1799 SP140 3' AGTATCTCATCAGCCAGGGA 24326 T CAG
TCCCTGGCT ATGAG GCT
||||||| ||||| |||
AGGGACCGA TACTC TGA
C TA_

GAM1799 VI 3' CAGCCGCTAGGCCAGGGA 26486 ATG A
TCCCTGGCTT AGC GGCTG
||||||| ||| |||||
AGGGACCGGA TCG CCGAC

GAM1799 LOC112817 5' CAGTGGCCACAAGTCAGGGA 57319 A A AG
TCCCTGGCTT TG GC GCTG
||||||| || || |||||
AGGGACTGAA AC CG TGAC
C _ G_

GAM1799 LOC129676 5' CTCAGCCTGCAGACACAGGGA 76232 GCTTATGA
TCCCTG GCAGGCTGAG
||||| |||||
AGGGAC CGTCCGACTC
ACAGA_

GAM1799 LOC134266 3' CTCAGCCTACCAAGTAGCCAGG 75644 TATGAGC
CCTGGCT AGGCTGAG
||||| |||||
GGACCGA TCCGACTC
TGAACCA

GAM1799 LOC150248 3' CCACCTCATCAGCCAGGGA 86126 T CA
TCCCTGGCT ATGAG GG
||||||| ||||| ||
AGGGACCGA TACTC CC
C CA

GAM1799 LOC155179 3' CAGGCTCAGAAGCCAGGGA 82225 A AGG
TCCCTGGCTT TGAGC CTG
||||||| ||||| |||
AGGGACCGAA ACTCG GAC
G _

GAM1799 LOC158056 5' CTCAGCCCAGGAGAGCCAGGGG 82589 ATGAGCA
TCCCTGGCTT GGCTGAG
||||||| |||||
GGGGACCGAG CCGACTC
AGGAC_

GAM1799 LOC219405 3' CAGCCTGCTCTACCCAGAGA 92450 C CTTAT
TC CTGG GAGCAGGCTG
|| ||| |||||
AG GACC CTCGTCCGAC
A CAT_

GAM1799 LOC221496 3' TCAGCCTGCTCCCTGGGA 93643 T CTTAT
TCCC GG GAGCAGGCTGA
||| || |||||

AGGG CC CTCGTCCGACT
 T _____
 GAM1799 LOC222031 3' CAGCCTGTCTAACCCAAAGA 95672 CC C T G
 TC TGG TTA GA CAGGCTG
 || ||| ||| || |||||
 AG ACC AAT CT GTCCGAC
 AA C _ _
 GAM1799 LOC51320 3' CTGCAACTAATAAGCCAAGGA 34028 C GA____
 TCC TGGCTTAT GCAG
 ||| ||||| |||
 AGG ACCGAATA CGTC
 A ATCAA
 GAM1800 GALGT 3' AATCTTTGGGTCAGTGAGCTC 9416 C C
 GA CTCACTGACCCAGA GTT
 || ||||| ||||| |||
 CT GAGTGACTGGGTTT TAA
 C C
 GAM1800 HKR3 5' CGGAGCAGGGGGGCCAGTG GGG 19269 A AGAC
 CCTCACTG CCC GTTCCG
 ||||| ||| |||||
 GGGGTGAC GGG CGAGGC
 C GGA_
 GAM1800 MAN2A2 3' GAACCGTG GGCAGTGAGGTC 21510 A GAC
 GACCTCACTG CCCA GTTC
 ||||| ||| |||
 CTGGAGTGAC GGGT CAAG
 _ GC_
 GAM1800 MTIF2 5' GAACGTCTGGGTTCTAGTC 11713 CTCACT
 GAC GACCCAGACGTTT
 ||| ||||| |||||
 CTG TTGGGTCTGCAAG
 ATC____
 GAM1800 PLAUR 5' AACGTCTGGGAGGAGTC 12154 C A GA
 GAC TC CT CCCAGACGTT
 ||| || ||| |||||
 CTG AG GA GGGTCTGCAA
 _ _ _
 GAM1800 C9orf14 3' CGGAGTGTTGAGTCATAAAGTC 87956 CTCAC CCA
 GAC TGAC GACGTTCCG
 ||| ||| |||||
 CTG ACTG TTGTGAGGC
 AAAT_ AG_
 GAM1800 FLJ32734 5' AGCTGCCTGGGCCGTGAGGTC 59036 T A A_
 GACCTCAC G CCCAG C GTT
 ||||| | |||| | |||
 CTGGAGTG C GGGTC G CGA
 _ C C T
 GAM1800 HS6ST 3' CGAAGCTGGGGTCAGGTGAGGT 62729 _ AGAC C
 C GACCTCAC TGACCC GTT CG
 ||||| ||||| ||| ||

			CTGGAGTG ACTGGG CGA GC		
			G GT__ A		
GAM1800	LOC153546	5'	CGCTGGGTCAGCGAGGTC 81743	A	A
			GACCTC CTGACCCAG CG		
			CTGGAG GACTGGGTC GC		
			C _		
GAM1800	LOC160954	5'	GAACACCGATCAGTGAGGTC 88446		CCCAGAC
			GACCTCACTGA GTTC		
			CTGGAGTGACT CAAG		
			AGCCA__		
GAM1800	LOC254848	5'	AACGTCTGAGGTCGAGCTC 98877	C ACT	_
			GA CTC GACC CAGACGTT		
			CT GAG CTGG GTCTGCAA		
			C __ A		
GAM1801	LIMK1	3'	GGAGGTGGCCCTCAGCTGGGAC 11337		TTTG
	A		TGTCCCAGCTGAGGGCC TCC		
			ACAGGGTCGACTCCCGG AGG		
			TGG_		
GAM1801	LIMK1	3'	GGAGGTGGCCCTCAGCTGGGAC 11338		TTTG
	A		TGTCCCAGCTGAGGGCC TCC		
			ACAGGGTCGACTCCCGG AGG		
			TGG_		
GAM1801	LOXL1	5'	GGACAAAGCTAGAGCTGGGGCA 60821	GAG	C
			TGTCCCAGCT GGC TTTGTCC		
			ACGGGGTCGA TCG AAACAGG		
			GA_ _		
GAM1801	MEF2D	3'	GCTTCTCCCTCAGCTGAGCA 20986	CC	CCTTT
			TGT CAGCTGAGGG GT		
			ACG GTCGACTCCC CG		
			A_ TCTT_		
GAM1801	MTMR3	3'	ACAATCTCTTCCTCAGCCAGCA 41159	CCCA	CCT__
	CA		TGT GCTGAGGG TTGT		
			ACA CGACTCCT AACA		
			CGAC TCTCT		
GAM1801	NTRK2	3'	ACAAAGACAACCACTGGGAT 21632	CTGA	GC__
			GTCCCAG GG CTTTGT		
			TAGGGTC CC GAAACA		
			A__ AACA		
GAM1801	PRKR	5'	GGACAAAGCTTCCAACCAGGAT 12349	CAGC	AG C
	A		TGTCC TG GGC TTTGTCC		

		ATAGG AC TCG AAACAGG		
		ACCA CT _		
GAM1801	RGS19IP1 3'	GGGCCCCCAGCAGGGACA 63171	A A	
		TGTCCC GCTG GGGCCT		
		ACAGGG CGAC CCCGGG		
		A C		
GAM1801	FLJ20160 3'	AGGCTCCTCAGCCAGGACA 35162	CA _	
		TGTCC GCTGAGG GCCT		
		ACAGG CGACTCC CGGA		
		AC T		
GAM1801	FLJ23537 3'	ACAAAGGCAGAGAGCTAAAGCA 88916	CCC GAGG	
		TGT AGCT GCCTTTGT		
		ACG TCGA CGGAAACA		
		AAA GAGA		
GAM1801	GS3955 3'	GGACAAAAACCCTCAGTAGAGA 41622	CCA CC	
	CA	TGTC GCTGAGGG TTTGTCC		
		ACAG TGA TCCC AAACAGG		
		AGA AA		
GAM1801	KIAA0375 5'	ACAGTGTCTCAGCTGGAAC 71576	C G CT	
		GT CCAGCTGAGG C TTGT		
		CA GGTCGACTCT G GACA		
		A _ T _		
GAM1801	KIAA0981 3'	GACAAAAAATTAGCTGGGCA 62087	T GGGCC	
		TG CCCAGCTGA TTTGTC		
		AC GGGTCGATT AAACAG		
		_ AAA _		
GAM1801	KIAA1932 5'	ACAGTGGCCCTCAGCCTGGGAC 73820	_ T	
	A	TGTCCCAG CTGAGGGCC TTGT		
		ACAGGGTC GACTCCCGG GACA		
		C T		
GAM1801	NPTXR 3'	GGACAAAGACCC CAGGAGG 27438	AG A C	
		CC CTG GGG CTTTGTCC		
		GG GAC CCC GAAACAGG		
		AG _ A		
GAM1801	QSCN6 3'	GGTCTTGGCCCTCAACTGGGGC 12570	C TTTGT	
	A	TGTCCCAG TGAGGGCC CC		
		ACGGGGTC ACTCCCGG GG		
		A TTCT _		
GAM1801	REPRIMO 3'	GGACAAAGACCCAGAATAGA 39531	CCAG A GC	
		TC CTG GG CTTTGTCC		

	AG GAC CC GAAACAGG	
	ATAA _ A_	
GAM1801 LOC145757 3'	GGACAAAGACTCCTGGGACA 77937	CTGA C
	TGTCCCAAG GGG CTTTGTCC	
	ACAGGGTC CTC GAAACAGG	
	_____ A	
GAM1801 LOC147042 3'	GGACAAAGACCCCAAAGTGGGG 84994	G GA_ C
CA	TGTCCCA CT GGG CTTTGTCC	
	ACGGGGT GA CCC GAAACAGG	
	_ AAC A	
GAM1801 LOC150094 3'	GAAGCCCCCAGCTGGACA 86005	C A
	TGTCC AGCTG GGGCCTTT	
	ACAGG TCGAC CCCGGAAG	
	_ C	
GAM1801 LOC152286 5'	GGACAAAGCAGAGAACTGGGA 86811	CTGAGG C
	TCCAG GC TTTGTCC	
	AGGGTC CG AAACAGG	
	AAGAGA _	
GAM1801 LOC155376 5'	GGACACAGCCTCTGCTGGGACA 82246	T GC T
	TGTCCCAAGC GAGG CT TGTCC	
	ACAGGGTCG CTCC GA ACAGG	
	T _ C	
GAM1801 LOC222183 5'	GAAGCCCCTCAGCCGGGACA 95827	A C
	TGTCCC GCTGAGGG CTTT	
	ACAGGG CGACTCCC GAAG	
	C C	
GAM1801 LOC222233 5'	GGACACAGCCTCTGCTGGGACA 95906	T GC T
	TGTCCCAAGC GAGG CT TGTCC	
	ACAGGGTCG CTCC GA ACAGG	
	T _ C	
GAM1801 LOC253532 5'	GGACACAGCCTCTGCTGGGACA 97735	T GC T
	TGTCCCAAGC GAGG CT TGTCC	
	ACAGGGTCG CTCC GA ACAGG	
	T _ C	
GAM1801 LOC254875 5'	GGACACAGCCTCTGCTGGGACA 97780	T GC T
	TGTCCCAAGC GAGG CT TGTCC	
	ACAGGGTCG CTCC GA ACAGG	
	T _ C	
GAM1801 LOC90342 5'	GGCTGGCCCCCAACAAGGACA 63014	CAGC A TTT
	TGTCC TG GGGCC GTC	

			ACAGG AC CCCGG CGG	
			AACA C T__	
GAM1802	CLCN6	3'	ACGGTATCCTCGCTAGTTT 41692	TC
			AAACTAGCGAGG TGCTGT	
			TTTGATCGCTCC ATGGCA	
			T_	
GAM1802	CLCN6	3'	ACGGTATCCTCGCTAGTTT 41699	TC
			AAACTAGCGAGG TGCTGT	
			TTTGATCGCTCC ATGGCA	
			T_	
GAM1802	CLCN6	3'	ACGGTATCCTCGCTAGTTT 8900	TC
			AAACTAGCGAGG TGCTGT	
			TTTGATCGCTCC ATGGCA	
			T_	
GAM1802	EFEMP1	3'	TACAACATGCTGGTTT 15913	AGGTC C
			AAACTAGCG TG TGTA	
			TTTGGTCGT AC ACAT	
			_____ A	
GAM1802	EFEMP1	3'	TACAACATGCTGGTTT 38774	AGGTC C
			AAACTAGCG TG TGTA	
			TTTGGTCGT AC ACAT	
			_____ A	
GAM1802	IL12RB2	3'	ACAGCAGATCAGTACTGTT 9560	TA_ GA
			AAC GC GGTCTGCTGT	
			TTG TG CTAGACGACA	
			TCA A_	
GAM1802	RNF6	3'	GTACAGCAGACTTTAGCTTC 21087	T _
			C AGC GAGGTCTGCTGTAC	
			C TCG TTTCAGACGACATG	
			T A	
GAM1802	SCAMP1	3'	ACAACAGGTGCTAGTTT 54498	AGG C
			AAACTAGCG TCTG TGT	
			TTTGATCGT GGAC ACA	
			_____ A	
GAM1802	SORCS1	3'	ACAGCAGGGTTCAGTTT 54675	AGC G
			AAACT GAG TCTGCTGT	
			TTTGA CTT GGACGACA	
			_____ G	
GAM1802	TRRAP	3'	GTACGTTTCCTTCGCTAG 14493	TCT T
			CTAGCGAGG GC GTAC	

GATCGCTTC TG CATG
 CT_ _
 GAM1802 BS69 3' ACAGCAGGGCTAGTCC 22778 A GAGG
 A ACTAGC TCTGCTGT
 | ||||| |||||
 C TGATCG GGACGACA
 C _ _
 GAM1802 COASTER 3' GTACAAATGATGCTAGTTT 32082 GAG TGC
 AA ACTAGC GTC TGTAC
 ||||| || ||||
 TTTGATCG TAG ACATG
 _ TAA
 GAM1802 COQ7 3' GCAGCCTGGACCTCCTAG 32856 C _
 CTAG GAGGTCT GCTGT
 ||| ||||| ||||
 GATC CTCCAGG CGACG
 _ TC
 GAM1802 DKFZP434B044 3' ACAGCAGTGCTGGTTT 49707 AGGT
 AA ACTAGCG CTGCTGT
 ||||| |||||
 TTTGGTCGT GACGACA
 _
 GAM1802 FLJ23441 3' TACAGCAGAATGCATGTTT 45493 TA GAGG
 AA AC GC TCTGCTGTA
 ||| || |||||
 TTTG CG AGACGACAT
 TA TA_ _
 GAM1802 ICB-1 3' GTACAGCAAGATTCCTGC 17934 G _ _
 GC AGG TCT GCTGTAC
 || ||| || |||||
 CG TCC AGA CGACATG
 _ TT A
 GAM1802 KIAA0275 3' ACCTCACACCTCGCTGTT 29322 T C CT
 AAC AGCGAGGT TG GT
 ||| ||||| || ||
 TTG TCGCTCCA AC CA
 _ C TC
 GAM1802 KIAA0276 3' GTACAGCAAACCTGGTTTTAGGT 71522 _ G GTC
 TT AA ACT AGC AG TGCTGTAC
 |||| ||| || |||||
 TTTGG TTG TC ACGACATG
 ATT G AA_ _
 GAM1802 KIAA0280 3' ACAGCTGGACCTCACAGTT 93285 AGC _
 AA CT GAGGTCT GCTGT
 ||| ||||| ||||
 TTGA CTCCAGG CGACA
 CA_ T
 GAM1802 KIAA0293 3' ACACAGGTCTCACTAGTT 61233 C GT C
 AA CTAG GAG CTG TGT
 ||||| ||| ||| |||

			TTGATC CTC GAC ACA		
			A TG _		
GAM1802	KIAA0660	3'	ACACAGATTTTCATAGTTT 25467	GC	C
			AAACTA GAGGTCTG TGT		
			TTTGAT TTTTAGAC ACA		
			AC _		
GAM1802	KIAA1530	3'	GTACAGCAATTTATCTGTTT 68565	T CG	C
			AAAC AG AGGT TGCTGTAC		
			TTTG TC TTTA ACGACATG		
			_ TA _		
GAM1802	KIAA1678	3'	GTACAGCAGACATGCCGCT 72767	AG__	
			AGCG GTCTGCTGTAC		
			TCGC CAGACGACATG		
			CGTA		
GAM1802	KIAA1855	3'	ACACGCGGCGCCCCGCCAG 93945	A A _ _	
			CT GCG GGT CTGC TGT		
			GA CGC CCG GGCG ACA		
			C C C C		
GAM1802	MAP2K3	3'	ACAGCAGGCTGCCAGT 59682	A GA	
			ACT GC GGTCTGCTGT		
			TGA CG TCGGACGACA		
			C _		
GAM1802	MAP2K3	3'	ACAGCAGGCTGCCAGT 12320	A GA	
			ACT GC GGTCTGCTGT		
			TGA CG TCGGACGACA		
			C _		
GAM1802	MEGF10	3'	GTACAGCAAACCTGCCCGTT 51608	A C__	
			AGCG GGT TGCTGTAC		
			TTGC CCG ACGACATG		
			_ TCAA		
GAM1802	MGC2454	3'	GTACAGCAGAAGTTTGCTG 48285	G_	
			TAGCGAG TCTGCTGTAC		
			GTCGTTT AGACGACATG		
			GA		
GAM1802	MKP-7	3'	GCACAGACCTCACTAGTT 67013	C	C
			AACTAG GAGGTCTG TGT		
			TTGATC CTCCAGAC ACG		
			A _		
GAM1802	LOC143146	5'	GCAGCGCCACCTCGCTTGTTT 60765	T	C_
			AAAC AGCGAGGT TGCTGT		

TTTG TCGCTCCA GCGACG
 T CC
 GAM1802 LOC148077 5' ATGGAGACCTCGTAGTCC 85250 A G G
 A ACTA CGAGGTCT CTGT
 I IIII IIIIIII IIII
 C TGAT GCTCCAGA GGTA
 C _ _
 GAM1802 LOC148229 5' GTACAGCACCCCTGCCAGTT 79490 A G TC
 AACT GC AGG TGCTGTAC
 IIII II III IIIIIII
 TTGA CG TCC ACGACATG
 C _ C_
 GAM1802 LOC253970 3' TACAGCAGCTGGTGCTAGTCA 98316 A A_ T
 A ACTAGCG GG CTGCTGTA
 I IIIII II IIIIIII
 A TGATCGT TC GACGACAT
 C GG _
 GAM1802 LOC257222 5' TACAGCAGCCTCACTAG 99446 C T
 CTAG GAGG CTGCTGTA
 IIII IIII IIIIIII
 GATC CTCC GACGACAT
 A _
 GAM1802 LOC56965 3' GTACAGCAGCTGAGGCTG 39926 GA_ T
 TAGC GG CTGCTGTAC
 IIII II IIIIIII
 GTCG TC GACGACATG
 GAG _
 GAM1802 LOC56965 3' GTACAGCAGCTGAGGCTG 39932 GA_ T
 TAGC GG CTGCTGTAC
 IIII II IIIIIII
 GTCG TC GACGACATG
 GAG _
 GAM1802 LOC64182 3' TACAGCAGCTGTCCTGTT 42555 T C _ T
 AAC AG GA GG CTGCTGTA
 III II II IIIIIII
 TTG TC CT TC GACGACAT
 _ _ G _
 GAM1802 LOC92539 3' ACAGCAATCTTTGCTGTT 70219 T TC
 AAC AGCGAGG TGCTGT
 III IIIII IIIII
 TTG TCGTTTC ACGACA
 _ TA
 GAM1803 TERF1 3' CCCAAATCCTGTTCCAATGA 34391 C TA C
 TCATTGGA ACG GATT GGG
 IIIIIII III IIII III
 AGTAACCT TGT CTAA CCC
 _ C_ A
 GAM1803 FLJ10159 3' CCATGTCACGCCATCCAATGAC 36334 CA_ A TC
 GTCATTGGA CGT GAT GG
 IIIIIII III III II

		CAGTAACCT GCA CTG CC	
		ACC _ TA	
GAM1803	FLJ14213 3'	CCGATGCTCCCAATGACG 46216	ACAC GAT
		CGTCATTGG GTA TCGG	
		GCAGTAACC CGT AGCC	
		CT_ _	
GAM1803	MGC10715 3'	ATTTACCAGACATCCAATGAC 44495	CAC_
		GTCATTGGA GTAGAT	
		CAGTAACCT CATTTA	
		ACAGAC	
GAM1803	MOST2 5'	CCAGGACTGCCCAATGAC 40059	ACAC A _
		GTCATTGG GTAG TTC GG	
		CAGTAACC CGTC AGG CC	
		_ _ A	
GAM1803	LOC150370 3'	CCGGGTCTACGTGCCCATGAC 86123	T A
		GTCAT GG CACGTAGATTTCGG	
		CAGTA CC GTGCATCTGGGCC	
		C _	
GAM1803	LOC152620 3'	CCCAAATCCTGTTCCAATGA 60707	C TA C
		TCATTGGA ACG GATT GGG	
		AGTAACCT TGT CTAA CCC	
		_ C_ A	
GAM1803	LOC158668 3'	CCCAAATCCTGTTCCAATGA 69896	C TA C
		TCATTGGA ACG GATT GGG	
		AGTAACCT TGT CTAA CCC	
		_ C_ A	
GAM1804	ABR 3'	GATGTGGCCGAAGCAGGTGTCC 42003	ATATGA_
	AG	TTGGATGCTTG ACATC	
		GACCTGTGGAC TGTAG	
		GAAGCCGG	
GAM1804	AMACR 3'	GGTGTTTCATGATCTCCCTCTAA 69102	TGCTT _
		TTGGA GAT ATGAACATC	
		AATCT CTA TACTTGTGG	
		CCCT_ G	
GAM1804	ATF5 3'	GGTGTTTCATTTAGCTCTAA 24824	T TGAT
		TTGGA GCT ATGAACATC	
		AATCT CGA TACTTGTGG	
		_ TTT_	
GAM1804	ATP1B3 3'	GGTTTAATTGCCAAGTGTCTAA 9843	A _ ATC
		TTGGATGCTTG TA TGAAC	

AATCTGTGAAC GT ATTTG
 C TA G
 GAM1804 ATRX 3' GTTCTGTATTGAGTATCT 57079 TG _
 GGATGCT ATAT GAAC
 ||||| ||| |||
 TCTATGA TATG CTTG
 GT T
 GAM1804 B3GALT5 3' GGTGTTTCATGAAGTCACTGA 53734 TG A _ GA
 T G TG CTT TATGAACATC
 | | ||| |||||
 A C AC GAA GTACTTGTGG
 GT _ T _
 GAM1804 B3GALT5 3' TTCATACTAAGTGTTTGA 53739 TG A
 T GATGCTTG TATGAA
 | ||||| |||||
 A TTGTGAAT ATA CTT
 GT C
 GAM1804 BCL3 3' GATGTAAATTATTAAGCATTT 18992 TGA_
 GGATGCTTGATA ACATC
 ||||| |||
 TTTACGAATTAT TGTAG
 TAAA
 GAM1804 CD2AP 3' GGTGTTTCATAATGTTCCAG 25079 T TTGA
 TTGGA GC TATGAACATC
 |||| || |||||
 GACCT TG ATACTTGTGG
 _ TA_
 GAM1804 CDH13 3' GGTGTATGTATGAGTATCT 8837 G A
 GGATGCTT ATATG ACATC
 ||||| ||| |||
 TCTATGAG TATGT TGTGG
 _ A
 GAM1804 CENTD1 3' GTCTATGCTTAGGCATTAA 58278 _ A
 TTGGATGCTTGA TATG AC
 ||||| ||| |||
 AATTTACGGATT GTAT TG
 C C
 GAM1804 CHST1 3' GGTGAGTGGTCGGGTATCTAG 14702 ATGAA
 TTGGATGCTTGAT CATC
 ||||| |||
 GATCTATGGGCTG GTGG
 GTGA_
 GAM1804 CLCA1 5' CGGTGTTGAGGTTATGTCAAGC 8898 TG _____
 ATCTGG T GATGCTTGATATGA ACATC G
 | ||||| ||| |
 G CTACGAACTGTATT TGTGG C
 GT GGAGT
 GAM1804 CLOCK 3' GATGCAGTATTGAGTGTTT 18114 TG GAA
 GGATGCT ATAT CATC
 ||||| ||| |||

CTTGTGA TATG GTAG
 GT AC_
 GAM1804 CNTNAP2 3' GGTGGATAAAGTATTAAGTAAC 27093 A GAA____
 TAA TTGG TGCTTGATAT CATC
 |||| ||||| ||||
 AATC ATGAATTATG GTGG
 A AAATAG
 GAM1804 CORT 3' GATGTTTCATTATGGTGCTGG 8942 TG A TGAT
 T G TGCT ATGAACATC
 | |||| |||||
 G C GTGG TACTTGTAG
 GT_ TAT_
 GAM1804 CRH 3' GGTGTTTATAGTGGTGTTT 7482 TGA
 GGATGCT TATGAACATC
 ||||| |||||
 TTTGTGG ATATTTGTGG
 TG_
 GAM1804 CRHR2 3' GATGTCTGCAGGCATTT 10302 ATAT A
 GGATGCTTG GA CATC
 ||||| || ||||
 TTTACGGAC CT GTAG
 GT__ _
 GAM1804 CUL5 3' GGTGTTTATGAAAATCATTTAG 14431 C GA
 TTGGATG TT TATGAACATC
 ||||| || |||||
 GATTTAC AA GTATTTGTGG
 T AA
 GAM1804 CYP4F3 3' ATGTGCATGTTAAGTATTCAA 7993 A C
 TTGGATGCTTGATATG ACAT
 ||||| ||||| ||||
 AACTTATGAATTGTAC TGTA
 G A
 GAM1804 DAB2 5' GGTGTCACCAAGTGTCCA 9037 ATA A
 TGGATGCTTG TGA CATC
 ||||| || ||||
 ACCTGTGAAC ACT GTGG
 C__ _
 GAM1804 DPYSL3 3' GGTGTTTCAGTTCTGTGTCTGG 9128 TG TT TA
 T GATGC GA TGAACATC
 | |||| || |||||
 G CTGTG CT ACTTGTGG
 GT T_ TG
 GAM1804 EGFL4 3' GGTGAAGTCAGCTGGGCATTCA 62472 ATA A__
 A TTGGATGCTTG TGA CATC
 ||||| || ||||
 AACTTACGGGT ACT GTGG
 CG_ GAA
 GAM1804 EHF 3' GATGTTTCAGCAGTATCCA 25123 TGATA
 TGGATGCT TGAACATC
 ||||| |||||

		ACCTATGA ACTTGTAG	
		CG__	
GAM1804 EIF2B1	3'	GATGTTTAGCAACAGTATTC 60391	TGATA
		GGATGCT TGAACATC	
		CTTATGA ATTTGTAG	
		CAACG	
GAM1804 EZH1	3'	GGTTCTAAGTACAGGCATTCAA 10555	_ AT_ ATC
		TTGGATGCTTG AT GAAC	
		AACTTACGGAC TG CTTG	
		A AAT G	
GAM1804 FCAR	3'	GATGTGATTAGGTATTTAG 56575	ATGA
		TTGGATGCTTGAT ACATC	
		GATTATGGATTA TGTAG	
		G__	
GAM1804 FCMD	3'	GTTCTGTGGAGTGTCCAG 23044	G T
		TTGGATGCTT ATA GAAC	
		GACCTGTGAG TGT CTTG	
		G _	
GAM1804 FEN1	3'	GATGTTACCTGGCAATCAG 15923	A TGATA
		TTGG TGCT TGAACATC	
		GA CT ACGG ACTTG TAG	
		A TCC__	
GAM1804 FPRL1	3'	GAGTCATATTGAGGCATTCAA 9394	_ ACATC
		TTGGATGCTT GATATGA	
		AACTTACGGA TTATACT	
		G GAG	
GAM1804 FTSJ2	3'	AAATTTATATCAGTGTCTGG 26342	TG T CATC
		T GATGCT GATATGAA	
		G CTGTGA CTATATTT	
		GT _ AAAG	
GAM1804 GAS41	3'	GATGTGTCCAGTAAGTATTCAA 22554	ATATGA
		TTGGATGCTTG ACATC	
		AACTTATGAAT TGTAG	
		GACCTG	
GAM1804 GBAS	3'	GGTGGTGCATGTTGAGATTTAA 9435	G TG AA_
		TTGGAT CT ATATG CATC	
		AATTTA GA TGTAC GTGG	
		_ GT GTG	
GAM1804 GCA	3'	GATGATATGTCAACATTCAA 25178	C AA
		TTGGATG TTGATATG CATC	

			AACTTAC AACTGTAT GTAG	
			— A—	
GAM1804	GLO1	3'	GATGTTTATATTTCTCAT 22962 CTT	
			ATG GATATGAACATC	
			TAC TTATATTTGTAG	
			TCT	
GAM1804	GNG2	5'	GATGATACTGTGAAGTGTTTCAG 96597 G TGAA	
			TTGGATGCTT ATA CATC	
			GACTTGTGAA TGT GTAG	
			G CATA	
GAM1804	GPR85	3'	TCATGGTCATGCATCTAA 39106 T —	
			TTGGATGC TGAT ATGA	
			AATCTACG ACTG TACT	
			T G	
GAM1804	GRB10	3'	GGTGTCACTGTGGTAGGCATTT 19197 TG — _ A	
	GG		T GATGCTTG ATA TGA CATC	
			G TTACGGAT TGT ACT GTGG	
			GT GG C _	
GAM1804	GRIK1	5'	GGTGCATCTCTCGGGCGTCCG 7717 TAT A_	
			TGGATGCTTGA GA CATC	
			GCCTGCGGGCT CT GTGG	
			CT_ AC	
GAM1804	GUCY1B2	3'	GATGTTTCAGAGGCATCCAA 15946 TGATA	
			TTGGATGCT TGAACATC	
			AACCTACGG ACTTGTAG	
			AG__	
GAM1804	HDGF	3'	GGTGGGAGTGTTGAGCATCT 16900 TG GAA	
			GGATGCT ATAT CATC	
			TCTACGA TGTG GTGG	
			GT AGG	
GAM1804	HELLS	5'	GGTCCCCGGGTGAGTGTCCAG 36513 ATAT_ ATC	
			TTGGATGCTTG GAAC	
			GACCTGTGAGT CTTG	
			GGGCC G	
GAM1804	HGF	3'	GGTGTTTACATGTATTCA 95893 T ATA	
			TGGATGC TG TGAACATC	
			ACTTATG AC ATTTGTGG	
			T _	
GAM1804	HLA-G	3'	GACTTCAATGTATTGAGCATGT 10937 G TG _ CATC	
	GA		TTG ATGCT ATA TGAA	

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AGT TACGA TAT ACTT
G GT GTA CAG
GAM1804 HLF 3' GATGTTTATATCAAATGAGCAT 10934 ____
CT          GGATGCT TGATATGAACATC
           ||||| |||||
           TCTACGA ACTATATTTGTAG
           GTAA
GAM1804 HLX1 3' GGTTCGACTGTGAGGTGTTTGA 41985 TG G _ ATC
           T GATGCTT ATA TGAAC
           | ||||| || ||||
           A TTGTGGA TGT GCTTG
           GT G CA G
GAM1804 HNRPK 3' GATGTTTTGTGTAGTATCT 49191 TG T
           GGATGCT ATA GAACATC
           ||||| || |||||
           TCTATGA TGT TTTGTAG
           TG _
GAM1804 HNRPK 3' GATGTTTTGTGTAGTATCT 49192 TG T
           GGATGCT ATA GAACATC
           ||||| || |||||
           TCTATGA TGT TTTGTAG
           TG _
GAM1804 HRH1 3' GGTGTTTATGTTGCAATCTGG 7825 TG _ TT
           T GAT GC GATATGAACATC
           | ||| || |||||
           G CTA CG TTGTATTTGTGG
           GT A _
GAM1804 HSPA4 3' GTACGTGTTAAGCAGCTGA 90654 TG A A
           T G TGCTTGATATG AC
           | | ||||| || ||
           A C ACGAATTGTGC TG
           GT G A
GAM1804 HUNK 3' GGTGTTCCAATAATGAGGCATT 28188 TG G AT__
TGG          T GATGCTT AT GAACATC
           | ||||| || |||||
           G TTACGGA TA CTTGTGG
           GT G ATAAC
GAM1804 ITGA6 3' GATGTTTATTTTCAGGCATTGGA 5789 G T
           TT GATGCTTGA ATGAACATC
           || ||||| |||||
           AG TTACGGA CT TATTTGTAG
           G T
GAM1804 KAL1 3' GGTGTCATTACCAGCATCTGA 5837 TG TGAT A
           T GATGCT ATGA CATC
           | ||||| || ||||
           A CTACGA TACT GTGG
           GT CCAT _
GAM1804 KCNA6 3' GGTGTTCCGGTCTACATTTAG 11142 CTT A
           TTGGATG GAT TGAACATC
           ||||| || |||||

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			GATTTAC CTG GCTTGTGG		
			AT_ _		
GAM1804 KIF13A	3'	GGTGTGAATGAAGTGTTCA	42342	G ATG	
		TTGGATGCTT AT AACATC			
		GACTTGTGAA TA TTGTGG			
		G AG_			
GAM1804 KIN	3'	GGTGTTCGCCAAGGCATT	25538	GATA	
		GATGCTT TGAACATC			
		TTACGGA GCTTGTGG			
		ACC_			
GAM1804 LARS2	3'	GATGTTGCCTCCGGTGTCCAA	31695	T TATG	
		TTGGATGCT GA AACATC			
		AACCTGTGG CT TTGTAG			
		C CCG_			
GAM1804 LGI1	3'	GATGTGTAAATAAGCGTTTAA	18734	ATATGA	
		TTGGATGCTTG ACATC			
		AATTTGCGAAT TGTAG			
		AAATG_			
GAM1804 MAGEA2	3'	GATGAACCTCAGCATCCAA	61109	T TATGAA	
		TTGGATGCT GA CATC			
		AACCTACGA CT GTAG			
		_ TCAA__			
GAM1804 MAGEL2	3'	GGTGTGTTGTGTTCCAGTTCCA	39329	T T_ TG	
		TGGA GCT GATA AACATC			
		ACCT TGA TTGT TTGTGG			
		_ CC GT			
GAM1804 MLC1	5'	GATGGATCAATGAGGCATTTAA	58292	G A A_	
		TTGGATGCTT AT TGA CATC			
		AATTTACGGA TA ACT GTAG			
		G _ AG			
GAM1804 MMP15	3'	GGTGCCACAGTGTGTCAGGCACT	11613	TG A	GAA__
	GG	T G TGCTTGATAT CATC			
		G C ACGGACTGTG GTGG			
		GT_ ACACCC			
GAM1804 MPHOSPH1	3'	GATGTAATAGGTCAGGTATTTG	33004	TG	ATGA_
	G	T GATGCTTGAT ACATC			
		G TTATGGACTG TGTAG			
		GT GATAA			
GAM1804 MSR1	3'	GGTGTAATTTTAAGTATCC	11704	T GA	
		GGATGCTTGA AT ACATC			

CCTATGAATT TA TGTGG
 T AA
 GAM1804 NDN 3' GGTGGGTCATTATAGTATTCAG 11760 TGAT A_
 TTGGATGCT ATGA CATC
 ||||| ||| |||
 GACTTATGA TACT GTGG
 TAT_ GG
 GAM1804 NOC4 3' GATGTCGTCCAGGCGTCC 21374 AT A
 GGATGCTTG ATGA CATC
 ||||| ||| |||
 CCTGCGGAC TGCT GTAG
 C_ _
 GAM1804 OPHN1 3' GGTGTTTATATCTCCTTTGTAT 11910 TT____
 TC GGATGC GATATGAACATC
 |||| | |||||
 CTTATG CTATATTTGTGG
 TTTCT
 GAM1804 PAFAH1B2 3' GATGTTTCATATCTAGTGTGTTGA 11955 TG T
 T GATGCT GATATGAACATC
 | |||| | |||||
 A TTGTGA CTATACTTGTAG
 GT T
 GAM1804 PCLO 3' GGTGTCATTTTGGCATTGTA 95888 TG TGAT A
 T GATGCT ATGA CATC
 | |||| ||| |||
 A TTACGG TACT GTGG
 GT TTT_ _
 GAM1804 PEX10 3' GATGTTTCCAGGTTTTCAG 12040 T ATAT
 TTGGA GCTTG GAACATC
 |||| ||| |||||
 AACCT TGGAC TTTGTAG
 T C_
 GAM1804 PIGR 3' GATGTTTGAAGAGTTCCAA 73003 T GATA
 TTGGA GCTT TGAACATC
 |||| ||| |||||
 AACCT TGAG GTTTGTAG
 _ AA_
 GAM1804 PIR51 3' CGGTGTTTATATTTGATTTGTG 22395 TT____
 TTTA TGGATGC GATATGAACATC G
 |||| | ||||| |
 ATTTGTG TTATATTTGTGG C
 TTTAGT
 GAM1804 PK428 5' GATGTTTAATTCAGCACCAG 14602 A T TA
 TTGG TGCT GA TGAACATC
 ||| ||| || |||||
 GACC ACGA CT ATTTGTAG
 _ _ TA
 GAM1804 PLA2G2D 3' GGTGTTTGGACCAAAGCATC 25721 GATA_
 GATGCTT TGAACATC
 |||| | |||||

		CTACGAA	GTTTGTGG		
		ACCAG			
GAM1804	PLAGL1	3'	GATGTTTTAAGAAGCATTT	12152	GATAT
			GGATGCTT	GAACATC	
			TTTACGAA	TTGTAG	
			GAAT_		
GAM1804	POH1	5'	GGTCCATATCGCGGCATCCG	20545	_ A ATC
			TGGATGCT	TGATATG AC	
			GCCTACGG	GCTATAC TG	
			C	C G	
GAM1804	PPARGC1	3'	GATGTAGTTAAGTATTTA	26081	ATGA
			TGGATGCTTGAT	ACATC	
			ATTTATGAATTG	TGTAG	
			A_		
GAM1804	PRPS1	3'	GATGTTGTGTGAGGGTGTTTGA	12401	TG G_ G
			T	GATGCTT ATAT AACATC	
			A	TTGTGGG TGTG TTGTAG	
			GT	AG _	
GAM1804	PTP4A2	3'	GGTGTTTCATGTTAGTTTCT	14442	T T
			GGA GCT	GATATGAACATC	
			TCT TGA	TTGTACTTGTGG	
			T _		
GAM1804	PX19	3'	GATGTGTCTCAGTATCTAG	26016	T TATGA
			TTGGATGCT	GA ACATC	
			GATCTATGA	CT TGTAG	
			_ CTG_		
GAM1804	PYGB	3'	GATGTCTTTAGTGTTGAGCCTC	12691	TG T TG GA_
	TGG		T	GA GCT ATAT ACATC	
			G	CT CGA TGTG TGTAG	
			GT	C GT ATTTC	
GAM1804	RAB23	3'	GGTGTGTCCTTGTTAAGTGATC	33253	A T_ _
	AA		TTGG	TGCTTGATA GA ACATC	
			AACT	GTGAATTGT CT TGTGG	
			A	TC G	
GAM1804	RAB27A	3'	GATGTTTCATATTGAAGCAGTCA	17149	GA _
			TG	TGCTT GATATGAACATC	
			AC	ACGAA TTATACTTGTAG	
			TG	G	
GAM1804	RAB2L	3'	GGTGTTTCATACCAGATGT	17670	GC A
			AT	TTG TATGAACATC	

			TG GAC ATACTTGTGG		
			TA C		
GAM1804	RAB4A	3'	GGTGTTCATACAGTGGCATTG 17147	TG	___ A
	G		T GATGCT TG TATGAACATC		
			G TTACGG AC ATACTTGTGG		
			GT TG _		
GAM1804	RAD54B	3'	GTAAATATTAAGTGTTTAA 25769		GA
			TTGGATGCTTGATAT AC		
			AATTTGTGAATTATA TG		
			AA		
GAM1804	RAD54B	3'	GTAAATATTAAGTGTTTAA 25770		GA
			TTGGATGCTTGATAT AC		
			AATTTGTGAATTATA TG		
			AA		
GAM1804	RANBP3	3'	GATGCTCTCGAGCGTTGAG 24632	G	TAT A
			TT GATGCTTGA GA CATC		
			GA TTGCGAGCT CT GTAG		
			G ___ C		
GAM1804	RASGRP1	3'	GATGTTCATCAAAAGTATGCGA 20417	G	GAT
			TTG ATGCTT ATGAACATC		
			AGC TATGAA TACTTGTAG		
			G AAC		
GAM1804	RERE	3'	GGTGTTCCTGGGGTGTCT 25018		GATAT
			GGATGCTT GAACATC		
			TCTGTGGG CTTGTGG		
			GT___		
GAM1804	RNASEH1	5'	GTGCGGTGTTAAGCGCCG 12877	A	GAA C
			TGG TGCTTGATAT CAT		
			GCC GCGAATTGTG GTG		
			_ GC_ A		
GAM1804	RNMT	3'	GTTTTGAGTCGAGTATCCAG 15057		AT_
			TTGGATGCTTGAT GAAC		
			GACCTATGAGCTG TTTG		
			AGT		
GAM1804	SART2	3'	GGTGTTTTTGGAAGTATTTGG 26251	TG	GA T
			T GATGCTT TA GAACATC		
			G TTATGAA GT TTTGTGG		
			GT G_ T		
GAM1804	SDC2	3'	GATGTTCATGGAATTGGTTTAA 67716		GCTTGA
			TTGGAT TATGAACATC		

AATTTG GTACTTGTAG
 GTTAAG
 GAM1804 SERPIND1 3' GGTGGAGGTCTAGGTGTCTGA 5743 TG _ ATGAA
 T GATGCTT GAT CATC
 | ||||| ||| ||||
 A CTGTGGA CTG GTGG
 GT T GAG__
 GAM1804 SFRS2IP 5' TAGTGCATATATTAAGTAGCTA 17546 A AA C
 G TTGG TGCTTGATATG CAT
 |||| ||||| |||
 GATC ATGAATTATAT GTG
 G AC ATG
 GAM1804 SH3BP5 3' GGTGTTTCAGAGGGGGCTTTTAA 17919 T GATA
 TTGGA GCTT TGAACATC
 |||| ||| |||||
 AATTT CGGG ACTTGTGG
 T GGAG
 GAM1804 SLC10A2 3' GAGTCTATTTCAAGTGTTTGG 6593 TG T A ATC
 T GATGCTTGA ATG AC
 | ||||| ||| ||
 G TTGTGAACT TAT TG
 GT T C AG
 GAM1804 SLC20A1 3' TTTGTATCAGGCTTCAA 60098 T TG
 TTGGA GCTTGATA AA
 |||| ||||| ||
 AACTT CGGACTAT TT
 _ GT
 GAM1804 SLC21A2 3' TTTATGTCAATGTCCAA 20090 C
 TTGGATG TTGATATGAA
 ||||| |||||
 AACCTGT AACTGTATTT
 _
 GAM1804 SLC25A4 3' GATGCTTCATTGAGTGTTCA 60266 TG TA _
 TGGATGCT A TGAA CATC
 ||||| | ||| ||||
 ACTTGTGA T ACTT GTAG
 GT__ C
 GAM1804 SLC26A2 3' GGTAAAAATTTCAAGTGTCCAA 5476 TATG__ ATC
 TTGGATGCTTGA AAC
 ||||| |||
 AACCTGTGAACT TTG
 TAAAA G
 GAM1804 SLC30A4 5' GGTGGCTGTGGGCGTCCG 26157 TGA AA
 TGGATGCT TATG CATC
 ||||| ||| ||||
 GCCTGCGG GTGT GTGG
 _ CG
 GAM1804 SLC38A2 3' GGTTCAAAATCAAGTGCCTAG 39115 AT A_ ATC
 TTGG GCTTGAT TGAAC
 |||| ||||| ||||

			GATC TGAACTA ACTTG		
			CG AA G		
GAM1804	SLC4A4	3'	GATGACTAAGTCAAGTGTCT 14994	A AA	
			GGATGCTTGAT TG CATC		
			TCTGTGAACTG AT GTAG		
			A CA		
GAM1804	SMARCC2	3'	GGTGTTTATACAAGGTTCTA 13257	TG A	
			TGGA CTTG TATGAACATC		
			ATCT GAAC ATATTTGTGG		
			TG _		
GAM1804	SNX13	3'	GGTGTTCATTTTGTCCAG 31395	GCTT T	
			TTGGAT GA ATGAACATC		
			GACCTG TT TACTTGTGG		
			____ T		
GAM1804	SOX11	3'	AATTCTTTATTGAGTGTCTAA 13307	TG T_ CATC	
			TTGGATGCT ATA GAA		
			AATCTGTGA TAT CTT		
			GT TT AAG		
GAM1804	SOX11	3'	GATGTCTTCTATGCATCCGA 13318	TT_ TATGA	
			TTGGATGC GA ACATC		
			AGCCTACG CT TGTAG		
			TAT TC__		
GAM1804	SP3	5'	GGTACAGTGTCCAGTGTTCAA 83385	T GA_ ATC	
			TTGGATGCT GATAT AC		
			AACTTGTGA CTGTG TG		
			C ACA G		
GAM1804	TAF4	3'	GGTGTGAATCAAGTGTTGAA 13516	G ATGA	
			TT GATGCTTGAT ACATC		
			AA TTGTGAACTA TGTGG		
			G AG__		
GAM1804	TCTA	3'	GATGGTACCAAGCATTTAG 42497	A GAA	
			TTGGATGCTTG TAT CATC		
			GATTTACGAAC ATG GTAG		
			C ____		
GAM1804	TMEM1	3'	GATGTTTATTGTTTTTATCTAA 13800	CTT _	
			TTGGATG GATA TGAACATC		
			AATCTAT TTGT ATTTGTAG		
			TT_ T		
GAM1804	TRAP240	3'	GATTATAGTATCTAGTATTCAA 18874	T GAAC	
			TTGGATGCT GATAT ATC		

			AACTTATGA CTATG TAG	
			T ATAT	
GAM1804	TYROBP	5'	GGTGTCCAGCAGCATCCG 13924	TGATA A
			TGGATGCT TG ACATC	
			GCCTACGA AC TGTGG	
			CG__ C	
GAM1804	UC28	3'	GATGTTTACTAGGCGTTT 41586	ATA
			GGATGCTTG TGAACATC	
			TTTGCGGAT ATTTGTAG	
			C__	
GAM1804	WEE1	5'	GGTGTTCGGGCGGCGCCG 14112	A T ATA
			TGG TGCT G TGAACATC	
			GCC GCGG C GCTTGTGG	
			_ _GG_	
GAM1804	YWHAE	3'	GTGATGCAAGCATCTAA 23137	A GA
			TTGGATGCTTG TAT AC	
			AATCTACGAAC GTA TG	
			_ G_	
GAM1804	ZNF134	3'	GATGTTGAATTTTCATGTATCTG 14304	TG T T G_
	A		T GATGC TGA AT AACATC	
			A CTATG ACT TA TTGTAG	
			GT T T AG	
GAM1804	ZNFN2A1	5'	GGTGTTCTTTTTTAAAGTGTTT 61395	GATAT__
	AG		TTGGATGCTT GAACATC	
			GACTTGTGAA CTTGTGG	
			ATTTTTT	
GAM1804	ADAMTSL1	3'	GGTGCAATCTACATTGGGCATC 54612	TG TG AT_ A__
	TGG		T GATGCT AT GA CATC	
			G CTACGG TA CT GTGG	
			GT GT CAT AAC	
GAM1804	ADNP	3'	GTATTCATTTTAAGCATCTAA 31691	T CATC
			TTGGATGCTTGA ATGAA	
			AATCTACGAATT TACTT	
			T ATG	
GAM1804	AP3M1	3'	GATGTATCACTATTAGGTACCA 24936	A _ _
	A		TTGG TGCTTGATA TGA ACATC	
			AACC ATGGATTAT ACT TGTAG	
			_ C A	
GAM1804	ARHGEF9	3'	GATGTTTGGGCAGCATT 31486	T ATA
			GATGCT G TGAACATC	

TTACGA C GTTTGTAG
 _ GG_
 GAM1804 ARP3BETA 3' GATGTTTATATTTCTATC 40338 CTT
 GATG GATATGAACATC
 |||| |||||
 CTAT TTATATTTGTAG
 CCT
 GAM1804 ATF3 3' GATGTTTGTGTACACAACA 15731 GA CT TG
 TG TG TGATA AACATC
 || || |||| ||||
 AC AC ACTGT TTGTAG
 A_ AC GT
 GAM1804 ATIP1 3' GATGTCACAGAGTGTGTCATGTGT 40773 TG T GA____
 CTGA T GATGC TGATAT ACATC
 | |||| |||| ||||
 A CTGTG ACTGTG TGTAG
 GT T AGACAC
 GAM1804 BC008967 5' GATGCGGAGGTGCGAGCGGTAA 61416 A ATGAA
 TTGG TGCTTGAT CATC
 |||| ||||| ||||
 AATT GCGAGCTG GTAG
 G GAGGC
 GAM1804 BCCIP 3' GTACAATGTCTAGCATCCAG 33807 T GA_
 TTGGATGCT GATAT AC
 ||||| |||| ||
 GACCTACGA CTGTA TG
 T ACA
 GAM1804 BM045 5' GATGTTACAGTCTAAGCGTCCA 78583 _ TA
 G TTGGATGCTT GA TGAACATC
 ||||| || |||||
 GACCTGCGAA CT ACTTG TAG
 T GC
 GAM1804 BM045 5' GATGTTACAGTCTAAGCGTCCA 78584 _ TA
 G TTGGATGCTT GA TGAACATC
 ||||| || |||||
 GACCTGCGAA CT ACTTG TAG
 T GC
 GAM1804 C20orf97 3' GTGCTTATCAGGTGCCAA 41265 A TGA
 TTGG TGCTTGATA AC
 |||| ||||| ||
 AACC GTGGACTAT TG
 _ TCG
 GAM1804 C21orf100 3' AATTGTCTGTGTGTGGGCATTC 59503 _ GA TC
 AG TTGGATGCTT ATAT ACA
 ||||| |||| ||
 GACTTACGGGT TGTG TGT
 G TC TAAG
 GAM1804 C8orf4 3' AATTTTATATCTGAGTGTTC 39690 _ CATC
 A TTGGATGCTT GATATGAA
 ||||| |||||

			AACTTGTGAG CTATATTT		
			T TTAAG		
GAM1804	CCNE2	3'	GGTGTTC AACCTGTGCTCTAA 55166	T	TTGATA
			TTGGA GC TGAACATC		
			AATCT CG ACTTGTGG		
			_ TGTCCA		
GAM1804	CIDEB	3'	GATGTCCCCCAGGCATCT 27797	ATAT	A
			GGATGCTTG GA CATC		
			TCTACGGAC CT GTAG		
			CCC_ _		
GAM1804	CLIC5	5'	CCTTTTCATGTGAGCATCTGG 34185	TG	G CATC
			T GATGCTT ATATGAA		
			G CTACGAG TGTACTT		
			GT _ TTCCT		
GAM1804	COQ7	3'	GATGTTTATAAGCCACCCAG 32855	AT_	TGA
			TTGG GCT TATGAACATC		
			GACC CGA ATATTTGTAG		
			CAC _		
GAM1804	D2S448	3'	GGTTCAGGGTGGCAGGTGTCCA 73892	ATA_	ATC
	G		TTGGATGCTTG TGAAC		
			GACCTGTGGAC ACTTG		
			GGTGGG G		
GAM1804	DECR2	3'	GGTGCCACGCAGGTGTCTGA 40702	TG	ATA AA
			T GATGCTTG TG CATC		
			A CTGTGGAC AC GTGG		
			GT GC_ C_		
GAM1804	DIO2	3'	GATGTGAAGAAATAAGTATCCA 26553	ATATGA_	
	G		TTGGATGCTTG ACATC		
			GACCTATGAAT TGTAG		
			AAAGAAG		
GAM1804	DKFZp434L0850	3'	GGTGTTTATATCGACACTCTGG 34524	TG _	C
			T GA TG TTGATATGAACATC		
			G CT AC AGCTATATTTGTGG		
			GT C _		
GAM1804	DKFZP434P0316	5'	GGTGGGCGTGCGGGCGTTCGA 50452	A	AA
			TTGGATGCTTG TATG CATC		
			AGCTTGCGGGC GTGC GTGG		
			_ GG		
GAM1804	DKFZp547D155	3'	GATGGGTATGTGTTAGGTATGT 70949	G	_ AA
	GA		TTG ATGCTTGATAT G CATC		

		AGT TATGGATTGTG T GTAG		
		G TA GG		
GAM1804	DKFZP564F0522 3'	GTACATGTAGGCATTTAG	69139	G A
		TTGGATGCTT ATATG AC		
		GATTTACGGA TGTAC TG		
		_ A		
GAM1804	DKFZP564I052 3'	ATCTATTTATTTCAAGCATCCA	67278	T CATC
	G	TTGGATGCTTGA ATGAA		
		GACCTACGAACT TATTT		
		T ATCTAA		
GAM1804	DKFZP566H073 5'	AGTCCTTCATCTCAAGCATCCA	32030	T CATC
	A	TTGGATGCTTGA ATGAA		
		AACCTACGAACT TACTT		
		C CCTGAA		
GAM1804	DRIL2 3'	GGTGGGGGTCTGTGGGTGTCCA	22354	___ ATGAA
	G	TTGGATGCTT GAT CATC		
		GACCTGTGGG CTG GTGG		
		TGT GGG__		
GAM1804	ELL2 3'	GATGTTTGTCTCCAGCATCCAG	24895	T T TG
		TTGGATGCT GA A AACATC		
		GACCTACGA CT T TTGTAG		
		C C GT		
GAM1804	ENPP4 3'	GATGTTTTTGAAGTATCTAA	30717	GATAT
		TTGGATGCTT GAACATC		
		AATCTATGAA TTTGTAG		
		GTT__		
GAM1804	ERO1L 3'	ATGTGACAAGCATTTAA	28156	ATATGA C
		TTGGATGCTTG ACAT		
		AATTTACGAAC TGTA		
		AG__ A		
GAM1804	FAM8A1 3'	GTTAATTTAGGCGTCTAG	33201	TATG
		TTGGATGCTTGA AAC		
		GATCTGCGGATT TTG		
		TAA_		
GAM1804	FIGN 3'	GTTTGTGTTAGTGTCTAG	36577	T TG
		TTGGATGCT GATA AAC		
		GATCTGTGA TTGT TTG		
		_ GT		
GAM1804	FLJ10697 3'	CATGTTTGTATCAGTATTTAG	36956	T TG C
		TTGGATGCT GATA AACAT		

GATTTATGA CTAT TTGTA
 _ GT CA
 GAM1804 FLJ10701 3' GGTTCATATCATGCATTCAG 36965 T _ ATC
 TTGGATGC TGATATG AAC
 ||||| ||||| ||
 GACTTACG ACTATAC TTG
 T G G
 GAM1804 FLJ10971 3' GGTGTTTCATGAACATATATC 37485 CT A_
 GATG TG TATGAACATC
 ||| || |||||
 CTAT AC GTACTTGTGG
 AT AA
 GAM1804 FLJ10980 3' GATGTTTGTCTCTAGTGTTT 65253 T T TG
 GGATGCT GA A AACATC
 ||||| || | |||||
 CTTGTGA CT T TTGTAG
 T C GT
 GAM1804 FLJ11259 3' GATGAAAGCTATGTCAAGCATT 37767 AA____
 CA TGGATGCTTGATATG CATC
 ||||| ||||| |||||
 ACTTACGAACTGTAT GTAG
 CGAAA
 GAM1804 FLJ12078 3' GTATGTATCAAGCTCCAA 47084 T A
 TTGGA GCTTGATATG AC
 ||||| ||||| || ||
 AACCT CGAACTATGT TG
 _ A
 GAM1804 FLJ12389 3' GGTGTTTCACGTGTGTCT 60902 T ATA
 GGATGC TG TGAACATC
 ||||| || |||||
 TCTGTG GC ACTTGTGG
 T ____
 GAM1804 FLJ12542 3' GATGTTTGTCTAAGGGTTTGA 46602 TG G AT TG
 T GAT CTTG A AACATC
 | ||| ||| | |||||
 A TTG GAAT T TTGTAG
 GT G C_ GT
 GAM1804 FLJ12707 5' GTTCAGAACGAGCATTAA 42203 ATA
 TTGGATGCTTG TGAAC
 ||||| ||||| |||||
 AATTTACGAGC ACTTG
 AAG
 GAM1804 FLJ12750 3' TCACTTGTCGGGCATCCAG 45443 ____
 TTGGATGCTTGATA TGA
 ||||| ||||| |||||
 GACCTACGGGCTGT ACT
 TC
 GAM1804 FLJ12787 3' AGTGTTCTGTATCAACATTTGG 50688 TG C _ C
 T GATG TTGATAT GAACAT
 | ||| ||||| |||||

		G TTAC AACTATG CTTGTG		
		GT _ T AG		
GAM1804	FLJ13441	3' TTTTTTTCATATTAAGTCTTCA 43925	T	CATC
	A	TTGGA GCTTGATATGAA		
		AACTT TGAATTATACTT		
		C TTTTGT		
GAM1804	FLJ13576	3' GTCTATTTTAAGTATTCAG 42811	T	A
		TTGGATGCTTGA ATG AC		
		GACTTATGAATT TAT TG		
		T C		
GAM1804	FLJ13984	3' GATTTTTTATAAGCATTCAA 45808	TGA	C
		TTGGATGCT TATGAA ATC		
		AACTTACGA ATATTT TAG		
		_ T		
GAM1804	FLJ14124	3' ATGTCCCGAGGTGTCCAG 46354	_	
		TTGGATGCTT GATAT		
		GACCTGTGGA CTGTA		
		GCC		
GAM1804	FLJ14166	3' GATGTACATGGGCGTTTGA 44988	TG	TGA A
		T GATGCT TATG ACATC		
		A TTGCGG GTAC TGTA		
		GT _ A		
GAM1804	FLJ14251	3' GTGTTTATGTTAGGATCTGA 46490	TG	G
		T GAT CTTGATATGAACAT		
		A CTA GGATTGTATTTGTG		
		GT _		
GAM1804	FLJ14326	3' GTTGTGGTCAGGTGTTTA 50782	ATG	
		TGGATGCTTGAT AAC		
		ATTTGTGGACTG TTG		
		GTG		
GAM1804	FLJ14399	3' GGTGTGGTGTTGAGTATCT 52341	TG	GA
		GGATGCT ATAT ACATC		
		TCTATGA TGTG TGTGG		
		GT G_		
GAM1804	FLJ20040	3' GATGTTTACAGAGCATCACAA 39159	_	GATA
		TTG GATGCTT TGAACATC		
		AAC CTACGAG ATTTGTAG		
		A AC_		
GAM1804	FLJ20232	3' GGTGTTTGCTGAGCGCTCCG 39188	_	ATA
		TGGA TGCTTG TGAACATC		

GCCT GCGAGT GTTTGTGG
 C C__
 GAM1804 FLJ20315 3' GATGTTTCAGGCCTAGCTCCAA 35415 T TGATA
 TTGGA GCT TGAACATC
 ||||| ||| |||||
 AACCT CGA ACTTGTAG
 _ TCCGG
 GAM1804 FLJ20513 3' GATGAAGTAAAATAAGTATCTA 35785 A__ GAA
 A TTGGATGCTTG TAT CATC
 ||||| ||| |||
 AATCTATGAAT ATG GTAG
 AAA AA_
 GAM1804 FLJ21313 3' GATGTCTGTATTCAGCATTCAA 43932 T GA
 TTGGATGCT GATAT ACATC
 ||||| ||| |||
 AACTTACGA TTATG TGTAG
 C TC
 GAM1804 FLJ21657 3' GGTGTTTATATTATTTAGTT 42803 GCT_
 GAT TGATATGAACATC
 ||| |||||
 TTG ATTATATTTGTGG
 ATTT
 GAM1804 FLJ22029 3' GAATTTGCATTAAGTGTTCOA 46909 AT CATC
 TTGGATGCTTGAT GAA
 ||||| |||
 AACTTGTGAATTA TTT
 CG AAG
 GAM1804 FLJ22408 5' GGTGTTTACCTGGCACTCAG 45986 GA TGATA
 TTG TGCT TGAACATC
 ||| ||| |||||
 GAC ACGG ATTTGTGG
 TC TCC__
 GAM1804 FLJ23510 3' GGTGTTTATGTCTCTGCA 45627 TT_
 TGC GATATGAACATC
 ||| |||||
 ACG CTGTATTTGTGG
 TCT
 GAM1804 FN5 3' GATGTTTCATGTTGCTGAGC 39817 ____
 GCTT GATATGAACATC
 ||| |||||
 CGAG TTGTACTTGTAG
 TCG
 GAM1804 GFPT1 3' GTGTACATGTTGGGTATCC 10788 TG A C
 GGATGCT ATATG ACAT
 ||||| ||| |||
 CCTATGG TGTAC TGTG
 GT A T
 GAM1804 GOLGA1 3' GGTGTTCTTAAAATCAGAGCGT 10851 _ AT____
 CCAG TTGGATGCT TGAT GAACATC
 ||||| ||| |||||

GACCTGCGA ACTA CTTGTGG
 G AAATT
 GAM1804 GOLGA1 3' TATTTTGTACAAGTGTCTAA 10852 A TG CATC
 TTGGATGCTTG TA AA
 ||||| || ||
 AATCTGTGAAC AT TT
 _ GT TATG
 GAM1804 HARP11 3' TTCATATCAAATATTTAA 38073 C
 TTGGATG TTGATATGAA
 ||||| |||||
 AATTTAT AACTATACTT
 A
 GAM1804 HOMER-2B 3' GATGTTTATATCTTTTCAT 17908 CTT
 ATG GATATGAACATC
 || |||||
 TAC CTATATTTGTAG
 TTT
 GAM1804 HSPCAL3 3' GATGTTT TAGAAAAGTATTT 77065 GATA
 GGATGCTT TGAACATC
 ||||| |||||
 TTTATGAA ATTTGTAG
 AAG_
 GAM1804 HTGN29 3' GTTTAATCAGGTGTCCAA 39886 A
 TTGGATGCTTGAT TGAAC
 ||||| |||||
 AACCTGTGGACTA ATTTG
 _
 GAM1804 KIAA0052 3' GGTGTACAGATTAAGCAT 68444 A A
 ATGCTTGAT TG ACATC
 ||||| || |||||
 TACGAATTA AC TGTGG
 G A
 GAM1804 KIAA0092 3' GATGACTCAATGTAAAGCATT 28650 _ _ A_
 TAA TTGGATGCTT GATAT GA CATC
 ||||| ||||| || |||||
 AATTTACGAA TTGTA CT GTAG
 A A CA
 GAM1804 KIAA0143 3' GATGTTTGTGTTTATGGCTATT 65410 TG _ T__ TG
 TGG T GAT GCT GATA AACATC
 | ||| ||| |||||
 G TTA CGG TTGT TTGTAG
 GT T TAT GT
 GAM1804 KIAA0179 3' GTACAATTAGGTATCTGA 65457 TG A A
 T GATGCTTGAT TG AC
 | ||||| || ||
 A CTATGGATTA AC TG
 GT _ A
 GAM1804 KIAA0232 3' TTGTTTATTTCAGTATCTGA 73126 TG T T TC
 T GATGCT GA ATGAACA
 | ||||| || |||||

A CTATGA CT TATTTGT
 GT _ _ TG
 GAM1804 KIAA0240 3' TTGTTATTAAGCATTGTA 94042 TG TGA TC
 T GATGCTTGATA ACA
 | ||||| |||
 A TTACGAATTAT TGT
 GT _ _ TT
 GAM1804 KIAA0318 3' GTATGTGTCGTGCATTCAG 69531 T A
 TTGGATGC TGATATG AC
 ||||| ||||| ||
 GACTTACG GCTGTGT TG
 T A
 GAM1804 KIAA0321 3' GGTTTTCAGGTGCAGGCATCTG 63061 TG ATA_ C
 A T GATGCTTG TGAA ATC
 | ||||| ||| |||
 A CTACGGAC ACTT TGG
 GT GTGG T
 GAM1804 KIAA0420 3' GGTGTTTACCTTGGCATCTGA 64092 TG TGATA
 T GATGCT TGAACATC
 | |||| |||||
 A CTACGG ATTTGTGG
 GT TTCC_
 GAM1804 KIAA0515 3' GGTGGTCTTCGGGCATGTGA 64554 G TAT A
 TTG ATGCTTGA GA CATC
 || ||||| || |||
 AGT TACGGGCT CT GTGG
 G T_ G
 GAM1804 KIAA0534 3' GGTGTGCATGCCAGTGTTCAA 71933 T A A
 TTGGATGCT G TATG ACATC
 ||||| | ||| |||||
 AACTTGTGA C GTAC TGTGG
 _C G
 GAM1804 KIAA0628 3' GATGAGGGTGTCAACATTTGG 29531 TG C GAA
 T GATG TTGATAT CATC
 | ||| ||||| |||
 G TTAC AACTGTG GTAG
 GT _ GGA
 GAM1804 KIAA0710 5' GTTGGGTCAGGCATCTAA 30188 ATG
 TTGGATGCTTGAT AAC
 ||||| |||
 AATCTACGGA CTG TTG
 GG_
 GAM1804 KIAA0836 3' GCATTTGTAATGAGCATTCAA 65168 A TG CATC
 TTGGATGCTTG TA AA
 ||||| || ||
 AACTTACGAGT AT TT
 A GT ACG
 GAM1804 KIAA1010 3' GATGTTTATATTTAAGTA 72543 _
 TGCTTGA TATGAACATC
 ||||| ||||| |||

ATGAATT ATATTTGTAG
 T
 GAM1804 KIAA1024 3' GATGTAAGGTCAGTATTTGA 69618 TG T ATGA
 T GATGCT GAT ACATC
 | ||||| ||| |||||
 A TTATGA CTG TGTAG
 GT _ GAA_
 GAM1804 KIAA1034 3' GATGTTTAATGGGATGAGCATT 63130 GA__ _
 GATGCTT TAT GAACATC
 ||||| || |||||
 TTACGAG GTA TTTGTAG
 TAGG A
 GAM1804 KIAA1074 5' TTGTTATGTTGGGCTCCG 30544 T TG A TC
 TGGA GCT ATATGA CA
 ||| ||| ||||| ||
 GCCT CGG TGTATT GT
 _ GT _ TC
 GAM1804 KIAA1157 3' GGTGTTTGTGCAAGTGTT 72705 A TG
 GATGCTTG TA AACATC
 ||||| || |||||
 TTGTGAAC GT TTGTGG
 _ GT
 GAM1804 KIAA1239 3' GTTTAACATGTAAGCGTTCAA 71849 ATA__ ATC
 TTGGATGCTTG TGAAC
 ||||| || |||||
 AACTTGCGAAT ATTTG
 GTACA
 GAM1804 KIAA1243 3' GATGAATAGTTTAAGTGTTTCAG 74026 TATGAA
 TTGGATGCTTGA CATC
 ||||| || |||||
 GACTTGTGAATT GTAG
 TGATAA
 GAM1804 KIAA1254 3' GATGTTTGTGTAAATTTGCA 70562 ____ TG
 TGC TTGATA AACATC
 ||| ||||| |||||
 ACG AATTGT TTGTAG
 TTTA GT
 GAM1804 KIAA1280 5' GGTGTTTAACGAAGTGTTTCAG 70286 GATA
 TTGGATGCTT TGAACATC
 ||||| || |||||
 GACTTGTGAA ATTTGTGG
 GCA_
 GAM1804 KIAA1323 3' GGTGTTTACATAGTGTCTA 63725 TGATA
 TGGATGCT TGAACATC
 ||||| || |||||
 ATCTGTGA ATTTGTGG
 TAC_
 GAM1804 KIAA1365 3' GATGTTTCATGTGGTTATGTATT 40815 TTG____
 GATGC ATATGAACATC
 ||||| ||||| |||||

TTATG TGTACTTGTAG
 TATTGG
 GAM1804 KIAA1416 3' GTTCCAGTTCAAGTGTTTAA 87757 TAT_
 TTGGATGCTTGA GAAC
 ||||| |||
 AATTTGTGAACT CTTG
 TGAC
 GAM1804 KIAA1437 5' GGTGTTTAAGTTGGAGTCTGG 61215 TG GC TG A
 T GAT T AT TGAACATC
 | ||| | || |||||
 G CTG G TG ATTTGTGG
 GT A_GT A
 GAM1804 KIAA1463 3' TTCATATTAGGCCTTTGA 72744 TG T
 T GA GCTTGATATGAA
 | || |||||
 A TT CGGATTATACTT
 GT C
 GAM1804 KIAA1500 3' GATGAGTGTGAGTTTTCAG 64811 T GAA
 TTGGA GCTTGATAT CATC
 |||| ||||| |||
 GACTT TGGACTGTG GTAG
 T A__
 GAM1804 KIAA1508 3' GATGTGACTCATGTATCCAA 62552 T TATGA
 TTGGATGC TGA ACATC
 ||||| || |||||
 AACCTATG ACT TGTAG
 T CAG__
 GAM1804 KIAA1524 5' GGTGTTTTTGCAGTGCATTCAA 73839 _ ATAT
 TTGGATGC TTG GAACATC
 ||||| || |||||
 AACTTACG GAC TTTGTGG
 T GTT_
 GAM1804 KIAA1576 3' GTTTATATTCAGCATCTGA 66493 TG T
 T GATGCT GATATGAAC
 | ||||| |||||
 A CTACGA TTATATTTG
 GT C
 GAM1804 KIAA1673 3' TTGATGTTAAGTGTTTGA 71332 TG G
 T GATGCTTGATAT AA
 | ||||| ||||| ||
 A TTGTGAATTGTA TT
 GT G
 GAM1804 KIAA1708 3' GGTTTGCTTGTGTCAGGTATTTA 67592 _ ATC
 TGGATGCTTGATA TGAAC
 ||||| ||||| |||||
 ATTTATGGACTGT GTTTG
 TC G
 GAM1804 KIAA1853 5' GTTGCGCATGGCGAGCGTTTCAG 69925 A GAA TC
 TTGGATGCTTG TAT CA
 ||||| ||||| || ||

GACTTGCGAGC GTA GT
 G GCG TGG
 GAM1804 KIAA1893 3' GGTGTTCTTGGGTATTGGG 73590 G TG TAT
 TT GATGCT A GAACATC
 || ||||| | |||||
 GG TTATGG T CTTGTGG
 G GT ____
 GAM1804 KIAA1908 3' GGTGTTTATATCCCAGCTCT 73795 T T_
 GGA GCT GATATGAACATC
 ||| ||| |||||
 TCT CGA CTATATTTGTGG
 _ CC
 GAM1804 KIAA1915 3' GGTGTTTATGAAGGTATTCA 73669 GA
 TGGATGCTT TATGAACATC
 ||||| |||||
 ACTTATGGA GTATTTGTGG
 A_
 GAM1804 KLHL6 3' GTAATATTTAGCATTCAAG 56175 T GA
 TTGGATGCT GATAT AC
 ||||| ||||| ||
 GACTTACGA TTATA TG
 T A_
 GAM1804 MAD4 3' GTCCATGTTGGGCACTAG 22277 A TG A
 TTGG TGCT ATATG AC
 ||| ||| ||||| ||
 GATC ACGG TGTAC TG
 _ GT C
 GAM1804 MBIP 3' CATATAATAAGCATTCAA 33894 ____
 TTGGATGCTTG ATATG
 ||||| |||||
 AACTTACGAAT TATAC
 AA
 GAM1804 MCAM 3' GTTTTGTCAGGTGTGTAA 22465 G T
 TTG ATGCTTGATA GAAC
 ||| ||||| |||||
 AAT TGTGGACTGT TTTG
 G _
 GAM1804 MCC2 3' GGTGCACATGGGTGTCCAG 72528 TGA AA
 TTGGATGCT TATG CATC
 ||||| |||||
 GACCTGTGG GTAC GTGG
 ____ AC
 GAM1804 MESDC2 3' GATGGACACTTGAGTGTTCAG 72916 TG TA AA
 TTGGATGCT A TG CATC
 ||||| | |||
 GACTTGTGA T AC GTAG
 GT C_ AG
 GAM1804 MGC12760 3' GGTGTGTCACACGCGTCCAG 52161 T ATA _
 TTGGATGC TG TGA ACATC
 ||||| || ||| |||||

		GACCTGCG AC ACT TGTGG		
		C _ G		
GAM1804	MGC14161	5' GCTGTTGGATCAGGTATTTAG 52911	ATG	TC
		TTGGATGCTTGAT AACA		
		GATTTATGGACTA TTGT		
		GG_ CGT		
GAM1804	MGC14376	3' GATGTTTCATCCCAGCATTGCAA 52916	_	T AT
		TTG GATGCT G ATGAACATC		
		AAC TTACGA C TACTTGTAG		
		G _ CC		
GAM1804	MGC17330	3' GGTGGTCCTGCGGGCGTCCAG 54630	A	T A
		TTGGATGCTTG TA GA CATC		
		GACCTGCGGGC GT CT GTGG		
		_ C G		
GAM1804	MGC20235	3' GATGAAGCTATCAGTATCCAG 59554	T	TGAA
		TTGGATGCT GATA CATC		
		GACCTATGA CTAT GTAG		
		_ CGAA		
GAM1804	MGC27171	3' GATGTTTGTCTGTGTTCA 58701	TT	AT
		TGGATGC GAT GAACATC		
		ACTTGTG CTG TTTGTAG		
		T_ _		
GAM1804	MGC3035	5' GGTGCGGGGTCAGGCGCCCG 44405	A	ATGAA
		TGG TGCTTGAT CATC		
		GCC GCGGACTG GTGG		
		C GGGC_		
GAM1804	MGC4399	3' TTCAGGGTTAAGCACCAA 89882	A	A_
		TTGG TGCTTGAT TGAA		
		AACC ACGAATTG ACTT		
		_ GG		
GAM1804	MGC4399	3' TTCAGGGTTAAGCACCAA 89883	A	A_
		TTGG TGCTTGAT TGAA		
		AACC ACGAATTG ACTT		
		_ GG		
GAM1804	MGC5309	3' GTTCTATTGTATTATGGTGTCC 81681	_	ATC
	GA	TTGGATGCT TGATAT GAAC		
		AGCCTGTGG ATTATG CTTG		
		T TTAT C		
GAM1804	MKRN2	3' GGTGAACAAATGGGGCATTCAA 72849	G	A AA
		TTGGATGCTT AT TG CATC		

		AACTTACGGG TA AC GTGG G A AA	
GAM1804 MSP	3'	GATGTTCTACAGGAGTGTCCA 50244 TGGATGCTT TA GAACATC ACCTGTGAG AT CTTGTAG GAC C	GA_ T
GAM1804 MYL6	3'	GATGTTTGCCGTCAGCATTCA 55325 TGGATGCT GAT TGAACATC ACTTACGA CTG GTTTGTAG _ CC	T A_
GAM1804 MYL6	3'	GATGTTTGCCGTCAGCATTCA 55326 TGGATGCT GAT TGAACATC ACTTACGA CTG GTTTGTAG _ CC	T A_
GAM1804 MYL6	3'	GATGTTTGCCGTCAGCATTCA 55327 TGGATGCT GAT TGAACATC ACTTACGA CTG GTTTGTAG _ CC	T A_
GAM1804 MYO18B	3'	GTGTGTACAAGCATTCAA 51882 TTGGATGCTTG TATG AC AACTTACGAAC ATGT TG _ G	A A
GAM1804 N4BP3	3'	GGTGGGGGCTTAGGCATCCA 66860 TGGATGCTTGA CATC ACCTACGGATT GTGG CGGGG_	TATGAA
GAM1804 NMNAT G	5'	GATGTTCCACTCGCTGGCGTCC 43287 TGGATGCT TGA GAACATC GCCTGCGG GCT CTTGTAG TC CAC	_ TAT
GAM1804 NMT1	3'	GGTGTTCCAGCCAAGTGACCG 41150 TGG TGCTTG TGAACATC GCC GTGAAC ACTTGTGG A CG_	A ATA
GAM1804 OAZ2	3'	GATGTTTATGAACTGGCATT 11877 GATGCT TATGAACATC TTACGG GTATTTGTAG TCAA	TGA_
GAM1804 PADI3 G	3'	GATGGTTAATATTAGGTGTCTG 33175 T GATGCTTGATAT CATC 	TG GAA_

			G CTGTGGATTATA	GTAG	
			GT	ATTG	
GAM1804	PCQAP	3'	GGTGTGTTAGAGCGTCT	32459	GAT G
			GGATGCTT	AT AACATC	
			TCTGCGAG	TG TTGTGG	
			AT_ _		
GAM1804	PEX11A	3'	TGTTTCATGTGAGCATTAA	15242	G
			TTGGATGCTT	ATATGAACA	
			AATTTACGAG	TGTA	CTTGT
GAM1804	PIP3-E	3'	GGTGTTCATTTTGTCC	67357	CTT T
			GGATG	GA ATGAACATC	
			CCTGT	TT TACTTGTGG	
				T	
GAM1804	PPFIBP2	3'	GATGTTTCATCTTCAGCACCAG	77100	A T T_
			TTGG TGCT	GA ATGAACATC	
			GACC	ACGA CT TACTTGTAG	
				TC	
GAM1804	PPP1R14C	3'	GATGGGGGTCAGGCATT	48927	ATGAA
			GGATGCTTGAT	CATC	
			TTTACG	GA	CTGTG
			GGG_		
GAM1804	PRO0132	5'	GATGGAATGAATGTAAAGTATG	26938	G GAA_
			TAA	TTG ATGCTTGATAT	CATC
			AAT	TATGAATTGTA	GTAG
			G	AGTAAG	
GAM1804	PRO0902	5'	GATGATCATCAAGTGTCT	54966	TA A
			GGATGCTTGA	TGA CATC	
			TCTGTGA	ACT	GTAG
				A	
GAM1804	PRO1430	3'	AATTTTATATCTGAGTGTTC	38354	_ CATC
			A	TTGGATGCTT	GATATGAA
			AACTTGTGAG	CTATATTT	
			T	TTAAG	
GAM1804	PRO2859	5'	GGTGTTCATATCAGCCTC	38213	T T
			GA GCT	GATATGAACATC	
			CT	CGA CTATACTTGTGG	
			C		
GAM1804	RANBP6	3'	GATGTTTATATTCTGACCAA	62311	ATGCTT
			TTGG	GATATGAACATC	

			AACC TTATATTTGTAG			
			AGTC__			
GAM1804	RBM14	3'	GATGATCCTGTTAAGTGTTCTG 21993		T	A
			TGGATGCTTGATA GA CATC			
			GCTTGTGAATTGT CT GTAG			
			C A			
GAM1804	RGS17	3'	GTATATATCAGATGTCCAA 25772	GC	A	
			TTGGAT TTGATATG AC			
			AACCTG GACTATAT TG			
			TA A			
GAM1804	RGS18	3'	ATGTTTATGTTAAGATTTGG 56260	TG	G	C
			T GAT CTTGATATGAACAT			
			G TTA GAATTGTATTTGTA			
			GT _ C			
GAM1804	RRN3	3'	GGTTCGACTGAATCAAGCATCT 37960	TG	A__	ATC
	GA		T GATGCTTGAT TGAAC			
			A CTACGAACTA GCTTG			
			GT AGTCA G			
GAM1804	SEC14L2	3'	GGTGTTTGCCAGTCTGAGTGTC 25797		_ A__	
	C		GGATGCTT GAT TGAACATC			
			CCTGTGAG CTG GTTTGTGG			
			T ACC			
GAM1804	SEMA3E	3'	AATGTTTGTAAATGAGTGTTCTGA 25800	A	TG	C
			TTGGATGCTTG TA AACAT			
			AGCTTGTGAGT AT TTGTA			
			A GT AG			
GAM1804	SENP7	3'	GATGTCATATGTGAGTATCT 40673		_	A
			GGATGCTTG ATATGA CATC			
			TCTATGAGT TATACT GTAG			
			G _			
GAM1804	SERF1B	5'	TGTTGTCGGGCCTCCAG 43709	T	TGA	
			TTGGA GCTTGATA ACA			
			GACCT CGGGCTGT TGT			
			C _			
GAM1804	SES2	3'	GTGGTATCCAGTGTTCAA 49591	T	GA	
			TTGGATGCT GATAT AC			
			AACTTGTGA CTATG TG			
			C G_			
GAM1804	SIMRP7	3'	GGTGAGCGTCGAGCGGCTGG 93979	TG	A	AT AA
			T G TGCTTGAT G CATC			

G C GCGAGCTG C GTGG
 GT G ____ GA
 GAM1804 SLC31A2 3' GATGGCCGTGGGTGTCTGG 60758 TG TGA AA
 T GATGCT TATG CATC
 | ||||| ||| ||||
 G CTGTGG GTGC GTAG
 GT ____ CG
 GAM1804 STAM2 3' GATGTGTGATAAAGCATTTAG 20703 G ATGA
 TTGGATGCTT AT ACATC
 ||||| || ||||
 GATTACGAA TA TGTAG
 A GTG_
 GAM1804 STAM2 3' TTTGTGTGTAAGCATTTAG 20711 _ TG
 TTGGATGCTTG ATA AA
 ||||| || ||
 GATTACGAAT TGT TT
 G GT
 GAM1804 STIP-1 3' GTGCATTTAAGTATCCAA 70240 T A
 TTGGATGCTTGA ATG AC
 ||||| || ||
 AACCTATGAATT TAC TG
 _ G
 GAM1804 T2BP 3' GTCTATATTCAGCATCTAA 70539 T A
 TTGGATGCT GATATG AC
 ||||| || ||
 AATCTACGA TTATAT TG
 C C
 GAM1804 TBC1D2 5' GATGTTTATGTCCAACCTGA 37931 TG A CTT
 T G TG GATATGAACATC
 | | || |||||
 A C AC CTGTATTTGTAG
 GT A ____
 GAM1804 TOLLIP 3' GGTGTTTGTGGTTCAAGTGTCT 39199 _ TG
 GGATGCTTGA TA AACATC
 ||||| || ||||
 TCTGTGAACT GT TTGTGG
 TG GT
 GAM1804 TP53INP1 3' GATGTCTTTTCATGGCATCTGA 53870 TG _ TAT A
 T GATGCT TGA GA CATC
 | |||| || ||||
 A CTACGG ACT CT GTAG
 GT T TT_ _
 GAM1804 TU12B1-TY 3' GATGTTTGTGCGACTATTTGG 33852 TG C A TG
 T GATG TTG TA AACATC
 | |||| || ||||
 G TTAT AGC GT TTGTAG
 GT C _ GT
 GAM1804 TUCAN 5' GTTAGTGCAAGCATCTGG 30986 TG A G
 T GATGCTTG TAT AAC
 | ||||| || ||

			G CTACGAAC GTG TTG		
			GT _ A		
GAM1804 UBAP	3'	GGTGT	TTATGTCCTCAGC 76842	T__	
			GCT GATATGAACATC		
			CGA CTGTATTTGTGG		
			CTC		
GAM1804 USP15	3'	TTTATG	TTAGCATTTAA 21966	T	
			TTGGATGCT GATATGAA		
			AATTTACGA TTGTATTT		
GAM1804 WBP4	5'	GGTGGGC	CATCGGGCGGCTGG 24201	TG A	TA AA
			T G TGCTTGA TG CATC		
			G C GCGGGCT AC GTGG		
			GT G _ GG		
GAM1804 WBP4	3'	GTATTATG	TTCAGTGTCTAA 24202	T _	
			TTGGATGCT GATATGA AC		
			AATCTGTGA TTGTATT TG		
			C A		
GAM1804 WDR7	3'	GGTGTT	CATTATGCTTCTAA 31612	T TTGAT	
			TTGGA GC ATGAACATC		
			AATCT CG TACTTGTGG		
			T TAT__		
GAM1804 YAP1	3'	GATGCTT	CATGTCACAGCATTT 21460	_	_
AG			TTGGATGCT TGATATGAA CATC		
			GATTTACGA ACTGTACTT GTAG		
			C C		
GAM1804 ZFD25	5'	GATGTCT	TTTGGTTGGTATCCG 33112	TGA TGA	
			TGGATGCT TA ACATC		
			GCCTATGG GT TGTAG		
			TTG TTC		
GAM1804 ZNF258	3'	GGTGTT	CCCCGCTGAAGTATTTG 24134	TG	GATAT_
G			T GATGCTT GAACATC		
			G TTATGAA CTTGTGG		
			GT GTCGCC		
GAM1804 ZNF262	3'	GGTTCCT	ATATAAAGCATTTGG 18725	TG	G _ ATC
			T GATGCTT ATAT GAAC		
			G TTACGAA TATA CTTG		
			GT A TC G		
GAM1804 ZNF364	3'	TCAAATT	CAGGTATCTAA 67312	TA_	
			TTGGATGCTTGA TGA		

	AATCTATGGACT ACT	
	TAA	
GAM1804 ZSIG11 5'	GGTGCAGTGTGGGGATCCAG 32494	G TG GAA
	TTGGAT CT ATAT CATC	
	GACCTA GG TGTG GTGG	
	G GT AC_	
GAM1804 LOC115294 3'	GTTCACTGTATAAAGTATTTGG 73382	TG G ____ ATC
	T GATGCTT ATA TGAAC	
	G TTATGAA TAT ACTTG	
	GT A GTC	
GAM1804 LOC115648 3'	GGTGTTCCTCAGTGTAGGTATCT 60029	ATA ____
	GGATGCTTG TGA ACATC	
	TCTATGGAT ACT TGTGG	
	GTG TT	
GAM1804 LOC116143 3'	GGTGTCATGGCGGGCATCT 74191	A A
	GGATGCTTG TATGA CATC	
	TCTACGGGC GTACT GTGG	
	G _	
GAM1804 LOC119035 3'	GATGGGGCTCTGGCATCCGA 74400	T TATGAA
	TTGGATGCT GA CATC	
	AGCCTACGG CT GTAG	
	T CGGG__	
GAM1804 LOC119214 3'	GATGGGGCTCTGGCATCCGA 74406	T TATGAA
	TTGGATGCT GA CATC	
	AGCCTACGG CT GTAG	
	T CGGG__	
GAM1804 LOC119548 3'	GGTGTTCCCTTGGTGTTCAG 74452	TGATAT
	TTGGATGCT GAACATC	
	GACTTGTGG CTTGTGG	
	TTC__	
GAM1804 LOC120114 3'	TTTGTGTTGTGTTAAGCATCCAA 76058	TG TC
	TTGGATGCTTGATA AACA	
	AACCTACGAATTGT TTGT	
	GT TTG	
GAM1804 LOC121441 3'	TTCATATTAGGTACTAA 74505	A
	TTGG TGCTTGATATGAA	
	AATC ATGGATTATACTT	
	_	
GAM1804 LOC127262 3'	GGTGTTCCTTGAGTATCTA 76603	TG TAT
	TGGATGCT A GAACATC	

	ATCTATGA T TTTGTGG		
	GT CCT		
GAM1804 LOC127428 3'	GATGTACAGTATAAGCATCTAA 75160	ATA A	
	TTGGATGCTTG TG ACATC		
	AATCTACGAAT AC TGTAG		
	ATG A		
GAM1804 LOC130162 3'	TTTTGGATTATTTCAAGTGTCT 75420	TG	T A_ TC
GA	T GATGCTTGA ATGA CA		
	A CTGTGAACT TATT GT		
	GT T AG TTTG		
GAM1804 LOC132235 5'	GCAATCAGTGTTAAGCATTCAG 76664	_	ACATC
	TTGGATGCTTGATA TGA		
	GACTTACGAATTGT ACT		
	G AACG		
GAM1804 LOC132321 3'	GGTGGCAGTGTTAGGCATCT 75572	GAA	
	GGATGCTTGATAT CATC		
	TCTACGGATTGTG GTGG		
	ACG		
GAM1804 LOC143154 3'	GCAGTTTTTATATCAAAGTATT 76991	_	CATC
TAA	TTGGATGCTT GATATGAA		
	AATTTATGAA CTATATTT		
	A TTGACGT		
GAM1804 LOC143154 3'	TATATTTTATATTAGGAATTCA 76994	G	CATC
A	TTGGAT CTTGATATGAA		
	AACTTA GGATTATATTT		
	A TATATT		
GAM1804 LOC144742 3'	GTTGGAAATGTCAGGTATTTGA 77465	TG	GAA TC
	T GATGCTTGATAT CA		
	A TTATGGACTGTA GT		
	GT AAG TGG		
GAM1804 LOC145566 5'	GATGTTCATACGTTTTTTCAG 77789	TGCT A	
	TTGGA TG TATGAACATC		
	GACTT GC ATACTTGTAG		
	TTTT _		
GAM1804 LOC145786 3'	GATGCCATTTGTTGAGCATCTA 84493	TG TGAA_	
	TGGATGCT ATA CATC		
	ATCTACGA TGT GTAG		
	GT TTACC		
GAM1804 LOC145988 3'	GATGTTCAATTACAGAATTCAG 78067	GC AT	
	TTGGAT TTG ATGAACATC		

		GA	CTTA	GAC	TACTTGTAG		
		A_	AT				
GAM1804	LOC146159 5'	GGTGTAGCTCAGGCATTTA	78180		TATGA		
		TGGATGCTTGA	ACATC				
		ATTTACGGA	CT TGTGG				
		CGA_					
GAM1804	LOC146489 5'	GATGTTTGTAGAGTTGTCTA	71343		_ GA TG		
		TGGATG CTT TA	AACATC				
		ATCTGT GAG AT	TTGTAG				
		T _	GT				
GAM1804	LOC146565 5'	GATGAACCTTGTGTTGGGCATT	61123		TG TGAA_		
		CAG	TTGGATGCT ATA	CATC			
		GA	CTTACGG TGT GTAG				
		GT	TGTTCAA				
GAM1804	LOC146714 5'	GATGGGTCACAGGTGTTTGG	84747	TG	ATA A_		
		T GATGCTTG	TGA CATC				
		G	TTGTGGAC ACT GTAG				
		GT _	GG				
GAM1804	LOC146733 3'	GGTGTTCCTGAGCGTTTGG	84787	TG	ATAT		
		T GATGCTTG	GAACATC				
		G	TTGCGAGT TTTGTGG				
		GT	CC_				
GAM1804	LOC146823 3'	GTTACCATCAGCATCCAG	84828	T	ATG		
		TTGGATGCT GAT	AAC				
		GACCTACGA	CTA TTG				
		_	CCA				
GAM1804	LOC146895 5'	GATGGGCTCAAGCATCTA	84868		TATGAA		
		TGGATGCTTGA	CATC				
		ATCTACGAACT	GTAG				
		CGG_					
GAM1804	LOC148014 3'	GGTCTTTGGGTCGGGTATTCA	79312		A C		
		TTGGATGCTTGAT	TGAA ATC				
		GA	CTTATGGGCTG GTTT TGG				
		G	C				
GAM1804	LOC148089 3'	GTCAATGTCAGGTGGCCAA	79334	AT	GA		
		TTGG	GCTTGATAT AC				
		AACC	TGGACTGTA TG				
		GG	AC				
GAM1804	LOC148250 5'	GATGTTTGGTTCAGTGCTTCAA	79494	T _	TA		
		TTGGA GC TTGA	TGAACATC				

			AACTT CG GACT GTTTGTAG		
			_ T TG		
GAM1804	LOC148490	5'	GGTGTTTGTGTTGGGGACACC	79623	A _ TG TG
			GG TG CT ATA AACATC		
			CC AC GG TGT TTGTGG		
			_ AG GT GT		
GAM1804	LOC148529	5'	TTTATATTAAGATGTTCAA	85324	_
			TTGGATG CTTGATATGAA		
			AACTTGT GAATTATATTT		
			A		
GAM1804	LOC149127	3'	GATGTTTCGAGGGGAGGTATTGA	85501	G GATA_
		G	TT GATGCTT TGAACATC		
			GA TTATGGA GCTTGTAG		
			G GGGGA		
GAM1804	LOC149420	3'	GATGAAGTAAGTGTTAAGTGTC	80154	GAA_
			GATGCTTGATAT CATC		
			CTGTGAATTGTG GTAG		
			AATGAA		
GAM1804	LOC150333	5'	GATGTTCTTCTTCGAGTATTT	86213	TAT_
			GGATGCTTGA GAACATC		
			TTTATGAGCT CTTGTAG		
			TCTT		
GAM1804	LOC150538	3'	GATGTTTATTTGCAACTAA	80739	A TTGAT
			TTGG TGC ATGAACATC		
			AATC ACG TATTTGTAG		
			A TT_		
GAM1804	LOC150933	3'	GATGTTTCATTGCTCCA	86338	T TTGAT
			TGGA GC ATGAACATC		
			ACCT CG TACTTGTAG		
			_ T_		
GAM1804	LOC151127	5'	GATGTTTATGGGCTAACC	80937	AT_ TGA
			GG GCT TATGAACATC		
			CC CGG GTATTTGTAG		
			AAT _		
GAM1804	LOC151465	3'	GGTTTAATTGCCAAGTGTCTAA	63444	A _ ATC
			TTGGATGCTTG TA TGAAC		
			AATCTGTGAAC GT ATTTG		
			C TA G		
GAM1804	LOC151623	3'	GATGTTTAGCAGCATCCG	86634	TGATA
			TGGATGCT TGAACATC		

	GCCTACGA	ATTTGTAG	
	CG__		
GAM1804 LOC152220 3'	GGTGTGTTCAAGTATCT	86768	TATG
	GGATGCTTGA AACATC		
	TCTATGAACT TTGTGG		
	TG__		
GAM1804 LOC153561 3'	GATGTTCAGTGAAGAGTACCAG	81750	A GATA_
	TTGG TGCTT TGAACATC		
	GACC ATGAG ACTTGTAG		
	_ AAGTG		
GAM1804 LOC153592 3'	GGTGGAACCTCAGGCATCCG	87248	TATGAA
	TGGATGCTTGA CATC		
	GCCTACGGA CTGG		
	CCAAG_		
GAM1804 LOC153642 3'	GTTGTATGTGAGCATTTGA	81790	TG G _
	T GATGCTT ATATG AAC		
	A TTACGAG TGTAT TTG		
	GT _ G		
GAM1804 LOC157273 3'	GATGTTTAAACAGAGATCTGA	87722	TG G GATA
	T GAT CTT TGAACATC		
	A CTA GAG ATTTGTAG		
	GT _ ACAA		
GAM1804 LOC157931 3'	ATGCTGTGTTAGGCTCCAA	87936	T GAA C
	TTGGA GCTTGATAT CAT		
	AACCT CGGATTGTG GTA		
	_ TC_ C		
GAM1804 LOC158219 3'	GTATGTGTTGTGGCATCCAG	82691	_ A
	TTGGATGCT TGATATG AC		
	GACCTACGG GTTGTGT TG		
	T A		
GAM1804 LOC158328 5'	GATGTTTTCTTGATTAGGTGTC	88119	AT__
T	GGATGCTTGAT GAACATC		
	TCTGTGGATTA TTTGTAG		
	GTTCT		
GAM1804 LOC158427 3'	GGTGTTTTCAAAAGTATTTGG	58355	TG GATAT
	T GATGCTT GAACATC		
	G TTATGAA TTTGTGG		
	GT AACT_		
GAM1804 LOC160646 3'	GATGTGGGGTATAGGGCATTTA	83114	TG GA_
A	TTGGATGCT ATAT ACATC		

	AATTTACGG TATG TGTAG		
	GA GGG		
GAM1804 LOC160675 5'	GATGCCATTCAAGTGTC 88443	T AA	
	GATGCTTGA ATG CATC		
	CTGTGAACT TAC GTAG		
	_ C_		
GAM1804 LOC161527 5'	TTGTTTCATGTTGGGCACTTAG 83152	GA TG TC	
	TTG TGCT ATATGAACA		
	GAT ACGG TGTACTTGT		
	TC GT T		
GAM1804 LOC169026 3'	GATGTTTACACATTAAGCATC 83603	A__	
	GATGCTTGAT TGAACATC		
	CTACGAATTA ATTTGTAG		
	CAC		
GAM1804 LOC170082 3'	GGTGTTTATGTTTTGCTTTGG 83447	TG T TT	
	T GA GC GATATGAACATC		
	G TT CG TTGTATTTGTGG		
	GT _ TT		
GAM1804 LOC196214 3'	GATGTTTGTATCCAACCTCCGG 91178	TGCTT TG	
	TTGGA GATA AACATC		
	GGCCT CTAT TTGTAG		
	CAAC_ GT		
GAM1804 LOC196283 3'	GGTGTTTATGAATAGATTCCAA 88998	TG TGA	
	TTGGA CT TATGAACATC		
	AACCT GA GTATTTGTGG		
	TA TAA		
GAM1804 LOC197342 3'	AGTGTGCCGTGCCAGGTGTCCA 89350	A A_ C	
G	TTGGATGCTTG TATG ACAT		
	GACCTGTGGAC GTGC TGTG		
	C CG AG		
GAM1804 LOC199858 3'	TTCATATCAGCATTAA 89804	T	
	TTGGATGCT GATATGAA		
	AATTTACGA CTATACTT		
	-		
GAM1804 LOC200235 5'	GGTTTCACATTGAGTGTTTAG 91571	TG A CATC	
	TTGGATGCT AT TGAA		
	GATTTGTGA TA ACTT		
	GT C TGG		
GAM1804 LOC201562 3'	GATGTGCATTAAGTATT 90414	ATGA	
	GATGCTTGAT ACATC		

	TTATGAATTA TGTAG		
	CG__		
GAM1804 LOC201696 5'	GGTGGAATGATGTCAAGAGTT 63823	G	GAA__
CAG	TTGGAT CTTGATAT CATC		
	GACTTG GAACTGTA GTGG		
	A GTAAAG		
GAM1804 LOC202266 3'	GGTGTTAGCAGGGTCAGGTGTT 91937	A_ _	
	GATGCTTGAT TG AACATC		
	TTGTGGACTG AC TTGTGG		
	GG GA		
GAM1804 LOC219294 3'	GCAGTTTTTATATCAAAGTATT 94595	_	CATC
TAA	TTGGATGCTT GATATGAA		
	AATTTATGAA CTATATTT		
	A TTGACGT		
GAM1804 LOC219294 3'	TACATTTTATATTAGGAATTCA 94599	G	CATC
A	TTGGAT CTTGATATGAA		
	AACTTA GGATTATATTT		
	A TACATT		
GAM1804 LOC219296 3'	GATGGGGCTCTGGCATCCGA 92896	T	TATGAA
	TTGGATGCT GA CATC		
	AGCCTACGG CT GTAG		
	T CGGG__		
GAM1804 LOC219654 3'	CGGTGTTTACCCCATATGAAGT 92930	G	_____
ATTCAA	TTGGATGCTT ATATG AACATC G		
	AACTTATGAA TATAC TTGTGG C		
	G CCCAT		
GAM1804 LOC219654 3'	GATGCCCATCTGGTGTCCAG 92935	T	TA AA
	TTGGATGCT GA TG CATC		
	GACCTGTGG CT AC GTAG		
	T __ CC		
GAM1804 LOC219730 3'	GATATTGGTGTGTCATAGCATTTG 94670	TG	_ G C
G	T GATGCT TGATAT AA ATC		
	G TTACGA ACTGTG TT TAG		
	GT T G A		
GAM1804 LOC220115 5'	GATGTTCTTCTTCGAGTATTT 93402	TAT_	
	GGATGCTTGA GAACATC		
	TTTATGAGCT CTTGTAG		
	TCTT		
GAM1804 LOC220469 5'	GATGTTTACTAAGCACTCTGA 76892	TG	_ ATA
	T GA TGCTTG TGAACATC		

A CT ACGAAT ATTTGTAG
 GT C C__
 GAM1804 LOC220758 3' GATGCCATGATCAGCATTCG 92467 T _ AA
 TGGATGCT GAT ATG CATC
 ||||| ||| ||| ||||
 GCTTACGA CTA TAC GTAG
 _ G C_
 GAM1804 LOC221322 5' GGCTCAGTATCAGGTATCTGA 93583 TG _ ACATC
 T GATGCTTGATA TGA
 | ||||| ||| |||
 A CTATGGACTAT ACT
 GT G CGG
 GAM1804 LOC221663 5' GGTGCTTTTAAGGCATCTAA 95466 GATAT _
 TTGGATGCTT GAA CATC
 ||||| ||| ||| |||
 AATCTACGGA TTT GTGG
 AT__ C
 GAM1804 LOC222193 3' GATGTTGAAGATCAAGCAGCCA 95843 A ATG_
 A TTGG TGCTTGAT AACATC
 ||| ||||| |||||
 AACC ACGAACTA TTGTAG
 G GAAG
 GAM1804 LOC222234 3' GATGTTTATGTCAGCCAACTGG 95901 TG A C
 T G TG TTGATATGAACATC
 | | ||||| |||||
 G C AC GACTGTATTTGTAG
 GT A C
 GAM1804 LOC253187 5' GATGTTTACCAGGAGGCATCT 98903 GATA_
 GGATGCTT TGAACATC
 ||||| |||||
 TCTACGGA ATTTGTAG
 GGACC
 GAM1804 LOC253351 5' GGTGTTTCATGGGGAAGTGGTGT 98035 TGA____
 TCAG TTGGATGCT TATGAACATC
 ||||| |||||
 GACTTGTGG GTACTTGTGG
 TCAAGGG
 GAM1804 LOC254065 5' GATGTTTCGCCAAATATTCAA 99291 C ATA
 TTGGATG TTG TGAACATC
 ||||| ||| |||||
 AACTTAT AAC GCTTGTAG
 A C_
 GAM1804 LOC254431 5' GATGTTTCCAGGTTTTCAA 98649 T ATAT
 TTGGA GCTTG GAACATC
 |||| |||| |||||
 AACTT TGGAC TTTGTAG
 T C_
 GAM1804 LOC255520 3' GGGTATATATCAAGTGTTTAA 97553 A ATC
 TTGGATGCTTGATATG AC
 ||||| ||||| ||| ||

AATTTGTGAACTATAT TG
 A GG
 GAM1804 LOC256021 3' GGTGTCTTATCAAGTTCCG 98279 T T A
 TGGA GCTTGATA GA CATC
 ||| ||||| || |||
 GCCT TGAACATAT CT GTGG
 _ T _
 GAM1804 LOC256158 5' GATGTTTATGTCCCACC 99495 A CTT
 GG TG GATATGAACATC
 || || |||||
 CC AC CTGTATTTGTAG
 _ C _
 GAM1804 LOC256338 3' GATGTGTCTCAGTATCTAG 96252 T TATGA
 TTGGATGCT GA ACATC
 ||||| || |||
 GATCTATGA CT TGTAG
 _ CTG _
 GAM1804 LOC256789 5' GGTGTTCAAGAGCAGCCAG 99310 A GATA
 TTGG TGCTT TGAACATC
 ||| ||| |||||
 GACC ACGAG ACTTGTGG
 G A _
 GAM1804 LOC256830 5' GTGCAGCTCAAGTATGCAG 96195 G TA A
 TTG ATGCTTGA TG AC
 || ||||| || ||
 GAC TATGAACT AC TG
 G CG G
 GAM1804 LOC257354 3' GGTGTTTACCTTGGCATCTGA 96794 TG TGATA
 T GATGCT TGAACATC
 | ||||| |||||
 A CTACGG ATTTGTGG
 GT TTCC _
 GAM1804 LOC257471 5' GGTACAGTGTCCAGTGTTCAG 97391 T GA_ ATC
 TTGGATGCT GATAT AC
 ||||| ||| ||
 AACTTGTGA CTGTG TG
 C ACA G
 GAM1804 LOC51014 3' GCTATTCATGTAAATATTCAA 66425 C CATC
 TTGGATG TTGATATGAA
 ||||| |||||
 AACTTAT AATTGTACTT
 A ATCGG
 GAM1804 LOC51622 3' GATGTTTCAGCCTTGCTTCCAG 32208 T TTGATA
 TTGGA GC TGAACATC
 |||| || |||||
 GACCT CG ACTTGTAG
 T TTCCG _
 GAM1804 LOC51696 3' GTTCTATATGAAGTATTTGA 33088 TG G _
 T GATGCTT ATAT GAAC
 | ||||| ||| |||

	A TTATGAA TATA CTTG	
	GT G T	
GAM1804 LOC63920 5'	GGTGTTCATAACTTGTCTAA 42265	GCTTGA
	TTGGAT TATGAACATC	
	AATCTG ATACTTGTGG	
	TTCA__	
GAM1804 LOC89919 3'	GTTTGGCTCAGGTGTCTGG 61380	TG TA
	T GATGCTTGA TGAAC	
	G CTGTGGACT GTTTG	
	GT CG	
GAM1804 LOC90231 3'	GATGTCCATCTCGGCGTTTCG 62529	T T A
	TGGATGCT GA ATG ACATC	
	GCTTGCGG CT TAC TGTAG	
	_ C C	
GAM1804 LOC90381 3'	GGTGAGTATTTGTGTATCTAA 63214	TT_ GA ATC
	TTGGATGC GATAT AC	
	AATCTATG TTATG TG	
	TGT AG G	
GAM1804 LOC90459 3'	GTTGGATCAAGTATTTAA 63561	ATG
	TTGGATGCTTGAT AAC	
	AATTTATGAACTA TTG	
	GG_	
GAM1804 LOC91012 5'	GGTGTTCATATCTATTACCAA 65247	ATGCTT
	TTGG GATATGAACATC	
	AACC CTATACTTGTGG	
	ATTAT_	
GAM1804 LOC91050 3'	GATGTTTTTGTATTAGCATTTA 65375	TG_ T
A	TTGGATGCT ATA GAACATC	
	AATTTACGA TGT TTTGTAG	
	TTA T	
GAM1804 LOC91768 3'	GTGTGTGAATGTGCAAGTGTCT 67708	TG _ GA C
GA	T GATGCTTG ATAT ACAT	
	A CTGTGAAC TGTA TGTG	
	GT G AG TGG	
GAM1804 LOC91948 3'	GATGTTCAGATGTGTTTCGG 68237	TTGATA
	TTGGATGC TGAACATC	
	GGCTTGTG ACTTGTAG	
	TAG__	
GAM1804 LOC91963 3'	GGTGTTTACCACCACATCCAG 68324	CTTGATA
	TTGGATG TGAACATC	

			GACCTAC	ATTTGTGG		
			ACCACC_			
GAM1804	LOC92078	5'	GATGTCTGCAGGTATTCA	68603	ATAT	A
			TGGATGCTTG	GA CATC		
			ACTTATGGAC	CT GTAG		
			GT__ _			
GAM1805	AQP6	5'	CCCCATCAGGTCAGCTCA	54995	ACGAGGCG	_
			TGAGCTGAC	GA GGGG		
			ACTCGACTG	CT CCCC		
			GA_____A			
GAM1805	AQP6	5'	CCCCATCAGGTCAGCTCA	9727	ACGAGGCG	_
			TGAGCTGAC	GA GGGG		
			ACTCGACTG	CT CCCC		
			GA_____A			
GAM1805	BCAT1	3'	CTCCACCTCTTGTGTCAGCTCA	66784	C	C
			TGAGCTGACA	GAGG GGAG		
			ACTCGACTGT	CTCC CCTC		
			T	A		
GAM1805	ENO1	3'	ACCCCTCCCCTCGTGTGTCAGCTC	9278		C
	A		TGAGCTGACACGAGG	GGAGGGGT		
			ACTCGACTGTGCTCC	CCTCCCCA		
GAM1805	FABP5	5'	CCTCTCTGCACGCCAGCCCG	9343	A	ACA AG
			TG GCTG	CG GCGGAGGGG		
			GC CGAC	GC CGTCTCTCC		
			C	C_ A_		
GAM1805	RAB5C	3'	ACCCCTCCACCCTCGGTCA	60525	A	C_
			TGAC CGAGG	GGAGGGGT		
			ACTG GCTCC	CCTCCCCA		
				CA		
GAM1805	RAD18	3'	ACCCCTCTGCCATCACCCAGCC	39802	A	ACAC _
	CA		TG GCTG	GA GGCGGAGGGGT		
			AC CGAC	CT CCGTCTCCCCA		
			C	CCA_ A		
GAM1805	RBMX	5'	ACCCCTCCGACTACCGGCCCA	68771	A	ACAC G
			TG GCTG	GAG CGGAGGGGT		
			AC CGGC	CTC GCCTCCCCA		
			C	CA_ A		
GAM1805	RCV1	3'	ACCCCTCCCTCTGTCCACCAGC	12800	A	____ C CG
	CCA		TG GCT	GACA GAGG GAGGGGT		

AC CGA CTGT CTCC CTCCCCA
 C CCAC _ _
 GAM1805 FLJ20195 3' ACCCCTCCACCCCGCAAGCTC 35210 GACA A C
 GAGCT CG GG GGAGGGGT
 |||| | || |||||
 CTCGA GC CC CCTCCCCA
 AC_ C A
 GAM1805 FLJ25193 5' CCCCTCCACCCAGCCAGCTCA 59356 ACACGA C
 TGAGCTG GG GGAGGGG
 ||||| | |||||
 ACTCGAC CC CCTCCCC
 CGACC_ A
 GAM1805 FOXP1 3' ACCCCTCCACACTTCAGCTC 52042 CACG GC_
 GAGCTGA AG GGAGGGGT
 ||||| | |||||
 CTCGACT TC CCTCCCCA
 _ ACA
 GAM1805 ISL2 3' CCCCTCCCTGCCAGCCCG 71398 A ACACGA C
 TG GCTG GG GGAGGGG
 || ||| | |||||
 GC CGAC TC CCTCCCC
 C CG_ _
 GAM1805 MGC16703 3' CCCCTTTTCACGTCAGCT 73491 AC GCG
 AGCTGAC GAG GAGGGG
 ||||| || |||||
 TCGACTG CTT TTCCCC
 CA _
 GAM1805 MTCH1 3' CCCCTCCAGTCAGCCCA 27562 A ACGAGGC
 TG GCTGAC GGAGGGG
 || ||||| |||||
 AC CGACTG CCTCCCC
 C A_ _
 GAM1805 PCBP3 3' ACCCTTCCCCCGCGTCA 40442 A A C
 TGAC CG GG GGAGGGGT
 ||| || || |||||
 ACTG GC CC CCTTCCA
 C _ _
 GAM1805 TUBB5 3' ACCCCCCACAGCGTCAGCTC 21409 ACGAGGC A
 GAGCTGAC GG GGGT
 ||||| | |||||
 CTCGACTG CC CCCCCA
 CGACA_ _
 GAM1805 LOC124225 5' CCCTTTTCCTCGTGCAGCCCA 74759 A A CG
 TG GCTG CACGAGG GAGGG
 || ||| ||||| |||||
 AC CGAC GTGCTCC TTCCC
 C _ TT
 GAM1805 LOC149302 5' CCCCTCCGTGGCAGCCCA 80039 A ACACGAG
 TG GCTG GCGGAGGGG
 || ||| |||||

		AC CGAC	TGCCTCCCC		
		C	GG_____		
GAM1805	LOC151178 3'	CCCACCTGCGTCAGCTCA	80955	ACGAG	AG
		TGAGCTGAC	GCGG GGG		
		ACTCGACTG	CGTC CCC		
		_____	CA		
GAM1805	LOC220776 3'	CCACCTCGTGTCTGCTCA	68919	T	C
		TGAGC GACACGAGG	GG		
		ACTCG CTGTGCTCC	CC		
		T	A		
GAM1805	LOC256072 3'	ACCCCTCCCCTCGTGTGCTC	96157		C
	A	TGAGCTGACACGAGG	GGAGGGGT		
		ACTCGACTGTGCTCC	CCTCCCCA		

GAM1805	LOC256374 3'	ACCCCTCCACCCCATTTGCTCA	96272	TGACACGA	C
		TGAGC	GG GGAGGGGT		
		ACTCG	CC CCTCCCCA		
		TTTACC_	A		
GAM1806	HSPC126 3'	TTGACTTTCTTTTAAAGCCAA	27178	CAAG	T
		TTGGTT	GGA GGAAAGTCAA		
		AACCGA	TTT TCTTTCAGTT		
		AA_	T		
GAM1806	FLJ23142 5'	ACTTTCCATAACAACCAA	45024	CAAGGG	
		TTGGTT	ATGGAAAGT		
		AACCAA	TACCTTTCA		
		CAA_			
GAM1806	KIAA0618 3'	TGACCTGTACCTTGAAC	29860	G	AAA
		GTTCAAGG ATGG	GTCA		
		CAAGTTCC TGTC	CAGT		
		A	_____		
GAM1806	KIAA0793 3'	TGACCTTCCATCTGGTGAACCA	29695	AG	A
	A	TTGGTTCA	GGATGGAA GTCA		
		AACCAAGT	TCTACCTT CAGT		
		GG	C		
GAM1806	KIAA1228 3'	ACTTTTCTACCTTGAGCCAA	65663	GAT	
		TTGGTTCAAGG	GGAAAGT		
		AACCGAGTTCC	CTTTTCA		
		AT_			
GAM1806	MGC22014 3'	ACTTCAACATACCCTGGACCAA	65107	A _	GA_
		TTGGTTCA	GGG ATG AAGT		

AACCAGGT CCC TAC TTCA
 _ A AAC
 GAM1806 SCAND2 3' TCAACCCTCTACTGAACCAG 54435 ____ A
 TTGGTTCA AGGG TGG
 ||||| |||||
 GACCAAGT TCCC ACT
 CATC A
 GAM1806 STAF65(gamma) 3' TTGACTCCTGTTCTTAAACACA 30078 _ CA AA
 A TTG GTT AGGGATGG AGTCAA
 ||| ||| ||||| |||||
 AAC CAA TTCTTGTC TCAGTT
 A A_ C_
 GAM1807 GPD1 3' TCATGCCACCACATTTG 60398 C C
 TAAATG GGTGGCAT GA
 ||||| ||||| ||
 GTTTAC CCACCGTA CT
 A _
 GAM1807 IL5RA 5' TCGCATGGCCACCGCATTT 6906 AT__
 AAATGCGGTGGC CGA
 ||||| ||||| ||
 TTTACGCCACCG GCT
 GTAC
 GAM1807 MYO1C 3' TGCCGATGCCAAATATTTG 61873 CGG A
 TAAATG TGGCATCG CA
 ||||| ||||| ||
 GTTTAT ACCGTAGC GT
 AA_ C
 GAM1807 C6orf37 3' TGTCACACTGCATTTA 68097 GCATC
 TAAATGCGGTG GACA
 ||||| ||||| ||
 ATTTACGTAC CTGT
 A____
 GAM1807 DNAJC6 3' TTGCAGAACCACCGCATT 29498 CA GA
 AATGCGGTGG TC CAA
 ||||| || |||||
 TTACGCCACC AG GTT
 A_ AC
 GAM1807 FLJ11210 3' GTCGATGTGCATGCTTTTA 60319 T GTG
 TAAA GCG GCATCGAC
 ||||| ||||| |||||
 ATTT CGT TG TAGCTG
 T ACG
 GAM1807 FLJ12476 3' TCGATCTTCTGCATTTA 43270 T C
 TAAATGCGG GG ATCGA
 ||||| || |||||
 ATTTACGTC TC TAGCT
 T _
 GAM1807 KIAA1034 3' TCGATGGCATCCGCATTTG 63134 _ G
 TAAATGCGG TG CATCGA
 ||||| || |||||

		GTTTACGCC AC GTAGCT		
		T G		
GAM1807	KIAA1987	3' TCATGTAAGTGCATTTA	89391	G C
		TAAATGCGGT GCAT GA		
		ATTTACGTCA TGTA CT		
		A _		
GAM1807	MGC16063	3' TGTCCTGGCCACTGCATT	54929	ATC
		AATGCGGTGGC GACA		
		TTACGTCACCG CTGT		
		GTC		
GAM1807	LOC147949	3' TGTCAGATGTCCACATTGCA	79279	_ _ _
		TGCG GTGG CATC GACA		
		ACGT CACC GTAG CTGT		
		TA T A		
GAM1807	LOC150577	3' GTCCTCACCGCATTTG	86258	CATC
		TAAATGCGGTGG GAC		
		GTTTACGCCACT CTG		
		C_		
GAM1807	LOC158219	3' TGTGTGTCACCACATTT	82694	C CG
		AAATG GGTGGCAT ACA		
		TTTAC CCACTGTG TGT		
		A _		
GAM1807	LOC202020	3' TGTCTCACACATTTA	90605	C CATC
		TAAATG GGTGG GACA		
		ATTTAC CCACT CTGT		
		A _		
GAM1807	LOC90826	5' TGTCGATGCAGTTTATTTG	64788	CGGTG
		TAAATG GCATCGACA		
		GTTTAT CGTAGCTGT		
		TTGGA		
GAM1807	LOC93587	3' TTGTCTTTACCTGCATTTA	73042	_ CATC
		TAAATGC GGTGG GACAA		
		ATTTACG CCATT CTGTT		
		T T_		
GAM1808	ELF3	3' TGACCTTGACCTTGACCAA	16685	T GAT AAA
		TTGGT CAAGG GG GTCA		
		AACCA GTTCC TC CAGT		
		_ AGT _		
GAM1808	JAK2	3' TGACCTTCATTCTGAGACCAA	18318	CAA AA
		TTGGTT GGGATGGA GTCA		

			AACCAG TCTTACTT CAGT		
			AG_ C_		
GAM1808	SLC10A2	5'	ACTCTCTGTCTTGACCAA 6590	CAA	A
			TTGGTT GGGATGGA AGT		
			AACCAG TTCTGTCT TCA		
			___ C		
GAM1808	FLJ10803	3'	GTGACTTTTCAGTTAAAGCCAA 37205	CAAGG	G
			TTGGTT GAT GAAAGTCAC		
			AACCGA TTG CTTTCAGTG		
			AA___ A		
GAM1808	KIAA1958	5'	GTGACTTTGAACCCCAAACC 82788	CAA	ATGG
			GGTT GGG AAAGTCAC		
			CCAA CCC TTTTCAGTG		
			A___ CAAG		
GAM1808	MARCKS	3'	ACTTTCCACCCTGCCCA 11411	TTCA	A
			TGG AGGG TGGAAAGT		
			ACC TCCC ACCTTTCA		
			CG___ _		
GAM1808	TUB	5'	GTGGGACCATCCCTTAAACC 13898	C	AAAG
			GGTT AAGGGATGG TCAC		
			CCAA TTCCCTACC GGTG		
			A AG___		
GAM1808	LOC80298	3'	ACTTTTACCTTGAACCA 48062	GATG	
			TGGTTCAAGG GAAAGT		
			ACCAAGTTCC TTTTCA		
			A___		
GAM1809	GPD1	3'	TCATGCCACCACATTTG 60398	C	C
			TAAATG GGTGGCAT GA		
			GTTTAC CCACCGTA CT		
			A _		
GAM1809	IL5RA	5'	TCGCATGGCCACCGCATTT 6906	AT___	
			AAATGCGGTGGC CGA		
			TTTACGCCACCG GCT		
			GTAC		
GAM1809	MYO1C	3'	TGCCGATGCCAAATATTTG 61873	CGG	A
			TAAATG TGGCATCG CA		
			GTTTAT ACCGTAGC GT		
			AA_ C		
GAM1809	C6orf37	3'	TGTCACACTGCATTTA 68097	GCATC	
			TAAATGCGGTG GACA		

		ATTTACGTCAC	CTGT	
		A_____		
GAM1809	DNAJC6	3'	TTGCAGAACCACCGCATT	29498 CA GA
			AATGCGGTGG TC CAA	
			TTACGCCACC AG GTT	
			A_ AC	
GAM1809	FLJ11210	3'	GTCGATGTGCATGCTTTTA	60319 T GTG
			TAAA GCG GCATCGAC	
			ATTT CGT TGTAGCTG	
			T ACG	
GAM1809	FLJ12476	3'	TCGATCTTCTGCATTTA	43270 T C
			TAAATGCGG GG ATCGA	
			ATTTACGTC TC TAGCT	
			T _	
GAM1809	KIAA1034	3'	TCGATGGCATCCGCATTTG	63134 _ G
			TAAATGCGG TG CATCGA	
			GTTTACGCC AC GTAGCT	
			T G	
GAM1809	KIAA1987	3'	TCATGTAACTGCATTTA	89391 G C
			TAAATGCGGT GCAT GA	
			ATTTACGTCA TGTA CT	
			A _	
GAM1809	MGC16063	3'	TGTCCTGGCCACTGCATT	54929 ATC
			AATGCGGTGGC GACA	
			TTACGTCACCG CTGT	
			GTC	
GAM1809	LOC147949	3'	TGTCAGATGTCCACATTGCA	79279 _ _ _
			TGCG GTGG CATC GACA	
			ACGT CACC GTAG CTGT	
			TA T A	
GAM1809	LOC150577	3'	GTCCTCACCGCATTTG	86258 CATC
			TAAATGCGGTGG GAC	
			GTTTACGCCACT CTG	
			C_____	
GAM1809	LOC158219	3'	TGTGTGTCACCACATTT	82694 C CG
			AAATG GGTGGCAT ACA	
			TTTAC CCACTGTG TGT	
			A _	
GAM1809	LOC202020	3'	TGTCTCACACATTTA	90605 C CATC
			TAAATG GGTGG GACA	

		ATTTAC CCACT CTGT		
		A ____		
GAM1809	LOC90826	5' TGTCGATGCAGGTTTATTTG	64788	CGGTG
		TAAATG GCATCGACA		
		GTTTAT CGTAGCTGT		
		TTGGA		
GAM1809	LOC93587	3' TTGTCTTTACCTGCATTTA	73042	_ CATC
		TAAATGC GGTGG GACAA		
		ATTTACG CCATT CTGTT		
		T T__		
GAM1810	ESPL1	5' ACACCTGGCTTTCCAAACTGA	25436	AACTTT
		TCAGT AAGCCAGGTGT		
		AGTCA TTCGGTCCACA		
		AACCT_		
GAM1810	HNT	3' CACCCGGCTTGACCCACT	33697	AAC A
		AGT TTTAAGCC GGTG		
		TCA AGGTTCCG CCAC		
		CCC C		
GAM1810	PRO2325	5' CCCGGCTTAAACCACTGAC	98037	AAC A
		GTCAGT TTTAAGCC GG		
		CAGTCA AAATTCGG CC		
		CCA C		
GAM1810	LOC219673	5' CACCTGGCCTAAATGC	94615	AC A
		GTA TTTA GCCAGGTG		
		CGT AAAT CGGTCCAC		
		_ C		
GAM1810	LOC89944	3' ACACCTGGCTTGGGCTCACTG	93173	AAC
		CAGT TTTAAGCCAGGTGT		
		GTCA GGGTTCGGTCCACA		
		CTC		
GAM1811	DYRK1A	3' CTCTAAACACACTTGGGCAC	9161	C G _
		G TG CTA TGTGTTTAGAG		
		C AC GGT ACACAAATCTC		
		_ G TC		
GAM1811	DYRK1A	3' CTCTAAACACACTTGGGCAC	56077	C G _
		G TG CTA TGTGTTTAGAG		
		C AC GGT ACACAAATCTC		
		_ G TC		
GAM1811	IGSF1	5' TCAGAGCACACAGCCAGCA	9559	A A
		TGCTGGCT TGTGTTT GA		

	ACGACCGA ACACGAG CT	
	C A	
GAM1811 PACSIN1	3' CTACGGCAAAGCCAGCAA 93881	A GTT
	TTGCTGGCT TGT TAG	
	AACGACCGA ACG ATC	
	A GC_	
GAM1811 KIAA0352	3' CTCCAACTGGGATGACCAGCAA 29825	C GT__ TA
	TG CATTGCTGG TAT GTT GAG	
	GTAACGACC GTA CAA CTC	
	A GGGT C_	
GAM1811 KIAA0438	3' TCCAAACTCAACCAGCAATG 29733	CTA T A
	CATTGCTGG TG GTTT GA	
	GTAACGACC AC CAAA CT	
	A__ T C	
GAM1811 PHRET1	3' CTCTAAACACAACAGGGCA 41350	GGCTA
	TGCT TGTGTTTAGAG	
	ACGG ACACAAATCTC	
	GACA_	
GAM1811 PLAGL2	3' CTCCAGCCTCTGCCAGCAATG 70959	TATGT TA
	CATTGCTGGC GTT GAG	
	GTAACGACCG CGA CTC	
	TCTC_ C_	
GAM1811 RAB22A	3' TCTCCAAAGACTGCAGCAATG 60610	GCTAT G A
	CATTGCTG GT TTT GAGA	
	GTAACGAC CA AAA CTCT	
	GT__ G C	
GAM1811 RGS18	3' CTCTAGTTATAAGCCAGCAA 56261	A T
	TTGCTGGCT TGTG TTAGAG	
	AACGACCGA ATAT GATCTC	
	_ T	
GAM1811 LOC126669	3' TCTCTAAACAAACCAACAA 75952	C CTATG
	TTG TGG TGTTTAGAGA	
	AAC ACC ACAAATCTCT	
	A AA__	
GAM1811 LOC144438	3' TCTCCAGTTGCAAACAGCAATG 77327	GCTA GT A
	CATTGCTG TGT TT GAGA	
	GTAACGAC ACG GA CTCT	
	AA__ TT C	
GAM1811 LOC149127	3' CTCTGCACACAGCCAGAATG 85499	G A TT
	CATT CTGGCT TGTGT AGAG	

GTAA GACCGA ACACG TCTC
 _ C _
 GAM1811 LOC150596 3' TCTCTAAACACTAACAACA 80749 C GCTAT
 TG TG GTGTTTAGAGA
 || || |||||
 AC AC CACAAATCTCT
 A AAT_
 GAM1811 LOC153338 5' TCTCTCATCATAGCCAGCA 87199 _ TTT
 TGCTGGCTATG TG AGAGA
 ||||| || ||||
 ACGACCGATAC AC TCTCT
 T _
 GAM1811 LOC201194 5' AAACACATAACCAAAATG 91347 GC C
 CATT TGG TATGTGTTT
 ||| || |||||
 GTAA ACC ATACACAAA
 A_ A
 GAM1811 LOC253983 3' CTCCAGCCTCAGCCAGCAA 98429 ATGT TA
 TTGCTGGCT GTT GAG
 ||||| || |||
 AACGACCGA CGA CTC
 CTC_ C_
 GAM1812 GPD1 3' TCATGCCACCACATTTG 60398 C C
 TAAATG GGTGGCAT GA
 |||| ||||| ||
 GTTTAC CCACCGTA CT
 A _
 GAM1812 IL5RA 5' TCGCATGGCCACCGCATTT 6906 AT_
 AAATGCGGTGGC CGA
 ||||| |||
 TTTACGCCACCG GCT
 GTAC
 GAM1812 MYO1C 3' TGCCGATGCCAAATATTTG 61873 CGG A
 TAAATG TGGCATCG CA
 |||| ||||| ||
 GTTTAT ACCGTAGC GT
 AA_ C
 GAM1812 C6orf37 3' TGTCACACTGCATTTA 68097 GCATC
 TAAATGCGGTG GACA
 ||||| |||
 ATTTACGTCAC CTGT
 A_
 GAM1812 DNAJC6 3' TTGCAGAACCACCGCATT 29498 CA GA
 AATGCGGTGG TC CAA
 ||||| || |||
 TTACGCCACC AG GTT
 A_ AC
 GAM1812 FLJ11210 3' GTCGATGTGCATGCTTTTA 60319 T GTG
 TAAA GCG GCATCGAC
 ||| || |||||

	ATTT CGT TGTAGCTG	
	T ACG	
GAM1812 FLJ12476 3'	TCGATCTTCTGCATTTA 43270	T C
	TAAATGCGG GG ATCGA	
	ATTTACGTC TC TAGCT	
	T _	
GAM1812 KIAA1034 3'	TCGATGGCATCCGCATTTG 63134	_ G
	TAAATGCGG TG CATCGA	
	GTTTACGCC AC GTAGCT	
	T G	
GAM1812 KIAA1987 3'	TCATGTAAGTGCATTTA 89391	G C
	TAAATGCGGT GCAT GA	
	ATTTACGTCA TGTA CT	
	A _	
GAM1812 MGC16063 3'	TGTCCTGGCCACTGCATT 54929	ATC
	AATGCGGTGGC GACA	
	TTACGTCACCG CTGT	
	GTC	
GAM1812 LOC147949 3'	TGTCAGATGTCCACATTGCA 79279	_ _ _
	TGCG GTGG CATC GACA	
	ACGT CACC GTAG CTGT	
	TA T A	
GAM1812 LOC150577 3'	GTCCTCACCGCATTTG 86258	CATC
	TAAATGCGGTGG GAC	
	GTTTACGCCACT CTG	
	C _	
GAM1812 LOC158219 3'	TGTGTGTCACCACATTT 82694	C CG
	AAATG GGTGGCAT ACA	
	TTTAC CCACTGTG TGT	
	A _	
GAM1812 LOC202020 3'	TGTCTCACACATTTA 90605	C CATC
	TAAATG GGTGG GACA	
	ATTTAC CCACT CTGT	
	A _	
GAM1812 LOC90826 5'	TGTCGATGCAGGTTTATTTG 64788	CGGTG
	TAAATG GCATCGACA	
	GTTTAT CGTAGCTGT	
	TTGGA	
GAM1812 LOC93587 3'	TTGTCTTTACCTGCATTTA 73042	_ CATC
	TAAATGC GGTGG GACAA	

ATTTACG CCATT CTGTT
 T T___
 GAM1813 CDC6 3' TGACCTTTTTTACTTGAAGCCA 8831 _ GGAT A
 A TTGGTT CAAG GGAAA GTCA
 ||||| ||| ||||| |||||
 AACCGA GTTC TTTT CAGT
 A AT___ C
 GAM1813 ELF3 3' GACCTTGACCTTGACCAA 16682 T GAT AAAA
 TTGGT CAAGG GG GTC
 ||||| ||||| || |||
 AACCA GTTCC TC CAG
 _ AGT ____
 GAM1813 SLC10A2 5' ACTCTCTGTCTTGACCAA 6591 CAA AA
 TTGGTT GGGATGGA AGT
 ||||| ||||| ||||| |||
 AACCA G TTCTGTCT TCA
 ____ C_
 GAM1813 FLJ10829 3' ACTTTTCCACCAAAGCTA 37252 CAAG A
 TGGTT GG TGGAAAAGT
 ||||| ||||| ||||| |||||
 ATCGA CC ACCTTTTCA
 AA___ _
 GAM1813 HEAB 3' TGACTCTTCTAATCTTGAACCA 23363 GA A
 A TTGGTTCAAGG TGGAA AGTCA
 ||||| ||||| ||||| |||||
 AACCAAGTTCT ATCTT TCAGT
 A_ C
 GAM1813 HEMK 5' TGACCTCTCCATCTCCACC 32966 TCAA AAA
 GGT GGGATGGA GTCA
 ||| ||||| ||||| |||||
 CCA CTCTACCT CAGT
 C___ CTC
 GAM1813 KIAA0298 3' TCCAAGTTCATGAGCCAA 77080 A A_
 TTGGTTCA GGG TGGA
 ||||| ||| ||||| |||||
 AACCGAGT CTT ACCT
 A GA
 GAM1813 KIAA1228 3' ACTTTTCTACCTTGAGCCAA 65664 GA
 TTGGTTCAAGG TGGAAAAGT
 ||||| ||||| ||||| |||||
 AACCGAGTTCC ATCTTTTCA

 GAM1813 KIAA1486 3' TGACTTTTCTCTCTTATACCAA 67982 TC TG
 TTGGT AAGGGA GAAAAGTCA
 ||||| ||||| ||||| |||||
 AACCA TTCTCT CTTTTCAGT
 TA ____
 GAM1813 MGC21854 3' ACTTTTCAATTTGATCCAA 54601 T GGATG
 TTGG TCAAG GAAAAGT
 ||||| ||||| ||||| |||||

		AACC AGTTT CTTTCA		
		T AA__		
GAM1813	LOC148697 3'	ACTTTTCCTGCTCAAACC 79671	CAA	AT
		GGTT GGG GGAAAAGT		
		CCAA CTC CCTTTTCA		
		A__ GT		
GAM1813	LOC80298 3'	ACTTTTACCTTGAACCA 48063	GATGG	
		TGGTTCAAGG AAAAGT		
		ACCAAGTTCC TTTTCA		
		A__		
GAM1814	ELF3 3'	TGACCTTGACCTTGACCAA 16685	T	GAT AAA
		TTGGT CAAGG GG GTCA		
		AACCA GTTCC TC CAGT		
		_ AGT _		
GAM1814	JAK2 3'	TGACCTTCATTCTGAGACCAA 18318	CAA	AA
		TTGGTT GGGATGGA GTCA		
		AACCAG TCTTACTT CAGT		
		AG_ C_		
GAM1814	SLC10A2 5'	ACTCTCTGTCTTGACCAA 6590	CAA	A
		TTGGTT GGGATGGA AGT		
		AACCAG TTCTGTCT TCA		
		_ C		
GAM1814	FLJ10803 3'	GTGACTTTCAGTTAAAGCCAA 37205	CAAGG	G
		TTGGTT GAT GAAAGTCAC		
		AACCGA TTG CTTTCAGTG		
		AA__ A		
GAM1814	KIAA1958 5'	GTGACTTTGAACCCCAAACC 82788	CAA	ATGG
		GGTT GGG AAAGTCAC		
		CCAA CCC TTTCAGTG		
		A__ CAAG		
GAM1814	MARCKS 3'	ACTTTCCACCCTGCCCA 11411	TTCA	A
		TGG AGGG TGGAAAGT		
		ACC TCCC ACCTTTCA		
		CG_ _		
GAM1814	TUB 5'	GTGGGACCATCCCTTAAACC 13898	C	AAAG
		GGTT AAGGGATGG TCAC		
		CCAA TTCCCTACC GGTG		
		A AG_		
GAM1814	LOC80298 3'	ACTTTTACCTTGAACCA 48062	GATG	
		TGGTTCAAGG GAAAGT		

			ACCAAGTTCC	TTTTCA		
			A__			
GAM1815	ELF3	3'	TGACCTTGACCTTGACCAA	16685	T	GAT AAA
			TTGGT CAAGG GG	GTCA		
			AACCA GTTCC TC	CAGT		
			_ AGT _			
GAM1815	JAK2	3'	TGACCTTCATTCTGAGACCAA	18318	CAA	AA
			TTGGTT GGGATGGA	GTCA		
			AACCAG TCTTACTT	CAGT		
			AG_ C_			
GAM1815	SLC10A2	5'	ACTCTCTGTCTTGACCAA	6590	CAA	A
			TTGGTT GGGATGGA	AGT		
			AACCAG TTCTGTCT	TCA		
			_ C			
GAM1815	FLJ10803	3'	GTGACTTTCAGTTAAAGCCAA	37205	CAAGG	G
			TTGGTT GAT	GAAAGTCAC		
			AACCGA TTG CTTTCAGTG			
			AA_ A			
GAM1815	KIAA1958	5'	GTGACTTTGAACCCCAAACC	82788	CAA	ATGG
			GGTT GGG AAAGTCAC			
			CCAA CCC TTTCAGTG			
			A_ CAAG			
GAM1815	MARCKS	3'	ACTTTCCACCCTGCCCA	11411	TTCA	A
			TGG AGGG TGGAAAGT			
			ACC TCCC ACCTTTCA			
			CG_ _			
GAM1815	TUB	5'	GTGGGACCATCCCTTAAACC	13898	C	AAAG
			GGTT AAGGGATGG TCAC			
			CCAA TTCCCTACC GGTG			
			A AG_			
GAM1815	LOC80298	3'	ACTTTTACCTTGAACCA	48062	GATG	
			TGGTTCAAGG GAAAGT			
			ACCAAGTTCC TTTCA			
			A_			
GAM1816	GPD1	3'	TCATGCCACCACATTTG	60398	C	C
			TAAATG GGTGGCAT	GA		
			GTTTAC CCACCGTA	CT		
			A _			
GAM1816	IL5RA	5'	TCGCATGGCCACCGCATTT	6906	AT_	
			AAATGCGGTGGC	CGA		

		TTTACGCCACCG GCT		
		GTAC		
GAM1816 MYO1C	3'	TGCCGATGCCAAATATTTG 61873	CGG	A
		TAAATG TGGCATCG CA		
		GTTTAT ACCGTAGC GT		
		AA_ C		
GAM1816 C6orf37	3'	TGTCACACTGCATTTA 68097	GCATC	
		TAAATGCGGTG GACA		
		ATTTACGTCAC CTGT		
		A_____		
GAM1816 DNAJC6	3'	TTGCAGAACCACCGCATT 29498	CA GA	
		AATGCGGTGG TC CAA		
		TTACGCCACC AG GTT		
		A_ AC		
GAM1816 FLJ11210	3'	GTCGATGTGCATGCTTTTA 60319	T GTG	
		TAAA GCG GCATCGAC		
		ATTT CGT TG TAGCTG		
		T ACG		
GAM1816 FLJ12476	3'	TCGATCTTCTGCATTTA 43270	T C	
		TAAATGCGG GG ATCGA		
		ATTTACGTC TC TAGCT		
		T _		
GAM1816 KIAA1034	3'	TCGATGGCATCCGCATTTG 63134	_ G	
		TAAATGCGG TG CATCGA		
		GTTTACGCC AC GTAGCT		
		T G		
GAM1816 KIAA1987	3'	TCATGTAAGTGCATTTA 89391	G C	
		TAAATGCGGT GCAT GA		
		ATTTACGTCA TGTA CT		
		A _		
GAM1816 MGC16063	3'	TGTCCTGGCCACTGCATT 54929	ATC	
		AATGCGGTGGC GACA		
		TTACGTCACCG CTGT		
		GTC		
GAM1816 LOC147949	3'	TGTCAGATGTCCACATTGCA 79279	_ _ _	
		TGCG GTGG CATC GACA		
		ACGT CACC GTAG CTGT		
		TA T A		
GAM1816 LOC150577	3'	GTCCTCACCGCATTTG 86258	CATC	
		TAAATGCGGTGG GAC		

		GTTTACGCCACT	CTG		
		C___			
GAM1816	LOC158219	3'	TGTGTGTCACCACATTT	82694	C CG
			AAATG GGTGGCAT ACA		
			TTTAC CCACTGTG TGT		
			A _		
GAM1816	LOC202020	3'	TGTCTCACCACATTTA	90605	C CATC
			TAAATG GGTGG GACA		
			ATTTAC CCACT CTGT		
			A _		
GAM1816	LOC90826	5'	TGTCGATGCAGGTTTATTTG	64788	CGGTG
			TAAATG GCATCGACA		
			GTTTAT CGTAGCTGT		
			TTGGA		
GAM1816	LOC93587	3'	TTGTCTTTACCTGCATTTA	73042	_ CATC
			TAAATGC GGTGG GACAA		
			ATTTACG CCATT CTGTT		
			T T__		
GAM1817	GPD1	3'	TCATGCCACCACATTTG	60398	C C
			TAAATG GGTGGCAT GA		
			GTTTAC CCACCGTA CT		
			A _		
GAM1817	IL5RA	5'	TCGCATGGCCACCGCATTT	6906	AT__
			AAATGCGGTGGC CGA		
			TTTACGCCACCG GCT		
			GTAC		
GAM1817	MYO1C	3'	TGCCGATGCCAAATATTTG	61873	CGG A
			TAAATG TGGCATCG CA		
			GTTTAT ACCGTAGC GT		
			AA_ C		
GAM1817	C6orf37	3'	TGTCACACTGCATTTA	68097	GCATC
			TAAATGCGGTG GACA		
			ATTTACGTCAC CTGT		
			A__		
GAM1817	DNAJC6	3'	TTGCAGAACCACCGCATT	29498	CA GA
			AATGCGGTGG TC CAA		
			TTACGCCACC AG GTT		
			A_ AC		
GAM1817	FLJ11210	3'	GTCGATGTGCATGCTTTTA	60319	T GTG
			TAAA GCG GCATCGAC		

	ATTT CGT TGTAGCTG	
	T ACG	
GAM1817 FLJ12476 3'	TCGATCTTCTGCATTTA 43270	T C
	TAAATGCGG GG ATCGA	
	ATTTACGTC TC TAGCT	
	T _	
GAM1817 KIAA1034 3'	TCGATGGCATCCGCATTTG 63134	_ G
	TAAATGCGG TG CATCGA	
	GTTTACGCC AC GTAGCT	
	T G	
GAM1817 KIAA1987 3'	TCATGTAAGTGCATTTA 89391	G C
	TAAATGCGGT GCAT GA	
	ATTTACGTCA TGTA CT	
	A _	
GAM1817 MGC16063 3'	TGTCCTGGCCACTGCATT 54929	ATC
	AATGCGGTGGC GACA	
	TTACGTCACCG CTGT	
	GTC	
GAM1817 LOC147949 3'	TGTCAGATGTCCACATTGCA 79279	_ _ _
	TGCG GTGG CATC GACA	
	ACGT CACC GTAG CTGT	
	TA T A	
GAM1817 LOC150577 3'	GTCCTCACCGCATTTG 86258	CATC
	TAAATGCGGTGG GAC	
	GTTTACGCCACT CTG	
	C _	
GAM1817 LOC158219 3'	TGTGTGTCACCACATTT 82694	C CG
	AAATG GGTGGCAT ACA	
	TTTAC CCACTGTG TGT	
	A _	
GAM1817 LOC202020 3'	TGTCTCACACATTTA 90605	C CATC
	TAAATG GGTGG GACA	
	ATTTAC CCACT CTGT	
	A _	
GAM1817 LOC90826 5'	TGTCGATGCAGGTTTATTTG 64788	CGGTG
	TAAATG GCATCGACA	
	GTTTAT CGTAGCTGT	
	TTGGA	
GAM1817 LOC93587 3'	TTGTCTTTACCTGCATTTA 73042	_ CATC
	TAAATGC GGTGG GACAA	

		ATTACG CCATT CTGTT		
		T T__		
GAM1818 ADAM20	5'	TCCAGCTCCACCAGGACA 15103	AGC	A
		TGTCC TGGTGA CTGGA		
		ACAGG ACCACCT GACCT		
		__ C		
GAM1818 ATP1B2	3'	CCAACCTCAGATCAGTCAGACA 9829	CA	G_ AC_
		TGTC GCTGGT GA TGG		
		ACAG TACTA CT ACC		
		AC GA CCA		
GAM1818 BIRC7	5'	TCCAGAAGGGCCAGCTGGGCA 42466	GGAA	
		TGTCCAGCTGGT CTGGA		
		ACGGGTCGACCG GACCT		
		GGAA		
GAM1818 BIRC7	5'	TCCAGAAGGGCCAGCTGGGCA 58443	GGAA	
		TGTCCAGCTGGT CTGGA		
		ACGGGTCGACCG GACCT		
		GGAA		
GAM1818 BRCA2	3'	TCCAGTTTATAAGACTGGA 5346	_ GGTG	
		TCCAG CT GAACTGGA		
		AGGTC GA TTTGACCT		
		A ATA_		
GAM1818 CD74	3'	CCAGACCCAGGCTGGACA 16379	_ T AA	
		TGTCCAGC TGG GG CTGG		
		ACAGGTCG ACC CC GACC		
		G _ A_		
GAM1818 DCK	5'	CCAGCCCTCTTTGCCGGACG 7629	A T_ T AA	
		TGTCC GC GG GG CTGG		
		GCAGG CG TC CC GACC		
		C TT T C_		
GAM1818 DLEC1	3'	CCAGGCCCCAGCTGGA 24718	T AA	
		TCCAGCTGG GG CTGG		
		AGGTCGACC CC GACC		
		_ G_		
GAM1818 DLEC1	3'	CCAGTTCCACTGGGGCA 24719	AGC	
		TGTCC TGGTGGAACTGG		
		ACGGG GTCACCTTGACC		
		__		
GAM1818 DLEC1	3'	CCAGGCCCCAGCTGGA 24729	T AA	
		TCCAGCTGG GG CTGG		

			AGGTCGACC CC GACC		
			— G—		
GAM1818 DLEC1	3'	CCAGTTCCACTGGGGCA	24730	AGC	
		TGTCC TGGTGGAACTGG			
		ACGGG GTCACCTTGACC			
GAM1818 ENO3	3'	TCCAGGACTCCACTGGACA	10522	C T AA	
		TGTCCAG TGG GG CTGGA			
		ACAGGTC ACC TC GACCT			
GAM1818 ENO3	3'	TCCAGGACTCCACTGGACA	54870	C T AA	
		TGTCCAG TGG GG CTGGA			
		ACAGGTC ACC TC GACCT			
GAM1818 EPB49	3'	TCCAGCACTAAGCCAGGCA	10529	CA _ GAA	
		TGTC GCT GGTG CTGGA			
		ACGG CGA TCAC GACCT			
GAM1818 FGF7	3'	CCAGTTCCAGCAGGGA	10630	AG G	
		TCC CTG TGGA ACTGG			
		AGG GAC ACCTTGACC			
GAM1818 FGFR3	3'	TCCAGCATTTAGCTGGCCA	5570	T TGGAA	
		TG CCAGCTGG CTGGA			
		AC GGTCGATT GACCT			
GAM1818 GCGR	3'	CCAGCTAGGGCTGGAC	5675	GG AA	
		GTCCAGCT TGG CTGG			
		CAGGTCGG ATC GACC			
GAM1818 HR	5'	TCCAGTTCCCGGGCTTGGA	18918	C GGT	
		TGTC AGCT GGA ACTGGA			
		ACGG TCGG CCTTGACCT			
GAM1818 IL2RB	3'	TCCAGTTGCAGCTGGAC	7945	GTGG	
		GTCCAGCTG AACTGGA			
		CAGGTCGAC TTGACCT			
GAM1818 IPP	3'	TCCAGTTTAAGTGTAGACA	20908	CA_ GGTG	
		TGTC GCT GAACTGGA			

			ACAG TGA TTTGACCT			
			ATG A__			
GAM1818 KCNJ16	5'	CCAATCTCTGCTGGTCA	38484	T	T T	AC
		TG CCAGC GG GGA TGG				
		AC GGTCG TC TCT ACC				
		T _ _ A_				
GAM1818 MAML1	3'	CCAGCCCATCTGCTGGCA	29273	T	T	AA
		TG CCAGC GGTGG CTGG				
		AC GGTCG CTACC GACC				
		_ T C_				
GAM1818 NR1I2	5'	CCAGTCCCCACTGCTGGCA	15298	T	T	A_
		TG CCAGC GGTGG ACTGG				
		AC GGTCG TCACC TGACC				
		_ _ CC				
GAM1818 ORC5L	3'	TCCAGCTACTTAGCTGGCCA	11914	T	_	AA
		TG CCAGCTG GTGG CTGGA				
		AC GGTCGAT CATC GACCT				
		C T _				
GAM1818 OVOL1	5'	CCAGTTTCCGCTAAGACA	17063		CAGC	_
		TGTC TGGTGGAA CTGG				
		ACAG ATCGCCTT GACC				
		A__ T				
GAM1818 PLAB	5'	TCAGAGCACCAGTTAGACA	66427		C	GAA
		TGTC AGCTGGTG CTGG				
		ACAG TTGACCAC GACT				
		A GA_				
GAM1818 PML	3'	TCCAGTGACCTCCAGCTGGA	53822		T	A_
		TCCAGCTGG GG ACTGGA				
		AGGTCGACC CC TGACCT				
		T AG				
GAM1818 PSCD4	3'	TCCAGCTTCCAGCTGGA	26326		T	AA
		TCCAGCTGG GG CTGGA				
		AGGTCGACC TC GACCT				
		T _				
GAM1818 RAB26	3'	CCAGTCCCTAGAAGGCTGGACA	27600		GGT__	A
		TGTCCAGCT GG ACTGG				
		ACAGGTCGG CC TGACC				
		AAGAT C				
GAM1818 RBMS3	5'	TCCAGTTCCTGCCTCGGA	27921	_	CT	T
		TCC AG GG GGAAGTGA				

AGG TC TC CCTTGACCT
 C CG _
 GAM1818 SLC13A4 5' CCAGTTCCTTTTGTGGTCA 25862 T TGGT_
 TG CCAGC GGAAGTGG
 || |||| |||||
 AC GGTCG CCTTGACC
 T TTTT
 GAM1818 SLC26A2 3' CCAGTTCACAGTGGA 5474 A G
 TCC GCTG TGGAAGTGG
 ||| ||| |||||
 AGG TGAC ACCTTGACC
 G _
 GAM1818 SMAP 3' CCAGTTCAGAGGTGGA 22931 G GG
 TCCA CT TGGAAGTGG
 |||| || |||||
 AGGT GG ACCTTGACC
 _ AG
 GAM1818 SOX10 5' CCAGCCCCGAGCTGGAC 23668 _ T AA
 GTCCAGCT GG GG CTGG
 ||||| || || |||
 CAGGTCGA CC CC GACC
 G _ _
 GAM1818 SOX10 3' CCAGGAGAACAGGCTGGACA 23669 G GGAA
 TGTCCAGCT GT CTGG
 ||||| || |||
 ACAGGTCGG CA GACC
 A AGAG
 GAM1818 SRM 3' TCCAGCCCCGGGCCGGAC 13401 A _ T AA
 GTCC GCT GG GG CTGGA
 |||| || || |||
 CAGG CGG CC CC GACCT
 C G _ _
 GAM1818 SYNGR3 3' CCAGAGGCTCCAGCTGGCCA 16117 T T AA_
 TG CCAGCTGG GG CTGG
 || ||||| || |||
 AC GGTCGACC TC GACC
 C _ GGA
 GAM1818 TEM6 3' TCCAGGGCTCCCGCTGGACA 43042 T TG AA
 TGTCCAGC GG G CTGGA
 ||||| || | ||||
 ACAGGTCG CC C GACCT
 _ CT GG
 GAM1818 C20orf149 5' CCAGATCCCACCAGCCAGCA 44425 CCA AA_
 TGT GCTGGTGG CTGG
 ||| ||||| |||
 ACG CGACCACC GACC
 AC_ CTA
 GAM1818 C5orf4 3' CCAGTAGGCCAGCTGAGCA 51486 TC GGA
 TG CAGCTGGT ACTGG
 || ||||| ||||

AC GTCGACCG TGACC
 GA GA_
 GAM1818 C5orf4 3' CCAGTAGGCCAGCTGAGCA 33424 TC GGA
 TG CAGCTGGT ACTGG
 || ||||| ||||
 AC GTCGACCG TGACC
 GA GA_
 GAM1818 CABIN1 3' CCACACCCAGCTGGCCA 25453 T _ GAAC
 TG CCAGCTGG TG TGG
 || ||||| || |||
 AC GGTCGACC AC ACC
 C C ____
 GAM1818 CCNE1 3' CCATAGCCAGCTGGGCA 8789 GGAAC
 TGTCCAGCTGGT TGG
 ||||| || |||
 ACGGGTCGACCG ACC
 AT____
 GAM1818 CCNE1 3' CCATAGCCAGCTGGGCA 55163 GGAAC
 TGTCCAGCTGGT TGG
 ||||| || |||
 ACGGGTCGACCG ACC
 AT____
 GAM1818 DKFZP434O047 5' TCCAGCTCACCCTGGCA 32125 T T AA
 TG CCAGC GGTGG CTGGA
 || |||| |||| ||||
 AC GGTCG CCACT GACCT
 _ _ C_
 GAM1818 DKFZp547I224 5' CCAGCACGCAGCTGGA 39953 _ GAA
 TCCAGCTG GTG CTGG
 ||||| || |||
 AGGTCGAC CAC GACC
 G ____
 GAM1818 DKFZP761F241 3' CCAGCTCCCCAGTCCAGGACA 49580 A__ T A
 TGTCC GCTGG GGA CTGG
 |||| |||| || ||||
 ACAGG TGACC CCT GACC
 ACC _ C
 GAM1818 DNAJB5 3' CCAGCTTGATGTCCACTGGACA 25353 C ____ G A
 TGTCCAG TGG T GA CTGG
 ||||| || | ||||
 ACAGGTC ACC A TT GACC
 _ TGT G C
 GAM1818 ERAL1 3' TCCAGCTCAAGCTGCTGGCA 63313 T T G_ A
 TG CCAGC GGT GA CTGGA
 || |||| || ||||
 AC GGTCG TCG CT GACCT
 _ _ AA C
 GAM1818 ERN1 3' CCAGCCATCTACTGGATA 9321 CT AA
 TGTCCAG GGTGG CTGG
 ||||| |||| ||||

ATAGGTC CTACC GACC
 AT _
 GAM1818 ET 3' TCAGAAACACAGCTGGACA 44473 G GAA
 TGTCCAGCTG TG CTGG
 ||||| || ||||
 ACAGGTCGAC AC GACT
 _ AAA
 GAM1818 FLJ10159 3' TCCAATGACACCAGCTGGTCA 36337 T GAAC
 TG CCAGCTGGTG TGGA
 || ||||| ||||
 AC GGTGACAC ACCT
 T AGTA
 GAM1818 FLJ11078 3' CCAGCCCCACGGTTTCAGGCA 37593 C_ G AA
 TGTC AGCTG TGG CTGG
 ||| |||| || ||||
 ACGG TTGGC ACC GACC
 ACT _ CC
 GAM1818 FLJ11252 3' TCCAGTTTTTATTGCTGCACA 68220 C TGGT
 TGT CAGC GGAAGTGA
 ||| ||| |||||
 ACA GTCG TTTTGACCT
 C TTAT
 GAM1818 FLJ11370 3' CCAGCTCAGTGGCTGAGCA 46963 TC G AA
 TG CAGCTG TGG CTGG
 || |||| || ||||
 AC GTCGGT ACT GACC
 GA G C_
 GAM1818 FLJ12681 3' CCAGCCCAAGCTGGGCA 43184 GG AA
 TGTCCAGCT TGG CTGG
 ||||| || ||||
 ACGGGTCGA ACC GACC
 _ C_
 GAM1818 FLJ14084 3' TCCAGTGTTCCTACTGCCAAACA 41596 CCA T _
 TGT GC GGTGGA ACTGGA
 ||| || ||||| |||||
 ACA CG TCACTT TGACCT
 AAC _ TG
 GAM1818 FLJ14166 3' CCAGCTCTCGGTTCCGGA 44986 _ GT A
 TCC AGCTG GGA CTGG
 ||| |||| || ||||
 AGG TTGGC TCT GACC
 CC _ C
 GAM1818 FLJ20202 5' CCAGTTTCCCAGCCAGA 35235 CA T
 TC GCTGG GGAAGTGG
 || |||| |||||
 AG CGACC CTTTGACC
 AC C
 GAM1818 FLJ20208 3' TCCAGTTCCGATGCTGGCA 35246 T TGG
 TG CCAGC TGGAAGTGA
 || |||| |||||

AC GGTCTG GCCTTGACCT
 _ TA_
 GAM1818 FLJ20225 5' CCAGCGGCGCCAGCTGACA 39322 C GAA
 TGTC AGCTGGTG CTGG
 |||| ||||| ||||
 ACAG TCGACCGC GACC
 _ GGC
 GAM1818 FLJ21657 3' TCCAGTTCATTTTCTGGA 42804 CT G
 TCCAG GGTG AACTGGA
 |||| ||| |||||
 AGGTC TTAC TTGACCT
 TT _
 GAM1818 FUT10 5' TCCAGTTTGCAAGATGGACA 51992 G G TG A
 TGTCCA CT G GA CTGGA
 ||||| || | || ||||
 ACAGGT GA C TT GACCT
 A A GT _
 GAM1818 GPA33 5' TCCAGCTGAGGCTGGGCA 20573 GG AA
 TGTCCAGCT TGG CTGGA
 ||||| || |||||
 ACGGGTCGG GTC GACCT
 A_ _
 GAM1818 IAN4L1 5' TCAGTTTCCAGCCAACA 37800 CCA TG
 TGT GCTGG GAACTGG
 || |||| |||||
 ACA CGACC TTTGACT
 AC_ _
 GAM1818 KIAA0063 3' TCCAACCACCACCAGCCAGACA 30263 CA AAC_
 TGTC GCTGGTGG TGGA
 |||| ||||| ||||
 ACAG CGACCACC ACCT
 AC ACCA
 GAM1818 KIAA0700 3' CCAACTCCAGCAGCTGGAC 72515 G AC
 GTCCAGCTG TGGA TGG
 ||||| |||| |||
 CAGGTCGAC ACCT ACC
 G CA
 GAM1818 KIAA1190 3' TCCAACCCCATCACTGGCA 71655 T C AAC_
 TG CCAG TGGTGG TGGA
 || |||| ||||| ||||
 AC GGTC ACTACC ACCT
 _ _ CCCA
 GAM1818 KIAA1416 3' TCCAGTCGCTCCAGCTGGCA 87758 T TGGA
 TG CCAGCTGG ACTGGA
 || ||||| |||||
 AC GGTCGACC TGACCT
 _ TCGC
 GAM1818 KIAA1644 3' CCAGGGCCAGCTGGACA 86218 GGAA
 TGTCCAGCTGGT CTGG
 ||||| ||||| ||||

ACAGGTCGACCG GACC
 G____
 GAM1818 KIAA1952 5' TCCAGTTCCAGTTCTACA 73548 CC GGT
 TGT AGCT GGAAGTGA
 ||| ||| |||||
 ACA TTGA CCTTGACCT
 TC ____
 GAM1818 MAD4 3' CCAGCCCACGCCGAGCTGGGCA 22272 _ GAA_
 TGTCCAGCT GGTG CTGG
 ||||| ||| |||
 ACGGGTCGA CCGC GACC
 G ACCC
 GAM1818 MANBAL 3' CCAGGCTCCAGCTGGGCA 42215 TGGAA
 TGTCCAGCTGG CTGG
 ||||| ||| |||
 ACGGGTCGACC GACC
 TCG____
 GAM1818 MASA 5' TCCAGTTCCAGGTGTGCA 65466 TC G GGT
 TG CA CT GGAAGTGA
 || ||| |||||
 AC GT GA CCTTGACCT
 GT G ____
 GAM1818 MGC11034 3' CCATGACCAGCTGGGCA 49571 GGAAC
 TGTCCAGCTGGT TGG
 ||||| |||
 ACGGGTCGACCA ACC
 GT____
 GAM1818 MGC11034 3' TCCAGTTCCAAGAAGGTACA 49577 _ AG GG
 TGT CC CT TGGAAGTGA
 ||| || |||||
 ACA GG GA ACCTTGACCT
 T AA ____
 GAM1818 MGC3222 3' TCCTGGGTCAACCAGCAGACA 44547 CA AACT
 TGTC GCTGGTGG GGA
 ||| ||||| |||
 ACAG CGACCACT CCT
 A_ GGGT
 GAM1818 NPTXR 3' TCAAGGCCACCCAGCTGGACA 55217 _ AAC
 TGTCCAGCTGG TGG TGG
 ||||| ||| |||
 ACAGGTCGACC ACC ACT
 C GGA
 GAM1818 NPTXR 3' TCAAGGCCACCCAGCTGGACA 27443 _ AAC
 TGTCCAGCTGG TGG TGG
 ||||| ||| |||
 ACAGGTCGACC ACC ACT
 C GGA
 GAM1818 PCBP4 3' CCAGTTCTCAGCAGCAGACA 40278 CA G _
 TGTC GCTG TG GAACTGG
 ||| ||| || |||||

		ACAG CGAC AC CTTGACC		
		A_ G T		
GAM1818	PCBP4	3' CCAGTTCTCAGCAGCAGACA 53392	CA	G _
		TGTC GCTG TG GAACTGG		
		ACAG CGAC AC CTTGACC		
		A_ G T		
GAM1818	PCBP4	3' CCAGTTCTCAGCAGCAGACA 53393	CA	G _
		TGTC GCTG TG GAACTGG		
		ACAG CGAC AC CTTGACC		
		A_ G T		
GAM1818	PDZ-GEF1	3' TCCAGTTTGTACAAGCTGGA 27284	G	_
		TCCAGCT GTG GAACTGGA		
		AGGTCGA CAT TTTGACCT		
		A G		
GAM1818	PF1	5' CCAGCCCCGGGATGGCA 96832	T	G_ T AA
		TG CCA CTGG GG CTGG		
		AC GGT GGCC CC GACC		
		_ AG _ _		
GAM1818	PLK	3' CCAGCCCCGGTGGCTGGGCA 18524	G	AA
		TGTCCAGCTG TGG CTGG		
		ACGGGTCGGT GCC GACC		
		G CC		
GAM1818	PLSCR2	5' CCTAAGCACCAGGCTGGACA 40148	_	GAACT
		TGTCCAGC TGGTG GG		
		ACAGGTCG ACCAC CC		
		G GAAT_		
GAM1818	RA-GEF-2	3' TCCAGTTCTCTGTCTGACA 33414	C	C T
		TGTC AG TGG GGAAGTGA		
		ACAG TC GTC TCTTGACCT		
		_ T _		
GAM1818	SGP28	3' CCAATCATCTGGCTGGCA 21346	T	_ AAC
		TG CCAGCT GGTGG TGG		
		AC GGTCCG CTACT ACC		
		_ T A_		
GAM1818	TRIM2	3' CCAGCCCCCCTTGCTGGACA 31597	T_	T AA
		TGTCCAGC GG GG CTGG		
		ACAGGTCG CC CC GACC		
		TT _ CC		
GAM1818	ZDHC5	5' TCCAGTTTTTAACTGTACA 93190	C	CTGGT
		TGT CAG GGAAGTGA		

ACA GTC TTTTGACCT
 T AAAT_
 GAM1818 LOC142941 5' TCCAATCTCCACTGGATA 83768 C T AC
 TGTCCAG TGG GGA TGGA
 ||||| ||| ||| ||||
 ATAGGTC ACC TCT ACCT
 _ _ A_
 GAM1818 LOC143308 5' CCAGTTCCTCCTGGCCA 83834 T CT
 TG CCAG GGTGGA ACTGG
 || ||| |||||
 AC GGTC CTACCTTGACC
 C _
 GAM1818 LOC145438 5' TCCAGTTCCTCAGGTAGACA 84317 CAG T
 TGTC CTGG GGA ACTGGA
 ||| ||| |||||
 ACAG GACT CCTTGACCT
 ATG _
 GAM1818 LOC145989 3' CCAGCCCCCAGGAGCTGGGCA 60288 _ T AA
 TGTCCAGCT GG GG CTGG
 ||||| || |||
 ACGGGTCGA CC CC GACC
 GGA _ CC
 GAM1818 LOC146895 5' CCAACCCGCCACTGGCCA 84864 T C AAC
 TG CCAG TGGTGG TGG
 || ||| ||||| |||
 AC GGTC ACCGCC ACC
 C _ CA_
 GAM1818 LOC149095 5' CCAGTTCGAGGACTGGA 79891 _ GG
 TCCAG CT TGGA ACTGG
 ||||| || |||||
 AGGTC GG GCCTTGACC
 A A_
 GAM1818 LOC150933 3' TCCAGTCCTGGAGCAGCTGGA 86340 GT_ A
 TCCAGCTG GGA CTGGA
 ||||| ||| |||||
 AGGTCGAC CCT GACCT
 GAGGT _
 GAM1818 LOC151098 5' CCACATCAAACAGCTGGACA 80930 GTG AC
 TGTCCAGCTG GA TGG
 ||||| || |||
 ACAGGTCGAC CT ACC
 AAA AC
 GAM1818 LOC151171 5' CCAGTTCAGACAGGGTCA 80946 T AG G_
 TG CC CTG TGGA ACTGG
 || || ||| |||||
 AC GG GAC ACCTTGACC
 T _ AG
 GAM1818 LOC152503 5' CCAGTCTCTGCTGGACA 86977 T T A
 TGTCCAGC GG GGA CTGG
 ||||| || ||| ||||

ACAGGTCG TC TCT GACC

GAM1818	LOC153910	5'	CCACTAAATCACCAGTAGACA	81903	CA	AAC__
			TGTC GCTGGTGG TGG			
			ACAG TGACCACT ACC			
			A_ AAATC			
GAM1818	LOC154789	5'	CCAATTCTAGCCAGCTGGA	82025	_	C
			TCCAGCTGG TGGAA TGG			
			AGGTCGACC ATCTT ACC			
			G A			
GAM1818	LOC158819	5'	CCAACCCCACTAAGCTGGACA	88272	_	AAC
			TGTCCAGCT GGTGG TGG			
			ACAGGTCGA TCACC ACC			
			A CCA			
GAM1818	LOC159989	5'	TCCAGCTCCTCCCAGCTGGA	83079	T_	A
			TCCAGCTGG GGA CTGGA			
			AGGTCGACC CCT GACCT			
			CT C			
GAM1818	LOC161734	3'	CCAGCACGCAGCTGGA	88463	_	GAA
			TCCAGCTG GTG CTGG			
			AGGTCGAC CAC GACC			
			G _			
GAM1818	LOC163688	5'	CCACTGAGCACCAGCTGGCCA	57748	T	GAAC_
			TG CCAGCTGGTG TGG			
			AC GGTCGACCAC ACC			
			C GAGTC			
GAM1818	LOC164397	5'	CCAGTCCGGAACAGCTGGA	83407	GT_	A
			TCCAGCTG GGA CTGG			
			AGGTCGAC CCT GACC			
			AAGG _			
GAM1818	LOC200953	3'	TCCAGTCCCAGGCCTGGA	91805	_	GG A
			TCCAG CT TGG ACTGGA			
			AGGTC GG ACC TGACCT			
			C _ C			
GAM1818	LOC201685	5'	TCCAGTTCCAATTCTGTAGAC	91848	_	CTGG
			GTC CAG TGGA ACTGGA			
			CAG GTC ACCTTGACCT			
			AT TTA_			
GAM1818	LOC202152	5'	CCAGCCCGCCGCCAGATA	90633	CA	AA
			TGTC GCTGGTGG CTGG			

	ATAG CGGCCGCC GACC		
	AC C_		
GAM1818 LOC203429 3'	CCAGTTCCTTTCCGTGGCA 90929	T GC T__	
	TG CCA TGG GGAAGTGG		
	AC GGT GCC CCTTGACC		
	_ _ TTT		
GAM1818 LOC205095 3'	CCAACCCCACCCAGTTGGG 92380	_ AAC	
	TCCAGCTGG TGG TGG		
	GGGTTGACC ACC ACC		
	C CCA		
GAM1818 LOC221100 5'	CCATCACCAGTTAAACA 94868	CC AAC	
	TGT AGCTGGTGG TGG		
	ACA TTGACCACT ACC		
	AA _		
GAM1818 LOC221431 3'	TCCAGTTCAGTGCCCTGGCA 93729	T CT G__	
	TG CCAG GGT GAACTGGA		
	AC GGTC CCG CTTGACCT		
	_ _ TGA		
GAM1818 LOC222031 3'	TCAGAGACCTGCTGGACA 95686	T GGAA	
	TGTCCAGC GGT CTGG		
	ACAGGTCG CCA GACT		
	T GA__		
GAM1818 LOC222631 5'	TCCAGAACACAGCTGGA 94408	G GAA	
	TCCAGCTG TG CTGGA		
	AGGTCGAC AC GACCT		
	_ AA_		
GAM1818 LOC253596 5'	CCAGTTCGAGGACTGGA 97230	_ GG	
	TCCAG CT TGGAAGTGG		
	AGGTC GG GCCTTGACC		
	A A_		
GAM1818 LOC254944 3'	TCCAGTTCGTCTTAGGACA 99005	AGCT GT	
	TGTCC G GGAAGTGG		
	ACAGG C CCTTGACCT		
	ATT_ TG		
GAM1818 LOC257450 5'	TCCAGTTTTAGCCAGGACA 91452	AGC _	
	TGTCC TGG TGGAAGTGG		
	ACAGG ACC ATTTTGACCT		
	_ G		
GAM1818 LOC51319 3'	TCTTGCCACCAGCTGAACA 34027	C AACT	
	TGT CAGCTGGTGG GGA		

		ACA GTCGACCACC TCT		
		A GT_		
GAM1818	LOC51716	3' CCAGTTTCACAGCCAGGCA	33261	CA G
		TGTC GCTG TGGAAGTGG		
		ACGG CGAC ACTTTGACC		
		AC _		
GAM1818	LOC58525	3' CCAGTTCCTGGGTTGAACG	79343	C GGT
		TGT CAGCT GGAAGTGG		
		GCA GTTGG CCTTGACC		
		A GT_		
GAM1818	LOC90786	5' CCAGTTCCCAGCTGGGCA	64729	TG
		TGTCCAGCTGG GAACTGG		
		ACGGGTCGACC CTTGACC		
		—		
GAM1818	LOC91759	3' TCCAGCCTCCACTGGAC	67697	C T AA
		GTCCAG TGG GG CTGGA		
		CAGGTC ACC CC GACCT		
		_ T _		
GAM1818	LOC92017	5' TCCAATCACGTTGCTGGCA	68493	T TG_ AAC
		TG CCAGC GTGG TGGA		
		AC GGTCG CACT ACCT		
		_ TTG A_		
GAM1818	LOC92078	3' CCAGCCCATCGCCAGCCAGATA	68593	CA AA_
		TGTC GCTGGTGG CTGG		
		ATAG CGACCGCT GACC		
		AC ACCC		
GAM1819	ELF3	3' TGACCTTGACCTTGACCAA	16685	T GAT AAA
		TTGGT CAAGG GG GTCA		
		AACCA GTTCC TC CAGT		
		_ AGT _		
GAM1819	JAK2	3' TGACCTTCATTCTGAGACCAA	18318	CAA AA
		TTGGTT GGGATGGA GTCA		
		AACCAG TCTTACTT CAGT		
		AG_ C_		
GAM1819	SLC10A2	5' ACTCTCTGTCTTGACCAA	6590	CAA A
		TTGGTT GGGATGGA AGT		
		AACCAG TTCTGTCT TCA		
		— C		
GAM1819	FLJ10803	3' GTGACTTTCAGTTAAAGCCAA	37205	CAAGG G
		TTGGTT GAT GAAAGTCAC		

AACCGA TTG CTTTCAGTG
 AA__ A
 GAM1819 KIAA1958 5' GTGACTTTGAACCCCAAACC 82788 CAA ATGG
 GGTT GGG AAAGTCAC
 ||| ||| |||||
 CCAA CCC TTTCAGTG
 A__ CAAG
 GAM1819 MARCKS 3' ACTTTCCACCCTGCCCA 11411 TTCA A
 TGG AGGG TGGAAAGT
 ||| ||| |||||
 ACC TCCC ACCTTTCA
 CG__ _
 GAM1819 TUB 5' GTGGGACCATCCCTTAAACC 13898 C AAAG
 GGTT AAGGGATGG TCAC
 ||| ||||| |||
 CCAA TTCCCTACC GGTG
 A AG__
 GAM1819 LOC80298 3' ACTTTTACCTTGAACCA 48062 GATG
 TGGTTCAAGG GAAAGT
 ||||| |||||
 ACCAAGTTCC TTTTCA
 A__
 GAM1820 SCAMP1 3' GCTAAATAAATATTCTCC 54500 T C
 GGA AATATT ATTTAGC
 ||| ||||| |||||
 CCT TTATAA TAAATCG
 C A
 GAM1820 SCAMP1 3' GCTAAATAAATATTCTCC 54501 T C
 GGA AATATT ATTTAGC
 ||| ||||| |||||
 CCT TTATAA TAAATCG
 C A
 GAM1820 NX-17 3' TGAATATCAGCCCCTAATA 40706 ATA_
 TATTAGGG ATATTCA
 ||||| |||||
 ATAATCCC TATAAGT
 CGAC
 GAM1820 LOC161589 3' GCTAAATGAATATTATCCCTAA 83159
 TA TATTAGGGATAATATTCATTTAGC
 |||||
 ATAATCCCTATTATAAGTAAATCG
 GAM1821 SCAMP1 3' GCTAAATAAATATTCTCC 18013 T C
 GGA AATATT ATTTAGC
 ||| ||||| |||||
 CCT TTATAA TAAATCG
 C A
 GAM1821 SCAMP1 3' GCTAAATAAATATTCTCC 54501 T C
 GGA AATATT ATTTAGC
 ||| ||||| |||||

CCT TTATAA TAAATCG
 C A
 GAM1821 NX-17 3' TGAATATCAGCCCCTAATA 40706 ATA_
 TATTAGGG ATATTCA
 ||||| |||||
 ATAATCCC TATAAGT
 CGAC
 GAM1821 LOC161589 3' GCTAAATGAATATTATCCCTAA 83159
 TA TATTAGGGATAATATTCATTTAGC
 |||||
 ATAATCCCTATTATAAGTAAATCG

 GAM1822 ENC1 3' AATCCTTAACATTTT 14645 GCCGT
 GAAATGTAA GGATT
 ||||| |||||
 CTTTACAATT CCTAA

 GAM1822 NEDD4 3' TGAATTTTGTCTTAACATTT 70547 CCGT
 AAATGTAAAG GGATTCA
 ||||| |||||
 TTTACAATTC TTAAAGT
 CTGT
 GAM1822 NOV 3' GAATCATACTTAACATTTT 11814 CCGTG
 GAAATGTAAAG GATTC
 ||||| |||||
 CTTTACAATTC CTAAG
 ATA__
 GAM1822 EDG2 3' TGAATCCACAACCTTCATTT 9179 TT CC
 AAATG AAG GTGGATTCA
 |||| ||| |||||
 TTTAC TTC CACCTAAGT
 __ AA
 GAM1822 EDG2 3' TGAATCCACAACCTTCATTT 55135 TT CC
 AAATG AAG GTGGATTCA
 |||| ||| |||||
 TTTAC TTC CACCTAAGT
 __ AA
 GAM1822 FLJ14153 3' GAATGGGCTTAACACATCGT 43012 AA GTGG
 ACGA TGTTAAGCC ATTC
 ||| ||||| |||||
 TGCT ACAATTCGG TAAG
 AC G__
 GAM1822 FLJ14751 3' TGAAAAGTTGCTTAACATTTT 52671 CG GGA
 GAAATGTAAAGC T TTCA
 ||||| ||| |||||
 CTTTACAATTCG G AAGT
 TT AA_
 GAM1822 FLJ20186 5' GAACCCACGGCCAGGCTTCCGT 35202 A T AA A
 ACG AA GTT GCCGTGG TTC
 ||| || ||| ||||| |||

			TGC TT CGG CGGCACC AAG	
			C _ AC C	
GAM1822	GL004	3'	GAACCACCTAATATTTTC 66596	AGCC A
			GAAATGTTA GTGG TTC	
			CTTTATAAT CACC AAG	
			C _ _	
GAM1822	GRP3	3'	AATCATATTTGATTAACATTTTC 31737	GCC_ _
			GAAATGTAA GTG GATT	
			CTTTACAATT TAT CTAA	
			AGTT A	
GAM1822	OLFM3	3'	AATCTCTTGCTAACATTTT 83023	A CGT
			GAAATGTTA GC GGATT	
			TTTTACAAT CG TCTAA	
			_ TTC	
GAM1822	PRO1575	5'	ATTCAGCTTAACATTTTC 26871	CG
			GAAATGTTAAGC TGGAT	
			CTTTACAATTCG ACTTA	
			_	
GAM1822	LOC145608	3'	CAAGGACTTAGCATTTTCGT 84373	_ G
			ACGAAATGTTAAG CC TG	
			TGCTTTACGATTC GG AC	
			A A	
GAM1822	LOC200058	3'	TGAATCCAGCTTCCAACACTC 89964	AA _ CG
			GA TGTT AAGC TGGATTCA	
			CT ACAA TTCG ACCTAAGT	
			C_ CC _	
GAM1823	FBN2	3'	ACAACCACTGTAGCAAAA 10575	CAT
			TTTTGCTACAG TTGT	
			AAAACGATGTC AACA	
			ACC	
GAM1823	LYPLA1	3'	ACAGATTAATATGTAGCAAAA 21997	GC_
			TTTTGCTACA ATTTGT	
			AAAACGATGT TAGACA	
			ATAAT	
GAM1823	MITF	3'	CAACTACAAATGCCTCCAAAG 6000	CTACA A
			TTTTG GCATTTGTA TTG	
			GAAAC CGTAAACAT AAC	
			CTC_ C	
GAM1823	MXI1	3'	GCAAATACTTAGCAAAA 56127	C C
			TTTTGCTA AG ATTTGT	

			AAAACGAT TC TAAACG		
			_ A		
GAM1823	MXI1	3'	GCAAATACTTAGCAAAA 21058	C C	
			TTTTGCTA AG ATTTGT		
			AAAACGAT TC TAAACG		
			_ A		
GAM1823	EREG	3'	GCAACCACAAATGCATAAATGC 9309	TACA__	AA
	A		TGC GCATTTGT TTGC		
			ACG CGTAAACA AACG		
			TAAATA CC		
GAM1823	MBLL39	3'	CAATATAAATGCTGCAGCAAAG 20447	A	A
			TTTTGCT CAGCATTTGTA TTG		
			GAAACGA GTCGTAAATAT AAC		
			C _		
GAM1823	MBLL39	3'	CAATATAAATGCTGCAGCAAAG 59257	A	A
			TTTTGCT CAGCATTTGTA TTG		
			GAAACGA GTCGTAAATAT AAC		
			C _		
GAM1823	LOC221760	3'	GCAACTCTGGCAGTAGCAAAA 95429	A ATTT	AAT
			TTTTGCTAC GC GT TGC		
			AAAACGATG CG CA ACG		
			A GTCT _		
GAM1823	LOC51195	3'	GCAACAGCCGTAGCAAAA 33406	A AT	
			TTTTGCTAC GC TTGT		
			AAAACGATG CG AACG		
			C AC		
GAM1824	ABCC12	3'	ATCCCCAAGGGTTCCTC 53789	AC	G_
			GAG GAGCT TGGGGAT		
			CTC CTTGG ACCCCTA		
			_ GA		
GAM1824	CD4	3'	AGATCCCCTTGCAGCCTCCCC 7043	AA	ACGA _
	A		TG GAG GCTGTG GGGATCT		
			AC CTC CGACGT CCCTAGA		
			CC _ TCA		
GAM1824	CUL3	3'	TCATGTCATCTCTTCA 14574	C G T	
			TGAAGAGA GA C GTGG		
			ACTTCTCT CT G TACT		
			A _ _		
GAM1824	EGR3	3'	AGATCCCCACTTTTCCCCTC 60300	AC	CT
			GAG GAG GTGGGGATCT		

CTC CTT CACCCCTAGA
 CC TT
 GAM1824 LPIN2 3' AGATCCCCACAGAGCATCCTCC 28427 A ACGAG_
 TC GA GAG CTGTGGGGATCT
 || ||| |||||
 CT CTC GACACCCCTAGA
 C CTACGA
 GAM1824 MUC3B 3' ATCCTCCCTCCTCTCCTCA 95918 A C CTGT
 TGA GAGA GAG GGGGAT
 ||| ||| ||| |||||
 ACT CTCT CTC CTCCTA
 C C C____
 GAM1824 C9orf7 3' AGAGGCCACAGTCACCTCCCCA 34578 AA AC G GGA
 TG GAG GA CTGTGG TCT
 || ||| ||||| |||
 AC CTC CT GACACC AGA
 CC CA _ GG_
 GAM1824 DCAMKL1 5' AGACCCCCGGCGGCGTCTCTCC 17598 A A_ T A
 G TG AGAGACG GCTG GGGG TCT
 || ||||| ||| ||| |||
 GC TCTCTGC CGGC CCCC AGA
 C GG _ _
 GAM1824 FLJ10761 3' GATCCCTCACCTTCTC 37130 CG CT _
 GAGA AG GTG GGGATC
 |||| || ||| |||||
 CTCT TC CAC CCCTAG
 _ _ T
 GAM1824 FLJ10813 3' GACAACTACATCTCTTCA 37230 CGAGC GGA
 TGAAGAGA TGTGG TC
 ||||| ||| ||
 ACTTCTCT ACATC AG
 _ AAC
 GAM1824 FLJ22795 3' CCCCACAGCCCCCTCCTCA 47631 A ACGA
 TGA GAG GCTGTGGGG
 ||| ||| |||||
 ACT CTC CGACACCCC
 C CCC_
 GAM1824 MGC10960 3' ATCCCCATGGTGCTTCCCTCCA 51980 A A CGA
 TG AG GA GCTGTGGGGAT
 || ||| |||||
 AC TC CT TGGTACCCCTA
 C C TCG
 GAM1824 POLE3 3' TCCGTTCTCTCTCTTCA 34320 C CTG
 TGAAGAGA GAG TGGG
 ||||| ||| |||
 ACTTCTCT CTC GCCT
 _ TT_
 GAM1824 WNT16 5' AGATCCCCAGGCTGCTCTCTCC 55146 A CG G
 A TG AGAGA AGCT TGGGGATCT
 || |||| ||| |||||

AC TCTCT TCGG ACCCCTAGA
 C CG _
 GAM1824 LOC130951 3' AGACCCCCCGCCATCTCTACA 57940 A CGA TT A
 TG AGAGA GC G GGGG TCT
 || |||| || |||| ||
 AC TCTCT CG C CCCC AGA
 A AC_ _C C
 GAM1824 LOC145717 3' CCCCACAGCCCCCTCCTCA 67370 A ACGA
 TGA GAG GCTGTGGGG
 ||| ||| |||||
 ACT CTC CGACACCCC
 C CCC_
 GAM1824 LOC197135 5' AGACCCAGGGTCTCTCTCCTC 89237 A C _ G A
 A TGA GAGA GAG CT TGGGG TCT
 ||| |||| ||| || ||||| ||
 ACT CTCT CTC GG ACCCC AGA
 C _ T G _
 GAM1824 LOC199704 5' CTCCAGCCCATCTCTTCA 89696 CGA T
 TGAAGAGA GCTG GGG
 ||||| ||| ||
 ACTTCTCT CGAC CTC
 ACC _
 GAM1824 LOC200933 3' ATCCTTGCTCCCTCCCTTCA 91789 A C_ TGT
 TGAAG GA GAGC GGGGAT
 ||||| || ||| |||||
 ACTTC CT CTCG TTCCTA
 C CC _
 GAM1824 LOC220537 3' CCCCACAGCCCCCTCCTCA 92420 A ACGA
 TGA GAG GCTGTGGGG
 ||| ||| |||||
 ACT CTC CGACACCCC
 C CCC_
 GAM1824 LOC221830 3' AGATCCCTTACCCTCTCTC 94102 C CTGT
 GAGA GAG GGGGATCT
 |||| ||| |||||
 CTCT CTC TCCCTAGA
 _ CCAT
 GAM1824 LOC245806 3' AGATCCCTTCCTGCCCATCCCT 93539 A CGA TGT_
 TC GAAG GA GC GGGGATCT
 |||| || || |||||
 CTTC CT CG TCCCTAGA
 C ACC TCCT
 GAM1825 GPD1 3' TCATGCCACCACATTTG 60398 C C
 TAAATG GGTGGCAT GA
 ||||| ||||| ||
 GTTTAC CCACCGTA CT
 A _
 GAM1825 IL5RA 5' TCGCATGGCCACCGCATTT 6906 AT_
 AAATGCGGTGGC CGA
 ||||| |||

		TTTACGCCACCG GCT		
		GTAC		
GAM1825 MYO1C	3'	TGCCGATGCCAAATATTTG 61873	CGG	A
		TAAATG TGGCATCG CA		
		GTTTAT ACCGTAGC GT		
		AA_ C		
GAM1825 C6orf37	3'	TGTCACACTGCATTTA 68097	GCATC	
		TAAATGCGGTG GACA		
		ATTTACGTCAC CTGT		
		A_____		
GAM1825 DNAJC6	3'	TTGCAGAACCACCGCATT 29498	CA GA	
		AATGCGGTGG TC CAA		
		TTACGCCACC AG GTT		
		A_ AC		
GAM1825 FLJ11210	3'	GTCGATGTGCATGCTTTTA 60319	T GTG	
		TAAA GCG GCATCGAC		
		ATTT CGT TG TAGCTG		
		T ACG		
GAM1825 FLJ12476	3'	TCGATCTTCTGCATTTA 43270	T C	
		TAAATGCGG GG ATCGA		
		ATTTACGTC TC TAGCT		
		T _		
GAM1825 KIAA1034	3'	TCGATGGCATCCGCATTTG 63134	_ G	
		TAAATGCGG TG CATCGA		
		GTTTACGCC AC GTAGCT		
		T G		
GAM1825 KIAA1987	3'	TCATGTAAGTGCATTTA 89391	G C	
		TAAATGCGGT GCAT GA		
		ATTTACGTCA TGTA CT		
		A _		
GAM1825 MGC16063	3'	TGTCCTGGCCACTGCATT 54929	ATC	
		AATGCGGTGGC GACA		
		TTACGTCACCG CTGT		
		GTC		
GAM1825 LOC147949	3'	TGTCAGATGTCCACATTGCA 79279	_ _ _	
		TGCG GTGG CATC GACA		
		ACGT CACC GTAG CTGT		
		TA T A		
GAM1825 LOC150577	3'	GTCCTCACCGCATTTG 86258	CATC	
		TAAATGCGGTGG GAC		

			GTTTACGCCACT	CTG		
			C___			
GAM1825	LOC158219	3'	TGTGTGTCACCACATTT	82694	C	CG
			AAATG GGTGGCAT	ACA		
			TTTAC CCACTGTG	TGT		
			A	___		
GAM1825	LOC202020	3'	TGTCTCACCACATTTA	90605	C	CATC
			TAAATG GGTGG	GACA		
			ATTTAC CCACT	CTGT		
			A	_____		
GAM1825	LOC90826	5'	TGTCGATGCAGGTTTATTTG	64788		CGGTG
			TAAATG	GCATCGACA		
			GTTTAT	CGTAGCTGT		
			TTGGA			
GAM1825	LOC93587	3'	TTGTCTTTACCTGCATTTA	73042	_	CATC
			TAAATGC GGTGG	GACAA		
			ATTTACG CCATT	CTGTT		
			T	T___		
GAM1826	CKAP1	5'	GAAGGCCCTCTGGATTGG	73900	A	TCAA
			CCAG TCGGGG	GGCCTTC		
			GGTT GGTCTC	CCGGAAG		
			A	C___		
GAM1826	F2R	3'	GCCTCTGTTTTGATATGG	10569	G	T A
			CCA ATCGGGG	CA AGGC		
			GGT TAGTTTT	GT TCCG		
			A	_ C		
GAM1826	IGFBP3	3'	GGAAAACCTTTAAACCCCGGT	7001	C_	CC
			ATCGGGGT	AAAGG TTCC		
			TGGCCCCA	TTTCC AAGG		
			AA	AA		
GAM1826	LIG4	3'	AAAGCCTCTGATCTGG	11318	GGTCAA	C
			CCAGATCGG	AGGC TT		
			GGTCTAGTC	TCCG AA		
			_____	A		
GAM1826	MYBL2	5'	GGTCCTGACCCCGGCCCGG	11728	AGA	AA
			CC TCGGGGTCA	GGCC		
			GG	GGCCCCAGT CTGG		
			CCC	C_		
GAM1826	RXRA	3'	GGAAGGCCCTCCCTTTGGCCTG	12921	AT__	TCAA
			CAG C GGGG	GGCCTTCC		

GTC G TCCC CCGGAAGG
 CG TT TC____
 GAM1826 FLJ10199 5' GAAGGGGACCCCGGCCTG 71754 AT AAAGG
 CAG CGGGGTC CCTTC
 ||| ||||| ||||
 GTC GCCCCAG GGAAG
 CG G____
 GAM1826 FLJ12221 3' AGACCCCCACCCCGATCTGG 63216 TCAAA C
 CCAGATCGGGG GG CT
 ||||| || ||
 GGTCTAGCCCC CC GA
 CACCC A
 GAM1826 GRWD 3' GAAGGCCTGGCTCTGATC 49781 AA
 GATCGGGGTCA GGCCTTC
 ||||| |||||
 CTAGTCTCGGT CCGGAAG
 —
 GAM1826 KIAA0515 5' GGAAGGCCCTGGGTCCGA 64552 G AA
 TCGGG TCA GGCCTTCC
 |||| || |||||
 AGCCT GGT CCGGAAGG
 G C_
 GAM1826 KIAA0978 3' GGAAGGCCTTCCAGATCTGG 70996 GG TCA
 CCAGATC GG AAGGCCTTCC
 |||| || |||||
 GGTCTAG CC TTCCGGAAGG
 A_ ____
 GAM1826 KIAA1280 5' GAAGGCCTCCAAGGAGATCT 70278 GG____ TCAA
 AGATC GG AGGCCTTC
 |||| || |||||
 TCTAG CC TCCGGAAG
 AGGAA ____
 GAM1826 KIAA1421 3' GGAAGGCCTTTACATGAGCT 65144 A GG C
 AG TCG GT AAAGGCCTTCC
 || || || |||||
 TC AGT CA TTTCCGGAAGG
 G A_ _
 GAM1826 KIAA1466 5' GAAGGCCTTTAATGAGATC 72409 GGG C
 GATC GT AAAGGCCTTC
 || || |||||
 CTAG TA TTTCCGGAAG
 AG_ A
 GAM1826 KIAA1485 3' GCTCCTTGACCCCATCT 90768 C A_
 AGAT GGGGTCAA GGC
 ||| ||||| ||
 TCTA CCCCAGTT TCG
 C CC
 GAM1826 MGC11266 5' GGAAGGCCCTTGGAATCTG 44489 CGGGG A
 CAGAT TCAA GGCCTTCC
 |||| ||| |||||

GTCTA GGTT CCGGAAGG
 AG__ C
 GAM1826 PCDH19 5' GCTCGCGACCCCGACCTGG 64444 A AAA
 CCAG TCGGGGTC GGC
 ||| ||||| ||
 GGTC AGCCCCAG TCG
 C CGC
 GAM1826 PRO0233 5' GCCTAGAGTCCTGATCTGG 26953 _ AA
 CCAGATCGGGG TC AGGC
 ||||| || |||
 GGTCTAGTCCT AG TCCG
 G A_
 GAM1826 PROL1 3' GAACCAACCCTGATCT 41404 CAAA CC
 AGATCGGGGT GG TTC
 ||||| || |||
 TCTAGTCCCA CC AAG
 A__ _
 GAM1826 SAMHD1 3' GAAGGCCTCCCCTGACCTG 61984 A TCAA
 CAG TCGGGG AGGCCTTC
 || ||||| |||||
 GTC AGTCCC TCCGGAAG
 C C_
 GAM1826 SARM 3' GGTTTTGACCCACCTG 31302 ATC G
 CAG GGGGTCAAAG CC
 || ||||| ||
 GTC CCCAGTTTT GG
 CA_ _
 GAM1826 SLC21A11 5' GGCCCGACCCCGACCTCA 65095 C A AAA
 C AG TCGGGGTC GGCC
 || ||||| |||
 A TC AGCCCCAG CCGG
 C C C_
 GAM1826 TUB 3' GAAGGCCTCACTCAAGCCTG 13894 ATCG CAA
 CAG GGGT AGGCCTTC
 || ||| |||||
 GTC CTCA TCCGGAAG
 CGAA C_
 GAM1826 XYLT1 3' GAAAGCCTTTTGATGTGG 78413 G GGGTC C
 CCA ATCG AAAGGC TTC
 || ||| ||||| |||
 GGT TAGT TTTCCG AAG
 G _ _ A
 GAM1826 LOC122618 3' CCTCTGACCCCGGCCTGG 57902 AT A
 CCAG CGGGGTCA AGG
 ||| ||||| |||
 GGTC GCCCCAGT TCC
 CG C
 GAM1826 LOC145978 3' GGAAGGCCTGGTTCCACCTG 78051 ATC TCAA
 CAG GGGG AGGCCTTCC
 || ||| |||||

		GTC CCCT TCCGGAAGG		
		CA_ TGG_		
GAM1826	LOC158267 3'	GGAAATGACCCCGATTTG	82722	AAGG
		CAGATCGGGGTCA CC		
		GTTTAGCCCCAGT GG		
		AAA_		
GAM1826	LOC161498 5'	GGAAGACCGCCGCCCGACTCTG	88453	_ GTCAAA C
	G	CCAGA TCGGG GG CTTCC		
		GGTCT AGCCC CC GAAGG		
		C GCCG_ A		
GAM1826	LOC163255 3'	GAAGACCTTTAGATTTGG	83343	GGGGTC C
		CCAGATC AAAGG CTTC		
		GGTTTAG TTTCC GAAG		
		A_ A		
GAM1826	LOC201616 5'	GAAAGCCTTTCATTCTGA	91821	C C
		TCGGGGT AAAGGC TTC		
		AGTCTTA TTTCCG AAG		
		C A		
GAM1826	LOC221288 5'	AAGGCCTTCATTAGATATGG	95251	G GG CA
		CCA ATC GGT AAGGCCTT		
		GGT TAG TTA TTCCGGAA		
		A A_ C_		
GAM1826	LOC221596 3'	AAGGCCTTTAGTTACTGCTCTG	93622	T _ TC
	G	CCAGA CGG GG AAAGGCCTT		
		GGTCT GTC TT TTTCCGGAA		
		C A GA		
GAM1826	LOC222237 3'	GGAATAACCAACCCTGATCTGG	95947	CAAA CC_
		CCAGATCGGGGT GG TTCC		
		GGTCTAGTCCCA CC AAGG		
		A_ AAT		
GAM1826	LOC255480 3'	GGAGGCCAAACCCCAATCTGG	98287	C CAAA
		CCAGAT GGGGT GGCCTTC		
		GGTCTA CCCCCA CCGGAGG		
		A AA_		
GAM1826	LOC255535 3'	CTTTCTGACCCAGCCTGG	97417	ATC _
		CCAG GGGGTCA AAGG		
		GGTC CCCCAGT TTTC		
		CGA C		
GAM1826	LOC91115 3'	GGAAAGCCTTTAACTAGCCCTG	65571	C_ C
	G	TCGGGGT AAAGGC TTCC		

			GGTCCCG TTTCCG AAGG	
			ATCAA A	
GAM1827	AQP6	3'	CACTCTCAGGCAGGAACA 54986	CA
			TGTTCTTGCC AGAGTG	
			ACAAGGACGG TCTCAC	
			AC	
GAM1827	AQP6	3'	CACTCTCAGGCAGGAACA 54987	CA
			TGTTCTTGCC AGAGTG	
			ACAAGGACGG TCTCAC	
			AC	
GAM1827	PRKCB1	3'	CAGACCTTGAAAAGAACA 71025	GCC A G
			TGTTCTT CAAG GT TG	
			ACAAGAA GTTC CA AC	
			AA_ _ G	
GAM1827	DCNP1	3'	CAGACATACACTAAACACGAAC 56456	T CCCA A
	A		TGTTT TG AG GTGTGTCTG	
			ACAAG AC TC CATAACAGAC	
			C AAA_ A	
GAM1827	FLJ10349	3'	CAGACATGGTGCCAAGCAGAAC 36534	T CCAAGAGT
	A		TGTTCT GC GTGTCTG	
			ACAAGA CG TACAGAC	
			_ AACCGTGG	
GAM1827	FLJ12389	3'	CAGACACACTCCTGAGCCAAG 60897	_ C A
			CTTG C CA GAGTGTGTCTG	
			GAAC G GT CTCACACAGAC	
			C A C	
GAM1827	FLJ20967	3'	CAGAAGTGCTTAGACAAGAACA 42206	CCCAA TG G
			TGTTCTTG GAG T TCTG	
			ACAAGAAC TTC G AGAC	
			AGA_ GT A	
GAM1827	GFR	3'	AGAAACTGGGCAAAAACA 25443	C AGAGT G
			TGTT TTGCCCA GT TCT	
			ACAA AACGGGT CA AGA	
			A _ _ _ A	
GAM1827	KIAA1925	5'	ACTTTCCTGACCAAGAACA 93712	CC A T
			TGTTCTTG CA GAG GT	
			ACAAGAAC GT CTT CA	
			CA C T	
GAM1827	SE57-1	3'	CAGACATACAGTCAGGAAAGAA 48165	G CAAGA
	CA		TGTTCTT CC GTGTGTCTG	

		ACAAGAA GG CATAACAGAC	
		A ACTGA	
GAM1827	STK29	3' GACCCCTCAGCAAGAACA 88964	CCAA TGT
		TGTTCTTGC GAG GTC	
		ACAAGAACG CTC CAG	
		A__ CC_	
GAM1827	LOC222031	3' ACCTCTAAGCAAGAACA 95666	CCA T
		TGTTCTTGC AGAG GT	
		ACAAGAACG TCTC CA	
		AA_ _	
GAM1828	ARF3	3' ATTTCTGCCCACTCCCTCT 9769	CATCT A
		AGGGGGAGT GGCA AAAT	
		TCTCCCTCA CCGT TTTA	
		C__ C	
GAM1828	BTG2	3' CATTCCTGCCAGCTCTGCCTCC 23143	_ TCAT AA
	T	AGGGGG AG CTGGCA AATG	
		TCCTCC TC GACCGT TTAC	
		G TC__ CC	
GAM1828	CYP27A1	3' CATTTTTGAGCAACTCCCTCT 7601	CATC G_
		AGGGGGAGT TG CAAAAATG	
		TCTCCCTCA AC GTTTTTAC	
		__ GA	
GAM1828	FGF5	3' CATTTCTCTTTTTATCTCCCCC 16759	TCATCT CAA
	T	AGGGGGAG GG AAATG	
		TCCCCCTC TC TTTAC	
		TATTTT TC_	
GAM1828	FGF5	3' CATTTCTCTTTTTATCTCCCCC 53654	TCATCT CAA
	T	AGGGGGAG GG AAATG	
		TCCCCCTC TC TTTAC	
		TATTTT TC_	
GAM1828	HIP2	3' CATTCTTGCTTGCATTCCCCT 19268	_ TCT A
		AGGGGGAGT CA GGCAA AATG	
		TCCCCTTCA GT TCGTT TTAC	
		C __ C	
GAM1828	PRDM2	3' TTTTATGCCTCCCCCT 32422	GTCATCT _
		AGGGGGA GGCA AAAA	
		TCCCCCT CCGT TTTT	
		__ A	
GAM1828	PTPRZ1	5' ATTCCTTCGCTCCCCCT 12633	CATCT CAA
		AGGGGGAGT GG AAAT	

		TCCCCCTCG CC TTTA	
		CTT__ __	
GAM1828	SNTB1	3' ATTTTACCTACTCCTCCT 41045	CATCT C
		AGGGGGAGT GG AAAAAT	
		TCCTCCTCA CC TTTTTA	
		T__ A	
GAM1828	TAP2	3' CATTTTCTGCTCGACTCGCCCC 6776	_ ATCT _
	T	AGGGG GAGTC GGCA AAAATG	
		TCCCC CTCAG TCGT TTTTAC	
		G C__ C	
GAM1828	TP53	3' CATTTTCACCCACCCCTTCCCC 6796	TCATCT CA
	T	AGGGGGAG GG AAAATG	
		TCCCCTTC CC TTTTAC	
		CCACC_ AC	
GAM1828	YWHAG	3' CATTTTGTGCCAAAATACCACT 25940	GA CATC
		GG GT TGGCAAAAATG	
		TC CA ACCGTTTTTAC	
		AC TAAA	
GAM1828	ARH2	3' CATTTCTGCCACTTTCCCCCT 57374	TCATC A
		AGGGGGAG TGGCA AAATG	
		TCCCCCTT ACCGT TTTAC	
		TC__ C	
GAM1828	CLSTN3	5' CATTCTGCCCCTCTCTGCCCC 28874	_ TCATCT AA
	CT	AGGGGG AG GGCA AATG	
		TCCCC TC CCGT TTAC	
		G TCTCC_ CC	
GAM1828	CNNM4	3' TTTTACCAAAGGTTCTCCCT 39876	GT ATC C
		AGGGGGA C TGG AAAA	
		TCCCTCT G ACC TTTT	
		TG AA_ A	
GAM1828	FLJ13352	3' CATTTCCATTATCTCCCCCT 45051	TCATC CAA
		AGGGGGAG TGG AAATG	
		TCCCCCTC ACC TTTAC	
		TACTT __	
GAM1828	FLJ21916	3' CATCTTTGCCAGACAAGTCTCC 43891	GTCA A
		GGGGA TCTGGCAA ATG	
		CCTCT AGACCGTTT TAC	
		GAAC C	
GAM1828	GABBR1	3' CATTTCTGCTCAGATTCCCCC 41860	GTC _ A
		GGGGGA ATCTG GCA AAATG	

		CCCCCT TAGAC CGT TTTAC	
		___ T C	
GAM1828	GABBR1	3' CATTTCTGCTCAGATTCCCCC 9410	GTC _ A
		GGGGGA ATCTG GCA AAATG	
		CCCCCT TAGAC CGT TTTAC	
		___ T C	
GAM1828	GMPPB	5' ATTCTTCCAGACTCCCCCT 97436	ATC C A
		AGGGGGAGTC TGG AA AAT	
		TCCCCCTCAG ACC TT TTA	
		___ _ C	
GAM1828	HSJ001348	3' TTTTCCTTGACTCCCCCT 62863	TCT C
		GGGGGAGTCA GG AAAA	
		TCCCCTCAGT CC TTTT	
		T___ _	
GAM1828	HTGN29	5' TTTCGCCTAGCGGCAACTCCCT 39887	CAT___ _ A
	C	GGGGGAGT CT GGC AAA	
		CTCCCTCA GA CCG TTT	
		ACGGC T C	
GAM1828	KIAA0563	3' TTTGCTTGTCAACTCTCCCT 29892	CATCT
		AGGGGGAGT GGCAAA	
		TCCCTCTCA TCGTTT	
		ACTGT	
GAM1828	KIAA0939	3' TGCCAGAACTCACTCTCCC 62724	CA___
		GGGGGAGT TCTGGCA	
		CCCTCTCA AGACCGT	
		CTCA	
GAM1828	MARK2	3' TGCCCAGAGATTCCCCCT 66223	A _
		AGGGGGAGTC TCTGG CA	
		TCCCCCTTAG AGACC GT	
		_ C	
GAM1828	MARK2	3' TGCCCAGAGATTCCCCCT 34403	A _
		AGGGGGAGTC TCTGG CA	
		TCCCCCTTAG AGACC GT	
		_ C	
GAM1828	LOC147071	3' TTTGCTTGTCAACTCTCCCT 73375	CATCT
		AGGGGGAGT GGCAAA	
		TCCCTCTCA TCGTTT	
		ACTGT	
GAM1828	LOC153937	3' CATTTTTACCAAATACATTTCC 81917	C_ C C
	TC	GGGGGAGT AT TGG AAAAATG	

	CTCCTTTA TA ACC TTTTAC	
	CA A A	
GAM1828 LOC201173 3'	TTTGCTTGTCAACTCTCCCT 88696	CATCT
	AGGGGGAGT GGCAAA	
	TCCCTCTCA TCGTTT	
	ACTGT	
GAM1828 LOC201220 3'	TTTGCTTGTCAACTCTCCCT 88730	CATCT
	AGGGGGAGT GGCAAA	
	TCCCTCTCA TCGTTT	
	ACTGT	
GAM1828 LOC202775 5'	CATTTCTGACCTGCCTCCCC 91962	T TCT _ A_
T	AGGGGGAG CA GG CA AAATG	
	TCCCCCTC GT CC GT TTTAC	
	C _ A CC	
GAM1828 LOC253805 3'	TGCCAATGGCCACTCCCCTT 98189	_ C
	AGGGGGAGT CAT TGGCA	
	TTCCCCTCA GTA ACCGT	
	CCG _	
GAM1828 LOC254220 5'	CATTCTTATTAGTGACTCCTCC 98009	T C A
	GGGGGAGTCA CTGG AA AATG	
	CCTCCTCAGT GATT TT TTAC	
	_ A C	
GAM1829 GALNT2 3'	CCGCACACACAGATGCTCAGT 16814	C _ AA
	ACTGAGCA CTG GTG TGG	
	TGACTCGT GAC CAC GCC	
	A A AC	
GAM1829 NCSTN 3'	CGCCCACAGTGCTCAGT 74135	CTG AAT C
	ACTGAGCAC GTG GGC G	
	TGACTCGTG CAC CCG C	
	A _ _ A	
GAM1829 PPP1R11 3'	CCGGCAGCCCAGATGTTTCAGT 41986	C TGAATG
	ACTGAGCA CTGG GCCGG	
	TGACTTGT GACC CGGCC	
	A CGA _	
GAM1829 GP5 3'	CCTTCCCTCCAGGTGCCCAGT 16873	A T _ T
	ACTG GCACCTGG GAA GG	
	TGAC CGTGGACC CTT CC	
	C TCC _	
GAM1829 HRH3 3'	CCGGCCACTCTGTTTGCTCA 24316	CCTGGT A
	TGAGCA GA TGGCCGG	

	ACTCGT CT ACCGGCC	
	TTGT__ C	
GAM1829 KIAA0574 3'	CCAGCCACCCAGTGGACTCGGT 69809	__ CT AA
	ACTGAG CAC GGTG TGG	
	TGGCTC GTG CCAC ACC	
	AG AC CG	
GAM1829 LOC145622 5'	CCATCACCCAGGTGCTCAGT 77807	_ A
	ACTGAGCACCTGG TGA TGG	
	TGACTCGTGGACC ACT ACC	
	C _	
GAM1829 LOC145622 5'	CCATCAGCCAGGTGCTCAG 77808	GA
	CTGAGCACCTGGT ATGG	
	GACTCGTGGACCG TACC	
	AC	
GAM1829 LOC145622 5'	CCATCAGCCAGGTGCTCAG 77809	GA
	CTGAGCACCTGGT ATGG	
	GACTCGTGGACCG TACC	
	AC	
GAM1829 LOC145622 5'	CCATCAGCCAGGTGCTCAG 77810	GA
	CTGAGCACCTGGT ATGG	
	GACTCGTGGACCG TACC	
	AC	
GAM1829 LOC145622 5'	CCATCATCCAGGTGCTCAG 77811	_ A
	CTGAGCACCTGG TGA TGG	
	GACTCGTGGACC ACT ACC	
	T _	
GAM1829 LOC145622 5'	TGTACGTCAGCCAGGTGCTCAG 77827	GA GC
	CTGAGCACCTGGT ATG CG	
	GACTCGTGGACCG TGC GT	
	AC AT	
GAM1829 LOC145622 5'	TGTCTGTCAGCCAGGTGCTCAG 77828	GA C
	CTGAGCACCTGGT ATGG CG	
	GACTCGTGGACCG TGTC GT	
	AC T	
GAM1829 LOC154995 5'	CGGCCTCCAGGTGCTCA 82104	TGAAT
	TGAGCACCTGG GGCCG	
	ACTCGTGGACC CCGGC	
	T__	
GAM1829 LOC155036 5'	CCAGCTGGCCAAGTGTTTCAG 87611	C GAA C
	CTGAGCAC TGGT TGGC GG	

			GA	CTTGTG	ACCG	GTCG	CC		
			A	___	A				
GAM1829	LOC203248	3'	CCAGCCATT	CATCGACAGTCAG	90842	G	ACC		C
			CTGA	C TGGTGAATGGC	GG				
			GA	CT G GCTACTTACCG	CC				
			_	ACA	A				
GAM1829	LOC221362	3'	CCAAAAGACACCAATGCTCAGT	95398		CC		AA	___
			ACTGAGCA	TGGTG TGG					
			TGACTCGT	ACCAC ACC					
			A	_ AGAAA					
GAM1829	LOC57821	5'	CCGGCCATCTCTGTGATCCCAG	41301		AG	___	CT	T A
			CTG	CAC GG GA TGGCCGG					
			GAC	GTG TC CT ACCGGCC					
			CCTA	___ T _					
GAM1830	ABCB11	3'	CTTGAGCTAGACCAAGGTC	14975		G		A	C
			GACCTTGGT	TAG CTC AG					
			CTGGAACCA	ATC GAG TC					
			G	_ T					
GAM1830	BACE	3'	CTGGAGCTCACCCAAGGTC	58082		T	_	A	
			GACCTTGG	GT AG CTCCAG					
			CTGGAACC	CA TC GAGGTC					
			_	C _					
GAM1830	BACE	3'	CTGGAGCTCACCCAAGGTC	25030		T	_	A	
			GACCTTGG	GT AG CTCCAG					
			CTGGAACC	CA TC GAGGTC					
			_	C _					
GAM1830	C8B	3'	CTGGAGTTCATGCAAGG	5351		G		AG	
			CCTTG	TGT ACTCCAG					
			GGAAC	GTA TGAGGTC					
			_	CT					
GAM1830	CLDN14	5'	CTGGAGTCCAGCCAGGCTC	58470		C		GTA	
			GA	CTTGGT GACTCCAG					
			CT	GGACCG CTGAGGTC					
			C	AC_					
GAM1830	COL17A1	3'	CTGGAGTCTGTCAATGTC	6686		C		TG	
			GAC	TTGG TAGACTCCAG					
			CTG	AACT GTCTGAGGTC					
			T	___					
GAM1830	DAB2	5'	CTGGTGTACCAAGTGTC	9035		_		GTA	T
			GAC	CTTGGT GAC CCAG					

			CTG GAACCA CTG GGTC		
			T _ T		
GAM1830 EMP1	3'	CTGGAGTTTCTCTAAAGTC	9237	C	TGT
		GAC TTGG AGACTCCAG			
		CTG AATC TTTGAGGTC			
		A TC_			
GAM1830 ESR1	3'	CTGGGTGTGCACCAAGGTT	5514		G T
		GACCTTGGTGTA AC CCAG			
		TTGGAACCACGT TG GGTC			
		G _			
GAM1830 FOXD2	3'	CTGAAGCCTAAACCAGTGTC	16789	C	G A C
		GAC TTGGT TAG CT CAG			
		CTG GACCA ATC GA GTC			
		T A C A			
GAM1830 IHPK3	5'	CTGGAGCCCTTCCTGCACCAGG	55094	T	A_____
TC		GACCT GGTGTAG CTCCAG			
		CTGGA CCACGTC GAGGTC			
		_ CTTCCC			
GAM1830 LAMA4	3'	CTGAAGTTATCAAGGTT	11260		GTA C
		GACCTTGGT GACT CAG			
		TTGGA ACTA TTGA GTC			
		_ A			
GAM1830 LEP	3'	CTGGGATTCCCACCAAGGTC	5861		TA CT
		GACCTTGGTG GA CCAG			
		CTGGAACCAC TT GGTC			
		CC AG			
GAM1830 MECP2	3'	CTGGAGTCCACTGGGGT	18401	TG	TA
		ACCT GTG GACTCCAG			
		TGGG CAC CTGAGGTC			
		GT _			
GAM1830 MOCS1	3'	CTGGAGTCCAGGCAGCCAAGGT	93667	_	A__
		ACCTTGG TGT GACTCCAG			
		TGGAACC ACG CTGAGGTC			
		G GAC			
GAM1830 PCOLN3	3'	GGAGGCACCACAGGTC	12415	_	AGA
		GACCT TGGTGT CTCC			
		CTGGA ACCACG GAGG			
		C _			
GAM1830 PPP2R5A	5'	GGAGCTGCCAAGCGTC	21795	_	GT A
		GAC CTTGGT AG CTCC			

CTG GAACCG TC GAGG
 C _ _
 GAM1830 STK24 5' CTGGAGCATGTTGCCAAGGC 14548 A TAGA_
 G CCTTGGTG CTCCAG
 | ||||| |||||
 C GGAACCGT GAGGTC
 _ TGTAC
 GAM1830 TCF2 3' CTGGAGTCTAGGAAGGGC 22406 A GGTG
 G CCTT TAGACTCCAG
 | ||| |||||
 C GGGA ATCTGAGGTC
 _ AGG_
 GAM1830 TMEM4 5' CTGGAGTCCCGCTTAGGT 27300 T TA
 ACCT GGTG GACTCCAG
 ||| ||| |||||
 TGGATCGC CTGAGGTC
 T C_
 GAM1830 TRIM14 3' GAGTCACTTGCCCAAGGTC 29514 T _
 GACCTTGG GTA GACTC
 ||||| ||| |||||
 CTGGAACC CGT CTGAG
 _ TCA
 GAM1830 UMPS 3' CTGGAGTTCTCATGGTC 6331 TTG TA
 GACC GTG GACTCCAG
 ||| ||| |||||
 CTGG TAC TTGAGGTC
 _ TC
 GAM1830 ZNF144 3' CTGGAGTCTCAATAAAGCTC 24073 C GG_ T
 GA CTT TG AGACTCCAG
 || ||| |||||
 CT GAA AC TCTGAGGTC
 C ATA _
 GAM1830 BICD2 3' CTGAAGTCTGAGCCACCAAGG 70910 _ C
 CCTTGGTG TAGACT CAG
 ||||| ||||| |||
 GGAACCAC GTCTGA GTC
 CGA A
 GAM1830 BPES 3' CTGGAGCCAGCGCCCAAGGTC 43796 _ AGA
 GACCTTGG TGT CTCCAG
 ||||| ||| |||||
 CTGGGACC GCG GAGGTC
 C ACC
 GAM1830 BTEB5 3' GAGTCATTACACCAAGGC 57713 A _
 G CCTTGGTGTA GACTC
 | ||||| |||||
 C GGAACCACAT CTGAG
 _ TA
 GAM1830 C20orf60 3' CTGGGAAGGCCCAAGGTC 54806 T AGAC
 GACCTTGG GT TCCAG
 ||||| || |||||

		CTGGAACC CG GGGTC		
		C GAA_		
GAM1830	CARD14	3' CTGGGTGGTCCCCAAGGTC 44352	TGTA	__
		GACCTTGG GACT CCAG		
		CTGGAACC CTGG GGTC		
		C__ TG		
GAM1830	CBX1	3' CTGAAACCTATAAGCCAAGGT 23310	__	ACTC
		ACCTTGGT GTAG CAG		
		TGGAACCG TATC GTC		
		AA CAAA		
GAM1830	CST8	5' CTGAAAGTCCACCAAGG 19712	TA	C_
		CCTTGGTG GACT CAG		
		GGAACCAC CTGA GTC		
		__ AA		
GAM1830	DKFZp434N035	3' CTGAGAGTGTAGACCAAGGTC 51061	G G	_
		GACCTTGGT TA ACTC CAG		
		CTGGAACCA AT TGAG GTC		
		G G A		
GAM1830	DOCK3	3' CTGGACTCCATCAAGG 67094	TA	C
		CCTTGGTG GA TCCAG		
		GGAACTAC CT AGGTC		
		__ C		
GAM1830	ENDOGLYX1	5' CTGGAGCTACTTGCCAAGG 45732	__	A
		CCTTGGT GTAG CTCCAG		
		GGAACCG CATC GAGGTC		
		TT _		
GAM1830	FAPP2	3' CTGGTGGTGAACCAAGGTC 51956	GTAG	_
		GACCTTGGT ACT CCAG		
		CTGGAACCA TGG GGTC		
		AG__ T		
GAM1830	FLJ10761	3' CTGAAGCTGACCCGAGGTC 37129	TG	A C
		GACCTTGG TAG CT CAG		
		CTGGAGCC GTC GA GTC		
		CA _ A		
GAM1830	FLJ13855	3' CTGGGACTTAACCAAGGTC 43849	GT	A T
		GACCTTGGT AG C CCAG		
		CTGGAACCA TC G GGTC		
		AT A _		
GAM1830	FLJ20694	5' GGATCATCACCAAGGTC 35977	TA	C
		GACCTTGGTG GA TCC		

CTGGAACCAC CT AGG
 TA _
 GAM1830 FLJ23277 5' CTGAAGGAGCGCCAGGTC 50916 T AGA C
 GACCT GGTGT CT CAG
 ||||| ||||| |||||
 CTGGA CCGCG GA GTC
 _ AG_ A
 GAM1830 HIC2 3' CTGAAGTGGGCTCTCAAGGTC 65867 _T AG C
 GACCTTG G GT ACT CAG
 ||||| || |||||
 CTGGAAC C CG TGA GTC
 TT GG A
 GAM1830 IMAGE3510317 3' CTGGAGTCTCCCGAGG 68038 TGT
 CCTTGG AGACTCCAG
 ||||| |||||
 GGAGCC TCTGAGGTC
 C_
 GAM1830 KHDRBS3 5' CTGGAGTCCACATCCCGGG 22656 T _ A
 CCT GG TGT GACTCCAG
 ||| || |||||
 GGG CC ACA CTGAGGTC
 C T C
 GAM1830 KIAA0298 3' CTGGAGCGACTCAAGATC 77078 C T AGA
 GA CTTGG GT CTCCAG
 || ||||| || |||||
 CT GAACT CA GAGGTC
 A _ GC_
 GAM1830 KIAA0561 3' CTGGAACTGCCAAGGC 66476 A GT AC
 G CCTTGGT AG TCCAG
 | ||||| || |||||
 C GGAACCG TC AGGTC
 _ _ A_
 GAM1830 KIAA0939 3' CTGGCTTACACCAAAGG 62714 _ ACT
 CCTT GGTGTAG CCAG
 ||||| ||||| |||||
 GGAA CCACATT GGTC
 A C_
 GAM1830 KIAA1036 3' CTGGAGTCTTAGGAGGTT 30489 GGTGT
 GACCTT AGACTCCAG
 ||||| |||||
 TTGGAG TCTGAGGTC
 GAT_
 GAM1830 KIAA1318 3' TGGGTCTCCAGGGTC 67879 TGT T
 GACCTTGG AGAC CCA
 ||||| ||||| |||||
 CTGGGACC TCTG GGT
 _ _
 GAM1830 KLK15 3' CTGGTGTCTATACCAAAGTC 57515 C T
 GAC TTGGTGTAGAC CCAG
 ||| ||||| ||||| |||||

CTG AACCATATCTG GGTC
 A T
 GAM1830 KLK15 3' CTGGTGTCTATACCAAAGTC 43713 C T
 GAC TTGGTGTAGAC CCAG
 ||| ||||| ||||
 CTG AACCATATCTG GGTC
 A T
 GAM1830 LIMK2 5' CTGGAGTCCTCAGGCTC 34119 C TGTA
 GA CTTGG GACTCCAG
 || |||| |||||
 CT GGA CTGAGGTC
 C C__
 GAM1830 MGC15504 3' CTGAAGTTAGCCAAGGTT 52217 GTA C
 GACCTTGGT GACT CAG
 ||||| ||| |||
 TTGGAACCG TTGA GTC
 A__ A
 GAM1830 MGC2477 5' CTGGAACAAACACTCAAAGTC 44301 C _ AGAC
 GAC TTG GTGT TCCAG
 ||| ||| ||| ||||
 CTG AAC CACA AGGTC
 A T AACA
 GAM1830 p25 3' CTGGAGTCTACCTGCGG 23832 T T
 CC TGG GTAGACTCCAG
 || ||| |||||
 GG GTC CATCTGAGGTC
 C _
 GAM1830 PIP5K2B 3' CTGGAATACACCAGGTC 14529 T GAC
 GACCT GGTGTA TCCAG
 |||| |||| ||||
 CTGGA CCACAT AGGTC
 _ A__
 GAM1830 RAB35 3' CTGGAGAACAACCAGGGTC 23414 GTAGA
 GACCTTGGT CTCCAG
 ||||| |||||
 CTGGGACCA GAGGTC
 ACAA_
 GAM1830 TRIM26 3' CTGGAGTCCATGAGGG 14348 G TA
 CCTT GTG GACTCCAG
 |||| ||| |||||
 GGA TAC CTGAGGTC
 G _
 GAM1830 TTTY8 3' CTGGAGTCTGCTTAAAGG 51832 GGT
 CCTT GTAGACTCCAG
 ||| |||||
 GGAA CGTCTGAGGTC
 ATT
 GAM1830 USP24 3' CTGGAGTCCTCACACGGTC 92792 TTG TA
 GACC GTG GACTCCAG
 ||| ||| |||||

CTGG CAC CTGAGGTC
 CA_ TC
 GAM1830 LOC115708 3' CTGGGTGAGTCACCAGGGTC 73915 TAG_ T
 GACCTTGGTG AC CCAG
 ||||| |||||
 CTGGGACCAC TG GGTC
 TGAG _
 GAM1830 LOC123591 3' CTGGAGGCTGCCAAGG 76129 GT A
 CCTTGGT AG CTCCAG
 ||||| |||||
 GGAACCG TC GAGGTC
 _ G
 GAM1830 LOC147071 5' GCTGGAGTCCTGGGACCACCAG 73367 _ _ _
 GGTC GACCTTGGTG TAG ACTCCAG C
 ||||| ||||| |
 CTGGGACCAC GTC TGAGGTC G
 CAGG C _
 GAM1830 LOC147495 5' CTGTGAGTGCACCAAGG 85142 AG _
 CCTTGGTGT ACTC CAG
 ||||| |||||
 GGAACCACG TGAG GTC
 _ T
 GAM1830 LOC149935 3' CTGGCCTCACCAAGGT 60935 T ACT
 ACCTTGGTG AG CCAG
 ||||| |||||
 TGGAACCAC TC GGTC
 _ C_
 GAM1830 LOC151201 3' CTGGAGTCCAATGGGGC 86473 A GG TA
 G CCTT TG GACTCCAG
 | |||| |||||
 C GGGG AC CTGAGGTC
 _ TA _
 GAM1830 LOC151996 5' CTGGAGGACATGCACCAAGG 86718 GA_
 CCTTGGTGTA CTCCAG
 ||||| |||||
 GGAACCACGT GAGGTC
 ACAG
 GAM1830 LOC157943 5' CTGGAGTCCATGAGCGTC 87947 C G TA
 GAC TT GTG GACTCCAG
 ||||| |||||
 CTG GA TAC CTGAGGTC
 C G _
 GAM1830 LOC165693 3' CTGGTGTTTACACAAGG 83488 G T
 CCTTG TGTAGAC CCAG
 ||||| ||||| |||||
 GGAAC ACATTTG GGTC
 _ T
 GAM1830 LOC196707 3' TTGGGTACACCACAGG 88927 _ GAC
 CCT TGGTGTA TCCAG
 ||||| ||||| |||||

GGA ACCACAT GGGTT
 C _
 GAM1830 LOC196759 5' CTGGAGTCTCACCAAATC 88910 CC T
 GA TTGGTG AGACTCCAG
 || ||||| |||||
 CT AACCAC TCTGAGGTC
 A_ _
 GAM1830 LOC199864 5' CTGGAGTCTCACCAAATC 91457 CC T
 GA TTGGTG AGACTCCAG
 || ||||| |||||
 CT AACCAC TCTGAGGTC
 A_ _
 GAM1830 LOC201173 5' GCTGGAGTCCTGGGACCACCAG 88687 _ _ _
 GGTC GACCTTGGTG TAG ACTCCAG C
 ||||| || ||||| |
 CTGGGACCAC GTC TGAGGTC G
 CAGG C _
 GAM1830 LOC201220 5' GCTGGAGTCCTGGGACCACCAG 88722 _ _ _
 GGTC GACCTTGGTG TAG ACTCCAG C
 ||||| || ||||| |
 CTGGGACCAC GTC TGAGGTC G
 CAGG C _
 GAM1830 LOC203504 5' CTGGAGCTTCACCAAGG 92323 T A
 CCTTGGTG AG CTCCAG
 ||||| || |||||
 GGAACCAC TC GAGGTC
 T _
 GAM1830 LOC220776 3' CTGGAGCCCATGCCAGGT 68928 T AGA
 GACCT GGTGT CTCCAG
 ||||| |||||
 TTGGA CCGTA GAGGTC
 _ CCC
 GAM1830 LOC221955 3' CTGGGCGTCACCAAGG 58267 GTA _
 CCTTGGT GAC TCCAG
 ||||| || |||||
 GGAACCA CTG GGGTC
 _ C
 GAM1830 LOC256310 5' CTGGAGTCCATCACAGT 98098 CT TA
 AC TGGTG GACTCCAG
 || ||||| |||||
 TG ACTAC CTGAGGTC
 AC _
 GAM1830 LOC256848 5' CTGGGCTTCACCAAGGT 99378 T A T
 ACCTTGGTG AG C CCAG
 ||||| || |||||
 TGGAACCAC TC G GGTC
 T _ _
 GAM1830 LOC257169 3' CTGGAGCCTTTACCAGGG 97862 T A
 CCTTGGTG AG CTCCAG
 ||||| || |||||

		GGGACCAT TC GAGGTC		
		T C		
GAM1830	LOC257494 3'	CTGGAGTCCATGAGGG	99633	G TA
		CCTT GTG GACTCCAG		
		GGGA TAC CTGAGGTC		
		G _		
GAM1830	LOC90019 5'	CTGGAGCTTTGGCCAGGGTC	57528	GT_ A
		GACCTTGGT AG CTCCAG		
		CTGGGACCG TC GAGGTC		
		GTT _		
GAM1830	LOC90019 5'	CTGGAGTCATGGCAGGGTC	57529	G A
		GACCTTG TGT GACTCCAG		
		CTGGGAC GTA CTGAGGTC		
		G _		
GAM1830	LOC91272 3'	CTGAAGATAGGCCAAGGTC	66034	G GA C
		GACCTTGGT TA CT CAG		
		CTGGAACCG AT GA GTC		
		G A_ A		
GAM1830	LOC91516 5'	CTGTGAACACCAATGTC	66906	C AGAC _
		GAC TTGGTGT TC CAG		
		CTG AACCACA AG GTC		
		T _ _ _ T		
GAM1831	SLC7A5 3'	CCCACCCTGGGCTCCACACAGC	14463	GTAATCTT A
	A	TGCTG TCCAGGGT GG		
		ACGAC GGGTCCCA CC		
		ACACCTC_ C		
GAM1831	C1orf34 3'	CTTTAGAAAGCCCACCAGCA	61309	AAT C
		TGCTGGT CTTTC AGGG		
		ACGACCA GAAAG TTTC		
		CCC A		
GAM1831	ELOVL2 3'	CTTGGAAGATTCCAGCA	35438	T
		TGCTGG AATCTTTCCAGG		
		ACGACC TTAGAAAGGTTTC		
		_		
GAM1831	KIAA0193 3'	CCCACCTTACTAAATTACCAGC	29314	CTTTCC A
	A	TGCTGGTAAT AGGGT GG		
		ACGACCATTA TTCCA CC		
		AATCA_ C		
GAM1831	KIAA0543 3'	CCTACCCTGGGCTCCCACAGCA	69520	GTAATCTTT
		TGCTG CCAGGGTAGG		

ACGAC GGTCCCATCC
 ACCCTC___
 GAM1831 KIAA0889 3' CCCACCAGAGACTGCCAGCA 31768 A CCA
 TGCTGGTA TCTTT GGG
 ||||| |||| |
 ACGACCGT AGAGA CCC
 C CCA
 GAM1831 KIAA0993 3' CCTTATTTGGAAAAACCAACA 64818 C AATC GT
 TG TGGT TTTCCAGG AGG
 || ||| ||||| ||
 AC ACCA AAAGGTTT TCC
 A A___ AT
 GAM1831 KLHL8 3' CCTACCCTGAAAAATGCT 63512 ATC C
 GGTA TTTC AGGGTAGG
 ||| ||| |||||
 TCGT AAAG TCCCATCC
 AA_ _
 GAM1831 METL 5' CCTACCCTGAAGGTGCACCTGC 37840 T A_ TC
 A TGC GGT ATCTT CAGGGTAGG
 ||| ||| ||||| |||||
 ACG CCA TGGAA GTCCCATCC
 T CG _
 GAM1831 MGC27382 5' CCTACCCTATTTATTCCCAGCA 59125 T CTTTCC
 TGCTGG AAT AGGGTAGG
 ||||| ||| |||||
 ACGACC TTA TCCCATCC
 C TTAA___
 GAM1831 TDRKH 3' CTACCCTGGAAAATGAGTA 23423 G AATC
 TGCT GT TTTCCAGGGTAG
 |||| || |||||
 ATGA TA AAAGTCCCATC
 G _
 GAM1831 LOC148089 3' ACCCAGTTACCAGCA 79323 T TTCCA
 TGCTGGTAA CT GGGT
 ||||| || |||
 ACGACCATT GA CCCA
 _ _
 GAM1831 LOC150197 3' CCCACCCTGGACAACAACCAGC 80421 AATCTT A
 A TGCTGGT TCCAGGGT GG
 ||||| ||||| ||
 ACGACCA AGGTCCCA CC
 ACAAC_ C
 GAM1831 LOC200325 5' CCTACGATGAGGACTACCAGCA 91578 A TC GG
 TGCTGGTA TCTT CA GTAGG
 ||||| ||| || ||||
 ACGACCAT AGGA GT CATCC
 C _ AG
 GAM1832 DLEC1 3' CATCTGGCCCTCCCTTG 24716 A A C
 CAAGG AGGGC GG GTG
 |||| |||| || |||

			GTTCC TCCCG TC TAC			
			C G _			
GAM1832	DLEC1	3'	CATCTGGCCCTCCCTTG	24728	A A C	
			CAAGG AGGGC GG GTG			
			GTTCC TCCCG TC TAC			
			C G _			
GAM1832	PIP5K1A	3'	TATCCCACCCTGCCTTGATA	14520	A CA C	
			TATCAAGG AGGG GG GTG			
			ATAGTTCC TCCC CC TAT			
			G A_ C			
GAM1832	SOX11	3'	ACCCACCCCCCCTTGGA	13308	AA CA C	
			TATCAAGG GGG GG GT			
			ATGGTTCC CCC CC CA			
			CC A_ _			
GAM1832	CHL1	3'	TGTTACCTTTCCTCAATA	22768	CA CA	
			TAT AGGAAGGG GGCG			
			ATA TCCTTTCC TTGT			
			AC A_			
GAM1832	EPB41L1	3'	CATTCTGCCCTTCCCTGA	71104	A C	
			TCA GGAAGGGCAGG GTG			
			AGT CCTTCCCGTCT TAC			
			C _			
GAM1832	FLJ00060	3'	CATACCCCCTGCCCTCCTCTGA	61741	_ A CGTG	
			TCA AGGA GGGCAGG ATG			
			AGT TCCT CCCGTCC TAC			
			C _ CCCA			
GAM1832	FLJ10898	5'	CACCACAGCCCTTTCTCAATA	60126	CA AGGC	
			TAT AGGAAGGGC GTG			
			ATA TCTTTCCCG CAC			
			AC ACAC			
GAM1832	FLJ22557	3'	ATCATCCCATCCTTAATA	45581	C A CAGGC	
			TAT AAGGA GGG GTGAT			
			ATA TTCCT CCC TACTA			
			A A _			
GAM1832	KIAA0574	3'	CATCCCCTGCCCTCCCCTGA	69808	A A CGT	
			TCA GG AGGGCAGG GATG			
			AGT CC TCCCGTCC CTAC			
			C C C_			
GAM1832	KIAA0632	3'	CACCTCAGAAACCCTTCCTTGA	32071	CA_ C	
			TCAAGGAAGGG GG GTG			

AGTTCCTTCCC CT CAC
 AAAGA C
 GAM1832 KIAA1045 3' CATCACATGTCCTTCC 71599 GGC
 GGAAGGGCA GTGATG
 ||||| ||||
 CCTTCCTGT CACTAC
 A__
 GAM1832 KIAA1354 5' CAGTGA CTGCCTTCCCTTGATA 61572 A G _
 TATCAAGG AGGGCAG CG TG
 ||||| ||||| || ||
 ATAGTTCC TTCCGTC GT AC
 C A G
 GAM1832 MGC20460 5' CACCGCCTCCTACCCTTCTT 54901 C__ _
 AGGAAGGG AGGCG TG
 ||||| |||| ||
 TTCTTCCC TCCGC AC
 ATCC C
 GAM1832 LOC158476 3' CACGCCCGCCCCCCCCATTGA 88186 _ AA_ A
 TCAA GG GGGC GGC GTG
 ||| || ||| |||||
 AGTT CC CCG CCGCAC
 A CCC C
 GAM1832 LOC90459 3' CACACCCGCCTAATTTTGT 63550 A_ A C
 CAAGGA GGGC GG GTG
 |||| ||| || |||
 GTTTTT TCCG CC CAC
 AA C A
 GAM1833 ATP11A 3' GAGCACGGCCAGCCTTCCGCCA 77555 A_ C TG
 CG CGTGGCGGAAG TG GTT GCTC
 ||||| || ||| ||||
 GCACCGCCTTC AC CGG CGAG
 CG _ CA
 GAM1833 FN14 3' GAGCCAAGCTCCTCCAACCAC 34042 C_ A TGC
 GTGG GGA GA GTTTGGCTC
 ||| ||| || |||||
 CACC CCT CT CGAACCGAG
 AA C ____
 GAM1833 GYP A 3' AGCCAAACACATCCTTTCATCA 88838 GC _ C
 TG GGAAG ATG GTTTGGCT
 || |||| || |||||
 AC CTTTC TAC CAAACCGA
 TA C A
 GAM1833 MEF2D 3' AGCCAAATTCGCCTCCAC 98695 C AA TGC
 GTGG GG GA GTTTGGCT
 ||| || || |||||
 CACC CC CT TAAACCGA
 T G_ ____
 GAM1833 POLR2E 3' GAGCCCAGTGT CATCCGCCCGC 60595 AA_ _ T
 CACG CGTGGCGG GATG CGTT GGCTC
 ||||| ||| ||| |||||

GCACCGCC CTAC GTGA CCGAG
 CGC T C
 GAM1833 SORBS1 3' AAACCTCTCATCTTCCCCCAC 31800 C C__
 GTGG GGAAGATG GTTT
 ||| ||||| |||
 CACC CCTTCTAC CAAA
 C TCT
 GAM1833 TNFRSF1B 3' AGCCAAACTCTGCCAGCCAC 8382 _ A TGC
 GTGGC GG AGA GTTTGGCT
 |||| || ||| |||||
 CACCG CC TCT CAAACCGA
 A G ____
 GAM1833 AF9Q34 5' CCACAGCTTCCGCCAC 51713 A CGTT
 GTGGCGGAAG TG TGG
 ||||| || |||
 CACCGCCTTC AC ACC
 G ____
 GAM1833 BDG-29 3' AGCCCTATCTTCCACTAC 72801 C CGTTT
 GTGG GGAAGATG GGCT
 ||| ||||| |||
 CATC CCTTCTAT CCGA
 A C____
 GAM1833 FLJ21916 3' AGCCAAACACATCACCAC 43890 CGGAA C
 GTGG GATG GTTTGGCT
 ||| ||| |||||
 CACC CTAC CAAACCGA
 A____ A
 GAM1833 KIAA0483 3' GCTTAACATCTTCCACCGC 31474 C CGTTT
 GTGG GGAAGATG GGC
 ||| ||||| |||
 CGCC CCTTCTAC TCG
 A AAT__
 GAM1833 KIAA1009 3' TTGAACATACTCCGCCAC 30320 A A C TG
 GTGGCGGA G TG GTT G
 ||||| | || ||| |
 CACCGCCT C AT CAA T
 __ A GT
 GAM1833 KIAA1484 3' GAGCCGGGACCCTCCGCCGC 70522 AGATGCG
 GTGGCGGA TTTGGCTC
 ||||| |||||
 CGCCGCCT GGGCCGAG
 CCCA____
 GAM1833 MGC2749 3' GAGCCAGATGTCCCCCACCAC 44170 C AAGAT
 GTGG GG GCGTTTGGCTC
 ||| || |||||
 CACC CC TGTAGACCGAG
 A CCC__
 GAM1833 MRPS34 3' AGCTCACCTTCCGCGACG 43976 G A CGTTT
 CGT GCGGAAG TG GGCT
 || ||||| || |||

		GCA CGCCTTC AC	TCGA		
		G C _____			
GAM1833	PRKWNK4	3' AGCCATGTATCTCCCCAC	51502	C A	TT
		GTGG GG AGATGCG TGGCT			
		CACC CC TCTATGT ACCGA			
		_ C _			
GAM1833	RAB3IL1	3' GACGCATCCCTCACCACG	26367	C AA	
		CGTGG GG GATGCGTT			
		GCACC CT CTACGCAG			
		A CC			
GAM1833	SEMA6B	3' GAGTGGGGGGCCCCCTCCGCCA	50403	AGAT G G	
	C	GTGGCGGA GC TTT GCTC			
		CACCGCCT CG GGG TGAG			
		CCCC G G			
GAM1833	LOC125058	3' GAGCCAAACACACTTCC	60547	A C	
		GGAAG TG GTTTGGCTC			
		CCTTC AC CAAACCGAG			
		_ A			
GAM1833	LOC146733	5' AGCCAAACACAACAGCCCCACG	84781	C AAGA C	
		CGTGG GG TG GTTTGGCT			
		GCACC CC AC CAAACCGA			
		_ GACA A			
GAM1833	LOC197287	3' GAGCACGGCCAGCCTTCCGCCA	61547	A_ C TG	
	CG	CGTGGCGGAAG TG GTT GCTC			
		GCACCGCCTTC AC CGG CGAG			
		CG _ CA			
GAM1833	LOC219942	3' GAACCATTTGCCCTTCGCCAC	94992	G AT TT C	
		GTGGCG AAG GCG TGG TC			
		CACCGC TTC CGT ACC AG			
		_ C_ TT A			
GAM1833	LOC221540	3' GCTCCATCTTCCACCAC	95479	C	CGTTT
		GTGG GGAAGATG GGC			
		CACC CCTTCTAC TCG			
		A C_____			
GAM1833	LOC257545	3' GCTCCATCTTCCACCAC	99643	C	CGTTT
		GTGG GGAAGATG GGC			
		CACC CCTTCTAC TCG			
		A C_____			
GAM1833	LOC257598	3' GCTCCATCTTCCACCAC	99751	C	CGTTT
		GTGG GGAAGATG GGC			

CACC CTTCTAC TCG
 A C____
 GAM1834 ACLY 3' AGATTCTGGGCAGCTGCCA 65684 A CT AGT
 TG CAGC TCT AGAATCT
 || ||| || |||||
 AC GTCG GGG TCTTAGA
 C AC ____
 GAM1834 CCNDBP1 3' AGAGATTCCTAGGAAAGCTG 25116 C_ TA
 CAGC TTCTAG GAATCTCT
 ||| ||||| |||||
 GTCG AGGATC CTTAGAGA
 AA ____
 GAM1834 CCNDBP1 3' AGAGATTCCTAGGAAAGCTG 54470 C_ TA
 CAGC TTCTAG GAATCTCT
 ||| ||||| |||||
 GTCG AGGATC CTTAGAGA
 AA ____
 GAM1834 CST1 3' AGAGACAGACAGAGAAGGCTGC 10327 A A_ AGAA
 A TG CAGCCTTCT GT TCTCT
 || ||||| || |||||
 AC GTCGGAAGA CA AGAGA
 _ GA GAC_
 GAM1834 CST4 3' AGAGACAGACAGAGAAGGCTGC 10333 A A_ AGAA
 A TG CAGCCTTCT GT TCTCT
 || ||||| || |||||
 AC GTCGGAAGA CA AGAGA
 _ GA GAC_
 GAM1834 EGFL5 5' AGACTGCTGGAAGACTTCA 87903 C C AA
 TGA AG CTTCTAGTAG TCT
 ||| || ||||| |||
 ACT TC GAAGGTCGTC AGA
 _ A ____
 GAM1834 HIS1 3' GAGATTCATAAGATTGTCA 22339 CCT A A
 TGACAG TCT GT GAATCTC
 ||||| ||| || |||||
 ACTGTT AGA TA CTTAGAG
 ____ A ____
 GAM1834 LGALS3BP 3' AGAAATTACTGGAAGGCTTC 69855 C AA
 GA AGCCTTCTAGTAG TCT
 || ||||| ||||| |||
 CT TCGGAAGGTCATT AGA
 _ AA ____
 GAM1834 SLC6A6 3' AGAGATCCAAGAAGGCTG 13181 AGTA A
 CAGCCTTCT GA TCTCT
 ||||| || |||||
 GTCGGAAGA CT AGAGA
 AC__ _
 GAM1834 SPS2 3' AGAAATTTCCAAGAAGGCTG 25311 AGTA C
 CAGCCTTCT GAAT TCT
 ||||| ||| |||

		GTCGGAAGA	TTTA AGA		
		AACC	A		
GAM1834	C21orf25	3'	AGACATGTAAAAGGCTGTTA	64279	C G GAA
			TGACAGCCTT TA TA	TCT	
			ATTGTCGGAA AT GT	AGA	
			A _ AC_		
GAM1834	FLJ10276	3'	AGATTCTAACAGCTGTTA	36419	CTTCTAG
			TGACAGC	TAGAATCT	
			ATTGTCG	ATCTTAGA	
			ACA_____		
GAM1834	FLJ10853	3'	AGAGATTTTTTCAGAAGATTGTC	37314	GC AGT
	A		TGACA CTTCT	AGAATCTCT	
			ACTGT GAAGA	TTTTAGAGA	
			TA	CT_	
GAM1834	FLJ10898	3'	GAGATAAGAAGGCTGCA	60135	A AGTAGA
			TG CAGCCTTCT	ATCTC	
			AC GTCGGAAGA	TAGAG	
			_	A_____	
GAM1834	FLJ12903	3'	AGAGATTCTTTACCAGGCTGT	43064	TC T
			ACAGCCT TAG	AGAATCTCT	
			TGTCGGA ATT	TCTTAGAGA	
			CC	_	
GAM1834	LOC150378	3'	AGAGACAGAGAGAAGGCTGCA	80554	A AGTAGAA
			TG CAGCCTTCT	TCTCT	
			AC GTCGGAAGA	AGAGA	
			_	GAGAC_	
GAM1834	LOC200310	3'	AGAGACTAAAGGGAAGGCTG	66320	AG_ AA
			CAGCCTTCT TAG	TCTCT	
			GTCGGAAGG ATC	AGAGA	
			GAA	_	
GAM1834	LOC255465	3'	AGAACTCTACTAGGGCAGTGC	99098	_ A TT ATC
	A		TG AC GCC	CTAGTAGA TCT	
			AC TG CGG	GATCATCT AGA	
			G A _	CAA	
GAM1835	ACTB	5'	CGATCCGCCGCCCGTCCACA	8464	A A A GG
			TGTGGACG GC	GG GGA CG	
			ACACCTGC CG	CC CCT GC	
			C _ G A_		
GAM1835	AP1B1	3'	CCAGCCTTCTGCCCGCCCCA	8517	T A A A_
			TG GG CG	GCAGGAGG GG	

AC CC GC CGTCTTCC CC
 _ C C GA
 GAM1835 AR 5' CCTCCTCCTGCCTTCCCCAC 5274 AC _
 GTGG GAG CAGGAGGAGG
 |||| ||| |||||
 CACC TTC GTCCTCCTCC
 CC C
 GAM1835 B4GALT1 5' CGCCTCCCCTCCTGTAGCCAC 9469 ACGA _
 A TGTGG GCAGGA GGAGGCG
 |||| ||||| |||||
 ACACC TGTCTCCT CCTCCGC
 CGA_ CC
 GAM1835 CAPN1 3' CGCCTCCTACCACACCACA 19007 ACGAGCA _
 TGTGG GG AGGAGGCG
 |||| || |||||
 ACACC CC TCCTCCGC
 ACA_ A
 GAM1835 COL5A1 3' CGCCCCACGCTCTGTCCACA 5408 _ AGGA A
 TGTGGAC GAGC GG GGCG
 ||||| ||| || |||
 ACACCTG CTCG CC CCGC
 T CA_ _
 GAM1835 CTF1 3' CGCCTCCTCCCGCTGGGTTC 9012 G_ A
 GGAC AGC GGAGGAGGCG
 |||| ||| |||||
 CTTG TCG CCTCCTCCGC
 GG C
 GAM1835 DLK1 5' CGCCCCCTTTTCGCGTCCGCA 15176 GA AG A
 TGTGGAC GC GAGG GGCG
 ||||| || ||| |||
 ACGCCTG CG TTCC CCGC
 _ CT C
 GAM1835 FCN3 3' CCTCTGCTTGCCTGTCCACA 14752 A A
 TGTGGACG GCAGG GGAGG
 ||||| ||||| |||||
 ACACCTGT CGTTC TCTCC
 C G
 GAM1835 GP1BB 3' CGCCTCCTCCGCTGCCCA 6393 A G A
 TGG C AGC GGAGGAGGCG
 ||| ||| |||||
 ACC G TCG CCTCCTCCGC
 C _ _
 GAM1835 HDAC2 5' CGCCCCCTCCTCTCCTCCCA 92629 T C C A
 TG GGA GAG AGGAGG GGCG
 || ||| ||| ||||| |||
 AC CCT CTC TCCTCC CCGC
 _ C _ C
 GAM1835 HR 3' CCTCCTCCTGCTGCTCAC 37908 GA G
 GTG C AGCAGGAGGAGG
 ||| ||| |||||

CAC G TCGTCCTCCTCC
TC _
GAM1835 L1CAM 3' CCTCCTCCCACTGCCCAC 43987 A G CA
GTGG C AG GGAGGAGG
|||| | || |||||
CACC G TC CCTCCTCC
C _ AC
GAM1835 NAV2 3' CGCCTCCTCCTGCTAGGGCT 60793 ACG_
GG AGCAGGAGGAGGCG
|| |||||
TC TCGTCCTCCTCCGC
GGGA
GAM1835 ODF2 5' CCCCTGTCCACGTCCACA 11885 A__ A
TGTGGACG GCAGG GG
||||| |||| |
ACACCTGC TGTCC CC
ACC _
GAM1835 PDE4A 3' CCTCCTCCTCTGCCTCA 21680 T A G C
TG GG C AG AGGAGGAGG
|| || | |||||
AC CC G TC TCCTCCTCC
T _ _ _
GAM1835 PPFIA3 5' CGCCTCCTCCCGCACTTCCACA 61668 CGA A
TGTGGA GC GGAGGAGGCG
|||| | |||||
ACACCT CG CCTCCTCCGC
TCA C
GAM1835 PTGS2 5' CGCCTCCTTCAGCTCCACA 8245 CGA A
TGTGGA GC GGAGGAGGCG
|||| | |||||
ACACCT CG CTCCTCCGC
_ A
GAM1835 SOX12 3' CGCCCCCTCCTGCACAGCCAC 23683 ACGA A
GTGG GCAGGAGG GGCG
||| ||||| |||
CACC CGTCCTCC CCGC
GACA C
GAM1835 TITF1 3' CGCTTCCTCCTGCCCCGCCACA 13890 A A _
TGTGG CG GCAGGAGG AGGCG
|||| | ||||| |||||
ACACC GC CGTCCTCC TTCGC
_ C C
GAM1835 BRUNOL6 5' CGCCCCTTTCCTGCCCGCCCCA 54520 T A A _ A
TG GG CG GCAGGA GG GGCG
|| || | ||||| || |||
AC CC GC CGTCCT CC CCGC
_ C C TT _
GAM1835 C20orf150 3' CGCCTCCTCCTGCCAGCAC 66010 GACGA
GTG GCAGGAGGAGGCG
|| | |||||

CAC CGTCCTCCTCCGC
GAC__
GAM1835 CYP2S1 3' CCCCCAACCATTGTCCACA 48369 CA A_ A
TGTGGACGAG GG GG GG
||||||| || ||
ACACCTGTTC CC CC CC
A_ AA C
GAM1835 DJ159A19.3 3' CCTCCCACCCATCTCCTCCAC 32281 C CA_ A_
GTGGA GAG GG GGAGG
||||| || ||||
CACCT CTC CC CCTCC
C TAC AC
GAM1835 FLJ20257 5' CCTCCTCCAGTGGTCCCCA 39484 T GA A
TG GGAC GC GGAGGAGG
|| ||| || |||||
AC CCTG TG CCTCCTCC
C G_ A
GAM1835 FLJ20294 3' CCTCCTCCTCTTCCTCA 35351 T CG C
TG GGA AG AGGAGGAGG
|| ||| || |||||
AC CCT TC TCCTCCTCC
T _ _
GAM1835 FLJ20306 5' CCTCCTCCCGCCCGTCCCA 35389 T A A
TG GGACG GC GGAGGAGG
|| |||| || |||||
AC CCTGC CG CCTCCTCC
_ C C
GAM1835 FLJ21172 5' CGCCGTCGCCCGTCCACA 46070 AGCA A GA
TGTGGACG GG G GGCG
|||||| || | |||
ACACCTGC CC C CCGC
C__ G TG
GAM1835 GABBR1 5' CGCCCCCTCCTCCCCACA 9411 ACGAGC A
TGTGG AGGAGG GGCG
|||| ||||| |||
ACACC TCCTCC CCGC
CC__ C
GAM1835 H2BFQ 3' CGCCTCTTTACCCGCCCCCA 60077 T A AGCAG
TG GG CG GAGGAGGCG
|| ||| |||||
AC CC GC TTTCTCCGC
C C CCA__
GAM1835 ILF3 3' CGCCCCCATCCCGTCCAC 16923 AGCA _ A
GTGGACG GGA GG GGCG
||||| ||| || |||
CACCTGC CCT CC CCGC
__ A C
GAM1835 ILF3 3' CGCCCCCATCCCGTCCAC 25233 AGCA _ A
GTGGACG GGA GG GGCG
||||| ||| || |||

CACCTGC CCT CC CCGC
____ A C
GAM1835 KIAA1678 3' CCTTCTCTATCATCCACA 72766 C GCA
TGTGGA GA GGAGGAGG
||||| || |||||
ACACCT CT TCTCTTCC
A A__
GAM1835 KIAA1706 3' CCTCCTCCCTCCTCCCCA 94364 T C CA
TG GGA GAG GGAGGAGG
|| ||| || |||||
AC CCT CTC CCTCCTCC
C C __
GAM1835 KIAA1975 5' CGCCTCCTGGGTTACCCCCA 74420 T AC AGG
TG GG GAGC AGGAGGCG
|| || ||| |||||
AC CC CTTG TCCTCCGC
_ CA GG_
GAM1835 LRP15 5' CGCCTCCTCCCTGAGCCACG 54755 ACGAG _
TGTGG CAGG AGGAGGCG
|||| | ||| |||||
GCACC GTCC TCCTCCGC
GA__ C
GAM1835 MGC14859 3' CGCCCCCTCCCTGGGCTCGTCC 62600 A__ A
A TGGACGAGC GGAGG GGCG
||||| ||| |||
ACCTGCTCG CCTCC CCGC
GGTC C
GAM1835 ROBO4 3' CTTCTCCTGTCCACCCACA 39311 ACGA
TGTGG GCAGGAGGAG
|||| |||||
ACACC TGTCTCTTC
CACC
GAM1835 SCGF 3' CGCCTCCTTGCCCATCCCA 12945 T CGA GG
TG GGA GCA AGGAGGCG
|| ||| || |||||
AC CCT CGT TCCTCCGC
_ ACC _
GAM1835 SCMH1 3' CCCACTCGCCTGTCCACA 25282 A AG GA
TGTGGACG GC GAG GG
||||| || ||| ||
ACACCTGT CG CTC CC
C __ AC
GAM1835 SEC24A 5' CGCCCCCCCCTCTTCTCCCA 83565 T C C A A
TG GGA GAG AGG GG GGCG
|| ||| ||| || |||
AC CCT TTC TCC CC CCGC
_ C _ C C
GAM1835 WIT-1 5' CGCCCCCTTCTTTACCCAC 32396 AC C A
GTGG GAG AGGAGG GGCG
|||| ||| ||||| |||

	CACC CTT TCTTCC CCGC		
	CA _ C		
GAM1835 LOC144278 5'	CCAGGTCTGTTCGTCCACA 77273	AGGA	
	TGTGGACGAGCAGG GG		
	ACACCTGCTTGTCT CC		
	GGA_		
GAM1835 LOC146108 5'	CGCCCCCTCCTGCCCCCTTCAT 78148	CGA A	
	GTGGA GCAGGAGG GGCG		
	TACTT CGTCCTCC CCGC		
	CCC C		
GAM1835 LOC149506 3'	CCCCCTTCTGCCATCCAC 85629	CGA A	
	GTGGA GCAGGAGG GG		
	CACCT CGTCTTCC CC		
	AC_ C		
GAM1835 LOC152992 3'	CCTCCTCCAGCTTTCTCCACA 81643	C_ A_	
	TGTGGA GAGC GGAGGAGG		
	ACACCT TTCG CCTCCTCC		
	CT AC		
GAM1835 LOC200316 3'	CCTCCTCCCCGCTCTCCCA 90176	T C A_	
	TG GGA GAGC GGAGGAGG		
	AC CCT CTCG CCTCCTCC		
	_ _ CC		
GAM1835 LOC200734 3'	TGTTTCCAGCTCGTCCACA 90285	AGGA	
	TGTGGACGAGC GGAGGCG		
	ACACCTGCTCG CCTTTGT		
	A_		
GAM1835 LOC203652 5'	CGCCGTGCTTCCTGCCCCTCCA 92334	CGA A_	
CA	TGTGGA GCAGGAGG GGCG		
	ACACCT CGTCCTTC CCGC		
	CCC GTG		
GAM1835 LOC204515 5'	CGCCCCCTCTCCTTCCGC 92345	CG CA A	
	GTGGA AG GGAGG GGCG		
	CGCCT TC TCTCC CCGC		
	_ C_ C		
GAM1835 LOC205948 5'	CGCCTCCTCCCCGGCGGCCCA 91087	T A AGCA	
	TG GG CG GGAGGAGGCG		
	AC CC GC CCTCCTCCGC		
	C G GGCC		
GAM1835 LOC219920 5'	CCTCCCAACCCTGTCCACA 94944	G CA A_	
	TGTGGAC AG GG GGAGG		

ACACCTG TC CC CCTCC
 _ _ AAC
 GAM1835 LOC89944 3' CCCCTCCTGCTGGTGCCA 93174 _ G A
 TGG AC AGCAGGAGG GG
 ||| || ||||| ||
 ACC TG TCGTCCTCC CC
 G G C
 GAM1835 LOC90410 5' CCTCCTCCTGACTGCCAC 63352 A AG
 GTGG CG CAGGAGGAGG
 ||| || ||||| ||
 CACC GT GTCCTCCTCC
 _ CA
 GAM1836 SCAMP1 3' GCTAAATAAATATTCTCC 54500 T C
 GGA AATATT ATTTAGC
 ||| ||||| |||||
 CCT TTATAA TAAATCG
 C A
 GAM1836 SCAMP1 3' GCTAAATAAATATTCTCC 54501 T C
 GGA AATATT ATTTAGC
 ||| ||||| |||||
 CCT TTATAA TAAATCG
 C A
 GAM1836 NX-17 3' TGAATATCAGCCCCTAATA 40706 ATA_
 TATTAGGG ATATTCA
 ||||| |||||
 ATAATCCC TATAAGT
 CGAC
 GAM1836 LOC161589 3' GCTAAATGAATATTATCCCTAA 83159
 TA TATTAGGGATAATATTCATTTAGC
 |||||
 ATAATCCCTATTATAAGTAAATCG
 GAM1837 SCAMP1 3' GCTAAATAAATATTCTCC 18013 T C
 GGA AATATT ATTTAGC
 ||| ||||| |||||
 CCT TTATAA TAAATCG
 C A
 GAM1837 SCAMP1 3' GCTAAATAAATATTCTCC 54501 T C
 GGA AATATT ATTTAGC
 ||| ||||| |||||
 CCT TTATAA TAAATCG
 C A
 GAM1837 NX-17 3' TGAATATCAGCCCCTAATA 40706 ATA_
 TATTAGGG ATATTCA
 ||||| |||||
 ATAATCCC TATAAGT
 CGAC
 GAM1837 LOC161589 3' GCTAAATGAATATTATCCCTAA 83159
 TA TATTAGGGATAATATTCATTTAGC
 |||||

ATAATCCCTATTATAAGTAAATCG

GAM1838 LOC115219 3' GTCAGTACAAACGAGATCA 73703 GCC CC
TGA CGTTTGTGAG GC
||| ||||| ||
ACT GCAAACAGTC TG
AGA AC

GAM1838 LOC135763 3' ATCTGCGGCCGGTGAAGAAGCC 57555 A CCG TG A
CA TG GC TT TC GCCGCAGAT
|| || || || |||||
AC CG AA GG CGGCGTCTA
C AAG GT C

GAM1838 LOC219743 3' GGCTGACAAAGGACTCA 94748 C G
TGAG CC TTTGTGAGCC
||| || |||||
ACTC GG AAACAGTCGG
A _

GAM1839 ELF3 3' TGACCTTGACCTTGACCAA 16685 T GAT AAA
TTGGT CAAGG GG GTCA
||| ||| || |||
AACCA GTTCC TC CAGT
_ AGT _

GAM1839 JAK2 3' TGACCTTCATTCTGAGACCAA 18318 CAA AA
TTGGTT GGGATGGA GTCA
||| ||||| |||
AACCAG TCTTACTT CAGT
AG_ C_

GAM1839 SLC10A2 5' ACTCTCTGTCTTGACCAA 6590 CAA A
TTGGTT GGGATGGA AGT
||| ||||| |||
AACCAG TTCTGTCT TCA
_ C

GAM1839 FLJ10803 3' GTGACTTTCAGTTAAAGCCAA 37205 CAAGG G
TTGGTT GAT GAAAGTCAC
||| || |||||
AACCGA TTG CTTTCAGTG
AA_ A

GAM1839 KIAA1958 5' GTGACTTTGAACCCCAAACC 82788 CAA ATGG
GGTT GGG AAAGTCAC
||| || |||||
CCAA CCC TTTCAGTG
A_ CAAG

GAM1839 MARCKS 3' ACTTTCCACCCTGCCCA 11411 TTCA A
TGG AGGG TGGAAAGT
|| ||| |||||
ACC TCCC ACCTTTCA
CG_ _

GAM1839 TUB 5' GTGGGACCATCCCTTAAACC 13898 C AAAG
GGTT AAGGGATGG TCAC
||| ||||| |||

CCAA TTCCCTACC GGTG
 A AG__
 GAM1839 LOC80298 3' ACTTTTACCTTGAACCA 48062 GATG
 TGGTTCAAGG GAAAGT
 ||||| |||||
 ACCAAGTTCC TTTTCA
 A__
 GAM1840 ARHGEF7 3' TAAAAGTCTTGT TTTTCCAG 15326 T T_
 CTGGAAA GC GACTTTTA
 ||||| || |||||
 GACCTTT TG CTGAAAAT
 T TT
 GAM1840 BAALC 3' GTCAAAAGTCAGATACGCA 46094 T GAAATG A
 TGC G CTGACTTTT AC
 ||| ||||| ||
 ACG C GACTGAAAA TG
 _ATA__ C
 GAM1840 CACNA1G 3' GTTAAAAGCAGCAGCCCCGGCA 38776 AAA A
 TGCTGG TGCTG CTTTTAAC
 |||| |||| |||||
 ACGGCC ACGAC GAAAATTG
 CCG _
 GAM1840 DIAPH2 3' GTTAAAAGGTTTGT TTTCCAG 24594 _ GCTGA
 CTGG AAAT CTTTTAAC
 ||| ||| |||||
 GACC TTTG GAAAATTG
 C TTTG_
 GAM1840 ENTPD3 3' TAAAAATCAGCATTATTTCA 8808 _ C
 TGGAA ATGCTGA TTTTA
 |||| ||||| |||||
 ACTTT TACGACT AAAAT
 AT A
 GAM1840 RANBP3 5' GGGGTCAGCCTCCAGCA 24635 AAAT
 TGCTGG GCTGACTTT
 |||| |||||
 ACGACC CGACTGGGG
 CTC_
 GAM1840 ARPC3 3' GGGCAGCATTTTCCAGCA 20363 _ A
 TGCTGGAAA TGCTG CTT
 ||||| |||| |||
 ACGACCTTT ACGAC GGG
 T _
 GAM1840 C1orf2 3' GGTTGGGACCAGCAGCCCCCAG 22729 AAA_ AC
 CA TGCTGG TGCTG TTTTAACC
 |||| |||| |||||
 ACGACC ACGAC AGGGTTGG
 CCCG C_
 GAM1840 FBXO8 5' GGTAAAAGTCCCCGCCAG 25159 AAAT T__ A
 CTGG GC GACTTTTA CC
 ||| || ||||| ||

			GACC CG CTGAAAAT GG		
			____ CCC C		
GAM1840	FLJ11127	3'	AAAGCTAGCATTTTCAGCA 39228	G	A
			TGCTG AAATGCTG CTTT		
			ACGAC TTTACGAT GAAA		
			____ C		
GAM1840	KIAA0826	3'	AGTTAAACATTTCCAGTA 83525	C_	
			TGCTGGAAATG TGA		
			ATGACCTTTAC ATTGA		
			AA		
GAM1840	KIAA0939	3'	GGTCAAAAGTCAGCTGCCAGC 62719	AAAT	A
			GCTGG GCTGACTTTT ACC		
			CGACC CGACTGAAAA TGG		
			GT__ C		
GAM1840	KIAA0976	3'	GGTATTTTCTCAGATTTCCAGC 30553	G	CTTTTA
	A		TGCTGGAAAT CTGA ACC		
			ACGACCTTTA GACT TGG		
			____ CTTTTA		
GAM1840	KIAA1332	3'	AAGGCGAGCATTTCCACA 71703	C	GA
			TG TGGAAATGCT CTTT		
			AC ACCTTTACGA GGAA		
			____ GC		
GAM1840	LEC3	3'	AGTCAGAATATTTCCAACA 31531	C	____
			TG TGGAAATG CTGACT		
			AC ACCTTTAT GACTGA		
			A AA		
GAM1840	MGC4643	3'	GTAAAAAGTTCATTTCCAG 52145	CT	
			CTGGAAATG GACTTTTAAC		
			GACCTTTAC TTGAAAATTG		

GAM1840	VIAAT	3'	GTCCAGCCATTTCCAGCA 55453	__	__
			TGCTGGAAATG CTG AC		
			ACGACCTTTAC GAC TG		
			C C		
GAM1840	LOC115939	3'	GGTTCTCCCCACACTTCCAGCA 74034	A C	ACTTTT
			TGCTGGAA TG TG AACC		
			ACGACCTT AC AC TTGG		
			C _ CCCTC_		
GAM1840	LOC196264	3'	GTAAAAAGCCTTCCAG 88993	AT	GACT
			CTGGAA GCT TTAAAC		

GACCTT CGA AAATTG
 C_ ____
 GAM1840 LOC199729 3' AAAATTCATTGTTCCAGCA 73391 ATGC C
 TGCTGGAA TGA TTTT
 ||||| ||| ||||
 ACGACCTT ACT AAAA
 GTT_ T
 GAM1840 LOC204804 3' AAGGTGGCATTTCCTGCA 91028 T G
 TGC GGAAATGCT ACTTT
 ||| ||||| ||||
 ACG CCTTTACGG TGGAA
 T _
 GAM1840 LOC91050 3' TAAAAGTCATCCAGC 65379 AATGC
 GCTGGA TGA CTTTTA
 ||||| |||||
 CGACCT ACTGAAAAT

 GAM1841 ELF3 3' TGACCTTGACCTTGACCAA 16685 T GAT AAA
 TTGGT CAAGG GG GTCA
 ||||| ||||| |||
 AACCA GTTCC TC CAGT
 _ AGT _
 GAM1841 JAK2 3' TGACCTTCATTCTGAGACCAA 18318 CAA AA
 TTGGTT GGGATGGA GTCA
 ||||| ||||| ||||
 AACCAG TCTTACTT CAGT
 AG_ C_
 GAM1841 SLC10A2 5' ACTCTCTGTCTTGACCAA 6590 CAA A
 TTGGTT GGGATGGA AGT
 ||||| ||||| |||
 AACCAG TTCTGTCT TCA
 _ C
 GAM1841 FLJ10803 3' GTGACTTTCAGTTAAAGCCAA 37205 CAAGG G
 TTGGTT GAT GAAAGTCAC
 ||||| ||| |||||
 AACCGA TTG CTTTCAGTG
 AA_ A
 GAM1841 KIAA1958 5' GTGACTTTGAACCCCAAACC 82788 CAA ATGG
 GGTT GGG AAAGTCAC
 ||||| ||| |||||
 CCAA CCC TTTCAGTG
 A_ CAAG
 GAM1841 MARCKS 3' ACTTTCCACCCTGCCCA 11411 TTCA A
 TGG AGGG TGGAAAGT
 ||| ||||| |||||
 ACC TCCC ACCTTTCA
 CG_ _
 GAM1841 TUB 5' GTGGGACCATCCCTTAAACC 13898 C AAAG
 GGTT AAGGGATGG TCAC
 ||||| ||||| ||||

			CCAA TTCCCTACC	GGTG		
			A	AG__		
GAM1841	LOC80298	3'	ACTTTTACCTTGAACCA	48062	GATG	
			TGGTTCAAGG	GAAAGT		
			ACCAAGTTCC	TTTTCA		
			A__			
GAM1842	IER5	3'	TTCCCGGCTGCGAGGACGC	33747	A	CGAC A
			GC TCCTCGCG	CCG GAG		
			CG AGGAGCGT	GGC CTT		
			C	C__ C		
GAM1842	AQP10	3'	CTCCCTGCAGAGGATGCT	55394	GC	ACCC
			AGCATCCTC	GCG GAG		
			TCGTAGGAG	CGT CTC		
			A_ CC__			
GAM1842	C20orf28	3'	CGGGCCGCGCGGGGACGC	31844	A	A
			GC TCCTCGCGCG	CCCG		
			CG AGGGGCGCGC	GGGC		
			C	C		
GAM1842	CBCIP2	3'	CTCTCGGGCCGCACATGC	52656	CCTCGC	A
			GCAT	GCG CCCGAGAG		
			CGTA	CGC GGGCTCTC		
			CA__ C			
GAM1842	CCR5	3'	CTCAGGTCAGGGTGAGGATG	6962	GC_	C
			CATCCTCGC	GACC GAG		
			GTAGGAGTG	CTGG CTC		
			GGA	A		
GAM1842	DNAJC5	3'	CTCTCGGGCCGCAGACAATGCT	62136	CC GC	A
			AGCAT TC	GCG CCCGAGAG		
			TCGTA AG	CGC GGGCTCTC		
			AC A_ C			
GAM1842	FLJ12517	3'	CTCTTGCAGAGGATGC	43719	GC	CCC
			GCATCCTC	GCGA GAG		
			CGTAGGAG	CGTT CTC		
			A_ __			
GAM1842	STK36	3'	CTCCCAGATGCAGGATGTTT	72581	C	CGACCC
			AAGCATCCT	GCG GAG		
			TTTGTAGGA	CGT CTC		
			_ AGACC_			
GAM1842	LOC132617	5'	CGGTGCGCGAGGACGC	76412	A	AC
			GC TCCTCGCGCG	CCG		

CG AGGAGCGCGT GGC
C _

GAM1842 LOC199680 5' CTCCCAGGTCAAGGGATGGCT 91374 _ CGCGC C_

AGC ATCCT GACC GAG
||| ||| ||| |||
TCG TAGGG CTGG CTC
G AA_ ACC

GAM1842 LOC200845 5' CTCTCGGGTTCAAGTGATGCT 90315 CTC GC_

AGCATC GC GACCCGAGAG
||||| || |||||
TCGTAG TG TTGGGCTCTC
_ AAC

GAM1842 LOC201522 3' CTCCCGGGCCCCTTCGAGGGTG 89636 CGCGA_ A

C GCATCCTCG CCCG GAG
||||| ||| |||
CGTGGGAGC GGGC CTC
TTCCCC C

GAM1842 LOC253430 5' CTCTCGGGCCTGCCTGGACGC 97973 A TC CGA

GC TCC GCG CCCGAGAG
|| ||| ||| |||||
CG AGG CGT GGGCTCTC
C TC CC_

GAM1842 LOC254722 5' CTCCCGAAGGCGAGGATGC 99425 GCGACC A

GCATCCTCGC CG GAG
||||| || |||
CGTAGGAGCG GC CTC
GAA_ C

GAM1843 GAK 3' GGAACAGCTGATTCATGCTCC 19141 A_ AC

GGAGCATGAG AG GTTCC
||||| || |||
CCTCGTACTT TC CAAGG
AG GA

GAM1843 PRLR 3' AGCTCCTTTCATGCTCC 8143 A C

GGAGCATGAGA GA GTT
||||| || |||
CCTCGTACTTT CT CGA
C _

GAM1843 TIMM23 3' GGGAGCGCCTCTGCCCG 21989 A T AAGA

CGG GCA GAG CGTTCCC
||| ||| ||| |||||
GCC CGT CTC GCGAGGG
C _ C_

GAM1843 TRPV1 3' GGGAACACCAGTGCTCTGT 55678 GAGAAGAC

ACGGAGCAT GTTCCC
||||| |||||
TGTCTCGTG CAAGGG
ACCA_

GAM1843 UBE2B 3' GAGTTTCTTCTCATATCC 13936 GC CG

GGA ATGAGAAGA TTC
||| ||||| |||

CCT TACTCTTCT GAG
 A_ TT
 GAM1843 C11orf25 3' GAGAGGTTCTCATGCTCC 49465 GACG
 GGAGCATGAGAA TTC
 ||||| |||
 CCTCGTACTCTT GAG
 GGA_
 GAM1843 FLJ14735 3' GGAGAACGTTTAATACTTC 52668 C GAGAA _
 GGAG AT GACGTTC CC
 ||| || ||||| ||
 CTTC TA TTGCAAG GG
 A AT_ A
 GAM1843 JM11 3' GGGACATCTCATGCCCC 54365 A AGAC
 GG GCATGAGA GTTCC
 || ||||| ||||
 CC CGTACTCT CAGGG
 C A_
 GAM1843 KIAA1036 3' AGCCTGGCTCCTCATGCTCAGT 30483 G A AC_
 AC GAGCATGAG AG GTT
 || ||||| || |||
 TG CTCGTACTC TC CGA
 A C GGTC
 GAM1843 KIAA1045 3' GGGGAACGTCCCCAAGCCCTGT 71606 A A AGAA
 ACGG GC TG GACGTTCCCC
 ||| || ||||| |||
 TGTC CG AC CTGCAAGGGG
 C A CC_
 GAM1843 KIAA1492 3' GGAATCGTGTCTTCCATGCTCC 65126 A _
 GGAGCATG GAAGAC GTTCC
 ||||| ||||| |||||
 CCTCGTAC CTTCTG TAAGG
 _ TGC
 GAM1843 KIAA1674 3' GAGTTTCCTCTCACCTCCGT 69340 CA A CG
 ACGGAG TGAGA GA TTC
 ||||| ||||| || |||
 TGCCTC ACTCT CT GAG
 C_ C TT
 GAM1843 KIAA1674 3' GAGTTTCCTCTCACCTCCGT 69341 CA A CG
 ACGGAG TGAGA GA TTC
 ||||| ||||| || |||
 TGCCTC ACTCT CT GAG
 C_ C TT
 GAM1843 KIAA1674 3' GAGTTTCCTCTCACCTCCGT 69342 CA A CG
 ACGGAG TGAGA GA TTC
 ||||| ||||| || |||
 TGCCTC ACTCT CT GAG
 C_ C TT
 GAM1843 KIAA1751 3' GGGCCACATTTACATGCTCC 72163 A ACGTT
 GGAGCATG GAAG CCC
 ||||| ||| |||

			CCTCGTAC CTTT	GGG		
			A	ACACC		
GAM1843	KIAA1822	3'	GGACTCCTCATACTCTGT	68188	C	AA C
			ACGGAG ATGAG	GA GTTC		
			TGTCTC TACTC	CT CAGG		
			A	__ _		
GAM1843	SYT12	5'	GGA ACTCTCATGCCC	96384	A	AGAC
			GG GCATGAGA	GTTCC		
			CC CGTACTCT	CAAGG		
			__	_____		
GAM1843	LOC115207	3'	GGGAAATAAACCTCGTCATGCT	57398		GA ACG__
			CC	GGAGCATGA AG	TTCCC	
			CCTCGTACT TC	AAGGG		
			GC CAAATA			
GAM1843	LOC154789	5'	GAACTCTCACTTCTCATCTCC	82028	C	AC__
			GGAG ATGAGAAG	GTTCC		
			CCTC TACTCTTC	CAAG		
			__	ACTCT		
GAM1843	LOC170395	5'	GAGTTTCCTCTCACCTCCGT	76869	CA	A CG
			ACGGAG TGAGA	GA TTC		
			TGCCTC ACTCT CT	GAG		
			C_	C TT		
GAM1843	LOC170395	5'	GAGTTTCCTCTCACCTCCGT	76870	CA	A CG
			ACGGAG TGAGA	GA TTC		
			TGCCTC ACTCT CT	GAG		
			C_	C TT		
GAM1843	LOC92973	5'	GAAGTTTTATTCTCATGCT	71592	__	G
			AGCATGAGAA	GAC TTC		
			TCGTA CTCTT	TTG AAG		
			TATT	__		
GAM1844	DLEC1	3'	CATCTGGCCCTCCCTTG	24716	A	A C
			CAAGG AGGGC	GG GTG		
			GTTCC TCCCG TC	TAC		
			C	G _		
GAM1844	DLEC1	3'	CATCTGGCCCTCCCTTG	24717	A	A C
			CAAGG AGGGC	GG GTG		
			GTTCC TCCCG TC	TAC		
			C	G _		
GAM1844	PIP5K1A	3'	TATCCCACCCTGCCTTGATA	14520	A	CA C
			TATCAAGG AGGG	GG GTG		

			ATAGTTCC TCCC CC TAT			
			G A_ C			
GAM1844	SOX11	3'	ACCCACCCCCCTTGGTA 13308	AA	CA	C
			TATCAAGG GGG GG GT			
			ATGGTTCC CCC CC CA			
			CC A_ _			
GAM1844	CHL1	3'	TGTTACCTTTCCTCAATA 22768	CA		CA
			TAT AGGAAGGG GGCG			
			ATA TCCTTTCC TTGT			
			AC A_			
GAM1844	EPB41L1	3'	CATTCTGCCCTTCCCTGA 71104	A		C
			TCA GGAAGGGCAGG GTG			
			AGT CCTTCCCGTCT TAC			
			C _			
GAM1844	FLJ00060	3'	CATACCCCCTGCCCTCCTCTGA 61741	_	A	CGTG
			TCA AGGA GGGCAGG ATG			
			AGT TCCT CCCGTCC TAC			
			C _ CCCA			
GAM1844	FLJ10898	5'	CACCACAGCCCTTTCTCAATA 60126	CA		AGGC
			TAT AGGAAGGGC GTG			
			ATA TCTTTCCCG CAC			
			AC ACAC			
GAM1844	FLJ22557	3'	ATCATCCCATCCTTAATA 45581	C	A	CAGGC
			TAT AAGGA GGG GTGAT			
			ATA TTCCT CCC TACTA			
			A A _			
GAM1844	KIAA0574	3'	CATCCCCTGCCCTCCCCTGA 69808	A	A	CGT
			TCA GG AGGGCAGG GATG			
			AGT CC TCCCGTCC CTAC			
			C C C_			
GAM1844	KIAA0632	3'	CACCTCAGAAACCCTTCTTGA 32071		CA_	C
			TCAAGGAAGGG GG GTG			
			AGTTCCTTCCC CT CAC			
			AAAGA C			
GAM1844	KIAA1045	3'	CATCACATGTCCTTCC 71599		GGC	
			GGAAGGGCA GTGATG			
			CCTTCCTGT CACTAC			
			A_			
GAM1844	KIAA1354	5'	CAGTGA CTGCCCTTCCCTTGATA 61572	A		G _
			TATCAAGG AGGGCAG CG TG			

	ATAGTTCC TTCCGTC GT AC		
	C A G		
GAM1844 MGC20460 5'	CACCGCCTCCTACCCTTCTT 54901	C___ _	
	AGGAAGGG AGGCG TG		
	TTCTTCCC TCCGC AC		
	ATCC C		
GAM1844 LOC158476 3'	CACGCCCGCCCCCCCCATTGA 88186	_ AA_ A	
	TCAA GG GGGC GGC GTG		
	AGTT CC CCGC CCGCAC		
	A CCC C		
GAM1844 LOC90459 3'	CACACCCGCCTAATTTTTTG 63550	A_ A C	
	CAAGGA GGGC GG GTG		
	GTTTTT TCCG CC CAC		
	AA C A		
GAM1845 PIP5K1A 3'	TATCCCACCCTGCCTTGATA 14520	A CA C	
	TATCAAGG AGGG GG GTG		
	ATAGTTCC TCCC CC TAT		
	G A_ C		
GAM1845 SOX11 3'	ACCCACCCCCCCTTG GTA 13308	AA CA C	
	TATCAAGG GGG GG GT		
	ATGGTTCC CCC CC CA		
	CC A_ _		
GAM1845 CHL1 3'	TGTTACCTTTCCTCAATA 22768	CA CA	
	TAT AGGAAGGG GCG		
	ATA TCCTTTCC TTGT		
	AC A_		
GAM1845 EPB41L1 3'	CATTCTGCCCTTCCCTGA 71104	A C	
	TCA GGAAGGGCAGG GTG		
	AGT CCTTCCCGTCT TAC		
	C _		
GAM1845 FLJ00060 3'	CATACCCCCTGCCCTCCTCTGA 61741	_ A CGTG	
	TCA AGGA GGGCAGG ATG		
	AGT TCCT CCGTCC TAC		
	C _ CCCA		
GAM1845 FLJ10898 5'	CACCACAGCCCTTTCTCAATA 60126	CA AGGC	
	TAT AGGAAGGGC GTG		
	ATA TCTTTCCCG CAC		
	AC ACAC		
GAM1845 FLJ22557 3'	ATCATCCCATCCTTAATA 45581	C A CAGGC	
	TAT AAGGA GGG GTGAT		

ATA TTCCT CCC TACTA
 A A ____
 GAM1845 KIAA0574 3' CATCCCCTGCCCTCCCCTGA 69808 A A CGT
 TCA GG AGGGCAGG GATG
 ||| || ||||| |||
 AGT CC TCCCGTCC CTAC
 C C C__
 GAM1845 KIAA0632 3' CACCTCAGAAACCCTTCCTTGA 32071 CA__ C
 TCAAGGAAGGG GG GTG
 ||||| || |||
 AGTTCCTTCCC CT CAC
 AAAGA C
 GAM1845 KIAA1354 5' CAGTGA CTGCCTTCCCTTGATA 61572 A G _
 TATCAAGG AGGGCAG CG TG
 ||||| ||||| || ||
 ATAGTTCC TTCCGTC GT AC
 C A G
 GAM1845 MGC20460 5' CACCGCCTCCTACCCTTCTT 54901 C__ _
 AGGAAGGG AGGCG TG
 ||||| |||| ||
 TTCTTCCC TCCGC AC
 ATCC C
 GAM1845 LOC158476 3' CACGCCCGCCCCCCCCATTGA 88186 _ AA_ A
 TCAA GG GGGC GGC GTG
 ||| || ||| |||||
 AGTT CC CCG CCGCAC
 A CCC C
 GAM1845 LOC90459 3' CACACCCGCCTAATTTTTTG 63550 A_ A C
 CAAGGA GGGC GG GTG
 ||||| |||| || |||
 GTTTTT TCCG CC CAC
 AA C A
 GAM1846 ABCD4 5' CTATGGGGTCTCTGGGAAACA 40101 GC GGA C
 TG TCCCAGGA CAT AG
 || ||||| || ||
 AC AGGGTCCT GTA TC
 AA GGG _
 GAM1846 ACK1 5' CTGAGCTCTGGGAGCCA 20512 AGGACA
 TGGCTCCCAGG TCAG
 ||||| || |||
 ACCGAGGGTCT AGTC
 CG__
 GAM1846 AMD1 3' CTGATGTTTTTGGAACA 9683 GC CAG
 TG TCC GAGGACATCAG
 || ||| |||||
 AC AGG TTTTGTAGTC
 AA _
 GAM1846 AVP 5' GTGGGCTCCTGGGGAGCCA 6678 _ GA
 TGGCTCCC AGGAG CAT
 ||||| |||| |||

			ACCGAGGG TCCTC GTG		
			G GG		
GAM1846 BMP1	3'	ATGTCCCCAGGAGCCA	21520	CA A	
		TGGCTCC GG GGACAT			
		ACCGAGG CC CCTGTA			
		AC _			
GAM1846 CD4	3'	GCAGAACCTCCTGGAAGC	7047	C	ACA A
		GCT CCAGGAGG TC GC			
		CGA GGTCTCC AG CG			
		A A__ A			
GAM1846 CLCN7	3'	GCTATCGGCCTCTTGGGAGCCA	8909		ACATC
		TGGCTCCAGGAGG AGC			
		ACCGAGGGTTCTCC TCG			
		GGCTA			
GAM1846 COG3	3'	GCTGATGTTAAGGCAGCCA	49499	C	AGGAG
		TGGCT CC GACATCAGC			
		ACCGA GG TTGTAGTCG			
		C AA__			
GAM1846 EFNB1	5'	GCTCGATCGCCCGGAGCCA	16671		A AG CA _
		TGGCTCCC GG GA TC AGC			
		ACCGAGGG CC CT AG TCG			
		C G_ _ C			
GAM1846 ENPP3	3'	GCTGAACAGCCCTGGGAGACA	18471	G	AGGACA
		TG CTCCCAGG TCAGC			
		AC GAGGGTCC AGTCG			
		A CGACA_			
GAM1846 FRAT2	3'	GCCGACGTGCGCAGCCTGGGAG	24902		AG__ A A
C		GCTCCCAGG GAC TC GC			
		CGAGGGTCC CTG AG CG			
		GACCG C C			
GAM1846 GLP1R	3'	GTGCCTCCTGGGACCA	10799	C	A
		TGG TCCCAGGAGG CAT			
		ACC AGGGTCCTCC GTG			
		- -			
GAM1846 GNAT1	5'	GCAGGTCCTCCTGGGGCCA	5722	T	ATCA
		TGGC CCCAGGAGGAC GC			
		ACCG GGGTCCTCCTG CG			
		- GA__			
GAM1846 HM13	3'	GCTTCCCCCTCCCCGGGAGCC	70572		A_ ACATC
A		TGGCTCCC GGAGG AGC			

			ACCGAGGG CCTCC TCG			
			CC CCCCT			
GAM1846	HOXC13	3'	CTGCATTTCTGCGGGCCA 60417	T		ACAT
			TGGC CCCAGGAGG CAG			
			ACCG GGGTCCTTT GTC			
			AC__			
GAM1846	IL2RB	3'	GCTAACTCTGACCTGGGAGCC 7942		A_	CATC
			GGCTCCCAGG GGA AGC			
			CCGAGGGTCC TCT TCG			
			AG CAA_			
GAM1846	ITGB4	3'	GCTAGGTGTCTCCTGGGAGGCA 5807	G	G	_
			TG CTCCCAGGAG ACATC AGC			
			AC GAGGGTCCTC TGTGG TCG			
			G _ A			
GAM1846	LDLR	3'	CTGATGTCCGAGAGACA 6736	G	_	AGGA
			TG CTC CC GGACATCAG			
			AC GAG GG CCTGTAGTC			
			A A ____			
GAM1846	PPT2	3'	CTGATACCAGGCGAGGGGGCCA 58036		AGGA__	AC
			TGGCTCCC GG ATCAG			
			ACCGGGGG CC TAGTC			
			AGCGGA A_			
GAM1846	ROCK2	5'	GCCGGGCGGGCCCCTGGGAGC 66620		A ACA__	A
			GCTCCCAGG GG TC GC			
			CGAGGGTCC CC GG CG			
			_ GGGCG C			
GAM1846	TGFBR2	3'	CTGATGCTTCCTGGAAAACCA 13729	CTC_		A
			TGG CCAGGAGG CATCAG			
			ACC GGTCTTC GTAGTC			
			AAAA _			
GAM1846	ZNF257	5'	GCCAGGTCTCCTGGAAGCC 54235	C		ATCA
			GGCT CCAGGAGGAC GC			
			CCGA GGTCTCTCTG CG			
			A GAC_			
GAM1846	APBA3	3'	TGTCCTTCCTGGAAGCCA 18087	C		_
			TGGCT CCAGGA GGACA			
			ACCGA GGTCCT CCTGT			
			A T			
GAM1846	C9orf16	3'	ATGCCCTCCTGGGGCCA 44357	T		A
			TGGC CCCAGGAGG CAT			

ACCG GGGTCCTCC GTA
 _ C
 GAM1846 CLONE24945 3' GCTGGAATCCCCTAGGAGCC 32252 C A CA
 GGCTCC AGG GGA TCAGC
 ||||| ||| ||| |||||
 CCGAGG TCC CCT GGTCC
 A _ AA
 GAM1846 CNM2 3' GCTCCTCCTCCCAGGGAGCCA 34941 A_ CATC
 TGGCTCCC GGAGGA AGC
 ||||| ||||| |||
 ACCGAGGG CCTCCT TCG
 AC CC_
 GAM1846 DKFZp434F054 5' CTGACCAGCCCGGGACCA 51046 C A A_ ACA
 TGG TCCC GG GG TCAG
 || ||| || || |||
 ACC AGGG CC CC AGTC
 _ C GA _
 GAM1846 DKFZp547J036 3' GCCGGAGCCCCTGGGAGCC 51121 A ACA A
 GGCTCCCAGG GG TC GC
 ||||| || || |||
 CCGAGGGTCC CC GG CG
 _ GA_ C
 GAM1846 FLJ10846 5' GCTGCTCTCCTGGAAGCCA 37287 C ACAT
 TGGCT CCAGGAGG CAGC
 |||| ||||| |||
 ACCGA GGTCCTCT GTCG
 A C_
 GAM1846 FLJ10936 3' GCTGATGTGTATGGGAGCC 37446 GGAGG
 GGCTCCCA ACATCAGC
 ||||| |||||
 CCGAGGGT TGTAGTCG
 ATG_
 GAM1846 FLJ12089 3' CTGGACAGATCTGGGAGCCA 44950 AGGACA
 TGGCTCCCAGG TCAG
 ||||| |||
 ACCGAGGGTCT GGTC
 AGACA_
 GAM1846 FLJ13868 3' GCTGATGTCCTCCAGCC 43028 CCCA
 GGCT GGAGGACATCAGC
 ||| |||||
 CCGA CCTCCTGTAGTCG
 _
 GAM1846 FLJ14721 3' GCTGATGCCACAGGGGAGCCA 52642 AGGA A
 TGGCTCCC GG CATCAGC
 ||||| || |||||
 ACCGAGGG CC GTAGTCG
 GACA C
 GAM1846 FLJ14753 5' GCTGATGTCACTCAGGAGC 51764 CAG _
 GCTCC GAG GACATCAGC
 |||| ||| |||||

		CGAGG CTC CTGTAGTCG		
		A__ A		
GAM1846	FLJ20647	5' GCTGACGCCTGCGGGAGCC	35919	AGG ACA
		GGCTCCC AGG TCAGC		
		CCGAGGG TCC AGTCG		
		CG_ GC_		
GAM1846	FLJ20825	3' GCTGATGTGTGGAGAAGCC	36146	__ GGAGG
		GGCT C CCA ACATCAGC		
		CCGA G GGT TGTAGTCG		
		A A G__		
GAM1846	KCNMB3L	5' GCTGATGTCTTCAGATACCA	27714	CTCCCAG
		TGG GAGGACATCAGC		
		ACC CTTCTGTAGTCG		
		ATAGA__		
GAM1846	KIAA0152	3' CTGACTCCTGGGGCCA	28974	T GACA
		TGGC CCCAGGAG TCAG		
		ACCG GGGTCCTC AGTC		
		— —		
GAM1846	KIAA0317	3' GCCTTGGCCTCCTGGAAGC	29744	C A TCA
		GCT CCAGGAGG CA GC		
		CGA GGTCTCC GT CG		
		A G TC_		
GAM1846	KIAA0544	3' GTGTCTGCTGGGAGCCA	71475	GA
		TGGCTCCCAG GGACAT		
		ACCGAGGGTC TCTGTG		
		G_		
GAM1846	KIAA0563	5' CTGGAGTCCTGGGACCA	29882	C GGA AT
		TGG TCCA GGAC CAG		
		ACC AGGGT CCTG GTC		
		— — AG		
GAM1846	KIAA1025	3' CTGGCCTCCCGGGAGCCA	64676	A ACA
		TGGCTCCC GGAGG TCAG		
		ACCGAGGG CCTCC GGTC		
		C _		
GAM1846	KIAA1169	3' TGATTCCCCCGGGAGTCA	35886	A A C
		TGGCTCCC GG GGA ATCA		
		ACTGAGGG CC CCT TAGT		
		C _ _		
GAM1846	KIAA1671	3' CTGATGATTGGGAGCC	66279	GAGGA
		GGCTCCCAG CATCAG		

		CCGAGGGTT	GTAGTC		
		A__			
GAM1846	KIAA1870	5'	CTGCACCCCCGGGAGTCA	52900	A A ACAT
			TGGCTCCC GG GG CAG		
			ACTGAGGG CC CC GTC		
			C _ AC__		
GAM1846	KIAA1908	5'	GCAGGTTCTCCTGGGAGTCA	73789	C A
			TGGCTCCCAGGAGGA ATC GC		
			ACTGAGGGTCCTCCT TGG CG		
			_ A		
GAM1846	NYD-SP22	5'	CTGATGTCCAGCAGGAGCC	51858	CAGGA
			GGCTCC GGACATCAG		
			CCGAGG CCTGTAGTC		
			ACGA_		
GAM1846	PB1	3'	GCTAATGTACCTCCTGGACACC	36877	CTC _ C
	A		TGG CCAGGAGG ACAT AGC		
			ACC GGTCTCC TGTA TCG		
			ACA A A		
GAM1846	PDZD2	5'	CTCGTGACTCTTGGGAGCCA	81721	GA C
			TGGCTCCCAGGAG CAT AG		
			ACCGAGGGTTCTC GTG TC		
			A_ C		
GAM1846	RABEX5	3'	CTGATGTCTTTTACAAACCA	27960	CTCCCA
			TGG GGAGGACATCAG		
			ACC TTTTCTGTAGTC		
			AAACA_		
GAM1846	RAI	3'	CTGGATATTCCTGGGAGTCA	22854	GACA
			TGGCTCCCAGGAG TCAG		
			ACTGAGGGTCCTT GGTC		
			ATA_		
GAM1846	SCYA14	5'	GCTGGTATCCCGGGGAGCCA	53107	AGGA C
			TGGCTCCC GGA ATCAGC		
			ACCGAGGG CCT TGGTCG		
			GC_ A		
GAM1846	SCYA14	5'	GCTGGTATCCCGGGGAGCCA	16052	AGGA C
			TGGCTCCC GGA ATCAGC		
			ACCGAGGG CCT TGGTCG		
			GC_ A		
GAM1846	SCYA15	5'	GCTGGTATCCCGGGGAGCCA	53109	AGGA C
			TGGCTCCC GGA ATCAGC		

		ACCGAGGG CCT TGGTCG		
		GC__ A		
GAM1846	TIMM9	5' CTGATGTCGGCTGCGAGAGCC 25870	CCA_ AG	
		GGCTC GG GACATCAG		
		CCGAG TC CTGTAGTC		
		AGCG GG		
GAM1846	TSGA14	3' GATATTTCTGGAGCCA 38668	C AC	
		TGGCTCC AGGAGG ATC		
		ACCGAGG TCCTTT TAG		
		_ A_		
GAM1846	ZAK	5' GCTCACGCCCCGCCCCGGGAGCC 34105	A A ACATC_	
	A	TGGCTCCC GG GG AGC		
		ACCGAGGG CC CC TCG		
		C G CCGCAC		
GAM1846	ZAK	5' GCTCACGCCCCGCCCCGGGAGCC 56943	A A ACATC_	
	A	TGGCTCCC GG GG AGC		
		ACCGAGGG CC CC TCG		
		C G CCGCAC		
GAM1846	LOC146429	3' CTGGTGGCCCTGGGAGCCA 84665	AGGA	
		TGGCTCCCAGG CATCAG		
		ACCGAGGGTCC GTGGTC		
		CG__		
GAM1846	LOC147071	5' CTGGAGTCCTGGGACCA 73364	C GGA AT	
		TGG TCCA GGAC CAG		
		ACC AGGT CCTG GTC		
		_ _ AG		
GAM1846	LOC154761	3' CTCTCCCCAGGGAGCCA 82021	A A CATC	
		TGGCTCCC GG GGA AG		
		ACCGAGGG CC CCT TC		
		A _ C__		
GAM1846	LOC200301	3' GCTCTCATCTGCTGGGAGCCA 90143	G ACATC	
		TGGCTCCCAG AGG AGC		
		ACCGAGGGTC TCT TCG		
		G ACTC_		
GAM1846	LOC200310	3' GCCAATGCCCTCTGAGCCA 66328	CC A A CA	
		TGGCTC AGG GG CAT GC		
		ACCGAG TCC CC GTA CG		
		TC _ _ AC		
GAM1846	LOC201173	5' CTGGAGTCCTGGGACCA 88684	C GGA AT	
		TGG TCCA GGAC CAG		

		ACC AGGGT CCTG GTC		
		— — AG		
GAM1846	LOC201220 5'	CTGGAGTCCTGGGACCA 88719	C	GGA AT
		TGG TCCCA GGAC CAG		
		ACC AGGGT CCTG GTC		
		— — AG		
GAM1846	LOC203427 3'	CTGATGTCCCTGTGAACA 90919	GC C	AG
		TG TC CAGG GACATCAG		
		AC AG GTCC CTGTAGTC		
		A_ T _		
GAM1846	LOC255299 5'	CTGACGTCCTCTTCAGTCCA 99335	_ CCC	A
		TGG CT AGGAGGAC TCAG		
		ACC GA TTCTCCTG AGTC		
		T C_ C		
GAM1846	LOC90309 3'	GCTGTGTTCCCTGAGAACA 62874	GC C A	T
		TG TC CAGG GGACA CAGC		
		AC AG GTCC CTTGT GTCG		
		A_ A _ _		
GAM1846	LOC93070 3'	GCTGATGTGTATGGGAGCC 71811		GGAGG
		GGCTCCCA ACATCAGC		
		CCGAGGGT TGTAGTCG		
		ATG_		
GAM1847	CDH12 3'	CTTATCATTTAAAGTGGTGTA 15777	CCCAA	GA
		TACACCACT GAA ATAAG		
		ATGTGGTGA TTT TATTC		
		AA_ AC		
GAM1847	GOCAP1 3'	ATTGTTCTTGGGAGCAGTGTA 43007	CA	G
		TACAC CTCCCAAGAA AAT		
		ATGTG GAGGGTTCTT TTA		
		AC G		
GAM1847	DKFZp434N2435 5'	CTTATTACTGTGGGGTGGT 98090	T	AGAAG
		ACCAC CCCA AATAAG		
		TGGTG GGGT TTATTC		
		_ GTCA_		
GAM1847	DKFZP564I122 3'	CTTATTCTTCTCCCTCATGTGT 63877	CACTCCCA	
	A	TACAC AGAAGAATAAG		
		ATGTG TCTTCTTATTC		
		TACTCC_		
GAM1847	FLJ21791 3'	CTTATTTGCAGAAAGTGGTGTA 62126	CCCAAGAA	
		TACACCACT GAATAAG		

		ATGTGGTGA	TTTATTC	
		AGACG__		
GAM1847	HMP19	3' CTTATTCTTTGTTAGGAAAATG 88860	CCAC CAA_	
	TA	TACA TCC GAAGAATAAG		
		ATGT AGG TTTCTTATTC		
		AAA_ ATTG		
GAM1847	KIAA1719	3' TCTGTCTTGGGAGTGGTGTA 68742	_	
		TACACCACTCCCAAGA AGA		
		ATGTGGTGAGGGTTCT TCT		
		G		
GAM1847	KIAA1853	3' TTTTCTTGGAAGCAGTG 69929	CA C	
		CAC CT CCAAGAAGAA		
		GTG GA GGTTCCTTTT		
		AC A		
GAM1847	KIAA1877	3' CTTATTCTTCTGCCATGAGT 66748	CCA_	
		ACTC AGAAGAATAAG		
		TGAG TCTTCTTATTC		
		TACCG		
GAM1847	KIAA1906	3' CTTATTCTTCTTGACTTTTGG 73571	CTCC_	
		CCA CAAGAAGAATAAG		
		GGT GTTCTTCTTATTC		
		TTTCA		
GAM1847	OSBPL11	3' CTTAATTTCCCAAGAGTGGTG 43206	CCAA AA	
		CACCACTC GAAG TAAG		
		GTGGTGAG CTTT ATTC		
		AACC A_		
GAM1847	YME1L1	3' TCATTCTTGATGTGGTGTA 58438	TCC _	
		TACACCAC CAAGAA GA		
		ATGTGGTG GTTCTT CT		
		TA_ A		
GAM1847	ZNF262	3' CTTATTTTGTGTTGGGAGT 18723	A	
		ACTCCCAAG AGAATAAG		
		TGAGGGTTT TTTTATTC		
		G		
GAM1847	LOC91960	3' TGTGGCTTGGAACGTGGTGTA 68294	TC_ AAGA	
		TACACCAC CCAAG ATA		
		ATGTGGTG GGTTT TGT		
		CAA GG_		
GAM1848	ALPP	3' CCTCCAGCCCGAGTCGTCAT 69413	_ C	
		GTGGC TTCGGGC GGAGG		

			TACTG GAGCCCG CCTCC		
			CT A		
GAM1848	BACE	5'	CCTCTCCTGAGAAGCCACCAGC 25029	AACA	___ CC
			GC GTGGCTTC GGG GGAGG		
			CG CACCGAAG TCC TCTCC		
			AC___ AG ___		
GAM1848	BACE	5'	CCTCTCCTGAGAAGCCACCAGC 58081	AACA	___ CC
			GC GTGGCTTC GGG GGAGG		
			CG CACCGAAG TCC TCTCC		
			AC___ AG ___		
GAM1848	CDK5R2	3'	CCCCGGGACCACAAAGCCACCG 15446	AACA	C___ G_ A
			CCGC GC GTGGCTT GG CCGG GG		
			CG CACCGAA CC GGCC CC		
			CCGC ACA AG _		
GAM1848	CLN5	5'	CCGGCTACCGAAGCCACCTTGC 22429	CA	___
			GCAA GTGGCTTCGG GCCGG		
			CGTT CACCGAAGCC CGGCC		
			C_ AT		
GAM1848	CNGB3	3'	CCCCCAAAGATGGTCACTGTT 39388	_ _	___ CC
			AACAGTGGCT TC GGG GG		
			TTGTCACTGG AG CCC CC		
			T AAA _		
GAM1848	FOX E1	5'	CCGGTCACGAGGCCACCGCCGC 16778	AACA	_
			GC GTGGCTTCG GGCCGG		
			CG CACCGGAGC CTGGCC		
			CCGC A		
GAM1848	GATA6	5'	CCCCGGCCCCGCTCGCTGCTGC 19144	A	CTT A
			GCA CAGTGG CGGGCCGG GG		
			CGT GTCGCT GCCCGGCC CC		
			C C_ _		
GAM1848	HMGA2	5'	CCTCCGGGCACCCACCCACCGCC 14451	AACA	CTTC _
			GC GC GTGG GG GCCGGAGG		
			CG CACC CC CGGCCTCC		
			CCGC CAC_ A		
GAM1848	JAM3	3'	CCCCCGCTCTAGCTCACTGTTG 52487	_ TC	C A
			GCAACAGTG GCT GGGC GG GG		
			CGTTGTCAC CGA CTCG CC CC		
			T T_ C _		
GAM1848	LMO7	3'	CCTCCATACGAAAGCACTGTTG 32367	GC	GGCC
			GCAACAGTG TTCG GGAGG		

			CGTTGTCAC AAGC CCTCC			
			GA ATA_			
GAM1848 LMO7	3'	CCTCCATACGAAAGCACTGTTG 19304		GC	GGCC	
	C	GCAACAGTG TTCG GGAGG				
		CGTTGTCAC AAGC CCTCC				
		GA ATA_				
GAM1848 MRPL49	3'	CCTCCGAAGCTCACTGTTGC 70165		_	CC	
		GCAACAGTG GCTTCGGG GG				
		CGTTGTCAC CGAAGCCT CC				
		T _				
GAM1848 POLR2E	3'	CCTCCAGCTGCTCCTCACTGCC 60594	AA	CTTCG	C	
	GC	GC CAGTGG GGC GGAGG				
		CG GTCACT TCG CCTCC				
		CC CCTCG A				
GAM1848 REPS2	5'	CCCCGGCACGGCCACTGCGGC 17554	AA	TCGG	A	
		GC CAGTGGCT GCCGG GG				
		CG GTCACCGG CGGCC CC				
		GC CA_ _				
GAM1848 STK11	3'	CCCCCAAGGCCACTGCGC 6598	AA	C	CC	
		GC CAGTGGCTT GGG GG				
		CG GTCACCGGA CCC CC				
		C_ A _				
GAM1848 TBX1	3'	CCCCAGCCCCAGGGGCCACCGC 55543	AACA	_	C A	
	GGC	GC GTGGCTTC GGGC GG GG				
		CG CACCGGGG CCCG CC CC				
		GCGC AC A _				
GAM1848 UBL1	5'	CCCCGGGTGAAGCCACCGT 13975	A	GG	A	
		AC GTGGCTTCG CCGG GG				
		TG CACCGAAGT GGCC CC				
		C G_ _				
GAM1848 BCL2L12	5'	CCTCCAGCGTCGGCCACTGTAG 57642	A	TT	_ C	
	C	GC ACAGTGGC CGG GC GGAGG				
		CG TGTCACCG GCT CG CCTCC				
		A _ G A				
GAM1848 CRF	3'	CCCCGGCCCGTGCTCAACACCG 22912	AACAG	_ TT	A	
	C	GC TG GC CGGGCCGG GG				
		CG AC CG GCCCGGCC CC				
		CCACA T T_ _				
GAM1848 DKFZP434P211	5'	CCTCCAGCTCAGCCACTG 28027	TC	C		
		CAGTGGCT GGGC GGAGG				

GTCACCGA CTCG CCTCC
 _ A
 GAM1848 DKFZP564B147 5' CCTCCGGCCCCGCGCGCGTCGC 82954 A A G T
 GC AC GTG CT CGGGCCGGAGG
 || ||| || |||||
 CG TG CGC GG GCCCGGCCTCC
 C _ _ C
 GAM1848 DKFZP564D0478 3' CCTCCAGCCCGTGCAGTCCGCT 50442 _ T_ C
 AGTGG CT CGGGC GGAGG
 ||||| || |||||
 TCGCC GA GCCCG CCTCC
 T CGT A
 GAM1848 FLJ10737 3' CCTCCAGCCCACCCACAGCTGT 37053 GGCTTC_ C
 TGC GCAACAGT GGGC GGAGG
 ||||| ||| |||||
 CGTTGTCG CCGG CCTCC
 ACACCCA A
 GAM1848 FLJ14146 3' CCCCCAGTAGGCCACTGTT 45568 C_ CC
 AACAGTGGCTT GGG GG
 ||||| ||| ||
 TTGTCACCGGA CCC CC
 TGA _
 GAM1848 FLJ20320 3' CCTCCAGCTTTGGGAGCCAC 35423 _ C
 GTGGCTTC GGGC GGAGG
 ||||| ||| |||||
 CACCGAGG TTCG CCTCC
 GT A
 GAM1848 FLJ21919 3' CCTCCAGCCCCTCACACTGCTG 43735 A GCTTC C
 T GCA CAGTG GGGC GGAGG
 || |||| ||| |||||
 TGT GTCAC CCGG CCTCC
 C ACTC_ A
 GAM1848 KIAA0329 5' CCCCCGGCGGAGCCAGCTGCTGC 29939 A _ GG A
 GCA CAG TGGCTTC GCCGG GG
 || ||| ||||| ||||| ||
 CGT GTC ACCGAGG CGGCC CC
 C G _ _
 GAM1848 KIAA0914 5' CCCCCAACCAGCTTAGCCACTG 30295 TC_ CC A
 T ACAGTGGCT GGG GG GG
 ||||| ||| |||
 TGTACCGA CCC CC CC
 TTCGA AA _
 GAM1848 KIAA1018 3' CTCCAGGGGGCCACTGCGC 31056 AA GGGCC
 GC CAGTGGCTTC GGAG
 || ||||| |||
 CG GTCACCGGGG CCTC
 C_ GA_
 GAM1848 T1A-2 5' CCTCCGGCCCCCCCCACCGTCGC 22390 A A CTTC
 GC AC GTGG GGGCCGGAGG
 || ||| |||||

		CG TG CACC CCCGGCCTCC		
		C C CC__		
GAM1848	TCEA3	5' CCCCCGAGGCCCTACTGC	89894	AC T CC
		GCA AG GGCTTCGGG GG		
		CGT TC CCGGAGCCC CC		
		CA _ _		
GAM1848	ZNF317	3' CCCCCAAACGTCACTGTTGC	72475	_ C CC
		GCAACAGTGGC TT GGG GG		
		CGTTGTCACTG AA CCC CC		
		C A _		
GAM1848	LOC122970	5' CCCCCAGGCGCTGCTGC	74641	A C CC
		GCA CAGTGGCTT GGG GG		
		CGT GTCGCCGGA CCC CC		
		C _ _		
GAM1848	LOC127702	3' CCTAGGTCAAAGCCACT	75985	CG GG
		AGTGGCTT GGCC AGG		
		TCACCGAA CTGG TCC		
		A_ A_		
GAM1848	LOC149668	5' CCCCACCTCCAGCCACTGTC	85698	A TC_ C A
	C	C ACAGTGGCT GGG CGG GG		
		C TGTCACCGA TCC GCC CC		
		C CCC A _		
GAM1848	LOC150174	5' CCTCCAGCTCAGCCACTG	80435	TC C
		CAGTGGCT GGGC GGAGG		
		GTCACCGA CTCG CCTCC		
		_ A		
GAM1848	LOC150213	5' CCTCCAGCTCAGCCACTG	75354	TC C
		CAGTGGCT GGGC GGAGG		
		GTCACCGA CTCG CCTCC		
		_ A		
GAM1848	LOC200093	3' CCTCCGGTGGCTGGCCACTCTG	63768	AC TCGG
	C	GCA AGTGGCT GCCGGAGG		
		CGT TCACCGG TGGCCTCC		
		C_ TCGG		
GAM1848	LOC203503	5' CCTCCGGCCCGCGGCGGTCGC	90935	A A G T
		GC AC GTG CT CGGGCCGGAGG		
		CG TG CGC GG GCCCGGCCTCC		
		C _ _ C		
GAM1848	LOC221362	5' CCCCCAAAAAGCCACTGT	95400	C_ CC
		ACAGTGGCTT GGG GG		

TGTACCGAA CCC CC
 AAA ____
 GAM1848 LOC221935 3' GCCCAAAGCCACTTCTGC 94203 AC C
 GCA AGTGGCTT GGGC
 ||| ||||| |||
 CGT TCACCGAA CCGG
 CT A
 GAM1848 LOC222488 3' CTCCGGCCCACACTGATGC 96008 A GCTTC
 GCA CAGTG GGGCCGGAG
 ||| ||| |||||
 CGT GTCAC CCCGGCCTC
 A A____
 GAM1848 LOC254048 3' CCCAGTCAACCACTGTT 99058 CTTCG C A
 AACAGTGG GGC GG GG
 ||||| ||| ||
 TTGTCACC CTG CC CC
 AA____ A _
 GAM1848 LOC255941 5' CCCAGCCCGGAGCCACCACCG 99298 AACAC C A
 C GC GTGGCTTCGGGC GG GG
 || ||||| ||| ||
 CG CACCGAGGCCCG CC CC
 CCAC A _
 GAM1849 BRCA1 3' TGCCAAAGTAGCTGATGT 24581 CG GCC
 ACATCAGC AC TGGCA
 ||||| || |||
 TGTAGTCG TG ACCGT
 A_ AA_
 GAM1849 CD72 3' AGTGCCAGCCACCGGCTGA 10118 ACGC
 TCAGCCG CTGGCACT
 ||||| |||||
 AGTCGGC GACCGTGA
 CACC
 GAM1849 DDX5 5' AGTGCAGCTTCGGCTGGTGTCA 16562 C CTG
 TGACATCAGCCGA GC GCACT
 ||||| ||| |||
 ACTGTGGTCGGCT CG CGTGA
 T A____
 GAM1849 DLEC1 5' AGTGCCAGGCCAGTGACCTCA 24714 CA G CGAC
 TGA TCA C GCCTGGCACT
 ||| ||| |||||
 ACT AGT G CGGACCGTGA
 CC _AC____
 GAM1849 DLEC1 3' AGTGCCAGGCCAGTGACCTCA 96276 CA G CGAC
 TGA TCA C GCCTGGCACT
 ||| ||| |||||
 ACT AGT G CGGACCGTGA
 CC _AC____
 GAM1849 DLEC1 3' AGTGCCAGGCCAGTGACCTCA 96277 CA G CGAC
 TGA TCA C GCCTGGCACT
 ||| ||| |||||

			ACT AGT G	CGGACCGTGA		
			CC _ AC__			
GAM1849	FACL4	5'	AGTGCCAGGCGCCGCGCGGCTG	16743	A _ A A	
	CG		TG CA TC GCCG CGCCTGGCACT			
			GC GT GG CGGC GCGGACCGTGA			
			_ C C C			
GAM1849	GAGEC1	3'	GCTACACACATGGCTGATGTCA	23787	ACGCC_	
			TGACATCAGCCG TGGC			
			ACTGTAGTCGGT ATCG			
			ACACAC			
GAM1849	MRC1	3'	AGTGATGGGTAGCTGATGTCA	11681	CGAC GG	
			TGACATCAGC GCCT CACT			
			ACTGTAGTCG TGGG GTGA			
			A__ TA			
GAM1849	DDX35	3'	GTGCCAGGTCCTGGTGCCA	41929	A CCGAC	
			TG CATCAG GCCTGGCAC			
			AC GTGGTC TGGACCGTG			
			C C__			
GAM1849	FLJ14735	3'	GTGCCATCAGCTAATGCCA	52669	A C C CGCC	
			TG CAT AGC GA TGGCAC			
			AC GTA TCG CT ACCGTG			
			C A A __			
GAM1849	MGC11316	3'	AGTGCCATTAAATACCAACTGA	53045	CCGACGCC__	
	TGTCA		TGACATCAG TGGCACT			
			ACTGTAGTC ACCGTGA			
			AACCATAAATT			
GAM1849	LOC146488	5'	AGTGCCAGCCTGGCCAACCTCA	71354	CATCA AC C	
			TGA GCCG GC TGGCACT			
			ACT CGGT CG ACCGTGA			
			CCAAC C_ _			
GAM1850	FBXW7	3'	TGACAGCTAGACACCTAGAAAG	54410	TC A _ G	
	GAA		TTCCTTT AG TGT GGCTG TCA			
			AAGGAAA TC ACA TCGAC AGT			
			GA C GA _			
GAM1850	FBXW7	3'	TGACAGCTAGACACCTAGAAAG	37592	TC A _ G	
	GAA		TTCCTTT AG TGT GGCTG TCA			
			AAGGAAA TC ACA TCGAC AGT			
			GA C GA _			
GAM1850	HAS3	3'	AGTGCACATTAAAAAGGAA	19232	CA _	
			TTCCTTTT GATGTG GCT			

AAGGAAAA TTACAC TGA
 A_ G
 GAM1850 IL18RAP 5' ACCAACTGAAAGGGAA 15249 ATGTGGC
 TTCCTTTTCAG TGGT
 ||||| |||
 AAGGAAAAGTC ACCA
 A_____
 GAM1850 MAL 3' GACCGTGACCTGAGAAGGAA 11432 AT G T
 TTCCTTTTCAG GT GC GGTC
 ||||| || |||
 AAGGAAGAGTC CA TG CCAG
 _ G _
 GAM1850 NFKBIL1 3' TGGTTCCACATCTCAAAA 18447 C CT GT
 TTTT AGATGTGG G CA
 ||| ||||| | ||
 AAAA TCTACACC T GT
 C _ TG
 GAM1850 SLC25A19 3' TGACCAGCCCACACTGCAAAGG 41691 T A _
 AA TTCCTTT CAG TGTGG CTGGTCA
 ||||| ||| ||||| |||||
 AAGGAAA GTC ACACC GACCAGT
 C _ C
 GAM1850 TP53 3' GACCTTAGTACCTAAAAGGAA 6800 C ATGTG _
 TTCCTTTT AG GCT GGTC
 ||||| || ||| |||
 AAGGAAAA TC TGA CCAG
 _ CA_ TT
 GAM1850 TPX1 3' AGCTTTACATCTGCAAAA 13841 _ _
 TTTT CAGATGT GGCT
 ||| ||||| |||
 AAAA GTCTACA TCGA
 C TT
 GAM1850 ARV1 3' TGACCAGCTGTATCTGAAAGAG 43273 C TG
 AA TTC TTTTCAGATG GCTGGTCA
 || ||||| |||||
 AAG GAAAGTCTAT CGACCAGT
 A GT
 GAM1850 COL21A1 3' ACCAACAGTATCCCTTGAAAAG 48771 _ _ GC
 CTTTTCAGATG TG TGGT
 ||||| ||| || |||
 GAAAAGT CTAT AC ACCA
 TCC G A_
 GAM1850 CXorf1 3' ACACAGCTAAAAAGGAA 17484 CAGATG _
 TTCCTTTT TGGCTG GT
 ||||| ||||| ||
 AAGGAAAA ATCGAC CA
 _ A
 GAM1850 FLJ10898 3' GGGAACATCTGGAAAGGAA 60137 GG
 TTCCTTTTCAGATGT CT
 ||||| ||

	AAGGAAAGGTCTACA GG	
	AG	
GAM1850 FLJ11186 3'	ACCACTAAATCCAAAAAGGA 37722	CA G C
	TCCTTTT GAT TGG TGGT	
	AGGAAAA CTA ATC ACCA	
	AC A _	
GAM1850 FLJ13187 3'	ACCAACATATCTGAAAAGGA 45160	GC
	TCCTTTTCAGATGTG TGGT	
	AGGAAAAGTCTATAC ACCA	
	A_	
GAM1850 KIAA0895 3'	TGACCATGCTCTGAAAA 94289	TGTG _
	TTTTCAGA GC TGGTCA	
	AAAAGTCT CG ACCAGT	
	_____ T	
GAM1850 MANBAL 5'	GACCAGGCTGAAAGGGAA 42216	ATGTGG
	TTCCTTTTCAG CTGGTC	
	AAGGGAAAGTC GACCAG	
	G_____	
GAM1850 pcnp 3'	TGACCAATGGCCTCTGAAAA 40145	TGT _
	TTTTCAGA GGCT GTCA	
	AAAAGTCT CCGG CCAGT	
	_____ TAA	
GAM1850 LOC157697 5'	TGACCAGCCAAAGAGAAG 82464	AGATG
	CTTTTC TGGCTGGTCA	
	GAAGAG ACCGACCAGT	
	AA_____	
GAM1850 LOC219972 3'	TGACCTCAAACATCTGAAAAG 93280	GGCT
	CTTTTCAGATGT GGTCA	
	GAAAAGTCTACA CCAGT	
	AACT	
GAM1850 LOC220936 3'	TGACCAGCCTGCAAAAAGGGA 93047	CAGA _
	TTCCTTTT TGT GGCTGGTCA	
	AGGGAAAA ACG CCGACCAGT	
	_____ T	
GAM1850 LOC221463 3'	GGCCTCGCATCTGAAAAGGAA 93707	CT
	TTCCTTTTCAGATGTGG GGTC	
	AAGGAAAAGTCTACGCT CCGG	

GAM1850 LOC253792 3'	ACCAGCTTTTGAAAAG 99023	TGT
	CTTTTCAGA GGCTGGT	

GAAAAGTTT TCGACCA

GAM1850 LOC92181 5' ACCAGCCTTTGAAAAAGGAG 68939 _ TGT
TTCTTTT CAGA GGCTGGT
||||| ||| |||||
GAGGAAAA GTTT CCGACCA

A _

GAM1851 CST2 3' ACCCCCACCTCCTGCAATTAAA 8995 T CC
TTT ATTGC GAGGTGGGGGT
||| ||| |||||
AAA TAACG CTCCACCCCA

T TC

GAM1851 CST3 3' ACCCCCACCTCCTGCAATAAAA 5432 CC
TA TATTTTATTGC GAGGTGGGGGT
||||||| |||||
ATAAAATAACG CTCCACCCCA

TC

GAM1851 CST4 3' ACCCCCACCTCCTGCAATTAAA 10332 T CC
TTT ATTGC GAGGTGGGGGT
||| ||| |||||
AAA TAACG CTCCACCCCA

T TC

GAM1851 IL10RA 3' ACCCCCACCCCTCTGCCAAAGT 60377 ATT CCGA_
A TATTTT GC GGTGGGGGT
||||| || |||||
ATGAAA CG CCACCCCA

C_ TCTCC

GAM1851 LIMK1 3' ACCCAGACGCAGAACAATAAAA 11327 CCCGAG GG
TA TATTTTATTG GT GGGT
||||||| || |||
ATAAAATAAC CA CCA

AAGACG GA

GAM1851 LIMK1 3' ACCCAGACGCAGAACAATAAAA 11328 CCCGAG GG
TA TATTTTATTG GT GGGT
||||||| || |||
ATAAAATAAC CA CCA

AAGACG GA

GAM1851 WSX1 3' ACCCCTCACTACAAAAATAAAA 17912 GCCCGA _
TTTTATT GGTG GGGGT
||||| ||| |||||
AAAATAA TCAC CCA

AAACA_ T

GAM1851 FLJ10305 3' ACCCCCACCCCAATAAAG 68901 CCCGA
TTTTATTG GGTGGGGGT
||||| |||||
GAAATAAC CCACCCCA

C_

GAM1851 FLJ14466 3' CCCCATCTCAAACAAAAAATA 52427 A CCC
TATTTT TTG GAGGTGGGG
||||| ||| |||||

		ATAAAA AAC CTCTACCCC	
		_ AAA	
GAM1851	FLJ21603	3' CCCTGTTTCAAAAATAAAATA 45770	GCCC TG
		TATTTTATT GAGG GGG	
		ATAAAATAA CTTT CCC	
		AAA_ GT	
GAM1851	ICAM4	3' CCCTGTCTCCAAAAATAAAATA 9540	GCCC TG
		TATTTTATT GAGG GGG	
		ATAAAATAA CTCT CCC	
		AAAC GT	
GAM1851	ICAM4	3' CCCTGTCTCCAAAAATAAAATA 42592	GCCC TG
		TATTTTATT GAGG GGG	
		ATAAAATAA CTCT CCC	
		AAAC GT	
GAM1851	LOC153222	3' ACTTCCACCAGACAACAAAATA 81659	A CCCGA
		TATTTT TTG GGTGGGGGT	
		ATAAAA AAC CCACCTTCA	
		C AGA__	
GAM1851	LOC221474	5' TCCCCAGAAAATAAAATA 94001	GCCCGAGG
		TATTTTATT TGGGGG	
		ATAAAATAA ACCCCT	
		AAG_____	
GAM1851	LOC91191	3' ACCCCCACCCCAAATTAAAATG 65800	TTGCCCGA
		TATTTTA GGTGGGGGT	
		GTAAAAT CCACCCCA	
		TAAACC__	
GAM1852	BCHE	3' CACCATAGTTTACAAT 5341	GTCTC
		ATTGTGAA TTATGGTG	
		TAACATTT GATACCAC	

GAM1852	FLG	3' ATCAAGAACTTCATAAT 71446	C TA
		ATTGTGAAGT TCT TGGT	
		TAATACTTCA AGA ACTA	
		A _	
GAM1852	ZNF141	3' TGCTGGAGAGAACTTCACA 14315	_ ATGGT
		TGTGAAG TCTCTT GCA	
		ACACTTC AGAGAG CGT	
		AA GT__	
GAM1852	DDX34	3' TGCACCATAAGACCCACTCACA 28681	A C__
	AT	ATTGTGA GT TCTTATGGTGCA	

TAACACT CA AGAATACCACGT
 _ CCC
 GAM1852 DKFZp434F142 3' CACCAGCTCCTGCCTCACAATG 51031 A CTCTTA
 CATTGTGA GT TGGTG
 ||||| || ||||
 GTAACACT CG ACCAC
 C TCCTCG
 GAM1852 KIAA0418 3' TGCACCATAGGGACTTCACCAA 28301 _ T
 TG CATTG TGAAGTC CTTATGGTGCA
 |||| ||||| |||||
 GTAAC ACTTCAG GGATACCACGT
 C _
 GAM1852 KIAA1560 3' TGCACCTGGAAACTTACAATG 64853 A C TAT
 CATTGTGA GT TCT GGTGCA
 ||||| || ||| |||||
 GTAACATT CA AGG CCACGT
 _ A T__
 GAM1852 KIAA1871 3' CACCAGAACTTCACATTG 61894 T C TAT
 CA TGTGAAGT TCT GGTG
 || ||||| ||| ||||
 GT ACACTTCA AGA CCAC
 T A ____
 GAM1852 MGC32104 3' TACTGGAGAGACTTCACAAT 59070 A
 ATTGTGAAGTCTCTT TGGTG
 ||||| ||||| |||||
 TAACACTTCAGAGAG GTCAT
 _
 GAM1852 ZFD25 3' TACTGGTGAGAAACCTTACAAT 33115 A C _
 G CATTGTGA GT TCTTAT GGTG
 ||||| || ||||| ||||
 GTAACATT CA AGAGTG TCAT
 C A G
 GAM1853 HRH1 3' CTCAAACATGTTTAGAGTGGA 7819 A TGG
 TCCA TCTGA GCATGTTTGAG
 ||| |||| |||||
 AGGT AGATT TGTACAACTC
 G ____
 GAM1853 TRIM37 3' CTCAAATTTGTCATCAG 31625 G T
 CTGATGG CA GTTTGAG
 ||||| || |||||
 GACTACT GT TAAACTC
 _ T
 GAM1853 HTMP10 3' CTCAAAAAAGCCATCAGATCTG 53758 CA G ATG
 A TC ATCTGATGG C TTTGAG
 || ||||| | |||||
 AG TAGACTACC G AAACCTC
 TC _ AAA
 GAM1853 PAK2 5' CTCAAATATCACCAAACTAGA 67140 A__ GC
 TCTG TGG ATGTTTGAG
 ||| ||| |||||

AGAT ACC TATAAACTC
 CAA AC
 GAM1853 SEMA6A 3' CTCGAGTACCCACCAGA 40818 A CA
 TCTG TGGG TGTTTGAG
 |||| ||| |||||
 AGAC ACCC ATGAGCTC
 C _
 GAM1853 TTY7 3' TCAAACATGCAGGCTGGA 50019 AT GATGG
 TCCA CT GCATGTTTGA
 |||| || |||||
 AGGT GA CGTACAACT
 CG _
 GAM1853 LOC144766 3' CTCAAACATGAGAAGACTGGG 77481 A GATGGG
 TCCA TCT CATGTTTGAG
 |||| || |||||
 GGGT AGA GTACAAACTC
 C AGA_
 GAM1853 LOC201685 5' TAAACACCCATCAGATGGA 91845 A CA
 TCCA TCTGATGGG TGTTTG
 |||| ||||| ||||
 AGGT AGACTACCC ACAAAT
 _ _
 GAM1853 LOC221596 5' CTCAAACAAAACCTCAGATT 93623 TG GCA
 AATCTGA G TGTTTGAG
 ||||| | |||||
 TTAGACT C ACAAACCTC
 _ AAA
 GAM1853 LOC93622 3' CTCTGCAGACCATCAGAT 57729 GCA TT
 ATCTGATGG TGT GAG
 ||||| ||| |||
 TAGACTACC ACG CTC
 AG_ T_
 GAM1854 ALDH3A2 3' GGATCCCCTGAGCAAGTCA 69801 T A _
 TG CTTGCTCAG GG CC
 || ||||| || ||
 AC GAACGAGTC CC GG
 T C TA
 GAM1854 FGFR1 3' GTGCCGGCTGCCAAGACA 43889 CTCAGA
 TGTCTTG GGCCGGCAC
 ||||| |||||
 ACAGAAC TCGGCCGTG
 CG_
 GAM1854 HR 5' GCGCGCTGAGCAGACA 18917 T AG CG
 TGTCT GCTCAG GC GC
 |||| |||| || ||
 ACAGA CGAGTC CG CG
 _ G_ _
 GAM1854 MTMR6 5' AGTACCGGCCTCCTCCAGCA 95198 CA_ C
 TGCT GAGGCCGG ACT
 |||| ||||| |||

ACGA CTCCGGCC TGA
 CCTC A
 GAM1854 SELE 3' TGCCTGTGTGAGCAAGCA 6554 T GAG C
 TG CTTGCTCA GC GGCA
 || ||||| || ||||
 AC GAACGAGT TG CCGT
 _ G_ T
 GAM1854 UBQLN1 3' GGCTCTCTGAGCAAAACA 26477 C _
 TGT TTGCTCAGAG GCC
 ||| ||||| |||
 ACA AACGAGTCTC CGG
 A T
 GAM1854 BRAL1 5' CCTCTTCCTCAAGCAAGACA 41807 CA CC_
 TGTCTTGCT GAGG GG
 ||||| ||| ||
 ACAGAACGA CTCC CC
 A_ TTCT
 GAM1854 C16orf5 3' GGCGCACCCTTAAGCAAGACA 26355 CA CCG A
 TGTCTTGCT GAGG GC CT
 ||||| ||| |||
 ACAGAACGA TTCC CG GG
 A_ CA_ C
 GAM1854 C8orf17 3' AGCGCACAGCCTTGAACAAAAC 39987 C C G CG_ A
 A TGT TTG TCA AGGC GC CT
 ||| ||| ||| ||| |||
 ACA AAC AGT TCCG CG GA
 A A _ ACA C
 GAM1854 CPLX1 3' GCCAGCTCTGAGCAGACA 22822 T G C
 TGTCT GCTCAGAG C GGC
 |||| ||||| |||
 ACAGA CGAGTCTC G CCG
 _ _ A
 GAM1854 KIAA0350 3' AGTGCCGCTGACTGGCAAGACA 61824 T A_ C
 TGTCTTGC CAG GGC GGCCT
 ||||| ||| ||| |||||
 ACAGAACG GTC TCG CCGTGA
 _ AG _
 GAM1854 KIAA1322 3' GTTGGCCTTAAACAAAACA 73116 C CTCA
 TGT TTG GAGGCCGGC
 ||| ||| |||||
 ACA AAC TTCCGGTTG
 A AAA_
 GAM1854 KIAA1497 5' GTGCACTATAGCAAGACA 68127 CAG GCCG
 TGTCTTGCT AG GCAC
 ||||| || |||
 ACAGAACGA TC CGTG
 TA_ A_
 GAM1854 LGI4 3' AGCGCCAACCTCGAAGACA 58409 TGC A CC A
 TGTCT TC GAGG GGC CT
 |||| || ||| ||| |||

			ACAGA AG CTCC CCG GA		
			___ _ AA C		
GAM1854	PRO2133	5'	TGCCAACATCTGAGCAAACA 38401	C	GGCC
			TGT TTGCTCAGA GGCA		
			ACA AACGAGTCT CCGT		
			___ ACAA		
GAM1854	Tenr	5'	GGCCGGCCTCCGAGAC 58341	CTCA	A
			GTCTTG GAGGCCGGC C		
			CAGAGC CTCCGGCCG G		
			___ C		
GAM1854	UBE2D1	3'	TGTGTTTCTGAAGCAAGACA 13944	___	CG
			TGTCTTGCT CAGAGGC GCA		
			ACAGAACGA GTCTTTG TGT		
			A ___		
GAM1854	LOC116437	3'	GCACCCTGATGAGAAGACA 74325	G	G_ CCG
			TGTCTT CTCA AGG GC		
			ACAGAA GAGT TCC CG		
			___ AG CA_		
GAM1854	LOC142893	5'	CTGACTCTGAGCAAGCA 83760	T	GC
			TG CTTGCTCAGAG CGG		
			AC GAACGAGTCTC GTC		
			___ A_		
GAM1854	LOC146756	3'	GCAGCTCTGAGCAGGACA 84804		GCCG
			TGTCTTGCTCAGAG GC		
			ACAGGACGAGTCTC CG		
			GA_		
GAM1854	LOC200982	3'	TGCACCCCTGAGCAGGACA 91816	A	CCG
			TGTCTTGCTCAG GG GCA		
			ACAGGACGAGTC CC CGT		
			___ CA_		
GAM1854	LOC204084	5'	TGGTACCTGAGCAAGGCA 91002	AG	
			TGTCTTGCTCAG GCCG		
			ACGGAACGAGTC TGGT		
			CA		
GAM1854	LOC90462	5'	GCCCTCTGGAACAAGACA 63571	C_	CCG
			TGTCTTG TCAGAGG GC		
			ACAGAAC GGTCTCC CG		
			AA ___		
GAM1855	AGL	3'	ATCAGTAGATATCTTAA 5253	T	___
			TTGAG TATCTACTGA T		

			AATTC ATAGATGACT	A	
			T	_____	
GAM1855	AGL	3'	ATCAGTAGATATCTTAA	7197	T _____
			TTGAG TATCTACTGA	T	
				I	
			AATTC ATAGATGACT	A	
			T	_____	
GAM1855	AGL	3'	ATCAGTAGATATCTTAA	7201	T _____
			TTGAG TATCTACTGA	T	
				I	
			AATTC ATAGATGACT	A	
			T	_____	
GAM1855	AGL	3'	ATCAGTAGATATCTTAA	7204	T _____
			TTGAG TATCTACTGA	T	
				I	
			AATTC ATAGATGACT	A	
			T	_____	
GAM1855	AGL	3'	ATCAGTAGATATCTTAA	7207	T _____
			TTGAG TATCTACTGA	T	
				I	
			AATTC ATAGATGACT	A	
			T	_____	
GAM1855	AGL	3'	ATCAGTAGATATCTTAA	7212	T _____
			TTGAG TATCTACTGA	T	
				I	
			AATTC ATAGATGACT	A	
			T	_____	
GAM1855	DAZL	3'	TCAGTGGAAGTCAATA	68700	TA
			TATTGAGT TCTACTGA		
			ATAACTCA AGGTGACT		

GAM1855	DISC1	3'	TCAGTGCGGTACTCAGTA	38517	T _
			TATTGAGT ATC TACTGA		
			ATGACTCA TGG GTGACT		
			_ C		
GAM1855	HOXB6	5'	TCAGTATCAGCTCGATA	60542	ATC
			TATTGAGTT TACTGA		
			ATAGCTCGA ATGACT		
			CT_		
GAM1855	LEF1	3'	TCAGTAGAGCTAAATA	33225	G TA
			TATT AGT TCTACTGA		
			ATAA TCG AGATGACT		
			A _		
GAM1855	RAG1	3'	TCAGGGATTGAACTCAGTA	6547	_ A
			TATTGAGTT ATCT CTGA		

		ATGACTCAA TAGG GACT		
		GT _		
GAM1855	CTRP5	3' TCAGAGATCACTCAATA	32231	T A
		TATTGAGT ATCT CTGA		
		ATAACTCA TAGA GACT		
		C _		
GAM1855	DKFZP566G1424	3' CAGTAAATGTGGCTTAATA	85940	C__
		TATTGAGTTAT TACTG		
		ATAATTCGGTG ATGAC		
		TAA		
GAM1855	FLJ12587	3' TCAGTTTTCTAACTTAATA	42784	TCT_
		TATTGAGTTA ACTGA		
		ATAATTCAAT TGACT		
		CTTT		
GAM1855	FLJ20619	3' CAGTAGAGGTCATTTAATA	35891	TA__
		TATTGAGT TCTACTG		
		ATAATTTA AGATGAC		
		CTGG		
GAM1855	FLJ21302	3' TCAGTAGATAGAGCAATG	43515	AG
		TATTG TTATCTACTGA		
		GTAAC GATAGATGACT		
		GA		
GAM1855	HSPC129	3' TCAGCACAGTGACTCAGTA	33509	CTA_
		TATTGAGTTAT CTGA		
		ATGACTCAGTG GACT		
		ACAC		
GAM1855	KIAA1492	3' TCAGTAGATACAATA	65127	AGT
		TATTG TATCTACTGA		
		ATAAC ATAGATGACT		
		—		
GAM1855	KIAA1915	3' TCAGTAGAAATTCAGTA	73671	A
		TATTGAGTT TCTACTGA		
		ATGACTTAA AGATGACT		
		—		
GAM1855	KR18	3' TCAGTAGGATACTCCATA	53895	T TA
		TAT GAGT TCTACTGA		
		ATA CTCA GGATGACT		
		C TA		
GAM1855	PMAIP1	3' TCAGTAGACTGAACATTCAATA	41212	TA_____
		TATTGAGT TCTACTGA		

		ATAACTTA AGATGACT		
		CAAGTC		
GAM1855	STARD7	3' CAGTGCAAGATAATTCAATA 39737	_____	
		TATTGAGTTATCT ACTG		
		ATAACTTAATAGA TGAC		
		ACG		
GAM1855	STARD7	3' CAGTGCAAGATAATTCAATA 58369	_____	
		TATTGAGTTATCT ACTG		
		ATAACTTAATAGA TGAC		
		ACG		
GAM1855	LOC145009	5' TCAGAAGTCAACTCAATG 60982		AT A
		TATTGAGTT CT CTGA		
		GTAAGTCAA GA GACT		
		CT A		
GAM1855	LOC255265	5' ATCAGTAGATGATGAACTCAA 97091	_____	_____
	T	ATTGAGT TATCTACTGA T		
		TAAGTCA GTAGATGACT A		
		AAGTA		
GAM1856	DDX11	3' GACTTTCTCTTCCAGAGCCA 48387		G CAA T
		TGG TC GGA GAAAGTC		
		ACC AG CCTT TCTTCAG		
		G A_ C		
GAM1856	IKBKB	3' GTGACTTTCACCCAGGACCCA 63905		AA ATG
		TGGGTCC GGG GAAAGTCAC		
		ACCCAGG CCC CTTTCAGTG		
		A_ A_		
GAM1856	NOTCH2	3' GTGACTCTCTGCCCTTGGACCC 44579		A A
	A	TGGGTCCAAGGG TGGA AGTCAC		
		ACCCAGGTTCCC GTCT TCAGTG		
		_ C		
GAM1856	PRODH	3' GTGACCCCATGTCCTTGGACC 33397		_ AAA
	TA	TGGGTCCAAGGG ATGG GTCAC		
		ATCCAGGTTCTTACC CAGTG		
		G CC_		
GAM1856	UBASH3A	3' ACTCCCATCTGTGGACCCA 39047		AG AA
		TGGGTCCA GGATGG AGT		
		ACCCAGGT TCTACC TCA		
		G_ C_		
GAM1856	UNG	3' ACTTTCCAGAATCTGGCCCA 56023		T A GA_
		TGGG CCA GG TGGAAAGT		

		ACCC GGT CT ACCTTTCA		
		— — AAG		
GAM1856	UNG	3' ACTTTCCAGAATCTGGCCCA 14012	T A GA_	
		TGGG CCA GG TGGAAAGT		
		ACCC GGT CT ACCTTTCA		
		— — AAG		
GAM1856	FLJ23598	3' GACACCCCCCTGGACCCA 45864	A AT AAA	
		TGGGTCCA GGG GG GTC		
		ACCCAGGT CCC CC CAG		
		— C_ A_		
GAM1856	KIAA1025	3' TGA CTCCTCATTCCTGGCCCA 64680	T A AA	
		TGGG CCA GGGATGG AGTCA		
		ACCC GGT CCTTACT TCAGT		
		— — CC		
GAM1856	KIAA1958	5' GTGACTTTGAACCCCAAACCCA 82789	CCAA ATGG	
		TGGGT GGG AAAGTCAC		
		ACCCA CCC TTTCAGTG		
		AA_ CAAG		
GAM1856	LASP1	3' TGACCTCCCCTCCCAGCCCA 21580	CCAA T AAA	
		TGGGT GGGA GG GTCA		
		ACCCG CCCT CC CAGT		
		AC_ C CTC		
GAM1856	MARCKS	3' ACTTTCCACCCTGCCCA 11411	CCA A	
		TGGGT AGGG TGGAAAGT		
		ACCCG TCCC ACCTTTCA		
		— —		
GAM1856	TSGA14	3' ACTTTCAGATTCAGCCCA 38664	CCAAG G_	
		TGGGT GGAT GAAAGT		
		ACCCG CTTA CTTTCA		
		A_ GA		
GAM1856	TUB	5' GTGGGACCATCCCTTAAACCCA 13900	CC AAAG	
		TGGGT AAGGGATGG TCAC		
		ACCCA TTCCCTACC GGTG		
		AA AG_		
GAM1856	LOC131827	3' TGA CTGCTCTCTTGGACCCA 75503	TGGAA	
		TGGGTCCAAGGGA AGTCA		
		ACCCAGGTTCTCT TCAGT		
		CG_		
GAM1856	LOC145870	3' ACTGAACTCCCTTGGTCCCA 78018	T TGGAA	
		TGGG CCAAGGGA AGT		

		ACCC GGTTCCT TCA	
		T CAAG_	
GAM1856	LOC149041 3'	ACTTTGGACGCCTTGGATCCA 79869	GATGG
		TGGGTCCAAGG AAAGT	
		ACCTAGGTTCC TTTCA	
		GCAGG	
GAM1856	LOC254428 3'	TGACTTTGTCTCCCTGGGCCCA 97199	A T _
		TGGGTCCA GGGA GG AAAGTCA	
		ACCCGGGT CCCT CT TTTCAGT	
		_ _ G	
GAM1856	LOC256073 5'	ACCTTCCATCCCCCATCCA 98483	CCAA A
		TGGGT GGGATGGAA GT	
		ACCTA CCCTACCTT CA	
		CCC_ C	
GAM1856	LOC92017 5'	TGACATTCCCTTGGGCCCA 68494	TGGAAA
		TGGGTCCAAGGGA GTCA	
		ACCCGGGTTCCT CAGT	
		TA____	
GAM1857	GALNT2 3'	TGGAAACCATCCTTGAAA 16822	G AAAAG
		TTTCAAGG ATGG TCA	
		AAAGTTCC TACC GGT	
		_ AAA_	
GAM1857	GOT1 3'	TGAAGAGAACATCCCTTGAGA 10854	GAAAAG
		TTTCAAGGGATG TCA	
		AGAGTTCCCTAC AGT	
		AAGAGA	
GAM1857	GRINL1A 3'	GTGACTTTCATGTGCTTGAAA 70068	GG_ AA
		TTTCAAG ATGGA AGTCAC	
		AAAGTTC TACTT TCAGTG	
		GTG _	
GAM1857	HNRPH3 5'	GACTTCTCCCTTCTTTGAA 25209	T A
		TTCAAGGGA GGA AAGTC	
		AAGTTTCTT CCT TTCAG	
		C C	
GAM1857	AKL3L 3'	TGACTTGTTTCCTTTGAAA 33273	TGGAA
		TTTCAAGGGA AAGTCA	
		AAAGTTTCCT TTCAGT	
		TTG_	
GAM1857	C20orf36 3'	GTGACTTTTGTCTTGAAA 37335	GATGG
		TTTCAAGG AAAAGTCAC	

		AAAGTTCT	TTTTCAGTG		
		G_____			
GAM1857	CECR2	3'	TGACTTTTCCAAATCCTGAGA	49440	A A_
			TTTCA GGG TGGAAAAGTCA		
			AGAGT CCT ACCTTTTCAGT		
			_ AA		
GAM1857	CXorf12	3'	ACTTTTCTGTAGTTTGAAA	14486	GG
			TTTCAAG ATGGAAAAGT		
			AAAGTTT TGTCTTTTCA		
			GA		
GAM1857	DDO	3'	ACTTTTCCACTGCATGAAA	14681	AG_ A
			TTTCA GG TGGAAAAGT		
			AAAGT TC ACCTTTTCA		
			ACG _		
GAM1857	DMTF1	3'	TGACTTTTACCTCCTTT	41246	TG_
			AAGGGA GAAAAGTCA		
			TTTCCT TTTTTCAGT		
			CCA		
GAM1857	FLJ14800	3'	GTGACTTTTCCAGGGAGGAAG	52688	AAGGGA
			TTTC TGGAAAAGTCAC		
			GAAG ACCTTTTCAGTG		
			GAGGG_		
GAM1857	FLJ20086	3'	GTGACTTTTCTGTAATTG	35014	GGG
			CAA ATGGAAAAGTCAC		
			GTT TGTCTTTTCAGTG		
			AA_		
GAM1857	HCGIV.9	3'	GTGACTTTGGTCCCTTGA	39134	G AA
			TCAAGGGAT GA AGTCAC		
			AGTTCCCTG TT TCAGTG		
			G _		
GAM1857	KIAA0285	3'	ACTGGTTATCCTTTGAAA	29681	AAA
			TTTCAAGGGATGG AGT		
			AAAGTTTCCTATT TCA		
			GG_		
GAM1857	KIAA0731	3'	GACCTTTCCATCCTTGAAA	67480	G A
			TTTCAAGG ATGGAAA GTC		
			AAAGTTCC TACCTTT CAG		
			_ C		
GAM1857	P2RXL1	3'	CGTGACCCCCCAGCCCAACCCC	19561	A_ AAAA_____
			TTGGAA TTTCAAGGG TGG GTCAC G		

		AAGGTTCCC ACC CAGTG C	
		CA CGACCCCC _	
GAM1857	PROZ	3' GTGACCTTTCTTTCCCTGGAA 15307	A T A
		TTTCA GGGA GGAAA GTCAC	
		AAGGT CCCT TCTTT CAGTG	
		_ T C	
GAM1857	PSR	3' GTGAGATCCCATCTCTCAAAA 65791	CA AAAAG
		TTT AGGGATGG TCAC	
		AAA TCTCTACC AGTG	
		AC CTAG_	
GAM1857	SLC5A7	3' ACTTCAGTCACTCCCTTGAA 41803	_ AA_
		TTCAAGGGA TGG AAGT	
		AAGTCCCT ACT TTCA	
		C GAC	
GAM1857	TSSC1	3' ACTCTTCTTTCTCTTGAGA 13870	T A
		TTTCAAGGGA GGAA AGT	
		AGAGTTCTCT TCTT TCA	
		T C	
GAM1857	XYLT1	3' TGACCTTCTTTGATCCTTGAAA 78417	AT__ AA
		TTTCAAGGG GGAA GTCA	
		AAAGTTCCT TCTT CAGT	
		AGTT C_	
GAM1857	ZNF262	3' TGACCTTGTTGCCCTTGAAA 18729	ATGGA A
		TTTCAAGGG AA GTCA	
		AAAGTTCCC TT CAGT	
		GTTG_ C	
GAM1857	LOC221968	3' TGACTTTTAGTTCTTGAA 94156	ATGG
		TTCAAGGG AAAAGTCA	
		AAGTTCTT TTTTCAGT	
		GA_	
GAM1857	LOC222237	3' TGACCTTTCCAGACCTTGAAA 95949	GA A
		TTTCAAGG TGGAAA GTCA	
		AAAGTTCC ACCTTT CAGT	
		AG C	
GAM1857	LOC253336	3' ACTTTCTTCATCCCTTGAA 99178	_
		TTCAAGGGATGGA AAAGT	
		AAGTCCCTACTT TTTCA	
		C	
GAM1857	LOC256714	3' TGACCTTTTCTTCTTTGAAA 98048	T A
		TTTCAAGGGA GGAAA GTCA	

			AAAGTTTCTT CTTTT CAGT		
			— C		
GAM1857	LOC51313	3'	GTGACTTTTCATTTCTGAAA 33997	A	TG
			TTTCA GGGA GAAAAGTCAC		
			AAAGT CCTT CTTTTCAGTG		
			— TA		
GAM1858	GPD1	3'	TCATGCCACCACATTTG 60398	C	C
			TAAATG GGTGGCAT GA		
			GTTTAC CCACCGTA CT		
			A —		
GAM1858	IL5RA	5'	TCGCATGGCCACCGCATTT 6906	AT	—
			AAATGCGGTGGC CGA		
			TTTACGCCACCG GCT		
			GTAC		
GAM1858	MYO1C	3'	TGCCGATGCCAATATTTG 61873	CGG	A
			TAAATG TGGCATCG CA		
			GTTTAT ACCGTAGC GT		
			AA_ C		
GAM1858	C6orf37	3'	TGTCACACTGCATTTA 68097	GCATC	
			TAAATGCGGTG GACA		
			ATTTACGTCAC CTGT		
			A_		
GAM1858	DNAJC6	3'	TTGCAGAACCACCGCATT 29498	CA	GA
			AATGCGGTGG TC CAA		
			TTACGCCACC AG GTT		
			A_ AC		
GAM1858	FLJ11210	3'	GTCGATGTGCATGCTTTTA 60319	T	GTG
			TAAA GCG GCATCGAC		
			ATTT CGT TG TAGCTG		
			T ACG		
GAM1858	FLJ12476	3'	TCGATCTTCTGCATTTA 43270	T	C
			TAAATGCGG GG ATCGA		
			ATTTACGTC TC TAGCT		
			T _		
GAM1858	KIAA1034	3'	TCGATGGCATCCGCATTTG 63134	_	G
			TAAATGCGG TG CATCGA		
			GTTTACGCC AC GTAGCT		
			T G		
GAM1858	KIAA1987	3'	TCATGTAAGTGCATTTA 89391	G	C
			TAAATGCGGT GCAT GA		

		ATTACGTCA TGTA CT		
		A _		
GAM1858	MGC16063	3' TGTCCTGGCCACTGCATT	54929	ATC
		AATGCGGTGGC GACA		
		TTACGTCACCG CTGT		
		GTC		
GAM1858	LOC147949	3' TGTCAGATGTCCACATTGCA	79279	_ _ _
		TGCG GTGG CATC GACA		
		ACGT CACC GTAG CTGT		
		TA T A		
GAM1858	LOC150577	3' GTCCTCACCGCATTTG	86258	CATC
		TAAATGCGGTGG GAC		
		GTTTACGCCACT CTG		
		C_		
GAM1858	LOC158219	3' TGTGTGTCACCACATTT	82694	C CG
		AAATG GGTGGCAT ACA		
		TTTAC CCACTGTG TGT		
		A _		
GAM1858	LOC202020	3' TGTCTCACCATTTA	90605	C CATC
		TAAATG GGTGG GACA		
		ATTAC CCACT CTGT		
		A _		
GAM1858	LOC90826	5' TGTCGATGCAGGTTTATTTG	64788	CGGTG
		TAAATG GCATCGACA		
		GTTTAT CGTAGCTGT		
		TTGGA		
GAM1858	LOC93587	3' TTGTCTTTACCTGCATTTA	73042	_ CATC
		TAAATGC GGTGG GACAA		
		ATTACG CCATT CTGTT		
		T T_		
GAM1859	ELF3	3' TGACCTTGACCTTGACCAA	16685	T GAT CAA
		TTGGT CAAGG GG GTCA		
		AACCA GTTCC TC CAGT		
		_ AGT _		
GAM1859	KIAA1228	3' ACTTACACTTTGAACCA	65661	GA GC
		TGGTTCAAGG TG AAGT		
		ACCAAGTTTC AC TTCA		
		_ A_		
GAM1859	TUB	5' GTGGGACCATCCCTTAAACC	13898	C CAAG
		GGTT AAGGGATGG TCAC		

CCAA TTCCCTACC GGTG
 A AG__
 GAM1859 LOC197423 5' TGACTTGTGCCCTAAAC 78427 CA ATG
 GTT AGGG GCAAGTCA
 ||| ||| |||||
 CAA TCCC TGTTTCAGT
 A_ G__
 GAM1860 EHF 3' TCCAAAACCCAAGGTTGGCT 25127 AT _ C
 AGT GCCT GGGT TTGGA
 ||| ||| ||| |||
 TCG TGA CCCA AACCT
 GT A A
 GAM1860 EPHA2 3' CCATCGGCCAAGAATACTTGAA 16675 GC G T_
 G CTTCAAGTAT CT GGTC TGG
 ||||| || ||| |||
 GAAGTTCATA GA CCGG ACC
 A_ A CT
 GAM1860 ITGA5 3' CCCAGAGACATACTTGAAG 61933 C__
 CTTCAAGTATG CTGGG
 ||||| |||
 GAAGTTCATAC GACCC
 AGA
 GAM1860 TREM2 3' TCCAAGACTGTCATATTT 39098 CCTG
 AAGTATG GGTCTTGGA
 ||||| |||||
 TTTATAC TCAGAACCT
 TG__
 GAM1860 UQCRB 3' CCAACATAGGCATACTTAAG 21939 C GGTC
 CTT AAGTATGCCTG TTGG
 || ||||| |||
 GAA TTCATACGGAT AACC
 _ AC__
 GAM1860 ATP10D 3' CAGAGACCACTTGAAG 73526 ATGCCTG _
 CTTCAAGT GGTCT TG
 ||||| ||| ||
 GAAGTTCA CCAGA AC
 _ G
 GAM1860 B3GNT7 3' CCCTTCCAGGCAACCTGAA 71678 A A TCTT
 TTCA GT TGCCTGGG GG
 ||| || ||||| ||
 AAGT CA ACGGACCT CC
 C _ TC__
 GAM1860 DKFZp547I224 3' TCCAAAATTGACCACATACTTG 39963 CCTG ____
 GA TTCAAGTATG GGTC TTGGA
 ||||| ||| |||
 AGGTTCATAC CCAG AACCT
 A__ TTAA
 GAM1860 FLJ22341 3' CCAAGCTCAGGCACACCCAAG 45114 CAA A T
 CTT GT TGCCTGGG CTTGG
 || || ||||| |||

			GAA CA ACGGACTC GAACC		
			CC_ C _		
GAM1860	KIAA0779	3'	CCGAACAGCATACTTGAAG	86908	C GGTC
			CTTCAAGTATGC TG TTGG		
			GAAGTTCATACG AC AGCC		
			_ A _		
GAM1860	LOC144233	3'	CCAAGGCACATAATTGAA	77246	G CCTGG
			TTCAA TATG GTCTTG		
			AAGTT ATAC CGGAACC		
			A A _		
GAM1860	LOC147341	3'	ACCCAGGCATAACTGAAG	85116	AG
			CTTCA TATGCCTGGGT		
			GAAGT ATACGGACCCA		
			CA		
GAM1860	LOC221088	5'	TCCAAGGTGCTGGCCACTCGAA	94888	A AT TGGG
			G CTTC AGT GCC TCTTGGA		
			GAAG TCA CGG GGAACCT		
			C C_ TCGT		
GAM1861	ELF3	3'	TGACCTTGACCTTGACCAA	16685	T GAT CAA
			TTGGT CAAGG GG GTCA		
			AACCA GTTCC TC CAGT		
			_ AGT _		
GAM1861	KIAA1228	3'	ACTTACACTTTGAACCA	65661	GA GC
			TGGTTCAAGG TG AAGT		
			ACCAAGTTTC AC TTCA		
			_ A _		
GAM1861	TUB	5'	GTGGGACCATCCCTTAAACC	13898	C CAAG
			GGTT AAGGGATGG TCAC		
			CCAA TTCCCTACC GGTG		
			A AG_		
GAM1861	LOC197423	5'	TGACTTGTGCCCTAAAC	78427	CA ATG
			GTT AGGG GCAAGTCA		
			CAA TCCC TGTTCAGT		
			A_ G_		
GAM1862	DXYS155E	3'	TCCACCCCTGCAAAGCCAAG	18691	CCA A_
			CTTGGCTT AGG TGGA		
			GAACCGAA TCC ACCT		
			ACG CC		
GAM1862	HPGD	3'	GACCTCCCAGCTTGAAGCCAA	7810	C GA AAA
			TTGGCTTC AAG TGG GTC		

			AACCGAAG TTC ACC CAG		
			_ G_ CTC		
GAM1862	HSPC126	3'	GACTTTCTTTTAAAGCCAA 27176	CCAA	T
			TTGGCTT GGA GGAAAGTC		
			AACCGAA TTT TCTTTCAG		
			A__ T		
GAM1862	LAIR1	3'	CCTTCCTAGAAGTCAAG 41660	CA	T
			CTTGGCTTC AGGA GG		
			GAAGTGAAG TCCT CC		
			A_ T		
GAM1862	LAIR1	3'	CCTTCCTAGAAGTCAAG 11254	CA	T
			CTTGGCTTC AGGA GG		
			GAAGTGAAG TCCT CC		
			A_ T		
GAM1862	LPIN1	5'	GACTTTCCTCTGAAAGCTAAG 67988	CCAA	T
			CTTGGCTT GGA GGAAAGTC		
			GAATCGAA TCT CTTTTCAG		
			AG__ _		
GAM1862	OCLN	3'	CCATAACCCCGGAAGCCAA 11882	AA	_
			TTGGCTTCC GG ATGG		
			AACCGAAGG CC TACC		
			CC AA		
GAM1862	PCDH9	5'	GACCCCTCCCCTCCAAAGCCAA 83693	CCA	AT AA_
	G		CTTGGCTT AGG GGA GTC		
			GAACCGAA TCC CCT CAG		
			ACC _ CCC		
GAM1862	PTX3	3'	TCCAATTGAAGCCAA 12635	C	GA
			TTGGCTTC AAG TGGA		
			AACCGAAG TTC ACCT		
			- -		
GAM1862	SEL1L	3'	GATTTTCCCTAGAGGCCAA 18601	CA	ATG
			TTGGCTTC AGG GAAAGTC		
			AACCGGAG TCC CTTTTCAG		
			A_ _		
GAM1862	SLC1A5	5'	CCTCCTGGAGCCAAG 20067	T	A T
			CTTGGCT CCA GGA GG		
			GAACCGA GGT CCT CC		
			- - -		
GAM1862	SLC1A5	5'	CCTCCTGGAGCCAAG 79237	T	A T
			CTTGGCT CCA GGA GG		

GAACCGA GGT CCT CC

```

      _ _ _
GAM1862 TGFB2  3' ACTGATGCTTCCTGGAAAACCA 13726  C_  A  T AA__
      AG              CTTGG TTCCA GGA GG  AGT
                      |||| |||| ||| ||
                      GAACC AAGGT CCT TC  TCA
                      AA  _ _  GTAG
GAM1862 TNFSF4 3' CCAACCCCTGGAAGCCAA  13909  A_  A
                      TTGGCTTCCA GG TGG
                      ||||| |||
                      AACCGAAGGT CC ACC
                      CC A
GAM1862 ACYP2  3' ACTTTCTGTTCTGAAAGCTAAG 57405  CCA
                      CTTGGCTT AGGATGGAAAAGT
                      ||||| |||||
                      GAATCGAA TCTTGTCTTTCA
                      AG_
GAM1862 DAPK2  3' GACCTCCCAGAACCATGGAAGC 27513  A A__ AAA
      CAGG              CTTGGCTTCCA GG  TGG  GTC
                      ||||| ||| |||
                      GGACCGAAGGT CC  ACC  CAG
                      A AAG  CTC
GAM1862 DCTN4  3' ACTTTTTTCTTCAGAAGCCAA 68394  CA  T
                      TTGGCTTC AGGA GGAAAGT
                      ||||| ||| |||||
                      AACCGAAG TTCT TTTTCA
                      AC  _
GAM1862 DKFZP434F0318 3' GACTGTGTCCCAGAAGCCAA 48757  CAA  GGAA
                      TTGGCTTC GGAT  AGTC
                      ||||| ||| |||
                      AACCGAAG CCTG  TCAG
                      AC_  TG__
GAM1862 DKFZp762K2015 3' GACCCTCTGGATTTGGAAGGCA 72890  G    GA  AA
      A              TTG CTTCCAAG TGGA  GTC
                      ||| ||||| ||| |||
                      AAC GAAGGTTT GTCT CAG
                      G    AG  CC
GAM1862 FLJ10432 3' CCTGACCTGGAGGCCAAG  39350  A AT_
                      CTTGGCTTCCA GG  GG
                      ||||| ||| ||
                      GAACCGGAGGT CC  CC
                      _  AGT
GAM1862 FLJ10743 3' TGAAAGTCAAATCTTGGAACCA 37091  C    _____  GGAAA
      AA              TTGG TTCCAAG  GAT  G
                      ||| ||||| ||| |
                      AACC AAGGTTC  CTG  T
                      A    TAAA__  AAAGG
GAM1862 FLJ10826 5' TTCATCCAAAGCCAAG  37251  CCAA
                      CTTGGCTT  GGATGGA
                      ||||| |||||
```


		GAACCGAA CCTACTT	
		A__	
GAM1862	FLJ11053	3' TCTAAGTTCCTGGGAAGCCAA 90124	A ____
		TTGGCTTCC AGGA TGGA	
		AACCGAAGG TCCT ATCT	
		G TGA	
GAM1862	ICK	3' ACTTCCCTGGGGAAGCCAA 30590	AA AT A
		TTGGCTTCC GG GGAA GT	
		AACCGAAGG TC CCTT CA	
		GG __ _	
GAM1862	KIAA0172	5' ACTTCCTCATAGCCAGAAGTCA 65592	CAA AT____ A
		AG CTTGGCTTC GG GGAA GT	
		GAAGTGAAG CC CCTT CA	
		A__ GATACT _	
GAM1862	KIAA0426	3' GACCTTCACCCAGAAGCCAGG 28926	CAA ATG A
		CTTGGCTTC GG GAA GTC	
		GGACCGAAG CC CTT CAG	
		A__ CA_ C	
GAM1862	KIAA0793	3' GACCTTCCATCTGGTGAACCAA 29694	C CAA A
		G CTTGG TTC GGATGGAA GTC	
		GAACC AAG TCTACCTT CAG	
		_ TGG C	
GAM1862	KIAA1754	3' ACAGCCTCCAGAAGCCAA 63928	CAA T AAA
		TTGGCTTC GGA GG GT	
		AACCGAAG CCT CC CA	
		A__ _ GA_	
GAM1862	KIAA1843	3' GACTCTCCAGAAGGGAGCCAAG 62883	AAGGA A
		CTTGGCTTCC TGGA AGTC	
		GAACCGAGGG ACCT TCAG	
		AAG__ C	
GAM1862	KIAA1940	3' GACCTTCCATCCCTGAATACAA 80783	GC CAA A
		G CTTG TTC GGATGGAA GTC	
		GAAC AAG CCTACCTT CAG	
		AT TC_ C	
GAM1862	MGC12837	3' ACTTCCTCAAAGCCCAAAGCCA 52166	CCAA AT____ A
		AG CTTGGCTT GG GGAA GT	
		GAACCGAA CC CCTT CA	
		AC__ GAAACT _	
GAM1862	RAI17	3' GACCCCTGACCTATAAGCCAAG 92905	CCA AT_ AAA
		CTTGGCTT AGG GG GTC	

			GAACCGAA TCC CC CAG	
			TA_ AGT C__	
GAM1862	SCYA28	3'	ACCCTACCAGAAGCTAA 39534	CAA A AAA
			TTGGCTTC GG TGG GT	
			AATCGAAG CC ATC CA	
			A__ _ C__	
GAM1862	SYNCOILIN 3'		ACTCTTCTAGAAGCCAG 48628	CAAGGA _
			TTGGCTTC TGGAA AGT	
			GACCGAAG ATCTT TCA	
			_____ C	
GAM1862	TIEG	3'	ACTTGGACCCTTGGAACAA 20168	GC ATGGA
			TTG TTCCAAGG AAGT	
			AAC AAGGTTCC TTCA	
			AA CAGG_	
GAM1862	TOPK	5'	CTTTTGTAAAGCCAGG 38098	C AGGATG
			CTTGGCTT CA GAAAG	
			GGACCGAA GT TTTTC	
			A _____	
GAM1862	WWP1	5'	CTTTCCTTGGAACAAAG 81260	GC T
			CTTG TTCCAAGGA GG	
			GAAC AAGGTTCTCT TC	
			AA T	
GAM1862	ZFPL1	3'	GACCCCAGACCCAAAGCCAAG 60389	CCAA A_ AAA
			CTTGGCTT GG TGG GTC	
			GAACCGAA CC ACC CAG	
			AC__ AG C__	
GAM1862	ZNF294	3'	GACTTTCAATTTTGGAAGC 71383	ATG
			GCTTCCAAGG GAAAGTC	
			CGAAGGTTTT CTTTCAG	
			AA_	
GAM1862	LOC112448 3'		ACCTTTCGTCAGAAGTCAA 73182	CAAG A
			TTGGCTTC GATGGAA GT	
			AACTGAAG CTGCTTT CA	
			A__ C	
GAM1862	LOC120939 5'		CCATCCTCAAAGCCAAG 76759	CCA
			CTTGGCTT AGGATGG	
			GAACCGAA TCCTACC	
			AC_	
GAM1862	LOC151176 3'		CCTCCTGGGAGCCAAG 86440	A T
			CTTGGCTTCCA GGA GG	

GAACCGAGGGT CCT CC

GAM1862 LOC153139 3' ACTCTCAGTCAGAGGCCAA 87136 CAAG G A
TTGGCTTC GAT GA AGT
||||||| ||| |||
AACCGGAG CTG CT TCA
A__ A C

GAM1862 LOC169436 5' CCACCCGGAAGCCAAG 83617 AA A
CTTGGCTTCC GG TGG
||||||| |||
GAACCGAAGG CC ACC
__ C

GAM1862 LOC254922 3' ACTCTCAGTCAGAGGCCAA 98895 CAAG G A
TTGGCTTC GAT GA AGT
||||||| ||| |||
AACCGGAG CTG CT TCA
A__ A C

GAM1862 LOC256414 3' TCCATAGCTGGGAGCCAAG 98630 AGG
CTTGGCTTCCA ATGGA
||||||| ||||
GAACCGAGGGT TACCT
CGA

GAM1862 LOC51204 3' GACTTGCGACCTTGAAGCCA 33464 C A GA
TTGGCTTC AAGG TG AAGTC
||||||| |||| |||
AACCGAAG TTCC GC TTCAG
_ A G_

GAM1862 LOC51339 3' GACTCATGACTTGGAGGCCAA 34093 G_ GAA
TTGGCTTCCAAG ATG AGTC
||||||| ||| |||
AACCGGAGGTTT TAC TCAG
AG ____

GAM1862 LOC91445 3' CCATCCTCAGAAGCCAAG 61165 CA
CTTGGCTTC AGGATGG
||||||| |||||
GAACCGAAG TCCTACC
AC

GAM1862 LOC91445 3' GACCACCATCCTCAGAAGCCA 61170 CA AAA
G CTTGGCTTC AGGATGG GTC
||||||| ||||| |||
GAACCGAAG TCCTACC CAG
AC AC_

GAM1863 DMD 3' ACTTTCCACTGACAACGA 5460 GT_ GGGA
TTG TCAG TGGAAAGT
||| ||| |||||
AGC AGTC ACCTTTCA
AAC ____

GAM1863 DMD 3' ACTTTCCACTGACAACGA 15677 GT_ GGGA
TTG TCAG TGGAAAGT
||| ||| |||||

		AGC AGTC ACCTTTCA AAC _____		
GAM1863 DMD	3'	ACTTTCCACTGACAACGA 15680 TTG TCAG TGGAAAGT 	GT_	GGGA
		AGC AGTC ACCTTTCA AAC _____		
GAM1863 DMD	3'	ACTTTCCACTGACAACGA 15683 TTG TCAG TGGAAAGT 	GT_	GGGA
		AGC AGTC ACCTTTCA AAC _____		
GAM1863 DMD	3'	ACTTTCCACTGACAACGA 15687 TTG TCAG TGGAAAGT 	GT_	GGGA
		AGC AGTC ACCTTTCA AAC _____		
GAM1863 DMD	3'	ACTTTCCACTGACAACGA 15692 TTG TCAG TGGAAAGT 	GT_	GGGA
		AGC AGTC ACCTTTCA AAC _____		
GAM1863 DMD	3'	ACTTTCCACTGACAACGA 15695 TTG TCAG TGGAAAGT 	GT_	GGGA
		AGC AGTC ACCTTTCA AAC _____		
GAM1863 DMD	3'	ACTTTCCACTGACAACGA 15700 TTG TCAG TGGAAAGT 	GT_	GGGA
		AGC AGTC ACCTTTCA AAC _____		
GAM1863 DMD	3'	ACTTTCCACTGACAACGA 15704 TTG TCAG TGGAAAGT 	GT_	GGGA
		AGC AGTC ACCTTTCA AAC _____		
GAM1863 DMD	3'	ACTTTCCACTGACAACGA 15707 TTG TCAG TGGAAAGT 	GT_	GGGA
		AGC AGTC ACCTTTCA AAC _____		
GAM1863 DMD	3'	ACTTTCCACTGACAACGA 15710 TTG TCAG TGGAAAGT 	GT_	GGGA
		AGC AGTC ACCTTTCA AAC _____		
GAM1863 DMD	3'	ACTTTCCACTGACAACGA 15714 TTG TCAG TGGAAAGT 	GT_	GGGA

AGC AGTC ACCTTTCA
 AAC ____
 GAM1863 DMD 3' ACTTTCCACTGACAACGA 15719 GT_ GGGA
 TTG TCAG TGGAAAGT
 ||| ||| |||||
 AGC AGTC ACCTTTCA
 AAC ____
 GAM1863 JAK2 3' TGACCTTCATTCTGAGACCAA 18318 CAG AA
 TTGGTT GGGATGGA GTCA
 ||||| ||||| |||
 AACCAG TCTTACTT CAGT
 AG_ C_
 GAM1863 HSA250839 3' GTGACCCCCATTCCCCAAAGCA 37852 G CA AAA
 A TTG TT GGGGATGG GTCAC
 ||| || ||||| |||||
 AAC AA CCCTTACC CAGTG
 G AC CC_
 GAM1863 KIAA1958 5' GTGACTTTGAACCCCAAACC 82788 CA ATGG
 GGTT GGGG AAAGTCAC
 ||| ||| |||||
 CCAA CCCC TTTCAGTG
 A_ AAG_
 GAM1863 MARCKS 3' ACTTTCCACCCTGCCCA 11411 TT GA
 TGG CAGGG TGGAAAGT
 ||| ||||| |||||
 ACC GTCCC ACCTTTCA
 C_ _
 GAM1863 MGC16025 3' TGACCCTCCACCTGCACC 53028 T _ T AAA
 GGT CAGG GGA GG GTCA
 ||| ||||| ||| |||
 CCA GTCC CCT CC CAGT
 C A _ _
 GAM1863 LOC256073 5' ACCTTCCATCCCCCATCCA 98483 TTCA A
 TGG GGGGATGGAA GT
 ||| ||||| ||| |||
 ACC CCCCTACCTT CA
 TACC C
 GAM1864 VAT1 3' TAACCAAGGCTGCCTCTT 22091 A C C
 AAGA GC GCC TGGTTG
 ||||| ||| |||||
 TTCT CG CGG ACCAAT
 C T A
 GAM1864 AP3M2 3' CATGTGCAGAAGTAGCTTCT 23300 CG CCTGG
 AGAAGC C TTGCACATG
 ||||| | |||||
 TCTTCG G GACGTGTAC
 AT AA_
 GAM1864 FLJ12505 5' GTCAACAAGAGCGGCTTC 45717 C G C
 GAAGCCGC CT GTTG AC
 ||||| || ||| ||

CTTCGGCG GA CAAC TG
A A _
GAM1864 KIAA0275 3' CATGTGTTCAAAGAACGGTTTC 29324 CC GGTT
TT AAGAAGCCG CT GCACATG
||||||| || |||||
TTCTTTGGC GA TGTGTAC
AA AACT
GAM1864 KIAA0830 3' GCATCCAAACGGCTTCTT 70268 CCC T
AAGAAGCCG TGG TGC
||||||| ||| |||
TTCTTCGGC ACC ACG
AA_ T
GAM1864 KIAA1399 3' CATGTGCAATGCCAGCCCCTTC 70790 CC CC _
GAAG GC TGGT TGCACATG
||| || ||| |||||
CTTC CG ACCG ACGTGTAC
CC _ TA
GAM1864 KIAA1643 3' CATATGCATAGAAACGGCTTCT 65154 CC_ GT C
AGAAGCCG CTG TGCA ATG
||||||| ||| ||| |||
TCTTCGGC GAT ACGT TAC
AAA _ A
GAM1864 MAGE-E1 3' GCACCCTAGGCGGCTTCTT 48675 CT T
AAGAAGCCGCC GG TGC
||||||| ||| |||
TTCTTCGGCGG CC ACG
AT C
GAM1864 MRPS2 3' CATGTGCAGAACGGCCCCTT 32631 AA CCCTGG
AAG GCCG TTGCACATG
||| ||| |||||
TTC CGGC GACGTGTAC
CC AA____
GAM1864 SSTK 3' CATGCGCATCCGCGATTTC 50169 GC CCT T A
GAA CGC GG TGC CATG
||| ||| ||| ||| |||
CTT GCG CC ACG GTAC
A_ _ T C
GAM1864 LOC148887 3' CATGCGCATTAAAGCAGGGCGG 85396 A _ G _ _ A
GCTCCT AG AGCC GCCCTG T TGC CATG
|| ||| ||||| | ||| |||
TC TCGG CGGGAC A ACG GTAC
C G G AATT C
GAM1864 LOC152402 5' GTGCCAGAGCCGGCTTCT 86884 _ C TT
AGAAGCCG C CTGG GCAC
||||||| | ||| |||
TCTTCGGC G GACC CGTG
C A _
GAM1864 LOC158078 3' CATGTGTGTTGAGAGCTTCT 82600 CGCC GGT
AGAAGC CT TGCACATG
||||| || |||||

			TCTTCG GA GTGTGTAC		
			A__ GTT		
GAM1864	LOC163882	3'	CATAGGCAACCAAGGCTTC 83040	CC C	AC
			GAAG GC CTGGTTGC ATG		
			CTTC CG GACCAACG TAC		
			AC A GA		
GAM1864	LOC200138	3'	CATGTGCTTCCAGGGTGGCTTC 91539		TT
			GAAGCCGCCCTGG GCACATG		
			CTTCGGTGGGACC CGTGTAC		
			TT		
GAM1864	LOC51099	3'	CAACCAGGCAGCCTTCTT 32600	_ C C	
			AAGAAG C GCC TGGTTG		
			TTCTTC G CGG ACCAAC		
			C A _		
GAM1865	GCNT2	3'	CCTTAACAGTCACCACTGTGC 9453		CC
			GCACGGTGGTGA CTGT GGG		
			CGTGTCACCACTGACA TCC		
			AT		
GAM1865	MAPK7	3'	CCTGAGCCACCACCGAGC 12309	A	ACT TC
			GC CGGTGGTG G CGGG		
			CG GCCACCAC C GTCC		
			A __ GA		
GAM1865	MAPK7	3'	CCTGAGCCACCACCGAGC 58160	A	ACT TC
			GC CGGTGGTG G CGGG		
			CG GCCACCAC C GTCC		
			A __ GA		
GAM1865	MAPK7	3'	CCTGAGCCACCACCGAGC 58162	A	ACT TC
			GC CGGTGGTG G CGGG		
			CG GCCACCAC C GTCC		
			A __ GA		
GAM1865	MAPK7	3'	CCTGAGCCACCACCGAGC 58164	A	ACT TC
			GC CGGTGGTG G CGGG		
			CG GCCACCAC C GTCC		
			A __ GA		
GAM1865	PYGB	3'	CCCTGACCACCACTGTGC 12690	ACT C	
			GCACGGTGGTG GTC GGG		
			CGTGTCACCAC CAG CCC		
			__ T		
GAM1865	RORB	5'	CATCAAACAGTCACCACC 23586	CCGG	
			GGTGGTGA CTGT GATG		

CCACCACTGACA CTAC
 AAA_
 GAM1865 HMG17L1 5' CATCCCACTGCCATCATCACCA 41048 C CT CC_
 TGC GCA GGTGGTGA GT GGGATG
 ||| ||||| || |||||
 CGT CCACTACT CG CCCTAC
 A AC TCA
 GAM1865 KIAA1856 3' CCCAAGGCCTCCCACCGTGC 94228 T CT C_
 GCACGGTGG GA GTC GGG
 ||||| || ||| |||
 CGTGCCACC CT CGG CCC
 _ C_ AA
 GAM1865 KIAA1879 5' CTGTCTGCAGTCACCACCGGC 73940 A C_
 GC CGGTGGTGA CTGT CGG
 || ||||| ||||| |||
 CG GCCACCACTGACG GTC
 _ TCT
 GAM1865 SCYA22 3' CCCTTGGTCACCTCCGTGC 92586 T TCC
 GCACGG GGTGACTG GGG
 ||||| ||||| |||
 CGTGCC CCACTGGT CCC
 T T_
 GAM1865 LOC92609 3' CATCCAGACGCCACACCTGC 73206 C G AC C
 GCA GGTG TG TGTC GGGATG
 ||| ||| || ||| |||||
 CGT CCAC AC GCAG CCCTAC
 _ _ C_ A
 GAM1866 CHAD 3' GGAAGGCTGAGCCTCTC 8855 TA CTGC
 GAGAG CTC GTCTTCC
 |||| ||| |||||
 CTCTC GAG CGGAAGG
 C_ T_
 GAM1866 DSG1 5' AGGAAGGCAGAAACACCTC 10449 A ACTC GT
 GAG GT CTGC CTCCT
 ||| || ||| |||||
 CTC CA GACG GAAGGA
 _ CAAA _
 GAM1866 MID1 3' AAGATGTAGAAGTCCCTC 6351 T_ C
 GAG ACT CTGCGTCTT
 ||| ||| |||||
 CTC TGA GATGTAGAA
 CC A
 GAM1866 OTOF 3' AGGAAGACTCCTGAAACCCTC 17828 A AC CTGC
 GAG GT TC GTCTTCT
 ||| || ||| |||||
 CTC CA AG CAGAAGGA
 C A_ TCCT
 GAM1866 RNMT 3' AGGACATCCAAGGGTACTCTC 15047 T GCGTCT
 GAGAGTAC CCT TCCT
 ||||| ||| |||

		CTCTCATG GGA AGGA	
		_ ACCTAC	
GAM1866	SCN3A	5' AGGAAGACACGTTATACCCT	23612 A CTCC C
		AG GTA TG GTCTTCCT	
		TC CAT GC CAGAAGGA	
		C ATT_ A	
GAM1866	SFRS7	3' GGAAGGCGATACTCTC	60148 CTCCTG
		GAGAGTA CGTCTTCC	
		CTCTCAT GCGGAAGG	
		A_____	
GAM1866	SLC13A4	5' AAGACGAAGGAGGACTCTC	25857 A G
		GAGAGT CTCCT CGTCTT	
		CTCTCA GAGGA GCAGAA	
		G A	
GAM1866	SSX2	3' AGGAAGATGACGAGTAACTC	97962 _ CTG
		GAGT ACTC CGTCTTCCT	
		CTCA TGAG GTAGAAGGA	
		A CA_	
GAM1866	TGFBR2	3' AAGATTCAAGAGTATTCTC	13725 C C
		GAGAGTACTC TG GTCTT	
		CTCTTATGAG AC TAGAA	
		A T	
GAM1866	TNFRSF11A	3' AGGAAGACCCCGGCATTCTC	15187 A CC_ C
		GAGAGT CT TG GTCTTCCT	
		CTCTTA GG AC CAGAAGGA	
		C CCC _	
GAM1866	AP3M2	3' AGGAAGACCCGTA CTCTC	23299 TCCT C
		GAGAGTAC G GTCTTCCT	
		CTCTCATG C CAGAAGGA	
		____C	
GAM1866	CALN1	3' AGGAAGACACAGAATTCTTTC	49658 TACTC C
		GAGAG CTG GTCTTCCT	
		CTTTC GAC CAGAAGGA	
		TTAA_ A	
GAM1866	DAMS	5' AGGAAATTCAAGTACTCT	42084 CC C C
		AGAGTACT TG GT TTCCT	
		TCTCATGA AC TA AAGGA	
		__ T _	
GAM1866	DKFZP727M111	5' AGGCCAGGAGGACCCTC	32055 A A C
		GAG GT CTCCTG GTCT	

CTC CA GAGGAC CGGA
 C G _
 GAM1866 FLJ14486 5' AGGAAGGTTCAAGTCTCTC 52434 T CC CG
 GAGAG ACT TG TCTTCCT
 ||||| ||| || |||||
 CTCTC TGA AC GGAAGGA
 _ _ TT
 GAM1866 FUSIP1 3' AGGAAGACAGCCATAGTCTC 22780 T CCT _
 GAG ACT GC GTCTTCCT
 ||| ||| || |||||
 CTC TGA CG CAGAAGGA
 _ TAC A
 GAM1866 HIC 3' GAAGATTGAGTACTCT 68048 CTGC
 AGAGTACTC GTCTTC
 ||||| |||||
 TCTCATGAG TAGAAG
 T__
 GAM1866 IL22R 3' AGGAAATGCAGGGAAACTC 41467 AC C
 GAGT TCCTGCGT TTCCT
 ||| ||||| |||||
 CTCA GGGACGTA AAGGA
 AA _
 GAM1866 KIAA0472 3' AGGAGGGGTAAGTACTCTC 72334 CC G
 GAGAGTACT TGC TCTTCCT
 ||||| ||| |||||
 CTCTCATGA ATG GGGAGGA
 _ _
 GAM1866 KIAA1229 3' AGGATGTAAAAGTTCTCTC 62750 T CC
 GAGAG ACT TGC GTCTT
 ||||| ||| |||||
 CTCTC TGA ATGTAGGA
 T AA
 GAM1866 LAK-4P 3' AGGAAGACAGTTTCGCCTCTC 24394 TACTCCT _
 GAGAG GC GTCTTCCT
 |||| || |||||
 CTCTC TG CAGAAGGA
 CGCTT_ A
 GAM1866 MRPS35 3' AGGTCCTCAGGAGTATTCTC 41819 CGTCTT
 GAGAGTACTCCTG CCT
 ||||| ||||| |||
 CTCTTATGAGGAC GGA
 TCCT__
 GAM1866 OBTP 5' AGGATCTGCAAGGAGGACCCTC 34663 A A _ TCT
 GAG GT CTCCT GCG TCCT
 ||| || ||||| ||| |||||
 CTC CA GAGGA CGT AGGA
 C G A CT_
 GAM1866 RI58 3' AGATCAGGAATACTCTT 25774 C C
 GAGAGTA TCCTG GTCT
 ||||| ||||| |||||

		TTCTCAT AGGAC TAGA		
		A _		
GAM1866 SMBP	3'	AAGACAGAAAGTGTACTCTC 72620	TC GC_	
		GAGAGTAC CT GTCTT		
		CTCTCATG GA CAGAA		
		T_ AGA		
GAM1866 SNTG1	5'	AGGACTCTGAGGAGTACTCTT 39099	G TCT	
		GAGAGTACTCCT CG TCCT		
		TTCTCATGAGGA GT AGGA		
		_ CTC		
GAM1866 SNX11	3'	AGGACCAGGAGTATCTC 26169	G C	
		GAGA TACTCCTG GTCTT		
		CTCT ATGAGGAC CAGGA		
		- -		
GAM1866 TTY7	3'	AGGAAGACACAGGTAGCT 50015	ACT C	
		AGT CCTG GTCTTCCT		
		TCG GGAC CAGAAGGA		
		AT_ A		
GAM1866 LOC123872	5'	GGAAAGAGGGTACTCTC 74710	_ GCGTC	
		GAGAGTACTC CT TTCC		
		CTCTCATGGG GA AAGG		
		A _____		
GAM1866 LOC138389	3'	AGGAAGACTTGCAAGTCTCTC 76725	T CC _	
		GAGAG ACT TGC GTCTTCCT		
		CTCTC TGA ACG CAGAAGGA		
		- _ TT		
GAM1866 LOC143943	3'	AGGAAGATCAGCAGCCTCTC 83911	TA C C	
		GAGAG CT CTG GTCTTCCT		
		CTCTC GA GAC TAGAAGGA		
		C_ C _		
GAM1866 LOC145009	5'	AAGAAACAAAGGAGTACTTTC 60965	GCG_	
		GAGAGTACTCCT TCTT		
		CTTTCATGAGGA AGAA		
		AACAA		
GAM1866 LOC147976	5'	AGGAAGACTGGGGTACCCTC 79285	A TGC	
		GAG GTACTCC GTCTTCCT		
		CTC CATGGGG CAGAAGGA		
		C T_		
GAM1866 LOC151512	3'	AGGAAGACAATGCTTGTACCTC 86611	A TCCT _	
		GAG GTAC GC GTCTTCCT		

		CTC CATG CG CAGAAGGA		
		_ TT_ TAA		
GAM1866	LOC158801 3'	GAAAACACAAGAAGTATTCT 88255	_ C C C	
		AGAGTACT C TG GT TTC		
		TCTTATGA G AC CA AAG		
		A A A A		
GAM1866	LOC206426 3'	GAAGCGAGGTGCACTCTC 91099	ACT G T	
		GAGAGT CCT CG CTTC		
		CTCTCA GGA GC GAAG		
		CGT _ _		
GAM1866	LOC254337 5'	GGAAAGGGGAGTATCTC 98012	G GCGTC	
		GAGA TACTCCT TTCC		
		CTCT ATGAGGG AAGG		
		_ GA_		
GAM1866	LOC256790 5'	AGTGCAGGAGTGCCCTC 96489	A T	
		GAG GTACTCCTGCG CT		
		CTC CGTGAGGACGT GA		
		C _		
GAM1866	LOC256946 3'	AGGAAGACAGCCATAGTCTC 96182	T CCT _	
		GAG ACT GC GTCTTCCT		
		CTC TGA CG CAGAAGGA		
		_ TAC A		
GAM1866	LOC257396 5'	GAAATGTAGGAGCATCTC 98922	GTA C	
		GAGA CTCCTGCGT TTC		
		CTCT GAGGATGTA AAG		
		AC_ _		
GAM1866	LOC257408 3'	AGGGCACCAGGAGTACCTC 97797	A C CT	
		GAG GTACTCCTG GT TCCT		
		CTC CATGAGGAC CA GGGA		
		_ _ C_		
GAM1866	LOC257453 3'	AGGAAGATGACGAGTAACTC 82927	_ CTG	
		GAGT ACTC CGTCTTCCT		
		CTCA TGAG GTAGAAGGA		
		A CA_		
GAM1866	LOC51066 3'	AGGAAGATGGCCGACACTCTC 32500	AC CTG	
		GAGAGT TC CGTCTTCCT		
		CTCTCA AG GTAGAAGGA		
		C_ CCG		
GAM1867	IRS1 3'	CCATAGATGGTTCTCAATTGTA 19874	C TGAAC	
		TACA ATTGAGAACC ATGG		

		ATGT TAACTCTTGG	TACC	
		— TAGA_		
GAM1867	SERPINF1	3'	CCTGTAAGGTTTCAATG	12038 A GA T
			CATTGAGA CCT ACA GG	
			GTAAC TTT GGA TGT CC	
			— A_ —	
GAM1867	HSA243396	3'	CCATGTT CAGCAATGTCAATG	37844 GAAC_
			CATTGA CTGAACATGG	
			GTAAC T GACTTGTACC	
			GTAAC	
GAM1867	KIAA1387	3'	CAGGAATTTTCAATATGTA	71444 C —
			TACA ATTGAGAA CCTG	
			ATGT TAACTTTT GGAC	
			A AA	
GAM1867	MGC16063	3'	TTCAAATTC CAATGTGTA	54930 A CC
			TACACATTG GAA TGAA	
			ATGTGTAAC CTT ACTT	
			— AA	
GAM1867	SMCR8	3'	CCATGCTCAGGTTTGACTATGT	59253 TGA_ A
			ACAT GAACCTGA CATGG	
			TGTA TTTGGACT GTACC	
			TCAG C	
GAM1867	UPLC1	3'	CCATGCTAGGCCCAATGT	35227 AGAA AA
			ACATTG CCTG CATGG	
			TGTAAC GGAT GTACC	
			CCC_ C_	
GAM1867	ZNF334	3'	CCATAAGTCAACCCTCAATGT	36637 AACC AC_
			ACATTGAG TGA ATGG	
			TGTA ACTC ACT TACC	
			CCA_ GAA	
GAM1867	LOC145082	3'	TATGGAATGCCCTTAATGTGTA	84196 AACCTGAA
			TACACATTGAG CATG	
			ATGTGTAATTC GTAT	
			CCGTAAG_	
GAM1867	LOC157723	3'	CCAAGTAAGGTTCTCAAATGT	82465 — GA A
			ACATT GAGAACCT AC TGG	
			TGTAA CTCTTGGA TG ACC	
			A A_ A	
GAM1867	LOC219988	5'	CCATGTT CGGCCCAATG	93262 AGAAC
			CATTG CTGAACATGG	

			GTAAC GGCTTGTACC		
			CCCC_		
GAM1868	ABCE1	5'	GGGGATCGTTTTCTCCAGA 60261	C	CTG
			TCTGGAGAAA TG CCTC		
			AGACCTCTTT GC GGGG		
			T TA_		
GAM1868	AKAP13	3'	TGAGGCAGCTGCCTCCTGA 59238	T	AAACT
			TC GGAG GCTGCCTCA		
			AG CCTC CGACGGAGT		
			T CGT_		
GAM1868	AKAP13	3'	TGAGGCAGCTGCCTCCTGA 23090	T	AAACT
			TC GGAG GCTGCCTCA		
			AG CCTC CGACGGAGT		
			T CGT_		
GAM1868	AKAP13	3'	TGAGGCAGCTGCCTCCTGA 24220	T	AAACT
			TC GGAG GCTGCCTCA		
			AG CCTC CGACGGAGT		
			T CGT_		
GAM1868	ALOX12B	5'	GGGCAGCAGCTTTTCCAGA 8537	A	
			TCTGGAGAA CTGCTGCCT		
			AGACCTTTT GACGACGGG		
			C		
GAM1868	BCL7A	3'	GAGGCGGCGTTACCTCCAGA 40984	A_	T
			TCTGGAG AAC GCTGCCTC		
			AGACCTC TTG CGGCGGAG		
			CA _		
GAM1868	CEACAM1	3'	GAGGCTTTCTCCAGG 9930		CTGCT
			TCTGGAGAAA GCCTC		
			GGACCTCTTT CGGAG		

GAM1868	CLDN3	3'	TGGGGCAGCTTCCCCAG 8961	A	ACT
			CTGG GAA GCTGCCTCA		
			GACC CTT CGACGGGGT		
			C _		
GAM1868	COL10A1	5'	AGGCACCATCTCCAGG 6682	AAC	C
			TCTGGAGA TG TGCCT		
			GGACCTCT AC ACGGA		
			_ C		
GAM1868	CUTL1	3'	GAGCCCCAGTCTCTTCAGA 10348	A	CT C
			TCTGGAGA ACTG GC TC		

		AGACTTCT TGAC CG AG	
		C CC _	
GAM1868	CYBB	3' GAGAGTGTCTTCTCCA 76846	T GC
		TGGAGAAAC GCT CTC	
		ACCTCTTTG TGA GAG	
		— —	
GAM1868	DNASE1	5' GAAGTGCTTCTTCAGA 19072	ACT T C
		TCTGGAGAA GC GC TC	
		AGACTTCTT CG TG AG	
		— — A	
GAM1868	DXYS155E	3' GAGGATGGCTCTCCAGA 18688	AACT _
		TCTGGAGA GCTG CCTC	
		AGACCTCT CGGT GGAG	
		— — A	
GAM1868	EFNA1	3' TGGGGCAGCACTCCCCAGA 16666	A AAC
		TCTGG GA TGCTGCCTCA	
		AGACC CT ACGACGGGGT	
		C C_	
GAM1868	EGR1	3' TGAGCTTCGGTTCTCCAGA 10493	A CT C
		TCTGGAGAA CTG GC TCA	
		AGACCTCTT GGC CG AGT	
		— TT —	
GAM1868	FLT1	3' TGAGGAGAGTTTTCTCCA 10664	_ G G
		TGGAGAAA CT CT CCTCA	
		ACCTCTTT GA GA GGAGT	
		T _ _	
GAM1868	FRK	5' AGCCGGTAAGTCTCTCCAGG 10715	A _ C
		TCTGGAGA ACT GCTG CT	
		GGACCTCT TGA TGGC GA	
		C A C	
GAM1868	GAB2	3' GAGGCAGCATCTCCAGA 25458	AAC
		TCTGGAGA TGCTGCCTC	
		AGACCTCT ACGACGGAG	
		—	
GAM1868	GAB2	3' GAGGCAGCATCTCCAGA 55405	AAC
		TCTGGAGA TGCTGCCTC	
		AGACCTCT ACGACGGAG	
		—	
GAM1868	GP9	3' TGAGGCAGGTCCCCAGA 5725	A AACTG
		TCTGG GA CTGCCTCA	

			AGACC CT GACGGAGT		
			C G_____		
GAM1868	GPC6	5'	AGGCAGCAGCCTTCCCAG 20329	A A_	
			CTGG GAA CTGCTGCCT		
			GACC CTT GACGACGGA		
			_ CC		
GAM1868	GUCA2B	3'	TGAGGCAGCCCAGCTCCTGA 24020	T AAAC	
			TC GGAG GCTGCCTCA		
			AG CCTC CGACGGAGT		
			T GACC_		
GAM1868	GUCY1A3	5'	GAGTCAGTTTTCCAGA 64226	AACT C	
			TCTGGAGA GCTG CTC		
			AGACCTTT TGAC GAG		
			_____ T		
GAM1868	IL8RA	3'	TGAGGCAGGCACTGCCA 7153	_ AAAC _	
			TGG AG TGC TGCCTCA		
			ACC TC ACG ACGGAGT		
			G _____ G		
GAM1868	MADH6	5'	AGGCAGGGCTTTCCAGA 19972	AA TG	
			TCTGGAGA C CTGCCT		
			AGACCTTT G GACGGA		
			CG _		
GAM1868	MGAM	3'	GGGGCAGTTTCTCCAGG 72812	G	
			TCTGGAGAAACTGCT CC		
			GGACCTCTTTGACGG GG		

GAM1868	MYO7A	3'	GAGGCAGCAGTGGGTTTCAGG 6032	GAA	
			TCTGGA ACTGCTGCCTC		
			GGA CTT TGACGACGGAG		
			GGG		
GAM1868	NEUROD2	3'	AGGAGTGCTTCTCCAGG 21592	ACT G	
			TCTGGAGAA GCT CCT		
			GGACCTCTT TGA GGA		
			CG_ _		
GAM1868	NPY2R	3'	TGAACAGAAATTTCTCCAGG 8067	CTG CC	
			TCTGGAGAAA CTG TCA		
			GGACCTCTTT GAC AGT		
			AAA A_		
GAM1868	OXTR	3'	TGAATAGACATTTCTCCA 8083	C _ CC	
			TGGAGAAA TG CTG TCA		

			ACCTCTTT AC GAT AGT	
			_ A A_	
GAM1868	PARK2	3'	GAGGAGCCTTTCCAGA 17078	AACT G
			TCTGGAGA GCT CCTC	
			AGACCTTT CGA GGAG	
			C___ _	
GAM1868	PARK2	3'	GAGGAGCCTTTCCAGA 26542	AACT G
			TCTGGAGA GCT CCTC	
			AGACCTTT CGA GGAG	
			C___ _	
GAM1868	PARK2	3'	GAGGAGCCTTTCCAGA 26546	AACT G
			TCTGGAGA GCT CCTC	
			AGACCTTT CGA GGAG	
			C___ _	
GAM1868	PMCHL1	3'	GAGGTGTTCTCCAGA 49917	ACTGC
			TCTGGAGAA TGCCTC	
			AGACCTCTT GTGGAG	

GAM1868	PPP2R4	3'	TGAGGCATGTCTTTCCAGA 61184	A TGC
			TCTGGAGA AC TGCCTCA	
			AGACCTTT TG ACGGAGT	
			C T__	
GAM1868	PRX	3'	GAGGCAGCCCTTCCAGA 40896	AAACT
			TCTGGAG GCTGCCTC	
			AGACCTT CGACGGAG	
			CC___	
GAM1868	REV3L	5'	TGAGGAAGATTTCTCTCA 12825	_ CTG G
			TG GAGAAA CT CCTCA	
			AC CTCTTT GA GGAGT	
			T A__ A	
GAM1868	RXRA	3'	TGAGGCAGCAGCCTTC 12925	AAA
			GGAG CTGCTGCCTCA	
			CTTC GACGACGGAGT	
			C___	
GAM1868	SIRPB2	3'	GAGAAGCTTCTCTAGA 38272	ACT GC
			TCTGGAGAA GCT CTC	
			AGATCTCTT CGA GAG	
			__ A_	
GAM1868	SIRPB2	3'	GAGAAGCTTCTCTAGA 55858	ACT GC
			TCTGGAGAA GCT CTC	

			AGATCTCTT CGA GAG		
			___ A_		
GAM1868	SURF5	3'	TGAGGCAGCATTTCCTCCA 23130	A C	
			TGGAG AA TGCTGCCTCA		
			ACCTC TT ACGACGGAGT		
			C T		
GAM1868	TAF1C	5'	GAGGCCCATTTTCCAGA 20265	AC CT	
			TCTGGAGAA TG GCCTC		
			AGACCTTTT AC CGGAG		
			___ C_		
GAM1868	VANGL2	3'	TGAGACATCGACTCTCCGGA 72095	AA C C	
			TCTGGAGA CTG TG CTCA		
			AGGCCTCT GGC AC GAGT		
			CA T A		
GAM1868	WARS	3'	GAGGCAGCAGCCCTCGAGG 67865	G AAA	
			TCT GAG CTGCTGCCTC		
			GGA CTC GACGACGGAG		
			G CC_		
GAM1868	ZNF45	5'	GACTTGGCACTTCTCCAGA 14250	AC CC	
			TCTGGAGAA TGCTG TC		
			AGACCTCTT ACGGT AG		
			C_ TC		
GAM1868	ARHF	3'	GGGACAGTTTCTCAGA 39272	G CTG	
			TCTG AGAAACTG CCT		
			AGAC TCTTTGAC GGG		
			___ A_		
GAM1868	BLR1	3'	TGAGGCAGGGAAGTCCCCAGG 9940	A AA_ G	
			TCTGG GA CT CTGCCTCA		
			GGACC CT GG GACGGAGT		
			C GAA _		
GAM1868	BLR1	3'	TGAGGCAGGGAAGTCCCCAGG 53119	A AA_ G	
			TCTGG GA CT CTGCCTCA		
			GGACC CT GG GACGGAGT		
			C GAA _		
GAM1868	C20orf150	3'	TGAAGCCGAGCTCCTCCAGA 66017	AAACT _ C	
			TCTGGAG GCT GC TCA		
			AGACCTC CGA CG AGT		
			CT__ GC A		
GAM1868	C20orf4	3'	GGGCAGCAATCTCTCCAGG 31948	AAC	
			TCTGGAGA TGCTGCCT		

			GGACCTCT ACGACGGG		
			CTA		
GAM1868	C20orf7	3'	TGAATATGCACCTTCTCCAGA 44383	AC	TGCC
			TCTGGAGAA TGC TCA		
			AGACCTCTT ACG AGT		
			CC TATA		
GAM1868	C6orf26	3'	AGAAAGCAGCTTTCTCCA 48268	_	GC
			TGGAGAAA CTGCT CT		
			ACCTCTTT GACGA GA		
			C AA		
GAM1868	CASKIN1	3'	TGAGGCGGATTTCCCCAGA 40784	A	CTG
			TCTGG GAAA CTGCCTCA		
			AGACC CTTT GGCGGAGT		
			C A__		
GAM1868	CCR8	3'	TGAGGCAGATGCCTCTAGA 19041	AA	ACTG
			TCTGGAG CTGCCTCA		
			AGATCTC GACGGAGT		
			CGTA__		
GAM1868	CPGL2	5'	GAAGCCGCTTTGTTCTCCAGA 74884	ACT_	T C
			TCTGGAGAA GC GC TC		
			AGACCTCTT CG CG AG		
			GTTT C A		
GAM1868	CSRP2BP	5'	TGAAGCAGCAGTGGGACCAG 70657	AGAA	C
			CTGG ACTGCTGC TCA		
			GACC TGACGACG AGT		
			AGGG A		
GAM1868	DGKD	3'	TGAAACAACACTTTCTCCAG 60113	C C	CC
			CTGGAGAAA TG TG TCA		
			GACCTCTTT AC AC AGT		
			C A AA		
GAM1868	DKFZP434A043	3'	TGAGGTAGTAATTCCTCAGA 31823	GA	C
			TCTG GAAA TGCTGCCTCA		
			AGAC CTTT ATGATGGAGT		
			TC A		
GAM1868	DKFZP434P0111	3'	TGAGGGTGTCTTTCCAGA 67963	A T	TG
			TCTGGAGA AC GC CCTCA		
			AGACCTTT TG TG GGAGT		
			C _ _		
GAM1868	DKFZP586M1120	3'	TGAGGCAGCAGCTCCCAG 49287	A	AA
			CTGG GA CTGCTGCCTCA		

			GACC CT GACGACGGAGT		
			— C—		
GAM1868	ERG-1	3'	TGAGACATGTTTCTCCAGG 42102	TGC C	
			TCTGGAGAAAC TG CTCA		
			GGACCTCTTTG AC GAGT		
			T— A		
GAM1868	FASTK	3'	TGAGGCAGAAGCTCCAGG 47690	AAACTG	
			TCTGGAG CTGCCTCA		
			GGACCTC GACGGAGT		
			GAA—		
GAM1868	FLJ14855	5'	GGTTCCTCCAGTTTTCCAGA 53766	A CT—	
			TCTGGAGAA CTG GCC		
			AGACCTTTT GAC TGG		
			— CCT		
GAM1868	FLJ20249	3'	TGAGGAGTCCCTCCCAGA 80223	A AACT G	
			TCTGG GA GCT CCTCA		
			AGACC CT TGA GGAGT		
			— CCC—		
GAM1868	FLJ20730	3'	TGAAGAAGCAGTTTCTCAGA 36053	G GCC	
			TCTG AGAAACTGCT TCA		
			AGAC TCTTTGACGA AGT		
			— AGA		
GAM1868	FLJ21007	5'	TGAAGCTTGCACAAGCTCTCCA 48648	AAC— T— C	
	GA		TCTGGAGA TGC GC TCA		
			AGACCTCT ACG CG AGT		
			CGAAC TT A		
GAM1868	FLJ22938	5'	GAGGAGTTTTTCCAGA 45486	GCTG	
			TCTGGAGAAACT CCTC		
			AGACCTTTTTGA GGAG		
			—		
GAM1868	GPT2	3'	TGAGGCAGCAGCCTCTA 56772	AAA	
			TGGAG CTGCTGCCTCA		
			ATCTC GACGACGGAGT		
			C—		
GAM1868	KIAA0515	5'	GAGGAGCTTCTCCAG 64550	ACT G	
			CTGGAGAA GCT CCTC		
			GACCTCTT CGA GGAG		
			— —		
GAM1868	KIAA0542	3'	GGGGCAGCTCCTCCAGG 66665	AAACT	
			TCTGGAG GCTGCCTC		

GGACCTC CGACGGGG
CT___
GAM1868 KIAA0561 3' GAGGGAGCTTTCCAGA 66479 AACT G
TCTGGAGA GCT CCTC
||||||| ||| ||||
AGACCTTT CGA GGAG
___ G
GAM1868 KIAA0652 3' TGAGGCAGCAATCTTTGG 29125 TG AAC
C GAGA TGCTGCCTCA
| |||| |||||
G TTCT ACGACGGAGT
GT A___
GAM1868 KIAA1026 3' GAGACGGCTTTTTCCA 71738 CT C
TGGAGAAA GCTG CTC
||||||| |||||
ACCTTTTT CGGC GAG
___ A
GAM1868 KIAA1030 3' GAGGCAGCAGTGAGCCGAGA 94981 _ AGAA
TCT GG ACTGCTGCCTC
||| || |||||
AGA CC TGACGACGGAG
G GAG_
GAM1868 KIAA1086 3' TGAGGCAGGGGGTCCCCA 71291 A AA G
TGG GA CT CTGCCTCA
||| || |||||
ACC CT GG GACGGAGT
C GG _
GAM1868 KIAA1277 3' GAGGCAGGTTCTCAGA 65077 G ACTG
TCTG AGAA CTGCCTC
||||| |||||
AGAC TCTT GACGGAG
_ G___
GAM1868 KIAA1322 3' TGAGATAGTTTTTCCAGA 73118 CTGC
TCTGGAGAACTG CTCA
||||||| |||||
AGACCTTTTGTAT GAGT
A___
GAM1868 KIAA1634 3' GCATCAGTCTCTTCTCCAGA 64124 ___ C
TCTGGAGAA ACTG TGC
||||||| |||||
AGACCTCTT TGAC ACG
CTC T
GAM1868 KIAA1638 3' TGAAACAACGGTGACCTCTCCA 47824 A___ C CC
GG TCTGGAGA ACTG TG TCA
||||||| ||||| |||||
GGACCTCT TGGC AC AGT
CCAG A AA
GAM1868 KIAA1742 3' AGGTATTTCTCCAGA 78137 CTGC
TCTGGAGAAA TGCCT
||||||| |||||

AGACCTCTTT ATGGA

GAM1868 KIAA1771 5' GGGTTACCAGACCTCTCCAGA 79866 AA_ CT_
TCTGGAGA CTG GCCT
||||||| ||| ||||
AGACCTCT GAC TGGG
CCA CAT

GAM1868 KIAA1831 5' GGAGCAGTCTCTCCGGA 64525 A G
TCTGGAGA ACTGCT CC
||||||| ||||| ||
AGGCCTCT TGACGA GG
C _

GAM1868 KIAA1894 3' GAGGCAACCTTTGCCTTCTTCA 74285 ACT _____
GA TCTGGAGAA GC TGCCTC
||||||| || |||||
AGACTTCTT CG ACGGAG
C_ TTTCCA

GAM1868 KIAA1937 3' GAGGCAGTGTCCCCCAGG 74071 AGAA T
TCTGG AC GCTGCCTC
||||| || |||||
GGACC TG TGACGGAG
CCC_ _

GAM1868 KIAA1985 3' TGAAAAGCACTTTCTCCA 45018 C GCC
TGGAGAAA TGCT TCA
||||||| ||| |||
ACCTCTTT ACGA AGT
C AA_

GAM1868 LCHN 3' TGAGATGCTTTCTCCAGA 87480 CT TGC
TCTGGAGAAA GC CTCA
||||||| || |||
AGACCTCTTT CG GAGT
_ TA_

GAM1868 MGC13007 3' CAGTTCAGTTATCTCCAGA 51277 _ _
TCTGGAGA AACTG CTG
||||||| ||||| |||
AGACCTCT TTGAC GAC
A TT

GAM1868 MGC16385 5' TGAAGCAGCAGCTGGGCTAGG 59543 AGAAA C
TCTGG CTGCTGC TCA
||||| ||||| |||
GGATC GACGACG AGT
GGGTC A

GAM1868 MGC26914 3' TGAATAGACATTTCTCCA 59332 C _ CC
TGGAGAAA TG CTG TCA
||||||| || ||| |||
ACCTCTTT AC GAT AGT
_ A A_

GAM1868 MRPL20 3' AGGCATTTTTTCCAGA 36199 CTGC
TCTGGAGAAA TGCCT
||||||| |||||

		AGACCTTTTT	ACGGA		
		T__			
GAM1868	NCX	5'	GAGGCCACTCTCCGA	32944	AAC CT
			TCTGGAGA TG GCCTC		
			AGGCCTCT AC CGGAG		
			C__		
GAM1868	PPP1R13B	3'	TGAGGCCCTTTCTCCAG	31660	CTGCT
			CTGGAGAAA GCCTCA		
			GACCTCTTT CGGAGT		
			CC__		
GAM1868	PSKH1	3'	AGGCTCCAGCCTCTCCAGA	68791	AA CT
			TCTGGAGA CTG GCCT		
			AGACCTCT GAC CGGA		
			CC CT		
GAM1868	PTPLA	3'	AGGTGCTTTTTTCCAGA	27266	CT T
			TCTGGAGAAA GC GCCT		
			AGACCTTTTT CG TGGA		
			— —		
GAM1868	SEMA4G	5'	GGGCAGCTGTCTCCAGA	96330	AACT
			TCTGGAGA GCTGCCT		
			AGACCTCT CGACGGG		
			GT__		
GAM1868	SPAF	3'	TGAAGCGATTTCTTTTCCAGA	83521	CTGC_ C
			TCTGGAGAAA TGC TCA		
			AGACCTTTTT GCG AGT		
			CTTTA A		
GAM1868	SUN1	3'	TGAGTTTCCCAGTTTCTACAGA	47926	G CTGC_
			TCTG AGAAACTG CTCA		
			AGAC TCTTTGAC GAGT		
			A CCTTT		
GAM1868	TSPAN-2	3'	GGGTCAGTTTCTCAGA	20375	G CT
			TCTG AGAAACTG GCCT		
			AGAC TCTTTGAC TGGG		
			— —		
GAM1868	USP24	3'	TGAAAATGCTGTGTTCTCCAGA	92795	_ T TGCC
			TCTGGAGAA AC GC TCA		
			AGACCTCTT TG CG AGT		
			G T TAAA		
GAM1868	LOC123096	3'	TGAGGCAGACACTCCAG	74654	AAAC _
			CTGGAG TG CTGCCTCA		

	GACCTC AC GACGGAGT	
	_____ A	
GAM1868 LOC129831 5'	TGAGACAGCAGCGGTGGCAGA 75398	GAGAA _____
	TCTG ACTGCTGC CTCA	
	AGAC TGGCGACG GAGT	
	GG_____ ACA	
GAM1868 LOC134637 3'	TGAGAACACCTTCTCCAGG 75693	AC CTGC
	TCTGGAGAA TG CTCA	
	GGACCTCTT AC GAGT	
	CC AA_____	
GAM1868 LOC146420 3'	TGAACTTCCAGATTCTCCAGA 84653	A CTGCC
	TCTGGAGAA CTG TCA	
	AGACCTCTT GAC AGT	
	A CTTCA	
GAM1868 LOC147711 5'	TGAGCAGGCAAGTCTCTTCAGA 79117	A _ GC
	TCTGGAGA ACT GCT CTCA	
	AGACTTCT TGA CGG GAGT	
	C A AC	
GAM1868 LOC148753 3'	TGAGACTCCATTTTCTCCAGG 85373	C CTGC
	TCTGGAGAAA TG CTCA	
	GGACCTCTTT AC GAGT	
	T CTCA	
GAM1868 LOC150290 3'	TGAGGCAGATGGTGCCCAGA 80592	AGAA _
	TCTGG ACTG CTGCCTCA	
	AGACC TGGT GACGGAGT	
	CG_____ A	
GAM1868 LOC153218 5'	TGAAATAGAACTTTTCCAGA 81658	ACTG CC
	TCTGGAGAA CTG TCA	
	AGACCTTTT GAT AGT	
	CAA_ AA	
GAM1868 LOC153769 3'	AGGCAGCATTTCAGA 81805	AAAC
	TCTGGAG TGCTGCCT	
	AGACTTT ACGACGGA	

GAM1868 LOC157570 5'	TGAGGCTTTTCTTCAGA 82397	CTGCT
	TCTGGAGAAA GCCTCA	
	AGACTTCTTT CGGAGT	
	TT_____	
GAM1868 LOC197259 5'	TGAGGCAGTGGCCTCCGGA 89304	AAA TG
	TCTGGAG C CTGCCTCA	

	AGGCCTC G GACGGAGT	
	C__GT	
GAM1868 LOC199923 3'	TGAGTTAGCCAGTTTCTTCAGA 89879	_ C
	TCTGGAGAACTG CTG CTCA	
	AGACTTCTTTGAC GAT GAGT	
	C T	
GAM1868 LOC200940 3'	TGAGGCAGGCGGATCTCCTGA 90398	T AA _
	TC GGAGA CTGC TGCCTCA	
	AG CCTCT GGCG ACGGAGT	
	T A_ G	
GAM1868 LOC201685 3'	AGGAGCTATTTTCCAGA 91834	ACT G
	TCTGGAGAA GCT CCT	
	AGACCTTTT CGA GGA	
	AT_ _	
GAM1868 LOC205327 3'	AGTCAATGTTTCTCCAGA 91067	TGC C
	TCTGGAGAAAC TG CT	
	AGACCTCTTTG AC GA	
	TA_ T	
GAM1868 LOC221288 3'	TGAAGCAGCAGTATCTAGA 95264	GAA C
	TCTGGA ACTGCTGC TCA	
	AGATCT TGACGACG AGT	
	A__ A	
GAM1868 LOC222057 3'	AGGTCAGCCTCTCCAGG 94345	AACT _
	TCTGGAGA GCTG CCT	
	GGACCTCT CGAC GGA	
	C__ T	
GAM1868 LOC222057 3'	GAGTCAGCCTCTCCAGG 94354	AACT C
	TCTGGAGA GCTG CTC	
	GGACCTCT CGAC GAG	
	C__ T	
GAM1868 LOC253254 5'	TGAGAAGAACTTCTTCAGA 98908	ACTG GC
	TCTGGAGAA CT CTCA	
	AGACTTCTT GA GAGT	
	CAA_ A_	
GAM1868 LOC254672 3'	GAGGTGTTCTCCAGA 96295	ACTGC
	TCTGGAGAA TGCCTC	
	AGACCTCTT GTGGAG	

GAM1868 LOC255975 3'	GAGTCAGCCTCTCCAGG 97582	AACT C
	TCTGGAGA GCTG CTC	

		GGACCTCT CGAC GAG	
		C__ T	
GAM1868	LOC256789 3'	TGAGGCTGTACTCTCTAGA 99312	AAC T
		TCTGGAGA TGC GCCTCA	
		AGATCTCT ATG CGGAGT	
		C__ T	
GAM1868	LOC257336 5'	GGGCCCTAGTCCTCCAGA 97900	AA CT
		TCTGGAG ACTG GCCT	
		AGACCTC TGAT CGGG	
		C_ CC	
GAM1868	LOC257449 3'	AGGTATTTCTCCAGA 63373	CTGC
		TCTGGAGAAA TGCCT	
		AGACCTCTTT ATGGA	

GAM1868	LOC91923 5'	AGAGTTCCAGTTTCTCCA 68169	CT _
		TGGAGAAACTG GC CT	
		ACCTCTTTGAC TG GA	
		CT A	
GAM1868	LOC92876 5'	AGAGTTCCAGTTTCTCCA 71346	CT _
		TGGAGAAACTG GC CT	
		ACCTCTTTGAC TG GA	
		CT A	
GAM1868	LOC93496 3'	TGAAACAGACTTACACTTCTTC 72863	ACTG__ CC
	AGA	TCTGGAGAA CTG TCA	
		AGACTTCTT GAC AGT	
		CACATTCA AA	
GAM1869	HAL 5'	GCCACTCCTGCATAAAGCTC 10903	TGAAAA
		GAGCTTTATGC GGTGGC	
		CTCGAAATACG TCACCG	
		TCC__	
GAM1869	HMG2 3'	GGCCACCTTGGCACAAAAGC 19809	A C AA
		GCTTT TG TG AAGGTGGCC	
		CGAAA AC AC TTCCACCGG	
		_ _ GG	
GAM1869	NMI 5'	GGCCACCTCCTCAGGAAG 17436	ATG AA
		CTTT CTGA AGGTGGCC	
		GAAG GACT TCCACCGG	
		_ _ CC	
GAM1869	PACE 3'	GGCCACCTCTCCAAGGGCTT 11944	A CT AAA
		GAGCTTT TG GA GGTGGCC	

		TTCGGGA AC CT CCACCGG	
		_ CT _	
GAM1869 PYCR1	3'	CCACCTTCCTCTAGAGCTC 70639	TGCT A_
		GAGCTTTA GA AAGGTGG	
		CTCGAGAT CT TTCCACC	
		_ CC	
GAM1869 SDC1	3'	GGCCACCTCCCCAGCATTCCAG 12991	TT_ AAA
C		GCT ATGCTG AGGTGGCC	
		CGA TACGAC TCCACCGG	
		CCT CCC	
GAM1869 FLJ11560	5'	GCCCAGGCCCAGCATAAAG 48008	AAAA _
		CTTTATGCTG GGT GGC	
		GAAATACGAC CCG CCG	
		_ GAC	
GAM1869 KIAA0446	5'	CCACCTTTTGAAGAGCTC 69446	ATGCTG
		GAGCTTT AAAAGGTGG	
		CTCGAGA TTTTCCACC	
		AG_	
GAM1869 KIAA0971	3'	GTTGTTCTCAGCATAAAGT 30677	AAA TG
		GCTTTATGCTGA GG GC	
		TGAAATACGACT TT TG	
		C_ GT	
GAM1869 KIAA1393	3'	GGCCACCTTGGCACAAAAGC 72574	A C AA
		GCTTT TG TG AAGGTGGCC	
		CGAAA AC AC TTCCACCGG	
		_ _ GG	
GAM1869 KIAA1656	3'	GGCCACCTCCTCCTAGAAGCC 66377	A ATGCT AA
		G GCTTT GA AGGTGGCC	
		C CGAAG CT TCCACCGG	
		_ ATC_ CC	
GAM1869 KIAA1884	3'	GCCACCTTCATCTACCAAGGCT 73728	ATGCT A_
C		GAGCTTT GA AAGGTGGC	
		CTCGGAA CT TTCCACCG	
		CCAT_ AC	
GAM1869 PP3501	3'	GGCCACCGTTGACAGCATAAAG 41683	AAAA_
		CTTTATGCTG GGTGGCC	
		GAAATACGAC CCACCGG	
		AGTTG	
GAM1869 SDCCAG3	3'	GGTGTTCCTCAGCATGAAGCTC 22803	AAA TG
		GAGCTTTATGCTGA GG GCC	

			CTCGAAGTACGACT CT TGG		
			____ TG		
GAM1869	SP140	3'	GGCCACCTCCATGCAGAAGC 24327	A	TGAAA
			GCTTT TGC AGGTGGCC		
			CGAAG ACG TCCACCGG		
			_ TACC_		
GAM1869	LOC148760	3'	GGCCACCTTCTCCAACAAGCTC 85364	TA	CT A
			GAGCTT TG GA AAGGTGGCC		
			CTCGAA AC CT TTCCACCGG		
			CA _ C		
GAM1869	LOC150170	5'	ACCTGTTTCACATAAAGC 80414	C	_
			GCTTTATG TGAAA AGGT		
			CGAAATAC ACTTT TCCA		
			_ G		
GAM1869	LOC150175	5'	ACCTGTTTCACATAAAGC 80453	C	_
			GCTTTATG TGAAA AGGT		
			CGAAATAC ACTTT TCCA		
			_ G		
GAM1869	LOC150215	5'	ACCTGTTTCACATAAAGC 80456	C	_
			GCTTTATG TGAAA AGGT		
			CGAAATAC ACTTT TCCA		
			_ G		
GAM1869	LOC150218	5'	ACCTGTTTCACATAAAGC 80525	C	_
			GCTTTATG TGAAA AGGT		
			CGAAATAC ACTTT TCCA		
			_ G		
GAM1869	LOC152065	3'	GGCCACCTTCTCCTTGGCAGGC 86737	TTA	____ A
			TC GAGCT TGCT GA AAGGTGGCC		
			CTCGG ACGG CT TTCCACCGG		
			____ TTC C		
GAM1869	LOC152267	3'	GGCCACCTTGGCACAAAAGC 61036	A	C AA
			GCTTT TG TG AAGGTGGCC		
			CGAAA AC AC TTCCACCGG		
			_ _ GG		
GAM1869	LOC158292	5'	CCTCTGGACCCAGCATAAGGCT 88046	AAAA_	T
			C GAGCTTTATGCTG GG GG		
			CTCGGAATACGAC TC CC		
			CCAGG T		
GAM1869	LOC219997	3'	GCCACCTCTTCAGCCTC 93256	CTTTAT	A
			GAG GCTGAA AGGTGGC		

		CTC	CGACTT TCCACCG		
			C		
GAM1869	LOC256269	3'	GGCCACCTTGGCACAAAAGC	96608	A C AA
			GCTTT TG TG AAGGTGGCC		
			CGAAA AC AC TTCCACCGG		
			_ _ GG		
GAM1869	LOC91963	5'	GGCCACCTCCTCTGAGAAGC	68321	ATGCT AA
			GCTTT GA AGGTGGCC		
			CGAAG CT TCCACCGG		
			AGT_ CC		
GAM1870	CHRNA2	3'	GCTCAGTCCCACAGCCCCTTG	7443	AA T A
			CAGG GTT TGGGACT AGC		
			GTTC CGA ACCCTGA TCG		
			CC C C		
GAM1870	DSC3	3'	GCCTAGTTGCTGAAATTTCTG	44627	A TG_ A
	CTG		CA CAGGAAGTTT G GACTA GC		
			GT GTCCTTTAAA C TTGAT CG		
			C GT G C		
GAM1870	DSC3	3'	GCCTAGTTGCTGAAATTTCTG	44628	A TG_ A
	CTG		CA CAGGAAGTTT G GACTA GC		
			GT GTCCTTTAAA C TTGAT CG		
			C GT G C		
GAM1870	EHD4	3'	CCCTGGCAAAACTTCCCGTT	58364	A _
			AAC GGAAGTTTT GGG		
			TTG CCTTCAAAA CCC		
			C CGGT		
GAM1870	HCFC1	3'	AGCCCAACTTCCTGTTG	71544	TT A
			CAACAGGAAGT TGGG CT		
			GTTGTCCTTCA ACCC GA		
			_ _		
GAM1870	HOXD4	5'	GCCCAGTCCCAGCTCTGCCCT	28262	A_ TT AA
			AGG AG TTGGGACT GC		
			TCC TC GACCCTGA CG		
			CG TC CC		
GAM1870	KCNQ1	3'	GCCCAGTCCCAGCAGCCAGCC	5843	AA_ _ AA
			GG GTT TTGGGACT GC		
			CC CGA GACCCTGA CG		
			GAC C CC		
GAM1870	RFP	3'	CTCAGCCTGGCTTCCT	22508	TT A A
			AGGAAGTT GGG CT AG		

		TCCTTCGG TCC GA TC	
		— — C	
GAM1870	SCN4A	3' GCTCAACCTTCCAACCTCCTGT 6203	TT_ ACTA
		ACAGGAAGTT GGG AGC	
		TGTCCTTCAA TCC TCG	
		CCT AAC_	
GAM1870	SEPN1	3' CTCAGCCAGGCTCCCTGT 66969	A TG A A
		ACAGG AGTTT GG CT AG	
		TGTCC TCGGA CC GA TC	
		C — — C	
GAM1870	SLC14A1	3' GCTCAGTCCCCACTTCCTG 32414	TTT A
		CAGGAAGT GGGACT AGC	
		GTCCTTCA CCCTGA TCG	
		C_ C	
GAM1870	SLC16A2	3' CCTAGTTACTATCCTGTCA 22522	A _ T_
		C ACAGGA AGT TTGGG	
		A TGTCTTCA GATCC	
		C A TT	
GAM1870	SOCS4	5' CCCAGAAGAACTTCCTGCTG 55991	A _____
		CA CAGGAAGT TTTGGG	
		GT GTCCTTCA AGACCC	
		C AAGA	
GAM1870	TADA2L	3' TTAAAACACTCCTGTTG 56766	A_
		CAACAGGA GTTTTGGG	
		GTTGTCCT CAAAATTT	
		CA	
GAM1870	BTN1A1	3' AGTCTGTTTCTTCCTGTTG 9965	TTTTG
		CAACAGGAAG GGA CT	
		GTTGTCCTTC TCTGA	
		TTTG_	
GAM1870	EPB41L1	3' GCTTAGTCCTTATCTCCCT 71110	A TTTT
		AGG AG GGGACTAAGC	
		TCC TC TCCTGATTCG	
		C TAT_	
GAM1870	FLJ13224	3' TCCAAGACAAAACCTTCCTGT 46025	_____
		ACAGGAAGTTTTG GGA	
		TGTCCTTCAAAAC CCT	
		AGAA	
GAM1870	H-plk	5' CCTAAATAAAACCTTCCTGTTG 32378	T_____
		CAACAGGAAG TTTGGG	

		GTTGTCCTTC	AAATCC		
		CAAAAT			
GAM1870	KIAA0451	5'	GCCTGTCCAAAATCTCCCATTG 29774	CA AG	G TAA
			CAA GGA TTTTGG AC GC		
			GTT CCT AAAACC TG CG		
			AC CT _ TC_		
GAM1870	KIAA0775	5'	CTCAGCCAAGGACTTCCTGT 28954	G A A	
			ACAGGAAGTTTT GG CT AG		
			TGTCCTTCAGGA CC GA TC		
			A _ C		
GAM1870	KIAA0828	3'	GCTTCCTGAAACTTCCTG 82117	TG CTA	
			CAGGAAGTTT GGA AGC		
			GTCCTTCAAA CCT TCG		
			GT _		
GAM1870	KIAA1036	3'	GCTCAGTCCCAGCTCTGCCTGT 30493	A TT	A
		TG	CAACAGG AG TTGGGACT AGC		
			GTTGTCC TC GACCCTGA TCG		
			G TC C		
GAM1870	KIAA1492	3'	CTCAGTCACCCTCCTGTT 65125	A TTTT _	A
			AACAGGA G GG GACT AG		
			TTGTCCT C CC CTGA TC		
			_ _ _ A C		
GAM1870	KIAA1726	3'	CTTAATTATTACTCCTGTTG 67830	A TTTGG	C
			CAACAGGA GT GA TAAG		
			GTTGTCCT CA TT ATTC		
			_ TTA_ A		
GAM1870	KIAA1924	3'	GCCCAGTCCCCGGGGCTCTGCT 74050	A GA	_ AA
		G	CA CAG AGTTTTGGG ACT GC		
			GT GTC TCGGGGCC TGA CG		
			C _ C CC		
GAM1870	SARM	3'	GCCCAGCCCAGCAGCTTCTGTT 31295	G _	A AA
		G	CAACAG AAGTT TTGGG CT GC		
			GTTGTC TTCGA GACCC GA CG		
			_ C _ CC		
GAM1870	SHARP	3'	GCTCAGTCGGCCAGACTTCCT 31103	T _	A
			AGGAAGTTT GG GACT AGC		
			TCCTTCAGA CC CTGA TCG		
			_ GG C		
GAM1870	LOC126661	3'	GCCTAGCCCCAGCTTCT 75058	TT A A	
			GGAAGT TGGG CTA GC		

	TCTTCG ACCC GAT CG		
	— C C		
GAM1870 LOC130497 5'	CTCAGCCCCAGGACCTCT 75447	A	A A
	GGA GTTTTGGG CT AG		
	TCT CAGGACCC GA TC		
	C C C		
GAM1870 LOC146894 3'	CTTAGTCCCACGGTCTCCTG 59860	AG TT	
	CAGGA T TGGGACTAAG		
	GTCCT G ACCCTGATTC		
	CT GC		
GAM1870 LOC151242 3'	GCTTAATCCTTGATGTCCT 80978	A TT C	
	AGGA GTT GGGA TAAGC		
	TCCT TAG TCCT ATTCG		
	G T_ A		
GAM1870 LOC153277 3'	CTAGTCCTCTTCCTGT 87188	TTTT A	
	ACAGGAAG GGGACTA G		
	TGTCCTTC TCCTGAT C		
	— C		
GAM1870 LOC153743 3'	CCTTTAAAATTCCTGTTG 61131	G T_	
	CAACAGGAA TTT GGG		
	GTTGTCCTT AAA TCC		
	A TT		
GAM1870 LOC158572 3'	CTTAGTGATCAACTTCCTG 82850	TT G_	
	CAGGAAGT TGG ACTAAG		
	GTCCTTCA ACT TGATTC		
	— AG		
GAM1870 LOC197342 3'	CCCAACGACCTTCCTGTT 89355	— —	
	AACAGGAAG TT TTGGG		
	TTGTCCTTC AG AACCC		
	C C		
GAM1870 LOC254413 5'	CTTATCTACAAACTTCC 98912	— C	
	GGAAGTTTTG GGA TAAG		
	CCTTCAAAAC TCT ATTC		
	A _		
GAM1870 LOC255252 3'	GCTGAGTCAAAGCCTCCTGTTG 96708	A GG A	
	CAACAGGA GTTTT GACT AGC		
	GTTGTCCT CGAAA CTGA TCG		
	C _ G		
GAM1870 LOC90092 3'	GCTTAATCACACTTCCTG 62065	TTTGG C	
	CAGGAAGT GA TAAGC		

GTCCTTCA CT ATTCG
 CA__ A
 GAM1870 LOC90297 5' GCCCAGCCCCGGGGCCCTCACT 62850 _ A_ A AA
 G CAG GA GTTTTGGG CT GC
 ||| || ||||| || ||
 GTC CT CGGGGCCC GA CG
 A CC C CC
 GAM1870 LOC90362 5' GCTCAGTTCATGCAATTCCTG 63114 A TTG_ A
 CTG CA CAGGAAGTT GGA CT AGC
 || ||||| |||| ||
 GT GTCCTTTAA CTTGA TCG
 C CGTA C
 GAM1871 ALDH8A1 3' CCACTAGCATGGCTAATTGAT 42914 A TCTAC
 ATCAATTA CT AGTGG
 ||||| || ||||
 TAGTTAAT GG TCACC
 C TACGA
 GAM1871 PARK2 3' CCACTGTAAATTTAATAGAT 17076 A C C
 ATC ATTAA TT TACAGTGG
 ||| |||| || |||||
 TAG TAATT AA ATGTCACC
 A T _
 GAM1871 PARK2 3' CCACTGTAAATTTAATAGAT 26540 A C C
 ATC ATTAA TT TACAGTGG
 ||| |||| || |||||
 TAG TAATT AA ATGTCACC
 A T _
 GAM1871 PARK2 3' CCACTGTAAATTTAATAGAT 26544 A C C
 ATC ATTAA TT TACAGTGG
 ||| |||| || |||||
 TAG TAATT AA ATGTCACC
 A T _
 GAM1871 BCMP1 3' CCTCTGAAGTTAACTGATG 49537 A TAC T
 CATCA TTA ACTTC AG GG
 |||| ||||| || ||
 GTAGT AATTGAAG TC CC
 C _ T
 GAM1871 C3orf4 3' CTA CTGTAGCAATTGA 39592 AACTT
 TCAATT CTACAGTGG
 |||| |||||
 AGTTAA GATGTCATC
 C_
 GAM1871 CDC14B 3' CCACCTAAGAAGTTGATCAATG 53987 CA ACA
 CAT ATTA ACTTCT GTGG
 ||| ||||| ||||
 GTA TAGTTGAAGA CACC
 AC ATC
 GAM1871 CDC14B 3' CCACCTAAGAAGTTGATCAATG 14773 CA ACA
 CAT ATTA ACTTCT GTGG
 ||| ||||| ||||

		GTA TAGTTGAAGA CACC	
		AC ATC	
GAM1871	DKFZP434F0318	3' CCACTGTAGCAAAATTAATG	48748 C AACTT
		CAT AATT CTACAGTGG	
		GTA TTAA GATGTCACC	
		A AAC__	
GAM1871	FBX09	3' CCACTGTTACTTTTAATTGA	54243 CTTCT
		TCAATTAA ACAGTGG	
		AGTTAATT TGTCACC	
		TTCAT	
GAM1871	FLJ10520	3' CCACTAAAAGAGTAATTGATG	36701 A CTAC
		CATCAATTA CTT AGTGG	
		GTAGTTAAT GAG TCACC	
		_ AAAA	
GAM1871	KIAA0355	3' CCACTGTATATTAATTGA	28704 CTTC
		TCAATTAA TACAGTGG	
		AGTTAATT ATGTCACC	
		AT__	
GAM1871	NET-2	3' CCACCTGGACAATAATTGATG	25621 ACT CA
		CATCAATTA TCTA GTGG	
		GTAGTTAAT AGGT CACC	
		AAC C_	
GAM1871	PRO0971	3' CCACTATATTGACTTTTAATTGA	38316 CT TAC__
	T	ATCAATTAA TC AGTGG	
		TAGTTAATT AG TCACC	
		TC TTATA	
GAM1871	RGS13	3' TACTGTAGTAGTCAATTAATG	59237 C A T
		CAT AATT ACT CTACAGTG	
		GTA TTAA TGA GATGTCAT	
		A C T	
GAM1871	RGS13	3' TACTGTAGTAGTCAATTAATG	12868 C A T
		CAT AATT ACT CTACAGTG	
		GTA TTAA TGA GATGTCAT	
		A C T	
GAM1871	LOC115110	3' CCACTGTGGCGTTTCATCGAT	72174 AATT_ TT
		ATC AAC CTACAGTGG	
		TAG TTG GGTGTCACC	
		CTACT C_	
GAM1871	LOC147057	3' CCACTGTAAATTGAGGATAAT	84976 A ____
		ATTA CTTC TACAGTGG	

TAAT GGAG ATGTCACC
 A TTAA
 GAM1871 LOC222070 5' CCACTGTGGTACAGTCAAT 95810 A T__
 ATT ACT CTACAGTGG
 ||| ||| |||||
 TAA TGA GGTGTCACC
 C CAT
 GAM1871 LOC51134 5' AGAAAATGTTAATTGATG 32791 ____
 CATCAATTAAC TTCT
 ||||| |||
 GTAGTTAATTG AAGA
 TAA
 GAM1871 LOC90459 3' CCACTAGTGAAGTTAGTCAAT 63551 CA T _
 AT ATTA ACTTC AC AGTGG
 || ||||| || ||||
 TA TGATTGAAG TG TCACC
 AC _ A
 GAM1872 ELF3 3' TGACCTTGACCTTGACCAA 16685 T GAT AAA
 TTGGT CAAGG GG GTCA
 |||| |||| || ||||
 AACCA GTTCC TC CAGT
 _ AGT ____
 GAM1872 JAK2 3' TGACCTTCATTCTGAGACCAA 18318 CAA AA
 TTGGTT GGGATGGA GTCA
 |||| ||||| |||
 AACCAG TCTTACTT CAGT
 AG_ C_
 GAM1872 SLC10A2 5' ACTCTCTGTCTTGACCAA 6590 CAA A
 TTGGTT GGGATGGA AGT
 |||| ||||| |||
 AACCAG TTCTGTCT TCA
 ____ C
 GAM1872 FLJ10803 3' GTGACTTTCAGTTAAAGCCAA 37205 CAAGG G
 TTGGTT GAT GAAAGTCAC
 |||| || |||||
 AACCGA TTG CTTTCAGTG
 AA__ A
 GAM1872 KIAA1958 5' GTGACTTTGAACCCCAAACC 82788 CAA ATGG
 GGTT GGG AAAGTCAC
 ||| ||| |||||
 CCAA CCC TTTCAGTG
 A__ CAAG
 GAM1872 MARCKS 3' ACTTTCCACCCTGCCCA 11411 TTCA A
 TGG AGGG TGGAAAGT
 || ||| |||||
 ACC TCCC ACCTTTCA
 CG__ _
 GAM1872 TUB 5' GTGGGACCATCCCTTAAACC 13898 C AAAG
 GGTT AAGGGATGG TCAC
 ||| ||||| |||

			CCAA TTCCCTACC GGTG		
			A AG__		
GAM1872	LOC80298	3'	ACTTTTACCTTGAACCA 48062	GATG	
			TGGTTCAAGG GAAAGT		
			ACCAAGTTCC TTTTCA		
			A__		
GAM1873	GPD1	3'	TCATGCCACCACATTTG 60398	C C	
			TAAATG GGTGGCAT GA		
			GTTTAC CCACCGTA CT		
			A _		
GAM1873	IL5RA	5'	TCGCATGGCCACCGCATTT 6906	AT__	
			AAATGCGGTGGC CGA		
			TTTACGCCACCG GCT		
			GTAC		
GAM1873	MYO1C	3'	TGCCGATGCCAATATTTG 61873	CGG A	
			TAAATG TGGCATCG CA		
			GTTTAT ACCGTAGC GT		
			AA_ C		
GAM1873	C6orf37	3'	TGTCACACTGCATTTA 68097	GCATC	
			TAAATGCGGTG GACA		
			ATTTACGTAC CTGT		
			A__		
GAM1873	DNAJC6	3'	TTGCAGAACCACCGCATT 29498	CA GA	
			AATGCGGTGG TC CAA		
			TTACGCCACC AG GTT		
			A_ AC		
GAM1873	FLJ11210	3'	GTCGATGTGCATGCTTTTA 60319	T GTG	
			TAAA GCG GCATCGAC		
			ATTT CGT TGTAGCTG		
			T ACG		
GAM1873	FLJ12476	3'	TCGATCTTCTGCATTTA 43270	T C	
			TAAATGCGG GG ATCGA		
			ATTTACGTC TC TAGCT		
			T _		
GAM1873	KIAA1034	3'	TCGATGGCATCCGCATTTG 63134	_ G	
			TAAATGCGG TG CATCGA		
			GTTTACGCC AC GTAGCT		
			T G		
GAM1873	KIAA1987	3'	TCATGTAAGTGCATTTA 89391	G C	
			TAAATGCGGT GCAT GA		

	ATTACGTCA TGTA CT		
	A _		
GAM1873 MGC16063 3'	TGTCCTGGCCACTGCATT 54929	ATC	
	AATGCGGTGGC GACA		
	TTACGTCACCG CTGT		
	GTC		
GAM1873 LOC147949 3'	TGTCAGATGTCCACATTGCA 79279	— _ _	
	TGCG GTGG CATC GACA		
	ACGT CACC GTAG CTGT		
	TA T A		
GAM1873 LOC150577 3'	GTCCTCACCGCATTTG 86258	CATC	
	TAAATGCGGTGG GAC		
	GTTTACGCCACT CTG		
	C_		
GAM1873 LOC158219 3'	TGTGTGTCACCACATTT 82694	C CG	
	AAATG GGTGGCAT ACA		
	TTTAC CCACTGTG TGT		
	A _		
GAM1873 LOC202020 3'	TGTCTCACCATTTA 90605	C CATC	
	TAAATG GGTGG GACA		
	ATTAC CCACT CTGT		
	A _		
GAM1873 LOC90826 5'	TGTCGATGCAGGTTTATTTG 64788	CGGTG	
	TAAATG GCATCGACA		
	GTTTAT CGTAGCTGT		
	TTGGA		
GAM1873 LOC93587 3'	TTGTCTTTACCTGCATTTA 73042	_ CATC	
	TAAATGC GGTGG GACAA		
	ATTACG CCATT CTGTT		
	T T_		
GAM1874 ALDH3A2 5'	CAGCCCGCTGCCAGAGCCGGGG 69796	ATG_ A	
A	TCCCTGGCTT AGC GGCTG		
	AGGGGCCGAG TCG CCGAC		
	ACCG C		
GAM1874 CASP10 3'	CAGCCTGCTTTCACACTAAGGA 53245	C CTTAT	
	TCC TGG GAGCAGGCTG		
	AGG ATC TTCGTCCGAC		
	A ACACT		
GAM1874 DYT1 3'	CAGCCCACTCATCGCAGGG 5477	G TT CA	
	CCCTG C ATGAG GGCTG		

GGGAC G TACTC CCGAC
_ C_ AC
GAM1874 LPIN1 5' CAGCCTGCTGAGAACTAG 67985 C ATG
CTGG TT AGCAGGCTG
||||| || |||||
GATC AA TCGTCCGAC
_ GAG
GAM1874 TNXB 5' CTCAGCCTTGGGCCAAGCCTGG 51634 CT TA A ____
A TCC GGCT TG GC AGGCTGAG
||| |||| || || |||||
AGG CCGA AC CG TCCGACTC
T_ _ _ GGT
GAM1874 C20orf150 3' CAGCCTGCCCTCAAGCCAAGGA 66009 C ATGA
TCC TGGCTT GCAGGCTG
||| ||||| |||||
AGG ACCGAA CGTCCGAC
A CTCC
GAM1874 C20orf39 5' CAGCCTGCCGGCCAGGCGA 46571 _ TAT A
TC CCTGGCT G GCAGGCTG
|| ||||| | |||||
AG GGACCGG C CGTCCGAC
C _ _ _
GAM1874 CBX6 3' CAGCCTGCCTGAAGCAAAGGA 27407 CTG ATGA
TCC GCTT GCAGGCTG
||| |||| |||||
AGG CGAA CGTCCGAC
AAA GTC_
GAM1874 CD84 3' CTCAGCCTGTAAGCAAAGCAGG 81570 G A A ____
CCTG CTT TG GCAGGCTGAG
||||| || |||||
GGAC GAA AC TGTCCGACTC
_ _ GAA
GAM1874 CYP2D6 3' CAGCCTGCTCCTAGCCCAGAGG 5451 _ C T
CC CTGG TTA GAGCAGGCTG
|| |||| || |||||
GG GACC GAT CTCGTCCGAC
A C C
GAM1874 DKFZP586J0619 3' CTCAGCCTGCCCAGCAGGGA 82317 G TAT A
TCCCTG CT G GCAGGCTGAG
||||| || | |||||
AGGGAC GA C CGTCCGACTC
_ _ _ C
GAM1874 FKHL18 3' CAGCCCTGGTGAGCCAAGGA 80370 C G CA
TCC TGGCTTAT AG GGCTG
||| ||||| || |||||
AGG ACCGAGTG TC CCGAC
A G _
GAM1874 FLJ14800 3' CAACCTGCTCAGGCACACAGA 52684 CC CTTA C
TC TGG TGAGCAGG TG
|| ||| ||||| ||

AG ACC ACTCGTCC AC
 AC ACGG A
 GAM1874 FLJ14957 3' CTCAGCCCCACTCATACCTAGAG 52816 C CT CA
 A TC CTGG TATGAG GGCTGAG
 || ||| ||||| |||||
 AG GATC ATACTC CCGACTC
 A C_ AC
 GAM1874 KIAA1023 3' CAGGCTCAGAAGCCAGGGA 34677 A AGG
 TCCCTGGCTT TGAGC CTG
 ||||| ||| |||
 AGGGACCGAA ACTCG GAC
 G _
 GAM1874 KIAA1655 5' CTCAGCCCCACTCCCAAACCAG 67183 C AT CA
 CTGG TT GAG GGCTGAG
 ||| || ||| |||||
 GACC AA CTC CCGACTC
 A CC AC
 GAM1874 MGC35521 3' CTCAGGTGTCAGTAAGCCAG 59666 GA GG
 CTGGCTTAT GCA CTGAG
 ||||| || |||
 GACCGAATG TGT GACTC
 AC G_
 GAM1874 MGC5508 3' CAGCCTGCCTCACCAGGGA 44264 CTTA _
 TCCCTGG TGAG CAGGCTG
 ||||| ||| |||||
 AGGGACC ACTC GTCCGAC
 _ C
 GAM1874 RIN3 5' CTCAGCCTGCCTCCCCAAGGGA 46162 _ CTTAT _
 TCCCT GG GAG CAGGCTGAG
 |||| || ||| |||||
 AGGGA CC CTC GTCCGACTC
 A C_ C
 GAM1874 SP140 3' AGTATCTCATCAGCCAGGGA 24326 T CAG
 TCCCTGGCT ATGAG GCT
 ||||| ||| |||
 AGGGACCGA TACTC TGA
 C TA_
 GAM1874 VI 3' CAGCCGCTAGGCCAGGGA 26486 ATG A
 TCCCTGGCTT AGC GGCTG
 ||||| ||| |||
 AGGGACCGGA TCG CCGAC
 _ _
 GAM1874 LOC112817 5' CAGTGGCCACAAGTCAGGGA 57319 A A AG
 TCCCTGGCTT TG GC GCTG
 ||||| || |||
 AGGGACTGAA AC CG TGAC
 C _ G_
 GAM1874 LOC129676 5' CTCAGCCTGCAGACACAGGGA 76232 GCTTATGA
 TCCCTG GCAGGCTGAG
 |||| |||||

		AGGGAC	CGTCCGACTC		
		ACAGA__			
GAM1874	LOC134266 3'	CTCAGCCTACCAAGTAGCCAGG	75644	TATGAGC	
		CCTGGCT	AGGCTGAG		
		GGACCGA	TCCGACTC		
		TGAACCA			
GAM1874	LOC150248 3'	CCCCTCATCAGCCAGGGA	86127	T CA	
		TCCCTGGCT	ATGAG GG		
		AGGGACCGA	TACTC CC		
		C CA			
GAM1874	LOC155179 3'	CAGGCTCAGAAGCCAGGGA	82225	A AGG	
		TCCCTGGCTT	TGAGC CTG		
		AGGGACCGAA	ACTCG GAC		
		G _			
GAM1874	LOC158056 5'	CTCAGCCCAGGAGAGCCAGGGG	82589	ATGAGCA	
		TCCCTGGCTT	GGCTGAG		
		GGGGACCGAG	CCGACTC		
		AGGAC__			
GAM1874	LOC219405 3'	CAGCCTGCTCTACCCAGAGA	92450	C CTTAT	
		TC CTGG	GAGCAGGCTG		
		AG GACC	CTCGTCCGAC		
		A CAT__			
GAM1874	LOC221496 3'	TCAGCCTGCTCCCTGGGA	93643	T CTTAT	
		TCCC GG	GAGCAGGCTGA		
		AGGG CC	CTCGTCCGACT		
		T _			
GAM1874	LOC222031 3'	CAGCCTGTCTAACCCAAAGA	95672	CC C T G	
		TC TGG TTA	GA CAGGCTG		
		AG ACC AAT	CT GTCCGAC		
		AA C _ _			
GAM1874	LOC51320 3'	CTGCAACTAATAAGCCAAGGA	34028	C GA__	
		TCC TGGCTTAT	GCAG		
		AGG ACCGAATA	CGTC		
		A ATCAA			
GAM1875	ELF3 3'	TGACCTTGACCTTGACCAA	16685	T GAT AAA	
		TTGGT CAAGG	GG GTCA		
		AACCA GTTCC	TC CAGT		
		_ AGT _			
GAM1875	JAK2 3'	TGACCTTCATTCTGAGACCAA	18318	CAA AA	
		TTGGTT	GGGATGGA GTCA		

			AACCAG TCTTACTT CAGT		
			AG_ C_		
GAM1875	SLC10A2	5'	ACTCTCTGTCTTGACCAA 6590	CAA	A
			TTGGTT GGGATGGA AGT		
			AACCAG TTCTGTCT TCA		
			___ C		
GAM1875	FLJ10803	3'	GTGACTTTTCAGTTAAAGCCAA 37205	CAAGG	G
			TTGGTT GAT GAAAGTCAC		
			AACCGA TTG CTTTCAGTG		
			AA___ A		
GAM1875	KIAA1958	5'	GTGACTTTGAACCCCAAACC 82788	CAA	ATGG
			GGTT GGG AAAGTCAC		
			CCAA CCC TTTTCAGTG		
			A___ CAAG		
GAM1875	MARCKS	3'	ACTTTCCACCCTGCCCA 11411	TTCA	A
			TGG AGGG TGGAAAGT		
			ACC TCCC ACCTTTCA		
			CG___ _		
GAM1875	TUB	5'	GTGGGACCATCCCTTAAACC 13898	C	AAAG
			GGTT AAGGGATGG TCAC		
			CCAA TTCCCTACC GGTG		
			A AG___		
GAM1875	LOC80298	3'	ACTTTTACCTTGAACCA 48062	GATG	
			TGGTTCAAGG GAAAGT		
			ACCAAGTTCC TTTTCA		
			A___		
GAM1876	EHF	3'	TCCAAAACCCAAGGTTGGCT 25127	AT	_ C
			AGT GCCT GGGT TTGGA		
			TCG TGGG CCGA AACCT		
			GT A A		
GAM1876	EPHA2	3'	CCATCGGCCAAGAATACTTGAA 16675	GC G	T_
	G		CTTCAAGTAT CT GGTC TGG		
			GAAGTTCATA GA CCGG ACC		
			A_ A CT		
GAM1876	ITGA5	3'	CCCAGAGACATACTTGAAG 61933	C___	
			CTTCAAGTATG CTGGG		
			GAAGTTCATAC GACCC		
			AGA		
GAM1876	TREM2	3'	TCCAAGACTGTCATATTT 39098	CCTG	
			AAGTATG GGTCTTGGA		

TTTATAC TCAGAACCT
 TG__
 GAM1876 UQCRB 3' CCAACATAGGCATACTTAAG 21939 C GGTC
 CTT AAGTATGCCTG TTGG
 ||| ||||| |||
 GAA TTCATACGGAT AACC
 _ AC__
 GAM1876 ATP10D 3' CAGAGACCACTTGAAG 73526 ATGCCTG _
 CTTCAAGT GGTCT TG
 ||||| ||||| ||
 GAAGTTCA CCAGA AC
 G
 GAM1876 B3GNT7 3' CCCTTCCAGGCAACCTGAA 71678 A A TCTT
 TTCA GT TGCCTGGG GG
 ||| || ||||| ||
 AAGT CA ACGGACCT CC
 C _ TC__
 GAM1876 DKFZp547I224 3' TCCAAAATTGACCACATACTTG 39963 CCTG ____
 GA TTCAAGTATG GGTC TTGGA
 ||||| ||| |||||
 AGGTTCATAC CCAG AACCT
 A__ TTAA
 GAM1876 FLJ22341 3' CCAAGCTCAGGCACACCCAAG 45114 CAA A T
 CTT GT TGCCTGGG CTTGG
 ||| || ||||| |||||
 GAA CA ACGGACTC GAACC
 CC_ C _
 GAM1876 KIAA0779 3' CCGAACAGCATACTTGAAG 86908 C GGTC
 CTTCAAGTATGC TG TTGG
 ||||| || |||||
 GAAGTTCATACG AC AGCC
 _ A__
 GAM1876 LOC144233 3' CCAAGGCACATAATTGAA 77246 G CCTGG
 TTCAA TATG GTCTTGG
 |||| ||| |||||
 AAGTT ATAC CGGAACC
 A A__
 GAM1876 LOC147341 3' ACCCAGGCATAACTGAAG 85116 AG
 CTTCA TATGCCTGGGT
 |||| |||||
 GAAGT ATACGGACCCA
 CA
 GAM1876 LOC221088 5' TCCAAGGTGCTGGCCACTCGAA 94888 A AT TGGG
 G CTTC AGT GCC TCTTGGA
 ||| ||| ||| |||||
 GAAG TCA CGG GGAACCT
 C C_ TCGT
 GAM1877 ACP1 3' GAAGAGAGAAACATTTAT 16287 G C
 GTGAG GT TCTCTCTTC
 |||| || |||||

			TATTT CA AGAGAGAAG		
			A A		
GAM1877	ACP1	3'	GAAGAGAGAAACATTTAT 24013	G C	
			GTGAG GT TCTCTCTTC		
			TATTT CA AGAGAGAAG		
			A A		
GAM1877	AQP1	3'	AAGAAAGGGACCCACCTGCT 6357	TGA C	
			AGCAG GGGTCTCT TCTT		
			TCGTC CCCAGGGA AGAA		
			CA_ A		
GAM1877	ARHG	5'	GAAGAGAGAGGAGGCACTGC 9792	AGGG	
			GCAGTG TCTCTCTCTTC		
			CGTCAC GGAGAGAGAAG		
			GGA_		
GAM1877	ARHG	5'	GAAGAGAGAGGAGGCACTGC 77089	AGGG	
			GCAGTG TCTCTCTCTTC		
			CGTCAC GGAGAGAGAAG		
			GGA_		
GAM1877	ATP6V0A4	5'	GAAGAGAGAGAGACACAGC 40551	A AGGG	
			GC GTG TCTCTCTCTTC		
			CG CAC AGAGAGAGAAG		
			A AG__		
GAM1877	EN1	5'	GGAAGTCAAACCCCTCACTACT 9249	C TCTCTCT	
	G		CAG AGTGAGGG CTTCC		
			GTC TCACTCCC GAAGG		
			A CAACT_		
GAM1877	FSTL1	3'	AAGAGAACCACCCCACTCTG 24002	C A CTC	
			CAG AGTG GGGT TCTCTT		
			GTC TCAC CCCA AGAGAA		
			_ _ CCA		
GAM1877	GAPD	3'	GGAAGAGAGAGACCCTCACTGC 10756		
	TG		CAGCAGTGAGGGTCTCTCTCTTCC		
			GTCGTCACCTCCAGAGAGAGAAGG		
GAM1877	KCNAB1	3'	AAGAGAGGGCTACACTGCT 61582	AG T	
			AGCAGTG GGTC CTCTCTT		
			TCGTCAC TCGG GAGAGAA		
			A_ _		
GAM1877	KIF2	3'	GGATACCCAGAACCCTCACTAC 16931	C C CTCT_	
	TG		CAG AGTGAGGGT TCT TCC		

			GTC TCACTCCCA AGA AGG		
			A _ CCCAT		
GAM1877 LILRA3	3'	GAAGAGAGAACAATGCACCATT 97019	CA AGG_ C		
G		CAG GTG GT TCTCTCTTC			
		GTT CAC CA AGAGAGAAG			
		AC GTAA _			
GAM1877 MAL	3'	GAAAGAAAGATCCTCTGCTG 42601	GT C C		
		CAGCA GAGGGTCT TCT TTC			
		GTCGT CTCCTAGA AGA AAG			
		_ A _			
GAM1877 MAL	3'	GAAAGAAAGATCCTCTGCTG 42602	GT C C		
		CAGCA GAGGGTCT TCT TTC			
		GTCGT CTCCTAGA AGA AAG			
		_ A _			
GAM1877 MAL	3'	GAAAGAAAGATCCTCTGCTG 42603	GT C C		
		CAGCA GAGGGTCT TCT TTC			
		GTCGT CTCCTAGA AGA AAG			
		_ A _			
GAM1877 MAL	3'	GAAAGAAAGATCCTCTGCTG 11431	GT C C		
		CAGCA GAGGGTCT TCT TTC			
		GTCGT CTCCTAGA AGA AAG			
		_ A _			
GAM1877 MBNL	3'	AAGAGAGAAAGAACTATACT 41065	A G _		
		AGTG GG TC TCTCTCTT			
		TCAT TC AG AGAGAGAA			
		A A AA			
GAM1877 NHLH1	3'	GAAGAAATGAACTCACTGC 20018	GG TCTC		
		GCAGTGAG TC TCTTC			
		CGTCACTC AG AGAAG			
		A_ TAA_			
GAM1877 PAK4	3'	AGATGAGACCCTACTACTG 20824	C G _		
		CAG AGT AGGGTCTC TCT			
		GTC TCA TCCCAGAG AGA			
		A _ T			
GAM1877 PARK2	3'	GAAGAGAAAGTACAACCACT 17077	AGG _ C		
		AGTG GT CT TCTCTTC			
		TCAC CA GA AGAGAAG			
		CAA T A			
GAM1877 PARK2	3'	GAAGAGAAAGTACAACCACT 26541	AGG _ C		
		AGTG GT CT TCTCTTC			

		TCAC CA GA AGAGAAG		
		CAA T A		
GAM1877 PARK2	3'	GAAGAGAAAGTACAACCACT	26545	AGG _ C
		AGTG GT CT TCTCTTC		
		TCAC CA GA AGAGAAG		
		CAA T A		
GAM1877 PIK3C2B	5'	GAAGAGAGAGGTTCACTGT	12098	GG
		GCAGTGAG TCTCTCTCTTC		
		TGTCAC TT GGAGAGAGAAG		
		—		
GAM1877 RFC2	5'	GGAAGAGAGAGACCCTCACTGC	12843	
TG		CAGCAGTGAGGGTCTCTCTCTCC		
		GTCG TCACTCCCAGAGAGAGAAGG		
GAM1877 RNF28	3'	GGTAGGACCCTCACCGCTG	51851	A CT
		CAGC GTGAGGGTCT CT		
		GTCG CACTCCCAGG GG		
		C AT		
GAM1877 SELL	3'	GAAGAGAGAAATAGCCTGC	7229	TGAGG C
		GCAG GT TCTCTCTTC		
		CGTC TA AGAGAGAAG		
		CGA_ A		
GAM1877 SGT	3'	GGAAGAGAGAGACCTCGGACCT	13040	___ G
GC		GCAG TGAGG TCTCTCTCTCC		
		CGTC GCTCC AGAGAGAGAAGG		
		CAG _		
GAM1877 SYN2	3'	GGAAAACAGACCCTCCCACTG	13500	___ CTCTC
		CAGT GAGGGTCT TTCC		
		GTCA CTCCCAGA AAGG		
		CC CAA_		
GAM1877 TNFSF10	3'	GAGAGAAGAGGCACCACT	15092	AGG _
		AGTG GTCTCT CTCTT		
		TCAC CGGAGA GAGAG		
		CA_ A		
GAM1877 VANGL2	3'	GGAGAGACCCCATCACTG	72093	___
		CAGTGA GGGTCTCTCT		
		GTCAC T CCCAGAGAGG		
		ACC		
GAM1877 AIG-1	3'	AAGAACTCACCTCACTGT	32756	CTCTC
		GCAGTGAGGGT TCTT		

TGTCACTCCCA AGAA
 CTCA_
 GAM1877 C21orf100 3' GAAGAAAGCAATCCTGCTG 59505 T GG T CTC
 CAGCAG GA G CT TCTTC
 ||||| || | || |||||
 GTCGTC CT C GA AGAAG
 _ AA _ A_
 GAM1877 CPR2 3' AAGAAAAAGTCTAGTCACTGCT 48823 G_ T CTC
 AGCAGTGA GG CT TCTT
 ||||| || || |||||
 TCGTCACT TC GA AGAA
 GA T AAA
 GAM1877 DKFZp434E169 3' GAAGAAAGAGTAATTACTG 51077 GGGT C
 CAGTGA CTCT TCTTC
 ||||| |||| |||||
 GTCATT GAGA AGAAG
 AAT_ A
 GAM1877 DKFZP564D116 3' AAGAGAGAAACACTTCTGCTG 72668 T G C
 CAGCAG GAG GT TCTCTCTT
 ||||| ||| || |||||
 GTCGTC TTC CA AGAGAGAA
 _ A A
 GAM1877 ENPP4 3' GAAAAGAGAGACAAGTGCT 30716 GTGAGG C
 AGCA GTCTCTCT TTC
 ||| ||||| |||
 TCGT CAGAGAGA AAG
 GAA_ A
 GAM1877 FLJ12221 3' AGAGCCGGAGACCCCCAC 63217 A _
 GTG GGGTCTCT CTCT
 ||| ||||| |||
 CAC CCCAGAGG GAGA
 C CC
 GAM1877 FLJ20069 3' GGAAGAAAGGATCCACTACT 34954 A_ T C
 AGTG GGGTC CT TCTTCC
 ||| |||| || |||||
 TCAT CCTAG GA AGAAGG
 CA _ A
 GAM1877 FLJ20986 5' AAGAGAGAGAATACCTACAT 44833 _ G_
 GTG AGG TCTCTCTCTT
 ||| ||| |||||
 TAC TCC AGAGAGAGAA
 A ATA
 GAM1877 FLJ22362 3' GAAGAGAGATGCACTAAC 43379 G G C
 GT AG GT TCTCTCTTC
 || || || |||||
 CA TC CG AGAGAGAAG
 A A T
 GAM1877 GRO3 3' GGAAAAGAGAATTTATCATTAC 63185 C GG TC C
 TG CAG AGTGA G TCTCT TTCC
 ||| |||| | |||| |||||

		GTC T TACT T AGAGA AAGG		
		A AT TA A		
GAM1877	KCND1	3' GAAGAGAACCCTCACCTCTG 18345	CA	CTC
		CAG GTGAGGGT TCTCTTC		
		GTC CACTCCCA AGAGAAG		
		TC ____		
GAM1877	KIAA0326	3' GGAAGAAAAGGTCCCACTCACT 64965	_ TC	C_
	G	CAGTGAG GG TCT TCTTCC		
		GTCACTC CC GGA AGAAGG		
		A CT AA		
GAM1877	KIAA0451	3' GAAGAAAGGATCCTGCTG 29773	G	T C
		CAGT AGGGTC CT TCTTC		
		GTCG TCCTAG GA AGAAG		
		_ _ A		
GAM1877	KIAA0451	3' GGAAGAAAAAACGGCTTTCATT 29775		TCTC__
		AGTGAGGGTC TCTTCC		
		T TACTTTCGG AGAAGG		
		CAAAAA		
GAM1877	KIAA0537	3' AAGAGAGAAACTTGACTGC 29924	G	GTC
		GCAGT AGG TCTCTCTT		
		CGTCA TTC AGAGAGAA		
		G AA_		
GAM1877	KIAA0618	3' GAAAGAGAGATCAGACTGTT 29853	GAG	C
		AGCAGT GGTCTCTCT TTC		
		TTGTCA CTAGAGAGA AAG		
		GA_ _		
GAM1877	KIAA0940	3' GGAAAAGAGAGGGCACTGC 30533	AGGG	C
		GCAGTG TCTCTCT TTCC		
		CGTCAC GGAGAGA AAGG		
		G_ A		
GAM1877	KIAA0972	3' GAAGTAAACCCTCACTGT 30680		CTCTCT
		GCAGTGAGGGT CTTC		
		TGTCACTCCCA GAAG		
		AAT__		
GAM1877	KIAA1281	3' GAAGAGAGAGACTTTAACGC 90627	A	G
		GC GT AGGGTCTCTCTCTTC		
		CG CA TTTCAGAGAGAGAAG		
		_ A		
GAM1877	KIAA1573	3' GGAAGAGAGAAAAATCTGCT 63363		TGAGGGTC
		AGCAG TCTCTCTTCC		

TCGTC AGAGAGAAGG
TAAAA__

GAM1877 KIAA1867 5' GGAAGAGAACTAACCACAGC 96484 A AG_ CTC
GC GTG GGT TCTCTTCC
|| ||| ||| |||||
CG CAC TCA AGAGAAGG
A CAA A__

GAM1877 MGC4400 5' GAAGAGAGAGAACATACT 52038 AGGG
AGTG TCTCTCTCTTC
|||| |||||
TCAT AGAGAGAGAAG
ACA_

GAM1877 MGC4606 3' GAAGAGAGAAACCTCAAGCT 44792 AG GTC
AGC TGAGG TCTCTCTTC
||| |||| |||||
TCG ACTCC AGAGAGAAG
A_ AA_

GAM1877 NMT1 3' GGAAATGGAACCCCACTG 41148 CA A CT TCTC
CAG GTG GGGT C TTCC
||| ||| ||| | |||
GTC CAC CCA G AAGG
AC _ AG TA__

GAM1877 NYD-SP16 3' GAAGAGAATTCCATACTG 50058 A TCTC
CAGTG GGG TCTCTTC
|||| ||| |||||
GTCAT CCT AGAGAAG
A TA__

GAM1877 PDE10A 3' AAGAGAGAGAAGTACCACTGT 22841 AGGG_
GCAGTG TCTCTCTCTT
|||| |||||
TGTCAC AGAGAGAGAA
CATGA

GAM1877 RAP2B 5' GGAAGAGAAGTCCAGCCGC 97523 A GA T C
GC GT GGG CT TCTCTTCC
|| || ||| ||| |||||
CG CG CCT GA AGAGAAGG
C A_ _ _

GAM1877 RHOBTB2 5' GGAAGAGATGTGTTCTCACGC 61605 A TCTC_
T AGC GTGAGGG TCTCTTCC
||| ||||| |||||
TCG CACTCCT AGAGAAGG
_ TGTGT

GAM1877 SLC31A2 3' GAAAGAGAGAAAATCACTGCTG 60757 GGG C
CAGCAGTGA TCTCTCTTC
|||||| ||||| |||
GTCGTCCT AGAGAGA AAG
AAA _

GAM1877 SLC37A1 5' GAAGAGAGCAGAGCCACTGC 39090 GA G _
GCAGT GG TCT CTCTCTTC
|||| ||| |||||

CGTCA CC AGA GAGAGAAG
 _ G C
 GAM1877 SMOC1 3' GAAGAAAGAGATTTATATGCTG 42411 GTGA C
 CAGCA GGGTCTCT TCTTC
 |||| ||||| ||||
 GTCGT TTTAGAGA AGAAG
 ATA_ A
 GAM1877 TCL6 3' GAGAGATGGGATCCCACT 40511 A _
 AGTG GGGTCTC TCTCTT
 ||| ||||| |||||
 TCAC CCTAGGG AGAGAG
 _ T
 GAM1877 TCL6 3' GAGAGATGGGATCCCACT 40530 A _
 AGTG GGGTCTC TCTCTT
 ||| ||||| |||||
 TCAC CCTAGGG AGAGAG
 _ T
 GAM1877 TRIM26 5' AGAAGAAGTCCTCACCAGT 14341 A_ TC C
 GC GTGAGGG TCT TCT
 || ||||| ||| |||
 TG CACTCCT AGA AGA
 AC GA _
 GAM1877 TU3A 3' GGTTTGAAGACCCCACTGC 24184 A C TCTT
 GCAGTG GGGTCT TC CC
 ||||| ||||| || ||
 CGTCAC CCCAGA AG GG
 _ _ TTT_
 GAM1877 WBSCR18 3' GAAAGAGGCCCCACGCTG 51262 A A C
 CAGC GTG GGGTCTCT TC
 |||| ||| ||||| ||
 GTCG CAC CCCGGAGA AG
 _ _ A
 GAM1877 ZNF262 3' GGAAAATGACCTTCACTGCTG 18724 TCTCTC
 CAGCAGTGAGGGTC TTCC
 ||||| ||||| ||||
 GTCGTCACCTCCAG AAGG
 TAA_
 GAM1877 ZNF90 5' GGAAAAAACCCTTCACTGT 79468 _ CTCTCTC
 GCAGTGA GGGT TTCC
 ||||| |||| ||||
 TGTCACCT CCCA AAGG
 T AAAA_
 GAM1877 ZnTL2 3' AAGAGAGAAATTATCACT 56865 GG C
 AGTGA GT TCTCTCTT
 |||| || ||||| ||||
 TCACT TA AGAGAGAA
 AT A
 GAM1877 LOC116113 3' GAAGAAACAGCCCCCTCTGCTG 93838 TGA T CTC
 CAGCAG GGG CT TCTTC
 ||||| ||| || |||||

GTCGTC CCC GA AGAAG
 TCC _ CAA
 GAM1877 LOC124216 3' GAAGAGCACCTCACGC 74735 A CTCT
 GC GTGAGGGT CTCTTC
 || ||||| |||||
 CG CACTCCCA GAGAAG
 _ C_
 GAM1877 LOC126353 3' AAGAAAGAGACCCGCTCCT 74987 C GA C
 AG AGT GGGTCTCT TCTT
 || ||| ||||| |||||
 TC TCG CCCAGAGA AGAA
 C _ A
 GAM1877 LOC135293 3' GAAAAGAAAAGACACTGTTG 76683 GAGG C_ C
 CAGCAGT GTCT TCT TTC
 ||||| ||| ||| |||
 GTTGTCA CAGA AGA AAG
 _ AA A
 GAM1877 LOC143425 3' GGAATCAGAGACCCCCAACACT 89016 A_ CTC
 AGTG GGGTCTCT TTCC
 ||| ||||| |||
 TCAC CCCAGAGA AAGG
 AACC CT_
 GAM1877 LOC147976 3' GAATGAAGACCCTCACTGT 79289 _ TC
 GCAGTGAGGGTCT C TC
 ||||| ||| |||
 TGTCACTCCAGAG G AG
 A TA
 GAM1877 LOC148166 5' GAAAGAGAGATTCCAAC 79414 GA C
 GT GGGTCTCTCT TTC
 || ||||| |||
 CA CTTAGAGAGA AAG
 AC _
 GAM1877 LOC152317 3' GAAAAAAGAGACCTGGAGTTG 86828 AGTGA CTC
 CAGC GGGTCTCT TTC
 ||| ||||| |||
 GTTG TCCAGAGA AAG
 AGG_ AAA
 GAM1877 LOC152793 3' GGAGGAGACCCCCACCCTG 81549 CA A T
 CAG GTG GGGTCTC CTCT
 ||| ||| ||||| |||||
 GTC CAC CCCAGAG GAGG
 C_ C _
 GAM1877 LOC158833 3' AGAAGAGACTCATCTGC 82898 TGA C
 GCAG GGGTCTCT TCT
 ||| ||||| |||
 CGTC CTCAGAGA AGA
 TA_ _
 GAM1877 LOC159193 5' GAAAAAAGAGACCGGCGCCTG 83054 CA AG CTC
 CAG GTG GGTCTCT TTC
 ||| ||| ||||| |||

	GTC CGC CCAGAGA AAG		
	__ GG AAA		
GAM1877 LOC163081 3'	GAAAGCAACCCTCACTGT 83311	CT C	
	GCAGTGAGGGT CT TC		
	TGTCACTCCCA GA AG		
	AC A		
GAM1877 LOC196485 3'	GAAAGAGAGATCAGACTGTCA 89072	A GAG C	
	C GCAGT GGTCTCTCT TTC		
	A TGTCA CTAGAGAGA AAG		
	C GA_ _		
GAM1877 LOC200059 3'	AAGAGAGGTGAACTGTTG 89953	GAGGG _	
	CAGCAGT TC TCTCTCTT		
	GTTGTCA AG GGAGAGAA		
	_____ T		
GAM1877 LOC201595 3'	AAGAGAAAGGGTTTTTCCTGC 90418	T T _	
	GCAG GAGGG CTC TCTCTT		
	CGTC CTTTT GGG AGAGAA		
	_ T AA		
GAM1877 LOC201696 3'	AGAGAGACCTGCTGTT 63810	GA	
	AGCAGT GGGTCTCTCT		
	TTGTCTG TCCAGAGAGA		

GAM1877 LOC202986 3'	GAAAGAGAGATCAGACTGTCA 92065	A GAG C	
	C GCAGT GGTCTCTCT TTC		
	A TGTCA CTAGAGAGA AAG		
	C GA_ _		
GAM1877 LOC221354 3'	GAAAGAGAGATCAGACTGTT 94014	GAG C	
	AGCAGT GGTCTCTCT TTC		
	TTGTCA CTAGAGAGA AAG		
	GA_ _		
GAM1877 LOC221596 5'	GAAGAGAGAATGACTGCT 93624	GAGGGTC	
	AGCAGT TCTCTCTTC		
	TCGTCA AGAGAGAAG		
	GTA_____		
GAM1877 LOC253187 3'	GGAAGAGAGAAATGACTGGTG 98904	G GAGG C	
	CA CAGT GT TCTCTCTTCC		
	GT GTCA TA AGAGAGAAGG		
	G G_ A		
GAM1877 LOC256880 5'	GAAGAAAAAGATGCTGCTG 98888	GAGG CTC	
	CAGCAGT GTCT TCTTC		

				GTCTGTCG	TAGA	AGAAG			
				_____	AAA				
GAM1877	LOC257494	5'	AGAAGAAGTCCTCACCAGT	99626	A_	TC	C		
			GC GTGAGGG TCT TCT						
			TG CACTCCT AGA AGA						
			AC GA _						
GAM1877	LOC51027	3'	GAAAAGAGAAGAATCACTCACT	60081	C	_	_	_	C
			ACTG CAG AGTGAG GGT CT CTCT TTC						
			GTC TCACTC CTA GA GAGA AAG						
			A A A A A						
GAM1877	LOC91263	5'	GGAAAAGAGAGGAAAAATTGC	66000		GAGGG			C
			GCAGT TCTCTCT TTCC						
			CGTTA GGAGAGA AAGG						
			AAAA_ A						
GAM1878	SCAMP1	3'	GCTAAATAAATATTCTCC	18013	T	C			
			GGA AATATT ATTTAGC						
			CCT TTATAA TAAATCG						
			C A						
GAM1878	SCAMP1	3'	GCTAAATAAATATTCTCC	54501	T	C			
			GGA AATATT ATTTAGC						
			CCT TTATAA TAAATCG						
			C A						
GAM1878	NX-17	3'	TGAATATCAGCCCCTAATA	40706		ATA_			
			TATTAGGG ATATTCA						
			ATAATCCC TATAAGT						
			CGAC						
GAM1878	LOC161589	3'	GCTAAATGAATATTATCCCTAA	83159					
			TA TATTAGGGATAATATTCATTTAGC						
			ATAATCCCTATTATAAGTAAATCG						
GAM1879	CLECSF2	5'	GCTGATTA AAAAGAAGCAC	18878	A	C			
			GTGC TCTTTTAA CAGC						
			CACG AGAAAATT GTCG						
			A A						
GAM1879	EFNB2	3'	CATTCGGCCTTGTTGAACACAC	15841		CATCTTTTA			
			GTG ACCA GCCGAATG						
			CAC TGGT CGGCTTAC						
			ACAAG_____ TC						
GAM1879	NDUFA6	3'	ATTCAGTGGAAAGATGCAC	11763		TAA	G	C	
			GTGCATCTTT CCA C GAAT						

CACGTAGAAA GGT G CTTA
____ _A
GAM1879 ARTN 5' TTTGGCTAAAAGAGGCAC 55119 A AACC
GTGC TCTTTT AGCCGAA
||||| |||||
CACG AGAAAA TCGGTTT
G ____
GAM1880 CLTCL1 3' CTTGCGCAGCTTGTCTCTTCA 64421 T
TGAAGAGACGAGCTGCG GG
||||| ||
ACTTCTCTGTTCGACGC TC
T
GAM1880 CUL3 3' TCATGTCATCTCTTCA 14574 C AGCT
TGAAGAGA G GCGTGG
||||| | |||||
ACTTCTCT C TGTACT
A ____
GAM1880 GPR86 3' ATCCACATAGATCTATTCA 43901 G CGAG C
TGAA AGA CTG GTGGAT
||||| ||| |||||
ACTT TCT GAT CACCTA
A A__ A
GAM1880 STXBP1 3' AGATCCACACACATCCTC 13472 AC GC C
GAG GA TG GTGGATCT
||| || |||||
CTC CT AC CACCTAGA
__ AC A
GAM1880 YWHAG 3' CTGCTGCAGCTCCCTCCTCA 25941 A AC _TG
TGA GAG GAGCTGC G G
||||| ||||| |
ACT CTC CTCGACG C C
C C_ TGT
GAM1880 KIAA0084 3' CCACAGCCTGTCTCTTC 68705 A GC
GAAGAGACG GCT GTGG
||||| ||| |||
CTTCTCTGT CGA CACC
C ____
GAM1880 KIAA0748 3' AGACCTTAGGCACATCTCTTCA 29611 CGA GCGT A
TGAAGAGA GCT GG TCT
||||| ||| |||
ACTTCTCT CGG CC AGA
ACA ATT_ _
GAM1880 KIAA1463 3' AGATCTATACTCATTCCTTCA 72732 AG C CTGC
TGAAG A GAG GTGGATCT
||||| ||| |||||
ACTTC T CTC TATCTAGA
CT A A____
GAM1880 POLE3 3' ATCCGTTCTCTCTCTTCA 34311 C CT GT
TGAAGAGA GAG GC GGAT
||||| ||| |||

ACTTCTCT CTC TG CCTA
 _ T _
 GAM1880 LOC148898 5' AGATCCACTAGATCGTCGTCTC 85415 A _ G C
 CA TG AGA GACGA CTG GTGGATCT
 || ||| ||||| ||| |||||
 AC TCT CTGCT GAT CACCTAGA
 C G A _
 GAM1880 LOC199704 5' AGACTCCAGCCCATCTCTTCA 89694 CGA CGT GA
 TGAAGAGA GCTG G TCT
 ||||| ||| | |||
 ACTTCTCT CGAC C AGA
 ACC _ TC
 GAM1881 MAP3K4 3' GCGACTGAGAACCGTGACA 20992 AA_ C
 TGTCACGGT AGTC GC
 ||||| ||| ||
 ACAGTGCCA TCAG CG
 AGAG _
 GAM1881 MAP3K4 3' GCGACTGAGAACCGTGACA 22994 AA_ C
 TGTCACGGT AGTC GC
 ||||| ||| ||
 ACAGTGCCA TCAG CG
 AGAG _
 GAM1881 MKI67 5' GCGGACTTTGGGTGCGAC 11597 A G_
 GTC CG TAAAGTCCGC
 ||| || |||||
 CAG GT GTTTCAGGCG
 C GG
 GAM1881 DKFZp762A227 5' GCAGACTTGATTGTGACA 26882 A C
 TGTCACGGT AAGTC GC
 ||||| ||| ||
 ACAGTGTTA TTCAG CG
 G A
 GAM1881 FLJ22679 3' GCGAACTTTACCGTACA 50908 C C
 TGT ACGGTAAAGT CGC
 ||| ||||| |||
 ACA TGCCATTTCA GCG
 _ A
 GAM1881 GPT2 3' GCAGACTCTGACCTGTGGCA 56770 _ AA_ C
 TGTCAC GGT AGTC GC
 ||||| ||| ||| ||
 ACGGTG CCA TCAG CG
 T GTC A
 GAM1881 HSN44A4A 5' GCAGACTTCAGGTCGTGGCA 31735 TA_ C
 TGTCACGG AAGTC GC
 ||||| ||| ||
 ACGGTGCT TTCAG CG
 GGAC A
 GAM1881 LOC148189 5' GCAATTTTACTGCGACA 79450 A CC
 TGTC CGGTAAAGT GC
 ||| ||||| ||

			ACAG GTCATTTTA CG		
			C A_		
GAM1881	LOC200268	3'	GCTCCTTTACCGTGACA 90087	TCC	
			TGTCACGGTAAAG GC		
			ACAGTGCCATTTC CG		
			CT_		
GAM1882	ADAM17	3'	TCCAGCCTGGGTGACAGAGTGA 41847	TG	
	GA		TCTCGCTCTGT CCCAGGCTGGA		
			AGAGTGAGACA GGGTCCGACCT		
			GT		
GAM1882	ADAM17	3'	TCCAGCCTGGGTGACAGAGTGA 41848	TG	
	GA		TCTCGCTCTGT CCCAGGCTGGA		
			AGAGTGAGACA GGGTCCGACCT		
			GT		
GAM1882	ADAT1	3'	TCCAGCCTGGGTGATAGAGCAA 24919 C	TG	
	GA		TCT GCTCTGT CCCAGGCTGGA		
			AGA CGAGATA GGGTCCGACCT		
			A GT		
GAM1882	ADCY2	3'	CCTGGGCAACATAGCAAGA 65646 C C		
			TCT GCT TGTTGCCCAGG		
			AGA CGA ACAACGGGTCC		
			A T		
GAM1882	ADCY2	3'	TCCAGCCTGGGTGACAGAGCGA 65655	TG	
	GA		TCTCGCTCTGT CCCAGGCTGGA		
			AGAGCGAGACA GGGTCCGACCT		
			GT		
GAM1882	AICDA	3'	TCCAGCCTGGGCGACAAGAGC 40698 _		
			GCTCT GTTGCCCAGGCTGGA		
			CGAGA CAGCGGGTCCGACCT		
			A		
GAM1882	AK1	3'	TCCAGCCTGGGTGACAGAGCAA 6641 C	TG	
	GA		TCT GCTCTGT CCCAGGCTGGA		
			AGA CGAGACA GGGTCCGACCT		
			A GT		
GAM1882	ALDH3A2	3'	TCAGCTTGGGCAACAGAGCAAG 69803 C		
	A		TCT GCTCTGTTGCCCAGGCTGG		
			AGA CGAGACAACGGGTTCGACT		
			A		
GAM1882	ALPP	3'	CCTGGGCGACAGAGCGAGA 69415		
			TCTCGCTCTGTTGCCCAGG		

AGAGCGAGACAGCGGGTCC

GAM1882	ANKH	3'	TCCAGCCTGAGCAACAGAGC	55072	C
			GCTCTGTTGC CAGGCTGGA		
			CGAGACAACG GTCCGACCT		
			A		
GAM1882	ANKH	3'	TCCAGCCTGGGTGACAAGAGC	55074	_ TG
			GCTCT GT CCCAGGCTGGA		
			CGAGA CA GGGTCCGACCT		
			A GT		
GAM1882	APAF1	3'	TCCAGCCTGGGTGACATAGCAA	25984	C C TG
	GA		TCT GCT TGT CCCAGGCTGGA		
			AGA CGA ACA GGGTCCGACCT		
			A T GT		
GAM1882	APOC4	3'	CCTGGGCAACACAGCGAGA	9705	C
			TCTCGCT TGTTGCCCAGG		
			AGAGCGA ACAACGGGTCC		
			C		
GAM1882	APOL1	3'	TCCAGCCTGGGTGACAGAGCGA	14745	TG
	GA		TCTCGCTCTGT CCCAGGCTGGA		
			AGAGCGAGACA GGGTCCGACCT		
			GT		
GAM1882	ARHGEF6	3'	CCAACCTAGGTAACAGAG	68754	C C
			CTCTGTTGCC AGG TGG		
			GAGACAATGG TCC ACC		
			A A		
GAM1882	ARSD	3'	TCCAGCCTGGGCCACATAGCAA	9800	C C T
	GA		TCT GCT TGT GCCCAGGCTGGA		
			AGA CGA ACA CGGGTCCGACCT		
			A T C		
GAM1882	ATM	3'	TCCAGCCTGGGAGACAGAGCGA	5303	TG
	GA		TCTCGCTCTGT CCCAGGCTGGA		
			AGAGCGAGACA GGGTCCGACCT		
			GA		
GAM1882	ATM	3'	TCCAGCCTGGGTGACAAGAGCG	5304	_ TG
	A		TCGCTCT GT CCCAGGCTGGA		
			AGCGAGA CA GGGTCCGACCT		
			A GT		
GAM1882	BCAS1	3'	CCTGGGCGACAGAGCAAGA	14710	C
			TCT GCTCTGTTGCCCAGG		

			AGA CGAGACAGCGGGTCC		
			A		
GAM1882	BPHL	3'	TCCAACCTGGGCAACAGAGTAA 16336	CG	C
	GA		TCT CTCTGTTGCCAGG TGGA		
			AGA GAGACAACGGGTCC ACCT		
			AT A		
GAM1882	BRCA1	5'	TCCAGCCTGGGCGACAGAGCGA 24576		
	GA		TCTCGCTCTGTTGCCAGGCTGGA		
			AGAGCGAGACAGCGGGTCCGACCT		
GAM1882	BRCA1	3'	TCCAGCCTGGGTGACAGTGAGA 24577	CT TG	
			TCTCGCT GT CCCAGGCTGGA		
			AGAGTGA CA GGGTCCGACCT		
			— GT		
GAM1882	BRCA1	3'	TCCAGCCTGGGTGACAGTGAGA 24578	CT TG	
			TCTCGCT GT CCCAGGCTGGA		
			AGAGTGA CA GGGTCCGACCT		
			— GT		
GAM1882	BRCA1	3'	TCCAGCCTGGGTGACAGTGAGA 24579	CT TG	
			TCTCGCT GT CCCAGGCTGGA		
			AGAGTGA CA GGGTCCGACCT		
			— GT		
GAM1882	BRCA1	3'	TCCAGCCTGGGTGACAGTGAGA 24580	CT TG	
			TCTCGCT GT CCCAGGCTGGA		
			AGAGTGA CA GGGTCCGACCT		
			— GT		
GAM1882	C1orf1	3'	TCCAGCCTAGGCGACAGAGTGA 8683	C	
	GA		TCTCGCTCTGTTGCC AGGCTGGA		
			AGAGTGAGACAGCGG TCCGACCT		
			A		
GAM1882	CARKL	3'	TCCAGCCTGGGTGACAGAGCAA 26109	C TG	
	GA		TCT GCTCTGT CCCAGGCTGGA		
			AGA CGAGACA GGGTCCGACCT		
			A GT		
GAM1882	CASP10	3'	TCCAGCTTGGGCAACAGGGCGA 53264		
	GA		TCTCGCTCTGTTGCCAGGCTGGA		
			AGAGCGGGACAACGGGTTCGACCT		
GAM1882	CASP10	3'	TCCAGCTTGGGCAACAGGGCGA 53265		
	GA		TCTCGCTCTGTTGCCAGGCTGGA		

AGAGCGGGACAACGGGTTCGACCT

GAM1882 CASP6 3' TCCAGCCTGGGCAACGAGTGA 8735 T
TCGCTC GTTGCCCAGGCTGGA
||||| |||||||||
AGTGAG CAACGGGTCCGACCT

—
GAM1882 CD28 3' TCCAGCCTGGGCGACAGAGTGA 21558
GA TCTCGCTCTGTTGCCAGGCTGGA
|||||||||||||||
AGAGTGAGACAGCGGGTCCGACCT

GAM1882 CD68 3' TCCAGCCTGGGCGACAGAGCCA 60508 C
GA TCT GCTCTGTTGCCAGGCTGGA
||| |||||||||||||
AGA CGAGACAGCGGGTCCGACCT
C

GAM1882 CEACAM5 3' TCCAGTCTGGCAACAGAGCAAG 16425 C C
A TCT GCTCTGTTGCC AGGCTGGA
||| ||||||| |||||
AGA CGAGACAACGG TCTGACCT
A —

GAM1882 CENPB 3' TCCAGCCTAGGCCCCCTGCAAG 70119 C TCTGTT C
G TCT GC GCC AGGCTGGA
||| || ||| |||||
GGA CG CGG TCCGACCT
A TCCCC_ A

GAM1882 CNGB1 3' CTGGGCAACATAGCGAGA 8935 C
TCTCGCT TGTTGCCAG
||||| |||||||
AGAGCGA ACAACGGGTC
T

GAM1882 COPA 3' TCCAGCCTGGGTGACAGAGCAA 16480 C TG
GA TCT GCTCTGT CCCAGGCTGGA
||| ||||| |||||||||
AGA CGAGACA GGGTCCGACCT
A GT

GAM1882 CPM 3' TCCAGCTTGGGCAACAGAGTAA 60411 CG
GA TCT CTCTGTTGCCAGGCTGGA
||| |||||||||||||
AGA GAGACAACGGGTTCGACCT
AT

GAM1882 CPT2 3' CCTGGGCGACAGAGCGAGA 5424
TCTCGCTCTGTTGCCAGG
|||||||||||||||
AGAGCGAGACAGCGGGTCC

GAM1882 CTMP 3' TCCAACCTGGGCAACAGAACAA 54954 CGC C
GA TCT TCTGTTGCCAGG TGGA
||| ||||||||| |||

			AGA AGACAACGGGTCC ACCT	
			ACA A	
GAM1882	CUBN	3'	TCCAGCCTGGGCGAGACGGCAA 8425	C CTG
	GA		TCT GCT TTGCCAGGCTGGA	
			AGA CGG AGCGGGTCCGACCT	
			A CAG	
GAM1882	CYP4F3	3'	TCCAGCCTGGGTGAAAGAGCTA 8015	C G TG
	GA		TCT GCTCT T CCCAGGCTGGA	
			AGA CGAGA A GGGTCCGACCT	
			T A GT	
GAM1882	DBT	3'	TCCAGCCTGGGCGACAGAGCAA 10379	C
	GA		TCT GCTCTGTTGCCAGGCTGGA	
			AGA CGAGACAGCGGGTCCGACCT	
			A	
GAM1882	DBT	3'	TCCAGCCTGGGTGGCAGAGC 10380	TG
			GCTCTGT CCCAGGCTGGA	
			CGAGACG GGGTCCGACCT	
			GT	
GAM1882	DCLRE1C	3'	TCCAGCCTGGGCAACAAGAGC 42822	_
			GCTCT GTTGCCAGGCTGGA	
			CGAGA CAACGGGTCCGACCT	
			A	
GAM1882	DDOST	3'	TCCAGCCTGGGCAACAGTGT 19066	T
			GC CTGTTGCCAGGCTGGA	
			TG GACAACGGGTCCGACCT	
			T	
GAM1882	DFFA	3'	TCCAGCCTGGGCAACAGAGCGA 16598	
	GA		TCTCGCTCTGTTGCCAGGCTGGA	
			AGAGCGAGACAACGGGTCCGACCT	
GAM1882	DGKI	5'	TCCAGCCTGGGCGACAAAGCAA 17529	C C
	GA		TCT GCT TGTTGCCAGGCTGGA	
			AGA CGA ACAGCGGGTCCGACCT	
			A A	
GAM1882	DMC1	3'	TCCAGCCTAGGTGACAGAGTGA 23947	TG C
	GA		TCTCGCTCTGT CC AGGCTGGA	
			AGAGTGAGACA GG TCCGACCT	
			GT A	
GAM1882	DSC1	3'	TCCAGCCTGGGCAACAAGAGCG 44606	_
	A		TCGCTCT GTTGCCAGGCTGGA	

			AGCGAGA CAACGGGTCCGACCT		
			A		
GAM1882	DSC1	3'	TCCAGCCTGGGCAACAAGAGCG 44607	—	
	A		TCGCTCT GTTGCCCAGGCTGGA		
			AGCGAGA CAACGGGTCCGACCT		
			A		
GAM1882	DVL3	3'	TCCAGCCTGGGTGACAGAGTGA 16651	TG	
	GA		TCTCGCTCTGT CCCAGGCTGGA		
			AGAGTGAGACA GGGTCCGACCT		
			GT		
GAM1882	EGFL4	3'	TCCAACCTGGGTGACAGAGCGA 62475	TG	C
	GA		TCTCGCTCTGT CCCAGG TGGA		
			AGAGCGAGACA GGGTCC ACCT		
			GT A		
GAM1882	EGFL5	3'	TCCAGCCTGGGCGACAGAGCAA 87921	C	
	GA		TCT GCTCTGTTGCCCAGGCTGGA		
			AGA CGAGACAGCGGGTCCGACCT		
			A		
GAM1882	F2R	3'	TCCAGCCTGGGCAACAGAGCAA 10573	C	
	GA		TCT GCTCTGTTGCCCAGGCTGGA		
			AGA CGAGACAACGGGTCCGACCT		
			A		
GAM1882	F2RL3	3'	TCCAGCCTGGGCAACAGAGCAA 15527	C	
	GA		TCT GCTCTGTTGCCCAGGCTGGA		
			AGA CGAGACAACGGGTCCGACCT		
			A		
GAM1882	FANCC	3'	TCCAGCCTGGGCAACAGAGCGA 71049		
	GA		TCTCGCTCTGTTGCCCAGGCTGGA		
			AGAGCGAGACAACGGGTCCGACCT		
GAM1882	FCAR	3'	TCCAGCCTGGGTGACAGAACGA 56582	C	TG
	GA		TCTCG TCTGT CCCAGGCTGGA		
			AGAGC AGACA GGGTCCGACCT		
			A GT		
GAM1882	FCAR	3'	TCCAGCCTGGGTGACAGAACGA 56583	C	TG
	GA		TCTCG TCTGT CCCAGGCTGGA		
			AGAGC AGACA GGGTCCGACCT		
			A GT		
GAM1882	FGF2	3'	TCCAGCCTAGGCAACAGAGTGA 10622	C	
	GA		TCTCGCTCTGTTGCC AGGCTGGA		

			AGAGTGAGACAACGG TCCGACCT		
			A		
GAM1882	FGFR2	3'	TCCAGCCTTGGCGACAGAGCGA 5566	C	
	GA		TCTCGCTCTGTTGCC AGGCTGGA		
			AGAGCGAGACAGCGG TCCGACCT		
			T		
GAM1882	FLRT2	5'	TCCAGCCTAAGCAACAGAGCAA 26004	C	CC
	GA		TCT GCTCTGTTGC AGGCTGGA		
			AGA CGAGACAACG TCCGACCT		
			A AA		
GAM1882	FUT6	3'	TCCAACCTGGACGACAGAGCAA 5644	C	C C
	GA		TCT GCTCTGTTG CCAGG TGGA		
			AGA CGAGACAGC GGTCC ACCT		
			A A A		
GAM1882	GALNT7	3'	TCCAACCTGGGTGACAGAGTGA 55090	TG	C
	GA		TCTCGCTCTGT CCCAGG TGGA		
			AGAGTGAGACA GGGTCC ACCT		
			GT A		
GAM1882	GAMT	3'	CCTGGGCTACAGAGCAAGA 5672	C	T
			TCT GCTCTGT GCCCAGG		
			AGA CGAGACA CGGGTCC		
			A T		
GAM1882	GGCX	3'	CCTGGGCAACAGAGCAAGA 7703	C	
			TCT GCTCTGTTGCCCAGG		
			AGA CGAGACAACGGGTCC		
			A		
GAM1882	GM2A	3'	TCCAGCCTGGTGACAGAGTGAG 68390	TG	C
	A		TCTCGCTCTGT CC AGGCTGGA		
			AGAGTGAGACA GG TCCGACCT		
			GT _		
GAM1882	GP2	3'	TCCAGCCTGGGCAACAGAGCAA 9483	C	
	GA		TCT GCTCTGTTGCCCAGGCTGGA		
			AGA CGAGACAACGGGTCCGACCT		
			A		
GAM1882	GRAF	3'	TCCAGCCTGGGTGACAGAGCCA 31248	C	TG
	GA		TCT GCTCTGT CCCAGGCTGGA		
			AGA CGAGACA GGGTCCGACCT		
			C GT		
GAM1882	GRM3	3'	TCCAGAATATGGAAACAGAGC 7746	GC	GG__
			GCTCTGTT CCA CTGGA		

			CGAGACAA GGT GACCT	
			A_ ATAA	
GAM1882	GRM6	3'	TCCAGCCTGGGTGACAGAGCGA 7772	TG
	GA		TCTCGCTCTGT CCCAGGCTGGA	
			AGAGCGAGACA GGGTCCGACCT	
			GT	
GAM1882	GTF2F1	3'	TCCAGCCTGGGTGACAGAATGA 10893	C TG
			TCG TCTGT CCCAGGCTGGA	
			AGT AGACA GGGTCCGACCT	
			A GT	
GAM1882	GTF2F1	3'	TCCAGCCTGGGTGACAGTGAGA 10894	CT TG
			TCTCGCT GT CCCAGGCTGGA	
			AGAGTGA CA GGGTCCGACCT	
			___ GT	
GAM1882	HIP1	3'	TCCAGCCTGAGTGACAGAGCGA 19264	TG C
	GA		TCTCGCTCTGT C CAGGCTGGA	
			AGAGCGAGACA G GTCCGACCT	
			GT A	
GAM1882	HIP1	3'	TCCAGCCTGGGCAACAAGAGC 19265	_
			GCTCT GTTGCCCAGGCTGGA	
			CGAGA CAACGGGTCCGACCT	
			A	
GAM1882	HRH1	3'	TCCAGCCTGGGCAACAGAGCAA 7828	C
	GA		TCT GCTCTGTTGCCAGGCTGGA	
			AGA CGAGACAACGGGTCCGACCT	
			A	
GAM1882	HSPA5	3'	TCCAGCCTGGCGACAAGAGTGA 19290	_ C
	GA		TCTCGCTCT GTTGCC AGGCTGGA	
			AGAGTGAGA CAGCGG TCCGACCT	
			A _	
GAM1882	HTR2A	3'	TCCTCCTGGGCAACAGAGTGAG 7107	CT
	A		TCTCGCTCTGTTGCCAGG GGA	
			AGAGTGAGACAACGGGTCC CCT	
			T_	
GAM1882	IAPP	3'	TCCAGCCTGGGTGGCAGAGTGA 6443	TG
	GA		TCTCGCTCTGT CCCAGGCTGGA	
			AGAGTGAGACG GGGTCCGACCT	
			GT	
GAM1882	ICA1	3'	CCAGCCTGGGCAACAAAGTGAG 18310	C
	A		TCTCGCT TGTTGCCAGGCTGG	

			AGAGTGA ACAACGGGTCCGACC		
			A		
GAM1882	IFIT4	3'	TCCAGCCTGGGCAACAGAGCAA 71497	C	
	GA		TCT GCTCTGTTGCCCAGGCTGGA		
			AGA CGAGACAACGGGTCCGACCT		
			A		
GAM1882	IFRD1	3'	CCTGGGCAACATAGCGAGA 60753	C	
			TCTCGCT TGTTGCCCAGG		
			AGAGCGA ACAACGGGTCC		
			T		
GAM1882	IL10	3'	TCCAGCCTGGGTGACAGAGCAA 6929	C	TG
	GA		TCT GCTCTGT CCCAGGCTGGA		
			AGA CGAGACA GGGTCCGACCT		
			A GT		
GAM1882	IL1R1	3'	TCTAGCCTGGCAACAGAGCAAG 7925	C	C
	A		TCT GCTCTGTTGCC AGGCTGGA		
			AGA CGAGACAACGG TCCGATCT		
			A _		
GAM1882	IL2RA	3'	TCCAGCCTGGGCAACAGAGCAA 6453	C	
	GA		TCT GCTCTGTTGCCCAGGCTGGA		
			AGA CGAGACAACGGGTCCGACCT		
			A		
GAM1882	IL6R	3'	TCCAGCCTGGGGTGACAGAGC 6915	TG	_
			GCTCTGT CCC AGGCTGGA		
			CGAGACA GGG TCCGACCT		
			GT G		
GAM1882	IPP	3'	TCCACTCTGGGCAACAGAATGA 20907	C	GC
	GA		TCTCG TCTGTTGCCCAG TGGA		
			AGAGT AGACAACGGGTC ACCT		
			A TC		
GAM1882	IRAK1	3'	TCCAGCCTGGGTGACAGAGCAA 9618	C	TG
	GA		TCT GCTCTGT CCCAGGCTGGA		
			AGA CGAGACA GGGTCCGACCT		
			A GT		
GAM1882	IRAK4	3'	TCCAGCCTGGGTGACAGAGTGA 61847		TG
	GA		TCTCGCTCTGT CCCAGGCTGGA		
			AGAGTGAGACA GGGTCCGACCT		
			GT		
GAM1882	ITGAL	3'	TCCAGCCTGGGCAACACAGCGA 11050	C	
	GA		TCTCGCT TGTTGCCCAGGCTGGA		

			AGAGCGA ACAACGGGTCCGACCT		
			C		
GAM1882	KAI1	3'	TCCAGCCTGGGGGACAGAAAGA 11130	GC	G
	GA		TCTC TCTGTT CCCAGGCTGGA		
			AGAG AGACAG GGGTCCGACCT		
			AA G		
GAM1882	KCNA7	3'	TCCAGCCTGGGCAACAGAGGGA 49905	G	
	G		CTC CTCTGTTGCCCAGGCTGGA		
			GAG GAGACAACGGGTCCGACCT		
			G		
GAM1882	KCNA7	3'	TCCAGCCTGGGCAGCAGAGC 49906		
			GCTCTGTTGCCCAGGCTGGA		
			CGAGACGACGGGTCCGACCT		
GAM1882	KCNJ5	3'	TCCAGCCTGGGCGACAGAGCGA 7978		
	GA		TCTCGCTCTGTTGCCCAGGCTGGA		
			AGAGCGAGACAGCGGGTCCGACCT		
GAM1882	KCNK3	3'	TCCAGCCTGGGTGACAGGGCAA 11178	C	TG
	GA		TCT GCTCTGT CCCAGGCTGGA		
			AGA CGGGACA GGGTCCGACCT		
			A GT		
GAM1882	KCNK6	3'	TCCAGCCTGCGGGACAGAGTGA 17885	G	_
	GA		TCTCGCTCTGTT CC CAGGCTGGA		
			AGAGTGAGACAG GG GTCCGACCT		
			_ C		
GAM1882	KIF1B	3'	TCCAGCCTGGGTGACAGAGCAA 31271	C	TG
	GA		TCT GCTCTGT CCCAGGCTGGA		
			AGA CGAGACA GGGTCCGACCT		
			A GT		
GAM1882	KIF3B	3'	TCCAGCCTGGGTGACAGAGTGA 17810		TG
	GA		TCTCGCTCTGT CCCAGGCTGGA		
			AGAGTGAGACA GGGTCCGACCT		
			GT		
GAM1882	KLRG1	3'	TCCAGCCTGGGAGATAGAGCAA 20557	C	TG
	GA		TCT GCTCTGT CCCAGGCTGGA		
			AGA CGAGATA GGGTCCGACCT		
			A GA		
GAM1882	KNSL1	3'	TCCAGCCTGGGCAACAGAGCAA 16949	C	
	GA		TCT GCTCTGTTGCCCAGGCTGGA		

			AGA CGAGACAACGGGTCCGACCT		
			A		
GAM1882	LAMC2	3'	TCCAGCCTGGGGAACAGAGCAA 19909	C	G
	GA		TCT GCTCTGTT CCCAGGCTGGA		
			AGA CGAGACAA GGGTCCGACCT		
			A G		
GAM1882	LDLR	3'	CCTGGGCGACAGAGCGAGA 6733		
			TCTCGCTCTGTTGCCCAGG		
			AGAGCGAGACAGCGGGTCC		
GAM1882	LDLR	3'	TCCAGCCTGGGCAACAGATGAA 6744	_ C	
	GA		TCT CG TCTGTTGCCCAGGCTGGA		
			AGA GT AGACAACGGGTCCGACCT		
			A _		
GAM1882	LDLR	3'	TCCAGCCTGGGCAACATAGTAA 6745	CG C	
	GA		TCT CT TGTTGCCCAGGCTGGA		
			AGA GA ACAACGGGTCCGACCT		
			AT T		
GAM1882	LILRB1	3'	TCCAGCCTGGGCGACAGAGGGAG 22877	G	C
	A		TCTC CTCTGTTGCC AGGCTGGA		
			AGAG GAGACAGCGG TCCGACCT		
			G _		
GAM1882	LPIN1	3'	TCCAGCCTGGGTGACAGAGTAA 67992	CG	TG
	GA		TCT CTCTGT CCCAGGCTGGA		
			AGA GAGACA GGGTCCGACCT		
			AT GT		
GAM1882	LRRC2	3'	TCCAGCCTGGGCAACAGAGTGA 44759		
	GA		TCTCGCTCTGTTGCCCAGGCTGGA		
			AGAGTGAGACAACGGGTCCGACCT		
GAM1882	LRRC2	3'	TCCAGCCTGGGTGACAGAGCCA 44760	C	TG
	GA		TCT GCTCTGT CCCAGGCTGGA		
			AGA CGAGACA GGGTCCGACCT		
			C GT		
GAM1882	LRRC2	3'	TCCAGCCTGGGTGACAGAGTGA 44761		TG
	GA		TCTCGCTCTGT CCCAGGCTGGA		
			AGAGTGAGACA GGGTCCGACCT		
			GT		
GAM1882	LUZP1	3'	TCCAGCCTGGGCAACAAGAGTG 54405	_	
	A		TCGCTCT GTTGCCCAGGCTGGA		

		AGTGAGA CAACGGGTCCGACCT		
		A		
GAM1882 LY94	3'	CCTGGGCGACAGAGCGAGA 17897		
		TCTCGCTCTGTTGCCAGG		
		AGAGCGAGACAGCGGGTCC		
GAM1882 MAFF	3'	TCCAGCCTGGGCAACATAGC 25583	C	
		GCT TGTTGCCAGGCTGGA		
		CGA ACAACGGGTCCGACCT		
		T		
GAM1882 MDM4	3'	TCCAGCCTGGGTGACAGCGCGA 11514	T	TG
GA		TCTCGC CTGT CCCAGGCTGGA		
		AGAGCG GACA GGGTCCGACCT		
		C GT		
GAM1882 MEN1	5'	TCCAGCCTGGGCGAAAGAGAAA 56361	CG	G
GA		TCT CTCT TTGCCAGGCTGGA		
		AGA GAGA AGCGGGTCCGACCT		
		AA A		
GAM1882 MSH3	3'	TCCAGCTTGGGCAACAGAGCAA 11693	C	
GA		TCT GCTCTGTTGCCAGGCTGGA		
		AGA CGAGACAACGGGTTCGACCT		
		A		
GAM1882 MTMR8	3'	TCCAGCCTGAGCAACAGAGCGA 31917		C
GA		TCTCGCTCTGTTGC CAGGCTGGA		
		AGAGCGAGACAACG GTCCGACCT		
		A		
GAM1882 MTMR8	3'	TCCAGCCTGGGCGAAAGGGCAA 31918	C	G
GA		TCT GCTCT TTGCCAGGCTGGA		
		AGA CGGGA AGCGGGTCCGACCT		
		A A		
GAM1882 MYH11	3'	TCCAGCCTGGGCAACGTAGT 43448	C	
		GCT TGTTGCCAGGCTGGA		
		TGA GCAACGGGTCCGACCT		
		T		
GAM1882 MYH11	3'	TCCAGCCTGGGCAACAGAG 11744		
		CTCTGTTGCCAGGCTGGA		
		GAGACAACGGGTCCGACCT		
GAM1882 MYH11	3'	TCCAGCCTGGGCAACAGAG 11745		
		CTCTGTTGCCAGGCTGGA		

GAGACAACGGGTCCGACCT

GAM1882 MYH11 3' TCCAGCCTGGGCAACGTAGT 11747 C
GCT TGTTGCCCAGGCTGGA
||| |||||
TGA GCAACGGGTCCGACCT
T

GAM1882 MYO1B 3' TCCAGCCCGGGTGACAATACAA 25247 CGCTC TG A
GA TCT TGT CCC GGCTGGA
||| ||| ||| |||||
AGA ACA GGG CCGACCT
ACATA GT C

GAM1882 MYO1C 3' TCCAGCCTGGGCAACAGAGCGA 61870
GA TCTCGCTCTGTTGCCCAGGCTGGA
|||||
AGAGCGAGACAACGGGTCCGACCT

GAM1882 NCOA6 5' TCCAGCCCAGGCAACAGAGCGT 26849 T CA
GA TC CGCTCTGTTGCC GGCTGGA
|| ||||| |||||
AG GCGAGACAACGG CCGACCT
T AC

GAM1882 NESG1 5' CCAGCCCAGGGCCAGAGCGA 25619 TT A_
TCGCTCTG GCCC GGCTGG
||||| ||| |||||
AGCGAGAC CGGG CCGACC
_ AC

GAM1882 NFKBIL2 3' TCCAGCCTGGGCGACAGACCGA 26455 C
GA TCTCG TCTGTTGCCCAGGCTGGA
||||| |||||
AGAGC AGACAGCGGGTCCGACCT
C

GAM1882 NKX3A 3' TCCAGCCTGGGCAACGAGCAAG 21617 C T
A TCT GCTC GTTGCCCAGGCTGGA
||| ||| |||||
AGA CGAG CAACGGGTCCGACCT
A _

GAM1882 NPHP1 3' TCCAGCCTAGGCAACAAGAGTG 63150 _ C
A TCGCTCT GTTGCC AGGCTGGA
||||| ||||| |||||
AGTGAGA CAACGG TCCGACCT
A A

GAM1882 NPHS1 3' TCCAGCCTGGGCGACAGAGCGA 17374
GA TCTCGCTCTGTTGCCCAGGCTGGA
|||||
AGAGCGAGACAGCGGGTCCGACCT

GAM1882 NT5C2 3' TCCAGCCTGGGCAACAAGA 25268 _
TCT GTTGCCCAGGCTGGA
||| |||||

			AGA CAACGGGTCCGACCT		
			A		
GAM1882	NUP62	3'	TCCAGCCTAGGCAACAGAG 25652	C	
			CTCTGTTGCC AGGCTGGA		
			GAGACAACGG TCCGACCT		
			A		
GAM1882	OGG1	5'	TCCAGCCTAGGCGACAGAGTGA 34160	C	
	GA		TCTCGCTCTGTTGCC AGGCTGGA		
			AGAGTGAGACAGCGG TCCGACCT		
			A		
GAM1882	OPA3	3'	CTAGCCTGGGCAACAGAGCAAG 47843	C	
	A		TCT GCTCTGTTGCCAGGCTGG		
			AGA CGAGACAACGGGTCCGATC		
			A		
GAM1882	OPA3	3'	TCCAGCCCGGGTGACAGAGCAA 47848	C	TG A
	GA		TCT GCTCTGT CCC GGCTGGA		
			AGA CGAGACA GGG CCGACCT		
			A GT C		
GAM1882	OPTN	3'	TCCAGCCTGGGTGACAGAGGGA 42053	G	TG
	GA		TCTC CTCTGT CCCAGGCTGGA		
			AGAG GAGACA GGGTCCGACCT		
			G GT		
GAM1882	P53AIP1	3'	TCCAGCCTGGGCGACAGAGAGA 42340	G	
	GA		TCTC CTCTGTTGCCAGGCTGGA		
			AGAG GAGACAGCGGGTCCGACCT		
			A		
GAM1882	PA2G4	3'	TCCAGCCTGGGTGACAGAATGA 71831	C	TG
	GA		TCTCG TCTGT CCCAGGCTGGA		
			AGAGT AGACA GGGTCCGACCT		
			A GT		
GAM1882	PAICS	3'	TCCAACCTGGGCAGCAGAGCAA 22268	C	C
	GA		TCT GCTCTGTTGCCAGG TGGA		
			AGA CGAGACGACGGGTCC ACCT		
			A A		
GAM1882	PCDH11X	3'	TCCAGCCTGGGTGACAGAGCAA 53133	C	TG
	GA		TCT GCTCTGT CCCAGGCTGGA		
			AGA CGAGACA GGGTCCGACCT		
			A GT		
GAM1882	PCDH11Y	3'	TCCAGCCTGGGTGACAGAGCAA 53169	C	TG
	GA		TCT GCTCTGT CCCAGGCTGGA		

			AGA CGAGACA GGGTCCGACCT		
			A GT		
GAM1882	PCDHB9	3'	TCCAGCCTGGGCAATAAGAGC 39451	—	
			GCTCT GTTGCCCAGGCTGGA		
			CGAGA TAACGGGTCCGACCT		
			A		
GAM1882	PDCL	3'	CCAACCTGGGCGACAGAG 19395	C	
			CTCTGTTGCCCAGG TGG		
			GAGACAGCGGGTCC ACC		
			A		
GAM1882	PDE4C	3'	CCTGGGCAACATAGCAAGA 8101	C C	
			TCT GCT TGTTGCCCAGG		
			AGA CGA ACAACGGGTCC		
			A T		
GAM1882	PDE4C	3'	TCCAGCCTGGGCAACACAGCAA 8107	C C	
	GA		TCT GCT TGTTGCCCAGGCTGGA		
			AGA CGA ACAACGGGTCCGACCT		
			A C		
GAM1882	PDE4C	3'	TCCAGCCTGGGGCTGACAGAGC 8108	C	— —
	AAGA		TCT GCTCTGTT GCCC AGGCTGGA		
			AGA CGAGACAG CGGG TCCGACCT		
			A T G		
GAM1882	PIK3CD	3'	TCCAAAACTCAACAGAGCCAGA 18501	C	CCC GC_
			TCT GCTCTGTTG AG TGGA		
			AGA CGAGACAAC TC ACCT		
			C — AAA		
GAM1882	PIK3CG	3'	TCCAGCCTGGATAACAGAGCGA 12125	C	
	GA		TCTCGCTCTGTTG CCAGGCTGGA		
			AGAGCGAGACAAT GGTCCGACCT		
			A		
GAM1882	PLA2G2D	3'	TCCAGCCTGGGCAACAGAGTGA 25723		
			TCGCTCTGTTGCCCAGGCTGGA		
			AGTGAGACAACGGGTCCGACCT		
GAM1882	POLH	3'	TCCAGCCTGGGCAACAGAGCGA 22484		
	GA		TCTCGCTCTGTTGCCCAGGCTGGA		
			AGAGCGAGACAACGGGTCCGACCT		
GAM1882	POLH	3'	TCCAGCCTGGGCAACAGAGCGA 22485		
	GA		TCTCGCTCTGTTGCCCAGGCTGGA		

AGAGCGAGACAACGGGTCCGACCT

GAM1882 POLK 3' CCAGCCTGAAGAGCGAGA 33100 GTTGCC
TCTCGCTCT CAGGCTGG
||||||| |||||
AGAGCGAGA GTCCGACC

A_____

GAM1882 PPP1R12B 3' TCCAGCCTGGGTGACAGAGCAA 50366 C TG
GA TCT GCTCTGT CCCAGGCTGGA
||| ||||| |||||
AGA CGAGACA GGGTCCGACCT

A GT

GAM1882 PRKY 3' TCCAGCCTGGGTGACAGAGTGA 12384 TG
GA TCTCGCTCTGT CCCAGGCTGGA
||||||| |||||
AGAGTGAGACA GGGTCCGACCT

GT

GAM1882 PRKY 3' TCCAGGCTGGACGACAGAGCAA 12385 C C G
GA TCT GCTCTGTTG CCAG CTGGA
||| ||||| ||| |||||
AGA CGAGACAGC GGTC GACCT

A A G

GAM1882 PSMB2 3' TCCAGCCTGGCAACAGAGTGAG 12478 C
A TCTCGCTCTGTTGCC AGGCTGGA
||||||| |||||
AGAGTGAGACAACGG TCCGACCT

GAM1882 PSMB2 3' TCCAGCCTGGCTGACAGAGCAA 12479 C GC
GA TCT GCTCTGTT CCAGGCTGGA
||| ||||| |||||
AGA CGAGACAG GGTCCGACCT

A TC

GAM1882 PSMB9 3' TCCAGCCTGGGAAACAGAGCGA 12509 G
TCGCTCTGTT CCCAGGCTGGA
||||||| |||||
AGCGAGACAA GGGTCCGACCT

A

GAM1882 PSMB9 3' TCCAGCCTGGGCGACAAAGCGA 12510 C
GA TCTCGCT TGTTGCCAGGCTGGA
||||| |||||
AGAGCGA ACAGCGGGTCCGACCT

A

GAM1882 PSMD5 3' CCTGGGCAACACAGCAAGA 18557 C C
TCT GCT TGTTGCCAGG
||| ||| |||||
AGA CGA ACAACGGGTCC

A C

GAM1882 PTAFR 3' TCTAGCCTGGCAACAGAGCGAG 8168 C
A TCTCGCTCTGTTGCC AGGCTGGA
||||||| |||||

AGAGCGAGACAACGG TCCGATCT

GAM1882 PTGIS 3' TCCAGCCTGGGCGACAGAGCAA 8229 C
GA TCT GCTCTGTTGCCCAGGCTGGA
||| ||||||||||||
AGA CGAGACAGCGGGTCCGACCT
A

GAM1882 RABIF 3' TCCAGCCTGGGCAACAGAGTGA 12730
GA TCTCGCTCTGTTGCCCAGGCTGGA
||||||||||||||
AGAGTGAGACAACGGGTCCGACCT

GAM1882 RAD1 3' TCCAGCCTAGGCAATAAGAGC 12647 _ C
GCTCT GTTGCC AGGCTGGA
|||| ||||| |||||
CGAGA TAACGG TCCGACCT
A A

GAM1882 RANBP2L1 3' TCCAGCTCGGGGAACAGAGCGA 51052 G AG
GA TCTCGCTCTGTT CCC GCTGGA
||||||| || |||||
AGAGCGAGACAA GGG CGACCT
G CT

GAM1882 RBBP5 3' TCCAGCCTAGGTGACAGAATGA 18579 C TG C
GA TCTCG TCTGT CC AGGCTGGA
|||| |||| || |||||
AGAGT AGACA GG TCCGACCT
A GT A

GAM1882 RBBP9 3' CCAGGGCAACACAGCAAGA 70687 C C A
TCT GCT TGTTGCCC GG
||| || ||||| ||
AGA CGA ACAACGGG CC
A C A

GAM1882 RBL1 3' TCCAGCCTGGGCAACAAGAGT 12789 _
GCTCT GTTGCCCAGGCTGGA
|||| |||||||||
TGAGA CAACGGGTCCGACCT
A

GAM1882 RBM3 3' TCCAGCCTGGGCAACAGCGAGA 71013 CT
TCTCGCT GTTGCCCAGGCTGGA
||||| |||||||||
AGAGCGA CAACGGGTCCGACCT

GAM1882 RFC2 3' CCAGCCTGGGCGACAGAG 12839
CTCTGTTGCCCAGGCTGG
|||||||||||
GAGACAGCGGGTCCGACC

GAM1882 ROCK2 3' TCCAGCCTGGGCAGCTGAACAA 66625 CGC T
GA TCT TC GTTGCCCAGGCTGGA
||| || |||||||||

			AGA AG CGACGGGTCCGACCT	
			ACA T	
GAM1882	SCAP2	3'	TCCAGCCTGGGCGACAGAGTGA 15427	
	GA		TCTCGCTCTGTTGCCCAGGCTGGA	
			AGAGTGAGACAGCGGGTCCGACCT	
GAM1882	SFRS2IP	5'	TCCAGCCTGGGTGACAGAGTGA 17547	TG
	GA		TCTCGCTCTGT CCCAGGCTGGA	
			AGAGTGAGACA GGGTCCGACCT	
			GT	
GAM1882	SIGLEC11	3'	TCCAGCCTGGGCAACAGAGTGA 54657	
	GA		TCTCGCTCTGTTGCCCAGGCTGGA	
			AGAGTGAGACAACGGGTCCGACCT	
GAM1882	SIGLEC6	3'	CCAGCCTGGGCAACAGAGCGAG 60605	
	A		TCTCGCTCTGTTGCCCAGGCTGG	
			AGAGCGAGACAACGGGTCCGACC	
GAM1882	SIM2	3'	TCCAGCCTGGGTAACAGAGTGA 18624	
	GA		TCTCGCTCTGTTGCCCAGGCTGGA	
			AGAGTGAGACAATGGGTCCGACCT	
GAM1882	SLC14A2	3'	TCCAGCCTGGGCAACGGATTGA 24128	C
	GA		TCTCG TCTGTTGCCCAGGCTGGA	
			AGAGT AGGCAACGGGTCCGACCT	
			T	
GAM1882	SLC17A5	3'	TCCAGCCTGGGCGATGGAGCGA 25835	
	GA		TCTCGCTCTGTTGCCCAGGCTGGA	
			AGAGCGAGGTAGCGGGTCCGACCT	
GAM1882	SLC26A4	3'	TCCAGCCTGGGCGACAGAGCAA 6530	C
	GA		TCT GCTCTGTTGCCCAGGCTGGA	
			AGA CGAGACAGCGGGTCCGACCT	
			A	
GAM1882	SLC28A2	3'	TCCAGCCTGGGTGACAGAGCGA 16154	TG
	GA		TCTCGCTCTGT CCCAGGCTGGA	
			AGAGCGAGACA GGGTCCGACCT	
			GT	
GAM1882	SLC2A6	3'	TCCAGCCTGGGCAACGAGAGTG 34577	—
	A		TCGCTCT GTTGCCCAGGCTGGA	

			AGTGAGA CAACGGGTCCGACCT	
			G	
GAM1882	SMG1	3'	TCCAGCCTGGGCAACAGAGCTA 31352	C
	GA		TCT GCTCTGTTGCCCAGGCTGGA	
			AGA CGAGACAACGGGTCCGACCT	
			T	
GAM1882	SRGAP1	5'	TCCAGCCTGGGCAACAGAGCGA 72721	
	GA		TCTCGCTCTGTTGCCCAGGCTGGA	
			AGAGCGAGACAACGGGTCCGACCT	
GAM1882	STK38	5'	TCCAGCCTGGGCAACAAGAGCG 24401	_
	A		TCGCTCT GTTGCCCAGGCTGGA	
			AGCGAGA CAACGGGTCCGACCT	
			A	
GAM1882	SULT2A1	3'	TCCAGCCTGGGTGACAGAGCGA 72232	TG
	GA		TCTCGCTCTGT CCCAGGCTGGA	
			AGAGCGAGACA GGGTCCGACCT	
			GT	
GAM1882	SWAP70	3'	TCCAGCTTGGGCAACAGAGTGA 71874	
	GA		TCTCGCTCTGTTGCCCAGGCTGGA	
			AGAGTGAGACAACGGGTTCGACCT	
GAM1882	TADA2L	3'	TCCAGCCTGGGCAACAAAGTGA 56765	C
	GA		TCTCGCT TGTTGCCCAGGCTGGA	
			AGAGTGA ACAACGGGTCCGACCT	
			A	
GAM1882	TBX1	3'	TCCAGCCTGGGTGACAGAGTGA 55541	TG
	GA		TCTCGCTCTGT CCCAGGCTGGA	
			AGAGTGAGACA GGGTCCGACCT	
			GT	
GAM1882	TBX6	3'	TCCAGCCTAGGCAACACGAGC 55817	_ C
			GCTC TGTTGCC AGGCTGGA	
			CGAG ACAACGG TCCGACCT	
			C A	
GAM1882	TCF1	3'	CCAGCCTGGGCCTATGGAG 6783	T_
			CTCTGT GCCCAGGCTGG	
			GAGGTA CGGGTCCGACC	
			TC	
GAM1882	TCTA	3'	TCCAGCCTGGGCAACAGAGCAA 42503	C
	GA		TCT GCTCTGTTGCCCAGGCTGGA	

			AGA CGAGACAACGGGTCCGACCT	
			A	
GAM1882	TEM7	3'	TCCAGCCTGGGTGACAGAGCGA 40269	TG
	GA		TCTCGCTCTGT CCCAGGCTGGA	
			AGAGCGAGACA GGGTCCGACCT	
			GT	
GAM1882	TEM7	3'	TCCAGCCTGGGTGACAGAGTGA 40270	TG
	GA		TCTCGCTCTGT CCCAGGCTGGA	
			AGAGTGAGACA GGGTCCGACCT	
			GT	
GAM1882	TNFAIP6	3'	CTGGGCAACATAGCAAGA 60165 C C	
			TCT GCT TGTTGCCAG	
			AGA CGA ACAACGGGTC	
			A T	
GAM1882	TNFRSF1B	3'	TCCAGCCTGAGCAACAGAGTGA 8402	C
	GA		TCTCGCTCTGTTGC CAGGCTGGA	
			AGAGTGAGACAACG GTCCGACCT	
			A	
GAM1882	TNFRSF1B	3'	TCCAGCCTGGGCGACAGAGCGA 8403	
	GA		TCTCGCTCTGTTGCCAGGCTGGA	
			AGAGCGAGACAGCGGGTCCGACCT	
GAM1882	TNFSF10	3'	TCCAGCCTGGCGACAGAGCGAG 15094	C
	A		TCTCGCTCTGTTGCC AGGCTGGA	
			AGAGCGAGACAGCGG TCCGACCT	
GAM1882	TNFSF15	3'	TCCAGCCTGGGTAACAAGAGC 18870 _	
			GCTCT GTTGCCCAGGCTGGA	
			CGAGA CAATGGGTCCGACCT	
			A	
GAM1882	TPM4	3'	TCCAGCCTGGTCGACAGAGTGA 13834	C
	GA		TCTCGCTCTGTTG CCAGGCTGGA	
			AGAGTGAGACAGC GGTCCGACCT	
			T	
GAM1882	TPMT	3'	CCAGCCTGGGCAACAGAGCAAG 6307 C	
	A		TCT GCTCTGTTGCCAGGCTGG	
			AGA CGAGACAACGGGTCCGACC	
			A	
GAM1882	TRIM14	3'	TCCAGCCTGGGCAATAGAGTGA 53778	
	GA		TCTCGCTCTGTTGCCAGGCTGGA	

AGAGTGAGATAACGGGTCCGACCT

GAM1882 TRIM14 3' TCCAGCCTGGGGACAGAGCAAG 29517 C G
A TCT GCTCTGTT CCCAGGCTGGA
||| ||||| |||||
AGA CGAGACAG GGGTCCGACCT
A _

GAM1882 TSN 3' CCAGCCTGGGCAACAAAGTGAG 17297 C
A TCTCGCT TGTTGCCCAGGCTGG
||||| |||||
AGAGTGA ACAACGGGTCCGACC
A

GAM1882 TSNAX 3' TCCAGCCTGGGTAACAGAGCAA 21160 C
GA TCT GCTCTGTTGCCCAGGCTGGA
||| |||||
AGA CGAGACAATGGGTCCGACCT
A

GAM1882 UBE2B 3' TCCAGCCTGGGTGACAGAGC 13938 TG
GCTCTGT CCCAGGCTGGA
||||| |||||
CGAGACA GGGTCCGACCT
GT

GAM1882 UBE2G2 3' TCCAGCCTGGGCAACAGAGCGA 65495
GA TCTCGCTCTGTTGCCCAGGCTGGA
|||||
AGAGCGAGACAACGGGTCCGACCT

GAM1882 UBE2G2 3' TCCAGCCTGGGCAACAGAGTGA 65496
GA TCTCGCTCTGTTGCCCAGGCTGGA
|||||
AGAGTGAGACAACGGGTCCGACCT

GAM1882 UC28 3' TCCAGCCTGGGCAACAGGAGT 41590 _
GCTC TGTTGCCCAGGCTGGA
||| |||||
TGAG ACAACGGGTCCGACCT
G

GAM1882 USP14 3' TCCAGCCTGGGTGACAGAGAGA 18940 G TG
TC CTCTGT CCCAGGCTGGA
|| ||||| |||||
AG GAGACA GGGTCCGACCT
A GT

GAM1882 VHL 3' CCAGCCTGGGAAACAAGAG 6841 _ G
CTCT GTT CCCAGGCTGG
||| ||| |||||
GAGA CAA GGGTCCGACC
A A

GAM1882 VHL 3' TCCAGCCTGGGGGACAGAGCAA 6876 C G
GA TCT GCTCTGTT CCCAGGCTGGA
||| ||||| |||||

			AGA CGAGACAG GGGTCCGACCT		
			A G		
GAM1882	VHL	3'	TCCAGCCTGTGTGACAGAGC 6877	TG C	
			GCTCTGT C CAGGCTGGA		
			CGAGACA G GTCCGACCT		
			GT T		
GAM1882	VPS41	3'	TCCAGCCTGGGCAACAAGAGC 27697	—	
			GCTCT GTTGCCCAGGCTGGA		
			CGAGA CAACGGGTCCGACCT		
			A		
GAM1882	WIG1	3'	TCCAGCCTGGGTGACAGAGCGA 96105	TG	
	GA		TCTCGCTCTGT CCCAGGCTGGA		
			AGAGCGAGACA GGGTCCGACCT		
			GT		
GAM1882	XT3	3'	TCCAGTCTGGGCGACAGAGCAA 39918	C	
	GA		TCT GCTCTGTTGCCAGGCTGGA		
			AGA CGAGACAGCGGGTCTGACCT		
			A		
GAM1882	ZNF14	3'	TCCAGCCTGTGCGACAGAATGA 41058	C C	
	GA		TCTCG TCTGTTGC CAGGCTGGA		
			AGAGT AGACAGCG GTCCGACCT		
			A T		
GAM1882	ZNF264	3'	TCCAGCCTGGGCAACAGAGCGA 14232		
	GA		TCTCGCTCTGTTGCCAGGCTGGA		
			AGAGCGAGACAACGGGTCCGACCT		
GAM1882	ZNF264	3'	TCCAGCCTGGGCAGCAGAGCGA 14233		
	GA		TCTCGCTCTGTTGCCAGGCTGGA		
			AGAGCGAGACGACGGGTCCGACCT		
GAM1882	ZNF36	3'	TCCAGCCTGGGTGACTAGC 95587	CT TG	
			GCT GT CCCAGGCTGGA		
			CGA CA GGGTCCGACCT		
			T_ GT		
GAM1882	ZNF91	3'	CCTGGGCGACAGAGCGAGA 14280		
			TCTCGCTCTGTTGCCAGG		
			AGAGCGAGACAGCGGGTCC		
GAM1882	AF020591	3'	TCCAGCCTGGGCAACAGAGCAA 27916	C	
	GA		TCT GCTCTGTTGCCAGGCTGGA		

			AGA CGAGACAACGGGTCCGACCT		
			A		
GAM1882	ALTE	3'	TCCAGCCTGGAGGCCAGAGTGA 61006	_	GC
	GA		TCTCGCTCTG TT CCAGGCTGGA		
			AGAGTGAGAC GG GGTCCGACCT		
			C A_		
GAM1882	ALTE	3'	TCCAGCCTGGGCGACAAGAGCG 61007	_	
	AGA		TCTCGCTCT GTTGCCAGGCTGGA		
			AGAGCGAGA CAGCGGTCCGACCT		
			A		
GAM1882	AP1GBP1	3'	TCTGAGCGACAGAGCAAGA 24356	C	C
			TCT GCTCTGTTGC CAGG		
			AGA CGAGACAGCG GTCT		
			A A		
GAM1882	AP4S1	3'	TCCAATCTGGCAACAGAGCGAG 23965		C GC
	A		TCTCGCTCTGTTGCC AG TGGA		
			AGAGCGAGACAACGG TC ACCT		
			_ TA		
GAM1882	APOF	3'	TCCAGCCTGGGTGACAGAGCGA 9696		TG
	GA		TCTCGCTCTGT CCCAGGCTGGA		
			AGAGCGAGACA GGGTCCGACCT		
			GT		
GAM1882	APXL2	3'	TCCAGCCTGGGCGACAGAGCAA 75686	C	
	GA		TCT GCTCTGTTGCCAGGCTGGA		
			AGA CGAGACAGCGGGTCCGACCT		
			A		
GAM1882	ARNTL2	3'	CCAGCCTGGGCGACAGAGCGAG 39843		
	A		TCTCGCTCTGTTGCCAGGCTGG		
			AGAGCGAGACAGCGGGTCCGACC		
GAM1882	ARNTL2	3'	TCCAGTCTGGGCAACAGAGTGA 39858		
	GA		TCTCGCTCTGTTGCCAGGCTGGA		
			AGAGTGAGACAACGGGTCTGACCT		
GAM1882	ASAH	3'	TCTAGCCTGGGCAACAGAGCGA 64321		
	GA		TCTCGCTCTGTTGCCAGGCTGGA		
			AGAGCGAGACAACGGGTCCGATCT		
GAM1882	ATP1B4	3'	TCCAGCCTGGGTGACAGAGTGA 24852		TG
	GA		TCTCGCTCTGT CCCAGGCTGGA		

			AGAGTGAGACA GGGTCCGACCT	
			GT	
GAM1882	BANP	3'	TCCAGACTGTGCGACAGAGCGA 66805	C G
	GA		TCTCGCTCTGTTGC CAG CTGGA	
			AGAGCGAGACAGCG GTC GACCT	
			T A	
GAM1882	BIRC1	3'	TCCAGCCTGGGCAACAGAGCAA 16995	C
	GA		TCT GCTCTGTTGCCCAGGCTGGA	
			AGA CGAGACAACGGGTCCGACCT	
			A	
GAM1882	BIVM	3'	TCCAGCCTGGGCAACAGGGCAA 35160	C
	GA		TCT GCTCTGTTGCCCAGGCTGGA	
			AGA CGGGACAACGGGTCCGACCT	
			A	
GAM1882	BLOV1	3'	TCCAGCCTGGGCAACAAGAGCG 76799	—
	A		TCGCTCT GTTGCCCAGGCTGGA	
			AGCGAGA CAACGGGTCCGACCT	
			A	
GAM1882	BLOV1	3'	TCCAGCCTGGGCGACAGAGCAA 76800	C
	GA		TCT GCTCTGTTGCCCAGGCTGGA	
			AGA CGAGACAGCGGGTCCGACCT	
			A	
GAM1882	BTN3A2	3'	TCCAGCCTGGGAGACAGAGCGA 23880	TG
	GA		TCTCGCTCTGT CCCAGGCTGGA	
			AGAGCGAGACA GGGTCCGACCT	
			GA	
GAM1882	C12orf2	3'	TCCAGCCTGGGTAACAGAGTGA 83688	
	GA		TCTCGCTCTGTTGCCCAGGCTGGA	
			AGAGTGAGACAATGGGTCCGACCT	
GAM1882	C13orf1	3'	TCCAGCCTAGGCAACAGAGTGA 40372	C
	GA		TCTCGCTCTGTTGCC AGGCTGGA	
			AGAGTGAGACAACGG TCCGACCT	
			A	
GAM1882	C1orf33	3'	TCCAGCCTGGGCAACAGAGT 32987	
			GCTCTGTTGCCCAGGCTGGA	
			TGAGACAACGGGTCCGACCT	
GAM1882	C1orf34	3'	CCTGGGCGACAGAGCGAGA 61304	
			TCTCGCTCTGTTGCCCAGG	

AGAGCGAGACAGCGGGTCC

GAM1882 C1QTNF2 3' TCCAGCCTGGGCAACAGAGTGA 49977
GA TCTCGCTCTGTTGCCCAGGCTGGA
|||||
AGAGTGAGACAACGGGTCCGACCT

GAM1882 C20orf106 3' TCCAGCCCAGGTGACAGAGTGA 55914 TG CA
GA TCTCGCTCTGT CC GGCTGGA
||||| || |||||
AGAGTGAGACA GG CCGACCT
GT AC

GAM1882 C20orf108 3' TCCAGCCTGGGCGACAGAGGGA 55883 G
GA TCTC CTCTGTTGCCCAGGCTGGA
||| |||||||
AGAG GAGACAGCGGGTCCGACCT
G

GAM1882 C20orf112 3' TCCAGCCTGGGCAACAAGAGC 36850 _
GCTCT GTTGCCCAGGCTGGA
|||| |||||||
CGAGA CAACGGGTCCGACCT
A

GAM1882 C20orf142 3' TCCAGCCTGAGCGACAGAGTGA 75289 C
GA TCTCGCTCTGTTGC CAGGCTGGA
||||| |||||
AGAGTGAGACAGCG GTCCGACCT
A

GAM1882 C20orf154 3' CTTGGGCAACATAGCAAGA 90049 C C
TCT GCT TGTTGCCCAGG
||| ||| |||||||
AGA CGA ACAACGGGTTC
A T

GAM1882 C20orf172 3' TCCAGCCTGAGCGACAGAGTGA 46768 C
GA TCTCGCTCTGTTGC CAGGCTGGA
||||| |||||
AGAGTGAGACAGCG GTCCGACCT
A

GAM1882 C20orf177 3' TCCAGCCTGGGCAACAAGAGGG 62841 G _
A TC CTCT GTTGCCCAGGCTGGA
|| ||| |||||||
AG GAGA CAACGGGTCCGACCT
G A

GAM1882 C20orf183 3' TCCAGGCTGGGCGACAGAGCGA 48537 G
GA TCTCGCTCTGTTGCCCAG CTGGA
||||| |||||
AGAGCGAGACAGCGGGTC GACCT
G

GAM1882 C20orf29 3' TCCAGCCTGGGCAACAGAGTGA 37712
GA TCTCGCTCTGTTGCCCAGGCTGGA
|||||

AGAGTGAGACAACGGGTCCGACCT

GAM1882 C21orf108 3' TCCAGCCTAGGTGACAGAGCAA 90121 C TG C
GA TCT GCTCTGT CC AGGCTGGA

||| ||||| || |||||
AGA CGAGACA GG TCCGACCT
A GT A

GAM1882 C22orf19 3' TCTGGACAACAGAGCAAGA 14831 C C
TCT GCTCTGTTG CCAGG

||| ||||| ||||
AGA CGAGACAAC GGTCT
A A

GAM1882 C22orf20 3' TCCAGCCTGGGCAACATGAGTG 48200 _
A TCGCTC TGTTGCCCAGGCTGGA

||||| |||||||||
AGTGAG ACAACGGGTCCGACCT
T

GAM1882 C6orf5 3' TCCAGCCTGGGCAATAGAGTGA 32004
GA TCTCGCTCTGTTGCCCAGGCTGGA

||||| |||||||||
AGAGTGAGATAACGGGTCCGACCT

GAM1882 C8orf17 3' CAGCCTGGGCAACAGAATGAGA 39990 C
TCTCG TCTGTTGCCCAGGCTG

||||| |||||||||
AGAGT AGACAACGGGTCCGAC
A

GAM1882 C9orf5 3' TCCAGCCTGGGTGAGAGAGTGA 50108 G TG
GA TCTCGCTCT T CCCAGGCTGGA

||||| | |||||
AGAGTGAGA A GGGTCCGACCT
G GT

GAM1882 CAMKK2 5' TCCAGCCTGGGCAACACAGAGA 22630 G C
GA TCTC CT TGTTGCCCAGGCTGGA

||| || |||||||||
AGAG GA ACAACGGGTCCGACCT
A C

GAM1882 CAMKK2 5' TCCAGCGTGGGCGACAGAGCGA 22631 G
GA TCTCGCTCTGTTGCCCA GCTGGA

||||| |||||
AGAGCGAGACAGCGGGT CGACCT
G

GAM1882 CBCIP2 3' TCCAGCCTGGGCGACAGAGCCA 52661 C
GA TCT GCTCTGTTGCCCAGGCTGGA

||| |||||||||
AGA CGAGACAGCGGGTCCGACCT
C

GAM1882 CCR6 3' TCCAGCCTGGGTGACAGAGCGA 49408 TG
GA TCTCGCTCTGT CCCAGGCTGGA

||||| |||||

			AGAGCGAGACA GGGTCCGACCT		
			GT		
GAM1882	CDT1	3'	TCCAGCCTGGGTGACAGAGCGA 78166	TG	
	GA		TCTCGCTCTGT CCCAGGCTGGA		
			AGAGCGAGACA GGGTCCGACCT		
			GT		
GAM1882	CENTA2	3'	TCCAGCCTGGGTGACAGAGCGA 37868	TG	
	GA		TCTCGCTCTGT CCCAGGCTGGA		
			AGAGCGAGACA GGGTCCGACCT		
			GT		
GAM1882	cerk	3'	TCCAGCCTGGGCAACAGAGGGA 43169	G	
	GA		TCTC CTCTGTTGCCAGGCTGGA		
			AGAG GAGACAACGGGTCCGACCT		
			G		
GAM1882	CG012	5'	TCCAGCCCAGGTGACAGAGGGA 84166	G	TG CA
	GA		TCTC CTCTGT CC GGCTGGA		
			AGAG GAGACA GG CCGACCT		
			G GT AC		
GAM1882	CG012	3'	TCCAGCCTCGCCGACAAAGCGA 84167	C	CCC
	GA		TCTCGCT TGTG AGGCTGGA		
			AGAGCGA ACAGC TCCGACCT		
			A CGC		
GAM1882	CG012	5'	TCCAGCCTGGGCAACAGAACGA 84168	C	
	GA		TCTCG TCTGTTGCCAGGCTGGA		
			AGAGC AGACAACGGGTCCGACCT		
			A		
GAM1882	CGI-203	3'	TCCAGCCTGGGTGACAGAGTGA 40277	TG	
	GA		TCTCGCTCTGT CCCAGGCTGGA		
			AGAGTGAGACA GGGTCCGACCT		
			GT		
GAM1882	CHRFAM7A	3'	CCTGGGCGACAAAGCAAGA 96717	C	C
			TCT GCT TGTTGCCAGG		
			AGA CGA ACAGCGGGTCC		
			A A		
GAM1882	CNNM1	3'	CCTAGGCAACAGAGCGAGA 40117	C	
			TCTCGCTCTGTTGCC AGG		
			AGAGCGAGACAACGG TCC		
			A		
GAM1882	CPR2	3'	TCCAGCCATACAGAACAGAGA 48838	GC_	TGCCCA
			TCTC TCTGT GGCTGGA		

			AGAG AGACA CCGACCT		
			ACA TA_____		
GAM1882	CPR2	3'	TCCAGCCTGGGCGACAGAGTGA 48839		
	GA		TCTCGCTCTGTTGCCCAGGCTGGA		
			AGAGTGAGACAGCGGGTCCGACCT		
GAM1882	CPR2	3'	TCCAGCCTGGGTAACAGAGCAA 48840	C	
	GA		TCT GCTCTGTTGCCCAGGCTGGA		
			AGA CGAGACAATGGGTCCGACCT		
			A		
GAM1882	CRTAM	3'	TCCAGCCTGGGCGACAGAGGGA 39476	G	
	GA		TCTC CTCTGTTGCCCAGGCTGGA		
			AGAG GAGACAGCGGGTCCGACCT		
			G		
GAM1882	CSAD	3'	TCCAGGCTGGGCAACAGTACGA 32585	CT	G
	GA		TCTCG CTGTTGCCCAG CTGGA		
			AGAGC GACAACGGGTC GACCT		
			AT G		
GAM1882	CXYorf1	3'	CCAGCCCAAACGTGTGACAGGAG 82906	GCT	TG CCA_____
	A		TCTC CTGT C GGCTGG		
			AGAG GACA G CCGACC		
			_____ GT TCAAAC		
GAM1882	CYB5-M	3'	CCTGGGCAACATAGCGAGA 96201	C	
			TCTCGCT TGTTGCCCAGG		
			AGAGCGA ACAACGGGTCC		
			T		
GAM1882	D21S2056E	3'	TCCAGCCTGGGCAACGAGAGGG 14873	G	T
	A		TCTC CTC GTTGCCCAGGCTGGA		
			AGGG GAG CAACGGGTCCGACCT		
			A _		
GAM1882	DCOHM	3'	TCCAGCCTGGGTGACGGAACGG 50537	C	TG
	GA		TCTCG TCTGT CCCAGGCTGGA		
			AGGGC AGGCA GGGTCCGACCT		
			A GT		
GAM1882	DDX34	3'	TCCAGCCTGGTTGACAGAGCAA 28678	C	GC
	GA		TCT GCTCTGTT CCAGGCTGGA		
			AGA CGAGACAG GGTCCGACCT		
			A TT		
GAM1882	DEGS	3'	TCCACCCTGGGCAACAGAGCAA 59270	C	C
	GA		TCT GCTCTGTTGCCCAGG TGGA		

			AGA CGAGACAACGGGTCC ACCT		
			A C		
GAM1882	DEGS	3'	TCCACCCTGGGCAACAGAGCAA 59271	C	C
	GA		TCT GCTCTGTTGCCCAGG TGGA		
			AGA CGAGACAACGGGTCC ACCT		
			A C		
GAM1882	DIS3	3'	TCCAGCCTGGGTGACAGAACAA 30922	CGC	TG
	GA		TCT TCTGT CCCAGGCTGGA		
			AGA AGACA GGGTCCGACCT		
			ACA GT		
GAM1882	dJ383J4.3	3'	TCCAGCCTGGGCAACAAAGTGA 67498	C	
	GA		TCTCGCT TGTTGCCCAGGCTGGA		
			AGAGTGA ACAACGGGTCCGACCT		
			A		
GAM1882	DKFZP434A0131	3'	TCCAGCCTGGGTGACAGAGCAA 39154	C	TG
	GA		TCT GCTCTGT CCCAGGCTGGA		
			AGA CGAGACA GGGTCCGACCT		
			A GT		
GAM1882	DKFZP434B168	3'	TCCAGCCTGGGCGACAGAGCGA 31872		
	GA		TCTCGCTCTGTTGCCCAGGCTGGA		
			AGAGCGAGACAGCGGGTCCGACCT		
GAM1882	DKFZP434C171	3'	TCCAGCCCGGGTGACAGAGCAA 32199	C	TG A
	GA		TCT GCTCTGT CCC GGCTGGA		
			AGA CGAGACA GGG CCGACCT		
			A GT C		
GAM1882	DKFZp434E0519	3'	TCTGGGCAACACAGCAAGA 51001	C	C
			TCT GCT TGTTGCCCAGG		
			AGA CGA ACAACGGGTCT		
			A C		
GAM1882	DKFZp434E169	3'	CCTGGGCGACAGAGCGAGA 51076		
			TCTCGCTCTGTTGCCCAGG		
			AGAGCGAGACAGCGGGTCC		
GAM1882	DKFZP434F1735	3'	TCCAGCCTGGGCAGTATAGCAA 32117	C	C
	GA		TCT GCT TGTTGCCCAGGCTGGA		
			AGA CGA ATGACGGGTCCGACCT		
			A T		
GAM1882	DKFZp434G171	3'	TCCAGCCTGGGAGACACAGCGA 80247	C	TG
	GA		TCTCGCT TGT CCCAGGCTGGA		

		AGAGCGA ACA GGGTCCGACCT		
		C GA		
GAM1882	DKFZp434G171 3'	TCCAGCCTGGGCAACAAGAGGG 80248	G	_
	A	TC CTCT GTTGCCCAGGCTGGA		
		AG GAGA CAACGGGTCCGACCT		
		G A		
GAM1882	DKFZP434I1735 3'	TCCAGCCTGGGCGACAGAGTGA 89173		
	GA	TCTCGCTCTGTTGCCAGGCTGGA		
		AGAGTGAGACAGCGGGTCCGACCT		
GAM1882	DKFZP434K1421 3'	TCCAACCTGGGCAACAGAATGA 50468	C	C
	GA	TCTCG TCTGTTGCCAGG TGA		
		AGAGT AGACAACGGGTCC ACCT		
		A A		
GAM1882	DKFZP434N1511 3'	TCCAGCCTGGGCAACAGAGCAA 93063	C	
	GA	TCT GCTCTGTTGCCAGGCTGGA		
		AGA CGAGACAACGGGTCCGACCT		
		A		
GAM1882	DKFZP434N161 3'	CCTGGGCAACACAGCAAGA 79214	C	C
		TCT GCT TGTTGCCAGG		
		AGA CGA ACAACGGGTCC		
		A C		
GAM1882	DKFZp547C176 3'	TCCAGCCTGGCGACAGAGCAAG 67806	C	C
	A	TCT GCTCTGTTGCC AGGCTGGA		
		AGA CGAGACAGCGG TCCGACCT		
		A		
GAM1882	DKFZp547G183 3'	TCCAGCCTGGGCGACAAGAGC 38649		_
		GCTCT GTTGCCCAGGCTGGA		
		CGAGA CAGCGGGTCCGACCT		
		A		
GAM1882	DKFZp547I094 3'	TCCAGCCTGGGCGGCAGAGTGA 50566		
	GA	TCTCGCTCTGTTGCCAGGCTGGA		
		AGAGTGAGACGGCGGGTCCGACCT		
GAM1882	DKFZP564A022 3'	TCCAGCCTGGGCAACAGAGTGA 48975		
	GA	TCTCGCTCTGTTGCCAGGCTGGA		
		AGAGTGAGACAACGGGTCCGACCT		
GAM1882	DKFZP564B1023 3'	TCCAGCCTGGACAACAGATTGA 49368	C	C
	GA	TCTCG TCTGTTG CCAGGCTGGA		

		AGAGT AGACAAC GGTCCGACCT		
		T A		
GAM1882	DKFZP564B1023 3'	TCCAGCCTGGGCAACAAGAGTG 49369	—	
	A	TCGCTCT GTTGCCCAGGCTGGA		
		AGTGAGA CAACGGGTCCGACCT		
		A		
GAM1882	DKFZP564I0422 5'	TCCAGCCTCTGCCAGAAGA 49518	GC	TT CC
		TC TCTG GC AGGCTGGA		
		AG AGAC CG TCCGACCT		
		A_ _ TC		
GAM1882	DKFZP564I0422 3'	TCCAGCCTGGGCAATGGAGTGA 49519		
	GA	TCTCGCTCTGTTGCCAGGCTGGA		
		AGAGTGAGGTAACGGGTCCGACCT		
GAM1882	DKFZP564I052 3'	TCCAGGCTGGGCAACAGAGTGA 67286		G
	GA	TCTCGCTCTGTTGCCAG CTGGA		
		AGAGTGAGACAACGGGTC GACCT		
		G		
GAM1882	DKFZp564K142 3'	TCCAGCCTGAGTGATAGAGTGA 50436		TG C
	GA	TCTCGCTCTGT C CAGGCTGGA		
		AGAGTGAGATA G GTCCGACCT		
		GT A		
GAM1882	DKFZp564K142 3'	TCCAGCCTGGCAACAGAGCGAG 50437		C
	A	TCTCGCTCTGTTGCC AGGCTGGA		
		AGAGCGAGACAACGG TCCGACCT		
GAM1882	DKFZP564M182 3'	TCCAGCCTGATGACAGAGCAAG 78642	C	CC
	A	TCT GCTCTGTTG CAGGCTGGA		
		AGA CGAGACAGT GTCCGACCT		
		A A_		
GAM1882	DKFZP564M182 3'	TCCAGCCTGGGCAACAGAGAGA 78643		G
	GA	TCTC CTCTGTTGCCAGGCTGGA		
		AGAG GAGACAACGGGTCCGACCT		
		A		
GAM1882	DKFZP564M182 3'	TCCAGCCTGGGCGGCAGAGC 78644		
		GCTCTGTTGCCAGGCTGGA		
		CGAGACGGCGGGTCCGACCT		
GAM1882	DKFZp566H0824 3'	TCCAGCCTGGGCAACAGAGCAA 34492		C
	GG	TCT GCTCTGTTGCCAGGCTGGA		

			GGA CGAGACAACGGGTCCGACCT	
		A		
GAM1882	DKFZp566H0824	5'	TCCAGCCTGGGCGACAGAGCGA 34493	
	GA		TCTCGCTCTGTTGCCCAGGCTGGA	
			AGAGCGAGACAGCGGGTCCGACCT	
GAM1882	DKFZP586D2223	3'	CCTGGGCAACATAGCGAGA 38288	C
			TCTCGCT TGTTGCCCAGG	
			AGAGCGA ACAACGGGTCC	
		T		
GAM1882	DKFZP586D2223	3'	TCTAGCCTGGGCAACAGAGTGA 38297	
	GA		TCTCGCTCTGTTGCCCAGGCTGGA	
			AGAGTGAGACAACGGGTCCGATCT	
GAM1882	DKFZP586M1120	3'	TCCAGCCTGGGCAACAGAGTGA 49286	
			TCGCTCTGTTGCCCAGGCTGGA	
			AGTGAGACAACGGGTCCGACCT	
GAM1882	DKFZP667O116	3'	CCTGGGCAACATAGCGAGA 95940	C
			TCTCGCT TGTTGCCCAGG	
			AGAGCGA ACAACGGGTCC	
		T		
GAM1882	DKFZp727G131	3'	TCCAGCCTGGGCAACAGCGTGA 59698	T
	GA		TCTCGC CTGTTGCCCAGGCTGGA	
			AGAGTG GACAACGGGTCCGACCT	
		C		
GAM1882	DKFZP761G1913	3'	TCCAGCCTGGGTGAAGGAGTGA 49699	G TG
	GA		TCTCGCTCT T CCCAGGCTGGA	
			AGAGTGAGG A GGGTCCGACCT	
		A GT		
GAM1882	DRF1	3'	TCCAGCCTGGGCGATAGAGCTA 47757	C
	GA		TCT GCTCTGTTGCCCAGGCTGGA	
			AGA CGAGATAGCGGGTCCGACCT	
		T		
GAM1882	DRF1	3'	TCCAGCCTGGGTGACAGAGCGA 47758	TG
	GA		TCTCGCTCTGT CCCAGGCTGGA	
			AGAGCGAGACA GGGTCCGACCT	
		GT		
GAM1882	DSCR6	3'	TCCAGCCTGGGCAACAAGAGCG 39076	—
	A		TCGCTCT GTTGCCCAGGCTGGA	

			AGCGAGA CAACGGGTCCGACCT		
			A		
GAM1882	EVI5	3'	TCCAACCTGGGCAACATGGCAA 20218	C C	C
	GA		TCT GCT TGTTGCCAGG TGGA		
			AGA CGG ACAACGGGTCC ACCT		
			A T A		
GAM1882	FADS1	3'	TCCAGCCTGGGCGACAGAGCAA 26386	C	
	GA		TCT GCTCTGTTGCCAGGCTGGA		
			AGA CGAGACAGCGGGTCCGACCT		
			A		
GAM1882	FADS1	3'	TCCAGCCTGGGGTGATAGAACA 26387	CGC TG	_
	AGA		TCT TCTGT CCC AGGCTGGA		
			AGA AGATA GGG TCCGACCT		
			ACA GT G		
GAM1882	FBXO26	3'	TCCAGCCTGGGTGAGAAAGCAA 46631	C CTG TG	
	GA		TCT GCT T CCCAGGCTGGA		
			AGA CGA A GGGTCCGACCT		
			A AAG GT		
GAM1882	FBXO27	3'	TCCAGCCTGGGCAACACAGCGA 75014	C	
	GA		TCTCGCT TGTTGCCAGGCTGGA		
			AGAGCGA ACAACGGGTCCGACCT		
			C		
GAM1882	FBXO27	3'	TCCAGCCTGGGTGACAGAGCGA 75015	TG	
	GA		TCTCGCTCTGT CCCAGGCTGGA		
			AGAGCGAGACA GGGTCCGACCT		
			GT		
GAM1882	FBXO6	3'	TCCAGCCTGGGTGACAGAGCGA 37997	TG	
	GA		TCTCGCTCTGT CCCAGGCTGGA		
			AGAGCGAGACA GGGTCCGACCT		
			GT		
GAM1882	FBXO9	3'	TCCAGCCTGAGCAACACAGTGA 25655	C C	
	GA		TCTCGCT TGTTGC CAGGCTGGA		
			AGAGTGA ACAACG GTCCGACCT		
			C A		
GAM1882	FBXO9	3'	CCTGGACAACATAGCAAGA 54244	C C C	
			TCT GCT TGTTG CCAGG		
			AGA CGA ACAAC GGTCC		
			A T A		
GAM1882	FBXO9	3'	TCCAGCATGGGCAACATAACAA 54254	CGCTC	G
	GA		TCT TGTTGCCCA GCTGGA		

			AGA ACAACGGGT CGACCT		
			ACAAT A		
GAM1882	FKBP14	3'	TCCAGCCTGGGTGACAGAGCAA 36070	C	TG
	GA		TCT GCTCTGT CCCAGGCTGGA		
			AGA CGAGACA GGGTCCGACCT		
			A GT		
GAM1882	FKSG17	3'	TCCAGCCTGGGTGACAGAGTGA 50159		TG
	GA		TCTCGCTCTGT CCCAGGCTGGA		
			AGAGTGAGACA GGGTCCGACCT		
			GT		
GAM1882	FKSG43	5'	TCCAGCCTGGGTGACAGAGCAA 50163	C	TG
	GA		TCT GCTCTGT CCCAGGCTGGA		
			AGA CGAGACA GGGTCCGACCT		
			A GT		
GAM1882	FKSG44	5'	TCCAGCCTGGGCGACAGAGCGA 49963		
	GA		TCTCGCTCTGTTGCCAGGCTGGA		
			AGAGCGAGACAGCGGGTCCGACCT		
GAM1882	FKSG83	3'	TCCAGCCTGGGAGACAGCAAGA 50146	GCT	TG
			TC CTGT CCCAGGCTGGA		
			AG GACA GGGTCCGACCT		
			AAC GA		
GAM1882	FLJ00060	3'	TCCAGCCTGGGCGATAGAGCAA 61755	C	
	GA		TCT GCTCTGTTGCCAGGCTGGA		
			AGA CGAGATAGCGGGTCCGACCT		
			A		
GAM1882	FLJ10008	3'	TCCAGCCTGGGCGACACAGCAA 36193	C C	
	GA		TCT GCT TGTTGCCAGGCTGGA		
			AGA CGA ACAGCGGGTCCGACCT		
			A C		
GAM1882	FLJ10043	3'	TCCAGCCTGGGTGACAGAGCGA 36237		TG
	GA		TCTCGCTCTGT CCCAGGCTGGA		
			AGAGCGAGACA GGGTCCGACCT		
			GT		
GAM1882	FLJ10058	3'	TCCAGCCTGGGCAACACAGTGA 36264	C	
	GA		TCTCGCT TGTTGCCAGGCTGGA		
			AGAGTGA ACAACGGGTCCGACCT		
			C		
GAM1882	FLJ10139	3'	TCCAGCCTGGGTGACAAAGTAA 36317	CG C	TG
	GA		TCT CT TGT CCCAGGCTGGA		


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          AGA GA ACA GGGTCCGACCT
          AT A  GT
GAM1882 FLJ10157 5' CCAGCCTGGACCAGAAGA 36329 GC TTGC
          TC TCTG CCAGGCTGG
          || ||| |||||
          AG AGAC GGTCCGACC
          A_ CA__
GAM1882 FLJ10159 3' CCATTTGGGAACAGAGCAAGA 36335 C G C
          TCT GCTCTGTT CCCAGG TGG
          ||| ||||| ||||| |||
          AGA CGAGACAA GGGTTT ACC
          A _ _
GAM1882 FLJ10244 3' TCCAGCCTGGGCAAAAAGAGC 36406 G_
          GCTCT TTGCCCAGGCTGGA
          |||| |||||
          CGAGA AACGGGTCCGACCT
          AA
GAM1882 FLJ10460 3' TCCAACCTGGGTGATGGAGCAA 36623 C TG C
          GA TCT GCTCTGT CCCAGG TGGA
          ||| ||||| ||||| |||
          AGA CGAGGTA GGGTCC ACCT
          A GT A
GAM1882 FLJ10520 3' TCCAGCCTCGGTGACAGAGCAA 36710 C TG C
          GA TCT GCTCTGT CC AGGCTGGA
          ||| ||||| ||| |||||
          AGA CGAGACA GG TCCGACCT
          A GT C
GAM1882 FLJ10547 3' TCCAGCCTGGGCTACAGAGCGA 36779 T
          GA TCTCGCTCTGT GCCCAGGCTGGA
          ||||| |||||
          AGAGCGAGACA CGGGTCCGACCT
          T
GAM1882 FLJ10597 3' CCAGCCTGGGCTGACAGG 36835 _
          TCTGTT GCCCAGGCTGG
          ||||| |||||
          GGACAG CGGGTCCGACC
          T
GAM1882 FLJ10607 3' TCCAGCCTGGCGACAGAGAGAG 77646 G C
          A TCTC CTCTGTTGCC AGGCTGGA
          ||| ||||| |||||
          AGAG GAGACAGCGG TCCGACCT
          A _
GAM1882 FLJ10613 3' TCTAGCCTGGGCAACAACACGA 39341 CTC
          TCG TGTTGCCCAGGCTGGA
          ||| |||||
          AGC ACAACGGGTCCGATCT
          ACA
GAM1882 FLJ10650 3' TCCAGCCTGGGCGACAGAATGA 36903 C
          GA TCTCG TCTGTTGCCCAGGCTGGA
          ||||| |||||

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AGAGT AGACAGCGGGTCCGACCT
A
GAM1882 FLJ10704 3' TCCAGCCTGGACGACAGAGTGA 36984 C
GA TCTCGCTCTGTTG CCAGGCTGGA
||||| |||||
AGAGTGAGACAGC GGTCCGACCT
A
GAM1882 FLJ10781 3' TCCAGCCTGGGCAGCAGAGTGA 37176
GA TCTCGCTCTGTTGCCAGGCTGGA
|||||
AGAGTGAGACGACGGGTCCGACCT

GAM1882 FLJ10803 3' TCCAGCCTGGGCAACAGAGCAA 37209 C
GA TCT GCTCTGTTGCCAGGCTGGA
||| |||||
AGA CGAGACAACGGGTCCGACCT
A
GAM1882 FLJ10826 3' TCCAGCCTGGGCAACAAGAGTG 37250 _
A TCGCTCT GTTGCCAGGCTGGA
||||| |||||
AGTGAGA CAACGGGTCCGACCT
A
GAM1882 FLJ10830 3' TCCAGCCTGGGCGACAGAACGA 37267 C
GA TCTCG TCTGTTGCCAGGCTGGA
|||| |||||
AGAGC AGACAGCGGGTCCGACCT
A
GAM1882 FLJ10901 3' CCAGCCTGGGCTGGGGGAGA 37355 G TGTT
TCTC CTC GCCAGGCTGG
|||| ||| |||||
AGAG GGG CGGGTCCGACC
G T__
GAM1882 FLJ10936 3' TCCAGCCTGGGCAACAGAGGGA 37450 G
GA TCTC CTCTGTTGCCAGGCTGGA
|||| |||||
AGAG GAGACAACGGGTCCGACCT
G
GAM1882 FLJ10989 3' TCCAGCCTGGGTGACAAAGCAA 37507 C C TG
GA TCT GCT TGT CCCAGGCTGGA
||| ||| ||| |||||
AGA CGA ACA GGGTCCGACCT
A A GT
GAM1882 FLJ10998 3' TCCAGCCTGGGTGACAGTGA 37523 CT TG
TCGCT GT CCCAGGCTGGA
|||| || |||||
AGTGA CA GGGTCCGACCT
__ GT
GAM1882 FLJ11016 3' CCTGGGCAACACAGCAAGA 37540 C C
TCT GCT TGTTGCCAGG
||| ||| |||||

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		AGA CGA ACAACGGGTCC	
		A C	
GAM1882	FLJ11036	3' TCCAGCCTGGGCGACAGAGCAA 37556	C
	GA	TCT GCTCTGTTGCCCAGGCTGGA	
		AGA CGAGACAGCGGGTCCGACCT	
		A	
GAM1882	FLJ11126	3' TCCAGCCTGGGTAACAGAGCGA 37655	
	GA	TCTCGCTCTGTTGCCCAGGCTGGA	
		AGAGCGAGACAATGGGTCCGACCT	
GAM1882	FLJ11149	3' TCTGGGCAACATAGCGAGA 37689	C
		TCTCGCT TGTTGCCCAGG	
		AGAGCGA ACAACGGGTCT	
		T	
GAM1882	FLJ11151	3' TCCAGCCTGGGCAACAGAGCAA 68482	C
	GA	TCT GCTCTGTTGCCCAGGCTGGA	
		AGA CGAGACAACGGGTCCGACCT	
		A	
GAM1882	FLJ11259	3' TCCAGTCTGGGCAACAGAGTGA 37772	
	GA	TCTCGCTCTGTTGCCCAGGCTGGA	
		AGAGTGAGACAACGGGTCTGACCT	
GAM1882	FLJ11301	3' TCCAGCCTGGGCGACAGAGTGA 37810	
	GA	TCTCGCTCTGTTGCCCAGGCTGGA	
		AGAGTGAGACAGCGGGTCCGACCT	
GAM1882	FLJ11577	3' TCCAGCCTGGGCAACAAGAGTG 47960	_
	AGA	TCTCGCTCT GTTGCCCAGGCTGGA	
		AGAGTGAGA CAACGGGTCCGACCT	
		A	
GAM1882	FLJ11700	3' TCCAGCCTGGGCAACAGAACAA 46567	CGC
	GA	TCT TCTGTTGCCCAGGCTGGA	
		AGA AGACAACGGGTCCGACCT	
		ACA	
GAM1882	FLJ11710	5' TCCAGCCTGGGCAACAGAGCAA 46252	C
	GA	TCT GCTCTGTTGCCCAGGCTGGA	
		AGA CGAGACAACGGGTCCGACCT	
		A	
GAM1882	FLJ11715	3' TCCAGCCTGGGTGATAGAGTGA 44983	TG
	GA	TCTCGCTCTGT CCCAGGCTGGA	

AGAGTGAGATA GGGTCCGACCT
 GT
 GAM1882 FLJ11722 3' TCCAGCCTGGCAACAGAGCAAG 47008 C C
 G TCT GCTCTGTTGCC AGGCTGGA
 ||| ||||| |||||
 GGA CGAGACAACGG TCCGACCT
 A _
 GAM1882 FLJ11722 3' TCCAGCCTGGCCACAGAGCGAG 47009 T C
 A TCTCGCTCTGT GCC AGGCTGGA
 ||||| ||| |||||
 AGAGCGAGACA CGG TCCGACCT
 C _
 GAM1882 FLJ11726 3' TCCAGCCTGGGCGACAGAGCAG 47031 TC
 GA TC GCTCTGTTGCCCAGGCTGGA
 || ||||| |||||
 AG CGAGACAGCGGGTCCGACCT
 GA
 GAM1882 FLJ11800 3' TCCAGCCTGGGCAACAGAG 47042
 CTCTGTTGCCCAGGCTGGA
 ||||| |||||
 GAGACAACGGGTCCGACCT

 GAM1882 FLJ11827 3' CCTGGGCAACATAGCAAGA 47681 C C
 TCT GCT TGTTGCCCAGG
 ||| ||| |||||
 AGA CGA ACAACGGGTCC
 A T
 GAM1882 FLJ11996 3' TCCAACCTGGGCAACAGAGTAA 47069 CG C
 GA TCT CTCTGTTGCCCAGG TGGA
 ||| ||||| |||||
 AGA GAGACAACGGGTCC ACCT
 AT A
 GAM1882 FLJ12056 3' TCAGCCCGGGCAACAAGAGCGA 46823 _ A
 GA TCTCGCTCT GTTGCCG GCTGG
 ||||| ||||| |||||
 AGAGCGAGA CAACGGG CCGACT
 A C
 GAM1882 FLJ12078 3' TCCAGCCTGGGTGGCAGAGAGA 47086 G TG
 GA TCTC CTCTGT CCCAGGCTGGA
 ||| ||||| |||||
 AGAG GAGACG GGGTCCGACCT
 A GT
 GAM1882 FLJ12190 3' TCCAGCCTGGGCAACAGAGC 47572
 GCTCTGTTGCCCAGGCTGGA
 ||||| ||||| |||||
 CGAGACAACGGGTCCGACCT

 GAM1882 FLJ12294 3' TCCAGCCTGGGTGACAGAGAGA 47721 G TG
 GA TCTC CTCTGT CCCAGGCTGGA
 ||| ||||| |||||

		AGAG GAGACA GGGTCCGACCT		
		A GT		
GAM1882	FLJ12298	3' TCCAGCCTGGGCAACAGAGCGA 50600		
	GA	TCTCGCTCTGTTGCCAGGCTGGA		
		AGAGCGAGACAACGGGTCCGACCT		
GAM1882	FLJ12331	3' TCCAGCCTGAGCTACAGAGCAA 47114	C	T C
	GA	TCT GCTCTGT GC CAGGCTGGA		
		AGA CGAGACA CG GTCCGACCT		
		A T A		
GAM1882	FLJ12363	3' TCCAGCCTGGGCAACAAGAGAG 50643	G	C
	A	TCTC CT TGTTGCCAGGCTGGA		
		AGAG GA ACAACGGGTCCGACCT		
		A _		
GAM1882	FLJ12586	3' TCCAGCCTGGGTGACAGAGCGA 45212		TG
	GA	TCTCGCTCTGT CCCAGGCTGGA		
		AGAGCGAGACA GGGTCCGACCT		
		GT		
GAM1882	FLJ12592	3' CCTGGGCAACATAGCGAGA 50650		C
		TCTCGCT TGTTGCCAGG		
		AGAGCGA ACAACGGGTCC		
		T		
GAM1882	FLJ12592	3' TCCAGCCTGGGTGACCGAGTGA 50655		T TG
	GA	TCTCGCTC GT CCCAGGCTGGA		
		AGAGTGAG CA GGGTCCGACCT		
		C GT		
GAM1882	FLJ12618	3' TCCAGCCTGGGTGACAGAGCAA 46508	C	TG
	GA	TCT GCTCTGT CCCAGGCTGGA		
		AGA CGAGACA GGGTCCGACCT		
		A GT		
GAM1882	FLJ12666	3' TCCAGCCTGGGCAACAAAACGA 45072		CTC
	GA	TCTCG TGTTGCCAGGCTGGA		
		AGAGC ACAACGGGTCCGACCT		
		AAA		
GAM1882	FLJ12671	3' TCCAGCCTGGGTGACAAGAGTG 49112		_ TG
	AGA	TCTCGCTCT GT CCCAGGCTGGA		
		AGAGTGAGA CA GGGTCCGACCT		
		A GT		
GAM1882	FLJ12687	3' TCCAGCCTGGGTGACAGAGTGA 46759		TG
	GA	TCTCGCTCTGT CCCAGGCTGGA		

		AGAGTGAGACA GGGTCCGACCT		
		GT		
GAM1882	FLJ12847	3' TCCAGCCTGGGCAACAGAGT 45079		
		GCTCTGTTGCCCAGGCTGGA		
		TGAGACAACGGGTCCGACCT		
GAM1882	FLJ12921	3' TCCAGCCTGGGCGACGGAGCGA 46400		
	GA	TCTCGCTCTGTTGCCCAGGCTGGA		
		AGAGCGAGGCAGCGGGTCCGACCT		
GAM1882	FLJ12949	3' TCCAGCCTGGGCAACAAAGCAA 43727	C	C
	GA	TCT GCT TGTTGCCCAGGCTGGA		
		AGA CGA ACAACGGGTCCGACCT		
		A A		
GAM1882	FLJ13117	3' TCCAGCCTGGGAGACAGAGCAA 43811	C	TG
	GA	TCT GCTCTGT CCCAGGCTGGA		
		AGA CGAGACA GGGTCCGACCT		
		A GA		
GAM1882	FLJ13193	3' TCCAGCCTGGCGACAGAGCGAG 50736		C
	A	TCTCGCTCTGTTGCC AGGCTGGA		
		AGAGCGAGACAGCGG TCCGACCT		
GAM1882	FLJ13241	3' TCCAGCCTGGGTGGCAGAGCCA 47656	C	TG
	GA	TCT GCTCTGT CCCAGGCTGGA		
		AGA CGAGACG GGGTCCGACCT		
		C GT		
GAM1882	FLJ13352	3' CTGGCCTGGGCAACAGAGCAAG 45053	C	TG
	A	TCT GCTCTGTTGCCAGGC G		
		AGA CGAGACAACGGGTCCG C		
		A GT		
GAM1882	FLJ13448	3' TCCAGCCTGGGCAACAGAGGGA 47885		G
	GA	TCTC CTCTGTTGCCAGGCTGGA		
		AGAG GAGACAACGGGTCCGACCT		
		G		
GAM1882	FLJ13456	3' CCTGGGAAACAGAGCGAGA 66542		G
		TCTCGCTCTGTT CCCAGG		
		AGAGCGAGACAA GGGTCC		
		A		
GAM1882	FLJ13456	3' TCCAGCCTGGACAACGGAGTGA 66563		C
	GA	TCTCGCTCTGTTG CCAGGCTGGA		

AGAGTGAGGCAAC GGTCCGACCT
 A
 GAM1882 FLJ13456 3' TCCAGCCTGGGTGACAGAGTAA 66564 CG TG
 GA TCT CTCTGT CCCAGGCTGGA
 ||| ||||| |||||
 AGA GAGACA GGGTCCGACCT
 AT GT
 GAM1882 FLJ13544 3' TCCAGCCTGGATGACAGAGTGA 47210 GC
 GA TCTCGCTCTGTT CCAGGCTGGA
 ||||| |||||
 AGAGTGAGACAG GGTCCGACCT
 TA
 GAM1882 FLJ13621 3' TCCAGCCTGGGCGACAGAGCGA 47226
 GA TCTCGCTCTGTTGCCAGGCTGGA
 |||||
 AGAGCGAGACAGCGGGTCCGACCT

 GAM1882 FLJ13659 3' TCCAGCCTGGGCAACAAGAGTG 48036 —
 G TCGCTCT GTTGCCCAGGCTGGA
 ||||| |||||
 GGTGAGA CAACGGGTCCGACCT
 A
 GAM1882 FLJ13769 3' TCCAGCCTGGGTGACAGAGCGA 47264 TG
 GA TCTCGCTCTGT CCCAGGCTGGA
 ||||| |||||
 AGAGCGAGACA GGGTCCGACCT
 GT
 GAM1882 FLJ13848 3' TCCAGCCTAGGCGACAGAGTGA 45831 C
 GA TCTCGCTCTGTTGCC AGGCTGGA
 ||||| |||||
 AGAGTGAGACAGCGG TCCGACCT
 A
 GAM1882 FLJ13902 3' CCTGGGCAATAGAGCGAGA 45380
 TCTCGCTCTGTTGCCAGG
 |||||
 AGAGCGAGATAACGGGTCC

 GAM1882 FLJ13952 3' TCCAGCCTGGGCAACAAGAGTG 46021 —
 A TCGCTCT GTTGCCCAGGCTGGA
 ||||| |||||
 AGTGAGA CAACGGGTCCGACCT
 A
 GAM1882 FLJ14011 3' TCCAGTCTGGGCAACAGAGCAA 42320 C
 GA TCT GCTCTGTTGCCAGGCTGGA
 ||| |||||
 AGA CGAGACAACGGGTCTGACCT
 A
 GAM1882 FLJ14100 3' TCCAGCCTGGGCGACAAAGCAA 47340 C C
 GA TCT GCT TGTTGCCAGGCTGGA
 ||| ||| |||||

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          AGA CGA ACAGCGGGTCCGACCT
          A A
GAM1882 FLJ14117 3' TCCAGCCTGGGCAACAGA 43233
          TCTGTTGCCCAGGCTGGA
          |||||
          AGACAACGGGTCCGACCT

GAM1882 FLJ14117 3' TCCAGCTTGGGCAACAGAGCAA 43235 C
          GA          TCT GCTCTGTTGCCCAGGCTGGA
          ||| |||||
          AGA CGAGACAACGGGTTCGACCT
          A

GAM1882 FLJ14154 3' CCAGCCTGAGGAGGAGGGAGA 46226 G GTTG _
          TCTC CTCT CC CAGGCTGG
          ||| ||| || |||||
          AGAG GAGG GG GTCCGACC
          G A__ A

GAM1882 FLJ14251 3' TCCAGCCTGGGTAACAGAGCGA 46491
          GA          TCTCGCTCTGTTGCCCAGGCTGGA
          |||||
          AGAGCGAGACAATGGGTCCGACCT

GAM1882 FLJ14326 3' TCCAGCTTGGGCAACGAGC 50784 T
          GCTC GTTGCCCAGGCTGGA
          ||| |||||
          CGAG CAACGGGTTCGACCT

GAM1882 FLJ14327 3' TCCAGCCTGGACAACAGAGCTA 46688 C C
          GA          TCT GCTCTGTTG CCAGGCTGGA
          ||| ||||| |||||
          AGA CGAGACAAC GGTCCGACCT
          T A

GAM1882 FLJ14327 3' TCCAGCCTGGATAATAGAGTGA 46689 C
          GA          TCTCGCTCTGTTG CCAGGCTGGA
          ||||| |||||
          AGAGTGAGATAAT GGTCCGACCT
          A

GAM1882 FLJ14345 3' TCCAGCCTGGGCAACAAGAGTG 45662 _
          A          TCGCTCT GTTGCCCAGGCTGGA
          ||||| |||||
          AGTGAGA CAACGGGTCCGACCT
          A

GAM1882 FLJ14346 3' CCTGGGCAACATAGCAAGA 47362 C C
          TCT GCT TGTTGCCCAGG
          ||| ||| |||||
          AGA CGA ACAACGGGTCC
          A T

GAM1882 FLJ14346 3' TCCAGCCTGGGCAACAGAGCAA 47372 C
          GA          TCT GCTCTGTTGCCCAGGCTGGA
          ||| |||||

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			AGA CGAGACAACGGGTCCGACCT		
			A		
GAM1882	FLJ14346	3'	TCCAGCCTGGGGGACAGAGCGA 47373	G	
	GA		TCTCGCTCTGTT CCCAGGCTGGA		
			AGAGCGAGACAG GGGTCCGACCT		
			G		
GAM1882	FLJ14397	3'	TCCAGCCTGGGCAACAAGGGC 52333	—	
			GCTCT GTTGCCCAGGCTGGA		
			CGGGA CAACGGGTCCGACCT		
			A		
GAM1882	FLJ14397	3'	TCCAGCCTGGGTGACAGAGCAA 52335	C	TG
	GA		TCT GCTCTGT CCCAGGCTGGA		
			AGA CGAGACA GGGTCCGACCT		
			A GT		
GAM1882	FLJ14431	3'	CCTGAGCAACATAGCAAGA 52367	C C	C
			TCT GCT TGTTGC CAGG		
			AGA CGA ACAACG GTCC		
			A T A		
GAM1882	FLJ14457	3'	TCCAGCCTGGGAGACAGAGTGA 52413		TG
	GA		TCTCGCTCTGT CCCAGGCTGGA		
			AGAGTGAGACA GGGTCCGACCT		
			GA		
GAM1882	FLJ14466	3'	TCCAACCTGGGCAACAGAGGGA 52431	G	C
	GA		TCTC CTCTGTTGCCAGG TGGA		
			AGAG GAGACAACGGGTCC ACCT		
			G A		
GAM1882	FLJ14466	3'	TCCAGCCTGGGCAACAACAGTG 52432	C_	
	A		TCGCT TGTTGCCAGGCTGGA		
			AGTGA ACAACGGGTCCGACCT		
			CA		
GAM1882	FLJ14490	3'	TCCAGCCTGGGCAACAGAGCAA 52448	C	
	GA		TCT GCTCTGTTGCCAGGCTGGA		
			AGA CGAGACAACGGGTCCGACCT		
			A		
GAM1882	FLJ14621	3'	TCCAGCCTGGGCAACAGAGC 52540		
			GCTCTGTTGCCAGGCTGGA		
			CGAGACAACGGGTCCGACCT		
GAM1882	FLJ14888	3'	CCTGGGCAACATAGCAAGA 52747	C C	
			TCT GCT TGTTGCCAGG		

			AGA CGA ACAACGGGTCC		
			A T		
GAM1882	FLJ20004	3'	TCCAGCCTAGGCAACAAGAGTG 34765	—	C
	A		TCGCTCT GTTGCC AGGCTGGA		
			AGTGAGA CAACGG TCCGACCT		
			A A		
GAM1882	FLJ20004	3'	TCCAGCCTGGCAACAGAGCAAG 34766	C	C
	A		TCT GCTCTGTTGCC AGGCTGGA		
			AGA CGAGACAACGG TCCGACCT		
			A —		
GAM1882	FLJ20004	3'	TCCAGCCTGGGCAACAGAGGGA 34767	G	
	GA		TCTC CTCTGTTGCCAGGCTGGA		
			AGAG GAGACAACGGGTCCGACCT		
			G		
GAM1882	FLJ20004	3'	TCCAGCCTGGGTGACAGAGTGA 34768		TG
	GA		TCTCGCTCTGT CCCAGGCTGGA		
			AGAGTGAGACA GGGTCCGACCT		
			GT		
GAM1882	FLJ20006	3'	TCCAGCCTGGGCGATAGAGTGA 34788		
	GA		TCTCGCTCTGTTGCCAGGCTGGA		
			AGAGTGAGATAGCGGGTCCGACCT		
GAM1882	FLJ20013	3'	TCCAGCCTCGGTGACAGAGCAA 34803	C	TG C
	GA		TCT GCTCTGT CC AGGCTGGA		
			AGA CGAGACA GG TCCGACCT		
			A GT C		
GAM1882	FLJ20019	3'	TCCAGCCTAGGTGACAGGGCAA 34816	C	TG C
	GA		TCT GCTCTGT CC AGGCTGGA		
			AGA CGGGACA GG TCCGACCT		
			A GT A		
GAM1882	FLJ20045	3'	TCCAGCCTGGGTGAGAAGAGCG 34893		G_ TG
	A		TCGCTCT T CCCAGGCTGGA		
			AGCGAGA A GGGTCCGACCT		
			AG GT		
GAM1882	FLJ20055	3'	TCCAGCTGGGCAACACAGCAAG 34914	C C	G
	A		TCT GCT TGTTGCCAG CTGGA		
			AGA CGA ACAACGGGTC GACCT		
			A C —		
GAM1882	FLJ20059	3'	TCCAGCCTGGACAGCAGGAGCG 34930	—	C
	A		TCGCTC TGTTG CCAGGCTGGA		

			AGCGAG ACGAC GGTCCGACCT		
			G A		
GAM1882	FLJ20069	3'	TCCAGCCTGGGGGACAGAGCAA 34957	C	G
	GA		TCT GCTCTGTT CCCAGGCTGGA		
			AGA CGAGACAG GGGTCCGACCT		
			A G		
GAM1882	FLJ20084	3'	TCCAGCCTGGGCAACAGAGCGA 34999		
	GA		TCTCGCTCTGTTGCCCAGGCTGGA		
			AGAGCGAGACAACGGGTCCGACCT		
GAM1882	FLJ20139	3'	TCCAGCCTGCGTGACAAAGTGA 35122	C	TG C
	GA		TCTCGCT TGT C CAGGCTGGA		
			AGAGTGA ACA G GTCCGACCT		
			A GT C		
GAM1882	FLJ20139	3'	TTGGGCAACAAAGCAAGA 35124	C	C
			TCT GCT TGTTGCCCAG		
			AGA CGA ACAACGGGTT		
			A A		
GAM1882	FLJ20170	3'	TCCAGCCTGGGTGACAGAGTGA 35166		TG
	GA		TCTCGCTCTGT CCCAGGCTGGA		
			AGAGTGAGACA GGGTCCGACCT		
			GT		
GAM1882	FLJ20211	3'	TCCAGCCTGGGCAACAGAGTGA 35266		
	GA		TCTCGCTCTGTTGCCCAGGCTGGA		
			AGAGTGAGACAACGGGTCCGACCT		
GAM1882	FLJ20211	3'	TCCAGCCTGGGCGACAGAGTGA 35267		
	GA		TCTCGCTCTGTTGCCCAGGCTGGA		
			AGAGTGAGACAGCGGGTCCGACCT		
GAM1882	FLJ20241	3'	TCCAGCCTGGACAACAGAGCGA 35291		C
	GA		TCTCGCTCTGTTG CCAGGCTGGA		
			AGAGCGAGACAAC GGTCCGACCT		
			A		
GAM1882	FLJ20280	3'	TCCAGCCTGGGTGACAGAGCGA 35334		TG
	GA		TCTCGCTCTGT CCCAGGCTGGA		
			AGAGCGAGACA GGGTCCGACCT		
			GT		
GAM1882	FLJ20306	3'	TCCAGCCTGGACGACTGAGTGA 35399	T	C
	GA		TCTCGCTC GTTG CCAGGCTGGA		

			AGAGTGAG CAGC GGTCCGACCT		
			T A		
GAM1882	FLJ20306	3'	TCCAGCCTGGCGACAGAGCAAG 35400	C	C
	A		TCT GCTCTGTTGCC AGGCTGGA		
			AGA CGAGACAGCGG TCCGACCT		
			A _		
GAM1882	FLJ20340	3'	TCCAGCCTGGTGACAGAGCGAG 35460	TG	C
	A		TCTCGCTCTGT CC AGGCTGGA		
			AGAGCGAGACA GG TCCGACCT		
			GT _		
GAM1882	FLJ20456	3'	TCCAGCCTGGGTAACAGAGCTA 35666	C	
	GA		TCT GCTCTGTTGCCAGGCTGGA		
			AGA CGAGACAATGGGTCCGACCT		
			T		
GAM1882	FLJ20546	3'	TCCAGCCTGGGCAACGAGCGA 35814	T	
			TCGCTC GTTGCCCAGGCTGGA		
			AGCGAG CAACGGGTCCGACCT		
			_		
GAM1882	FLJ20671	3'	TCCAGCCTGGGTGACAGAGCGA 35945	TG	
	GA		TCTCGCTCTGT CCCAGGCTGGA		
			AGAGCGAGACA GGGTCCGACCT		
			GT		
GAM1882	FLJ20694	3'	TCCAGCCTGGCGACAGAGCAAG 35979	C	C
	A		TCT GCTCTGTTGCC AGGCTGGA		
			AGA CGAGACAGCGG TCCGACCT		
			A _		
GAM1882	FLJ20700	3'	TCCAGCCTGGGCGACACAGCGA 36020	C	
	GA		TCTCGCT TGTTGCCAGGCTGGA		
			AGAGCGA ACAGCGGGTCCGACCT		
			C		
GAM1882	FLJ20802	3'	TCCAGCCTGGGCGACAGAGCGA 36114		
	GA		TCTCGCTCTGTTGCCAGGCTGGA		
			AGAGCGAGACAGCGGGTCCGACCT		
GAM1882	FLJ20825	3'	TCCAGCCTGGCCACAGAGTGA 36148	TGC	
	GA		TCTCGCTCTGT CCAGGCTGGA		
			AGAGTGAGACA GGTCCGACCT		
			CCC		
GAM1882	FLJ20825	3'	TCCAGCCTGGGCAACAAGAGCG 36149	_	
	A		TCGCTCT GTTGCCCAGGCTGGA		

AGCGAGA CAACGGGTCCGACCT
 A
 GAM1882 FLJ20972 3' TCCAGCCTGGGCAACAAGAGAA 47389 CG _
 GA TCT CTCT GTTGCCCAGGCTGGA
 ||| ||| |||||||||
 AGA GAGA CAACGGGTCCGACCT
 A_ A
 GAM1882 FLJ21144 3' TCCAGCCTGGGCAACAGAGTGA 43194
 GA TCTCGCTCTGTTGCCCAGGCTGGA
 |||||||||||||
 AGAGTGAGACAACGGGTCCGACCT

 GAM1882 FLJ21240 3' TCCAGCCTGGGCAAAAAGAGC 46268 G_
 GCTCT TTGCCCAGGCTGGA
 |||| |||||||||
 CGAGA AACGGGTCCGACCT
 AA
 GAM1882 FLJ21369 3' TCCAGCCTGGGTGACAGAGCAA 46056 C TG
 GA TCT GCTCTGT CCCAGGCTGGA
 ||| ||||| |||||||
 AGA CGAGACA GGGTCCGACCT
 A GT
 GAM1882 FLJ21687 3' TCCAGCCTGGGTGACAGAGCGA 46304 TG
 GA TCTCGCTCTGT CCCAGGCTGGA
 ||||||| |||||||
 AGAGCGAGACA GGGTCCGACCT
 GT
 GAM1882 FLJ21870 3' TCCAGCCTGGGCAACGGAG 43750
 CTCTGTTGCCCAGGCTGGA
 |||||||||||||
 GAGGCAACGGGTCCGACCT

 GAM1882 FLJ22009 3' TCCAGCTTGGGCGACAGAGCGA 60921
 GA TCTCGCTCTGTTGCCCAGGCTGGA
 |||||||||||||
 AGAGCGAGACAGCGGGTTCGACCT

 GAM1882 FLJ22054 3' TCCAGCCTGGGCAACAGAGCAA 96053 C
 GA TCT GCTCTGTTGCCCAGGCTGGA
 ||| |||||||||||||
 AGA CGAGACAACGGGTCCGACCT
 A
 GAM1882 FLJ22316 3' TCCAGCCTGGGCAACAGAGCCA 47619 C
 GG TCT GCTCTGTTGCCCAGGCTGGA
 ||| |||||||||||||
 GGA CGAGACAACGGGTCCGACCT
 C
 GAM1882 FLJ22415 3' TCCAGCCTGGGTGACAAAGCAA 93121 C C TG
 GA TCT GCT TGT CCCAGGCTGGA
 ||| ||| ||| |||||||

			AGA CGA ACA GGGTCCGACCT		
			A A GT		
GAM1882	FLJ22474	3'	TCCAGCCTGGGCAACAGAGTGA 45618		
	GA		TCTCGCTCTGTTGCCAGGCTGGA		
			AGAGTGAGACAACGGGTCCGACCT		
GAM1882	FLJ22644	3'	TCCAGCCTGGGCTACAGAGCGA 47703	T	
	GA		TCTCGCTCTGT GCCCAGGCTGGA		
			AGAGCGAGACA CGGGTCCGACCT		
			T		
GAM1882	FLJ22814	3'	TCCAACCTGGGTGACGAGTGAG 46731	T TG	C
	A		TCTCGCTC GT CCCAGG TGGA		
			AGAGTGAG CA GGGTCC ACCT		
			_ GT A		
GAM1882	FLJ22814	3'	TCCAGCCTGGGTGACAGAGGGA 46732	G TG	
			TC CTCTGT CCCAGGCTGGA		
			AG GAGACA GGGTCCGACCT		
			G GT		
GAM1882	FLJ23022	3'	TCCAGCCTGGGCGACAAGAGC 47499	_	
			GCTCT GTTGCCAGGCTGGA		
			CGAGA CAGCGGGTCCGACCT		
			A		
GAM1882	FLJ23040	3'	TCCAGCCTGGGCAATAGAGCAA 47992	C	
	GA		TCT GCTCTGTTGCCAGGCTGGA		
			AGA CGAGATAACGGGTCCGACCT		
			A		
GAM1882	FLJ23042	3'	CCTGAGCAACAGATCAAGA 47941	CGC	C
			TCT TCTGTTGC CAGG		
			AGA AGACAACG GTCC		
			ACT A		
GAM1882	FLJ23042	3'	TCCAGCCTGGGCAACAAGAGTG 47949	_	
	A		TCGCTCT GTTGCCAGGCTGGA		
			AGTGAGA CAACGGGTCCGACCT		
			A		
GAM1882	FLJ23120	3'	TCCAGCCTGGGTGACGGAGAAA 86330	CG TG	
	GA		TCT CTCTGT CCCAGGCTGGA		
			AGA GAGGCA GGGTCCGACCT		
			AA GT		
GAM1882	FLJ23185	3'	TCCAGCCTTGCGCAACAAGCAA 47522	C C C	
	GA		TCT GCT TGTTGCC AGGCTGGA		

			AGA CGA ACAACGG TCCGACCT	
			A A T	
GAM1882	FLJ23185	3'	TCCAGCCTTGGCAACAGAGTGA 47523	C
	GA		TCTCGCTCTGTTGCC AGGCTGGA	
			AGAGTGAGACAACGG TCCGACCT	
			T	
GAM1882	FLJ23209	3'	CCTGGGCAACATAGCAAGA 46586	C C
			TCT GCT TGTTGCCCAGG	
			AGA CGA ACAACGGGTCC	
			A T	
GAM1882	FLJ23229	3'	TCCAGCCTGGACAACAGAGCAA 47532	C C
	GA		TCT GCTCTGTTG CCAGGCTGGA	
			AGA CGAGACAAC GGTCCGACCT	
			A A	
GAM1882	FLJ23360	3'	TCCAGCCCGGGTGACAGAGCGA 43835	TG A
	GA		TCTCGCTCTGT CCC GGCTGGA	
			AGAGCGAGACA GGG CCGACCT	
			GT C	
GAM1882	FLJ23447	3'	CTGGGCAACAGAGCAAGA 46132	C
			TCT GCTCTGTTGCCCAG	
			AGA CGAGACAACGGGTC	
			A	
GAM1882	FLJ23499	3'	CCTGGGCAACATAGCAAGA 43132	C C
			TCT GCT TGTTGCCCAGG	
			AGA CGA ACAACGGGTCC	
			A T	
GAM1882	FLJ23499	3'	TCCAGCCTGGGCGACAAGAGCG 43140	—
	A		TCGCTCT GTTGCCCAGGCTGGA	
			AGCGAGA CAGCGGGTCCGACCT	
			A	
GAM1882	FLJ23537	3'	TCCAGCCTGGGCAACAAGAGGA 88921	G —
			TC CTCT GTTGCCCAGGCTGGA	
			AG GAGA CAACGGGTCCGACCT	
			— A	
GAM1882	FLJ23556	3'	CTGGGCAACAAAGCAAGA 46439	C C
			TCT GCT TGTTGCCCAG	
			AGA CGA ACAACGGGTC	
			A A	
GAM1882	FLJ23556	3'	TCCAGCCTGGGCGACTGTGAGA 46455	TCT
			TCTCGC GTTGCCCAGGCTGGA	

			AGAGTG CAGCGGGTCCGACCT		
			T__		
GAM1882	FLJ23878	3'	TCCAGCCTGGGTGACAGGGCGA 59373	TG	
	GA		TCTCGCTCTGT CCCAGGCTGGA		
			AGAGCGGGACA GGGTCCGACCT		
			GT		
GAM1882	FLJ25006	3'	TCCAGCCTGAGCAACAGAGTGA 58789	C	
	GA		TCTCGCTCTGTTGC CAGGCTGGA		
			AGAGTGAGACAACG GTCCGACCT		
			A		
GAM1882	FLJ30092	3'	TCCAGCCTGGGCAACAGAGTGA 59342		
	G		CTCGCTCTGTTGCCCAGGCTGGA		
			GAGTGAGACAACGGGTCCGACCT		
GAM1882	FLJ30681	3'	TCCAGCCTAGGCAACAGAGGGA 93440	G	C
	GA		TCTC CTCTGTTGCC AGGCTGGA		
			AGAG GAGACAACGG TCCGACCT		
			G A		
GAM1882	FLJ31168	3'	TCCAGCCTGGGCGACAGAGCGA 59186		
	GA		TCTCGCTCTGTTGCCCAGGCTGGA		
			AGAGCGAGACAGCGGGTCCGACCT		
GAM1882	FLJ31455	3'	TCCAGCCTGGGCGACAGAGCCA 59291	C	
	GA		TCT GCTCTGTTGCCCAGGCTGGA		
			AGA CGAGACAGCGGGTCCGACCT		
			C		
GAM1882	FLJ31455	3'	TCCAGCCTGGGTGACAGAGCAA 59292	C	TG
	GA		TCT GCTCTGT CCCAGGCTGGA		
			AGA CGAGACA GGGTCCGACCT		
			A GT		
GAM1882	FLJ31952	3'	TCCAGCCTGGGCAACAGAGTGA 59050		
	GA		TCTCGCTCTGTTGCCCAGGCTGGA		
			AGAGTGAGACAACGGGTCCGACCT		
GAM1882	FLJ32499	5'	TCCAGTGACCGACAGAGCAAGA 58782	C	CCCAG
			TCT GCTCTGTTG GCTGGA		
			AGA CGAGACAGC TGACCT		
			A CAG__		
GAM1882	FLJ32915	5'	TCCAGCCTGGGCGACAAGAGCG 59437		
	AGA		TCTCGCTCT GTTGCCCAGGCTGGA		

			AGAGCGAGA CAGCGGGTCCGACCT	
			A	
GAM1882	FRSB	3'	TCCAGCCTGGGTGACAGAGTGA 20293	TG
	GA		TCTCGCTCTGT CCCAGGCTGGA	
			AGAGTGAGACA GGGTCCGACCT	
			GT	
GAM1882	FUSIP1	3'	TCCAGCCTGGGCAACAGAGTGA 55043	
	GA		TCTCGCTCTGTTGCCAGGCTGGA	
			AGAGTGAGACAACGGGTCCGACCT	
GAM1882	GALNT6	3'	CCAGCCTGAGCAACAAGAGCGA 24244	_ C
			TCGCTCT GTTGC CAGGCTGG	
			AGCGAGA CAACG GTCCGACC	
			A A	
GAM1882	GALNT6	3'	TCCAGCCTGGGCAACAGGTAAG 24252	CG T
	A		TCT C CTGTTGCCAGGCTGGA	
			AGA G GACAACGGGTCCGACCT	
			AT _	
GAM1882	GCN2	3'	CCAGCCTGAGCAACAAAGCAAG 63437	C C C
	A		TCT GCT TGTTGC CAGGCTGG	
			AGA CGA ACAACG GTCCGACC	
			A A A	
GAM1882	GCN2	3'	TCCAGTCTGGGACAACAGAGCA 63440	C _
	AGA		TCT GCTCTGTTG CCCAGGCTGGA	
			AGA CGAGACAAC GGGTCTGACCT	
			A A	
GAM1882	GGA2	3'	TCCAGCCTGGGCTACATAGTGA 57683	C T
	GA		TCTCGCT TGT GCCCAGGCTGGA	
			AGAGTGA ACA CGGGTCCGACCT	
			T T	
GAM1882	GGA2	3'	TCCAGCCTGGGCTACATAGTGA 31172	C T
	GA		TCTCGCT TGT GCCCAGGCTGGA	
			AGAGTGA ACA CGGGTCCGACCT	
			T T	
GAM1882	GLTP	3'	TCCAGCCTGGGCAACAAGAGCG 33588	_
	A		TCGCTCT GTTGCCAGGCTGGA	
			AGCGAGA CAACGGGTCCGACCT	
			A	
GAM1882	GNB4	3'	TCCAGCCTAGGCGACAGAGTGA 41570	C
	GA		TCTCGCTCTGTTGCC AGGCTGGA	

			AGAGTGAGACAGCGG TCCGACCT		
			A		
GAM1882	GP5	3'	CCTGGGCGACAGAGCGAGA 16872		
			TCTCGCTCTGTTGCCAGG		
			AGAGCGAGACAGCGGGTCC		
GAM1882	GTPBP5	3'	TCCAGCCTGAGCGACAGAGCAA 65981	C	C
	GA		TCT GCTCTGTTGC CAGGCTGGA		
			AGA CGAGACAGCG GTCCGACCT		
			A A		
GAM1882	GTPBP5	3'	TCCAGCCTGAGTGACAGAGCGA 65982		TG C
	GA		TCTCGCTCTGT C CAGGCTGGA		
			AGAGCGAGACA G GTCCGACCT		
			GT A		
GAM1882	HCGIX	3'	TCCAGCCTGGGTGACAGCAAGA 20716	GCT	TG
	G		CTC CTGT CCCAGGCTGGA		
			GAG GACA GGGTCCGACCT		
			AAC GT		
GAM1882	HEI10	3'	TCCAGCCTGGGCAACAGAGTGA 41299		
	GA		TCTCGCTCTGTTGCCAGGCTGGA		
			AGAGTGAGACAACGGGTCCGACCT		
GAM1882	HES2	3'	TCCAGGCTGGGCGACAGAGCGA 39378		G
	GA		TCTCGCTCTGTTGCCAG CTGGA		
			AGAGCGAGACAGCGGGTC GACCT		
			G		
GAM1882	HIC	3'	TCCAGCCTGGGCAACAGAGCGA 68052		
	GA		TCTCGCTCTGTTGCCAGGCTGGA		
			AGAGCGAGACAACGGGTCCGACCT		
GAM1882	HIG2	3'	CCAGCCTGGGCCACAGTGCAAG 26198	C T	T
	A		TCT GC CTGT GCCCAGGCTGG		
			AGA CG GACA CGGGTCCGACC		
			A T C		
GAM1882	HRH4	3'	CCAGCCTGGCAACAGAGCAAGA 41530	C	C
			TCT GCTCTGTTGCC AGGCTGG		
			AGA CGAGACAACGG TCCGACC		
			A _		
GAM1882	HSA250303	3'	TCCAGCCTGGGCTACAGAGTGA 38023		T
	GA		TCTCGCTCTGT GCCCAGGCTGGA		

			AGAGTGAGACA CGGGTCCGACCT	
			T	
GAM1882	HSD17B7	3'	TCCAGCCTGGGTGACAGCGAGA 33484	CT TG
			TCTCGCT GT CCCAGGCTGGA	
			AGAGCGA CA GGGTCCGACCT	
			__ GT	
GAM1882	HSH2	3'	TCCAGCCTGGATGACAGAGTGA 52744	GC
	GA		TCTCGCTCTGTT CCAGGCTGGA	
			AGAGTGAGACAG GGTCCGACCT	
			TA	
GAM1882	HSMPP8	3'	TCCAGCCTGAGTGACAGAATGA 95141	C TG C
	GA		TCTCG TCTGT C CAGGCTGGA	
			AGAGT AGACA G GTCCGACCT	
			A GT A	
GAM1882	HSU79252	5'	TCCAGCCTGGGTGACAGAGTGA 26143	TG
	GA		TCTCGCTCTGT CCCAGGCTGGA	
			AGAGTGAGACA GGGTCCGACCT	
			GT	
GAM1882	HSU79266	3'	CCAGCCTGAGGAGGGAGCGTGA 26144	T GTTG _
			TC CGCTCT CC CAGGCTGG	
			AG GCGAGG GG GTCCGACC	
			T GA__ A	
GAM1882	HYPK	3'	TCCAGCCTGGGGGAAAGAGTGA 33516	G G
			TCTCTCT TT CCCAGGCTGGA	
			AGTGAGA AG GGGTCCGACCT	
			A G	
GAM1882	ICAM4	3'	TCCAGCCTGGGGGACAGAGC 9545	G
			GCTCTGTT CCCAGGCTGGA	
			CGAGACAG GGGTCCGACCT	
			G	
GAM1882	ICAM4	3'	TCCAGCCTGGGGGACAGAGC 9546	G
			GCTCTGTT CCCAGGCTGGA	
			CGAGACAG GGGTCCGACCT	
			G	
GAM1882	IL-23R	3'	TCCAGCCTGGGCAACAAGAGC 59132	_
			GCTCT GTTGCCCAGGCTGGA	
			CGAGA CAACGGGTCCGACCT	
			A	
GAM1882	IL10RB	3'	TCCAGCCTGGGTGACAAAGTGA 7129	C TG
	GA		TCTCGCT TGT CCCAGGCTGGA	

			AGAGTGA ACA GGGTCCGACCT		
			A GT		
GAM1882	IMAGE:4907098	3'	TCCAGCCTGGGCGACAGAGCAA 57758	C	
	GA		TCT GCTCTGTTGCCCAGGCTGGA		
			AGA CGAGACAGCGGGTCCGACCT		
			A		
GAM1882	KBRAS2	3'	TCCAGCCTGGTCAACAGAGCAA 34628	C	C
	GA		TCT GCTCTGTTG CCAGGCTGGA		
			AGA CGAGACAAC GGTCCGACCT		
			A T		
GAM1882	KCNH6	3'	TCCAGCCTGGGTGACAGAGTGA 48576		TG
	GA		TCTCGCTCTGT CCCAGGCTGGA		
			AGAGTGAGACA GGGTCCGACCT		
			GT		
GAM1882	KIAA0042	3'	TCCAGTCTGAGCAACAGAACGA 30239	C	C
	GA		TCTCG TCTGTTGC CAGGCTGGA		
			AGAGC AGACAACG GTCTGACCT		
			A A		
GAM1882	KIAA0057	3'	TCCAGCCTGGACAACAAGAGCG 25424		C
	A		TCGCTCT GTTG CCAGGCTGGA		
			AGCGAGA CAAC GGTCCGACCT		
			A A		
GAM1882	KIAA0184	3'	TCCAGCCTGGGTGACAGCACGA 65815	CT	TG
	GA		TCTCG CTGT CCCAGGCTGGA		
			AGAGC GACA GGGTCCGACCT		
			AC GT		
GAM1882	KIAA0186	3'	TCCAGCCTGGGTGACAAAGTGA 41119	C	TG
	GA		TCTCGCT TGT CCCAGGCTGGA		
			AGAGTGA ACA GGGTCCGACCT		
			A GT		
GAM1882	KIAA0226	3'	TCCAGCCTGGGTGACAGAGTGA 64264		TG
	GA		TCTCGCTCTGT CCCAGGCTGGA		
			AGAGTGAGACA GGGTCCGACCT		
			GT		
GAM1882	KIAA0336	3'	TCCAGCTCGGGGAACAGAGCGA 28324	G	AG
	GA		TCTCGCTCTGTT CCC GCTGGA		
			AGAGCGAGACAA GGG CGACCT		
			G CT		
GAM1882	KIAA0355	3'	TCCAGCCTGGGTGACAGAGTGA 28710		TG
	GA		TCTCGCTCTGT CCCAGGCTGGA		

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AGAGTGAGACA GGGTCCGACCT
GT
GAM1882 KIAA0391 3' CCTGGGCAACATAGCAAGA 28605 C C
TCT GCT TGTTGCCCAGG
||| ||| |||||
AGA CGA ACAACGGGTCC
A T
GAM1882 KIAA0391 3' TCCAGCCTAGGTGACAGAGTGA 28621 TG C
GA TCTCGCTCTGT CC AGGCTGGA
||||||| || |||||
AGAGTGAGACA GG TCCGACCT
GT A
GAM1882 KIAA0408 3' TCCAGCCTGGGTGACAGAGTGA 28802 TG
GA TCTCGCTCTGT CCCAGGCTGGA
||||||| |||||
AGAGTGAGACA GGGTCCGACCT
GT
GAM1882 KIAA0409 3' TCCAGCCTGGCTGTGAGCCAAG 31682 C_ TGTT C
A TCT GCTC GCC AGGCTGGA
||| ||| ||| |||||
AGA CGAG CGG TCCGACCT
AC TGT_ _
GAM1882 KIAA0427 3' CCAGCCTGGGAACACAGA 29375 TG_
TCTGT CCCAGGCTGG
|||| |||||
AGACA GGGTCCGACC
CAA
GAM1882 KIAA0431 3' TCCAACCTGGGTAACAGGGCAA 31554 C C
GA TCT GCTCTGTTGCCCAGG TGGA
||| ||||| ||||| |||
AGA CGGGACAATGGGTCC ACCT
A A
GAM1882 KIAA0445 5' TCCAGCCTGTGTGACAGAGCAA 28642 C TG C
GA TCT GCTCTGT C CAGGCTGGA
||| ||||| | |||||
AGA CGAGACA G GTCCGACCT
A GT T
GAM1882 KIAA0446 5' TCCAGCCTGGGCGACAGAGCGA 69460
GA TCTCGCTCTGTTGCCCAGGCTGGA
||||||| |||||
AGAGCGAGACAGCGGGTCCGACCT
GAM1882 KIAA0447 3' TCCAGCCTGGGCAACAGGGCAA 72129 C
GA TCT GCTCTGTTGCCCAGGCTGGA
||| ||||| |||||
AGA CGGGACAACGGGTCCGACCT
A
GAM1882 KIAA0451 5' TCAGCCTGGGCAACAGAGCAAG 29781 C
A TCT GCTCTGTTGCCCAGGCTGG
||| ||||| |||||

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		AGA CGAGACAACGGGTCCGACT		
		A		
GAM1882	KIAA0472	3' TCCAGCCTGGGCAACAGAGCGA 72367		
	GA	TCTCGCTCTGTTGCCCAGGCTGGA		
		AGAGCGAGACAACGGGTCCGACCT		
GAM1882	KIAA0472	3' TCCAGCCTGGGCAGCAGAGCAA 72368	C	
	GA	TCT GCTCTGTTGCCCAGGCTGGA		
		AGA CGAGACGACGGGTCCGACCT		
		A		
GAM1882	KIAA0472	3' TCCAGCCTGGGCGACAGAGTGA 72369		
	GA	TCTCGCTCTGTTGCCCAGGCTGGA		
		AGAGTGAGACAGCGGGTCCGACCT		
GAM1882	KIAA0475	3' TCCAGCCTGGGAGACAGAGCGA 30130		TG
	GA	TCTCGCTCTGT CCCAGGCTGGA		
		AGAGCGAGACA GGGTCCGACCT		
		GA		
GAM1882	KIAA0514	3' TCCAGCCTGGATGACGGAGCCA 28755	C	GC
	GA	TCT GCTCTGTT CCAGGCTGGA		
		AGA CGAGGCAG GGTCCGACCT		
		C TA		
GAM1882	KIAA0547	3' TCCAGCCTGGCAACAGAGCAAG 29600	C	C
	A	TCT GCTCTGTTGCC AGGCTGGA		
		AGA CGAGACAACGG TCCGACCT		
		A _		
GAM1882	KIAA0557	3' TCCAGCCTGGTGATAGAACGAG 78576	C	TG C
	A	TCTCG TCTGT CC AGGCTGGA		
		AGAGC AGATA GG TCCGACCT		
		A GT _		
GAM1882	KIAA0563	3' TCCAGCCTGGGCGACAGAGCAA 29890	C	
	GA	TCT GCTCTGTTGCCCAGGCTGGA		
		AGA CGAGACAGCGGGTCCGACCT		
		A		
GAM1882	KIAA0565	3' TCCAACCTGGGCGACAGAGCAA 67441	C	C
	GA	TCT GCTCTGTTGCCCAGG TGGA		
		AGA CGAGACAGCGGGTCC ACCT		
		A A		
GAM1882	KIAA0565	3' TCCAATCTGGGCAACATAGCAA 67442	C C	GC
	GA	TCT GCT TGTTGCCCAG TGGA		

		AGA CGA ACAACGGGTC ACCT	
		A T TA	
GAM1882 KIAA0643	3'	TCCAGCCTGGGTGACAGAGTGA 45980	TG
	GA	TCTCGCTCTGT CCCAGGCTGGA	
		AGAGTGAGACA GGGTCCGACCT	
		GT	
GAM1882 KIAA0694	3'	TCCAGCCTGGGCAACAGAGTGA 72974	
	GA	TCTCGCTCTGTTGCCAGGCTGGA	
		AGAGTGAGACAACGGGTCCGACCT	
GAM1882 KIAA0701	5'	CAGTGAGCAACAGGACGAGA 70094	CT C AG
		TCTCG CTGTTGC C GCTG	
		AGAGC GACAACG G TGAC	
		AG A _	
GAM1882 KIAA0738	3'	TCCAGCCTGGGGGACAGAGTGA 28887	G
	GA	TCTCGCTCTGTT CCCAGGCTGGA	
		AGAGTGAGACAG GGGTCCGACCT	
		G	
GAM1882 KIAA0752	3'	TCCAGCCTGGGCAACGAGCGA 67635	T
		TCGCTC GTTGCCAGGCTGGA	
		AGCGAG CAACGGGTCCGACCT	
GAM1882 KIAA0794	3'	TCCAGCCTGGGCGACAAAGCGA 81238	C
		TCGCT TGTTGCCAGGCTGGA	
		AGCGA ACAGCGGTCCGACCT	
		A	
GAM1882 KIAA0795	3'	TCCAGCCTGGTTGACAGAGTGA 47232	GC
	GA	TCTCGCTCTGTT CCAGGCTGGA	
		AGAGTGAGACAG GGTCCGACCT	
		TT	
GAM1882 KIAA0798	3'	TCCAGCCTGGGCAACAAGAGCG 28455	_
	A	TCGCTCT GTTGCCAGGCTGGA	
		AGCGAGA CAACGGGTCCGACCT	
		A	
GAM1882 KIAA0831	3'	TCCAGCCTGGGCAACAAGAGCG 30655	_
	AGG	TCTCGCTCT GTTGCCAGGCTGGA	
		GGAGCGAGA CAACGGGTCCGACCT	
		A	
GAM1882 KIAA0853	3'	TCCAACCTAGGTGACAGAGCAA 31215	C TG C C
	GA	TCT GCTCTGT CC AGG TGGA	

		AGA CGAGACA GG TCC ACCT	
		A GT A A	
GAM1882	KIAA0872	3' TCCAGCCTGGGTGACAGAGTGA 30762	TG
	GA	TCTCGCTCTGT CCCAGGCTGGA	
		AGAGTGAGACA GGGTCCGACCT	
		GT	
GAM1882	KIAA0876	3' TCCAGCCTGGGCAACAGAGCGA 65319	
	GA	TCTCGCTCTGTTGCCCAGGCTGGA	
		AGAGCGAGACAACGGGTCCGACCT	
GAM1882	KIAA0884	3' TCCAACCTGGGTAACAGAGTGA 70758	C
	GA	TCTCGCTCTGTTGCCCAGG TGGA	
		AGAGTGAGACAATGGGTCC ACCT	
		A	
GAM1882	KIAA0889	3' TCCAGCCTGGGTGACAGAGTGA 31786	TG
	GA	TCTCGCTCTGT CCCAGGCTGGA	
		AGAGTGAGACA GGGTCCGACCT	
		GT	
GAM1882	KIAA0894	3' TCCAGCCTGGGTGACAGAGCGA 30342	TG
	GA	TCTCGCTCTGT CCCAGGCTGGA	
		AGAGCGAGACA GGGTCCGACCT	
		GT	
GAM1882	KIAA0907	3' TCCAGCCTGGGCAATAGAGCAA 30882	C
	GA	TCT GCTCTGTTGCCCAGGCTGGA	
		AGA CGAGATAACGGGTCCGACCT	
		A	
GAM1882	KIAA0907	3' TCCAGCCTGGGCACTAGAGTGA 30883	T
	GA	TCTCGCTCTG TGCCCAGGCTGGA	
		AGAGTGAGAT ACGGGTCCGACCT	
		C	
GAM1882	KIAA0924	3' TCCAGCCTGGGCAACAGAGCGA 30376	
	GA	TCTCGCTCTGTTGCCCAGGCTGGA	
		AGAGCGAGACAACGGGTCCGACCT	
GAM1882	KIAA0961	3' TCCAGCCTGGGCAACAAGAGC 30409	—
		GCTCT GTTGCCCAGGCTGGA	
		CGAGA CAACGGGTCCGACCT	
		A	
GAM1882	KIAA0981	3' TCCAGCCTGGGCAACAGAGCAA 62093	C
	GA	TCT GCTCTGTTGCCCAGGCTGGA	


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          AGA CGAGACAACGGGTCCGACCT
          A
GAM1882 KIAA1001 3' TCCAGCCTGGGTGATGGAGCAA 31012   C   TG
          GA          TCT GCTCTGT CCCAGGCTGGA
          ||| ||||| |||||
          AGA CGAGGTA GGGTCCGACCT
          A   GT
GAM1882 KIAA1032 3' TCCAGCCTGGGCAACAGA   66732
          TCTGTTGCCCAGGCTGGA
          |||||
          AGACAACGGGTCCGACCT

GAM1882 KIAA1086 3' CCAGCCCAGACAACAGAGTGAG 71284       CCCA
          A          TCTCGCTCTGTTG   GGCTGG
          ||||| ||||
          AGAGTGAGACAAC   CCGACC
          AGAC
GAM1882 KIAA1086 3' TCCAGCCTGGGCAACAGAAGAA 71289   _GC
          GA          TCT C TCTGTTGCCCAGGCTGGA
          ||| | |||||
          AGA G AGACAACGGGTCCGACCT
          A A_
GAM1882 KIAA1086 3' TCCAGCCTGGGTTACAGAGCGA 71290       T
          GA          TCTCGCTCTGT GCCCAGGCTGGA
          ||||| |||||
          AGAGCGAGACA TGGGTCCGACCT
          T
GAM1882 KIAA1130 3' CCTGGGCAACATAGCAAGA   63085   C C
          TCT GCT TGTTGCCCAGG
          ||| ||| |||||
          AGA CGA ACAACGGGTCC
          A   T
GAM1882 KIAA1143 3' CCAGCCTGGGCGACAAAGC   69233   C
          GCT TGTTGCCCAGGCTGG
          ||| |||||
          CGA ACAGCGGGTCCGACC
          A
GAM1882 KIAA1143 3' TCCAGCCTGGGCAACAGAGTAA 69251   CG
          GA          TCT CTCTGTTGCCCAGGCTGGA
          ||| |||||
          AGA GAGACAACGGGTCCGACCT
          AT
GAM1882 KIAA1160 3' TCCAGCCTGGCGACAGAGTGAG 40762       C
          A          TCTCGCTCTGTTGCC AGGCTGGA
          ||||| |||||
          AGAGTGAGACAGCGG TCCGACCT

          -
GAM1882 KIAA1164 3' CCTGGGCAATAGAGCGAGA   70041
          TCTCGCTCTGTTGCCCAGG
          |||||

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AGAGCGAGATAACGGGTCC

GAM1882 KIAA1164 3' TCCAGCCTGGGTGACAGAGGGA 70051 G TG
GA TCTC CTCTGT CCCAGGCTGGA
||||| |||||
AGAG GAGACA GGGTCCGACCT
G GT

GAM1882 KIAA1191 3' TCCAGCCTGGGCGACAGAACGA 40336 C
GA TCTCG TCTGTTGCCCAGGCTGGA
||||| |||||
AGAGC AGACAGCGGGTCCGACCT
A

GAM1882 KIAA1202 3' TCCATCCTGGGCAACAGAGTGA 72492 C
GA TCTCGCTCTGTTGCCCAGG TGGA
||||| |||||
AGAGTGAGACAACGGGTCC ACCT
T

GAM1882 KIAA1204 3' CCTGGGCAACACAGCGAGA 69738 C
TCTCGCT TGTTGCCCAGG
||||| |||||
AGAGCGA ACAACGGGTCC
C

GAM1882 KIAA1228 3' TCCAGCCTGGGCAACAGAGTGA 65678
GA TCTCGCTCTGTTGCCCAGGCTGGA
||||| |||||
AGAGTGAGACAACGGGTCCGACCT

GAM1882 KIAA1253 3' TCTAGCCTGGGCAACAGAGTAA 93550 CG
GA TCT CTCTGTTGCCCAGGCTGGA
||| |||||
AGA GAGACAACGGGTCCGATCT
AT

GAM1882 KIAA1257 3' TCCAGCCTGGGCAGCAGAGCAA 63419 C
GA TCT GCTCTGTTGCCCAGGCTGGA
||| |||||
AGA CGAGACGACGGGTCCGACCT
A

GAM1882 KIAA1271 3' TCCAACCTGGGTGAGAGAGCGA 70145 G TG C
GA TCTCGCTCT T CCCAGG TGGA
||||| | |||||
AGAGCGAGA A GGGTCC ACCT
G GT A

GAM1882 KIAA1277 3' TCCAGCCTGGACAACAGAGCAA 65086 C C
GA TCT GCTCTGTTG CCAGGCTGGA
||| ||||| |||||
AGA CGAGACAAC GGTCCGACCT
A A

GAM1882 KIAA1328 3' TCCAGCCTGGGTGACAGAGCAA 62334 C TG
GA TCT GCTCTGT CCCAGGCTGGA
||| ||||| |||||

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          AGA CGAGACA GGGTCCGACCT
          A   GT
GAM1882 KIAA1340 3' TCCAGCCTGGGCGACAGTGCAA 69699   C T
          GA          TCT GC CTGTTGCCAGGCTGGA
          ||| || |||||
          AGA CG GACAGCGGGTCCGACCT
          A T
GAM1882 KIAA1348 3' TCCAGCCTGGGCAACAAGAGTG 69129   _
          A          TCGCTCT GTTGCCAGGCTGGA
          ||||| |||||
          AGTGAGA CAACGGGTCCGACCT
          A
GAM1882 KIAA1364 3' TCCAGCCTGTGTGACAGAATGA 64359   C   TG C
          GA          TCTCG TCTGT C CAGGCTGGA
          |||| |||| | |||||
          AGAGT AGACA G GTCCGACCT
          A   GT T
GAM1882 KIAA1423 3' TCCAGCCTGGGTGTCAGAGCGA 62398   T
          GA          TCTCGCTCTG TGCCAGGCTGGA
          ||||| |||||
          AGAGCGAGAC GTGGGTCCGACCT
          T
GAM1882 KIAA1456 3' CCTGGGCAACATAGCAAGA 67546   C C
          TCT GCT TGTTGCCAGG
          ||| ||| |||||
          AGA CGA ACAACGGGTCC
          A T
GAM1882 KIAA1456 3' CCTGGGCAACATAGCAAGA 67547   C C
          TCT GCT TGTTGCCAGG
          ||| ||| |||||
          AGA CGA ACAACGGGTCC
          A T
GAM1882 KIAA1456 3' TCCAACCTGGGCAACAAGAGTG 67568   _   C
          A          TCGCTCT GTTGCCAGG TGGA
          ||||| ||||| |||
          AGTGAGA CAACGGGTCC ACCT
          A   A
GAM1882 KIAA1456 5' TCCAGCCTGGGTGACTGAGGGA 67569   G T TG
          GA          TCTC CTC GT CCCAGGCTGGA
          |||| ||| || |||||
          AGAG GAG CA GGGTCCGACCT
          G T GT
GAM1882 KIAA1486 3' TCCAGCCTGGGTGACAGAGCGA 67979   TG
          GA          TCTCGCTCTGT CCCAGGCTGGA
          ||||| |||||
          AGAGCGAGACA GGGTCCGACCT
          GT
GAM1882 KIAA1497 5' TCCAGCCTGGGCGACAGAGCGA 68132
          GA          TCTCGCTCTGTTGCCAGGCTGGA
          |||||

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AGAGCGAGACAGCGGGTCCGACCT

GAM1882 KIAA1508 3' TCCAGCCTGGGTGACAGAGCGA 62564 TG
GA TCTCGCTCTGT CCCAGGCTGGA

||||||| |||||
AGAGCGAGACA GGGTCCGACCT
GT

GAM1882 KIAA1554 3' TCCAACCTGGGTGACAGAGTGA 96862 TG C
GA TCTCGCTCTGT CCCAGG TGA

||||||| |||||
AGAGTGAGACA GGGTCC ACCT
GT A

GAM1882 KIAA1559 3' TCCAGCCTGGGTAACAGAGCAA 73461 C
GA TCT GCTCTGTTGCCAGGCTGGA

||| |||||||||
AGA CGAGACAATGGGTCCGACCT
A

GAM1882 KIAA1559 3' TCCAGCCTGGGTGACAGAGTGA 73462 TG
GA TCTCGCTCTGT CCCAGGCTGGA

||||||| |||||
AGAGTGAGACA GGGTCCGACCT
GT

GAM1882 KIAA1586 5' CCTGGGCAACAGAGCAAGA 93938 C
TCT GCTCTGTTGCCAGG

||| |||||||||
AGA CGAGACAACGGGTCC
A

GAM1882 KIAA1614 3' TCCAGCCTGGGCAACAAGAGC 70668 _
GCTCT GTTGCCCAGGCTGGA

||||| |||||||||
CGAGA CAACGGGTCCGACCT
A

GAM1882 KIAA1630 3' TCCAGCCTGGGTGACAGAGCAA 38657 C TG
GA TCT GCTCTGT CCCAGGCTGGA

||| ||||| |||||
AGA CGAGACA GGGTCCGACCT
A GT

GAM1882 KIAA1641 3' TCCAGCCTGAGCAACAGAGTGA 81022 C
TCGCTCTGTTGC CAGGCTGGA

||||||| |||||
AGTGAGACAACG GTCCGACCT
A

GAM1882 KIAA1644 3' TCCAGCCTGGGCAACAGAGTGA 86223
GA TCTCGCTCTGTTGCCAGGCTGGA

|||||||
AGAGTGAGACAACGGGTCCGACCT

GAM1882 KIAA1649 3' TCCAGCCTGTGCAACAGAGCGA 51248 C
GG TCTCGCTCTGTTGC CAGGCTGGA

||||||| |||||

		GGAGCGAGACAACG GTCCGACCT	
		T	
GAM1882	KIAA1656	5' TCCAGCCTGGCAACAGAGTGAG 66385	C
	A	TCTCGCTCTGTTGCC AGGCTGGA	
		AGAGTGAGACAACGG TCCGACCT	
		—	
GAM1882	KIAA1674	3' TCCAGCCTGGGCGACAGAGCGA 69348	
	GA	TCTCGCTCTGTTGCCAGGCTGGA	
		AGAGCGAGACAGCGGGTCCGACCT	
		—	
GAM1882	KIAA1715	3' TCCAGCCTGGGCAACAAGAGTG 68691	—
	A	TCGCTCT GTTGCCAGGCTGGA	
		AGTGAGA CAACGGGTCCGACCT	
		A	
GAM1882	KIAA1727	3' TCCAGCCTGGATGACAGAGTGA 64765	GC
	GA	TCTCGCTCTGTT CCAGGCTGGA	
		AGAGTGAGACAG GGTCCGACCT	
		TA	
GAM1882	KIAA1771	3' TCCAGCCTGGACAACAGAGT 79867	C
		GCTCTGTTG CCAGGCTGGA	
		TGAGACAAC GGTCCGACCT	
		A	
GAM1882	KIAA1786	3' CCAGCCCGGGTGACAGAGCGAG 66630	TG A
	A	TCTCGCTCTGT CCC GGCTGG	
		AGAGCGAGACA GGG CCGACC	
		GT C	
GAM1882	KIAA1829	3' TCCAGCCTGGGCAACAAGAGCG 62656	—
	A	TCGCTCT GTTGCCAGGCTGGA	
		AGCGAGA CAACGGGTCCGACCT	
		A	
GAM1882	KIAA1871	3' TCCAGCCTGGGCAACAAGTGCG 61911	T —
	A	TCGC CT GTTGCCAGGCTGGA	
		AGCG GA CAACGGGTCCGACCT	
		T A	
GAM1882	KIAA1872	3' TCCAGCCTGGGAGACAGAGCAA 63620	C TG
	GA	TCT GCTCTGT CCCAGGCTGGA	
		AGA CGAGACA GGGTCCGACCT	
		A GA	
GAM1882	KIAA1872	3' TCCAGCCTGGGCAACAAGAGC 63621	—
		GCTCT GTTGCCAGGCTGGA	

			CGAGA CAACGGGTCCGACCT		
			A		
GAM1882	KIAA1872	3'	TCCAGCCTGGGCGACAGAGCAA 63623	C	
	GA		TCT GCTCTGTTGCCCAGGCTGGA		
			AGA CGAGACAGCGGGTCCGACCT		
			A		
GAM1882	KIAA1879	3'	TCCAGCCTGGGAGACAGAGCAA 73946	C	TG
	GA		TCT GCTCTGT CCCAGGCTGGA		
			AGA CGAGACA GGGTCCGACCT		
			A GA		
GAM1882	KIAA1948	3'	TCCAGCCTGGGTGACAGACCGA 83306	C	TG
	GA		TCTCG TCTGT CCCAGGCTGGA		
			AGAGC AGACA GGGTCCGACCT		
			C GT		
GAM1882	KIAA1948	5'	TCCAGCCTGGGTGACAGAGTGA 83307		TG
	GA		TCTCGCTCTGT CCCAGGCTGGA		
			AGAGTGAGACA GGGTCCGACCT		
			GT		
GAM1882	KIAA1951	3'	TCCAGCCTGGGCGACAGAGTGA 74165		
	GA		TCTCGCTCTGTTGCCCAGGCTGGA		
			AGAGTGAGACAGCGGGTCCGACCT		
GAM1882	KIAA1951	3'	TCCAGTCTGGGCAACAGTGCAA 74166	C	T
	GA		TCT GC CTGTTGCCCAGGCTGGA		
			AGA CG GACAACGGGTCTGACCT		
			A T		
GAM1882	KIAA1954	3'	TCCAGCCTGAGCAACAGAGCAA 78231	C	C
	GA		TCT GCTCTGTTGC CAGGCTGGA		
			AGA CGAGACAACG GTCCGACCT		
			A A		
GAM1882	KIAA1958	3'	TCCAGCCTGGGCAACAAAGCTA 82792	C	C
	GA		TCT GCT TGTTGCCCAGGCTGGA		
			AGA CGA ACAACGGGTCCGACCT		
			T A		
GAM1882	KIAA1969	3'	TCCAGTTTGGCAACAGAGTGAG 79482		C
	A		TCTCGCTCTGTTGCC AGGCTGGA		
			AGAGTGAGACAACGG TTTGACCT		
GAM1882	KR18	3'	TCCAGCCTGGGCAACAAGA 53896		
			TCT GTTGCCCAGGCTGGA		

			AGA CAACGGGTCCGACCT	
			A	
GAM1882	KR18	3'	TCCAGCCTGGGCACCAGGAACG 53898	C_ T
	A		TCG TCTG TGCCCAGGCTGGA	
			AGC GGAC ACGGGTCCGACCT	
			AA C	
GAM1882	KREMEN	3'	TCCAGCCTGAGCAGCAGAGCGG 50237	C
	GA		TCTCGCTCTGTTGC CAGGCTGGA	
			AGGGCGAGACGACG GTCCGACCT	
			A	
GAM1882	KREMEN	3'	TCCAGTGTAGGCAACAGAGTGA 50238	CAG
	GA		TCTCGCTCTGTTGCC GCTGGA	
			AGAGTGAGACAACGG TGACCT	
			ATG	
GAM1882	LANO	3'	TCCAGCCCGGGTGACAGAGCGA 47977	TG A
	GA		TCTCGCTCTGT CCC GGCTGGA	
			AGAGCGAGACA GGG CCGACCT	
			GT C	
GAM1882	LIAS	3'	TCCAGCCTGGGTGACAAGAGC 71169	_ TG
			GCTCT GT CCCAGGCTGGA	
			CGAGA CA GGGTCCGACCT	
			A GT	
GAM1882	LIM	3'	TCCAGCCTGGGTGACAGAGTGA 22334	TG
	GA		TCTCGCTCTGT CCCAGGCTGGA	
			AGAGTGAGACA GGGTCCGACCT	
			GT	
GAM1882	LIM	3'	TCCAGCCTGGTGACAGAGCAAG 22335	C TG C
	A		TCT GCTCTGT CC AGGCTGGA	
			AGA CGAGACA GG TCCGACCT	
			A GT _	
GAM1882	LIN-28	3'	TCCAGCCTGGTTACAGAGCGAG 45471	TGC
	A		TCTCGCTCTGT CCAGGCTGGA	
			AGAGCGAGACA GGTCCGACCT	
			TT_	
GAM1882	LRG	3'	CCTGGGCGACAGAGCAAGA 54817	C
			TCT GCTCTGTTGCCAGG	
			AGA CGAGACAGCGGGTCC	
			A	
GAM1882	LRRFIP1	3'	TCCAGCCTGGACAACAAGAGCG 17617	_ C
	A		TCGCTCT GTTG CCAGGCTGGA	

			AGCGAGA CAAC GGTCCGACCT	
			A A	
GAM1882	LSR68	3'	TCCAGCCTGGGCGACAGAATGA 38559	C
	GA		TCTCG TCTGTTGCCCAGGCTGGA	
			AGAGT AGACAGCGGGTCCGACCT	
			A	
GAM1882	MACF1	3'	TCCAACTTGGGCAACAGACAGA 53433	_____ C
	GCGAGA		TCTCGCTCTGT TGCCCAGG TGA	
			AGAGCGAGACA ACGGGTTC ACCT	
			GACA A	
GAM1882	MACF1	3'	TCCAGCCTGGGCAACAGACAGA 53435	_____
	GTGAGA		TCTCGCTCTGT TGCCCAGGCTGGA	
			AGAGTGAGACA ACGGGTCCGACCT	
			GACA	
GAM1882	MAWBP	3'	CCTGGGCAACACAGCGAGA 42382	C
			TCTCGCT TGTTGCCCAGG	
			AGAGCGA ACAACGGGTCC	
			C	
GAM1882	MAWBP	3'	TCCAGCCTGGGCAACAGAGTAA 42388	CG
	GA		TCT CTCTGTTGCCCAGGCTGGA	
			AGA GAGACAACGGGTCCGACCT	
			AT	
GAM1882	MCAM	3'	TCCAGCCTGGGCAACACAGCGA 22466	C
	GA		TCTCGCT TGTTGCCCAGGCTGGA	
			AGAGCGA ACAACGGGTCCGACCT	
			C	
GAM1882	METL	3'	TCCAGCCTGGGCAAAATAGCGA 37841	CTG
	GA		TCTCGCT TTGCCCAGGCTGGA	
			AGAGCGA AACGGGTCCGACCT	
			TAA	
GAM1882	MGC10200	3'	TCCAGTCTGGGCAACAGAGCGA 59649	
	GA		TCTCGCTCTGTTGCCCAGGCTGGA	
			AGAGCGAGACAACGGGTCTGACCT	
GAM1882	MGC10765	3'	TCCAGCCTAGGCGACAGAGCGA 44567	C
	GA		TCTCGCTCTGTTGCC AGGCTGGA	
			AGAGCGAGACAGCGG TCCGACCT	
			A	
GAM1882	MGC10814	3'	TCCAGCCTGGGCAACAAGAGC 52025	_
			GCTCT GTTGCCCAGGCTGGA	

CGAGA CAACGGGTCCGACCT
A
GAM1882 MGC10814 5' TCCAGCCTGGGCAACAGAGTGA 52027
GG TCTCGCTCTGTTGCCCAGGCTGGA
|||||
GGAGTGAGACAACGGGTCCGACCT

GAM1882 MGC11386 3' TCCAGCCTGGGCAACAGAGCGA 53072
GA TCTCGCTCTGTTGCCCAGGCTGGA
|||||
AGAGCGAGACAACGGGTCCGACCT

GAM1882 MGC12972 3' CCTGGGCAACATAGCAAGA 52052 C C
TCT GCT TGTTGCCCAGG
||| ||| |||||
AGA CGA ACAACGGGTCC
A T

GAM1882 MGC13008 3' TCCAGCCTGGGCAACAGAATGA 52059 C
GA TCTCG TCTGTTGCCCAGGCTGGA
|||| |||||
AGAGT AGACAACGGGTCCGACCT
A

GAM1882 MGC13017 3' TCCAGCCTAGGCAATAAGAGC 55578 _ C
GCTCT GTTGCC AGGCTGGA
|||| |||| |||||
CGAGA TAACGG TCCGACCT
A A

GAM1882 MGC13053 3' TCCAGCCTGGGCGACAGAGTGA 52114
GA TCTCGCTCTGTTGCCCAGGCTGGA
|||||
AGAGTGAGACAGCGGGTCCGACCT

GAM1882 MGC13053 3' TCCAGCCTGGGCGACAGCAAGA 52115 GCT
TC CTGTTGCCCAGGCTGGA
|| |||||
AG GACAGCGGGTCCGACCT
AAC

GAM1882 MGC14126 3' TCCAGCCTGGGCGATGAGC 52942 T
GCTC GTTGCCCAGGCTGGA
|||| |||||
CGAG TAGCGGGTCCGACCT
—

GAM1882 MGC14407 3' TCCAGCCTGGGTGACAGAGCAA 52977 C TG
GA TCT GCTCTGT CCCAGGCTGGA
||| ||||| |||||
AGA CGAGACA GGGTCCGACCT
A GT

GAM1882 MGC14436 3' TCCAGCCTGGGTGACAGAACGA 52931 C TG
GA TCTCG TCTGT CCCAGGCTGGA
|||| |||| |||||

		AGAGC AGACA GGGTCCGACCT		
		A GT		
GAM1882	MGC14799	3' TCCAGCCTGGGTGACAGTGAGA 51332	CT	TG
		TCTCGCT GT CCCAGGCTGGA		
		AGAGTGA CA GGGTCCGACCT		
		— GT		
GAM1882	MGC15397	3' TCCAGCCTGGGTGATAGAGTGA 55556	TG	
	GA	TCTCGCTCTGT CCCAGGCTGGA		
		AGAGTGAGATA GGGTCCGACCT		
		GT		
GAM1882	MGC15631	3' TCCAGCCTGTGCAACAGAGCCA 52235	C	C
	GA	TCT GCTCTGTTGC CAGGCTGGA		
		AGA CGAGACAACG GTCCGACCT		
		C T		
GAM1882	MGC16037	3' TCCAGCCTGGACAACAGAGTGG 52894	C	
	GA	TCTCGCTCTGTTG CCAGGCTGGA		
		AGGGTGAGACAAC GGTCCGACCT		
		A		
GAM1882	MGC16175	3' TCCAGCCTGGGCAATAGAGCAA 52279	C	
	GA	TCT GCTCTGTTGCCAGGCTGGA		
		AGA CGAGATAACGGGTCCGACCT		
		A		
GAM1882	MGC16332	3' TCCAGCCTGGTCAACAAAGCAA 57545	C	C C
	GA	TCT GCT TGTTG CCAGGCTGGA		
		AGA CGA ACAAC GGTCCGACCT		
		A A T		
GAM1882	MGC16703	3' TCCAGCCTGGGCAACAGAGCGA 73498		
	GA	TCTCGCTCTGTTGCCAGGCTGGA		
		AGAGCGAGACAACGGGTCCGACCT		
GAM1882	MGC20235	3' TCCAGCCTGGGCAAAAGAGC 59562	G	
		GCTCT TTGCCAGGCTGGA		
		CGAGA AACGGGTCCGACCT		
		A		
GAM1882	MGC22805	3' CCAGGGCAACACAGCGAGA 58699	C	A
		TCTCGCT TGTTGCC GG		
		AGAGCGA ACAACGGG CC		
		C A		
GAM1882	MGC23244	3' TCCAGCCTGGGCGACAGAGTGA 58838		
	GA	TCTCGCTCTGTTGCCAGGCTGGA		

AGAGTGAGACAGCGGGTCCGACCT

GAM1882 MGC2396 3' CCAGCCTGGGCAATAAGAG 54558 _
CTCT GTTGCCAGGCTGG
|||||
GAGA TAACGGGTCCGACC
A

GAM1882 MGC2562 3' CCACTAGGCAACAGAGCCAGA 51434 C C GC
TCT GCTCTGTTGCC AG TGG
||| ||||| || |||
AGA CGAGACAACGG TC ACC
C A _

GAM1882 MGC2562 3' TCCAGCCTGACGACAAAGCGAG 51449 C CC
A TCTCGCT TGTTG CAGGCTGGA
||||| ||||| |||||
AGAGCGA ACAGC GTCCGACCT
A A _

GAM1882 MGC2562 3' TCCAGCCTGGAAGACCAAACGA 51450 CTCT GC
GA TCTCG GTT CCAGGCTGGA
||||| ||| |||||
AGAGC CAG GGTCCGACCT
AAAC AA

GAM1882 MGC2562 3' TCCAGCCTGGGCGACAGAGC 51451
GCTCTGTTGCCAGGCTGGA
|||||
CGAGACAGCGGGTCCGACCT

GAM1882 MGC2663 3' TCCAGCCTGGGCGATGGAGTGA 44338
GA TCTCGCTCTGTTGCCAGGCTGGA
|||||
AGAGTGAGGTAGCGGGTCCGACCT

GAM1882 MGC26641 3' TCCAGCCTGGGCAATAGGGCAA 59326 C
GA TCT GCTCTGTTGCCAGGCTGGA
||| |||||
AGA CGGGATAACGGGTCCGACCT
A

GAM1882 MGC26877 5' CCAGCCTGGGTGACAGAGCGAG 58890 TG
A TCTCGCTCTGT CCCAGGCTGG
||||| |||||
AGAGCGAGACA GGGTCCGACC
GT

GAM1882 MGC2731 3' TCCAGCCTGGGCAATAAGAGCG 44164 _
A TCGCTCT GTTGCCAGGCTGGA
||||| |||||
AGCGAGA TAACGGGTCCGACCT
A

GAM1882 MGC29762 3' TCCAGCCTGGGCAACAAGAGC 59148 _
GCTCT GTTGCCAGGCTGGA
|||||

			CGAGA CAACGGGTCCGACCT	
			A	
GAM1882	MGC29891	3'	TCCAGCCTGGGCAACAGAGCCA 58871	C
	GA		TCT GCTCTGTTGCCCAGGCTGGA	
			AGA CGAGACAACGGGTCCGACCT	
			C	
GAM1882	MGC29937	3'	TCCAGCCTGGGCAACAAGAGTG 58734	—
	A		TCGCTCT GTTGCCCAGGCTGGA	
			AGTGAGA CAACGGGTCCGACCT	
			A	
GAM1882	MGC3101	5'	TCCAGCCTGGGTGACAGAGCGA 44105	TG
	GA		TCTCGCTCTGT CCCAGGCTGGA	
			AGAGCGAGACA GGGTCCGACCT	
			GT	
GAM1882	MGC3207	3'	TCCAGCCTGGGCAACAGAGCGA 63242	
	GA		TCTCGCTCTGTTGCCCAGGCTGGA	
			AGAGCGAGACAACGGGTCCGACCT	
GAM1882	MGC4368	3'	CCTGGGCAACACAGCAAGA 44725	C C
			TCT GCT TGTTGCCCAGG	
			AGA CGA ACAACGGGTCC	
			A C	
GAM1882	MGC4400	3'	CCTGGGCAACATAGCGAGA 52037	C
			TCTCGCT TGTTGCCCAGG	
			AGAGCGA ACAACGGGTCC	
			T	
GAM1882	MGC4562	3'	TCCAGCCTGGGCAACAGAGCGA 56743	
	GA		TCTCGCTCTGTTGCCCAGGCTGGA	
			AGAGCGAGACAACGGGTCCGACCT	
GAM1882	MGC4663	3'	TCCAGCCTGGGCAACAGAGCCA 44791	C
	GA		TCT GCTCTGTTGCCCAGGCTGGA	
			AGA CGAGACAACGGGTCCGACCT	
			C	
GAM1882	MGC4771	3'	TCCAGCCTGGGCAACAGAGTGA 52006	
	GA		TCTCGCTCTGTTGCCCAGGCTGGA	
			AGAGTGAGACAACGGGTCCGACCT	
GAM1882	MGC4840	3'	TCCAGCCTGGCTGACAGAGCGA 72029	GC
	GA		TCTCGCTCTGTT CCAGGCTGGA	

			AGAGCGAGACAG GGTCCGACCT	
			TC	
GAM1882	MGC5384	3'	TCCAGCCTGGGCGACAGAGTGA 49094	
	GA		TCTCGCTCTGTTGCCAGGCTGGA	
			AGAGTGAGACAGCGGGTCCGACCT	
GAM1882	MGC5457	3'	TCCAGCCTGGGTGACAGAGCGA 51943	TG
	GA		TCTCGCTCTGT CCCAGGCTGGA	
			AGAGCGAGACA GGGTCCGACCT	
			GT	
GAM1882	MKRN4	3'	CCAGCCTGGGTGACAGAGCGAG 48455	TG
	A		TCTCGCTCTGT CCCAGGCTGG	
			AGAGCGAGACA GGGTCCGACC	
			GT	
GAM1882	MOST2	5'	TCCAGCCTGGGCACCACAGCAA 40072	C C T
	GA		TCT GCT TG TGCCCAGGCTGGA	
			AGA CGA AC ACGGGTCCGACCT	
			A C C	
GAM1882	MRPL48	5'	TCCAGCCTGCGCAACAGAGCGA 32662	C
	GA		TCTCGCTCTGTTGC CAGGCTGGA	
			AGAGCGAGACAACG GTCCGACCT	
			C	
GAM1882	MRPS10	3'	TCCAGCCTGGCGACAGAGCGAG 36822	C
	A		TCTCGCTCTGTTGCC AGGCTGGA	
			AGAGCGAGACAGCGG TCCGACCT	
GAM1882	MRPS18B	3'	TCCAGCCTGGGTGACAGCTAGA 26755	C CT TG
			TCT GCT GT CCCAGGCTGGA	
			AGA CGA CA GGGTCCGACCT	
			T _ GT	
GAM1882	My015	3'	TCCAGCCTGGGAGACAGAGCAA 67235	C TG
	GA		TCT GCTCTGT CCCAGGCTGGA	
			AGA CGAGACA GGGTCCGACCT	
			A GA	
GAM1882	NCBP2	3'	CTGGGCAACATAGCAAGA 24767	C C
			TCT GCT TGTTGCCAG	
			AGA CGA ACAACGGGTC	
			A T	
GAM1882	NDUFC2	3'	TCCAGCCTGGGTGACAAAGGAG 17038	G C TG
	A		TCTC CT TGT CCCAGGCTGGA	

			AGAG GA ACA GGGTCCGACCT		
			_ A GT		
GAM1882	NMNAT	3'	TCCAGCCTGGCGACAGAGCAAG 43292	C	C
	A		TCT GCTCTGTTGCC AGGCTGGA		
			AGA CGAGACAGCGG TCCGACCT		
			A _		
GAM1882	NMNAT	3'	TCCAGCCTGGGCAAAAAAGC 43293	CTG	
			GCT TTGCCCAGGCTGGA		
			CGA AACGGGTCCGACCT		
			AAA		
GAM1882	NMNAT	3'	TCCAGCCTGGGTGACAGAGCGA 43295	TG	
	GA		TCTCGCTCTGT CCCAGGCTGGA		
			AGAGCGAGACA GGGTCCGACCT		
			GT		
GAM1882	NMT2	3'	TCCAGCCTGGGTGACAGAGCGT 17859	T	TG
	GA		TC CGCTCTGT CCCAGGCTGGA		
			AG GCGAGACA GGGTCCGACCT		
			T GT		
GAM1882	NPTXR	3'	TCCAGCCTGGGCAACAGAGCAA 27445	C	
	GA		TCT GCTCTGTTGCCCAGGCTGGA		
			AGA CGAGACAACGGGTCCGACCT		
			A		
GAM1882	Nup43	3'	TCCAGCCTGGGCAAAAGAGC 45355	G	
			GCTCT TTGCCCAGGCTGGA		
			CGAGA AACGGGTCCGACCT		
			A		
GAM1882	NY-BR-1	3'	TCCAGCCTAGGTGACAGAGTGA 54853	TG	C
	GA		TCTCGCTCTGT CC AGGCTGGA		
			AGAGTGAGACA GG TCCGACCT		
			GT A		
GAM1882	OR51E2	3'	TCCAGCCTGGGCAACGGAGCAA 48521	C	
	GA		TCT GCTCTGTTGCCCAGGCTGGA		
			AGA CGAGGCAACGGGTCCGACCT		
			A		
GAM1882	ORC6L	3'	TCCAGCCTGGGTGACAGAGCGA 27494	TG	
	GA		TCTCGCTCTGT CCCAGGCTGGA		
			AGAGCGAGACA GGGTCCGACCT		
			GT		
GAM1882	ORC6L	3'	TCCAGCCTGGGTGACAGAGCGA 27495	TG	
	GA		TCTCGCTCTGT CCCAGGCTGGA		

			AGAGCGAGACA GGGTCCGACCT		
			GT		
GAM1882	PAFAH2	3'	TCCAGCCTGGGTGACAGAGCAA 6508	C	TG
	GA		TCT GCTCTGT CCCAGGCTGGA		
			AGA CGAGACA GGGTCCGACCT		
			A GT		
GAM1882	PB1	3'	TCCAGCCTGGGCAACAAGAGCG 36880	_	
	A		TCGCTCT GTTGCCCAGGCTGGA		
			AGCGAGA CAACGGGTCCGACCT		
			A		
GAM1882	PB1	3'	TCCAGCCTGGGCAACAGAGTGA 36881		
	G		CTCGCTCTGTTGCCAGGCTGGA		
			GAGTGAGACAACGGGTCCGACCT		
GAM1882	PDCD7	3'	TCCAGCCTGGGAGACAGAGCAA 72611	C	TG
	GA		TCT GCTCTGT CCCAGGCTGGA		
			AGA CGAGACA GGGTCCGACCT		
			A GA		
GAM1882	PIWIL2	3'	TCCAGCCTGTTGACAAAGCAAG 36547	C C	GCC
	A		TCT GCT TGTT CAGGCTGGA		
			AGA CGA ACAG GTCCGACCT		
			A A TT_		
GAM1882	POFUT1	3'	TCCAGCCTGGGCAACAGAGCGA 70984		
	GA		TCTCGCTCTGTTGCCAGGCTGGA		
			AGAGCGAGACAACGGGTCCGACCT		
GAM1882	POLYDOM	3'	TCCAGCCTGGGCAATGGAGAGA 44691	G	
	G		CTC CTCTGTTGCCAGGCTGGA		
			GAG GAGGTAACGGGTCCGACCT		
			A		
GAM1882	PPP1R3B	3'	CCCGCCTGGGCAGCAGAGCGAG 45138		T
	A		TCTCGCTCTGTTGCCAGGC GG		
			AGAGCGAGACGACGGGTCCG CC		
			C		
GAM1882	PRIC285	3'	TCCAGCCTGGGTGACAGAGCGA 62120		TG
	GA		TCTCGCTCTGT CCCAGGCTGGA		
			AGAGCGAGACA GGGTCCGACCT		
			GT		
GAM1882	PRO0038	3'	TCCAGCCTGGGTGACAGACCGA 26931	C	TG
	GA		TCTCG TCTGT CCCAGGCTGGA		

			AGAGC AGACA GGGTCCGACCT		
			C GT		
GAM1882	PRO0478	5'	TCCAGCCTAGGCAACAAGAGCG 27035	—	C
	A		TCGCTCT GTTGCC AGGCTGGA		
			AGCGAGA CAACGG TCCGACCT		
			A A		
GAM1882	PRO0478	5'	TCCAGCCTGGACAACAGAGTGA 27036		C
	GA		TCTCGCTCTGTTG CCAGGCTGGA		
			AGAGTGAGACAAC GGTCCGACCT		
			A		
GAM1882	PRO0478	3'	TCCAGCCTGGCAACAGAGCGAG 27037		C
	A		TCTCGCTCTGTTGCC AGGCTGGA		
			AGAGCGAGACAACGG TCCGACCT		
			—		
GAM1882	PRO0478	3'	TCCAGCCTGGGGGACAGAGCAA 27038	C	G
	GG		TCT GCTCTGTT CCCAGGCTGGA		
			GGA CGAGACAG GGGTCCGACCT		
			A G		
GAM1882	PRO1048	5'	TCCAGCCTGGGTGACAGAGCGA 38119		TG
	GA		TCTCGCTCTGT CCCAGGCTGGA		
			AGAGCGAGACA GGGTCCGACCT		
			GT		
GAM1882	PRO1386	3'	TCCAGCCTGGGCAACAGAGTGA 49218		
	GA		TCTCGCTCTGTTGCCAGGCTGGA		
			AGAGTGAGACAACGGGTCCGACCT		
GAM1882	PRO1496	3'	TCCAACCTGGGTGACAGACCGA 38368	C	TG C
	GA		TCTCG TCTGT CCCAGG TGGA		
			AGAGC AGACA GGGTCC ACCT		
			C GT A		
GAM1882	PRO1942	5'	TCCAGCCTGGACAACAGAAAGA 38384	GC	C
	GA		TCTC TCTGTTG CCAGGCTGGA		
			AGAG AGACAAC GGTCCGACCT		
			AA A		
GAM1882	PRO2015	3'	TCCAGCCTGGGCCACACAGTGA 38166	C	T
	GA		TCTCGCT TGT GCCCAGGCTGGA		
			AGAGTGA ACA CGGGTCCGACCT		
			C C		
GAM1882	PRO2859	3'	TCCAGCCTGGGGAGACAGAGCG 38214		G_
	AGA		TCTCGCTCTGTT CCCAGGCTGGA		

			AGAGCGAGACAG GGGTCCGACCT		
			AG		
GAM1882	PRO2893	3'	TCCAACCTGGGCAATAAGAGC 38435	_	C
			GCTCT GTTGCCCAGG TGGA		
			CGAGA TAACGGGTCC ACCT		
			A A		
GAM1882	PRO2964	3'	CCAGCCTGGGCAAAAAGAG 38255	G_	
			CTCT TTGCCCAGGCTGG		
			GAGA AACGGGTCCGACC		
			AA		
GAM1882	PSR	3'	TCCAGCCTGGGTGACAGACCGA 65794	C	TG
	GA		TCTCG TCTGT CCCAGGCTGGA		
			AGAGC AGACA GGGTCCGACCT		
			C GT		
GAM1882	PTD012	3'	CCAGCTTGGGCAACATAGCAAG 26736	C C	
	A		TCT GCT TGTTGCCCAGGCTGG		
			AGA CGA ACAACGGGTTCGACC		
			A T		
GAM1882	PTK6	3'	TCCAGCCTGGGCGACAGAGCGA 21082		
	GA		TCTCGCTCTGTTGCCCAGGCTGGA		
			AGAGCGAGACAGCGGGTCCGACCT		
GAM1882	PTRF	3'	TCCAGCCTGGGTGACAGAGTGA 64245		TG
	GA		TCTCGCTCTGT CCCAGGCTGGA		
			AGAGTGAGACA GGGTCCGACCT		
			GT		
GAM1882	PTRF	3'	TCCATCCTAGGCAACAGAGTGA 64246	C C	
	GA		TCTCGCTCTGTTGCC AGG TGGA		
			AGAGTGAGACAACGG TCC ACCT		
			A T		
GAM1882	Rabip4R	3'	TCCAACCTGGGTGACAGAGCAA 36279	C	TG C
	GA		TCT GCTCTGT CCCAGG TGGA		
			AGA CGAGACA GGGTCC ACCT		
			A GT A		
GAM1882	RHOBTB3	3'	TCCAGCCTGGGTGACAAGAGCG 30432	_	TG
	A		TCGCTCT GT CCCAGGCTGGA		
			AGCGAGA CA GGGTCCGACCT		
			A GT		
GAM1882	RNO2	5'	TCCAGCCTAGACAACAGGGCAA 53941	C	CCC
	GG		TCT GCTCTGTTG AGGCTGGA		

			GGA CGGGACAAC TCCGACCT		
			A AGA		
GAM1882	RNO2	5'	TCCAGCCTGGGCAACAAGAGCG 53942	—	
	A		TCGCTCT GTTGCCCAGGCTGGA		
			AGCGAGA CAACGGGTCCGACCT		
			A		
GAM1882	RoXaN	3'	TCCAGCCTGAGAGACAGAATGA 47303	C	GCC
	GA		TCTCG TCTGTT CAGGCTGGA		
			AGAGT AGACAG GTCCGACCT		
			A AGA		
GAM1882	RoXaN	3'	TCCAGCCTGGGCTACAGAGTGA 47304	T	
	GA		TCTCGCTCTGT GCCCAGGCTGGA		
			AGAGTGAGACA CGGGTCCGACCT		
			T		
GAM1882	Rpo1-2	3'	TCCAGCCTGGGCGACAGAATGA 39225	C	
	GA		TCTCG TCTGTTGCCCAGGCTGGA		
			AGAGT AGACAGCGGGTCCGACCT		
			A		
GAM1882	Rpo1-2	3'	TCCAGCCTGGGTGACAGAGCAG 39226	TC	TG
	GA		TC GCTCTGT CCCAGGCTGGA		
			AG CGAGACA GGGTCCGACCT		
			GA GT		
GAM1882	RRP4	3'	TCCAGCCTGGGTGACAGAGCGA 27363	TG	
	GA		TCTCGCTCTGT CCCAGGCTGGA		
			AGAGCGAGACA GGGTCCGACCT		
			GT		
GAM1882	SAC2	3'	TCCAGCCTGGGGGACAGAGCAA 30728	C	G
	GA		TCT GCTCTGTT CCCAGGCTGGA		
			AGA CGAGACAG GGGTCCGACCT		
			A G		
GAM1882	SAMHD1	3'	TCCAGCCTGGGTGACAGAGTGA 61991	TG	
	GA		TCTCGCTCTGT CCCAGGCTGGA		
			AGAGTGAGACA GGGTCCGACCT		
			GT		
GAM1882	SC65	3'	TCCAGCCTGGGCGACAGAGCGA 22302		
	GA		TCTCGCTCTGTTGCCCAGGCTGGA		
			AGAGCGAGACAGCGGGTCCGACCT		
GAM1882	SC65	3'	TCCAGCCTGGGCGACAGAGTGA 22303		
	GA		TCTCGCTCTGTTGCCCAGGCTGGA		

AGAGTGAGACAGCGGGTCCGACCT

GAM1882 SCAND2 3' TCCAGCCTGGGCGACAGAGTGA 54423
GA TCTCGCTCTGTTGCCAGGCTGGA
|||||||
AGAGTGAGACAGCGGGTCCGACCT

GAM1882 SCAND2 3' TCCAGCCTGGGCGACAGAGTGA 54424
GA TCTCGCTCTGTTGCCAGGCTGGA
|||||||
AGAGTGAGACAGCGGGTCCGACCT

GAM1882 SCIN 3' TCCAGCCTGGGCAACAGAG 53605
CTCTGTTGCCAGGCTGGA
|||||||
GAGACAACGGGTCCGACCT

GAM1882 SCN12A 3' TCCAGCCTGGTGACAGAGTGAG 27083 TG C
A TCTCGCTCTGT CC AGGCTGGA
||||||| || |||||
AGAGTGAGACA GG TCCGACCT
GT _

GAM1882 SCYA5 3' TCCAGCCTGGGCGACAGAGCGA 12971
GA TCTCGCTCTGTTGCCAGGCTGGA
|||||||
AGAGCGAGACAGCGGGTCCGACCT

GAM1882 SCYA5 3' TCCAGCCTGGGTGACAAAGTGA 12972 C TG
GA TCTCGCT TGT CCCAGGCTGGA
||||| ||| |||||
AGAGTGA ACA GGGTCCGACCT
A GT

GAM1882 SEMA3E 3' CCTGGGCGACAGAGCGAGA 25806
TCTCGCTCTGTTGCCAGG
|||||||
AGAGCGAGACAGCGGGTCC

GAM1882 SMA3 3' TCCAGGAGATACAACAGAGGAG 23263 G CCCAGG
A TCTC CTCTGTTG CTGGA
||| ||||| |||
AGAG GAGACAAC GACCT
_ ATAGAG

GAM1882 SMCR5 3' TCTGGGCGACAGAGCAAGA 59251 C
TCT GCTCTGTTGCCAGG
||| |||||
AGA CGAGACAGCGGGTCT
A

GAM1882 SNAPC1 3' TCCAGCCTGGGCAACAGAGTGA 13279
GA TCTCGCTCTGTTGCCAGGCTGGA
|||||||

AGAGTGAGACAACGGGTCCGACCT

GAM1882 SPRY4 3' TCCAGCCTGGGTGACAGAGCAA 49032 C TG
GA TCT GCTCTGT CCCAGGCTGGA

||| ||||| |||||

AGA CGAGACA GGGTCCGACCT

A GT

GAM1882 SPRY4 3' TCCAGCCTGGGTGACAGAGTGA 49033 TG
GA TCTCGCTCTGT CCCAGGCTGGA

||||||| |||||

AGAGTGAGACA GGGTCCGACCT

GT

GAM1882 SPTLC2 3' CCTGGGCAACACAGCAAGA 17989 C C
TCT GCT TGTTGCCCAGG

||| ||| |||||

AGA CGA ACAACGGGTCC

A C

GAM1882 SPTLC2 3' TCCAGCCTGGGTGACAGAGTGA 18001 TG
GA TCTCGCTCTGT CCCAGGCTGGA

||||||| |||||

AGAGTGAGACA GGGTCCGACCT

GT

GAM1882 SYAP1 3' TCCAGCCTGGGTGATAGAGTGA 52475 TG
GA TCTCGCTCTGT CCCAGGCTGGA

||||||| |||||

AGAGTGAGATA GGGTCCGACCT

GT

GAM1882 SYT12 3' CCAGCCTGAGCAATGGCAGGA 96376 TC CT C
TC GCT GTTGC CAGGCTGG

|| ||| |||||

AG CGG TAACG GTCCGACC

GA _ A

GAM1882 TADA3L 3' TCCAGCCTGGGCAACAAGAGTG 22047 _
A TCGCTCT GTTGCCAGGCTGGA

||||| |||||

AGTGAGA CAACGGGTCCGACCT

A

GAM1882 TBPL1 5' CCGGAACAACAAAGCAAGG 18009 C C CCCAGG
TCT GCT TGTTG CTGG

||| ||| ||||| |||

GGA CGA ACAAC GGCC

A A AA_

GAM1882 THEA 3' TCCAGCCCAGGCAATAGAGTAA 66896 CG CA
GA TCT CTCTGTTGCC GGCTGGA

||| ||||| |||||

AGA GAGATAACGG CCGACCT

AT AC

GAM1882 TIP47 3' TCCAGCCTGGGGGACAAGAGTG 20608 _ G
AGA TCTCGCTCT GTT CCCAGGCTGGA

||||||| ||| |||||

			AGAGTGAGA CAG GGGTCCGACCT		
			A G		
GAM1882	TMG4	3'	TCCAGCCTGGGCGACAGAGCAA 44217	C	
	GA		TCT GCTCTGTTGCCCAGGCTGGA		
			AGA CGAGACAGCGGGTCCGACCT		
			A		
GAM1882	TOMM70A	3'	TCCAGCCTGGGCAATATAGCAA 29739	C C	
	GA		TCT GCT TGTTGCCCAGGCTGGA		
			AGA CGA ATAACGGGTCCGACCT		
			A T		
GAM1882	TRIAD3	3'	TCCAGCCTGAGCAACAAAAGC 96138	C_ C	
			GCT TGTTGC CAGGCTGGA		
			CGA ACAACG GTCCGACCT		
			AA A		
GAM1882	TSGA2	3'	TCCAGCCTGGGTGGCAGAGCGA 55956		TG
	GA		TCTCGCTCTGT CCCAGGCTGGA		
			AGAGCGAGACG GGGTCCGACCT		
			GT		
GAM1882	UBCE7IP5	3'	TCCAGCCTGGGCGACGGAGTGA 30856		
	GA		TCTCGCTCTGTTGCCCAGGCTGGA		
			AGAGTGAGGCAGCGGGTCCGACCT		
GAM1882	UST	3'	TCCAGCCTGGGTGACAGAGTGA 20354		TG
	GA		TCTCGCTCTGT CCCAGGCTGGA		
			AGAGTGAGACA GGGTCCGACCT		
			GT		
GAM1882	VIT1	5'	TCCAGCCTGGGTGGCAGAGTGA 38606		TG
	GA		TCTCGCTCTGT CCCAGGCTGGA		
			AGAGTGAGACG GGGTCCGACCT		
			GT		
GAM1882	VPS4B	3'	TCCAGCCTGGGCGACTGA 18024	T	
			TC GTTGCCCAGGCTGGA		
			AG CAGCGGGTCCGACCT		
			T		
GAM1882	WBSCR21	3'	TCCAGCCTAGGCAACAGAGCAA 49306	C C	
	GA		TCT GCTCTGTTGCC AGGCTGGA		
			AGA CGAGACAACGG TCCGACCT		
			A A		
GAM1882	WBSCR23	3'	TCCAGCCTGGGCGACAAAGTGA 47443		C
	GA		TCTCGCT TGTTGCCCAGGCTGGA		

			AGAGTGA ACAGCGGGTCCGACCT		
			A		
GAM1882	WBSCR23	3'	TCCAGCCTGGGCGACAGAGCAA 47444	C	
	GA		TCT GCTCTGTTGCCCAGGCTGGA		
			AGA CGAGACAGCGGGTCCGACCT		
			A		
GAM1882	WBSCR23	5'	TCCAGCCTGGGCGACAGAGCCA 47445	C	
	GA		TCT GCTCTGTTGCCCAGGCTGGA		
			AGA CGAGACAGCGGGTCCGACCT		
			C		
GAM1882	WBSCR23	3'	TCCAGCCTGGGTGATAGAGCAA 47446	C	TG
	GA		TCT GCTCTGT CCCAGGCTGGA		
			AGA CGAGATA GGGTCCGACCT		
			A GT		
GAM1882	WIRE	3'	TCCAGCCTGGGCGACAGAGCCA 78907	C	
	GA		TCT GCTCTGTTGCCCAGGCTGGA		
			AGA CGAGACAGCGGGTCCGACCT		
			C		
GAM1882	WSB1	3'	TCCAACCTGGACAACAGAGCGA 56978	C	C
	GA		TCTCGCTCTGTTG CCAGG TGGA		
			AGAGCGAGACAAC GGTCC ACCT		
			A A		
GAM1882	WSB1	3'	TCCAACCTGGACAACAGAGCGA 56979	C	C
	GA		TCTCGCTCTGTTG CCAGG TGGA		
			AGAGCGAGACAAC GGTCC ACCT		
			A A		
GAM1882	YME1L1	3'	TCCAGCCTGGGCAACAGAGCAA 58439	C	
	GA		TCT GCTCTGTTGCCCAGGCTGGA		
			AGA CGAGACAACCGGGTCCGACCT		
			A		
GAM1882	YME1L1	3'	TCCAGCCTGGGTGACAGAGTGA 58440		TG
	GA		TCTCGCTCTGT CCCAGGCTGGA		
			AGAGTGAGACA GGGTCCGACCT		
			GT		
GAM1882	ZAK	3'	CCTGGGCAAGAGAACAAGA 34103	CGC	G
			TCT TCT TTGCCCAGG		
			AGA AGA AACGGGTCC		
			ACA G		
GAM1882	ZAK	3'	TCCAGCCTGGATGACAGAGTGA 34109		GC
	GA		TCTCGCTCTGTT CCAGGCTGGA		

			AGAGTGAGACAG GGTCCGACCT		
			TA		
GAM1882	ZFP106	3'	CCAGCCTGGGCGACAAGAG 42720	—	
			CTCT GTTGCCCAGGCTGG		
			GAGA CAGCGGGTCCGACC		
			A		
GAM1882	ZFP106	3'	TCCAGCCTGGTGACAGAGTGAG 42742	TG C	
	A		TCTCGCTCTGT CC AGGCTGGA		
			AGAGTGAGACA GG TCCGACCT		
			GT —		
GAM1882	ZNF197	3'	TCCAGCCTGGGCAACAAGAGCG 23760	—	
	A		TCGCTCT GTTGCCCAGGCTGGA		
			AGCGAGA CAACGGGTCCGACCT		
			A		
GAM1882	ZNF271	3'	TCCAGCCTGGGCAACAGAGTGA 96968		
	GA		TCTCGCTCTGTTGCCAGGCTGGA		
			AGAGTGAGACAACGGGTCCGACCT		
			A		
GAM1882	ZNF271	3'	TCCAGTCTGGGCAACAGAGCAA 96969	C	
	GA		TCT GCTCTGTTGCCAGGCTGGA		
			AGA CGAGACAACGGGTCTGACCT		
			A		
GAM1882	ZNF297B	3'	TCCAGCCTGCGCGACAGATCGA 82707	C C	
	GA		TCTCG TCTGTTGC CAGGCTGGA		
			AGAGC AGACAGCG GTCCGACCT		
			T C		
GAM1882	ZNF297B	5'	TCCAGCCTGGGTAAAAGAGTGA 82708	G	
	GA		TCTCGCTCT TTGCCAGGCTGGA		
			AGAGTGAGA AATGGGTCCGACCT		
			A		
GAM1882	ZNF297B	5'	TCCAGCCTGGGCAACAAGAGC 26673	—	
			GCTCT GTTGCCCAGGCTGGA		
			CGAGA CAACGGGTCCGACCT		
			A		
GAM1882	ZNF297B	5'	TCCAGCCTGGGCAACAGAGCAA 26675	C	
	GA		TCT GCTCTGTTGCCAGGCTGGA		
			AGA CGAGACAACGGGTCCGACCT		
			A		
GAM1882	ZNF333	3'	TCCAGCCTGGGCAACAGAGTGA 51595		
			TCGCTCTGTTGCCAGGCTGGA		

AGTGAGACAACGGGTCCGACCT

GAM1882 ZNF339 3' TCCAGCCTGGGCAACAGAGTGG 41398
TCGCTCTGTTGCCCAGGCTGGA
|||||||
GGTGAGACAACGGGTCCGACCT

GAM1882 LOC112687 3' TCCAGCCTGGGCAACAGAGTGG 73243
GA TCTCGCTCTGTTGCCCAGGCTGGA
|||||||
AGGGTGAGACAACGGGTCCGACCT

GAM1882 LOC112868 3' TCCAGCCTGACCCAGAGCAGA 73271 C TTGCC
TCT GCTCTG CAGGCTGGA
||| |||||
AGA CGAGAC GTCCGACCT
_ CCCA_

GAM1882 LOC113201 3' TCCAGCTTGGGCACCAGAGCAA 57357 C T
GA TCT GCTCTG TGCCCAGGCTGGA
||| |||||
AGA CGAGAC ACGGGTTCGACCT
A C

GAM1882 LOC113523 3' TCCAGCCTGGGCGACAGGGCAA 73434 C
GA TCT GCTCTGTTGCCCAGGCTGGA
||| |||||
AGA CGGGACAGCGGGTCCGACCT
A

GAM1882 LOC114987 3' TCCAGCCTGGGCAACAAGAGCG 59800 _
A TCGCTCT GTTGCCCAGGCTGGA
||||| |||||
AGCGAGA CAACGGGTCCGACCT
A

GAM1882 LOC115129 3' TCCAGCCTGAGCGACAGAGTAA 73629 CG C
GA TCT CTCTGTTGC CAGGCTGGA
||| |||||
AGA GAGACAGCG GTCCGACCT
AT A

GAM1882 LOC115196 3' TCCAGCCTGGGAGACAGAGCGA 73661 TG
GA TCTCGCTCTGT CCCAGGCTGGA
||||||| |||||
AGAGCGAGACA GGGTCCGACCT
GA

GAM1882 LOC115273 3' TCCAGCCTGGGCAACAGAGTGA 73754
GA TCTCGCTCTGTTGCCCAGGCTGGA
|||||||
AGAGTGAGACAACGGGTCCGACCT

GAM1882 LOC115761 3' TCCAGTCTGGGCAACAGAGTGA 93398
GA TCTCGCTCTGTTGCCCAGGCTGGA
|||||||

AGAGTGAGACAACGGGTCTGACCT

GAM1882 LOC116113 3' CCAGCCTGGGGGAAGGAG 93832 G G
CTCT TT CCCAGGCTGG
|||||
GAGG AG GGGTCCGACC
A G

GAM1882 LOC116143 3' TCCAGCCTGGGCAACTGAGCAA 74194 C T
GA TCT GCTC GTTGCCCAGGCTGGA
|||||
AGA CGAG CAACGGGTCCGACCT
A T

GAM1882 LOC116236 3' TCCAGCCTGGGCGACAGAGTAA 74248 CG
GA TCT CTCTGTTGCCAGGCTGGA
|||||
AGA GAGACAGCGGGTCCGACCT
AT

GAM1882 LOC116349 3' TCCAGCCTGGGCAACAGAGCGA 74281
GG TCTCGCTCTGTTGCCAGGCTGGA
|||||
GGAGCGAGACAACGGGTCCGACCT

GAM1882 LOC119504 5' TCCAGCCTGGGCAACAAGAGGG 74449 G _
A TC CTCT GTTGCCCAGGCTGGA
|||||
AG GAGA CAACGGGTCCGACCT
G A

GAM1882 LOC120406 3' TCCAGCCTGGGTGACAGAGCGA 76066 TG
GA TCTCGCTCTGT CCCAGGCTGGA
|||||
AGAGCGAGACA GGGTCCGACCT
GT

GAM1882 LOC122704 3' TCCAACCTGGGCGACAGGGCGA 74611 C
GA TCTCGCTCTGTTGCCAGG TGGA
|||||
AGAGCGGGACAGCGGGTCC ACCT
A

GAM1882 LOC124225 5' CCAGCCTGAGAAACAAGC 74758 C GCC
GCT TGTT CAGGCTGG
|||||
CGA ACAA GTCCGACC
_ AGA

GAM1882 LOC126282 3' TCCAGCCTGGGTGACAGAGCAA 74967 C TG
GA TCT GCTCTGT CCCAGGCTGGA
|||||
AGA CGAGACA GGGTCCGACCT
A GT

GAM1882 LOC126669 3' TCCAGCCTGAGTGACAGAGTGA 75951 TG C
GA TCTCGCTCTGT C CAGGCTGGA
|||||

		AGAGTGAGACA G GTCCGACCT		
		GT A		
GAM1882	LOC127262 3'	TCCAGCCCCGGGCGACAGAGCGA 76605		A
	GA	TCTCGCTCTGTTGCCC GGCTGGA		
		AGAGCGAGACAGCGGG CCGACCT		
		C		
GAM1882	LOC127428 3'	TCCAGCCTGGGCAACAGAGTGA 75163		
	GA	TCTCGCTCTGTTGCCCAGGCTGGA		
		AGAGTGAGACAACGGGTCCGACCT		
GAM1882	LOC129880 3'	TCCAGCTTGGGCAACAGAGCAA 75409	C	
	GA	TCT GCTCTGTTGCCAGGCTGGA		
		AGA CGAGACAACGGGTTCGACCT		
		A		
GAM1882	LOC130026 3'	TCCAGCCTAGGCAACAGAGCAA 57441	C	C
	GA	TCT GCTCTGTTGCC AGGCTGGA		
		AGA CGAGACAACGG TCCGACCT		
		A A		
GAM1882	LOC130535 3'	TCCAGCCTGGGCAACAAGAATG 76655	C	_
	A	TCG TCT GTTGCCCAGGCTGGA		
		AGT AGA CAACGGGTCCGACCT		
		A A		
GAM1882	LOC130535 3'	TCCAGCCTGGGTGACAGAGCAA 76656	C	TG
	GA	TCT GCTCTGT CCCAGGCTGGA		
		AGA CGAGACA GGGTCCGACCT		
		A GT		
GAM1882	LOC131965 3'	TCCAGCCTGGGCGACAGAGTGA 75528		
	GA	TCTCGCTCTGTTGCCCAGGCTGGA		
		AGAGTGAGACAGCGGGTCCGACCT		
GAM1882	LOC133926 3'	TCCAGCCTGGGCGACAGAGCGA 75634		
	GA	TCTCGCTCTGTTGCCCAGGCTGGA		
		AGAGCGAGACAGCGGGTCCGACCT		
GAM1882	LOC134147 3'	TCCAGCCTGGACAACAGAGGGA 57967	G	C
	GA	TCTC CTCTGTTG CCAGGCTGGA		
		AGAG GAGACAAC GGTCCGACCT		
		G A		
GAM1882	LOC134265 3'	TCCAGCCTAAGCAAATAGCAAG 75657	C	CTG CC
	A	TCT GCT TTGC AGGCTGGA		

		AGA CGA AACG TCCGACCT	
		A TA_ AA	
GAM1882	LOC135154 3'	TCCAGCCTGGGCAACAAGAGCG 75736	—
	A	TCGCTCT GTTGCCCAGGCTGGA	
		AGCGAGA CAACGGGTCCGACCT	
		A	
GAM1882	LOC135818 3'	TCCAGCCTGGGCAATAGGGTAA 75749	CG
	GA	TCT CTCTGTTGCCAGGCTGGA	
		AGA GGGATAACGGGTCCGACCT	
		AT	
GAM1882	LOC137362 3'	TCCAGCCTGGGCAACAAGAGC 75787	—
		GCTCT GTTGCCCAGGCTGGA	
		CGAGA CAACGGGTCCGACCT	
		A	
GAM1882	LOC138389 3'	TCCAGCCTGGGCAACAAGAGTG 76744	—
	A	TCGCTCT GTTGCCCAGGCTGGA	
		AGTGAGA CAACGGGTCCGACCT	
		A	
GAM1882	LOC142937 3'	TCCAGCCTGGGCCACAGAACGA 57447	C T
	GA	TCTCG TCTGT GCCCAGGCTGGA	
		AGAGC AGACA CGGGTCCGACCT	
		A C	
GAM1882	LOC142948 3'	TCCAGCCTGGGTGACAGAGCGA 83780	TG
	GG	TCTCGCTCTGT CCCAGGCTGGA	
		GGAGCGAGACA GGGTCCGACCT	
		GT	
GAM1882	LOC143196 3'	TCCAGCTTGGAACAGAGCGAG 83805	C
	A	TCTCGCTCTGTTGCC AGGCTGGA	
		AGAGCGAGACAACGG TTCGACCT	
		—	
GAM1882	LOC143310 3'	CCAGCCTGGGTGACAGAGCGAG 77040	TG
	A	TCTCGCTCTGT CCCAGGCTGG	
		AGAGCGAGACA GGGTCCGACC	
		GT	
GAM1882	LOC143465 3'	TCCAGCCTGGGTGACGGAGTGA 83878	TG
	GA	TCTCGCTCTGT CCCAGGCTGGA	
		AGAGTGAGGCA GGGTCCGACCT	
		GT	
GAM1882	LOC143888 3'	TCCAGCCTGGGTGACAGAGTGA 77175	TG
	GA	TCTCGCTCTGT CCCAGGCTGGA	

		AGAGTGAGACA GGGTCCGACCT		
		GT		
GAM1882	LOC143943 3'	TCCAGCCTGGGTGACAGAGCGA 83921	TG	
	GA	TCTCGCTCTGT CCCAGGCTGGA		
		AGAGCGAGACA GGGTCCGACCT		
		GT		
GAM1882	LOC144289 3'	TCCAGCCTGGGTGACAGAGTGA 83962	TG	
	GA	TCTCGCTCTGT CCCAGGCTGGA		
		AGAGTGAGACA GGGTCCGACCT		
		GT		
GAM1882	LOC144308 5'	TCCAGCCTGGGTGACAGAGC 83985	TG	
		GCTCTGT CCCAGGCTGGA		
		CGAGACA GGGTCCGACCT		
		GT		
GAM1882	LOC144465 3'	TCCAGCCTGGGCAACAAGAGC 77350	—	
		GCTCT GTTGCCCAGGCTGGA		
		CGAGA CAACGGGTCCGACCT		
		A		
GAM1882	LOC144465 3'	TCCAGCCTGGGCAACAAGAGTG 77352	—	
	A	TCGCTCT GTTGCCCAGGCTGGA		
		AGTGAGA CAACGGGTCCGACCT		
		A		
GAM1882	LOC144481 3'	CCATCTTGGGCAACAGAATGAG 84015	C	C
	A	TCTCG TCTGTTGCCAGG TGG		
		AGAGT AGACAACGGGTTC ACC		
		A T		
GAM1882	LOC144519 5'	TCCAGCCTGGGCGACAGAGTGA 77380		
	GA	TCTCGCTCTGTTGCCAGGCTGGA		
		AGAGTGAGACAGCGGGTCCGACCT		
GAM1882	LOC144563 3'	TCCAGCTTGGGCAACAGAGTAA 77405	CG	
	GA	TCT CTCTGTTGCCAGGCTGGA		
		AGA GAGACAACGGGTTCGACCT		
		AT		
GAM1882	LOC144845 3'	TCCAGCCCAGGCGACAGAGCAA 57464	C	A
	GA	TCT GCTCTGTTGCC GGCTGGA		
		AGA CGAGACAGCGGG CCGACCT		
		A C		
GAM1882	LOC145216 3'	CCAGCCTAGCGACAGAGCAAGA 84219	C	CC
		TCT GCTCTGTTGC AGGCTGG		

AGA CGAGACAGCG TCCGACC
 A A_
 GAM1882 LOC145231 3' TCCAGCCTGAACAACATAACAA 84259 CGCTC CC
 GA TCT TGTTG CAGGCTGGA
 ||| |||| |||||
 AGA ACAAC GTCCGACCT
 ACAAT AA
 GAM1882 LOC145299 3' CCTGGGCGACAGAGCGAGA 84275
 TCTCGCTCTGTTGCCAGG
 |||||
 AGAGCGAGACAGCGGGTCC

 GAM1882 LOC145333 3' TCCAGCCTGGGCGACAGAGCGA 84304
 GA TCTCGCTCTGTTGCCAGGCTGGA
 |||||
 AGAGCGAGACAGCGGGTCCGACCT

 GAM1882 LOC145387 3' TCCAGCCTGGGCGACAGAGAGA 84344 G
 GA TCTC CTCTGTTGCCAGGCTGGA
 ||| |||||
 AGAG GAGACAGCGGGTCCGACCT
 A
 GAM1882 LOC145387 3' TCCAGCCTGGGTGGCAGAGTGA 84345 TG
 GA TCTCGCTCTGT CCCAGGCTGGA
 ||||| |||||
 AGAGTGAGACG GGGTCCGACCT
 GT
 GAM1882 LOC145438 3' TCCAGCCTGGGCGACAGAGCGA 84316
 GA TCTCGCTCTGTTGCCAGGCTGGA
 |||||
 AGAGCGAGACAGCGGGTCCGACCT

 GAM1882 LOC145453 3' TCAGCCTGGGCAACAGAGTGAG 77670
 A TCTCGCTCTGTTGCCAGGCTGG
 |||||
 AGAGTGAGACAACGGGTCCGACT

 GAM1882 LOC145482 3' CCAGCCTGGGCGACAAGAG 77741 _
 CTCT GTTGCCCAGGCTGG
 ||| |||||
 GAGA CAGCGGGTCCGACC
 A
 GAM1882 LOC145483 3' TCCAGCCTGGGCAGCAGAGC 77758
 GCTCTGTTGCCAGGCTGGA
 |||||
 CGAGACGACGGGTCCGACCT

 GAM1882 LOC145608 5' TCCAGCCTGGGTGACAGAGCAA 84386 C TG
 GA TCT GCTCTGT CCCAGGCTGGA
 ||| ||||| |||||

		AGA CGAGACA GGGTCCGACCT		
		A GT		
GAM1882	LOC145609 3'	TCCAGCCTGGGTGACAGAGCAA 84370	C	TG
	GA	TCT GCTCTGT CCCAGGCTGGA		
		AGA CGAGACA GGGTCCGACCT		
		A GT		
GAM1882	LOC145663 3'	TCCAGCCTGGGCGACAGAGCTA 84430	C	
	GA	TCT GCTCTGTTGCCAGGCTGGA		
		AGA CGAGACAGCGGGTCCGACCT		
		T		
GAM1882	LOC145757 3'	TCCAGCCTAGGTGACAGAGCGA 77942		TG C
	GA	TCTCGCTCTGT CC AGGCTGGA		
		AGAGCGAGACA GG TCCGACCT		
		GT A		
GAM1882	LOC145820 3'	TCCAGCCTGGGCGACAGAGCAA 77980	C	
	GA	TCT GCTCTGTTGCCAGGCTGGA		
		AGA CGAGACAGCGGGTCCGACCT		
		A		
GAM1882	LOC145945 5'	TCCAGCCTGAGCAACAGAGCAA 84571	C	C
	GA	TCT GCTCTGTTGC CAGGCTGGA		
		AGA CGAGACAACG GTCCGACCT		
		A A		
GAM1882	LOC145988 5'	TCCAGCCTGGAAGGCAGAGAGA 78072	G	GC
	GA	TCTC CTCTGTT CCAGGCTGGA		
		AGAG GAGACGG GGTCCGACCT		
		A AA		
GAM1882	LOC146059 3'	TCCAGTCTGGGTAACAGAGCGA 78090		
	GA	TCTCGCTCTGTTGCCAGGCTGGA		
		AGAGCGAGACAATGGGTCTGACCT		
GAM1882	LOC146229 3'	TCCAGCCTGGGCGACAGAGCGA 78317		
	GA	TCTCGCTCTGTTGCCAGGCTGGA		
		AGAGCGAGACAGCGGGTCCGACCT		
GAM1882	LOC146540 3'	TCCAGCCTGGGCTACAAAGCAG 78530	TC C T	
	GA	TC GCT TGT GCCCAGGCTGGA		
		AG CGA ACA CGGGTCCGACCT		
		GA A T		
GAM1882	LOC146713 3'	TCCAGCCTGGGCAACAGAGC 84739		
		GCTCTGTTGCCCAGGCTGGA		

CGAGACAACGGGTCCGACCT

GAM1882 LOC146713 3' TCCAGCCTGGTCAACAGAGCAA 84741 C C
GA TCT GCTCTGTTG CCAGGCTGGA

||| ||||| |||||

AGA CGAGACAAC GGTCCGACCT

A T

GAM1882 LOC146728 5' TCCAGACTGGACAACAGAGC 84772 C G
GCTCTGTTG CCAG CTGGA

||||| ||| |||

CGAGACAAC GGTC GACCT

A A

GAM1882 LOC146728 3' TCCAGCCTGGGAAGCAGAGTGA 84774 G
GA TCTCGCTCTGTT CCCAGGCTGGA

||||||| |||||

AGAGTGAGACGA GGGTCCGACCT

A

GAM1882 LOC146756 3' TCCAGCCTGGGCGACAGAGCGA 84813
GA TCTCGCTCTGTTGCCAGGCTGGA

||||||| |||||

AGAGCGAGACAGCGGGTCCGACCT

GAM1882 LOC146839 5' TCCAGCCTGGGCAACATAGC 84853 C
GCT TGTTGCCAGGCTGGA

||| |||||

CGA ACAACGGGTCCGACCT

T

GAM1882 LOC146895 3' TCCAGCCTGGGTGACAAGAGC 84874 _ TG
GCTCT GT CCCAGGCTGGA

|||| || |||||

CGAGA CA GGGTCCGACCT

A GT

GAM1882 LOC146901 3' CAGCCTAGACAACAGAGCAAGA 84894 C CCC
TCT GCTCTGTTG AGGCTG

||| ||||| |||

AGA CGAGACAAC TCCGAC

A AGA

GAM1882 LOC146923 3' TCCAGCCTGGGCGACAGAGTGA 78804
GA TCTCGCTCTGTTGCCAGGCTGGA

||||||| |||||

AGAGTGAGACAGCGGGTCCGACCT

GAM1882 LOC146958 3' TCCAGCCTGGGTGACACAGCGA 84946 C TG
GA TCTCGCT TGT CCCAGGCTGGA

||||| || |||||

AGAGCGA ACA GGGTCCGACCT

C GT

GAM1882 LOC146958 3' TCCAGCCTGGGTGACAGAGCGA 84948 TG
GA TCTCGCTCTGT CCCAGGCTGGA

||||||| |||||

AGAGCGAGACA GGGTCCGACCT
 GT
 GAM1882 LOC147063 5' CCAGCCTGGGCAACAGAGTGAG 85016
 A TCTCGCTCTGTTGCCCAGGCTGG
 |||||
 AGAGTGAGACAACGGGTCCGACC

 GAM1882 LOC147071 3' TCCAGCCTGGGCGACAGAGCAA 73373 C
 GA TCT GCTCTGTTGCCCAGGCTGGA
 ||| |||||
 AGA CGAGACAGCGGGTCCGACCT
 A
 GAM1882 LOC147180 5' TCCAGCCCGGGTGACAGAGTGA 85105 TG A
 TCGCTCTGT CCC GGCTGGA
 ||||| ||| |||||
 AGTGAGACA GGG CCGACCT
 GT C
 GAM1882 LOC147599 3' TCCAGCCTGGGCAACAGAGAGA 85166 G
 TC CTCTGTTGCCCAGGCTGGA
 || |||||
 AG GAGACAACGGGTCCGACCT
 A
 GAM1882 LOC147622 3' TCCAGCCTGGGTGACAGAGCTA 85172 C TG
 GA TCT GCTCTGT CCCAGGCTGGA
 ||| ||||| |||||
 AGA CGAGACA GGGTCCGACCT
 T GT
 GAM1882 LOC147649 3' CCTGGGCGACAGAGCGAGA 79060
 TCTCGCTCTGTTGCCCAGG
 |||||
 AGAGCGAGACAGCGGGTCC

 GAM1882 LOC147664 3' TCCAGCCTGGGCAACGAGAG 79049 _
 CTCT GTTGCCCAGGCTGGA
 ||||| |||||
 GAGA CAACGGGTCCGACCT
 G
 GAM1882 LOC147700 3' TCCAGCCTGTGCAACAAGCGA 59886 C C
 TCGCT TGTTGC CAGGCTGGA
 ||||| ||||| |||||
 AGCGA ACAACG GTCCGACCT
 _ T
 GAM1882 LOC147727 5' TCCAGCCTGGGCGATAGAGTGA 79139
 GA TCTCGCTCTGTTGCCCAGGCTGGA
 |||||
 AGAGTGAGATAGCGGGTCCGACCT

 GAM1882 LOC147727 5' TCCAGTCTGGGCGACAGAGCGA 79140
 GA TCTCGCTCTGTTGCCCAGGCTGGA
 |||||

AGAGCGAGACAGCGGGTCTGACCT

GAM1882 LOC147837 3' CCAGCCTGGGCGACAGAGCCAG 79204 C
A TCT GCTCTGTTGCCCAGGCTGG

||| ||||||||||||
AGA CGAGACAGCGGGTCCGACC
C

GAM1882 LOC147837 3' TCCAGCCTGGGCAGCAAGAGC 79209 _
GCTCT GTTGCCCAGGCTGGA

|||| ||||||||||||
CGAGA CGACGGGTCCGACCT
A

GAM1882 LOC147990 3' TCCAGCCTGGGCAACAGAGC 85235
GCTCTGTTGCCCAGGCTGGA

||||||||||||||
CGAGACAACGGGTCCGACCT

GAM1882 LOC148166 3' TCCAGCCTAGGCGACGGGGCAA 79424 C C
GA TCT GCTCTGTTGCC AGGCTGGA

||| |||||||| |||||
AGA CGGGGCAGCGG TCCGACCT
A A

GAM1882 LOC148206 3' TCCAGCCTGGGCCACAAGGCAA 79466 C TC T
GA TCT GC TGT GCCCAGGCTGGA

||| || ||| |||||||||
AGA CG ACA CGGGTCCGACCT
A GA C

GAM1882 LOC148397 3' CCAGCCTGGGCAACAAGAGT 79565 _
GCTCT GTTGCCCAGGCTGG

|||| ||||||||||||
TGAGA CAACGGGTCCGACC
A

GAM1882 LOC148534 3' TCCAGCCTGGGCGACAGAGCAA 79640 C
GA TCT GCTCTGTTGCCCAGGCTGGA

||| ||||||||||||||||
AGA CGAGACAGCGGGTCCGACCT
A

GAM1882 LOC148758 5' TCCAGCCTGGGCAACAAGAGC 79726 _
GCTCT GTTGCCCAGGCTGGA

|||| ||||||||||||
CGAGA CAACGGGTCCGACCT
A

GAM1882 LOC148809 3' TCCAGCCTGGGCGACAGAGCAA 79762 C
GA TCT GCTCTGTTGCCCAGGCTGGA

||| ||||||||||||||||
AGA CGAGACAGCGGGTCCGACCT
A

GAM1882 LOC148809 5' TCCAGCCTGGGTGACAGAGCAA 79763 C TG
GA TCT GCTCTGT CCCAGGCTGGA

||| ||||| |||||||||

AGA CGAGACA GGGTCCGACCT
 A GT
 GAM1882 LOC148823 3' TCCAGCTTGGGCAACAGAGTGA 59896
 GA TCTCGCTCTGTTGCCCAGGCTGGA
 |||||
 AGAGTGAGACAACGGGTTCGACCT

GAM1882 LOC148936 3' TCCAGGTTGGGCAACAGAGCAA 85459 C G
 GA TCT GCTCTGTTGCCCAG CTGGA
 ||| |||||
 AGA CGAGACAACGGGT GACCT
 A G

GAM1882 LOC148938 3' TCCAGGCTGGGCAACACAGCAA 85441 C C G
 GA TCT GCT TGTTGCCCAG CTGGA
 ||| ||| |||||
 AGA CGA ACAACGGGTC GACCT
 A C G

GAM1882 LOC148946 5' CCAACGAAAACAGAGCGAGA 85465 GC AGGC
 TCTCGCTCTGTT CC TGG
 ||||| || |||
 AGAGCGAGACAA GG ACC
 AA CA__

GAM1882 LOC149073 3' TCCAGCCTGGGCAACAGTGTGA 85487 T
 GA TCTCGC CTGTTGCCCAGGCTGGA
 ||||| |||||
 AGAGTG GACAACGGGTCCGACCT
 T

GAM1882 LOC149113 5' CCAGCCTGGGCTACAAGAG 79905 _ T
 CTCT GT GCCCAGGCTGG
 |||| || |||||
 GAGA CA CGGGTCCGACC
 A T

GAM1882 LOC149157 5' TCCAGCCTGGTCCAGAGAGAAA 79943 CG G C_
 GA TCT CTCT TTG CCAGGCTGGA
 ||| |||| ||| |||||
 AGA GAGA GAC GGTCCGACCT
 AA _ CT

GAM1882 LOC149175 3' TCCAGCCTGGGCGACAGAGCGA 79957
 GA TCTCGCTCTGTTGCCCAGGCTGGA
 |||||
 AGAGCGAGACAGCGGGTCCGACCT

GAM1882 LOC149194 5' TCCAGCCTGGGCAACAAGAGC 79990 _
 GCTCT GTTGCCCAGGCTGGA
 ||||| |||||
 CGAGA CAACGGGTCCGACCT
 A

GAM1882 LOC149271 3' TCCAGCCTGGGCAACAAGAGTG 80012 _
 A TCGCTCT GTTGCCCAGGCTGGA
 ||||| |||||

		AGTGAGA CAACGGGTCCGACCT		
		A		
GAM1882	LOC149464 3'	CCAGCCTGGGCAACAAGAG	85588	_
		CTCT GTTGCCCAGGCTGG		
		GAGA CAACGGGTCCGACC		
		A		
GAM1882	LOC149579 5'	TCCAGCCTGTGTGACAGAGCAA	71695	C TG C
	GA	TCT GCTCTGT C CAGGCTGGA		
		AGA CGAGACA G GTCCGACCT		
		A GT T		
GAM1882	LOC149606 3'	CCTGGGCAACATAGCGAGA	80258	C
		TCTCGCT TGTTGCCCAGG		
		AGAGCGA ACAACGGGTCC		
		T		
GAM1882	LOC149628 3'	TCCAGCCTGGGTGACAGAGCGA	80281	TG
	GA	TCTCGCTCTGT CCCAGGCTGGA		
		AGAGCGAGACA GGGTCCGACCT		
		GT		
GAM1882	LOC149672 5'	TCCAGCCTGGGCAACAGAGTGA	80339	
	GA	TCTCGCTCTGTTGCCCAGGCTGGA		
		AGAGTGAGACAACGGGTCCGACCT		
GAM1882	LOC149705 3'	TCCAGCCTGGGTGACGAGTGA	85787	T TG
		TCGCTC GT CCCAGGCTGGA		
		AGTGAG CA GGGTCCGACCT		
		_ GT		
GAM1882	LOC149711 3'	TCCAGCCTGGGTGACAGAGTGA	85856	TG
	GA	TCTCGCTCTGT CCCAGGCTGGA		
		AGAGTGAGACA GGGTCCGACCT		
		GT		
GAM1882	LOC149952 3'	TCCAGCCTGGGCAATAGAGTGA	80372	
	GA	TCTCGCTCTGTTGCCCAGGCTGGA		
		AGAGTGAGATAACGGGTCCGACCT		
GAM1882	LOC150095 3'	TCCAGCCTGGGCAACAGAGCGA	85996	
	GA	TCTCGCTCTGTTGCCCAGGCTGGA		
		AGAGCGAGACAACGGGTCCGACCT		
GAM1882	LOC150139 3'	CCTGAGCAACATAGCGAGA	80410	C C
		TCTCGCT TGTTGC CAGG		

		AGAGCGA ACAACG GTCC		
		T A		
GAM1882	LOC150139 3'	TCCAGCCTGGGTGACAGAGAGA 80413	G	TG
		TC CTCTGT CCCAGGCTGGA		
		AG GAGACA GGGTCCGACCT		
		A GT		
GAM1882	LOC150142 5'	CCAGCCTGGGCAACAAAGTAAG 80404	CG	C
	A	TCT CT TGTTGCCCAGGCTGG		
		AGA GA ACAACGGGTCCGACC		
		AT A		
GAM1882	LOC150174 3'	TCCAGCCTGGTCAACAGAGTGA 80441		C
	GA	TCTCGCTCTGTTG CCAGGCTGGA		
		AGAGTGAGACAAC GGTCCGACCT		
		T		
GAM1882	LOC150185 3'	TCCAGCCTGGGTGACAGAGCGA 86070		TG
	GA	TCTCGCTCTGT CCCAGGCTGGA		
		AGAGCGAGACA GGGTCCGACCT		
		GT		
GAM1882	LOC150213 3'	TCCAGCCTGGTCAACAGAGTGA 75360		C
	GA	TCTCGCTCTGTTG CCAGGCTGGA		
		AGAGTGAGACAAC GGTCCGACCT		
		T		
GAM1882	LOC150225 3'	TCCAGCCTGGGCGTCAGAGTGA 86206		T
	GA	TCTCGCTCTG TGCCCAGGCTGGA		
		AGAGTGAGAC GCGGGTCCGACCT		
		T		
GAM1882	LOC150236 3'	TCCAGCCTGGTCAACAGAGTGA 80503		C
	GA	TCTCGCTCTGTTG CCAGGCTGGA		
		AGAGTGAGACAAC GGTCCGACCT		
		T		
GAM1882	LOC150244 3'	TCCAGCCTGGGCGACAGAGCGA 80552		
	GA	TCTCGCTCTGTTGCCCAGGCTGGA		
		AGAGCGAGACAGCGGGTCCGACCT		
GAM1882	LOC150245 3'	TCCAGCCTGGGTGACAGAATAA 86119	CGC	TG
	GA	TCT TCTGT CCCAGGCTGGA		
		AGA AGACA GGGTCCGACCT		
		ATA GT		
GAM1882	LOC150299 3'	TCCAGCCTGGCGACAGAGCAAG 86170	C	C
	A	TCT GCTCTGTTGCC AGGCTGGA		

		AGA CGAGACAGCGG TCCGACCT		
		A _		
GAM1882	LOC150319 3'	TCCAGCCTGGGCAACAAGAGCG 80477		_
	A	TCGCTCT GTTGCCCAGGCTGGA		
		AGCGAGA CAACGGGTCCGACCT		
		A		
GAM1882	LOC150358 3'	TCCAGCCTGGGCGACAGAGCGA 86101		
	GA	TCTCGCTCTGTTGCCAGGCTGGA		
		AGAGCGAGACAGCGGGTCCGACCT		
GAM1882	LOC150481 3'	TCCAGCCTGGTGACAGAGCAAG 80714	C	TG C
	A	TCT GCTCTGT CC AGGCTGGA		
		AGA CGAGACA GG TCCGACCT		
		A GT _		
GAM1882	LOC150577 3'	TCCAGCCTGGATGACAGAGTGA 86260		GC
		TCGCTCTGTT CCAGGCTGGA		
		AGTGAGACAG GGTCCGACCT		
		TA		
GAM1882	LOC150622 3'	TCCAGCCTGGGCAACAAGAGC 80768		_
		GCTCT GTTGCCCAGGCTGGA		
		CGAGA CAACGGGTCCGACCT		
		A		
GAM1882	LOC150630 5'	TCCAGCCTGGGCAGCAGAGTGA 86307		
	GA	TCTCGCTCTGTTGCCAGGCTGGA		
		AGAGTGAGACGACGGGTCCGACCT		
GAM1882	LOC150889 3'	TCCAGCCTGCGGGACAGAGTGA 80819		G _
	GA	TCTCGCTCTGTT CC CAGGCTGGA		
		AGAGTGAGACAG GG GTCCGACCT		
		_ C		
GAM1882	LOC150960 3'	TCCAGCTTGGGCAACAAAGTGA 80879		C
	GA	TCTCGCT TGTTGCCAGGCTGGA		
		AGAGTGA ACAACGGGTTCGACCT		
		A		
GAM1882	LOC151196 3'	TCCAGCCTGGGCAACACAGCAA 86456	C	C
	GA	TCT GCT TGTTGCCAGGCTGGA		
		AGA CGA ACAACGGGTCCGACCT		
		A C		
GAM1882	LOC151248 5'	CCTGGGCGACAGAGCGAGA 80992		
		TCTCGCTCTGTTGCCAGG		

AGAGCGAGACAGCGGGTCC

GAM1882	LOC151248	3'	TCCAGCCCAGGTAACAGAGTGA	80998		CA
		GA	TCTCGCTCTGTTGCC	GGCTGGA		
			AGAGTGAGACAATGG	CCGACCT		
			AC			
GAM1882	LOC151248	3'	TCCAGCCTGGTGACAGAGCGAG	80999		TG C
		A	TCTCGCTCTGT	CC AGGCTGGA		
			AGAGCGAGACA	GG TCCGACCT		
			GT	_		
GAM1882	LOC151429	3'	TCCAGCCTGGGCGACAGAGCAA	86549	C	
		GA	TCT GCTCTGTTGCC	AGGCTGGA		
			AGA CGAGACAGCGGGTCCGACCT			
			A			
GAM1882	LOC151429	3'	TCCAGCCTGGGTGACAGAGCAA	86550	C	TG
		GA	TCT GCTCTGT	CCCAGGCTGGA		
			AGA CGAGACA	GGGTCCGACCT		
			A	GT		
GAM1882	LOC151438	3'	CCTGGGCAACACAGCAAGA	86555	C C	
			TCT GCT	TGTTGCCCAGG		
			AGA CGA	ACAACGGGTCC		
			A	C		
GAM1882	LOC151446	3'	TCTGAACAACAGAGCAAGA	86575	C	CC
			TCT GCTCTGTTG	CAGG		
			AGA CGAGACAAC	GTCT		
			A	AA		
GAM1882	LOC151556	3'	TCCAGCCTGAGCAACAGAGCAA	81085	C	C
		GA	TCT GCTCTGTTGC	CAGGCTGGA		
			AGA CGAGACAACG	GTCCGACCT		
			A	A		
GAM1882	LOC151632	3'	TCCAGCCTGGGCAACAGAGTAA	86651	CG	
		GA	TCT CTCTGTTGCC	CAGGCTGGA		
			AGA GAGACAACGGGTCCGACCT			
			AT			
GAM1882	LOC151720	3'	TCCAGCCTGGGCGACAGAGCGA	81158		
		GA	TCTCGCTCTGTTGCC	CAGGCTGGA		
			AGAGCGAGACAGCGGGTCCGACCT			
GAM1882	LOC151904	3'	TCCAGCCTGGGCAACAGAGCGA	81210		
		GA	TCTCGCTCTGTTGCC	CAGGCTGGA		

AGAGCGAGACAACGGGTCCGACCT

GAM1882	LOC152002	3'	TCCAGCCTGGACGACAGAGTGA	81268	C
		GA	TCTCGCTCTGTTG CCAGGCTGGA		
			AGAGTGAGACAGC GGTCCGACCT		
			A		
GAM1882	LOC152106	3'	TCCAGCCTGGTCGACAGAGTGA	70598	C
		GA	TCTCGCTCTGTTG CCAGGCTGGA		
			AGAGTGAGACAGC GGTCCGACCT		
			T		
GAM1882	LOC152271	3'	TCCAGCCTGGGCAACAGAGTAA	81365	CG
		GA	TCT CTCTGTTGCCCAGGCTGGA		
			AGA GAGACAACGGGTCCGACCT		
			AT		
GAM1882	LOC152283	3'	TCCAGCCTGGGCAACAAGAGTG	86875	—
		AGA	TCTCGCTCT GTTGCCCAGGCTGGA		
			AGAGTGAGA CAACGGGTCCGACCT		
			A		
GAM1882	LOC152313	3'	TCCAGCCTGGGTGACAGAGCGA	86853	TG
		GA	TCTCGCTCTGT CCCAGGCTGGA		
			AGAGCGAGACA GGGTCCGACCT		
			GT		
GAM1882	LOC152316	3'	TCCAGCCTAGGCAACAGAGCGA	86794	C
		GA	TCTCGCTCTGTTGCC AGGCTGGA		
			AGAGCGAGACAACGG TCCGACCT		
			A		
GAM1882	LOC152317	3'	TCCAGCCTGAGTGACAGA	86837	TG C
			TCTGT C CAGGCTGGA		
			AGACA G GTCCGACCT		
			GT A		
GAM1882	LOC152426	3'	TCCAGCCTGGGCGACAGAGTGA	86902	
		GA	TCTCGCTCTGTTGCCCAGGCTGGA		
			AGAGTGAGACAGCGGGTCCGACCT		
GAM1882	LOC152445	3'	TCCAGCCTGAGTGAGGAAGC	86964	— G TG C
			GCT CT T C CAGGCTGGA		
			CGA GG A G GTCCGACCT		
			A _ GT A		
GAM1882	LOC152453	3'	TCCAGCCTGGGCAACAAGAGCG	81480	—
		A	TCGCTCT GTTGCCCAGGCTGGA		

		AGCGAGA CAACGGGTCCGACCT		
		A		
GAM1882	LOC152627 5'	TCCAGCCTGGATAAAAGAGCAA 81515	C	G C
	GA	TCT GCTCT TTG CCAGGCTGGA		
		AGA CGAGA AAT GGTCCGACCT		
		A A A		
GAM1882	LOC152627 3'	TCCAGCCTGGGCCACAGAGTGA 81516		T
	GA	TCTCGCTCTGT GCCCAGGCTGGA		
		AGAGTGAGACA CGGGTCCGACCT		
		C		
GAM1882	LOC152804 3'	TCCAGCCTGGGCAACAGAGCGA 87088		
	GG	TCTCGCTCTGTTGCCCAGGCTGGA		
		GGAGCGAGACAACGGGTCCGACCT		
GAM1882	LOC152860 3'	CCAGCCTGGGCAGCAAGAG 81578		—
		CTCT GTTGCCCAGGCTGG		
		GAGA CGACGGGTCCGACC		
		A		
GAM1882	LOC152897 3'	CCAGCCTGGGAGACAGAGTGAG 81603		TG
	A	TCTCGCTCTGT CCCAGGCTGG		
		AGAGTGAGACA GGGTCCGACC		
		GA		
GAM1882	LOC153077 3'	TCCAGCCTGGGCTACAGAGCAA 87133	C	T
	GA	TCT GCTCTGT GCCCAGGCTGGA		
		AGA CGAGACA CGGGTCCGACCT		
		A T		
GAM1882	LOC153146 3'	TCCAGCCTGGGTGACAGAGGGA 87148	G	TG
	GA	TCTC CTCTGT CCCAGGCTGGA		
		AGAG GAGACA GGGTCCGACCT		
		G GT		
GAM1882	LOC153243 5'	CCTGGAGCAGCAGAACAAAGA 81662	CGC	—
		TCT TCTGTTGC CCAGG		
		AGA AGACGACG GGTCC		
		ACA A		
GAM1882	LOC153338 3'	TCCAGCCTGGGTGACAGAGCAA 87198	C	TG
	GA	TCT GCTCTGT CCCAGGCTGGA		
		AGA CGAGACA GGGTCCGACCT		
		A GT		
GAM1882	LOC153561 3'	AGCCTGGGCAACAGAGTGAGA 81748		
		TCTCGCTCTGTTGCCCAGGCT		

AGAGTGAGACAACGGGTCCGA

GAM1882 LOC153579 3' CCAGCCTGGGCCCGCAGA 81767 T_
TCTGT GCCCAGGCTGG
||||| |||||||||
AGACG CGGGTCCGACC
CC

GAM1882 LOC153579 3' TCCAGCCTGGGCGACAGAGCGA 81774
GA TCTCGCTCTGTTGCCCAGGCTGGA
||||| |||||||||
AGAGCGAGACAGCGGGTCCGACCT

GAM1882 LOC153642 3' TCCAGCCTGGCAACAGAGTGAG 81793 C
A TCTCGCTCTGTTGCC AGGCTGGA
||||| |||||||
AGAGTGAGACAACGG TCCGACCT

GAM1882 LOC153682 3' TCCAGCCTGAGCGACAGAGCAA 87276 C C
GA TCT GCTCTGTTGC CAGGCTGGA
||| ||||||| |||||||
AGA CGAGACAGCG GTCCGACCT
A A

GAM1882 LOC153688 3' TCCAGCCTGGGCGACAGAGGGA 87333 G
GA TCTC CTCTGTTGCCCAGGCTGGA
||| |||||||||
AGAG GAGACAGCGGGTCCGACCT
G

GAM1882 LOC154403 5' CCAGCCTGGGCTACAAGAG 81971 _ T
CTCT GT GCCCAGGCTGG
|||| || |||||||||
GAGA CA CGGGTCCGACC
A T

GAM1882 LOC154739 5' TCCAGCCTGGGCAACAGGTGAG 87443 T
A TCTCGC CTGTTGCCCAGGCTGGA
||||| |||||||||
AGAGTG GACAACGGGTCCGACCT

GAM1882 LOC154739 3' TCCAGCCTGGGTGACAGAGTGA 87444 TG
GA TCTCGCTCTGT CCCAGGCTGGA
||||||| |||||||||
AGAGTGAGACA GGGTCCGACCT
GT

GAM1882 LOC154791 3' TCCAGCCTGGGCAACAAGAGC 82055 _
GCTCT GTTGCCCAGGCTGGA
||||| |||||||||
CGAGA CAACGGGTCCGACCT
A

GAM1882 LOC154877 3' TCCAGCCTAGGTGATAGAGCAA 87576 C TG C
GA TCT GCTCTGT CC AGGCTGGA
||| |||||| || |||||||

		AGA CGAGATA GG TCCGACCT		
		A GT A		
GAM1882	LOC155006 3'	TCCAGCCTGGGCGGCAGAGCAA 82176	C	
	GA	TCT GCTCTGTTGCCCAGGCTGGA		
		AGA CGAGACGGCGGGTCCGACCT		
		A		
GAM1882	LOC155054 3'	TCCAGCCTGGGTGACAGAGCAA 82206	C	TG
	GA	TCT GCTCTGT CCCAGGCTGGA		
		AGA CGAGACA GGGTCCGACCT		
		A GT		
GAM1882	LOC155072 3'	TCCAACCTGGGTGACAGAGCGA 87672		TG C
		TCGCTCTGT CCCAGG TGGA		
		AGCGAGACA GGGTCC ACCT		
		GT A		
GAM1882	LOC155072 3'	TCCAGCCTGGGTGACTGAGCGA 87673		T TG
	GA	TCTCGCTC GT CCCAGGCTGGA		
		AGAGCGAG CA GGGTCCGACCT		
		T GT		
GAM1882	LOC155376 3'	TCCAGCCTGGGTGACAAAGCAA 82251	C C	TG
	GA	TCT GCT TGT CCCAGGCTGGA		
		AGA CGA ACA GGGTCCGACCT		
		A A GT		
GAM1882	LOC157247 5'	CCTGGGCAACATAGCAAGA 82294	C C	
		TCT GCT TGTTGCCCAGG		
		AGA CGA ACAACGGGTCC		
		A T		
GAM1882	LOC157464 5'	TCCAGCCTGGGCAACGGGCGAG 87752		T
	A	TCTCGC CTGTTGCCCAGGCTGGA		
		AGAGCG GGCAACGGGTCCGACCT		
		—		
GAM1882	LOC157562 5'	TCCAGCCTGGGCAACATAGTGA 87776		C
	GA	TCTCGCT TGTTGCCCAGGCTGGA		
		AGAGTGA ACAACGGGTCCGACCT		
		T		
GAM1882	LOC157657 3'	TCCAGCCTGGACAACACAGTGA 82437	C	C
	GA	TCTCGCT TGTTG CCAGGCTGGA		
		AGAGTGA ACAAC GGTCCGACCT		
		C A		
GAM1882	LOC157660 3'	TCCAGCGTGGGCAACAGAGTGA 87807		G
	GA	TCTCGCTCTGTTGCCCA GCTGGA		

		AGAGTGAGACAACGGGT CGACCT		
		G		
GAM1882	LOC157737 3'	TCCAGCCTGGGCAACAGAGAGA 87846	G	
	GA	TCTC CTCTGTTGCCAGGCTGGA		
		AGAG GAGACAACGGGTCCGACCT		
		A		
GAM1882	LOC157983 3'	TCCAGCCTGGCGACAGAGC 82543	C	
		GCTCTGTTGCC AGGCTGGA		
		CGAGACAGCGG TCCGACCT		
		—		
GAM1882	LOC158088 3'	TCCAGCCTGGCGACAGAGCAAG 87978	C	C
	A	TCT GCTCTGTTGCC AGGCTGGA		
		AGA CGAGACAGCGG TCCGACCT		
		A		
		—		
GAM1882	LOC158160 3'	TCCAGCCTGGGTGACAGCGAGA 73476	CT	TG
		TCTCGCT GT CCCAGGCTGGA		
		AGAGCGA CA GGGTCCGACCT		
		— GT		
GAM1882	LOC158187 3'	TCCAGCCTGGGTGACAGAGCAA 87998	C	TG
	GA	TCT GCTCTGT CCCAGGCTGGA		
		AGA CGAGACA GGGTCCGACCT		
		A GT		
GAM1882	LOC158191 3'	TCCAGCCTGGCGACAGAGCTAG 82682	C	C
	A	TCT GCTCTGTTGCC AGGCTGGA		
		AGA CGAGACAGCGG TCCGACCT		
		T		
		—		
GAM1882	LOC158235 3'	TCCAGCCTGGGCAACACAGAGA 88008	G	C
	GA	TCTC CT TGTTGCCAGGCTGGA		
		AGAG GA ACAACGGGTCCGACCT		
		A C		
GAM1882	LOC158292 5'	TCCAGCCTGGGCAACAGAGCAA 88056	C	
	GA	TCT GCTCTGTTGCCAGGCTGGA		
		AGA CGAGACAACGGGTCCGACCT		
		A		
GAM1882	LOC158292 5'	TCCAGCCTGGGCGACAGAGCGA 88057		
	GA	TCTCGCTCTGTTGCCAGGCTGGA		
		AGAGCGAGACAGCGGGTCCGACCT		
GAM1882	LOC158337 3'	TCCAGCCTGGGTGACAGAGCGA 88112		TG
	GA	TCTCGCTCTGT CCCAGGCTGGA		

		AGAGCGAGACA GGGTCCGACCT		
		GT		
GAM1882	LOC158677 5'	TCCAGCCTGGGTGACAGAGCAA 88252	C	TG
	GA	TCT GCTCTGT CCCAGGCTGGA		
		AGA CGAGACA GGGTCCGACCT		
		A GT		
GAM1882	LOC158819 3'	TCCAGCCTGGGTGACAGAGCGA 88286		TG
	GA	TCTCGCTCTGT CCCAGGCTGGA		
		AGAGCGAGACA GGGTCCGACCT		
		GT		
GAM1882	LOC158987 3'	TCCAGCCTGGGCAACAGAGGGA 88334	G	
	G	CTC CTCTGTTGCCAGGCTGGA		
		GAG GAGACAACGGGTCCGACCT		
		G		
GAM1882	LOC158987 3'	TCCAGCCTGGGCAACATAGTGA 88335	C	
	GA	TCTCGCT TGTTGCCAGGCTGGA		
		AGAGTGA ACAACGGGTCCGACCT		
		T		
GAM1882	LOC158987 3'	TCCAGCCTGGGTGACAGAGCGA 88337		TG
	GA	TCTCGCTCTGT CCCAGGCTGGA		
		AGAGCGAGACA GGGTCCGACCT		
		GT		
GAM1882	LOC159053 3'	TCCAGCCTGGGCAACAGTGAGA 88377		CT
		TCTCGCT GTTGCCAGGCTGGA		
		AGAGTGA CAACGGGTCCGACCT		
		—		
GAM1882	LOC159110 3'	CCAGCCTGGGCAACAGAACAGG 82986		CGC
	A	TCT TCTGTTGCCAGGCTGG		
		AGG AGACAACGGGTCCGACC		
		ACA		
GAM1882	LOC159116 3'	CCAGCCTGGGCAACAGAACAGG 82969		CGC
	A	TCT TCTGTTGCCAGGCTGG		
		AGG AGACAACGGGTCCGACC		
		ACA		
GAM1882	LOC161823 3'	TCCAGCCTGGGCAACAGAGTGA 83176		
		TCTGCTCTGTTGCCAGGCTGGA		
		AGTGAGACAACGGGTCCGACCT		
GAM1882	LOC162962 3'	TCCAGCCTGGGTGACAGCGAGA 83260		CT TG
		TCTCGCT GT CCCAGGCTGGA		

	AGAGCGA CA GGGTCCGACCT	
	— GT	
GAM1882 LOC170395 3'	TCAAGCCTGGGCAACAGAGTGA 76876	G
GA	TCTCGCTCTGTTGCCCAGGCT GA	
	AGAGTGAGACAACGGGTCCGA CT	
	A	
GAM1882 LOC170395 3'	TCCAGCCTGGGCAACAAGAGC 76877	—
	GCTCT GTTGCCCAGGCTGGA	
	CGAGA CAACGGGTCCGACCT	
	A	
GAM1882 LOC196047 5'	TCCAGCCTGGGTGACAGAGCGA 91167	TG
GA	TCTCGCTCTGT CCCAGGCTGGA	
	AGAGCGAGACA GGGTCCGACCT	
	GT	
GAM1882 LOC196540 3'	TCCAGCCTGGGTGACAGAGTGA 91208	TG
GA	TCTCGCTCTGT CCCAGGCTGGA	
	AGAGTGAGACA GGGTCCGACCT	
	GT	
GAM1882 LOC196761 3'	TCCAGCCTGGGCGATAGAGGGA 91121	G
GA	TCTC CTCTGTTGCCCAGGCTGGA	
	AGAG GAGATAGCGGGTCCGACCT	
	G	
GAM1882 LOC197196 3'	TCCAGCCTGGGCGACAAGAGCG 91306	—
A	TCGCTCT GTTGCCCAGGCTGGA	
	AGCGAGA CAGCGGGTCCGACCT	
	A	
GAM1882 LOC197201 3'	TCCAGCCTGGGCAACACAGCAA 89288	C C
GA	TCT GCT TGTTGCCCAGGCTGGA	
	AGA CGA ACAACGGGTCCGACCT	
	A C	
GAM1882 LOC197319 3'	TCCAGCCTGGCAACAGAGTGAG 89329	C
A	TCTCGCTCTGTTGCC AGGCTGGA	
	AGAGTGAGACAACGG TCCGACCT	
	—	
GAM1882 LOC197362 3'	TCCAGCCTGGGTGACAGAGTGA 91312	TG
GA	TCTCGCTCTGT CCCAGGCTGGA	
	AGAGTGAGACA GGGTCCGACCT	
	GT	
GAM1882 LOC199729 3'	TCCAGCCAGGGCAACAGAGTGA 73397	A
GA	TCTCGCTCTGTTGCC GGCTGGA	

		AGAGTGAGACAACGGG CCGACCT		
		A		
GAM1882	LOC199733 3'	TCCAACCTGGGCAACAGAGCCA 91443	C	C
	GA	TCT GCTCTGTTGCCCAGG TGGA		
		AGA CGAGACAACGGGTCC ACCT		
		C A		
GAM1882	LOC199786 3'	TCCAGCCTGGGTGATGGGAGTG 89767	_	TG
	AGA	TCTCGCTCT GT CCCAGGCTGGA		
		AGAGTGAGG TA GGGTCCGACCT		
		G GT		
GAM1882	LOC199858 3'	TCCAGCCTGGGCGACAGAGCGA 89803		
	GA	TCTCGCTCTGTTGCCCAGGCTGGA		
		AGAGCGAGACAGCGGGTCCGACCT		
GAM1882	LOC199923 3'	TCCAGCCTGGACGACAGAGCAA 89874	C	C
	GA	TCT GCTCTGTTG CCAGGCTGGA		
		AGA CGAGACAGC GGTCCGACCT		
		A A		
GAM1882	LOC199923 3'	TCCAGCCTGGGCAACTGAGC 89875	T	
		GCTC GTTGCCCAGGCTGGA		
		CGAG CAACGGGTCCGACCT		
		T		
GAM1882	LOC200014 3'	TCCAGCCTGGGCGACAGAGCAA 89948	C	
	GA	TCT GCTCTGTTGCCCAGGCTGGA		
		AGA CGAGACAGCGGGTCCGACCT		
		A		
GAM1882	LOC200251 3'	TCCAGCCTAGGCAACAAGAGC 90066	_	C
		GCTCT GTTGCC AGGCTGGA		
		CGAGA CAACGG TCCGACCT		
		A A		
GAM1882	LOC200316 3'	TCCAGTTTGAGCAACAGATCAA 90194	CGC	C
	GA	TCT TCTGTTGC CAGGCTGGA		
		AGA AGACAACG GTTTGACCT		
		ACT A		
GAM1882	LOC200317 3'	TCCAGCCTGGGCAACAAGAGTG 90229	_	
	A	TCGCTCT GTTGCCCAGGCTGGA		
		AGTGAGA CAACGGGTCCGACCT		
		A		
GAM1882	LOC200853 3'	TCCAGCCTGGGAGACAGAGCGA 90335		TG
		TCGCTCTGT CCCAGGCTGGA		

		AGCGAGACA GGGTCCGACCT		
		GA		
GAM1882	LOC200904 3'	TCTAGCCTGGGCAACAGAGTAA 91785	CG	
	GA	TCT CTCTGTTGCCCAGGCTGGA		
		AGA GAGACAACGGGTCCGATCT		
		AT		
GAM1882	LOC200918 3'	CCAGCCTGGGCGACAAGAG 90366	_	
		CTCT GTTGCCCAGGCTGG		
		GAGA CAGCGGGTCCGACC		
		A		
GAM1882	LOC200940 3'	TCCAGCCTGGGCGACAGAGTGA 90396		
	GA	TCTCGCTCTGTTGCCCAGGCTGGA		
		AGAGTGAGACAGCGGGTCCGACCT		
GAM1882	LOC201173 3'	TCCAGCCTGGGCGACAGAGCAA 88694	C	
	GA	TCT GCTCTGTTGCCCAGGCTGGA		
		AGA CGAGACAGCGGGTCCGACCT		
		A		
GAM1882	LOC201182 5'	TCCAGCCTGGTCAACAGAGCAA 91338	C	C
	GA	TCT GCTCTGTTG CCAGGCTGGA		
		AGA CGAGACAAC GGTCCGACCT		
		A T		
GAM1882	LOC201220 3'	TCCAGCCTGGGTGACAGAGCAA 88727	C	TG
	GA	TCT GCTCTGT CCCAGGCTGGA		
		AGA CGAGACA GGGTCCGACCT		
		A GT		
GAM1882	LOC201564 3'	TCCAGCCTGGGCAACAAGAGC 81276	_	
		GCTCT GTTGCCCAGGCTGGA		
		CGAGA CAACGGGTCCGACCT		
		A		
GAM1882	LOC201685 3'	TCAAGCCTGGACAACAGGGCAA 91846	C	C G
	GA	TCT GCTCTGTTG CCAGGCT GA		
		AGA CGGGACAAC GGTCCGA CT		
		A A A		
GAM1882	LOC201868 5'	CCAGCCTGGGCTACAAGAG 90518	_	T
		CTCT GT GCCCAGGCTGG		
		GAGA CA CGGGTCCGACC		
		A T		
GAM1882	LOC201895 3'	TCCAGCCTAAGCAATAGAGCGA 90548		CC
	GA	TCTCGCTCTGTTGC AGGCTGGA		

	AGAGCGAGATAACG TCCGACCT	
	AA	
GAM1882 LOC201911 3'	TCCAGCCTGGGCAACAAGAGC 91869	—
	GCTCT GTTGCCCAGGCTGGA	
	CGAGA CAACGGGTCCGACCT	
	A	
GAM1882 LOC201931 3'	TCCAGCCTGGGCGACAGAGCGA 90569	
GA	TCTCGCTCTGTTGCCAGGCTGGA	
	AGAGCGAGACAGCGGGTCCGACCT	
GAM1882 LOC202020 3'	TCCAGCCCGGGCGACAGAGTGA 90603	A
GA	TCTCGCTCTGTTGCC GGCTGGA	
	AGAGTGAGACAGCGGG CCGACCT	
	C	
GAM1882 LOC202781 3'	TCCAGCCTGGACGATATAGCCA 91975	C C C
GA	TCT GCT TGTTG CCAGGCTGGA	
	AGA CGA ATAGC GGTCCGACCT	
	C T A	
GAM1882 LOC202781 3'	TCCAGCCTGGGCGACAGAGCGA 91976	
GA	TCTCGCTCTGTTGCCAGGCTGGA	
	AGAGCGAGACAGCGGGTCCGACCT	
GAM1882 LOC202868 3'	TCCAACCTGGGTGACAGAGCGA 92009	TG C
	TCGCTCTGT CCCAGG TGGA	
	AGCGAGACA GGGTCC ACCT	
	GT A	
GAM1882 LOC202868 3'	TCCAGCCTGGGTGACAGAGCGA 92010	TG
GA	TCTCGCTCTGT CCCAGGCTGGA	
	AGAGCGAGACA GGGTCCGACCT	
	GT	
GAM1882 LOC203025 3'	TCCAGCCTGGGCAACAAGAGC 90749	—
	GCTCT GTTGCCCAGGCTGGA	
	CGAGA CAACGGGTCCGACCT	
	A	
GAM1882 LOC203083 3'	TCCAGCCTGGGCAACAGAGTAA 92095	CG
GA	TCT CTCTGTTGCCAGGCTGGA	
	AGA GAGACAACGGGTCCGACCT	
	AT	
GAM1882 LOC203246 3'	CCTGGGCGACAGAACGAGA 90830	C
	TCTCG TCTGTTGCCAGG	

		AGAGC AGACAGCGGGTCC		
		A		
GAM1882	LOC203276 3'	TCCAGCCTGGGCAACAGAGTGA 92130		
	GA	TCTCGCTCTGTTGCCCAGGCTGGA		
		AGAGTGAGACAACGGGTCCGACCT		
GAM1882	LOC203289 3'	TCCAGCCTGGCGACAGAGC 90870	C	
		GCTCTGTTGCC AGGCTGGA		
		CGAGACAGCGG TCCGACCT		
GAM1882	LOC203305 3'	TCCAGCCTGGGCAACAGAGTGA 92183		
	GA	TCTCGCTCTGTTGCCCAGGCTGGA		
		AGAGTGAGACAACGGGTCCGACCT		
GAM1882	LOC203350 3'	CCTGGGGCAACATAGCGAGA 92235	C	
		TCTCGCT TGTTGCC AGG		
		AGAGCGA ACAACGGG TCC		
		T G		
GAM1882	LOC203350 3'	TCCAGCCTGGATGACAGAGTGA 92250		GC
	GA	TCTCGCTCTGTT CCAGGCTGGA		
		AGAGTGAGACAG GGTCCGACCT		
		TA		
GAM1882	LOC203378 3'	TCCAGCCTGGGCGACAGAACAA 92303		CGC
	GA	TCT TCTGTTGCCCAGGCTGGA		
		AGA AGACAGCGGGTCCGACCT		
		ACA		
GAM1882	LOC205327 3'	TCCAACCTGGGCAACATAGTGG 91072	C	C
	GA	TCTCGCT TGTTGCCCAGG TGGA		
		AGGGTGA ACAACGGGTCC ACCT		
		T A		
GAM1882	LOC219347 3'	TCCAGCCTGGGCAACAGAGTGA 94581		
	GA	TCTCGCTCTGTTGCCCAGGCTGGA		
		AGAGTGAGACAACGGGTCCGACCT		
GAM1882	LOC219540 3'	TCCAGCCTGGGCGACAGAGCGA 95247		
	GA	TCTCGCTCTGTTGCCCAGGCTGGA		
		AGAGCGAGACAGCGGGTCCGACCT		
GAM1882	LOC219627 3'	TCCAGCCTGGGCAACAAGCGA 93812		C
		TCGCT TGTTGCCCAGGCTGGA		

AGCGA ACAACGGGTCCGACCT

GAM1882 LOC219627 3' TCCAGCTGGGCGACAGAGCGAG 93813 G
A TCTCGCTCTGTTGCCAG CTGGA
|||||
AGAGCGAGACAGCGGGTC GACCT

GAM1882 LOC219649 3' TCCAGCCTAGGCAACAAGAGC 94557 _ C
GCTCT GTTGCC AGGCTGGA
|||||
CGAGA CAACGG TCCGACCT
A A

GAM1882 LOC219649 3' TCCAGCCTGGGCGACAGAGTGA 94558
GA TCTCGCTCTGTTGCCAGGCTGGA
|||||
AGAGTGAGACAGCGGGTCCGACCT

GAM1882 LOC219672 5' TCCAGCCTGGGCAACAAGAGTG 92973 _
A TCGCTCT GTTGCCCAGGCTGGA
|||||
AGTGAGA CAACGGGTCCGACCT
A

GAM1882 LOC219722 5' CCAGCCTGGGCAACAGAACAAG 94677 CGC
A TCT TCTGTTGCCAGGCTGG
|||
AGA AGACAACGGGTCCGACC
ACA

GAM1882 LOC219722 5' TCAGCCTGGACAACAGAGTGAG 94685 C
A TCTCGCTCTGTTG CCAGGCTGG
|||||
AGAGTGAGACAAC GGTCCGACT
A

GAM1882 LOC219919 3' TCCAGCCTGGGCAACAGAGTAA 94933 CG
GA TCT CTCTGTTGCCAGGCTGGA
|||
AGA GAGACAACGGGTCCGACCT
AT

GAM1882 LOC220038 3' TCCAGCCTGGGCGATGGAGTGA 93377
GA TCTCGCTCTGTTGCCAGGCTGGA
|||||
AGAGTGAGGTAGCGGGTCCGACCT

GAM1882 LOC220506 3' TCCAGCCTGGGCAACAGAACAA 74521 CGC
GA TCT TCTGTTGCCAGGCTGGA
|||
AGA AGACAACGGGTCCGACCT
ACA

GAM1882 LOC220549 3' TCCAGCCTGGGTGACAGAATGA 94511 C TG
GA TCTCG TCTGT CCCAGGCTGGA
|||||

		AGAGT AGACA GGGTCCGACCT	
		A GT	
GAM1882	LOC220662 3'	TCCAGCCTGGGCAACACGAGCG 92831	—
	A	TCGCTC TGTTGCCCAGGCTGGA	
		AGCGAG ACAACGGGTCCGACCT	
		C	
GAM1882	LOC220692 3'	TCCAGCTCGGGGAACAGAGCGA 92866	G AG
	GA	TCTCGCTCTGTT CCC GCTGGA	
		AGAGCGAGACAA GGG CGACCT	
		G CT	
GAM1882	LOC220776 3'	CCAGCCCAGAGTAAGAGAGCAG 68920	C G CCA_
	A	TCT GCTCT TTGC GGCTGG	
		AGA CGAGA AATG CCGACC	
		— G AGAC	
GAM1882	LOC220906 3'	TCCAGCCTGGGCAACAAGCGA 93037	C
		TCGCT TGTTGCCCAGGCTGGA	
		AGCGA ACAACGGGTCCGACCT	
		—	
GAM1882	LOC220906 3'	TCCAGCTGGGCGACAGAGCGAG 93038	G
	A	TCTCGCTCTGTTGCCCAG CTGGA	
		AGAGCGAGACAGCGGGTC GACCT	
		—	
GAM1882	LOC220992 3'	TCCAGCCTGGGCAACATAGCAA 93110	C C
	GA	TCT GCT TGTTGCCCAGGCTGGA	
		AGA CGA ACAACGGGTCCGACCT	
		A T	
GAM1882	LOC221042 3'	TCCAGCCTGGGTGACAGAGCAA 94807	C TG
	GA	TCT GCTCTGT CCCAGGCTGGA	
		AGA CGAGACA GGGTCCGACCT	
		A GT	
GAM1882	LOC221069 3'	TCCAGCCTGGGCGACAGAGCAA 94821	C
	GA	TCT GCTCTGTTGCCCAGGCTGGA	
		AGA CGAGACAGCGGGTCCGACCT	
		A	
GAM1882	LOC221178 3'	TCCAGCCTGGGAGATACAGCGA 95176	C TG
	GA	TCTCGCT TGT CCCAGGCTGGA	
		AGAGCGA ATA GGGTCCGACCT	
		C GA	
GAM1882	LOC221271 3'	TCCAGCCTGGGCAACAGAGGGA 93530	G
	GA	TCTC CTCTGTTGCCCAGGCTGGA	

		AGAG GAGACAACGGGTCCGACCT	
		G	
GAM1882	LOC221271 3'	TCCAGCCTGGGTGACAGAGCGA 93532	TG
	GA	TCTCGCTCTGT CCCAGGCTGGA	
		AGAGCGAGACA GGGTCCGACCT	
		GT	
GAM1882	LOC221288 3'	TCCAGCCTGGGCGACAGAGTGA 95263	
	GA	TCTCGCTCTGTTGCCCAGGCTGGA	
		AGAGTGAGACAGCGGGTCCGACCT	
GAM1882	LOC221337 3'	TCCAGCCTGGGCAACAAGAGTG 93738	—
	A	TCGCTCT GTTGCCCAGGCTGGA	
		AGTGAGA CAACGGGTCCGACCT	
		A	
GAM1882	LOC221410 3'	TCCAGCCTGGGTGACAGAGCGA 93699	TG
	GA	TCTCGCTCTGT CCCAGGCTGGA	
		AGAGCGAGACA GGGTCCGACCT	
		GT	
GAM1882	LOC221477 3'	TCCAGCCTGGGCGACAGAGCGA 93776	
		TCGCTCTGTTGCCCAGGCTGGA	
		AGCGAGACAGCGGGTCCGACCT	
GAM1882	LOC221490 3'	CCTAGGCGACAGAGCAAGA 95304	C C
		TCT GCTCTGTTGCC AGG	
		AGA CGAGACAGCGG TCC	
		A A	
GAM1882	LOC221543 3'	TCCAGCCTGGGCAACAAGAGTA 95386	CG —
	AG	CT CTCT GTTGCCCAGGCTGGA	
		GA GAGA CAACGGGTCCGACCT	
		AT A	
GAM1882	LOC221543 5'	TCCAGCCTGGGCGACAGAGCAA 95388	C
	GA	TCT GCTCTGTTGCCCAGGCTGGA	
		AGA CGAGACAGCGGGTCCGACCT	
		A	
GAM1882	LOC221641 5'	TCCAGCCTGGGTGGCAGAGCGA 95348	TG
	GA	TCTCGCTCTGT CCCAGGCTGGA	
		AGAGCGAGACG GGGTCCGACCT	
		GT	
GAM1882	LOC221795 3'	TCCAGCCTGGGCAACAGAGTAA 94081	CG
	GA	TCT CTCTGTTGCCCAGGCTGGA	

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          AGA GAGACAACGGGTCCGACCT
          AT
GAM1882 LOC221931 3' CCAGAGCAACAGAGTGAGA 95630      CCAGG
          TCTCGCTCTGTTGC  CTGG
          |||||
          AGAGTGAGACAACG  GACC
          A____
GAM1882 LOC221943 5' TCCAGCCTGGGCGACAGAGCAA 95625  C
          GA          TCT GCTCTGTTGCCCAGGCTGGA
          ||| |||||
          AGA CGAGACAGCGGGTCCGACCT
          A
GAM1882 LOC221954 5' TCCAGCCTGGGCAACAGAGCGA 95651
          GA          TCTCGCTCTGTTGCCCAGGCTGGA
          |||||
          AGAGCGAGACAACGGGTCCGACCT

GAM1882 LOC221954 5' TCCAGCCTGGGTGACAGAGTAA 95652  CG  TG
          GA          TCT CTCTGT CCCAGGCTGGA
          ||| ||||| |||||
          AGA GAGACA GGGTCCGACCT
          AT  GT
GAM1882 LOC221954 5' TCCAGCTTGGGCGACAGAGCAA 95653  C
          GA          TCT GCTCTGTTGCCCAGGCTGGA
          ||| |||||
          AGA CGAGACAGCGGGTTCGACCT
          A
GAM1882 LOC222008 5' TCCAGCCTGGGCTCCGCAGG 95659  T__
          TCTGT  GCCCAGGCTGGA
          ||||| |||||
          GGACG  CGGGTCCGACCT
          CCT
GAM1882 LOC222060 5' TCCAGCCTGGGCGACAGAGCAA 95758  C
          GA          TCT GCTCTGTTGCCCAGGCTGGA
          ||| |||||
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          A
GAM1882 LOC222160 3' TCCAGCCTGGGCAGCAGAGGAA 95791  CG
          GA          TCT CTCTGTTGCCCAGGCTGGA
          ||| |||||
          AGA GAGACGACGGGTCCGACCT
          AG
GAM1882 LOC222160 5' TCCAGCCTGGGCGACAGAGCAA 95792  C
          GA          TCT GCTCTGTTGCCCAGGCTGGA
          ||| |||||
          AGA CGAGACAGCGGGTCCGACCT
          A
GAM1882 LOC222182 3' TCCAGCCTGGGCAATAGAGTGA 95862
          GA          TCTCGCTCTGTTGCCCAGGCTGGA
          |||||

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AGAGTGAGATAACGGGTCCGACCT

GAM1882 LOC222865 3' TCCAGCCTGAGTGACAGAGCGA 94450 TG C
GA TCTCGCTCTGT C CAGGCTGGA

||||||| | |||||
AGAGCGAGACA G GTCCGACCT
GT A

GAM1882 LOC245771 5' CCAGCCTGGGCTGGGGGAGA 94469 G TGTT
TCTC CTC GCCCAGGCTGG

||| ||| |||||
AGAG GGG CGGGTCCGACC
G T__

GAM1882 LOC253039 3' TCCAGCCTGGGCGACAGAGCAA 97867 C
GA TCT GCTCTGTTGCCCAGGCTGGA

|| |||||
AGA CGAGACAGCGGGTCCGACCT
A

GAM1882 LOC253532 3' TCCAGCCTGGGTGACAAAGCAA 97740 C C TG
GA TCT GCT TGT CCCAGGCTGGA

||| ||| ||| |||||
AGA CGA ACA GGGTCCGACCT
A A GT

GAM1882 LOC253612 5' TCCAGCCTAGGCAACAGAGTGA 98559 C
GA TCTCGCTCTGTTGCC AGGCTGGA

||||||| |||||
AGAGTGAGACAACGG TCCGACCT
A

GAM1882 LOC253639 3' TCCAGCCTGGGCGACAGAGTGA 97517
GA TCTCGCTCTGTTGCCCAGGCTGGA

|||||||
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GAM1882 LOC253778 5' TCCAGCCTGGGCGACAGAGTGA 96527
GA TCTCGCTCTGTTGCCCAGGCTGGA

|||||||
AGAGTGAGACAGCGGGTCCGACCT

GAM1882 LOC253786 3' TCCAGCCTGGGCAATAGAGCAA 98834 C
GA TCT GCTCTGTTGCCCAGGCTGGA

|| |||||
AGA CGAGATAACGGGTCCGACCT
A

GAM1882 LOC253832 3' TCCAGCCTGGGCGACGAGTGA 96593 T
TCGCTC GTTGCCCAGGCTGGA

|||| |||||
AGTGAG CAGCGGGTCCGACCT

GAM1882 LOC253840 5' TCCAGCCTGGGCAACAGAGCAA 97914 C
GA TCT GCTCTGTTGCCCAGGCTGGA

|| |||||

		AGA CGAGACAACGGGTCCGACCT			
		A			
GAM1882	LOC253906 3'	CAGCCTGGGCAACAAAGTGAGA 98299	C		
		TCTCGCT TGTTGCCCAGGCTG			
		AGAGTGA ACAACGGGTCCGAC			
		A			
GAM1882	LOC254041 5'	CCTGGACGACAGAGCAAGA 96554	C	C	
		TCT GCTCTGTTG CCAGG			
		AGA CGAGACAGC GGTCC			
		A A			
GAM1882	LOC254045 3'	CCATCTTGGGCAACAGAATGAG 98265	C	C	
	A	TCTCG TCTGTTGCCCAGG TGG			
		AGAGT AGACAACGGGTTC ACC			
		A T			
GAM1882	LOC254100 3'	TCCAGCCTGGGCAACAGAGTGA 98160			
	GA	TCTCGCTCTGTTGCCCAGGCTGGA			
		AGAGTGAGACAACGGGTCCGACCT			
GAM1882	LOC254176 3'	TCCAGCCTGGGCAACAGAGTAA 99176	CG		
	GA	TCT CTCTGTTGCCCAGGCTGGA			
		AGA GAGACAACGGGTCCGACCT			
		AT			
GAM1882	LOC254243 3'	TCCAGCCTGGGCAACAGAGTGA 99269			
	GA	TCTCGCTCTGTTGCCCAGGCTGGA			
		AGAGTGAGACAACGGGTCCGACCT			
GAM1882	LOC254531 5'	TCCAGCCTGGGTGACAGAGCAA 96673	C	TG	
	GA	TCT GCTCTGT CCCAGGCTGGA			
		AGA CGAGACA GGGTCCGACCT			
		A GT			
GAM1882	LOC254659 3'	TCCAGAGTGGGAAACAGAGCAA 96822	C	G	GG
	GA	TCT GCTCTGTT CCA CTGGA			
		AGA CGAGACAA GGGT GACCT			
		A A GA			
GAM1882	LOC254756 3'	TCCAGCCTGGGCAATAGAGTAA 99212	CG		
	GA	TCT CTCTGTTGCCCAGGCTGGA			
		AGA GAGATAACGGGTCCGACCT			
		AT			
GAM1882	LOC254808 3'	TCCAGCCTGGGCAACAGAGCAA 98810	C		
	GA	TCT GCTCTGTTGCCCAGGCTGGA			

		AGA CGAGACAACGGGTCCGACCT		
		A		
GAM1882	LOC254875 3'	TCCAGCCTGGGTGACAAAGCAA 97785	C C	TG
	GA	TCT GCT TGT CCCAGGCTGGA		
		AGA CGA ACA GGGTCCGACCT		
		A A GT		
GAM1882	LOC255030 5'	TCCAGCCTGGGTGACAGAGCGA 99086		TG
	GA	TCTCGCTCTGT CCCAGGCTGGA		
		AGAGCGAGACA GGGTCCGACCT		
		GT		
GAM1882	LOC255031 3'	TCCAGCCTGGCTACAGAGTGAG 99044	T C	
	A	TCTCGCTCTGT GCC AGGCTGGA		
		AGAGTGAGACA CGG TCCGACCT		
		T _		
GAM1882	LOC255042 3'	TCCAGCCTGGGCAACAAGAGCG 97056		_
	A	TCGCTCT GTTGCCCAGGCTGGA		
		AGCGAGA CAACGGGTCCGACCT		
		A		
GAM1882	LOC255042 3'	TCCAGCCTGGGCGACGAGC 97057	T	
		GCTC GTTGCCCAGGCTGGA		
		CGAG CAGCGGGTCCGACCT		
		_		
GAM1882	LOC255177 3'	TCCAGCCTAGGCAACAGAGTGA 98401		C
	GA	TCTCGCTCTGTTGCC AGGCTGGA		
		AGAGTGAGACAACGG TCCGACCT		
		A		
GAM1882	LOC255196 3'	CCTGGGCAACAGAGCCAGA 98952	C	
		TCT GCTCTGTTGCCAGG		
		AGA CGAGACAACGGGTCC		
		C		
GAM1882	LOC255196 5'	TCCAACCTGGGCAGCACGAAGA 98966	_ CTC	C
		TCT CG TGTTGCCAGG TGGA		
		AGA GC ACGACGGGTCC ACCT		
		A _ A		
GAM1882	LOC255231 3'	TCCAGCCTGGGTGACAGAGTGA 97123		TG
	GA	TCTCGCTCTGT CCCAGGCTGGA		
		AGAGTGAGACA GGGTCCGACCT		
		GT		
GAM1882	LOC255326 3'	TCCAGCCTGGGTGACAGAGCAA 98124	C	TG
	GA	TCT GCTCTGT CCCAGGCTGGA		


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          AGA CGAGACA GGGTCCGACCT
            A   GT
GAM1882 LOC255328 3' TCCAGCCTGGGTGATAAGAGC 98347   _ TG
          GCTCT GT CCCAGGCTGGA
          ||||| || |||||
          CGAGA TA GGGTCCGACCT
            A   GT
GAM1882 LOC255463 3' TCCAGCCTGGACAACATAGTGA 96543   C   C
          GA          TCTCGCT TGTG CCAGGCTGGA
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          AGAGTGA ACAAC GGTCCGACCT
            T   A
GAM1882 LOC255523 3' TCCAGCCTGGGCAACAGAGCAA 96737   C
          GA          TCT GCTCTGTTGCCAGGCTGGA
          ||| |||||
          AGA CGAGACAACGGGTCCGACCT
            A
GAM1882 LOC255565 5' CCAGCCTGAGAAACAAGC 96802   C   GCC
          GCT TGTT CAGGCTGG
          ||| |||||
          CGA ACAA GTCCGACC
            _   AGA
GAM1882 LOC255671 3' TCCAGCCTGGGTAACAGAGCAA 99076   C
          GA          TCT GCTCTGTTGCCAGGCTGGA
          ||| |||||
          AGA CGAGACAATGGGTCCGACCT
            A
GAM1882 LOC255671 5' TCCAGCCTGGGTGACAGAGTGA 99077   TG
          GA          TCTCGCTCTGT CCCAGGCTGGA
          ||||| |||||
          AGAGTGAGACA GGGTCCGACCT
            GT
GAM1882 LOC255792 5' CCAGCCCAAGGCTAGAAGA 98469   GC   TT   CA_
          TC TCTG GCC GGCTGG
          || ||||| ||| |||||
          AG AGAT CGG CCGACC
          A_   _   AAC
GAM1882 LOC256073 3' CCTGGGCAACATAGCGAGA 98485   C
          TCTCGCT TGTTGCCAGG
          ||||| |||||
          AGAGCGA ACAACGGGTCC
            T
GAM1882 LOC256207 3' TCCAACCTGGGCGACAGAGCAA 96880   C           C
          GA          TCT GCTCTGTTGCCAGG TGGA
          ||| ||||| ||||| |||
          AGA CGAGACAGCGGGTCC ACCT
            A           A
GAM1882 LOC256267 3' CCAGCCTGGAAAACAAGT 98608   C   GC
          GCT TGTT CCAGGCTGG
          ||| ||||| |||||

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		TGA ACAA GGTCCGACC		
		— AA		
GAM1882	LOC256267 5'	TCCAGCCTGGGAGACAGAGTGA 98613	TG	
	GA	TCTCGCTCTGT CCCAGGCTGGA		
		AGAGTGAGACA GGGTCCGACCT		
		GA		
GAM1882	LOC256515 3'	TCCAGCCTGGGCAACAGAGTAA 98218	CG	
	GA	TCT CTCTGTTGCCCAGGCTGGA		
		AGA GAGACAACGGGTCCGACCT		
		AT		
GAM1882	LOC256520 3'	TCCAGCCTGGGCGACAGAGCCA 97670	C	
	GA	TCT GCTCTGTTGCCCAGGCTGGA		
		AGA CGAGACAGCGGGTCCGACCT		
		C		
GAM1882	LOC256544 3'	TCCAGCCTGGGCGACAGAGC 97934	C	
		GCTCTGTTGCC AGGCTGGA		
		CGAGACAGCGG TCCGACCT		
		—		
GAM1882	LOC256594 3'	TCCAGCCTGGGCAACAGAGTAA 98868	CG	
	GA	TCT CTCTGTTGCCCAGGCTGGA		
		AGA GAGACAACGGGTCCGACCT		
		AT		
GAM1882	LOC256980 3'	TCCAGCCTGGTCGACAAGAGAG 96933	G C C	
	A	TCTC CT TGTTG CCAGGCTGGA		
		AGAG GA ACAGC GGTCCGACCT		
		A — T		
GAM1882	LOC257282 5'	TCAAGCCTGGGCAACAGAGCAA 98136	C	G
	GA	TCT GCTCTGTTGCCCAGGCT GA		
		AGA CGAGACAACGGGTCCGA CT		
		A A		
GAM1882	LOC257397 3'	TCCAGCCTGGACAGCAGAACAA 97953	CGC	C
	GA	TCT TCTGTTG CCAGGCTGGA		
		AGA AGACGAC GGTCCGACCT		
		ACA A		
GAM1882	LOC257596 3'	TCCAGCCTGGGCAACAAGAGTA 99789	CG	—
	AG	CT CTCT GTTGCCCAGGCTGGA		
		GA GAGA CAACGGGTCCGACCT		
		AT A		
GAM1882	LOC257596 5'	TCCAGCCTGGGCGACAGAGCAA 99791	C	
	GA	TCT GCTCTGTTGCCCAGGCTGGA		

AGA CGAGACAGCGGGTCCGACCT
 A
 GAM1882 LOC51145 3' TCCAGCCTGGGCGACAGAGTGA 32928 C TG
 GA TCTCGCTCTGTTGCCAGGCTGGA
 |||||
 AGAGTGAGACAGCGGGTCCGACCT

 GAM1882 LOC51212 3' TCCAGCCTGGGTGACAGAGCAA 33501 C TG
 GA TCT GCTCTGT CCCAGGCTGGA
 ||| ||||| |||||
 AGA CGAGACA GGGTCCGACCT
 A GT
 GAM1882 LOC51279 3' TCCAGCCTAAGCAACATAGTGA 33763 C CC
 TCGCT TGTTGC AGGCTGGA
 ||||| ||||| |||||
 AGTGA ACAACG TCCGACCT
 T AA
 GAM1882 LOC51279 3' TCCAGCCTGCGGACAGACCAAG 33764 CGC TG _
 A TCT TCTGT CC CAGGCTGGA
 ||| ||||| ||| |||||
 AGA AGACA GG GTCCGACCT
 ACC _ C
 GAM1882 LOC51333 3' TCCGGCCTGGGCAACAGAGGAA 34057 CG
 GA TCT CTCTGTTGCCAGGCTGGA
 ||| |||||
 AGA GAGACAACGGGTCCGGCCT
 AG
 GAM1882 LOC51336 3' TCCAGCCTGGGTGACAGCGT 34078 T TG
 GC CTGT CCCAGGCTGGA
 || ||||| |||||
 TG GACA GGGTCCGACCT
 C GT
 GAM1882 LOC51652 3' CCTGGGCAACATAGCAAGA 32700 C C
 TCT GCT TGTTGCCAGG
 ||| ||| |||||
 AGA CGA ACAACGGGTCC
 A T
 GAM1882 LOC51759 3' TCCAGCCTGGGCAACGAGC 73172 T
 GCTC GTTGCCCAGGCTGGA
 ||||| |||||
 CGAG CAACGGGTCCGACCT
 _
 GAM1882 LOC57107 5' CCAGCCTGGGCTGCTAGA 40182 _ T
 TCT GT GCCCAGGCTGG
 ||| || |||||
 AGA CG CGGGTCCGACC
 T T
 GAM1882 LOC63929 3' TCCAGCCTGGGTGACTGAGCAA 42285 C T TG
 GA TCT GCTC GT CCCAGGCTGGA
 ||| ||||| || |||||

		AGA CGAG CA GGGTCCGACCT		
		A T GT		
GAM1882	LOC64167 3'	TCCAGCCTGGGTGACTGAGCGA 42543	T TG	
	GA	TCTCGCTC GT CCCAGGCTGGA		
		AGAGCGAG CA GGGTCCGACCT		
		T GT		
GAM1882	LOC85479 5'	TCCAGCCTGGGCGACAGAGCAA 53571	C	
	GA	TCT GCTCTGTTGCCCAGGCTGGA		
		AGA CGAGACAGCGGGTCCGACCT		
		A		
GAM1882	LOC89890 3'	TCCAGCCTGGATGACAGAGTGA 61209	GC	
	GA	TCTCGCTCTGTT CCAGGCTGGA		
		AGAGTGAGACAG GGTCCGACCT		
		TA		
GAM1882	LOC90038 3'	TCCAGCCTGGGCAACAGAGTGA 61813		
	GA	TCTCGCTCTGTTGCCCAGGCTGGA		
		AGAGTGAGACAACGGGTCCGACCT		
GAM1882	LOC90072 3'	TCCAGCCTGGGGAACAGAGCAA 61963	C G	
	GA	TCT GCTCTGTT CCCAGGCTGGA		
		AGA CGAGACAA GGGTCCGACCT		
		A G		
GAM1882	LOC90072 5'	TCCAGCCTGGGTGACAGAACAA 61964	CGC TG	
	GA	TCT TCTGT CCCAGGCTGGA		
		AGA AGACA GGGTCCGACCT		
		ACA GT		
GAM1882	LOC90092 3'	TCCAGCCTGGCGACAAGAGCGA 62075	_ C	
	GA	TCTCGCTCT GTTGCC AGGCTGGA		
		AGAGCGAGA CAGCGG TCCGACCT		
		A _		
GAM1882	LOC90110 5'	TCCAGCCTGGGCAACGGAGTGA 62182		
	GA	TCTCGCTCTGTTGCCCAGGCTGGA		
		AGAGTGAGGCAACGGGTCCGACCT		
GAM1882	LOC90141 3'	TCCAGCCTGGATGATAGAGCAA 62310	C GC	
	GA	TCT GCTCTGTT CCAGGCTGGA		
		AGA CGAGATAG GGTCCGACCT		
		A TA		
GAM1882	LOC90155 5'	TCCAGCCTGGGCAACAAGAGTG 62368	_	
	A	TCGCTCT GTTGCCCAGGCTGGA		

		AGTGAGA CAACGGGTCCGACCT		
		A		
GAM1882	LOC90233 3'	TCCAGCCCAGGCAACAGAGTGA 57197	CA	
	GA	TCTCGCTCTGTTGCC GGCTGGA		
		AGAGTGAGACAACGG CCGACCT		
		AC		
GAM1882	LOC90321 3'	TCCAACCTGGGTGACAGAGCGA 62938	TG	C
	GA	TCTCGCTCTGT CCCAGG TGGA		
		AGAGCGAGACA GGGTCC ACCT		
		GT A		
GAM1882	LOC90393 5'	TCCAGCCTGGGTGACAGAGTGA 63309	TG	
	GA	TCTCGCTCTGT CCCAGGCTGGA		
		AGAGTGAGACA GGGTCCGACCT		
		GT		
GAM1882	LOC90538 3'	TCTGGGCAAAAAGCGAGA 63902	CTG	
		TCTCGCT TTGCCCAGG		
		AGAGCGA AACGGGTCT		
		AAA		
GAM1882	LOC90573 5'	TCCAGCCTGGGCGACAGAGTGA 63962		
	GA	TCTCGCTCTGTTGCCAGGCTGGA		
		AGAGTGAGACAGCGGGTCCGACCT		
GAM1882	LOC90624 3'	TCCAGCCTGGGGGACAGAGTGA 64373	G	
	GA	TCTCGCTCTGTT CCCAGGCTGGA		
		AGAGTGAGACAG GGGTCCGACCT		
		G		
GAM1882	LOC90639 3'	TCCAGCCTGAGCAACAGAGCCG 64416	C	C
	GA	TCT GCTCTGTTGC CAGGCTGGA		
		AGG CGAGACAACG GTCCGACCT		
		C A		
GAM1882	LOC90784 5'	TCCAGCCTGGGCAACAGAGTGA 64700		
	GA	TCTCGCTCTGTTGCCAGGCTGGA		
		AGAGTGAGACAACGGGTCCGACCT		
GAM1882	LOC90785 3'	TCCAGCCTGGGTGACAGAGCGA 64720	TG	
	GA	TCTCGCTCTGT CCCAGGCTGGA		
		AGAGCGAGACA GGGTCCGACCT		
		GT		
GAM1882	LOC90918 5'	TCCAGCCTAGGCAACAAGAGTG 65005	—	C
	A	TCGCTCT GTTGCC AGGCTGGA		

		AGTGAGA CAACGG TCCGACCT		
		A A		
GAM1882	LOC91035 3'	TCCAGCCTGGACAACAAGAGC 65306	—	C
		GCTCT GTTG CCAGGCTGGA		
		CGAGA CAAC GGTCCGACCT		
		A A		
GAM1882	LOC91056 3'	TCCAGCCTGGGCGACAGAGCAA 96410	C	
	GG	TCT GCTCTGTTGCCCAGGCTGGA		
		GGA CGAGACAGCGGGTCCGACCT		
		A		
GAM1882	LOC91064 3'	TCCAGCGTGGGCGACAGAGCAA 65391	C	G
	GA	TCT GCTCTGTTGCCA GCTGGA		
		AGA CGAGACAGCGGGT CGACCT		
		A G		
GAM1882	LOC91250 5'	TCCAGCCTGAGTGACAGAGTGA 65921		TG C
	GA	TCTCGCTCTGT C CAGGCTGGA		
		AGAGTGAGACA G GTCCGACCT		
		GT A		
GAM1882	LOC91250 5'	TCCAGCCTGGGCAACAGAGTGA 65922		
	GA	TCTCGCTCTGTTGCCCAGGCTGGA		
		AGAGTGAGACAACGGGTCCGACCT		
GAM1882	LOC91286 3'	TCCAGCCTGGACAACAGA 66061	C	
		TCTGTTG CCAGGCTGGA		
		AGACAAC GGTCCGACCT		
		A		
GAM1882	LOC91380 3'	TCCAGCCTGGGTGACAGAGTGA 66454		TG
	GA	TCTCGCTCTGT CCCAGGCTGGA		
		AGAGTGAGACA GGGTCCGACCT		
		GT		
GAM1882	LOC91442 3'	TCCAGCCTGGGCACCAGAGCGA 66648		T
	GA	TCTCGCTCTG TGCCCAGGCTGGA		
		AGAGCGAGAC ACGGGTCCGACCT		
		C		
GAM1882	LOC91547 3'	TCCAGCCTGGGCGACAGAGCGA 67006		
	GA	TCTCGCTCTGTTGCCCAGGCTGGA		
		AGAGCGAGACAGCGGGTCCGACCT		
GAM1882	LOC91750 3'	TCCAGCCTGGGCAACAGAGTGA 67657		
	GA	TCTCGCTCTGTTGCCCAGGCTGGA		

AGAGTGAGACAACGGGTCCGACCT

GAM1882 LOC91812 3' TCCAGCCTGGGCAACAGAACGA 67821 C
GA TCTCG TCTGTTGCCCAGGCTGGA

||||| |||||||

AGAGC AGACAACGGGTCCGACCT

A

GAM1882 LOC91813 3' TCCAGCCTGGGCAACAGAACGA 67848 C
GA TCTCG TCTGTTGCCCAGGCTGGA

||||| |||||||

AGAGC AGACAACGGGTCCGACCT

A

GAM1882 LOC91862 3' TCCAGCCCAGGTGACAGAGCGA 54574 TG CA
GA TCTCGCTCTGT CC GGCTGGA

||||| || |||

AGAGCGAGACA GG CCGACCT

GT AC

GAM1882 LOC91963 5' TCCAGCCTGGGCAACAGAGTGA 68327
TCGCTCTGTTGCCCAGGCTGGA

||||| |||||||

AGTGAGACAACGGGTCCGACCT

GAM1882 LOC92078 3' TCCAGCCTGGGTGACAGAGTGA 68612 TG
GA TCTCGCTCTGT CCCAGGCTGGA

||||| |||||||

AGAGTGAGACA GGGTCCGACCT

GT

GAM1882 LOC92223 3' TCCAGCCTGGGCAACAAGAGTG 69055 _
A TCGCTCT GTTGCCCAGGCTGGA

||||| |||||||

AGTGAGA CAACGGGTCCGACCT

A

GAM1882 LOC92228 3' CCAGCCTGGGCAACGGAGTGAG 69073
A TCTCGCTCTGTTGCCCAGGCTGG

||||| |||||||

AGAGTGAGGCAACGGGTCCGACC

GAM1882 LOC92267 3' TCCAGCCTGGGCAACAAGAGAG 69179 G C
A TCTC CT TGTTGCCCAGGCTGGA

||| || |||||||

AGAG GA ACAACGGGTCCGACCT

A _

GAM1882 LOC92299 3' TCCAGCCTGGCGACAAAGCGAG 69373 C C
A TCTCGCT TGTTGCC AGGCTGGA

||||| ||| |||

AGAGCGA ACAGCGG TCCGACCT

A _

GAM1882 LOC92340 3' TCCAGCCTAGTAATGGAGCAAG 69568 C CC
A TCT GCTCTGTTGC AGGCTGGA

||| ||||||| |||

AGA CGAGGTAATG TCCGACCT
 A A_
 GAM1882 LOC92360 3' TCCAGCCTGGGTGACAGAGCAA 69626 C TG
 GG TCT GCTCTGT CCCAGGCTGGA
 ||| ||||| |||||
 GGA CGAGACA GGGTCCGACCT
 A GT
 GAM1882 LOC92405 3' TCTAGCCTGGGCAACAGAGCAA 69718 C
 GG TCT GCTCTGTTGCCCAGGCTGGA
 ||| |||||
 GGA CGAGACAACGGGTCCGATCT
 A
 GAM1882 LOC92421 3' TCCAGACTGGGCAACAGAGGGA 69729 G G
 GA TCTC CTCTGTTGCCCAG CTGGA
 ||| |||||
 AGAG GAGACAACGGGTC GACCT
 G A
 GAM1882 LOC92465 5' TCCAGCCTGGGCGACAGAGCGA 69955
 GA TCTCGCTCTGTTGCCCAGGCTGGA
 |||||
 AGAGCGAGACAGCGGGTCCGACCT

 GAM1882 LOC92465 5' TCCAGTCTGGGCAACAGAGCAA 69956 C
 GA TCT GCTCTGTTGCCCAGGCTGGA
 ||| |||||
 AGA CGAGACAACGGGTCTGACCT
 A
 GAM1882 LOC92466 3' CCAGCCTGGAAAACAAGT 69964 C GC
 GCT TGTT CCAGGCTGG
 ||| ||| |||||
 TGA ACAA GGTCCGACC
 — AA
 GAM1882 LOC92466 5' TCCAGCCTGGGAGACAGAGTGA 69969 TG
 GA TCTCGCTCTGT CCCAGGCTGGA
 ||||| |||||
 AGAGTGAGACA GGGTCCGACCT
 GA
 GAM1882 LOC92482 3' CCAGCCTGGGCAACAGAGCAAG 70019 C
 A TCT GCTCTGTTGCCCAGGCTGG
 ||| |||||
 AGA CGAGACAACGGGTCCGACC
 A
 GAM1882 LOC92492 3' TCCAGCCTGGATGACAGCGAGA 70083 CT GC
 TCTCGCT GTT CCAGGCTGGA
 ||||| ||| |||||
 AGAGCGA CAG GGTCCGACCT
 — TA
 GAM1882 LOC92499 5' CCTGGACGACAGAGCAAGA 70105 C C
 TCT GCTCTGTTG CCAGG
 ||| ||||| |||||

		AGA CGAGACAGC GGTCC		
		A A		
GAM1882	LOC92568 3'	TCCAGCCTGGGTGACAGAGTGA 70331	TG	
	GA	TCTCGCTCTGT CCCAGGCTGGA		
		AGAGTGAGACA GGGTCCGACCT		
		GT		
GAM1882	LOC92573 3'	TCCAGCCTGGGTGACAGAGCGA 70379	TG	
	GA	TCTCGCTCTGT CCCAGGCTGGA		
		AGAGCGAGACA GGGTCCGACCT		
		GT		
GAM1882	LOC92659 3'	CCAGCCTGGGCGACAGAG 70609		
		CTCTGTTGCCAGGCTGG		
		GAGACAGCGGGTCCGACC		
GAM1882	LOC92771 3'	CCTGAGCAACATAGCGAGA 54210	C C	
		TCTCGCT TGTTGC CAGG		
		AGAGCGA ACAACG GTCC		
		T A		
GAM1882	LOC92771 3'	TCCAGCCTGGGCCACAGAATGA 54215	C T	
	GA	TCTCG TCTGT GCCCAGGCTGGA		
		AGAGT AGACA CGGGTCCGACCT		
		A C		
GAM1882	LOC92973 5'	TCCAGCCTGGGCAACAGAGTGA 71594		
	GG	TCTCGCTCTGTTGCCAGGCTGGA		
		GGAGTGAGACAACGGGTCCGACCT		
GAM1882	LOC93070 3'	TCCAGCCTGGGCAACAGAGGGA 71815	G	
	GA	TCTC CTCTGTTGCCAGGCTGGA		
		AGAG GAGACAACGGGTCCGACCT		
		G		
GAM1882	LOC93132 3'	TCCAGCTCGGGCAACAAAGTGA 72000	C AG	
	GA	TCTCGCT TGTTGCC GCTGGA		
		AGAGTGA ACAACGGG CGACCT		
		A CT		
GAM1882	LOC93613 3'	TCCAACCTGGGCGGCAGAGTGA 73082	C	
	GA	TCTCGCTCTGTTGCCAGG TGGA		
		AGAGTGAGACGGCGGGTCC ACCT		
		A		
GAM1882	LOC96597 5'	CCAGCCTGGGCGACAAGAG 67449	_	
		CTCT GTTGCCAGGCTGG		

GAGA CAGCGGGTCCGACC
 A
 GAM1883 FGF20 5' CATCCCACCCCCACAACA 39553 CGAT CTGT
 TGTTGTGGG GGTG TG
 ||||| ||| ||
 ACAACACCC CCAC AC
 ____ CCT_
 GAM1883 TMP21 3' CCAACAGCACCATCAAGGCAC 23354 GGC_
 GTG GATGGTGCTGTTGG
 ||| |||||
 CAC CTACCACGACAACC
 GGAA
 GAM1883 KIAA0478 3' CCAACAGCATCTGAGCCCTCAA 30173 T GAT
 CA TGTTG GGGC GGTGCTGTTGG
 ||||| ||| |||||
 ACAAC CCCG CTACGACAACC
 T AGT
 GAM1883 KIAA1831 5' CACCACCACCCGCAACA 64521 CGA C
 TGTTGTGGG TGGTG TG
 ||||| ||| ||
 ACAACGCCC ACCAC AC
 ____ C
 GAM1883 RFX3 5' CCATCTCCATCACCCACCAACA 57058 _ C TGCTGT
 TGTTG TGGG GATGG TGG
 ||||| ||| ||| |||
 ACAAC ACCC CTACC ACC
 C A TCT____
 GAM1883 RFX3 5' CCATCTCCATCACCCACCAACA 12853 _ C TGCTGT
 TGTTG TGGG GATGG TGG
 ||||| ||| ||| |||
 ACAAC ACCC CTACC ACC
 C A TCT____
 GAM1883 LOC118470 3' CAGTACCACCACTCACAACA 74346 CGA
 TGTTGTGGG TGGTGCTG
 ||||| |||||
 ACAACACTC ACCATGAC
 ACC
 GAM1884 LAMC1 3' TTGCAAAGTTTTACGTCA 11275 C CC_
 TGACGTGGA AT GCAA
 ||||| || |||
 ACTGCACTT TG CGTT
 T AAA
 GAM1884 OPA1 3' TTGCGGGTGGAACAGTCA 56430 G GA_
 TGAC TG CATCCGCAA
 ||| || |||||
 ACTG AC GTGGGCGTT
 _ AAG
 GAM1884 PITX2 5' TTGCGGAGGGTGCGCTCA 6161 C G A_
 TGA GTG AC TCCGCAA
 ||| ||| || |||||

	ACT CGC TG AGGCGTT		
	_ G GG		
GAM1884 LOC144848 3'	TGGAGGATGTCCACATCA	73961	C G_
	TGA GTGGACATCC CA		
	ACT CACCTGTAGG GT		
	A AG		
GAM1884 LOC221495 5'	TTGCAGGGGCATCACGTTA	95498	ACA _
	TGACGTGG TCC GCAA		
	ATTGCACT GGG CGTT		
	ACG A		
GAM1884 LOC256520 3'	GCAGATTTTGTCTACGTCA	97667	_ _ C
	TGACGTGGA CA TC GC		
	ACTGCATCT GT AG CG		
	T TTT A		
GAM1885 CDH12 3'	CTTATCATTTAAAGTGGTGTA	15777	CCCAA GA
	TACACCACT GAA ATAAG		
	ATGTGGTGA TTT TATTC		
	AA_ AC		
GAM1885 GOCAP1 3'	ATTGTTCTTGGGAGCAGTGTA	43007	CA G
	TACAC CTCCCAAGAA AAT		
	ATGTG GAGGGTTCTT TTA		
	AC G		
GAM1885 DKFZp434N2435 5'	CTTATTACTGTGGGGTGGT	98090	T AGAAG
	ACCAC CCCA AATAAG		
	TGGTG GGGT TTATTC		
	_ GTCA_		
GAM1885 DKFZP564I122 3'	CTTATTCTTCTCCCTCATGTGT	63877	CACTCCCA
A	TACAC AGAAGAATAAG		
	ATGTG TCTTCTTATTC		
	TACTCCC_		
GAM1885 FLJ21791 3'	CTTATTTGCAGAAGTGGTGTA	62126	CCCAAGAA
	TACACCACT GAATAAG		
	ATGTGGTGA TTTATTC		
	AGACG_		
GAM1885 HMP19 3'	CTTATTCTTTGTTAGGAAAATG	88860	CCAC CAA_
TA	TACA TCC GAAGAATAAG		
	ATGT AGG TTTCTTATTC		
	AAA_ ATTG		
GAM1885 KIAA1719 3'	TCTGTCTTGGGAGTGGTGTA	68742	_
	TACACCACTCCCAAGA AGA		

ATGTGGTGAGGGTTCT TCT
 G
 GAM1885 KIAA1853 3' TTTTCTTGGAAGCAGTG 69929 CA C
 CAC CT CCAAGAAGAA
 ||| || |||||
 GTG GA GGTTCTTTT
 AC A
 GAM1885 KIAA1877 3' CTTATTCTTCTGCCATGAGT 66748 CCA__
 ACTC AGAAGAATAAG
 |||| |||||
 TGAG TCTTCTTATTC
 TACCG
 GAM1885 KIAA1906 3' CTTATTCTTCTTGACTTTTGG 73571 CTCC_
 CCA CAAGAAGAATAAG
 ||| |||||
 GGT GTTCTTCTTATTC
 TTTCA
 GAM1885 OSBPL11 3' CTTAATTTCCCAAGAGTGGTG 43206 CCAA AA
 CACCACTC GAAG TAAG
 ||||| ||| |||
 GTGGTGAG CTTT ATTC
 AACC A_
 GAM1885 YME1L1 3' TCATTCTTGATGTGGTGTA 58438 TCC _
 TACACCAC CAAGAA GA
 ||||| |||||
 ATGTGGTG GTTCTT CT
 TA_ A
 GAM1885 ZNF262 3' CTTATTTTGTGTTGGGAGT 18723 A
 ACTCCCAAG AGAATAAG
 ||||| |||||
 TGAGGGTTT TTTTATTC
 G
 GAM1885 LOC91960 3' TGTGGCTTGGAACGTGGTGTA 68294 TC_ AAGA
 TACACCAC CCAAG ATA
 ||||| |||||
 ATGTGGTG GGTTG TGT
 CAA GG_
 GAM1886 CERD4 3' CCCTCGATATCCCATGGA 24877 T ACA A
 TCCATGGG TAT CGGG GG
 ||||| ||| |||
 AGGTACCC ATA GCTC CC
 T _ _
 GAM1886 PPFIA3 5' CTCCTCCCGCACTTCCACAGGA 61669 A _ TTATACA
 TCC TG GG CGGGAGGAG
 ||| ||| |||||
 AGG AC CC GCCCTCCTC
 _ A TTCAC_
 GAM1886 BANK 3' CTATTTGCATATAACCCTG 36030 T CA A
 CA GGGTTATA CGGG GG
 || ||||| ||| ||

		GT CCCAATAT GTTT TC	
		— AC A	
GAM1886	C8orf17	3' CCTCCGCTGTCTACCCATGGA 39994	TAT CG
		TCCATGGGT ACA GGAGG	
		AGGTACCCA TGT CCTCC	
		TC_ CG	
GAM1886	CX46.6	3' CCCTGCAGCAACCCATGGA 40311	ATA_ C
		TCCATGGGTT CA GGG	
		AGGTACCCAA GT CCC	
		CGAC _	
GAM1886	DDX39	3' CTCCCTTCCCACACAGCCCATG 58117	ATACAC _
	GA	TCCATGGGTT GGGA GGAG	
		AGGTACCCGA CCCT CCTC	
		CACA_ TC	
GAM1886	FLJ10193	3' TCCTCCCACCCCATAGGA 36350	_ TTATACAC
		TCC ATGGG GGGAGGA	
		AGG TACCC CCCTCCT	
		A CCA_____	
GAM1886	FLJ20277	3' CTGTGCCCAACCCATGGA 35313	ATA
		TCCATGGGTT CACGG	
		AGGTACCCAA GTGTC	
		CCC	
GAM1886	FLJ20306	5' CTCCTCCCGCCCGTCCCATTGA 35391	C TTATACA
		TC ATGGG CGGGAGGAG	
		AG TACCC GCCCTCCTC	
		T TGCCC_	
GAM1886	HSPC065	3' TCCTCTCAGAACCCACAGA 27164	CA ATACAC
		TC TGGGTT GGGAGGA	
		AG ACCCAA CTCTCCT	
		AC GA_____	
GAM1886	KIAA1189	3' CTCATTCTATACAACCTATGGA 72506	A CAC G
		TCCATGGGTT TA GGGA GAG	
		AGGTATCCAA AT TCTT CTC	
		C A_ A	
GAM1886	NKD2	3' CTCGTCTGTGTAACCCAT 53593	CGG G
		ATGGGTTATACA GA GAG	
		TACCCAATGTGT CT CTC	
		_ G	
GAM1886	PADI3	3' CTCCTGTGATTCAACACAACCC 33173	_____ A
	ATGGA	TCCATGGGTT AT CACGGGAG	

AGGTACCCAA TA GTGTCCTC
 CACAAC T _
 GAM1886 SSAT2 5' CTCCTCCCGTACGGCGCCGGA 56859 AT _ TA AC
 TCC GG GT T ACGGGAGGAG
 ||| ||| | |||||
 AGG CC CG A TGCCCTCCTC
 _ G GC _
 GAM1886 LOC146174 5' CTGTGTACAAACCATGGA 78199 G A
 TCCATGG TT TACACGG
 ||||| || |||||
 AGGTACC AA ATGTGTC
 A C
 GAM1886 LOC149153 3' CTCCTCCTCAGCTCACCCATGG 85527 TATACAC
 A TCCATGGGT GGGAGGAG
 ||||| |||||
 AGGTACCCA TCCTCCTC
 CTCGAC _
 GAM1886 LOC202134 5' CTCCTCCCAAAACAACCCAGGA 91920 A ATACAC
 TCC TGGGTT GGGAGGAG
 ||| ||||| |||||
 AGG ACCCAA CCCTCCTC
 _ CAAAA _
 GAM1887 ABCA9 3' AAAGGATGAGTTCATATTCTTC 55362 CG_ C
 ACA TGTGAAGAG GAGC CATCCTTT
 ||||| ||| |||||
 ACACTTCTT CTTG GTAGGAAA
 ATA A
 GAM1887 AP1S2 3' GTGTTGCTCTCTTCACA 15350 GCG C_
 TGTGAAGA GAGC CAT
 ||||| ||| |||
 ACACTTCT CTCG GTG
 _ TT
 GAM1887 DKFZP434F1735 5' AAAGGATGGACTCTGTTACCCA 32109 AAG C
 CA TGTG AGCGGAG CCATCCTTT
 ||| ||||| |||||
 ACAC TTGTCTC GGTAGGAAA
 CCA A
 GAM1887 DNAJA2 3' ATGGGCTTTGCACACA 60487 AAGA
 TGTG GCGGAGCCCAT
 ||| |||||
 ACAC CGTTTCGGGTA
 A _
 GAM1887 DRIL2 3' AAAGGATGGACTCTTCCCAC 22344 AA GC C
 GTG GA GGAG CCATCCTTT
 ||| || ||| |||||
 CAC CT TCTC GGTAGGAAA
 C_ _ A
 GAM1887 SLC26A9 3' AAAGGATGAGCCTGGGGTCACA 54708 AGAG A C
 TGTGA CGG GC CATCCTTT
 |||| ||| || |||||

		ACACT GTC CG GTAGGAAA		
		GGG_ _ A		
GAM1887	LOC150837 3'	ATGAGGCTTCGCTCTCCACA 80800	A	_
		TGTG AGAGCGGAGCC CAT		
		ACAC TCTCGCTTCGG GTA		
		C A		
GAM1888	CBFA2T2 3'	CCACACCTGGCCTTGGCTG 18705	A__	A
		CAGC GCCGG GTGTGG		
		GTCG CGGTC CACACC		
		GTTC _		
GAM1888	CD97 3'	CCACTGGTCCTGCTGCTG 55303	C	G_
		CAGCAGC GGA T GTGG		
		GTCGTCG CCT G CACC		
		T G T		
GAM1888	COLQ 3'	CCACACCTGGGCAGGCTGTTG 55419	_____	A
		CAGCAGCC GG GTGTGG		
		GTTGTCGG TC CACACC		
		ACGGG _		
GAM1888	COLQ 3'	CCACACCTGGGCAGGCTGTTG 55420	_____	A
		CAGCAGCC GG GTGTGG		
		GTTGTCGG TC CACACC		
		ACGGG _		
GAM1888	LETM1 3'	CCACACAGAGCTGGCTGCTG 25550	A__	
		CAGCAGCCGG GTGTGG		
		GTCGTCGGTC CACACC		
		GAGA		
GAM1888	MASP1 3'	CCACACTGTGTCCTGCTG 58211	C_	G
		CAGCAG CG AGTGTGG		
		GTCGTC GT TCACACC		
		CT G		
GAM1888	MAT1A 3'	CCAGACGCCTGGCTGCTG 92497	A_	G
		CAGCAGCCGG GT TGG		
		GTCGTCGGTC CA ACC		
		CG G		
GAM1888	PKD1 3'	CCACTGCTAAGGCTGCTG 6102	GG	_
		CAGCAGCC AGT GTGG		
		GTCGTCGG TCG CACC		
		AA T		
GAM1888	RNMT 3'	CCACACCTGCAGGCGCTG 15050	A	__ A
		CAGC GCC GG GTGTGG		

			GTCG CGG TC CACACC		
			— ACG —		
GAM1888	RPL30	5'	CCATCTTAGCGGCTGCTG 8271	—	T
			CAGCAGCCG GAG GTGG		
			GTCGTCGGC TTC TACC		
			GA —		
GAM1888	TEM5	3'	CCACATATGCTGGCTGCTG 52298	A	—
			CAGCAGCCGG GTGTGG		
			GTCGTCGGTC TACACC		
			GTA		
GAM1888	XT3	3'	CCAGCTACTCTGGCTGCTG 39906	—	
			CAGCAGCCGGAGTG TGG		
			GTCGTCGGTCTCAT ACC		
			CG		
GAM1888	AD034	3'	CCACAGTTCAGCTGGCTG 49747	—	C G
			CAGC AGC GGA TGTGG		
			GTCG TCG CTT ACACC		
			G A G		
GAM1888	ALLC	5'	CCTAATTTTCAGGCTGCTG 37980	—	GT
			CAGCAGCC GGAGT GG		
			GTCGTCGG CTTTA CC		
			A AT		
GAM1888	COLEC12	3'	CCACAGTTTTTGGCCTCTG 56101	CA	—
			CAG GCCGGAG TGTGG		
			GTC CGGTTTT ACACC		
			TC G		
GAM1888	DKFZP564C186	3'	CCACAACGTGTGGGCTGCTG 72841	—	G —
			CAGCAGCC G AGT GTGG		
			GTCGTCGG T TCA CACC		
			G G A		
GAM1888	FBXO26	5'	CCAGGACTCTGGCTACTG 46624	C	G_
			CAG AGCCGGAGT TGG		
			GTC TCGGTCTCA ACC		
			A GG		
GAM1888	FLJ21736	3'	CCACACTCTGTATCTGGCT 46780	—	C_
			AGC AG CGGAGTGTGG		
			TCG TC GTCTCACACC		
			G TAT		
GAM1888	ITGB5	3'	CCATGTCACCTGGCTGCT 60215	A	—
			AGCAGCCGG GTG TGG		

		TCGTCGGTC CAC ACC		
		_ TGT		
GAM1888 KIAA0084	5'	CCACCGCTCCAGCGGCTG 68706	A C	_
		CAGC GC GGAGTG TGG		
		GTCG CG CCTCGC ACC		
		G A C		
GAM1888 KIAA1582	5'	CCACAGGCTCCAGCTCTG 65987	C C	_
		CAG AGC GGAGT GTGG		
		GTC TCG CCTCG CACC		
		_ A GA		
GAM1888 KIAA1879	5'	CCACAGTGCTGCGGCTGCT 73933	G	___
		AGCAGCCG AGT GTGG		
		TCGTCGGC TCG CACC		
		G TGA		
GAM1888 LGI2	3'	GCCCACTCCAGGTCTGT 36926	- -	___
		GCAG CC GGAGTGTGG C		
		TGTC GG CCTCACACC G		
		T A		___
GAM1888 MAP-1	3'	CCACCTGCTTCGGCCTCTG 42437	CA	___
		CAG GCCGGAGT GTGG		
		GTC CGGCTTCG CACC		
		TC TC		
GAM1888 MGC2647	3'	CCACAGGCTGTGGCTGCT 74076	G	___
		AGCAGCCG AGT GTGG		
		TCGTCGGT TCG CACC		
		G GA		
GAM1888 SCAM-1	3'	CCAGCACCCCAGCTTGCTG 20501	_ C A	_
		CAGCA GC GG GTG TGG		
		GTCGT CG CC CAC ACC		
		T A C G		
GAM1888 XYLT1	5'	CCACAAGTTAGGGCTGCTG 78412	G_ G_	
		CAGCAGCC GA TGTGG		
		GTCGTCGG TT ACACC		
		GA GA		
GAM1888 LOC136120	3'	CCATCAACCTGGCTGCTG 76706	AG	_
		CAGCAGCCGG TG TGG		
		GTCGTCGGTC AC ACC		
		CA T		
GAM1888 LOC144486	5'	CCACCGACGCCGTTGCTG 84002	A	___
		CAGCAGCCGG GT GTGG		

			GTCGTTGGCC CA CACC			
			G GC			
GAM1888	LOC200471	5'	CCAGGCTGCTGGCTGCTG	91634	_	G
			CAGCAGCCGG AGT TGG			
			GTCGTCGGTC TCG ACC			
			G G			
GAM1888	LOC256905	5'	CCACAGCTCTGGCTCCTG	98658	C	_
			CAG AGCCGGAG TGTGG			
			GTC TCGGTCTC ACACC			
			C G			
GAM1889	ABL1	3'	GCCCCACCCAGGTCCC	18954	A	AA
			GGGA CCTGGGTG GGC			
			CCCT GGACCCAC CCG			
			_ CC			
GAM1889	ABL1	3'	GCCCCACCCAGGTCCC	24607	A	AA
			GGGA CCTGGGTG GGC			
			CCCT GGACCCAC CCG			
			_ CC			
GAM1889	LRP1	3'	AGGGCCCCCACCAGGTTCCC	11357	G	AA A
			GGGAACCT GGTG GGC CCT			
			CCCTTGGA CCAC CCG GGA			
			G CC _			
GAM1889	GMPPB	3'	AGGGCTCCCCACCCAGGCCCC	97434	AA	AA CA
	C		GGG CCTGGGTG GG CCTT			
			CCC GGACCCAC CC GGGA			
			CC CC TC			
GAM1889	KIAA1949	5'	GCCTGCACCCAGGTTCCC	99591	A	
			GGGAACCTGGGTG AGGC			
			CCCTTGACCCAC TCCG			
			G			
GAM1889	KIAA1949	5'	GCCTGCACCCAGGTTCCC	99697	A	
			GGGAACCTGGGTG AGGC			
			CCCTTGACCCAC TCCG			
			G			
GAM1889	KIAA1949	5'	GCCTGCACCCAGGTTCCC	93718	A	
			GGGAACCTGGGTG AGGC			
			CCCTTGACCCAC TCCG			
			G			
GAM1889	KIAA1977	5'	TGCCTTCACACATTGCC	74769	G CC	G
			GG AA TG GTGAAGGCA			

		CC TT AC CACTTCCGT		
		G _ A		
GAM1889	RNPC1	3' AAAGACGCAATCCCAGGTTCT 34407		TGAAG AC
		GGGAACCTGGG GC CTTT		
		TCCTTGGACCC CG GAAA		
		TAA_ CA		
GAM1889	LOC120526	3' GAGGTAGTCATCCAGGTTCCC 74465		AGGC
		GGGAACCTGGGTGA ACCTT		
		CCCTTGGACCTACT TGGAG		
		GA_		
GAM1889	LOC146909	3' AAGGTGCTGCCATGTTCCC 78754		CTG GAA
		GGGAAC GGT GGCACCTT		
		CCCTTG CCG TCGTGGAA		
		TA_ _		
GAM1889	LOC150622	3' AAAGGAGTTCACTCAAGTTCCC 80750		C AG A
		GGGAAC TGGGTGA GC CCTTT		
		CCCTTG ACTCACT TG GGAAA		
		A _ A		
GAM1889	LOC90750	3' AAGGACATCCAGGTTCCC 64624		AAGGCA
		GGGAACCTGGGTG CCTT		
		CCCTTGGACCTAC GGAA		
		A_		
GAM1889	LOC92017	3' CCACTCACCCAGGCTTCC 68489	A	A_
		GGGA CCTGGGTGA GG		
		CCTT GGACCCACT CC		
		C CA		
GAM1889	LOC92912	5' AAAGGAAGCGCCACCCAGGCC 71403	AA	AAG A_
		GG CCTGGGTG GC CCTTT		
		CC GGACCCAC CG GGAAA		
		_ CG_ AA		
GAM1890	BCKDHA	3' TCTTCACCCCTGCTCCTC 62944		TTGTCTGA
		GAGGAGCAG TGAAGA		
		CTCCTCGTC ACTTCT		
		CCC_		
GAM1890	CASP10	3' TCTCTAGACAACCTACCCCTT 53228	AGC	AT
		GAGG AGTTGTCTG GA		
		TTCC TCAACAGAT CT		
		CCA CT		
GAM1890	CASP10	3' TCTCTAGACAACCTACCCCTT 53267	AGC	AT
		GAGG AGTTGTCTG GA		

			TTCC TCAACAGAT CT		
			CCA CT		
GAM1890	FXVD6	3'	CTCCATCACCTTCTGCTCCT 42091	TTGTC	A
			AGGAGCAG TGATG AG		
			TCCTCGTC ACTAC TC		
			TTCC_ C		
GAM1890	LILRB4	3'	CTTCATCATCCGCCCTC 23386	A AGTT TC	
			GAGG GC G TGATGAAG		
			CTCC CG C ACTACTTC		
			_ _ _ CT		
GAM1890	NGB	3'	CTTCATCACCAACCCGCTCCC 41463	A A_ TC	
			G GGAGC GTTG TGATGAAG		
			C CCTCG CAAC ACTACTTC		
			_ CC C_		
GAM1890	OCLN	5'	TCTCCATCAGACACCCC 11883	AGCA T A	
			GG GT GTCTGATG AGA		
			CC CA CAGACTAC TCT		
			C_ _ C		
GAM1890	POU2F2	3'	CTCTTCATCCTCATCCTCCTCC 12214	C T_ TCT	
	TC		GAGGAG AG TG GATGAAGAG		
			CTCCTC TC AC CTACTTCTC		
			C CT TC_		
GAM1890	TJP1	5'	CTCCCCACCCTCACCTGCTGCT 13763	G T TCTGA AA	
	C		GAG AGCAG TG TG GAG		
			CTC TCGTC AC AC CTC		
			G C TCCC_ CC		
GAM1890	TRH	3'	CACAGGCCTGCTCCTT 24050	TT A	
			GAGGAGCAG GTCTG TG		
			TTCTCTCGTC CGGAC AC		
			_ _		
GAM1890	CDCA7	3'	CTCTATTTCCAATGCTCCTC 50040	G TCT TGA	
			GAGGAGCA TTG GA AGAG		
			CTCCTCGT AAC CT TCTC		
			_ _ _ TTA		
GAM1890	DOCK3	3'	CTTCTCCACTGCCCTC 67095	A TGTCT T	
			GAGG GCAGT GA GAAG		
			CTCC CGTCA CT CTTC		
			C C_ _		
GAM1890	ERF	3'	CTTCATCCCCAGCTGCTCCT 22440	TCT	
			AGGAGCAGTTG GATGAAG		

		TCCTCGTCGAC CTACTTC		
		CC_		
GAM1890 FKBP4	3'	CTCTCCACCAGCCCTACTCCT 10641	C TT T A A	
		AGGAG AG G CTG TG AGAG		
		TCCTC TC C GAC AC TCTC		
		A C__ C C		
GAM1890 HABP2	3'	CTCTAAGCAGAGACAAC TGCCA 15950	A_ GA A__	
CC		GG GCAGTTGTCT TG AGAG		
		CC CGTCAACAGA AC TCTC		
		AC G_ GAA		
GAM1890 KIAA0570	3'	CTAGTCAGACAACGCTCCTC 28850	A GA	
		GAGGAGC GTTGTCTGAT AG		
		CTCCTCG CAACAGACTG TC		
		_ A_		
GAM1890 KIAA0779	3'	TCATTTGAATGCTCCTC 86911	GTTG T	
		GAGGAGCA TC GATGA		
		CTCCTCGT AG TTACT		
		A__ T		
GAM1890 KIAA1742	3'	CTCTTCATCAGGACACTTCC 78139	GC T _	
		GGA AGT GTC TGATGAAGAG		
		CCT TCA CAG ACTACTTCTC		
		_ _ G		
GAM1890 MGC11335	3'	CTCCAGTGGCTCACCTGCTCCT 48769	TT__ TGA A	
C		GAGGAGCAG GTC TG AG		
		CTCCTCGTC CGG AC TC		
		CACT TG_ C		
GAM1890 MGC2668	3'	CGCCAGCAGCTGCTCCTC 61192	T A	
		GAGGAGCAGTTG CTG TG		
		CTCCTCGTCGAC GAC GC		
		_ C		
GAM1890 NIFU	5'	TCCCCAGCAACTGCGCCTC 67881	A T AT	
		GAGG GCAGTTG CTG GA		
		CTCC CGTCAAC GAC CT		
		G _ CC		
GAM1890 PDEF	3'	TCCTCAGGCCAGCTGCTCC 25680	_ T	
		GGAGCAGTT GTCTGA GA		
		CCTCGTCGA CGGACT CT		
		CC C		
GAM1890 SIMRP7	3'	TCTCCGCAGCTGCTCCTC 93980	CT T	
		GAGGAGCAGTTGT GA GA		

CTCCTCGTCGACG CT CT
 C_ _
 GAM1890 SNTA1 3' CTCTTCATCCTGTCTCTCTCCT 13296 C TTGTCT
 C GAGGAG AG GATGAAGAG
 ||||| || |||||
 CTCCTC TC CTACTTCTC
 _ TCTGTC
 GAM1890 LOC124222 3' CTCCTCACCTATCCTGTTTCCT 74747 TTGTCTGA A
 C GAGGAGCAG TGA GAG
 ||||| || |||||
 CTCCTTGTC ACT CTC
 CTATCCC_ C
 GAM1890 LOC200734 5' CTCTTCATCTCTAGCCGCCCC 90277 A A TCT
 GG GC GTTG GATGAAGAG
 || || || || |||||
 CC CG CGAT CTACTTCTC
 C C CT_
 GAM1890 LOC221718 5' CTTCTTCGACTGCTCCTC 95281 TCTGAT
 GAGGAGCAGTTG GAAG
 ||||| || |||||
 CTCCTCGTCAGC CTTC
 TT____
 GAM1890 LOC256950 3' TCCTCACCAACTGCTCC 97158 TC T
 GGAGCAGTTG TGA GA
 ||||| || |||||
 CCTCGTCAAC ACT CT
 C_ C
 GAM1890 LOC257442 5' CTCTTCATCCTAGCCCGCCCCC 97808 A_ A_ TCT
 TC GAGG GC GTTG GATGAAGAG
 || || || || |||||
 CTCC CG CGAT CTACTTCTC
 CC CC C_
 GAM1890 LOC257449 3' CTCTTCATCAGGACACTTCC 63375 GC T _
 GGA AGT GTC TGATGAAGAG
 || || || || |||||
 CCT TCA CAG ACTACTTCTC
 _ _ G
 GAM1890 LOC90381 3' CTCTTCATCCAGCTAATCCTC 63212 GC TCT
 GAGGA AGTTG GATGAAGAG
 || || || || |||||
 CTCCT TCGAC CTACTTCTC
 AA _
 GAM1890 LOC90678 3' TCTCCACAACTGTCCCTC 57205 AG CT T
 GAGG CAGTTGT GA GA
 || || || || |||||
 CTCC GTCAACA CT CT
 CT C_ _
 GAM1890 LOC90987 5' CTCTTCATCCTAGCCCGCCCCC 65149 A_ A_ TCT
 TC GAGG GC GTTG GATGAAGAG
 || || || || |||||

			CTCC CG CGAT CTACTTCTC	
			CC CC C__	
GAM1891	ABCC1	3'	CAGAGGCAGCCTCTGCACT 18434	AA TA
			AGTGCAGA CT CTTTG	
			TCACGTCT GA GAGAC	
			CC CG	
GAM1891	ABCC1	3'	CAGAGGCAGCCTCTGCACT 39598	AA TA
			AGTGCAGA CT CTTTG	
			TCACGTCT GA GAGAC	
			CC CG	
GAM1891	ABCC1	3'	CAGAGGCAGCCTCTGCACT 39601	AA TA
			AGTGCAGA CT CTTTG	
			TCACGTCT GA GAGAC	
			CC CG	
GAM1891	ADARB1	3'	TCTAGAAGCTTCTGTACT 32341	A A TT
			AGTGCAGAA CTT CT GA	
			TCATGTCTT GAA GA CT	
			C _ T_	
GAM1891	ADARB1	3'	TCTAGAAGCTTCTGTACT 8486	A A TT
			AGTGCAGAA CTT CT GA	
			TCATGTCTT GAA GA CT	
			C _ T_	
GAM1891	CYP4F3	3'	TTTCAAAGTAAGTCTCTGCCCT 8021	T A
			AG GCAGA ACTTACTTTGAAA	
			TC CGTCT TGAATGAACTTT	
			C C	
GAM1891	DSC3	3'	TTCAAGATTTCTGCAT 10448	CTTAC
			GTGCAGAAA TTTGAA	
			TACGTCTTT GAACTT	
			A__	
GAM1891	DSC3	3'	TTCAAGATTTCTGCAT 44638	CTTAC
			GTGCAGAAA TTTGAA	
			TACGTCTTT GAACTT	
			A__	
GAM1891	GDI2	3'	CAAATGATTTCTGTACT 9459	C C
			AGTGCAGAAA TTA TTTG	
			TCATGTCTTT AGT AAAC	
			- -	
GAM1891	IRF1	3'	CAGGGCTGGCTCTGCACT 64991	AA TA
			AGTGCAGA CT CTTTG	

		TCACGTCT GG GGGAC		
		C_ TC		
GAM1891 KLF7	5'	TTCCTGGCAGTCGTCTGCACT 14929	A_ TA TT	
		AGTGCAGA ACT CT GAA		
		TCACGTCT TGA GG CTT		
		GC C_ TC		
GAM1891 LIMD1	3'	TTTCAAGACCACTCTCTGCACT 27265	AACTTAC	
		AGTGCAGA TTTGAAA		
		TCACGTCT GAACTTT		
		CTCACCA		
GAM1891 PIK3R1	3'	TTCAGAATAAGCTTCCCCAC 69136	CA A C	
		GTG GAA CTTA TTTGAA		
		CAC CTT GAAT AGACTT		
		CC C A		
GAM1891 PLS1	3'	TTTCTGTAAGTTTCTATACT 12180	C TTT	
		AGTG AGAACTTAC GAAA		
		TCAT TCTTTGAATG CTTT		
		A T__		
GAM1891 RASGRP1	3'	TAGTGTAATTTCTGCAT 20419	C T	
		GTGCAGAAA TTAC TTG		
		TACGTCTTT AATG GAT		
		A T		
GAM1891 RB1	3'	TTTCATCATTGTTTCTGCAT 92557	TTACTT	
		GTGCAGAAAC TGAAA		
		TACGTCTTTG ACTTT		
		TTACT_		
GAM1891 RBMY1A1	3'	TTTCAAAGTAATTTCTATACT 18582	CA C	
		AGTG GAAA TTACTTTGAAA		
		TCAT CTTT AATGAACTTT		
		A_ _		
GAM1891 SERPINA4	3'	TTGGAGCAAGTTTCTGCCT 21705	T A TG	
		AG GCAGAACTT CTT A		
		TC CGTCTTTGAA GAG T		
		_ C GT		
GAM1891 TTC3	3'	TCAAAGATTCTGCATT 13886	ACTTA	
		AGTGCAGAA CTTTGA		
		TTACGTCTT GAAACT		
		A_____		
GAM1891 UBE2V1	3'	TCAAGTTCCTTTTTGCAC 13971	CTT T	
		GTGCAGAAA ACTT GA		

			CACGTTTTT TGAA CT		
			CCT _		
GAM1891	UBE2V1	3'	TCAAGTTCCTTTTTGCAC 42068	CTT	T
			GTGCAGAAA ACTT GA		
			CACGTTTTT TGAA CT		
			CCT _		
GAM1891	UBE2V1	3'	TCAAGTTCCTTTTTGCAC 42606	CTT	T
			GTGCAGAAA ACTT GA		
			CACGTTTTT TGAA CT		
			CCT _		
GAM1891	UTY	3'	TTCAGGAAATTCTGCAC 24064	C A	T
			GTGCAGAAA TT CTT GAA		
			CACGTCTTT AA GGA CTT		
			A _ _		
GAM1891	VIM	3'	TTTCAAGTGCCTTTCTGCA 94494	CT	T
			TGCAGAAA TACTT GAAA		
			ACGTCTTT GTGAA CTTT		
			CC _		
GAM1891	ZNF217	3'	TTCATAGTTTTGCACT 22550	AACTT	T
			AGTGCAGA ACT TGAA		
			TCACGTTT TGA ACTT		
			_____ T		
GAM1891	B7-H1	3'	TCAATTTGTTTTCTGCAT 27098	CT	CT
			GTGCAGAAA TA TTGA		
			TACGTCTTT GT AACT		
			T_ TT		
GAM1891	C20orf16	5'	TCATGATGTAGCTTCTGCACT 39242	A T TT	__
			AGTGCAGAA CT AC TGA		
			TCACGTCTT GA TG ACT		
			C _ TAGT		
GAM1891	C6orf10	3'	TTCATATCACAGTTTCTGCTCT 23265	T	TACTT_
			AG GCAGAACT TGAA		
			TC CGTCTTTGA ACTT		
			T CACTAT		
GAM1891	CACNG4	3'	TTCTGGAAGTTTCTGCCT 27712	T	A TT
			AG GCAGAACTT CT GAA		
			TC CGTCTTTGAA GG CTT		
			_ _ T_		
GAM1891	DKFZP434I1735	3'	TAGTGTAATTATCTGCACT 89172	_ C	T
			AGTGCAGA AA TTAC TTG		

TCACGTCT TT AATG GAT
A A T

GAM1891 DKFZp547I224 5' TCAAGTGGGTCCCTGAC 39962 G AA T
GT CAG ACTTACTT GA
|| ||| ||||| ||
CA GTC TGGGTGAA CT
_ CC _

GAM1891 DKFZP586I2223 5' TCTCTGTAGTCTCTGCACT 55773 A T TTT
AGTGCAGA ACT AC GA
||||| ||| || ||
TCACGTCT TGA TG CT
C _ TCT

GAM1891 DKFZp761K1423 3' TTCAAAGTTTTCTCCAC 37940 C CTT
GTG AGAAA ACTTTGAA
||| |||| |||||
CAC TCTTT TGAACTT
C _

GAM1891 DSCR6 3' TTTCAAAGCTCCTTCTGCATT 39080 ACTTA
AGTGCAGAA CTTTGAAA
||||| |||||
TTACGTCTT GAAACTTT
CCTC_

GAM1891 FLJ10718 3' CAAAGTGAGCTCCACT 37025 C AAA
AGTG AG CTTACTTTG
|||| || |||||
TCAC TC GAGTGAAAC
C _

GAM1891 FLJ10936 3' TCATGTGATTTCTGTAC 37449 C TT
GTGCAGAAA TTAC TGA
||||| ||| |||
CATGTCTTT AGTG ACT
_ T_

GAM1891 FLJ12568 3' TTTCAAAGGTTTTTATGCACT 47145 _ TTA
AGTGCA GAAAC CTTTGAAA
|||| |||| |||||
TCACGT TTTTG GAAACTTT
AT _

GAM1891 FLJ12572 3' TTTCAAAGTGCAGCCTGCCT 43547 T AAA _
AG GCAG CT TACTTTGAAA
|| ||| || |||||
TC CGTC GA GTGAAACTTT
_ C_ C

GAM1891 FLJ12985 3' TTCACAGTTTTTGCAC 46801 TACTT
GTGCAGAAACT TGAA
||||| |||
CACGTTTTTGA ACTT
C_

GAM1891 FLJ13909 5' TCAAAGAGTTGGAGTTTCTGAC 47783 G A_
GT CAGAAACTT CTTTGA
|| ||||| |||||

		CA GTCTTTGAG	GAAACT		
		—	GTTGA		
GAM1891	FLJ14466	3'	AGAGAAATTTCTGCACT	52415	C A
			AGTGCAGAAA TT CTTT		
			TCACGTCTTT AA GAGA		
			A —		
GAM1891	FLJ20281	5'	TTTCAAAGTAAATTGGTCTG	92624	AAC__
			CAGA TTACTTTGAAA		
			GTCT AATGAACTTT		
			GGTTA		
GAM1891	FLJ23598	5'	TCCTGGGAAGTTTCTGCTCT	96506	T A TT
			AG GCAGAACTT CT GA		
			TC CGTCTTTGAA GG CT		
			T G TC		
GAM1891	GL004	3'	TTTCATTTTAGTTTTGCACT	66597	A TACTT
			AGTGCAGAA CT TGAAA		
			TCACGTTTT GA ACTTT		
			— TTTT—		
GAM1891	KIAA1210	3'	TCCAAGAAAATTTCTGCAC	98084	C A T
			GTGCAGAAA TT CTT GA		
			CACGTCTTT AA GAA CT		
			A A C		
GAM1891	KIAA1391	3'	TTTCAAAGGTATCTCTGCCT	67855	T AACTTA
			AG GCAGA CTTTGAAA		
			TC CGTCT GAACTTT		
			— CTATG—		
GAM1891	KIAA1393	3'	TTTCAAAGTATGTGGCACT	72579	AGAA T
			AGTGC AC TACTTTGAAA		
			TCACG TG ATGAACTTT		
			G__ T		
GAM1891	KIAA1396	3'	TCAAGTGGGTCCCTGAC	63675	G AA T
			GT CAG ACTTACTT GA		
			CA GTC TGGGTGAA CT		
			— CC —		
GAM1891	KIAA1615	3'	TTCAATATCTTTTCTGCATT	69291	CTTACT
			AGTGCAGAAA TTGAA		
			TTACGTCTTT AACTT		
			TCTAT—		
GAM1891	KIAA1638	3'	TTCAAAGTCTTTCTTACAC	47825	C_ CTT
			GTG AGAAA ACTTTGAA		

CAC TCTTT TGAACTT
AT C__
GAM1891 KIAA1724 3' TTCAAAGGTGTGTTTCTGCCCT 67626 T TTA_
AG GCAGAAAC CTTTGAA
|| ||||| |||||
TC CGTCTTTG GAAACTT
C TGTG
GAM1891 MGC4473 5' TCAGAGTATTTCCGCA 55757 A CT
TGC GAAA TACTTTGA
||| ||| |||||
ACG CTTT ATGAGACT
C _
GAM1891 PPP2R3A 3' TCCAAGTGTGTATCATCTGCAC 12245 A__ T T
T AGTGCAGA AC TACTT GA
||||| || |||||
TCACGTCT TG GTGAA CT
ACTA T C
GAM1891 RAP140 5' TTCAGGGCCTCTGCATT 31526 AACTTA
AGTGCAGA CTTTGAA
||||| |||||
TTACGTCT GGGACTT
CC__
GAM1891 REG-IV 3' TCAGGAGTAAGCTTCTAGAC 50219 GC A _
GT AGAA CTTACTT TGA
|| ||| ||||| |||
CA TCTT GAATGAG ACT
GA C G
GAM1891 UBCE7IP5 3' TCAGGAGTCTCTGCCT 30853 T A ACT
AG GCAGA ACTT TTGA
|| |||| ||| |||
TC CGTCT TGAG GACT
_ C _
GAM1891 LOC115123 3' TTGGAAGTGTCTGCACT 73596 AACT G
AGTGCAGA TACTTT AA
||||| ||||| ||
TCACGTCT GTGAAG TT
_ G
GAM1891 LOC131368 3' TCAAAGTGTGTTTCTGCACT 76375 CT C
AGTGCAGAAA TA TTTGA
||||||| || |||||
TCACGTTTTT GT AAAGT
T_ C
GAM1891 LOC143310 5' TTCATGGAGCTTTGCACT 77054 AA ACTT
AGTGCAGA CTT TGAA
||||| ||| |||
TCACGTTT GAG ACTT
C_ GT_
GAM1891 LOC144970 3' TTTGGAGTGAGTTTCTGCAC 77533 TG
GTGCAGAACTTACTT AA
||||||| ||| ||

	CACGTCTTTGAGTGAG TT	
	GT	
GAM1891 LOC146540 3'	TTTCAAAGTAAGTTGCA 78532	GAA
	TGCA ACTTACTTTGAAA	
	ACGT TGAATGAACTTT	
	—	
GAM1891 LOC155032 3'	TAAAGGCAAGCTTCTGTAC 87599	A A_
	GTGCAGAA CTT CTTTG	
	CATGTCTT GAA GAAAT	
	C CG	
GAM1891 LOC157349 5'	TTCATTGAGCTCTCTGCACT 82351	AA_ CTT
	AGTGCAGA CTTA TGAA	
	TCACGTCT GAGT ACTT	
	CTC T_	
GAM1891 LOC158158 3'	TCAAGTGGGTCCCTGAC 82622	G AA T
	GT CAG ACTTACTT GA	
	CA GTC TGGGTGAA CT	
	_ CC _	
GAM1891 LOC159163 3'	TTTCAAAGTAATTTCACT 64617	CA C
	AGTG GAAA TTACTTTGAAA	
	TCAT CTTT AATGAACTTT	
	A_ _	
GAM1891 LOC159982 5'	TTCAGAGTCTCTGCATT 88436	AACTT
	AGTGCAGA ACTTTGAA	
	TTACGTCT TGAGACTT	
	C_	
GAM1891 LOC161734 3'	TCAAGTGGGTCCCTGAC 88468	G AA T
	GT CAG ACTTACTT GA	
	CA GTC TGGGTGAA CT	
	_ CC _	
GAM1891 LOC163126 3'	TTCAAGAGAACCTCTGCATT 83321	AAC AC
	AGTGCAGA TT TTTGAA	
	TTACGTCT AA GAACTT	
	CC_ GA	
GAM1891 LOC164295 5'	TTCAGCCAGGACTTCTGCAT 83399	A_ ACT
	GTGCAGAA CTT TTGAA	
	TACGTCTT GGA GACTT	
	CA CC_	
GAM1891 LOC165346 5'	CAGTGTGGGTTCTGCAC 83376	A T
	GTGCAGAA CTTAC TTG	

		CACGTCTT GGGTG GAC		
		— T		
GAM1891	LOC196410 3'	TCAACTGCAAGTTTCTGGACT 89033	G	ACT_
		AGT CAGAACTT TTGA		
		TCA GTCTTTGAA AACT		
		G CGTC		
GAM1891	LOC196513 3'	TTCAATGTTTCTGCCT 89096	T	TTACT
		AG GCAGAAAC TTGAA		
		TC CGTCTTTG AACTT		
		— T_____		
GAM1891	LOC197196 5'	CAAAGTGGGCCTCTGCAC 91296	AA	
		GTGCAGA CTTACTTTG		
		CACGTCT GGGTGAAAC		
		CC		
GAM1891	LOC199678 3'	TCAAAGAGAATGAACTTTTGC 91372	AC_ ____	
	AC	GTGCAGAA TTA CTTTGA		
		CACGTTTT AGT GAACT		
		CAA AAGA		
GAM1891	LOC203378 3'	CAAAGCAAGACTCTGCACT 92280	AA A	
		AGTGCAGA CTT CTTTG		
		TCACGTCT GAA GAAAC		
		CA C		
GAM1891	LOC203508 3'	AGGTAATAAAGTTCTGCACT 90937	AC____	
		AGTGCAGAA TTACTT		
		TCACGTCTT AATGGA		
		GAAAT		
GAM1891	LOC219942 3'	TCTAGAAGCCTCTGCGCT 94997	AA A TT	
		AGTGCAGA CTT CT GA		
		TCGCGTCT GAA GA CT		
		CC _ T_		
GAM1891	LOC253126 3'	TTTCAAAGTAATTTCACT 98087	CA C	
		AGTG GAAA TTACTTTGAAA		
		TCAT CTTT AATGAACTTT		
		A_ _		
GAM1891	LOC254557 5'	TTCAGCGCGTCTCTGCGCT 97980	A TTACT	
		AGTGCAGA AC TTGAA		
		TCGCGTCT TG GACTT		
		C CGC__		
GAM1891	LOC255624 3'	TTCACAGTTTTTGCAC 96168	TACTT	
		GTGCAGAACT TGAA		

CACGTTTTTTGA ACTT
C____
GAM1891 LOC256019 3' TTTGGAGTGAGTTTCTGCAC 97596 TG
GTGCAGAAACTTACTT AA
||||| ||
CACGTCTTTGAGTGAG TT
GT
GAM1891 LOC257486 3' TCCAAGAAAATTTCTGCAC 69783 C A T
GTGCAGAAA TT CTT GA
||||| || ||
CACGTCTTT AA GAA CT
A A C
GAM1891 LOC90233 3' TCAAACCTTTCTGTACT 57195 CTTAC
AGTGCAGAAA TTTGA
||||| ||||
TCATGTCTTT AACT
C____
GAM1891 LOC90233 3' TCAGAGAAGCAAACCTCTGTAC 57196 AA____ A
T AGTGCAGA CTT CTTTGA
||||| || |||||
TCATGTCT GAA GAGACT
CCAAAC _
GAM1891 LOC93070 3' TCATGTGATTTCTGTAC 71814 C TT
GTGCAGAAA TTAC TGA
||||| ||| ||
CATGTCTTT AGTG ACT
_ T_
GAM1892 CSH2 3' AAGTTTGACACAAACTCACACA 40974 CA AGGT_
A TTG TGGGTTTGT ACTT
||| ||||| ||||
AAC ACTCAAACA TGAA
AC CAGTT
GAM1892 SLC22A2 3' ATCACAAAGCCCATACAA 60276 C _ A
TTG ATGGGTTT GT GGT
||| ||||| || |||
AAC TACCCGAA CA CTA
A A _
GAM1892 CYLD 3' TTTACAAACCCTGCAATT 31543 T
AATTGCA GGGTTTGTAGG
||||| |||||
TTAACGT CCCAAACATTT
_
GAM1892 KIAA1095 3' ATTTGCAAACCCTACAA 68087 CAT
TTG GGGTTTGTAGGT
||| |||||
AAC CCCAAACGTTTA
AT_
GAM1892 ZNF397 3' AAGCACCTACAAGAACTTAT 51346 ____ A
ATGGGTT TGTAGGT CTT
||||| ||||| |||

		TATTCAA ACATCCA GAA		
		AGA C		
GAM1892	LOC116123	3' AAGTACCTACAATCAAACAA 57873	CA	GT
		TTG TGG TTGTAGGTACTT		
		AAC ACT AACATCCATGAA		
		AA _		
GAM1892	LOC120114	5' AAGCACCCACAAGCCCACAGC 76032	A_	A A
		GC TGGGTTTGT GGT CTT		
		CG ACCCGAACA CCA GAA		
		AC C C		
GAM1892	LOC158235	5' TACCCACAAGTCTAGGTAATT 88007	ATG	T A
		AATTGC GGTT GT GGTA		
		TTAATG TCAA CA CCAT		
		GA_ _ C		
GAM1893	A1BG	3' CCCAGCCCCAGCTTAGT 56284	C	A GAA
		ACT AGCTGG GCT GGG		
		TGA TCGACC CGA CCC		
		T C _		
GAM1893	AANAT	3' TCCTCTTAGCTCAGCTGAG 8439	G	A
		CTCAGCTG AGCTGA GGGGA		
		GAGTCGAC TCGATT CTCCT		
		_ _		
GAM1893	AKR1C3	3' CTTCAGTCAACTACAGCTGAGT 14966	GA_____	
		ACTCAGCTG GCTGAAG		
		TGAGTCGAC TGAAGTC		
		ATCAAC		
GAM1893	CHI3L1	3' CCCCTCTGGCTCCAGCTGG 8882	GA	
		TCAGCTGGAGCT AGGGG		
		GGTCGACCTCGG TCCCC		
		TC		
GAM1893	CHST6	3' CCAGCCAGCTCCAGCTGA 41498	AAG	
		TCAGCTGGAGCTG GG		
		AGTCGACCTCGAC CC		
		CGA		
GAM1893	CKM	5' CCCCTTCAGCCCAGCCCAG 10200	CA	A
		CT GCTGG GCTGAAGGGG		
		GA CGACC CGACTTCCCC		
		CC _		
GAM1893	DIO3	3' CTCTCAGCTCAGCTGAG 9071	G	A
		CTCAGCTG AGCTGA GGG		

GAGTCGAC TCGACT CTC

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GAM1893 KRT9   3' CCCAGCCCCAGCTGAG   76805   A   GAA
                  - -
                  CTCAGCTGG GCT GGG
                  ||||| ||| |||
                  GAGTCGACC CGA CCC
                  C _
GAM1893 LAMB3  3' CCCTGAGCTGCAGCTGAG   5855   G   GA
                  CTCAGCTG AGCT AGGG
                  ||||| ||| |||
                  GAGTCGAC TCGA TCCC
                  G G_
GAM1893 MAP3K14 3' CCCCTGCTCCAGTCGAGT   15545   A   TGA
                  ACTC GCTGGAGC AGGGG
                  ||| ||||| ||||
                  TGAG TGACCTCG TCCCC
                  C _
GAM1893 MFAP2  3' TCCCCCACCACAGCTGG   34361   AGC AA
                  TCAGCTGG TG GGGGA
                  ||||| || ||||
                  GGTCGACC AC CCCCT
                  CC_ C_
GAM1893 OPA1   3' TCCCCCTCTCAGCTGA   56429   _ CTGAA
                  TCAGCTG GAG GGGGA
                  ||||| ||| ||||
                  AGTCGAC CTC CCCCT
                  T _
GAM1893 PPP1R12B 3' TCCCTCAGGCTCCAGCTGAG   50368   GAA
                  CTCAGCTGGAGCT GGGGA
                  ||||| ||||
                  GAGTCGACCTCGG TCCCT
                  AC_
GAM1893 RABL2A 3' CCCCCCACCACAGCTGAGT   23994   GAGC AA
                  ACTCAGCTG TG GGGG
                  ||||| || |||
                  TGAGTCGAC AC CCCC
                  ACCC CC
GAM1893 RABL2B 3' CCCCCCACCACAGCTGAGT   23976   GAGC AA
                  ACTCAGCTG TG GGGG
                  ||||| || |||
                  TGAGTCGAC AC CCCC
                  ACCC CC
GAM1893 RBM10  5' CTCCGGCTCCGGCTGAG   20246   GAA
                  CTCAGCTGGAGCT GGGG
                  ||||| ||||
                  GAGTCGGCCTCGG CCTC
                  _
GAM1893 SLC12A4 3' CCCCCACCAAGCTGAG   18628   _ AGC AA
                  CTCAGCT GG TG GGGG
                  ||||| || || |||
```

GAGTCGA CC AC CCCC
 A _ C_
 GAM1893 SORBS1 3' TCCCCTGGAGCCAGCTGA 31808 AG GA
 TCAGCTGG CT AGGGGA
 ||||| || |||||
 AGTCGACC GG TCCCCT
 GA _
 GAM1893 TNFRSF12 3' CCCCTATCGCTCCAGCCAAG 15040 CA T _
 CT GCTGGAGC GA AGGGG
 || ||||| || |||||
 GA CGACCTCG CT TCCCC
 AC _ A
 GAM1893 TNNC1 3' CCAGCCTCCAACCTCCAGCTGAG 13819 C A _
 T ACTCAGCTGGAG TG AGG GG
 ||||| || || || ||
 TGAGTCGACCTC AC TCC CC
 A C GA
 GAM1893 ZNF274 5' TCCTGAGCTCCAGCTGG 33342 GA
 TCAGCTGGAGCT AGGG
 ||||| |||||
 GGTCGACCTCGA TCCT
 G_
 GAM1893 ATPW 5' CTCCAGCTCCAGCCGGGT 32257 A A
 ACTC GCTGGAGCTG AG
 ||| ||||| ||
 TGGG CGACCTCGAC TC
 C C
 GAM1893 BLCAP 3' GTTCTAGCAGTCCCCAGCTGAG 22946 A_ AAGG
 T ACTCAGCTGG GCTG GGAAC
 ||||| ||||| |||||
 TGAGTCGACC TGAC TCTTG
 CC GA_
 GAM1893 C16orf5 3' CCCCTCACCCAGCTGA 26348 AGC A
 TCAGCTGG TGA GGGG
 ||||| || |||||
 AGTCGACC ACT CCCC
 CC_ _
 GAM1893 CECR7 5' CCCCAGAGCTCCAGCCAGG 80446 CA GAA
 CT GCTGGAGCT GGGG
 || ||||| |||||
 GG CGACCTCGA CCCC
 AC GA_
 GAM1893 DKFZp761O17121 5' GTTCCCCTGGACTCCAGCCAAG 51134 CA _ GA
 CT GCTGGAG CT AGGGGAAC
 || ||||| || |||||
 GA CGACCTC GG TCCCCTTG
 AC A _
 GAM1893 FER1L4 3' TCCCTACACCAGCCCCAGCTGA 48138 A AA_
 TCAGCTGG GCTG GGGGA
 ||||| ||||| |||||

AGTCGACC CGAC TCCCT
 C CACA
 GAM1893 FLJ11413 3' CCCCTTCAACCCAGTTGATGT 44955 _ AGC
 AC TCAGCTGG TGAAGGGG
 || ||||| |||||
 TG AGTTGACC ACTTCCCC
 T CA_
 GAM1893 FLJ12229 5' CCCC GGCCCCAGCTGAGT 46402 A GAA
 ACTCAGCTGG GCT GGGG
 ||||| || |||
 TGAGTCGACC CGG CCCC
 C ____
 GAM1893 FLJ14326 3' CCTCTCCAGTCCAGCTGAG 50768 G A
 CTCAGCTGGA CTG AGGGG
 ||||| || |||
 GAGTCGACCT GAC TCTCC
 _ C
 GAM1893 FLJ14627 5' GTTCCCCTCCAGCCTGGTGCTG 52548 T__ A A
 GG CTCAGC GG GCTG AGGGGAAC
 |||| || ||| |||||
 GGGTCG TC CGAC TCCCCTTG
 TGG _ C
 GAM1893 FLJ20085 3' CCCTCGCTCCAGCTGA 35005 T A
 TCAGCTGGAGC GA GGG
 ||||| || |||
 AGTCGACCTCG CT CCC
 _ _
 GAM1893 FLJ21839 3' GTTCCCCTCCAGGCCGCTGA 41838 T AG A
 TCAGC GG CTG AGGGGAAC
 |||| || || |||||
 AGTCG CC GAC TCCCCTTG
 _ G_ C
 GAM1893 FLJ31164 3' CCCCTGTGTCGGCCCCAGCTGA 59394 A ____
 G CTCAGCTGG GCTGA AGGGG
 ||||| || |||
 GAGTCGACC CGGCT TCCCC
 C GTG
 GAM1893 HSPC065 3' CCCCCACCCAGGCTGAGT 27147 _ AGC AA
 ACTCAGC TGG TG GGGG
 ||||| || || |||
 TGAGTCG ACC AC CCCC
 G C_ C_
 GAM1893 HSU79275 3' TCCCCCTCCACTCAGCACTGAG 66922 CTG_ CT A
 T ACTCAG GAG GA GGGGA
 |||| || || |||||
 TGAGTC CTC CT CCCCT
 ACGA AC C
 GAM1893 KIAA0210 3' TCCCCTTCTCCCCAGCTAAG 29178 C AGCT
 CT AGCTGG GAAGGGGA
 || ||||| |||||

		GA TCGACC CTTCCCCT		
		A CCT_		
GAM1893 KIAA0350	3'	GTTCCCCTCCAGCTGCAAGGG	61833	AGC G A
		CTC TG AGCTG AGGGGAAC		
		GGG AC TCGAC TCCCCTTG		
		A_ G C		
GAM1893 KIAA0429	5'	TCCCTGCCCCAGCTGA	29246	A TGAA
		TCAGCTGG GC GGGGA		
		AGTCGACC CG TCCCT		
		C _		
GAM1893 KIAA0792	5'	CCAGAGACAGCTCCAAGTGA	28764	C AAGG_
		CTCAG TGGAGCTG GG		
		GAGTC ACCTCGAC CC		
		A AGAGA		
GAM1893 KIAA0930	3'	GTTCCAGAAAGGCCTCCAGCTG	71074	_ GAAGG
	AG	CTCAGCTGGAG CT GGAAC		
		GAGTCGACCTC GG CTTG		
		C AAAGA		
GAM1893 KIAA1171	3'	CTCCAGGGCTCCAAGCTGAGT	89343	_ GAA
		ACTCAGCT GGAGCT GGGG		
		TGAGTCGA CCTCGG CCTC		
		A GA_		
GAM1893 KIAA1183	3'	CTCCTGCAACCCCGGCTGAG	63191	AGC A
		CTCAGCTGG TG AGGGG		
		GAGTCGGCC AC TCCTC		
		CCA G		
GAM1893 KIAA1509	3'	CCCCCAGCCTCCAGCTGG	62294	_ AA
		TCAGCTGGAG CTG GGGG		
		GGTCGACCTC GAC CCCC		
		C _		
GAM1893 KIAA1571	5'	TTCCCCTTCAAGTTAGTGA	61626	CTGG_
		TCAG AGCTGAAGGGGAA		
		AGTC TTGACTTCCCCTT		
		AGTGA		
GAM1893 KIAA1710	5'	GTTCCGAGGAACTCCAGCTGA	63180	CTGAAGG
		TCAGCTGGAG GGAAC		
		AGTCGACCTC CCTTG		
		AAGGAG_		
GAM1893 KIAA1853	3'	TCCCCCTCACCAGCTGA	69926	AGC A
		TCAGCTGG TGA GGGGA		

AGTCGACC ACT CCCCT
 ____ C
 GAM1893 KIAA1862 3' CCCCGGCTCCAGCTCGAG 69508 _ GAA
 CTC AGCTGGAGCT GGGG
 ||| ||||| |||
 GAG TCGACCTCGG CCCC
 C ____
 GAM1893 KRTHB4 3' TCCATTAGCAGTTCCAGCTAAG 53500 C AAGG_
 CT AGCTGGAGCTG GGA
 || ||||| |||
 GA TCGACCTTGAC CCT
 A GATTA
 GAM1893 MANBAL 3' TCCCCAGGCTCCAGCTGGG 42221 GAA
 CTCAGCTGGAGCT GGGGA
 ||||| |||
 GGGTCGACCTCGG CCCCT
 A_
 GAM1893 MGC14697 5' CTTTGGCAGACCCAGCTGAGT 52206 AG AA
 ACTCAGCTGG CTG GGGG
 ||||| ||| |||
 TGAGTCGACC GAC TTTC
 CA GG
 GAM1893 MGC2731 3' TCCCTCATTGTCCAGCTGA 44165 G TGAA
 TCAGCTGGA C GGGGA
 ||||| | |||
 AGTCGACCT G TCCCT
 _TTAC
 GAM1893 NCX 5' CTCCAGGGGCCCCAGCTGG 32943 A GAA
 TCAGCTGG GCT GGGG
 ||||| ||| |||
 GGTCGACC CGG CCTC
 C GGA
 GAM1893 NFASC 3' CCCCTTCAGCCCCGGGTG 70852 G A
 CA CTGG GCTGAAGGGG
 || ||| |||||
 GT GGCC CGACTTCCCC
 G C
 GAM1893 PHACS 5' CCTCCAGCTCCGCCAAGT 51853 CA T A
 ACT GC GGAGCTG AGG
 ||| || ||||| |||
 TGA CG CCTCGAC TCC
 AC _ C
 GAM1893 PRO2389 3' CTCTGAGCCTCAGCTGAG 64476 GA GA
 CTCAGCTG GCT AGGG
 ||||| ||| |||
 GAGTCGAC CGA TCTC
 TC G_
 GAM1893 RASSF2 3' TCCCCAGCTCCGGCCAAG 29112 CA GAA
 CT GCTGGAGCT GGGGA
 || ||||| |||

		GA CGGCCTCGA CCCCT		
		AC ___		
GAM1893	SDC3	5' GTTCCCCTGCAAGCCCCAGC	28482	A GA_
		GCTGG GCT AGGGGAAC		
		CGACC CGA TCCCCTTG		
		C ACG		
GAM1893	SMARCF1	3' CCCCTTCAGCCGCCTGGAG	21183	AGCT A_
		CTC GG GCTGAAGGGG		
		GAG CC CGACTTCCCC		
		GT_ GC		
GAM1893	STOML1	3' TCCCGGTCCCCAGCTGAGT	17864	AGCT AG
		ACTCAGCTGG GA GGGA		
		TGAGTCGACC CT CCCT		
		C_ GG		
GAM1893	TNK1	3' CCCCTGCTCCAGCCCAGT	15649	CA TGA
		ACT GCTGGAGC AGGGG		
		TGA CGACCTCG TCCCC		
		CC ___		
GAM1893	LOC113730	5' TCCCCTGCCCCAGCTGA	73501	A TGA
		TCAGCTGG GC AGGGGA		
		AGTCGACC CG TCCCCT		
		C ___		
GAM1893	LOC128077	3' GTTCCCCTTATTCCCGCTAAGT	75230	C T GCTG
		ACT AGC GGA AAGGGGAAC		
		TGA TCG CCT TTCCCCTTG		
		A C TA_		
GAM1893	LOC148490	5' CCCCAGGTGAAGTCCAGCTGAG	79620	G GAA_
	T	ACTCAGCTGGA CT GGGG		
		TGAGTCGACCT GA CCCC		
		_ AGTGGA		
GAM1893	LOC155368	3' CCCCCAGCCCCAGCTGG	82263	A_ AA
		TCAGCTGG GCTG GGGG		
		GGTCGACC CGAC CCCC		
		CC ___		
GAM1893	LOC162427	3' TCCCCTCCCACCAGCTGG	83232	AGC A_
		TCAGCTGG TG AGGGGA		
		GGTCGACC AC TCCCCT		
		_ CC		
GAM1893	LOC170425	3' CCCCTGCAGAGCCCCAGCTGG	76884	A GA_
		TCAGCTGG GCT AGGGG		

		GGTCGACC CGA TCCCC		
		C GACG		
GAM1893	LOC196214 5'	CCCATGCAGCTCCAGCCCAG	91174	CA AAG
		CT GCTGGAGCTG GGG		
		GA CGACCTCGAC CCC		
		CC GTA		
GAM1893	LOC200731 3'	CTCCAGCCCCAGCTGGGT	91696	A A
		ACTCAGCTGG GCTG AG		
		TGGGTCGACC CGAC TC		
		C C		
GAM1893	LOC205418 5'	CCTGAGGCAGTTCCAGCTGAG	92371	AA__
		CTCAGCTGGAGCTG GGG		
		GAGTCGACCTTGAC TCC		
		GGAG		
GAM1893	LOC221927 3'	CCCCAGGGCTCCAGCCCAG	94221	CA GAA
		CT GCTGGAGCT GGGG		
		GA CGACCTCGG CCCC		
		CC GA_		
GAM1893	LOC253675 3'	CCTTCATCACCTCCAGCTGA	98573	C__
		TCAGCTGGAG TGAAGG		
		AGTCGACCTC ACTTCC		
		CACT		
GAM1893	LOC254219 3'	CCCCCAAGGCTCCAGATGA	98319	G GAA
		TCA CTGGAGCT GGGG		
		AGT GACCTCGG CCCC		
		A AAC		
GAM1893	LOC57228 3'	TCCAAGCTCCAGCCAGGT	40401	CA GAA
		ACT GCTGGAGCT GGG		
		TGG CGACCTCGA CCT		
		AC A__		
GAM1893	LOC91974 5'	TTCCCCCTCTTTAGCTGTGT	68367	T CTGAA
		AC CAGCTGGAG GGGGAA		
		TG GTCGATTTC CCCCTT		
		T TC__		
GAM1893	LOC92078 3'	CCCCACCAGCCCCGGCTGAG	68595	A AA
		CTCAGCTGG GCTG GGGG		
		GAGTCGGCC CGAC CCCC		
		C CA		
GAM1893	LOC92078 5'	CTCTTCCAGCCCCAGTTGAG	68600	A _
		CTCAGCTGG GCTG AAGGG		

GAGTTGACC CGAC TTCTC
 C C
 GAM1893 LOC95633 3' TCCCCTTCAGCCCCCGGCTGA 60560 A__
 TCAGCTGG GCTGAAGGGGA
 ||||| |||||
 AGTCGGCC CGACTTCCCCT
 CCC
 GAM1894 BCL7A 3' GGAAGCCAGGATTCCAT 40988 C C C
 ATGGAA CCTG GC TCT
 ||||| ||| ||
 TACCTT GGAC CG AGG
 A _ A
 GAM1894 CYP1A1 5' GATCCCAGGCTCCAAGAGTCCA 6690 A C GC__ CT
 TGGA C CT GCCT GGGATC
 ||| || ||| |||||
 ACCT G GA CGGA CCCTAG
 _ A ACCT _
 GAM1894 FGF23 3' GATCCCAGAAGCTTCTCCA 40558 ACCCTGC C
 TGGA GC TCTGGGATC
 ||| || |||||
 ACCT CG AGACCCTAG
 CTT__ A
 GAM1894 ITGA1 3' GATCCCAGAATGATAAGTTC 64275 CCTG CC
 GAAC CG TCTGGGATC
 ||| || |||||
 CTTG GT AGACCCTAG
 AATA A_
 GAM1894 LARS2 3' ATCCCAGGCAAGGCACCA 31693 AAC GC CT
 TGG CCT GCCT GGGAT
 ||| ||| ||| |||||
 ACC GGA CGGA CCCTA
 AC_ A_ _
 GAM1894 LOXL1 3' GATTCCGGACGCCAGACCCCAT 60819 AACC C C
 ATGG CTG GC TCTGGGATC
 ||| ||| |||||
 TACC GAC CG AGGCCTTAG
 CCA_ _ C
 GAM1894 RENT1 3' CTCGGCGCAGGGCCCCG 12811 AA TCT
 TGG CCCTGCGCC GGG
 ||| ||||| |||
 GCC GGGACGCGG CTC
 CC _
 GAM1894 SLC24A1 5' ATCCCAGAGTAGCCTCCAT 17559 ACCCT GC
 ATGGA GC CTCTGGGAT
 |||| || |||||
 TACCT CG GAGACCCTA
 C__ AT
 GAM1894 SORCS2 3' ATCCCAATGAGGGTCCC 40795 A G CCTC
 GG ACCCT CG TGGGAT
 || |||| || |||||

			CC TGGGA GT ACCCTA		
			C _ A__		
GAM1894	WNT3A	3'	CCCTGTAAGGTTCCAT 53610	C	CCTCT
			ATGGAACC TGCG GGG		
			TACCTTGG ATGT CCC		
			A _____		
GAM1894	ABTB1	3'	CCCAGGGGAGGATCCAT 51699	AC	GCG
			ATGGA CCT CCTCTGGG		
			TACCT GGA GGGGACCC		
			A_ _____		
GAM1894	FEM-2	3'	ATCCCAGAGGCAGTCCCA 28308	A	CCTGC
			TGG AC GCCTCTGGGAT		
			ACC TG CGGAGACCCTA		
			C A_____		
GAM1894	FLJ10824	3'	ATCCCAGAGATAGCAAATGCCA 72956	AACCC	GC_
			TGG TGC CTCTGGGAT		
			ACC ACG GAGACCCTA		
			GTAA_ ATA		
GAM1894	FLJ13102	3'	ATCCCTGGCACAGGGTTCC 46525	C	TCT
			GGAACCCTG GCC GGGAT		
			CCTTGGGAC CGG CCCTA		
			A T__		
GAM1894	FLJ21777	5'	TAGGGCGCAGGGCTCCA 50851	A	T
			TGGA CCCTGCGCC CTG		
			ACCT GGGACGCGG GAT		
			C _		
GAM1894	IGF2AS	3'	GATCCCAGTTCGAAGACTCC 33529	ACC	G CCT
			GGA CT CG CTGGGATC		
			CCT GA GC GACCCTAG		
			CA_ A TT_		
GAM1894	KIAA1724	3'	GATCCCAGAATTGGAAGGTGCC 67617	AAC	G_ CC
	A		TGG CCT CG TCTGGGATC		
			ACC GGA GT AGACCCTAG		
			GT_ AG TA		
GAM1894	KIAA1866	3'	GATCCCAGAGGAAGGCGCCAT 61589	AA	CTGCG
			ATGG CC CCTCTGGGATC		
			TACC GG GGAGACCCTAG		
			GC AA_____		
GAM1894	KIAA1922	3'	GATCCCAGAAGTTCACTCCAT 73995	ACCC	C C
			ATGGA TG GC TCTGGGATC		

TACCT AC TG AGACCCTAG
C__ T A
GAM1894 KIAA1951 3' GATCCCAGGAAACAGACCTCCA 74155 ACC CGCC
T ATGGA CTG TCTGGGATC
||||| ||| |||||
TACCT GAC GGACCCTAG
CCA AAA_
GAM1894 KIAA1975 5' ATCCCAGAGCACAGGCTC 74413 AC C C
GA CCTG GC TCTGGGAT
|| ||| || |||||
CT GGAC CG AGACCCTA
C_ A_
GAM1894 MGC13102 5' GATCCCAGAACTGAGGCCCCA 51292 AAC G CC
TGG CCT CG TCTGGGATC
||| ||| || |||||
ACC GGA GT AGACCCTAG
CC_ _ CA
GAM1894 RAB39 3' TAGACACAGGGTTTCAT 77126 CGCC
ATGGAACCCTG TCTG
||||||| |||
TACTTTGGGAC AGAT
AC_
GAM1894 SDF1 3' CCCAGAGGATTGCTGCCCCAT 92515 AACCCT _
ATGG GCG CCTCTGGG
||||| ||| |||||
TACC CGT GGAGACCC
CCGT_ TA
GAM1894 LOC112817 5' GATCCCAGAAACCAGTCC 57329 ACC CGCC
GGA CTG TCTGGGATC
||| ||| |||||
CCT GAC AGACCCTAG
_ CAA_
GAM1894 LOC146820 3' CCCAGGTGTAGAACTTCAT 78738 ACC CT
ATGGA CTGCGCCT GGG
||||| ||||| |||
TACTT GATGTGGA CCC
CAA _
GAM1894 LOC147054 5' ATCCCAGAGGGCCCAGCCCCA 85000 AACC C _
TGG CTG GCC TCTGGGAT
||| ||| ||| |||||
ACC GAC CGG AGACCCTA
CC_ C G
GAM1894 LOC149086 3' CCCAGAGGCAGGTCC 85492 AC GC
GGA CCT GCCTCTGGG
||| ||| |||||
CCT GGA CGGAGACCC
_ _
GAM1894 LOC220020 3' GATCCCAGGAGGCAGAAGCTCC 95046 ACC GC_ _
A TGGA CT GCCTC TGGGATC
||||| || ||||| |||||

ACCT GA CGGAG ACCCTAG
 C__ AGA G
 GAM1894 LOC220045 3' GATCCCAGACCTAGGGGCTCC 95034 A GCGCC
 GGA CCCT TCTGGGATC
 ||| ||| |||||
 CCT GGGG AGACCCTAG
 C ATCC_
 GAM1894 LOC51596 5' ATCCCAGAGGTTGGCCCC 32487 AA CTGC
 GG CC GCCTCTGGGAT
 || || |||||
 CC GG TGGAGACCCTA
 CC T__
 GAM1895 PCOLN3 3' CGACAGGGAGCCTGTCCA 12410 GACTT GA
 TGGGCA GGT CCTGTCTG
 ||||| ||| |||||
 ACCTGT CCG GGACAGC
 ____ AG
 GAM1895 KIAA0140 5' TCACCCCAAGTCTGCCCA 28520 ____
 TGGGCAGACTT GGTGA
 ||||| |||||
 ACCCGTCTGAA CCACT
 CC
 GAM1895 RAB33B 5' CGACAGGTCCACGCCTGCCTA 49323 ACT T
 TGGGCAG TGG GACCTGTCTG
 ||||| ||| |||||
 ATCCGTC ACC CTGGACAGC
 CGC _
 GAM1895 LOC147004 3' ACAAACATCTAACTCTGCCCA 84963 C _ ACC
 TGGGCAGA TTGG TG TGT
 ||||| ||||| |||
 ACCCGTCT AATC AC ACA
 C T AA_
 GAM1896 CELSR3 3' CAAGTTGATCTGAGTATCGTCA 9184 A TG _ C
 TGAC ATACT GG AAC TG
 ||||| ||| ||| |||
 ACTG TATGA CT TTG AC
 C GT AG A
 GAM1896 FY 5' TCTTCAGGCTCCCTGCTTTGTC 10740 TACTT A
 GACAA GGGG CCTGAAGA
 ||||| ||||| |||||
 CTGTT CCCT GGA CTTCT
 TCGT_ C
 GAM1896 KMO 3' CTTCAAATATAAGTATTATCA 14845 C GGAACC
 TGA AATACTTG TGAAG
 ||| ||||| |||||
 ACT TTATGAAT ACTTC
 A ATAA_
 GAM1896 RTN3 3' CTTCAGGTTCTCACTCATAGTC 74330 A ACT
 A TGAC AT TGGGAACCTGAAG
 ||||| ||| ||||| |||||

		ACTG TA ACTCTTGGACTTC		
		A CTC		
GAM1896	ZNF266	5' TCAGACTCTGTAGGTATTGCA 89692	A	_ AC
		TG CAATACTTG GGA CTGA		
		AC GTTATGGAT TCT GACT		
		_ G CA		
GAM1896	C1orf24	3' TCTCCAGTCCCAAGTATT 54796	AC	A
		AATACTTGGGA CTG AGA		
		TTATGAACCCT GAC TCT		
		_ C		
GAM1896	IGF2AS	3' CTTCAGGTCACCTTGTCA 33527	TACTT	GA
		TGACAA GG ACCTGAAG		
		ACTGTT CC TGGACTTC		
		_ AC		
GAM1896	LOC138046	3' TCTCCATTCCCAAGCATTGCCA 75811	A A	CC A
		TG CAAT CTTGGGAA TG AGA		
		AC GTTA GAACCCTT AC TCT		
		C C _ C		
GAM1896	LOC149132	5' TCTCCAGGCCCTGAACATTCTC 79929	C	AC TG AA A
	A	TGA AAT T GG CCTG AGA		
		ACT TTA A CC GGAC TCT		
		C CA GT C_ C		
GAM1896	LOC152905	3' CTTCAGGTTCTCACTCATAGTC 61094	A	ACT
	A	TGAC AT TGGGAACCTGAAG		
		ACTG TA ACTCTTGGACTTC		
		A CTC		
GAM1896	LOC158056	5' TCTCCAGGCCCCAGGTG 82596	AA	A
		TACTTGGG CCTG AGA		
		GTGGACCC GGAC TCT		
		C_ C		
GAM1896	LOC91069	3' CTTCCAGCCAGATATTGTCA 65401	C	GAAC _
		TGACAATA TTGG CTG AAG		
		ACTGTTAT GACC GAC TTC		
		A _ C		
GAM1896	LOC96597	5' CTTTGTCCCAAGTATTCCCA 67459	AC	ACC
		TG AATACTTGGGA TGAAG		
		AC TTATGAACCCT GTTTC		
		CC _		
GAM1897	ASTN	3' AGACCTCTGGAGTTTCCTCTTG 69866	TTTG	
		CAAGAGGA CCAGAGGTCT		

			GTTCTCCT	GGTCTCCAGA		
			TTGA			
GAM1897	BCAT2	3'	AGACCCCTGGT	GCTGCCGTTG	8649	GA ATT A
			CAA GG	TGCCAG GGTCT		
			GTT CC	GTGGTC CCAGA		
			G_ GTC	C		
GAM1897	CHST5	5'	GACCTCTGGCT	TTTCCTGG	25089	AGA TTT
			CCA GGA	GCCAGAGGTC		
			GGT CCT	CGGTCTCCAG		
			___ TT_			
GAM1897	DUSP5	3'	GACCCCTGCCCT	CCTTGG	16632	ATTT C A
			CCAAGAGG	GC AG GGTC		
			GGTTCTCC	CG TC CCAG		
			___ _ C			
GAM1897	FMR1	3'	GGAACAAATCTT	CCTGGT	10679	A _
			ACCA GAGG	ATTTG CC		
			TGGT CTTCTAAAC	GG		
			C	AA		
GAM1897	MFAP3	3'	AGACCTCTGTCA	ACCCTCCTG	21000	A AT C
			CA GAGG	TTG CAGAGGTCT		
			GT CTCC	AAC GTCTCCAGA		
			C C_ T			
GAM1897	PML	3'	AGACCTCTGGT	TTTTCTTT	53820	TTT
			GAGGA	GCCAGAGGTCT		
			TTTCT	TGGTCTCCAGA		
			TT_			
GAM1897	SCD	3'	AGACAAGGCTG	GCAAACCCTC	18589	A AG_
			GAGG TTTGCCAG	GTCT		
			CTCC AAACGGTC	CAGA		
			C	GGAA		
GAM1897	TNFAIP2	3'	AGACCTCCTGGG	TCCTCTCAGG	21918	A_ TTG _
			CC AGAGGAT	CCAG AGGTCT		
			GG TCTCCTG	GGTC TCCAGA		
			AC	___ C		
GAM1897	TPP2	3'	GACCTCTGACAT	CATGGT	13836	A GGATT C
			ACCA GA	TG CAGAGGTC		
			TGGT CT	AC GTCTCCAG		
			A	___ A		
GAM1897	BDG-29	3'	GACCTCTTCTC	CCTCATGGT	72804	A TTTGCC
			ACCA GAGGA	AGAGGTC		

TGGT CTCCT TCTCCAG
 A CT____
 GAM1897 BIRC5 3' ACCTCTGGAGGTCATCTCGG 8603 A G G
 CC AGA GATTT CCAGAGGT
 || ||| |||| |||||
 GG TCT CTGGA GGTCTCCA
 C A _
 GAM1897 DKFZP564I0422 3' GCCAACAAATCCTCTCTG 49516 _ CCAGA
 CA AGAGGATTTG GGT
 || ||||| |||
 GT TCTCCTAAAC CCG
 C AA____
 GAM1897 EZF-2 5' AGACCTCTTTGCCCCCTGG 37671 A A ATTT C_
 CCA G GG GC AGAGGTCT
 ||| || || |||||
 GGT C CC CG TCTCCAGA
 _ _ C _ TT
 GAM1897 FLJ00007 3' AGACCCCTGACCACCCCTGGG 71774 A A ATTTGC A
 T ACC AG GG CAG GGTCT
 ||| || ||| |||||
 TGG TC CC GTC CCAGA
 G _ CCACCA C
 GAM1897 FLJ10349 3' AGACCCAAGAGCAAGTCCTC 36533 CAGA_
 GAGGATTTGC GGTCT
 ||||| |||||
 CTCCTGAACG CCAGA
 AGAAC
 GAM1897 FLJ10687 3' AGACCTGACATTAAATCCTCTT 36944 CCAG_
 G CAAGAGGATTTG AGGTCT
 ||||| |||||
 GTTCTCCTAAAT TCCAGA
 TACAG
 GAM1897 FLJ22167 5' GACCTCTGGCTTTCCTGG 44871 AGA TTT
 CCA GGA GCCAGAGGTC
 ||| || |||||
 GGT CCT CGGTCTCCAG
 _ _ TT_
 GAM1897 H105E3 5' CTGGGCCAATCCTCTTGGT 32490 T AG
 ACCAAGAGGATT GCC AG
 ||||| ||| ||
 TGGTTCTCCTAA CGG TC
 C G_
 GAM1897 KIAA0014 3' ACCTCACAAGTCCTCT 28536 CCA
 AGAGGATTTG GAGGT
 ||||| |||||
 TCTCCTGAAC CTCCA
 A_
 GAM1897 KIAA1956 3' ACCTCTGTGCATCTTCTTG 79075 TT _
 CAAGAGGA TGC CAGAGGT
 ||||| ||| |||||

GTTCTTCT ACG GTCTCCA
 _ T
 GAM1897 MGC14407 5' AGACCTCTGGTTTTACTCTT 52967 GATTT
 AAGAG GCCAGAGGTCT
 |||| |||||
 TTCTC TGGTCTCCAGA
 ATTT_
 GAM1897 NFAT5 5' AGACCTCTCGCTTCTCTCGG 57782 A TTT C
 CC AGAGGA GC AGAGGTCT
 || |||| || |||||
 GG TCTCTT CG TCTCCAGA
 C _ C
 GAM1897 TM4SF11 3' AGACCTCTTCTCCATCCCCCTT 32586 A_ TTGCC
 AAG GGAT AGAGGTCT
 ||| ||| |||||
 TTC CTA TCTCCAGA
 CC CCTCT
 GAM1897 UBN1 3' AGACCTCTGTCTGCCCTTTGG 34193 A ATTTGC
 CCAAG GG CAGAGGTCT
 |||| || |||||
 GGTTT CC GTCTCCAGA
 C GTCT_
 GAM1897 LOC130250 3' AGACCCCTTGGCCCCTCCTT 75421 TTT A_
 GAGGA GCCAG GGTCT
 |||| |||| ||||
 TTCCT CGGTT CCAGA
 CCC CC
 GAM1897 LOC145216 3' AGACCCCTCACCCCTTCTGG 84214 AG ATT CC A
 CCA AGG TG AG GGTCT
 ||| ||| || |||||
 GGT TCC AC TC CCAGA
 CT CC_ _ C
 GAM1897 LOC150094 3' TTCTGGCAAATCCTGTCGG 86008 AAG
 CC AGGATTTGCCAGAG
 || |||||
 GG TCCTAAACGGTCTT
 CTG
 GAM1897 LOC169181 5' GACCTCTCCCCTACTTGG 83608 _ ATTTGCC
 CCAAG AGG AGAGGTC
 |||| ||| |||||
 GGTTC TCC TCTCCAG
 A CC_
 GAM1897 LOC199899 5' AGACCTCCTCGGGTCCTCCGG 91464 AA CCA
 CC GAGGATTG GAGGTCT
 || ||||| |||||
 GG CTCCTGGGC CTCCAGA
 C_ TC_
 GAM1897 LOC200301 5' AGACCCCTGGAGAGGCCCGTCC 90131 A _ A_ TG A
 TGGT ACCA GA GG TT CCAG GGTCT
 |||| ||| || |||||

		TGGT CT CC GA GGTC CCAGA		
		C G CG GA C		
GAM1897	LOC202025 5'	AGACCCCCAAAGAGCTTTTGGT 91882	GA_	CCAGA
		ACCAAGAG TTTG GGTCT		
		TGGTTTTC AAAC CCAGA		
		GAG CC__		
GAM1897	LOC220032 3'	AGACCTCTAAGAGATCCCCATG 93330	AGA	GCC
	G	CCA GGATTT AGAGGTCT		
		GGT CCTAGA TCTCCAGA		
		ACC GAA		
GAM1897	LOC222070 5'	AGATCTCTCAGCAAATCCCCTG 95807	A A	C_
	G	CCA G GGATTTGC AGAGGTCT		
		GGT C CCTAAACG TCTCTAGA		
		_ C AC		
GAM1897	LOC254105 3'	AGACCTCTGACCTTGACCCCT 96415	A A	TGC__
		AG GG TT CAGAGGTCT		
		TC CC AG GTCTCCAGA		
		_ C TTCCA		
GAM1897	LOC92218 3'	ACCTCCAATTACCTCTGG 69030	A	AT_ CCA
		CCA GAGG TTG GAGGT		
		GGT CTCC AAC CTCCA		
		_ ATT _		
GAM1898	BBS4 3'	ATTGCCCCAAAGGGAATCCAGA 53447	G_ G_	A
	ACA	TGTTCTGGA CT TTGG CAAAT		
		ACAAGACCT GG AACC GTTTA		
		AA GA C		
GAM1898	CENTD2 3'	CCAACAAACTCCAGAACA 58270	C_	
		TGTTCTGGAG TGTTGG		
		ACAAGACCTC ACAACC		
		AA		
GAM1898	CENTD2 3'	CCAACAAACTCCAGAACA 31539	C_	
		TGTTCTGGAG TGTTGG		
		ACAAGACCTC ACAACC		
		AA		
GAM1898	HAMP 3'	TCCTGCTGCCCCAGAACA 41289	A T T	
		TGTTCTGG GC GT GGA		
		ACAAGACC CG CG CCT		
		C T T		
GAM1898	ITGA11 3'	TCTGCCGGCCCCCAGGACA 25213	A_	TT
		TGTTCTGG GCTG GGA		

			ACAGGACC CGGC TCT		
			CC CG		
GAM1898 KITLG	3'	ATTTGCATGGCTCCAGAA	15671	TGGA	
		TTCTGGAGCTGT CAAAT			
		AAGACCTCGGTA GTTTA			
		C__			
GAM1898 KITLG	3'	ATTTGCATGGCTCCAGAA	8023	TGGA	
		TTCTGGAGCTGT CAAAT			
		AAGACCTCGGTA GTTTA			
		C__			
GAM1898 MAPK4	5'	CCTGGGCAGCTCCAGATCA	12300	T	__
		TG TCTGGAGCTGTT GG			
		AC AGACCTCGACGG CC			
		T GT			
GAM1898 MGAT2	3'	ATTTGTCCAAACAGGACA	11557	GAGCTG	
		TGTTCTG TTGGACAAAT			
		ACAGGAC AACCTGTTTA			
		A__			
GAM1898 PSPHL	5'	TTGTCATACAGCTCCAAACA	94499	C	TG
		TGTT TGGAGCTGT GACAA			
		ACAA ACCTCGACA CTGTT			
		TA			
GAM1898 TTC3	3'	TATTTGTCCAACAACTGTCAGA	13885	_	C
ATA		TGTTCTGG AG TGTTGGACAAATA			
		ATAAGACT TC ACAACCTGTTTAT			
		G A			
GAM1898 FLJ14213	3'	TGATAACAGCTCCAGAA	46218	GA	
		TTCTGGAGCTGTTG CA			
		AAGACCTCGACAAT GT			
		A_			
GAM1898 H2BFQ	3'	TTTAAGAGAACTCCAGGACA	60079	__	G
		TGTTCTGGAG CT TTGGA			
		ACAGGACCTC GA AATTT			
		AA G			
GAM1898 LRG	3'	TCCATCCATGCTTCCTAGAACA	54825	_ _ _	T_
		TGTTCT GGA GC TG TGGA			
		ACAAGA CCT CG AC ACCT			
		T T T CT			
GAM1898 NMT2	3'	ATTTGTCCATGTAACAGAACA	17852	GA	TGT
		TGTTCTG GC TGGA			

ACAAGAC TG ACCTGTTTA
 AA T__
 GAM1898 NYD-SP21 3' TATTTGTCCAATCTAGATTCAG 51863 G __
 AACA TGTTCTGGA CT GTTGGACAAATA
 ||||| || |||||
 ACAAGACTT GA TAACCTGTTTAT
 A TC
 GAM1898 PSPH 3' TTGTCGTACAGCTCCAAACA 17143 C TG
 TGTT TGGAGCTGT GACAA
 ||| ||||| ||||
 ACAA ACCTCGACA CTGTT
 _ TG
 GAM1898 LOC122258 3' CCACCAGCCTCCGGAACA 59820 _ T
 TGTTCTGGAG CTG TGG
 ||||| ||| |||
 ACAAGGCCTC GAC ACC
 C C
 GAM1898 LOC151826 3' ATTTGTCCAACCTAGCACA 81176 T AGCT
 TGT CTGG GTTGGACAAAT
 ||| ||| |||||
 ACA GATC CAACCTGTTTA
 C ____
 GAM1898 LOC169611 3' TCCAGTGGCAGCTCCAGAA 83663 ____
 TTCTGGAGCTGT TGGA
 ||||| |||
 AAGACCTCGACG ACCT
 GTG
 GAM1898 LOC196746 3' TCAGAGCAGCTCCAAGACA 88903 TC G_
 TGT TGGAGCTGTT GA
 ||| ||||| ||
 ACA ACCTCGACGA CT
 GA GA
 GAM1898 LOC204119 5' TGCCACAACCTCAGAACA 92343 G C T A
 TGTTCTG AG TGT GG CA
 ||||| || ||| ||
 ACAAGAC TC ACA CC GT
 _ A _ _
 GAM1898 LOC253142 5' TTGCTAGGATGCCCCAGAATA 99230 A TG_ A
 TGTTCTGG GC TTGG CAA
 ||||| || ||| |||
 ATAAGACC CG GATC GTT
 C TAG _
 GAM1899 ADCY6 3' CCCTTCTGACACCAGCTCC 40946 CCG CC__
 GGAGCTGG TGTT GGG
 ||||| ||| |||
 CCTCGACC ACAG CCC
 _ TCTT
 GAM1899 ALPL 3' CTGAACACACACGCCAGCTCCT 6649 C__ C
 AGGAGCTGGC GTGTTC GG
 ||||| ||||| ||

		TCCTCGACCG CACAAG TC	
		CACA _	
GAM1899 BARHL1	3'	CCCCCAGCCTCTGCCGGCTCC 39635	CGT_ CC
		GGAGCTGGC GTT GGG	
		CCTCGGCCG CGA CCC	
		TCTC CC	
GAM1899 CASQ2	3'	CCCACACCCAGCCAGCTCCTT 8781	C__ TCC
		AAGGAGCTGGC GTGT GGG	
		TTCCTCGACCG CACA CCC	
		ACC ____	
GAM1899 DLG5	5'	CCCAGGAGGCAGCAGCTCCTT 83813	G C G C
		AAGGAGCTG C GT TTC GGG	
		TTCCTCGAC G CG AGG CCC	
		_ A G A	
GAM1899 F12	3'	CCCCCAGTGCGGCCAGCTCC 6700	TG CC
		GGAGCTGGCCG TT GGG	
		CCTCGACCGGC GA CCC	
		GT CC	
GAM1899 GGA3	3'	CCCGCCAACCAGCTCCT 26584	CCG TTC
		AGGAGCTGG TG CGGG	
		TCCTCGACC AC GCCC	
		A__ C__	
GAM1899 GRAF	3'	CCCACCACTGGCCAGCCCC 31229	A _ TTCC
		GG GCTGGCC GTG GGG	
		CC CGACCGG CAC CCC	
		C T CA__	
GAM1899 GTF2I	5'	CTCCCGTCCGCTCGCCAGCTCC 53381	C_ TTC
		GGAGCTGGC GTG CGGGAG	
		CCTCGACCG CGC GCCCTC	
		CT CT_	
GAM1899 HDAC5	5'	CCCCAACGCCAGCTTCCT 19620	_ C GTTCC
		AGGA GCTGGC GT GGG	
		TCCT CGACCG CA CCC	
		T _ AC__	
GAM1899 HMX1	3'	CCCGGCGCCACGGCCACCCCC 38945	AGC TT_
		GG TGGCCGTG CCGGG	
		CC ACCGGCAC GGCCC	
		CCC CGC	
GAM1899 INHBB	5'	CCCGAGGCCCGGCCGGCCCC 11007	A T TC
		GG GCTGGCCG GT CGGG	

CC CGGCCGGC CG GCCC
 C C GA
 GAM1899 ITGAL 3' TCCCAGGCCAGGCTCCTT 11051 _ GTGTTCC
 AAGGAGC TGGCC GGA
 ||||| |||| ||||
 TTCCTCG ACCGG CCCT
 G A____
 GAM1899 NEURL 3' CTCCCGTCTCTGCACCCAGCTC 16129 CC TC____
 CT AGGAGCTGG GTGT CGGGAG
 ||||| |||| |||||
 TCCTCGACC CACG GCCCTC
 _ TCTCT
 GAM1899 OVOL1 3' CTCCCAGCTGCCTGGCCAGCCC 17067 A T TCC_
 GG GCTGGCCG GT GGGAG
 || ||||| || |||||
 CC CGACCGGT CG CCCTC
 _ C TCGA
 GAM1899 PCDH1 3' CCCCCAGCGCCGGCCAGCTCC 51576 _ CC
 GGAGCTGGCCG TGTT GGG
 ||||| |||| ||||
 CCTCGACCGGC GCGA CCC
 C CC
 GAM1899 PRSS8 5' CTCCCGTTGCGGCCGCTCC 12421 T TTC
 GGAGC GGCCGTG CGGGAG
 |||| ||||| |||||
 CCTCG CCGGCGT GCCCTC
 _ T____
 GAM1899 PRX 3' CTCCCGGAAGTGCAGCTCC 40893 _ CGTG
 GGAGCTG GC TTCCGGGAG
 ||||| || |||||
 CCTCGAC TG AAGGCCCTC
 G ____
 GAM1899 SCAMP2 3' CTCCCTCAGCGACCAGCTCTCC 20304 A C GTTCC
 A GGAGCTGG CGT GGGAG
 | ||||| || |||||
 C TCTCGACC GCG CCCTC
 C A ACT____
 GAM1899 SLC9A1 3' CCCCACCCCAGCACAGCTCCT 70921 _ C____ TTCC
 AGGAGCTG GC GTG GGG
 ||||| || |||||
 TCCTCGAC CG CAC CCC
 A ACCC ____
 GAM1899 SYNGR2 3' CTCCTGGAAGTGCAGCCCCT 17492 A CGT
 AGG GCTGGC GTTCCGGGAG
 || ||||| |||||
 TCC CGACCG CAAGGTCCTC
 C T____
 GAM1899 ZNF76 3' CTCCCAGCAATAACCACCTCC 14269 C CCG_ CC
 GGAG TGG TGTT GGGAG
 |||| || |||| |||||

CCTC ACC ACGA CCCTC
 C AATA ____
 GAM1899 ATP6V1B2 5' CTCCCAGCACGCTGGTCAGCTC 9885 _ TCC
 CT AGGAGCTGGCC GTGT GGGAG
 ||||| ||| ||||
 TCCTCGACTGG CGCA CCCTC
 T CGA
 GAM1899 BCMP1 3' TCCCAAACACAGTTCTT 49539 GGCC CC
 AGGAGCT GTGTT GGA
 ||||| ||| ||||
 TTCTTGA CACAA CCCT
 ____ AA
 GAM1899 C11orf25 5' CTCCCTCTCGGGCAGCTCC 49464 G TGTTC
 GGAGCTG CCG GGGAG
 ||||| ||| ||||
 CCTCGAC GGC CCCTC
 G TCT____
 GAM1899 DKFZP434N1511 3' CCCCAAGGTCAGCTCC 93055 G TTCC
 GGAGCTGGCC TG GGG
 ||||| || ||||
 CCTCGACTGG AC CCC
 A ____
 GAM1899 DKFZp547I094 5' CTCCCAAACCCAGCCAGCTTCC 50555 _ CGT CC
 T AGGA GCTGGC GTT GGGAG
 ||| ||||| ||| |||||
 TCCT CGACCG CAA CCCTC
 T ACC A_
 GAM1899 DKFZP566G1424 5' CTCCCAGAACAGGCACCCCTT 85942 AGCTG G C
 AAGG GCC TGTTTC GGGAG
 |||| ||| ||||| |||||
 TTCC CGG ACAAG CCCTC
 CCA__ _ A
 GAM1899 DKFZp761N0624 3' TCTGGCACAACCAGCTTCCT 51162 _ CC TT
 AGGA GCTGG GTG CCGGG
 |||| ||||| ||| |||||
 TCCT CGACC CAC GGTCT
 T AA ____
 GAM1899 FLJ12788 3' CCCAGATTACTCACAGCTCCT 42846 GCC T C
 AGGAGCTG GTG TC GGG
 ||||| ||| ||| ||||
 TCCTCGAC CAT AG CCC
 ACT T A
 GAM1899 FLJ13855 3' TCCACAGGGCCAGCTCCTT 43856 G TCCG
 AAGGAGCTGGCC TGT GGA
 ||||| ||||| ||| ||||
 TTCCTCGACCGG ACA CCT
 G ____
 GAM1899 FLJ14146 3' CTCCCGCCATTGGCTCAGCTCC 45569 _ TGTTTC
 T AGGAGCTG GCCG CGGGAG
 ||||| |||| |||||

			TCCTCGAC CGGT GCCCTC		
			T TACC_		
GAM1899	FLJ14154	5'	CCCCCAGCGGCCGCGGCTCC 46228	C _ CC	
			GGAGCTGGC GT GTT GGG		
			CCTCGGCCG CG CGA CCC		
			C G CC		
GAM1899	FLJ20257	5'	CCCGGGGCGAGCCGCTCC 39482	T CG	
			GGAGC GGC TGTTCCGGG		
			CCTCG CCG GCGGGGCC		
			_ A_		
GAM1899	FLJ22477	3'	CCCAGCCCACAGCCAGCTCC 45671	C TTCC	
			GGAGCTGGC GTG GGG		
			CCTCGACCG CAC CCC		
			A CCGA		
GAM1899	FYCO1	3'	CCCGGAGATCCTGACCAGCTCC 44768	C TG__	
	T		AGGAGCTGG CG TTCCGGG		
			TCCTCGACC GT GAGGCC		
			A CCTA		
GAM1899	GGA2	3'	CTCACCACAGCCAGCTCC 57662	C TTCC	
			GGAGCTGGC GTG GGG		
			CCTCGACCG CAC CTC		
			A CA__		
GAM1899	GRO2	5'	CCCGGGCCACAGGCAGCTCCTT 60252	G _ TT	
			AAGGAGCTG CC GTG CCGGG		
			TTCCTCGAC GG CAC GGCCC		
			_ A CG		
GAM1899	GTPBP1	5'	CCCCGAGCCCAGCTCC 16265	CCGT C	
			GGAGCTGG GTTC GGG		
			CCTCGACC CGAG CCC		
			_____ C		
GAM1899	HCGIV.9	5'	CCCCGCGGCCAGCCCC 39130	A TTCC	
			GG GCTGGCCGTG GGG		
			CC CGACCGGCGC CCC		
			C _____		
GAM1899	HSPC195	3'	CCTGCCCACGGCCAGCTTCCT 81864	_ TTC	
			AGGA GCTGGCCGTG CGGG		
			TCCT CGACCGGCAC GTCC		
			T CC_		
GAM1899	HYA22	5'	CCCGCGCGCGCGGCCGCCCT 20553	A T TC_	
			AGG GC GGCCGTGT CGGG		

		TCC CG CCGGCGCG	GCCC		
		C _	CGC		
GAM1899	KCNK17	5'	TCCCGGCGCCGGCTCC	49594	CGTGTT
			GGAGCTGGC	CCGGA	
			CCTCGGCCG	GGCCCT	
			C _		
GAM1899	KIAA1030	3'	CTCCCGGGCCTGGCCAGCATCC	94977	_ T T
			GGA GCTGGCCG	GT CCGGGAG	
			CCT CGACCGGT	CG GGCCCTC	
			A	C _	
GAM1899	KIAA1607	5'	TTCACATAGCCAGCTCCT	64540	CG TCCG
			AGGAGCTGGC	TGT GGA	
			TCCTCGACCG	ACA CTT	
			AT	_	
GAM1899	KIAA1831	3'	CTCCTCATCGGCCAGCCCCT	64524	A _ TTCC
			AGG GCTGGCCG	TG GGGAG	
			TCC CGACCGGC	AC TCCTC	
			C	T _	
GAM1899	KIAA1870	5'	TCCTACCACCAGCTCCT	50588	CC GTTCC
			AGGAGCTGG	GT GGGA	
			TCCTCGACC	CA TCCT	
			AC	_	
GAM1899	KIAA1908	5'	CTCCCAGAGTGGCCCCAGCTCC	73786	_ TG C
			GGAGCT GGCCG	TTC GGGAG	
			CCTCGA	CCGGT GAG CCCTC	
			CC	_ A	
GAM1899	KIAA1981	3'	CCCGGAGGCCAGCTCC	89711	GTGT
			GGAGCTGGCC	TCCGGG	
			CCTCGACCGG	AGGCC	
			_		
GAM1899	MGC2555	5'	CTCCCGCAGTCCAGCCGGCTCC	52290	CGTGTTT
		T	AGGAGCTGGC	CGGGAG	
			TCCTCGGCCG	GCCCTC	
			ACCTGAC		
GAM1899	MGC5508	3'	GGAACACAGGCAGCTCCTT	44268	G _
			AAGGAGCTG	CC GTGTTCC	
			TTCTCGAC	GG CACAAGG	
			_ A		
GAM1899	NCOR1	5'	CTCCCACGCTTAGCCAGCTCC	21956	C_ TCC
			GGAGCTGGC	GTGT GGGAG	

			CCTCGACCG CGCA CCCTC		
			ATT ____		
GAM1899 RBMS1	5'	CCCTGCACGGCAGCTCC	34182	G	TCC
		GGAGCTG CCGTGT GGG			
		CCTCGAC GGCACG CCC			
		__ T__			
GAM1899 SCGN	3'	CTCCCAAAGACTCAGCTCC	23776	CC G CC	
		GGAGCTGG GT TT GGGAG			
		CCTCGACT CA AA CCCTC			
		__ G A__			
GAM1899 SCYA14	5'	CTCCCACCAGGCCAGCTCTCC	16050	A	G TTCC
		A GGAGCTGGCC TG GGGAG			
		C TCTCGACCGG AC CCCTC			
		C __ CA__			
GAM1899 SIPL	3'	TCCCGAAATGCAGTTCCTT	37390	GC	GTTC
		AAGGAGCTG CGT CGGGA			
		TTCCTTGAC GTA GCCCT			
		__ AA__			
GAM1899 SSI-1	5'	CCCGGACGCTATGGCCACCCC	14983	AGCT	--
T		AGG GGCCGT GT TCCGGG			
		TCC CCGGTA CG AGGCC			
		CCAC T C			
GAM1899 TRAF3	3'	CCTGGGACAGCCAGCTGCCT	13849	_	CG
		AGG AGCTGGC TGTTCCGGG			
		TCC TCGACCG ACAGGGTCC			
		G __			
GAM1899 LOC112616	3'	CTCCCAGGAAGCCAGCTCC	57295	CGTG	_
		GGAGCTGGC TTCC GGGAG			
		CCTCGACCG AAGG CCCTC			
		__ A			
GAM1899 LOC116411	5'	CCCCACCCGGCCAGCCGCC	74297	A_	T TCC
		GG GCTGGCCG GT GGG			
		CC CGACCGGC CA CCC			
		GC C C__			
GAM1899 LOC116411	5'	CCCGCCCGGCCAGCCGCC	74298	A_	T TTC
		GG GCTGGCCG G CGGG			
		CC CGACCGGC C GCCC			
		GC C __			
GAM1899 LOC158435	3'	CCCATCAATACAACCAGCTCCT	57500	CC	CC_
		AGGAGCTGG GTGTT GGG			

	TCCTCGACC CATAA CCC		
	AA CTA		
GAM1899 LOC201868 3'	CCCAGAAGGAATGCAGCTCCT 90520	GGCC	_____
	AGGAGCT GTGTTCC GGG		
	TCCTCGA CGTAAGG CCC		
	_____ AAGA		
GAM1899 LOC219997 3'	CCCAGGGGCTGAGGCCAGCTCC 93254	GT_ _	
	GGAGCTGGCC GTTCC GGG		
	CCTCGACCGG CGGGG CCC		
	AGT A		
GAM1899 LOC221751 5'	CTCCACGTCCAGCTCCT 93677	C TTCC	
	AGGAGCTGG CGTG GGG		
	TCCTCGACC GCAC CTC		
	T _____		
GAM1899 LOC255313 5'	CCCTCAGCGGCCAGCTCCT 97940	GTTCC	
	AGGAGCTGGCCGT GGG		
	TCCTCGACCGGCG CCC		
	ACT_____		
GAM1899 LOC255565 3'	TCCCTCACCCAGCTCCT 96804	CC TTCC	
	AGGAGCTGG GTG GGGA		
	TCCTCGACC CAC CCCT		
	_____ T_____		
GAM1899 LOC256032 5'	CTCCCAAAGCCTGGGATCCAG 99358	A _____ T CC_	
CCCC	GG GCTGG CCG GTT GGGAG		
	CC CGACC GGT CGA CCCTC		
	C TAG C AAA		
GAM1899 LOC257426 3'	CTCCCATTTGCGCCGCCAGTCC 67218	AG _ TTCC	
CT	AGG CTGGCCG TG GGGAG		
	TCC GACCGGC GC CCCTC		
	CT C TTTA		
GAM1899 LOC56930 5'	CTCCCGCGGAGCCAGCCC 62743	A CGTG _	
	GG GCTGGC TTC CGGGAG		
	CC CGACCG AGG GCCCTC		
	_____ C		
GAM1899 LOC90550 3'	CCCCAGTCGTCAGCTCCTT 73480	CG GTTCC	
	AAGGAGCTGGC T GGG		
	TTCTCGACTG G CCC		
	CT AC_____		
GAM1899 LOC91450 3'	CTCCCTGGGCAGCAGCCCC 66655	A G CG C	
	GG GCTG C TGTTT GGGAG		

CC CGAC G ACGGG CCCTC
 C _ _ T
 GAM1899 LOC95633 3' CTCCCGCCCCAGCCACCTCC 60558 C CG TTC
 GGAG TGGC TG CGGGAG
 ||| ||| || |||||
 CCTC ACCG AC GCCCTC
 C _ CCC
 GAM1900 FLJ12787 3' ACTATTCTTCATATGTTTCAA 50687 C TCCA
 TTGAAGCATA TGG AATAGT
 ||||| ||| |||||
 AACTTTGTAT ACT TTATCA
 _ TC_
 GAM1900 FLJ13231 3' ACTAAGAACCAGTATCCTTCAA 43813 C CCAAA
 TTGAAG ATACTGGT TAGT
 ||||| ||||| |||
 AACTTC TATGACCA ATCA
 C AGA_
 GAM1900 MGC4655 3' ACTATTAATTTCCCATATGCT 53959 C TCCA_
 TCAA TTGAAGCATA TGG AATAGT
 ||||| ||| |||||
 AACTTCGTAT ACC TTATCA
 _ CCTTTAA
 GAM1900 LOC221337 3' TTGGACCAGCATTCTCAA 93740 AGC A
 TTGA ATCTGGTCCAA
 ||| || |||||
 AACT TA GACCAGGTT
 CCT C
 GAM1901 SCAMP1 3' GCTAAATAAATATTCTCC 54500 T C
 GGA AATATT ATTTAGC
 || ||||| |||||
 CCT TTATAA TAAATCG
 C A
 GAM1901 SCAMP1 3' GCTAAATAAATATTCTCC 54501 T C
 GGA AATATT ATTTAGC
 || ||||| |||||
 CCT TTATAA TAAATCG
 C A
 GAM1901 NX-17 3' TGAATATCAGCCCCTAATA 40706 ATA_
 TATTAGGG ATATTCA
 ||||| |||||
 ATAATCCC TATAAGT
 CGAC
 GAM1901 LOC161589 3' GCTAAATGAATATTATCCCTAA 83159
 TA TATTAGGGATAATATTCATTTAGC
 |||||
 ATAATCCCTATTATAAGTAAATCG
 GAM1902 ADORA1 3' GGTGGTAGCTCTGAGCCCT 7272 A T_ TG
 AG GCTCA GT TGCCACC
 || |||| || |||||

			TC CGAGT CG ATGGTGG		
			C CT _		
GAM1902	BCL10	5'	GGCGGCGCAGCCCGAGCTC 15371	AT	A
			GAGCTC GTTGTGCC CC		
			CTCGAG CGACGCGG GG		
			CC C		
GAM1902	CSNK1D	3'	GTGGTGGCCGCCCTGTACTC 58170	CT TGT T	
			GAG CA TG GCCACCAC		
			CTC GT GC CGGTGGTG		
			AT CCC _		
GAM1902	CSNK1D	3'	GTGGTGGCCGCCCTGTACTC 58171	CT TGT T	
			GAG CA TG GCCACCAC		
			CTC GT GC CGGTGGTG		
			AT CCC _		
GAM1902	CSNK1G3	3'	GGTGGTAAATGAATCTT 16511	GC GTTG	
			AAGA TCAT TGCCACC		
			TTCT AGTA ATGGTGG		
			A_ AA_		
GAM1902	DIAPH2	3'	GTGGTGCAAACATAGCTC 24593	C _TG	
			GAGCT ATGTT G CCAC		
			CTCGA TACAA C GGTG		
			_ A GT		
GAM1902	EIF2C1	3'	GGCAATGACAAGAAATGAGTTC 25197	_____ TG _	
	TT		AAGAGCTCA TGT T GCC		
			TTCTTGAGT ACA A CGG		
			AAAGA GT A		
GAM1902	EIF4G2	5'	GGTGGCAGCTGCTGAGTTCT 9220	T T_	
			AGAGCTCA GT G TGCCACC		
			TCTTGAGT CG C ACGGTGG		
			_ T G		
GAM1902	EYA1	3'	TGAAACAAAATGAGCTCT 6698	G GC	
			AGAGCTCAT TTGT CA		
			TCTCGAGTA AACA GT		
			A AA		
GAM1902	FBXL7	5'	GGGGCGGCGCGGTGAGCCTCT 25497	_ GT A A	
			AGAG CTCAT TGTGCC CC CC		
			TCTC GAGTG GCGCGG GG GG		
			C _ C C		
GAM1902	FSHPRH1	5'	GTGGCGCAATCACGGCTCT 23070	CAT	
			AGAGCT GTTGTGCCAC		

TCTCGG TAACGCGGTG
 CAC
 GAM1902 HIP1 3' GGTGGTAGCCATCAAGCACTT 19261 A CA T T C
 AAG GCT TG TG GC ACCACC
 ||| ||| || ||| |||||
 TTC CGA AC AC CG TGGTGG
 A _ T _ A
 GAM1902 HMG20A 3' GCAGCAACATGTATATGAGCTT 37068 A _ _
 CC A GAGCTCA TGTG TGC
 | ||||| ||||| |||
 C TTCGAGT ACAAC ACG
 C ATATGT G
 GAM1902 IDS 3' TGGCAAATGTGATGTGCTC 5778 _ G
 GAGC TCATGTT TGCCA
 ||| ||||| |||||
 CTCG AGTGTAACGCGT
 TGT _
 GAM1902 KRTHA5 5' GTGGTGGAGATGAGTCTT 11243 G G TGTG
 AAGA CTCAT T CCACCAC
 ||| ||||| | |||||
 TTCT GAGTA A GGTGGTG
 _ G _
 GAM1902 MYOG 5' GGTGGCAGGAACAAGCCTT 60069 A CATG G
 AAG GCT TT TGCCACC
 ||| ||| || |||||
 TTC CGA AG ACGGTGG
 _ ACA_ G
 GAM1902 NOX3 3' GGCCTGTTGATATGAGCTC 32314 T _
 GAGCTCATGTTG GCC
 ||||| ||||| |||
 CTCGAGTATAGT CGG
 TGTC
 GAM1902 PRPSAP2 5' GTAAAACATTGAGCTCTT 12407 _ G
 AAGAGCTCA TGTT TGC
 ||||| ||||| |||
 TTCTCGAGT ACAA ATG
 T A
 GAM1902 PTGFRN 3' GGTGATGGCATGCGGAGTTCTT 67772 A T C
 AAGAGCTC TGT GTGCCA CACC
 ||||| ||| ||||| |||||
 TTCTTGAG GCG TACGGT GTGG
 _ _ A
 GAM1902 RHCG 3' GGTGGGTGAACCTGAGCTCT 33331 T GTG
 AGAGCTCA GTT CCACC
 ||||| ||| |||||
 TCTCGAGT CAA GGTGG
 C GTG
 GAM1902 RP2 3' GGTGATAACTTTTATTAGCTCT 23604 C TT_ GC_
 T AAGAGCT ATG GT CACC
 ||||| ||| || |||||

		TTCTCGA TAT CA GTGG		
		T TTT ATA		
GAM1902 SAR1	3'	GTGGTGACATGTGCTCTT 39733	T	GT
		AAGAGC CATGTT GCCAC		
		TTCTCG GTACAG TGGTG		
		T _		
GAM1902 CHST8	5'	GGCGACGAGCAGATGAGTTC 42694	_ _ _	
		GAGCTCA TGTT GT GCC		
		CTTGAGT ACGA CA CGG		
		AG G G		
GAM1902 CLDN1	3'	GTGATGCCCTCAGAGCTCTT 41188	A TT_ GC	
		AAGAGCTC TG GT CAC		
		TTCTCGAG AC CG GTG		
		_ TCC TA		
GAM1902 CRELD1	3'	GGTGGATACCATGAGCTCTT 31954	T G	
		AAGAGCTCATG TGT CCACC		
		TTCTCGAGTAC ATA GGTGG		
		C _		
GAM1902 DCTD	3'	GGTGGTGGCACATTATCCCTC 10393	CTC T	
		GAG ATG TGTGCCACCACC		
		CTC TAT ACACGGTGGTGG		
		CC_ T		
GAM1902 FLJ10458	3'	GGCAGCAGTATGAGCTCT 36603	_	
		AGAGCTCATGTTG TGCC		
		TCTCGAGTATGAC ACGG		
		G		
GAM1902 FLJ10490	5'	GGCAGTGGCGCGCACTAGCCCT 36668	A CA T CA	
		AG GCT TGT GTGCCAC CC		
		TC CGA ACG CGCGGTG GG		
		C TC _ AC		
GAM1902 FLJ10535	3'	GGTAGCAGCCGGTGTGACTC 36753	C TG _ C	
		GAG TCA TTG TGC ACC		
		CTC AGT GGC ACG TGG		
		_ GT CG A		
GAM1902 FLJ10718	3'	GGTGGTGAACTACAACTCT 37031	CTCA T GC	
		AGAG TGT GT CACCACC		
		TCTC ACA CA GTGGTGG		
		A_ T AA		
GAM1902 FLJ11726	3'	GGTAGTGGCACATGGGCACTT 47026	A TGT C	
		AAG GCTCA TGTGCCAC ACC		

TTC CGGGT ACACGGTG TGG
 A _ A
 GAM1902 FLJ13848 3' GGCAGTGACTTGAGCTTTT 45826 T _
 AAGAGCTCA GTTG TGCC
 ||||| ||| |||
 TTTTCGAGT CAGT ACGG
 T G
 GAM1902 FLJ14393 5' GTGGTGGCAGAACTGCCT 52307 A TCAT G
 AG GC GTT TGCCACCAC
 || || || |||||
 TC CG CAA ACGGTGGTG
 _ T _ G
 GAM1902 FLJ20156 5' GTGGTGACGCACTGGGCTCT 35149 T T C
 AGAGCTCA GT GTG CACCAC
 ||||| || ||| |||||
 TCTCGGGT CA CGC GTGGTG
 _ _ A
 GAM1902 FLJ20373 3' GGTGGCAAGTACACAGCCCTT 35541 A CA TG_
 AAG GCT TGT TGCCACC
 ||| ||| ||| |||||
 TTC CGA ACA ACGGTGG
 C C_ TGA
 GAM1902 FLJ22059 5' GGCAGCCACACAGGAGCTCTT 43056 A _ _
 AAGAGCTC TGT TG TGCC
 ||||| ||| || |||
 TTCTCGAG ACA AC ACGG
 G C CG
 GAM1902 KIAA0090 3' GTGGCACAGTCATAGCTC 89819 C _
 GAGCT ATG TTGTGCCAC
 |||| ||| |||||
 CTCGA TAC GACACGGTG
 _ T
 GAM1902 KIAA1247 3' GTGGTGGTGTCAATAAACGCTC 62509 TCA _
 GAGC TGTTG TGCCACCAC
 ||| |||| |||||
 CTCG ATAAC GTGGTGGTG
 CAA T
 GAM1902 KIAA1582 5' GGTGGTGAACACATGAACTC 65992 C T GC
 GAG TCATGT GT CACCACC
 || ||||| || |||||
 CTC AGTACA CA GTGGTGG
 A _ A_
 GAM1902 MAPK8IP3 3' GGTGGCGGCACAGCCAGCCCTT 54144 A CAT A
 AAG GCT GTTGTGCC CCACC
 ||| ||| ||||| |||||
 TTC CGA CGACACGG GGTGG
 C C_ C
 GAM1902 MGC15429 3' GGTAATCCATTACATGAGCTT 52213 T CC_
 GAGCTCATGT GTG ACC
 ||||| ||| |||

TTCGAGTACA TAC TGG
 T CTA
 GAM1902 NAPG 5' GTGGCACAATCACGGCTC 15146 CAT
 GAGCT GTTGTGCCAC
 |||| |||||
 CTCGG TAACACGGTG
 CAC
 GAM1902 PAFAH2 3' GTGGCAGACAGCATGGCTCT 6507 T _
 AGAGC CATGTTGT GCCAC
 |||| ||||| ||||
 TCTCG GTACGACA CGGTG
 _ GA
 GAM1902 PBX4 3' GGTGGTGGTGCCCATGAGC 48256 TT TG
 GCTCATG G CCACCACC
 ||||| | |||||
 CGAGTAC C GGTGGTGG
 C_ GT
 GAM1902 PRDM8 5' GGCGGCAACACCAACACCTCTT 39975 CTCA _ A
 AAGAG TGTTG TGCC CC
 |||| |||| ||||
 TTCTC ACAAC ACGG GG
 C_ CACA C
 GAM1902 PRO2405 5' GGTGGTGGCCAGTGTCAAGCGC 38419 A C_ TG T
 TT AAG GCT A TTG GCCACCACC
 |||| | |||||
 TTC CGA T GAC CGGTGGTGG
 G AC GT _
 GAM1902 RNPC1 3' GGCGACAGCCCGGCTGAGCTTT 34410 T_ _
 AGAGCTCA GTTGT GCC
 ||||| |||||
 TTTTCGAGT CGACA CGG
 CGGCC G
 GAM1902 RPH3A 5' GGCAGTGGCACCTCCGCTGAGC 30934 T T_ CA
 TTTT AAGAGCTCA GT GTGCCAC CC
 ||||| || ||||| ||
 TTTTCGAGT CG CACGGTG GG
 _ CCTC AC
 GAM1902 SDCCAG43 3' GTGGGCACAACACAGCCCTT 70895 A CA AC
 AAG GCT TGTTGTGCC CAC
 |||| ||||| ||||
 TTC CGA ACAACACGG GTG
 C C_ _
 GAM1902 SYT12 3' GGTGACAGCATGGACCCTC 96385 C_ GC
 GAG TCATGTTGT CACC
 || ||||| ||||
 CTC GGTACGACA GTGG
 CCA _
 GAM1902 USP15 3' GGTAATTTGGCAACTTGAGCTC 21964 T TG CC_
 T AGAGCTCA GT TGCCA ACC
 ||||| || |||| ||

	TCTCGAGT CA ACGGT TGG		
	T _ TTA		
GAM1902 LOC146062 5'	GTGGTGACGGGTGAGCTC 78143	G GC	
	GAGCTCAT TTGT CACCAC		
	CTCGAGTG GGCA GTGGTG		
	- -		
GAM1902 LOC147042 3'	GTAGCAAAGAGATGAGCTC 84996	G G_ C	
	GAGCTCAT TT TGC AC		
	CTCGAGTA AG ACG TG		
	G AA A		
GAM1902 LOC148166 5'	TGGCGGCACAACATTGTAGT 79426	_ _ A	
	GCT CA TGTTGTGCC CCA		
	TGA GT ACAACACGG GGT		
	T T C		
GAM1902 LOC150587 3'	GGTGGCGCGATCATGGCTC 86245	T _	
	GAGC CATG TTGTGCCACC		
	CTCG GTAC AGCGCGGTGG		
	- T		
GAM1902 LOC150630 5'	GGCAATAGTATGTATGAGTTCT 86303	_____	
T	AAGAGCTCATG TTGT GCC		
	TTCTTGAGTAT GATA CGG		
	GTAT A		
GAM1902 LOC154881 3'	GGCAGCAAGCTGAGAGCTCTT 82073	AT_ _	
	AAGAGCTC GTT G TGCC		
	TTCTCGAG CGA C ACGG		
	AGT A G		
GAM1902 LOC155060 3'	GTGGTGGCAGGAGGCCTT 87606	A CATG G	
	AAG GCT TT TGCCACCAC		
	TTC CGG AG ACGGTGGTG		
	- _ G		
GAM1902 LOC155435 3'	GTGGTGA CTTTGGTAGCCCTT 82272	A CA TT GC	
	AAG GCT TG GT CACCAC		
	TTC CGA GT CA GTGGTG		
	C TG TT _		
GAM1902 LOC157584 3'	CCGGCAATAGCACAGCCATCCA 82403	AT_____	CA_____ ACC_____
GGAGCTCTT	AAGAGCTC GTTGTGC	CC G	
	TTCTCGAG CGACACG GG C		
	GACCTAC ATAAC _CC		
GAM1902 LOC157586 3'	CCGGCAATAGCACAGCCATCCA 82398	AT_____	CA_____ ACC_____
GGAGCTCTT	AAGAGCTC GTTGTGC	CC G	

		TTCTCGAG	CGACACG	GG	C	
		GACCTAC	ATAAC	__	CC	
GAM1902	LOC157858	5'	GCTACAACATGGGCCCTT	87891	A	—
			AAG GCTCATGTTGT	GC		
			TTC CGGGTACAACA	CG		
			C	T		
GAM1902	LOC197125	3'	GGCAGGTAACATTGAGCTCTT	89243		— —
			AAGAGCTCA TGTTG	TGCC		
			TTCTCGAGT ACAAT	ACGG		
			T	GG		
GAM1902	LOC202739	5'	GGTAGCAGCACAGCATCTC	91961	CTC	C__
			GAG ATGTTGTGC	ACC		
			CTC TACGACACG	TGG		
			—	ACGA		
GAM1902	LOC203080	5'	GTAGTGGCATGAGATCTT	90773	G	TGTTG C
			AAGA CTCA	TGCCAC AC		
			TTCT GAGT	ACGGTG TG		
			A	— A		
GAM1902	LOC203504	5'	GTGAAGTGGCACAAACCTC	92326	CTCATG	—
			GAG	TTGTGCCAC CAC		
			CTC AACACGGTG	GTG		
			CA	— AA		
GAM1902	LOC205795	5'	GTGGTGGCATGCAGAGCTCTT	92398	A	T
			AAGAGCTC TGT	GTGCCACCAC		
			TTCTCGAG ACG	TACGGTGGTG		
			— —			
GAM1902	LOC221715	3'	GGTAGCAAAGCATGAGCTT	95394	G	C
			GAGCTCATGTT	TGC ACC		
			TTCGAGTACGA	ACG TGG		
			A	A		
GAM1902	LOC255316	3'	GGTGGCACAACATCACAGC	99096	C	—
			GCT ATGTTGTGCCACC			
			CGA TACAACACGGTGG			
			CAC			
GAM1902	LOC255497	3'	GGCATTTCACAACATGACTCT	98987	C	—
			AGAG TCATGTTGT	GCC		
			TCTC AGTACAACA	CGG		
			—	CTTTA		
GAM1902	LOC256861	3'	GTGGTGAGAACATGAGCTCT	98601		GTGC
			AGAGCTCATGTT	CACCAC		

TCTCGAGTACAA GTGGTG
 GA__
 GAM1902 LOC256950 3' TGGCAGTTCTATGGGCTC 97160 TT_
 GAGCTCATG G TGCCA
 ||||| | ||||
 CTCGGGTAT T ACGGT
 CT G
 GAM1902 LOC83693 3' GGTGACTTAACATGGACTCTT 49605 CT TGC
 AAGAG CATGTTG CACC
 |||| ||||| |||
 TTCTC GTACAAT GTGG
 AG TCA
 GAM1902 LOC91574 5' GTGAGTAAACATGAGCCTCT 67115 _ G _
 AGAG CTCATGTT TGC CAC
 ||| ||||| ||| |||
 TCTC GAGTACAA ATG GTG
 C _ A
 GAM1902 LOC92710 3' TGGCACGGGCAGCGGGCTCTT 70872 A_ _
 AAGAGCTC TGTT GTGCCA
 ||||| ||| |||||
 TTCTCGGG ACGG CACGGT
 CG G
 GAM1903 CBFB 3' GATGGTACATTTTCCTCTA 43441 A C GAT
 TAGA GA AATG TACCATC
 ||| || ||| |||||
 ATCT CT TTAC ATGGTAG
 C T _
 GAM1903 CBFB 3' GATGGTACATTTTCCTCTA 43442 A C GAT
 TAGA GA AATG TACCATC
 ||| || ||| |||||
 ATCT CT TTAC ATGGTAG
 C T _
 GAM1903 DAF 3' GATGCTTTCATTGTCTTT 6954 TTAC
 GAAGACAATGGA CATC
 ||||| |||
 TTTCTGTTACTT GTAG
 TC_
 GAM1903 FCMD 3' ATGATAACCAACAGTCTTCTG 23026 AA_ A C
 TAGAAGAC TGG TTA CAT
 ||||| ||| ||| |||
 GTCTTCTG ACC AAT GTA
 ACA _ A
 GAM1903 ITPR2 3' GATGGTGGCATTGCCTTTTA 11081 A GA
 TAGAAG CAATG TTACCATC
 |||| |||| |||||
 ATTTTC GTTAC GGTGGTAG
 C _
 GAM1903 MOG 3' ATGGTGGTTGTTTCTTC 11667 C G
 GAAGA AATG ATTACCAT
 |||| ||| |||||

CTTCT TTGT TGGTGGTA

GAM1903 NCALD 3' ATGGTGATGCCGTCCTG 50192 AA AAT _
TAG GAC GG ATTACCAT
||| ||| || |||||
GTC CTG CC TAGTGGTA
CC _ G

GAM1903 PPP1R12B 3' GATGGTAATTATAGGCCTTCTA 50357 ACAATG
TAGAAG GATTACCATC
||||| |||||
ATCTTC TTAATGGTAG
CGGATA

GAM1903 BCMP1 3' ATGGTAATAAGTTGTTCCTA 49534 AA GG
TAG GACAAT ATTACCAT
||| ||||| |||||
ATC TTGTTG TAATGGTA
CC AA

GAM1903 BNIP-S 5' GGTAATCTGCTTCTA 57106 A ATG
TAGAAG CA GATTACC
||||| || |||||
ATCTTC GT CTAATGG

GAM1903 CED-6 3' ATGGTAATCAACTCTGCTA 33317 A CAATG
TAG AGA GATTACCAT
||| ||| |||||
ATC TCT CTAATGGTA
G CAA_

GAM1903 CHCR 3' GATGGTTGTAGTTGTCTTT 37825 GG T
GAAGACAAT AT ACCATC
||||||| || |||||
TTTCTGTTG TG TGGTAG
A_ T

GAM1903 CXorf1 3' ATGGTAATTCCCTTCTA 17485 ACAAT
TAGAAG GGATTACCAT
||||| |||||
ATCTTC CTTAATGGTA
C_

GAM1903 FLJ12806 3' GATGGGTTTACAATGTCTTCTA 43391 A GATTA
TAGAAGACA TG CCATC
||||||| || |||||
ATCTTCTGT AC GGTAG
A ATTTG

GAM1903 FLJ20533 3' ATGGTAAGTAGTGTCTTC 35802 GA_
GAAGACAATG TTACCAT
||||||| |||||
CTTCTGTTGT AATGGTA
GATG

GAM1903 GOLGA1 3' GATGCAGACCACCTGTCTTCTA 10849 A_ A AC
TAGAAGACA TGG TT CATC
||||||| ||| || |||||

		ATCTTCTGT ACC AG GTAG		
		CC _ AC		
GAM1903 HCC-4	3'	ATGGTAAATTAAGTTGTCTTC 57597	GGA__	
		GAAGACAAT TTACCAT		
		CTTCTGTTG AATGGTA		
		AATTA		
GAM1903 HHLA2	3'	ATGATAATCCATCACCTTC 23952	ACA_ C	
		GAAG ATGGATTA CAT		
		CTTC TACCTAAT GTA		
		CCAC A		
GAM1903 KIAA0562	3'	GATGTTGGCCATTATTTTCTA 28823	C A C	
		TAGAAGA AATGG TTA CATC		
		ATCTTTT TTACC GGT GTAG		
		A _ T		
GAM1903 KIAA1641	3'	GATGATATGTCATTGTCTCCTA 81019	A AT C	
		TAG AGACAATGG TA CATC		
		ATC TCTGTTACT AT GTAG		
		C GT A		
GAM1903 KIAA1674	3'	GATGGGCTCCACTGTCTTCTG 69343	A TTA	
		TAGAAGACA TGGA CCATC		
		GTCTTCTGT ACCT GGTAG		
		C CG_		
GAM1903 MESDC2	3'	GATGACATTCTAGTGTCTTCTA 72915	A TTAC	
		TAGAAGACA TGGA CATC		
		ATCTTCTGT ATCT GTAG		
		G TACA		
GAM1903 MGC14844	3'	GATAGTAACCTCAGTCTTTTA 51341	AAT A C	
		TAGAAGAC GG TTAC ATC		
		ATTTTCTG CC AATG TAG		
		ACT _ A		
GAM1903 MGC32043	3'	GATGGTACTTGCTGTCTTCTG 58666	ATG T	
		TAGAAGACA GA TACCATC		
		GTCTTCTGT TT ATGGTAG		
		CG_ C		
GAM1903 LOC124460	3'	ATGGTTTCATTGTATTCTA 76556	G TT	
		TAGAA ACAATGGA ACCAT		
		ATCTT TGTTACTT TGGTA		
		A _		
GAM1903 LOC144147	5'	ATGATACTTTATTGTCTTC 72195	T C	
		GAAGACAATGGA TA CAT		

CTTCTGTTATTT AT GTA
 C A
 GAM1903 LOC145783 3' GATGGTGGGTAGCCATCTTC 77948 CAA AT____
 GAAGA TGG TACCATC
 ||||| ||| |||||
 CTTCT ACC GTGGTAG
 ____ GATGG
 GAM1903 LOC147622 5' GATGGTAAACCATCCTCT 85169 CA A
 AGA ATGG TTACCATC
 ||| ||||| |||||
 TCT TACC AATGGTAG
 CC A
 GAM1903 LOC199899 3' GATGAAAAGTCCATTGTCT 91468 AC_
 AGACAATGGATT CATC
 ||||| ||||| |||||
 TCTGTTACCTGA GTAG
 AAA
 GAM1903 LOC91750 3' GATGGTGGGATTGTCCCCT 67654 AA GGA
 AG GACAAT TTACCATC
 || ||||| |||||
 TC CTGTTA GGTGGTAG
 CC G_
 GAM1903 LOC93333 5' GTGGGTTTCATTACCTTCTA 72530 AC TA
 TAGAAG AATGGAT CCAT
 ||||| ||||| |||||
 ATCTTC TTA CTTG GGTG
 CA _
 GAM1904 ABH 3' ATGGTAAATTGTGGTTCTGTG 60460 G GTCC_
 AA TTCACAGGAT GCAA CCGT
 ||||| ||||| |||||
 AAGTGTCTTG TGTT GGTA
 G AAAAT
 GAM1904 ADCY7 3' GGGGATAGAGTCCTGAGGA 8491 A GGCAA
 TTC CAGGAT GTCCCC
 ||| ||||| |||||
 AGG GTCCTG TAGGGG
 A AGA_
 GAM1904 ADORA1 3' GTGGGGGAAGGCCTTGCTGTCA 7273 G ____ GT
 TGTGAA TTCACA GATGGCAAG TCCCC
 ||||| ||||| |||||
 AAGTGT CTGTCGTT AGGGG
 A CGGA GTG
 GAM1904 APLP2 3' ACGGGGAGGTTTGTGTGTGA 92541 G TG _
 A TTCACA GA GCAAG TCCCCGT
 ||||| || ||||| |||||
 AAGTGT TT TGTTT AGGGGCA
 G _ GG
 GAM1904 ATP10C 3' GGCATGTCATCTTCTGAG 44669 C A
 TTCA AGGATGGCA GTC
 ||||| ||||| |||||

			GAGT TTCTACTGT CGG		
			C A		
GAM1904	ATP1B2	3'	ATGGGGGGTTTCTCCTTGT 9827	AT C GT	
			ACAGG GG AA CCCCCT		
			TGTTC TC TT GGGGTA		
			C _ _ TG		
GAM1904	ATP7A	3'	GGTGTGTCATTTGTGAA 5328	G AGT	
			TTCACAG ATGGCA CC		
			AAGTGTT TACTGT GG		
			_ GT _		
GAM1904	BACH2	3'	GATGCTGCCATTTTGTGAA 41784	A _	
			TTCACAGGATGGCA GTC		
			AAGTGTTTTACCGT TAG		
			CG		
GAM1904	BCKDHA	3'	GGCAGGTCAGCCTGTGGA 62942	A AA	
			TTCACAGG TGGC GTC		
			AGGTGTCC ACTG CGG		
			G GA		
GAM1904	BCL7A	3'	ATGGGTTTTTGTGTTTTTGG 40978	C TG TC	
			TCA AGGA GCAAG CCCGT		
			GGT TTTT TGTTT GGGTA		
			_ GT T _		
GAM1904	C1orf1	5'	ACGGGCTTATAATTGCCATTT 8676	G C _____	
			GTGAA TTCACAG ATGGCAAGT CCCGT		
			AAGTGTT TACCGTTTA GGGCA		
			_ ATATTC		
GAM1904	CAPS	3'	GGAGGCCATCCTGGAA 15767	A AAG	
			TTC CAGGATGGC TCC		
			AAG GTCCTACCG AGG		
			_ G _		
GAM1904	CDH13	3'	GATTTGTATTCTGTGAG 8835	G	
			TTCACAGGATG CAAGTC		
			GAGTGTCTTAT GTTTAG		
			_		
GAM1904	CHRNE	3'	GGCTGCCAGCTTGTGAG 5379	A A	
			TTCACAGG TGGCA GTC		
			GAGTGTTT ACCGT CGG		
			G _		
GAM1904	CLCN7	3'	GGAATTGCTGCCCTGTGGA 8911	AT G	
			TTCACAGG GGCAA TCC		

			AGGTGTCC TCGTT AGG		
			CG A		
GAM1904 CPNE7	3'	GCGGGGTCTGCCTGGCCTGTGG 27792	AT_ A T		
		TCACAGG GGCA G CCCCCT			
		GGTGTCC CCGT C GGGGCG			
		GGT _ T			
GAM1904 CPT2	3'	GGGTGCTATTCTGTGAA 5428	AGT		
		TTCACAGGATGGCA CCC			
		AAGTGTCTTATCGT GGG			
		—			
GAM1904 CRSP8	3'	GCGGGGTTCTTGTTTTGTGG 81858	G T_		
		TCACAGGATG CAAG CCCCCT			
		GGTGTTTTGT GTTC GGGGCG			
		_ TT			
GAM1904 CSHL1	3'	ATGGTGCAGTGCCGCTCTGTGG 42934	GA AGTCC		
A		TTCACAG TGGCA CCGT			
		AGGTGTC GCCGT GGTA			
		TC GACGT			
GAM1904 CSHL1	3'	ATGGTGCAGTGCCGCTCTGTGG 42935	GA AGTCC		
A		TTCACAG TGGCA CCGT			
		AGGTGTC GCCGT GGTA			
		TC GACGT			
GAM1904 CUL3	3'	GATTGCTGCTATTCTGGAA 14572	A _		
		TTC CAGGATGGCA AGTC			
		AAG GTCTTATCGT TTAG			
		_ CG			
GAM1904 DBN1	5'	GGGGACTCTGACCTGGGG 56020	A A CA		
		TTC CAGG TGG AGTCCCC			
		GGG GTCC GTC TCAGGGG			
		_ A _			
GAM1904 DDX11	3'	GGGTCCTGGCTGTCCTTGG 16580	C A TC GT		
		TCA AGGATGGC AG CCC			
		GGT TCCTGTCTG TC GGG			
		_ G CT T			
GAM1904 DDX11	3'	GGGTCCTGGCTGTCCTTGG 16581	C A TC GT		
		TCA AGGATGGC AG CCC			
		GGT TCCTGTCTG TC GGG			
		_ G CT T			
GAM1904 EMD	3'	ATGGTCCTCTTTGTCAATTTTGT 5487	_ TCC_		
TGA		TCA CAGGATGGCAAG CCGT			

			AGT GTTTTACTGTTT GGTA		
			T CTCCT		
GAM1904	EXTL3	3'	TGGGGAGCTCCTAGTTTGTGG 9338	AT_ CA _	GT
			TCACAGG GG AG TCCCC		
			GGTGTTC CC TC AGGGG		
			GAT _ G TG		
GAM1904	EYA2	3'	TGGGGACAATCATTCTTTGAA 19127	C CAA	GT
			TTCA AGGATGG GTCCCC		
			AAGT TCTTACT CAGGGG		
			T AA_ TG		
GAM1904	FKRP	3'	GCGGGGGCTCACGCCTGT 44436	A GCA	
			ACAGG TG AGTCCCCGT		
			TGTCC GC TCGGGGGCG		
			_ AC_		
GAM1904	FLRT2	3'	ATGGGGAATGCTTGTCACTGTG 25991	GA _	
	GA		TTACAG TGGCAAGT CCCCCGT		
			AGGTGTC ACTGTTCG GGGGTA		
			_ TAA		
GAM1904	FZD4	5'	GCGGCCGCGCGCCGGCTTGTGG 25174	A AA C_	
			TCACAGG TGGC GTC CCGT		
			GGTGTTC GCCG CGG GGCG		
			G _ CC		
GAM1904	FZD7	3'	GGGGGCCTGTTTCTGT 14506	TG A	
			ACAGGA GCA GTCCCC		
			TGTCTT TGT CGGGGG		
			_ C		
GAM1904	GAS7	3'	GCGGGTCTGGGCTATTCTTGAG 20852	C A_ TC	
			TTCA AGGATGGC AG CCCGT		
			GAGT TCTTATCG TC GGGCG		
			_ GG T_		
GAM1904	GCNT3	3'	GCTTTTCCATTCTGTGGA 17643	C_	
			TTACAGGATGG AAGT		
			AGGTGTCTTACC TTCG		
			TT		
GAM1904	GLDC	3'	GGAAGTGCCATCTGTGG 64896	G _	
			TCACAG ATGGCA AGTCC		
			GGTGTC TACCGT TCAGG		
			_ G		
GAM1904	HNMT	3'	GTTACTGATTTGGCCGTTTTGT 23554	_ CCCGT	
	GAA		TTACAGGATGGC AAGTC		

			AAGTGT	TTTTGCCG	TTTAG	
			G	TCATTGT		
GAM1904	HOXD4	5'	ATGGGGG	GCTTGCTTGTATTTG	28254	AT__
			CAGG	GGCAAGTCCCCGT		
			GTTT	TCGTTCGGGGGTA		
			ATGT			
GAM1904	HRAS	5'	ATGGGG	AATTGTGCCTGTTGGA	19272	_ ATGGCA
			TTC	ACAGG AGTCCCCGT		
			AGG	TGTCC TTAGGGGTA		
			T	GTG__		
GAM1904	HTR1D	3'	GGGTCT	CCATTCTGTG	7847	CA T
			CACAGG	ATGG AG CCC		
			GTGTCT	TACC TC GGG		
			__	T		
GAM1904	IL1RAP	3'	ATGAATCT	TGGTATCCTGTGAA	57068	G TCCC
			TTCACAGG	ATG CAAG CGT		
			AAGTGT	CCTAT GTTC GTA		
			G	TAA__		
GAM1904	KIF3B	3'	GGGCCT	GTTTTGTGGA	17808	CAA
			TTCACAGG	ATGG GTCC		
			AGGTGT	TTTGTGTC CGGG		
			__			
GAM1904	KLHL3	3'	GGCCAC	GGCTGCTTGTA	88849	A AA__
			TTCACAGG	TGGC GTC		
			AAGTGT	TGTCG CGG		
			__	GCAC		
GAM1904	KLK3	3'	ATGGGG	TGTCTGTGTTATTTGT	9707	G AGT__
	GG		TCACAG	ATGGCA CCCCCGT		
			GGTGTT	TATTGT GGGGTA		
			__	GTCTGT		
GAM1904	LDB2	3'	ATGGGG	ACTTTTCGTTTTTGG	8916	C C
			TCA	AGGATGG AAGTCCCCGT		
			GGT	TTTTGCT TTCAGGGGTA		
			__	T		
GAM1904	LRP1	3'	GCGGGC	AGCCCCGTTTTGGGGA	11361	A CAAGTC
			TTC	CAGGATGG CCCGT		
			AGG	GTTTTGCC GGGCG		
			G	CCGAC__		
GAM1904	MAGEA9	3'	ATGGGG	GAAATCCCTGTTATTTT	19320	AG__
	GTGAA		TTCACAGG	ATGGCA TCCCCGT		

AAGTGTTTTATTGT AGGGGTA

CCCTAA

GAM1904 MAML1 3' GGGGGTCCTGTATCCTGGAG 29280 A G AGT GT
TTC CAGGATG CA CCCC

||| ||||| || |||

GAG GTCCTAT GT GGGG

_ _ CCT GT

GAM1904 NDST1 5' GCGGGGGTTTGCCATGGTGA 9529 AGG GT
TCAC ATGGCAA CCCCCT

|||| ||||| |||||

AGTG TACCGTT GGGGCG

G_ TG

GAM1904 NFATC3 3' GGGACCCACCATTGTGG 17051 G CAA
TCACAG ATGG GTCCC

||||| ||| |||||

GGTGTT TACC CAGGG

_ ACC

GAM1904 NOVA1 3' ATTTGCATGTTTTGTGGA 22419 _
TTCACAGGATG GCAAGT

||||||| |||||

AGGTGTTTTGT CGTTTA

A

GAM1904 NSD1 3' TGGGGGCTTATGGTTGTGTGAA 42632 G GGC GT
TTCACA GAT AAGTCCCC

||||| ||| |||||

AAGTGT TTG TTCGGGGG

G GTA TG

GAM1904 NUP98 5' GTGGGGGCGCGCGCTGCTCTG 33328 GA AA_ GT
TGAG TTCACAG TGGC GTCCCC

||||| ||| |||||

GAGTGTC GTCG CGGGGG

TC CGCGC TG

GAM1904 OLIG2 3' TGGGGATTCCAGCATCTGCGAA 20550 A A_ CA GT
TTC CAGG TGG AGTCCCC

||| ||| ||| |||||

AAG GTCT ACC TTAGGGG

C ACG _ TG

GAM1904 PAIP2 5' GCGGGGGAGCGGCGCTGCCTGT 33644 ATG_ AAG_
GGA TTCACAGG GC TCCCCGT

||||| || |||||

AGGTGTCC CG GGGGGCG

GTCG GCGA

GAM1904 PCDHB5 5' GGGCTTCGTTCTTGTGGA 32245 TG _
TTCACAGGA GC AAGTCC

||||||| || |||||

AGGTGTTCT TG TTCGGG

_ C

GAM1904 PLCG1 3' ATGGATCCTTCCATCTTGTGG 12156 C TCC
TCACAGGATGG AAG CCGT

||||||| ||| |||

			GGTGTCTACC TTC GGTA		
			— CTA		
GAM1904	PMM2	3'	ATGGGGGTTTGGTAATGAGAA 72556	A GGA G GT	
			TTC CA TG CAA CCCCCGT		
			AAG GT AT GTT GGGGTA		
			A A__ G TG		
GAM1904	PPT2	3'	ATGGGGACAGTTCCGTTCTTGA 18946	C CAA_	
	A		TTCA AGGATGG GTCCCCGT		
			AAGT TCTTGCC CAGGGGTA		
			— TTGA		
GAM1904	PXR1	3'	GGTTCTGTCATTCTTGGA 6145	C A TC	
			TTCA AGGATGGCA G CC		
			AGGT TCTTACTGT C GG		
			— — TT		
GAM1904	PXR1	3'	GTGGGACGGGCTGCCCTGTGAG 6146	AT AA CGT	
			TTACACAGG GGC GTCCC		
			GAGTGTCC TCG CAGGG		
			CG GG TG		
GAM1904	RAB27A	3'	ATGCCTGTTTGCTATTTGGTGG 17148	AG TCCC	
	A		TTCAC GATGGCAAG CGT		
			AGGTG TTATCGTTT GTA		
			GT GTCC		
GAM1904	RAB6A	5'	CGGCTGCCAGTCTGTGGA 12715	GA AGTCC	
			TTACAG TGGCA CCG		
			AGGTGTC ACCGT GGC		
			TG C__		
GAM1904	RAD51L1	3'	ATGGGGGTGTGATTTGTGAA 56876	G G AG	
			TTACAG AT GCA TCCCCGT		
			AAGTGTT TA TGT GGGGGTA		
			— G —		
GAM1904	RALBP1	3'	ATGCCTTCTTGCTGTCCTGT 23270	TCCC	
			ACAGGATGGCAAG CGT		
			TGTCCTGTCGTTT GTA		
			TTCC		
GAM1904	RARB	5'	ATGGGGTCAGCGCCTGTGAG 32885	ATG AAGT	
			TTACAGG GC CCCCCGT		
			GAGTGTCC CG GGGGTA		
			G__ ACT_		
GAM1904	RET	3'	GGGGGCAGCTTTTGGGAA 40540	A AT AA	
			TTC CAGG GGC GTCCCC		

AAG GTTT TCG CGGGGG
 G _ A_
 GAM1904 RET 3' GGGGGCAGCTTTTGGGAA 40541 A AT AA
 TTC CAGG GGC GTCCCC
 ||| ||| ||| |||||
 AAG GTTT TCG CGGGGG
 G _ A_
 GAM1904 RET 3' GGGGGCAGCTTTTGGGAA 40542 A AT AA
 TTC CAGG GGC GTCCCC
 ||| ||| ||| |||||
 AAG GTTT TCG CGGGGG
 G _ A_
 GAM1904 RNMT 3' GTGGAAAGTATTGCAATTCTGT 15056 G G____ CCGT
 GAG TTCACAGGAT GCAA TCC
 ||||| ||| |||
 GAGTGTCTTA CGTT AGG
 A ATGAA TG
 GAM1904 SLC6A12 3' ATGGGGACCCCTTCTTG 13189 T CAA
 CAGGA GG GTCCCCGT
 |||| || |||||
 GTTCT CC CAGGGGTA
 T CC_
 GAM1904 SLC6A12 3' GGGGATGCCTCTTGT 13197 T AG
 ACAGGA GGCA TCCCC
 |||| ||| ||||
 TGTCT CCGT AGGGG
 _ _
 GAM1904 SLC6A3 3' TGGGAGCCGTGAGCCTGTGAA 8314 A AA TC GT
 TTCACAGG TGGC G CCC
 ||||| ||| | |||
 AAGTGTCC ACTG C GGG
 G C_GA TG
 GAM1904 SPI1 5' ACGGGCACCCCATCCTGAGG 13350 A CAA C
 TC CAGGATGG GT CCCGT
 || ||||| || |||||
 GG GTCCTACC CA GGGCA
 A C_ C
 GAM1904 TCFL4 3' CGGTGTTTGT TTTGTGAA 64210 TG_ AGTCC
 TTCACAGGA G CA CCG
 ||||| | || |||
 AAGTGT TTT T GT GGC
 GT T _
 GAM1904 TNFRSF11A 3' GACTATCCTGTTCTGTGG 15194 CA_
 TCACAGGATGG AGTC
 ||||| |||
 GGTGTCTTGTC TCAG
 CTA
 GAM1904 UBE2H 3' TGGCCCTATGTCTTCTGTGGA 13956 T _ TC CGT
 TTCACAGGA GGCA AG CC
 ||||| ||| || ||

AGGTGTCTT CTGT TC GG
 _ A CC TG
 GAM1904 UPK1B 3' GGGGGCTCATGCCTGT 23704 _ GCA
 ACAGG ATG AGTCCCC
 ||||| ||| |||||
 TGTCC TAC TCGGGGG
 G _
 GAM1904 WBSCR1 3' GGATATGGTATTTTGTGAA 42483 G A
 TTCACAGGATG CA GTCC
 ||||| ||| |||
 AAGTGTTTTAT GT TAGG
 G A
 GAM1904 WEE1 3' GGGATGATGATTCTGTGGA 14111 GGCAA
 TTCACAGGAT GTCCC
 ||||| |||
 AGGTGTCTTA TAGGG
 GTAG_
 GAM1904 XPC 3' GGGGGCTTCTCTGCTGAG 17332 _ GAT C
 TTCA CAG GG AAGTCCCC
 ||| ||| || |||||
 GAGT GTC TC TTCGGGGG
 C _ _
 GAM1904 ZNF146 3' TGGGAATGCTGTATCTGTGGA 24079 _ AG CGT
 TTCACAGG ATGGCA TCCC
 ||||| ||||| |||
 AGGTGTCT TGTCGT AGGG
 A A_ TA
 GAM1904 ZNF200 3' ATGGGGATTCACTTGAGAA 14366 A _ CAA
 TTC CAGG ATGG GTCCCCGT
 ||| ||| ||| |||||
 AAG GTTC TACT TAGGGGTA
 A A _
 GAM1904 ZNF278 5' GCGGGGGTTGGCTATGTGG 50270 GGA A GT
 TCACA TGGC A CCCC GT
 |||| |||| | |||||
 GGTGT ATCG T GGGGCG
 _ G TG
 GAM1904 ZNF76 3' ATGGGGACTGGCCCTGT 14267 ATG A
 ACAGG GC AGTCCCCGT
 |||| || |||||
 TGTCC CG TCAGGGGTA
 _ G
 GAM1904 AF093680 3' GGGGGTAAGCAGTCCTGTGAG 26019 G AAG GT
 TTCACAGGAT GC TCCC
 ||||| || |||
 GAGTGTCTG CG GGGGG
 A AAT T
 GAM1904 AP3S2 3' GGGCCGCTTCCTGTGGA 20653 T AA
 TTCACAGGA GGC GTCC
 ||||| ||| |||

AGGTGTCCT TCG CGGG
 _ C_
 GAM1904 Apg4B 3' GGCTGGCTGTCCTGGAG 26184 A A
 TTC CAGGATGGC AGTC
 ||| ||||| ||||
 GAG GTCCTGTCG TCGG
 _ G
 GAM1904 C11orf15 5' GCGGGGGGCTCCGGGCTGTGG 40594 GA CA
 TCACAG TGG AGTCCCCGT
 ||||| ||| |||||
 GGTGTC GCC TCGGGGGCG
 GG _
 GAM1904 C11orf9 3' ATGGGGGTTTCATGTTCTTG 26116 TG _GT
 CAGGA GCA A CCCCCGT
 ||||| ||| | |||||
 GTTCT TGT T GGGGTA
 _ AC TG
 GAM1904 C16orf7 3' GGGGGCTTGTCCTACTGTGG 18145 GAT GT
 TCACAG GGCAAGTCCCC
 ||||| |||||
 GGTGTC CTGTTCTGGGGG
 AC_ T
 GAM1904 C1orf34 3' ATGGGGGTTGTAACCCTCTGAG 61299 C ATG G
 TTCA AGG GCAA TCCCCGT
 ||||| ||| ||| |||||
 GAGT TCC TGTT GGGGGTA
 C CAA _
 GAM1904 C20orf177 3' ATGATTACTGCTGTTTGGTGG 62828 AG _ CCGT
 TCAC GATGGCA AGTC
 ||||| ||||| |||||
 GGTG TTGTCGT TTAG
 GT CA TA
 GAM1904 C20orf36 3' GAGTGCTATCTGTGAA 37334 G AG
 TTCACAG ATGGCA TC
 ||||| ||||| ||
 AAGTGTC TATCGT AG
 _ G_
 GAM1904 CASP9 5' GCGGGGGGCGGGTTCCTGGGGA 8774 A GGCAA
 TTC CAGGAT GTCCCCGT
 ||| ||||| |||||
 AGG GTCCTG CGGGGGCG
 G GG_
 GAM1904 CBCIP2 3' GCGGGGATTTGTCAGATG 52660 GGA
 CA TGGCAAGTCCCCGT
 || |||||
 GT ACTGTTTAGGGGCG
 AG_
 GAM1904 CFDP1 5' GCGGCTGCTGCGGTCTTGTGAG 21987 G A CC
 TTCACAGGAT GCA GT CCGT
 ||||| ||| || ||||

			GAGTGTTCCTG CGT CG GGCG			
			G _ TC			
GAM1904	CRMP5	3'	TACTTGTTCATCCTGTGA 39707	_____	CCCCGT	
	A		TTCACAGGATG GCAAGT			
			AAGTGCCTAC TGTTC			
			GTGTT TG			
GAM1904	DAPK2	3'	GGCTGTCTTCTGTGGA 27514	T	A	
			TTCACAGGA GGCA GTC			
			AGGTGTCTT CTGT CGG			
			— —			
GAM1904	DAPK3	3'	GGGGGCGCTTCCTGTGGA 9048	T	AA	
			TTCACAGGA GGC GTCCCC			
			AGGTGTCCT TCG CGGGGG			
			— —			
GAM1904	DCAMKL1	3'	ATGGGGATTACAGGTTCTGTG 17599	GGCA_		
			CACAGGAT AGTCCCCGT			
			GTGTCTTG TTAGGGGTA			
			GACAC			
GAM1904	DDX12	3'	TGGGTCCTGGCTGTCCTTGG 60426	C	A TC GT	
			TCA AGGATGGC AG CCC			
			GGT TCCTGTCTG TC GGG			
			_ G CT TG			
GAM1904	DIM1	3'	ACGAAGGTGTTTATCCTGTGAG 22947	_ AG_	CCCGT	
			TTCACAGGATGG CA TC			
			GAGTGCCTATT GT AG			
			T GGA CA			
GAM1904	dJ309H15.1	3'	GCGGCCTGGCCGTTCTTGG 57570	C	A TCC	
			TCA AGGATGGC AG CCGT			
			GGT TCTTGCCG TC GGCG			
			_ G C_			
GAM1904	DKFZP434C212	3'	GACATACTGTCTTGTGAA 69487	CAA		
			TTCACAGGATGG GTC			
			AAGTGTTCCTGTC CAG			
			ATA			
GAM1904	DKFZP434H132	5'	TCAAGGCTTCCCGTTCTGTGGA 31934	C	CCCGT	
			TTCACAGGATGG AAGTC			
			AGGTGTCTTGCC TTCGG			
			C AACTG			
GAM1904	DKFZp434K1210	3'	ATGGCCACGTTGTCAATTGTGAG 34687	GG	_ CC	
			TTCACA ATGGCAA GT CCGT			

GAGTGT TACTGTT CA GGTA
 — G CC
 GAM1904 DKFZP434P0721 3' GCGGCACCTGCCATCTTCTGAA 64462 C A CC
 TTCA AGGATGGCA GT CCGT
 ||| ||||| || |||
 AAGT TTCTACCGT CA GGCG
 C C C_

GAM1904 DKFZP564D1378 5' GCGGGGGCCCTTTCCTGAGGA 50440 A T CAA
 TTC CAGGA GG GTCCCCGT
 || |||| || |||||
 AGG GTCCT TC CGGGGGCG
 A T _

GAM1904 DKFZp761G2113 3' GTGGGGCTCACGCTGTCCTGTG 70469 A_ CGT
 G TCACAGGATGGC AGTCCC
 ||||| |||||
 GGTGTCCTGTG TCGGGG
 CAC TG

GAM1904 DKFZp761H2121 3' GGTGTGTGTGTGTGGA 57180 G T
 TTCACAGGATG CAAG CC
 ||||| |||||
 AGGTGTTTTGT GTTT GG

GAM1904 DKK2 5' GCGATTCGCTGTCTCTTGTGAG 27776 T A CCC_
 TTCACAGGA GGCA GT CGT
 ||||| |||| ||
 GAGTGTCT CTGT CG GCG
 _ _ CTTA

GAM1904 DNAJC5 3' GGGGTGCCCATCCTGGGG 62140 A _ AGT
 TTC CAGGATGG CA CCCC
 || ||||| || ||||
 GGG GTCCTACC GT GGGG
 C _

GAM1904 DOK4 3' GTGGGGTTTTTTGTTGTTTTTT 36662 C TG T_ GT
 GG TCA AGGA GCAAG CCCC
 || |||| |||| ||||
 GGT TTTT TGTTT GGGG
 T GT TTT TG

GAM1904 FBXO27 3' ATGGGGGAATGCCCATCCTGGA 75003 A _ AG
 G TTC CAGGATGG CA TCCCCGT
 || ||||| || |||||
 GAG GTCCTACC GT GGGGGTA
 _ C AA

GAM1904 FENS-1 3' GGGTTCTGTTTTTGTGG 40834 TG A TC
 TCACAGGA GCA G CCC
 ||||| ||| ||
 GGTGTTTT TGT C GGG
 _ _ TT

GAM1904 FGF19 3' GGATGCTGTCCTGAGAA 18855 A AG
 TTC CAGGATGGCA TCC
 || ||||| |||

		AAG GTCCTGTCGT AGG		
		A _		
GAM1904	PHOD2	3' ACGATTTTGTCTTTCTGTGGA 74260	T	TCCC
		TTCACAGGA GGCAAG CGT		
		AGGTGTCTT CTGTTT GCA		
		T TA_		
GAM1904	FLJ00001	3' ATGGGGACCTGACATCTTTGG 82710	C	G A
		TCA AGGATG CA GTCCCCGT		
		GGT TTCTAC GT CAGGGGTA		
		_ A C		
GAM1904	FLJ10044	3' GTGGCTCATGCTGTCCTGTGAG 36243	_	CCCGT
		TTCACAGGATGGCA AGTC		
		GAGTGTCTGTCGT TCGG		
		AC TG		
GAM1904	FLJ10193	3' CGGGTGGTCACCTGTGAG 36348	A	AAGTC
		TTCACAGG TGGC CCG		
		GAGTGTCC ACTG GGGC		
		_ GT_		
GAM1904	FLJ10232	3' ATGGGGCCCTGTTCTG GGG 36372	A	CAA T
		TTC CAGGATGG G CCCCCGT		
		GGG GTCTTGTC C GGGGTA		
		_ C_		
GAM1904	FLJ10415	3' GTGGGGACTCTGGATCTTTGTG 36589	_	GGCA GT
	AG	TTCACAG GAT AGTCCCC		
		GAGTGTT CTA TCAGGGG		
		T GGTC TG		
GAM1904	FLJ10482	3' GTGGACCAAGCCATCCTGAGG 36650	A	AA_ CCGT
		TC CAGGATGGC GTCC		
		GG GTCCTACCG CAGG		
		A AAC TG		
GAM1904	FLJ10751	3' TGGGGGCTGAAGTCCTGTG 37115	GG A	GT
		CACAGGAT CA GTCCCC		
		GTGTCCTG GT CGGGGG		
		AA _ TG		
GAM1904	FLJ10751	3' TGGGGGCTGAAGTCCTGTG 37116	GG A	GT
		CACAGGAT CA GTCCCC		
		GTGTCCTG GT CGGGGG		
		AA _ TG		
GAM1904	FLJ10904	3' GGATAGGCATCTTGTGAG 37383	G AA	
		TTCACAGGATG C GTCC		

GAGTGTCTAC G TAGG
 _ GA
 GAM1904 FLJ12484 3' TGGGGGTGTCAATATCCTGGAG 70231 A ____ AG GT
 TTC CAGGA TGGCA TCCCC
 ||| |||| |||| ||||
 GAG GTCCT ACTGT GGGGG
 _ ATA _ TG
 GAM1904 FLJ12783 3' TGGGGGCTCGTGTGTCCTGGGA 49492 A _ A GT
 TTC CAGGATG GC AGTCCCC
 ||| ||||| || |||||
 AGG GTCCTGT TG TCGGGGG
 _ G C TG
 GAM1904 FLJ13725 5' GGGCAGTGTCTCCTGTGAG 68833 T AGT
 TTCACAGGA GGCA CCC
 ||||| |||| |||
 GAGTGTCTCTCTGT GGG
 _ GAC
 GAM1904 FLJ13940 5' ACGGGGGGGGGGTGGTTCTGTG 47306 G AAG_
 GA TTCACAGGAT GC TCCCCGT
 ||||| || |||||
 AGGTGTCTTG TG GGGGGCA
 G GGGG
 GAM1904 FLJ14768 3' TGGGGACTTTGCAGTGAG 52677 AGGATG _
 TTCAC GCAA GTCCCCG
 |||| ||| |||||
 GAGTG CGTT CAGGGGT
 A_____ T
 GAM1904 FLJ14855 3' ATGGGGGAGGCTCCCAACCTGT 53762 A CAAG_
 GGA TTCACAGG TGG TCCCCGT
 ||||| || |||||
 AGGTGTCC ACC GGGGGTA
 A CTCGGA
 GAM1904 FLJ14855 3' GGAAGTGGTCCTGTGAA 53764 G AAG
 TTCACAGGAT GC TCC
 ||||| || |||
 AAGTGTCTTG TG AGG
 G A_
 GAM1904 FLJ20034 3' ATGGGGCGCTGTTGTTTGTGG 34836 G TG A _
 TCACAG A GCA GT CCCCCGT
 ||||| | ||| || |||||
 GGTGTT T TGT CG GGGGTA
 _ GT _ C
 GAM1904 FLJ20125 3' GGATGTGCTGTCTGAGAG 35075 A A
 TTC CAGGATGGCA GTCC
 ||| ||||| |||||
 GAG GTCCTGTCGT TAGG
 A G
 GAM1904 FLJ20136 3' GACACTGTGTTCTGTGAG 35097 G A_
 TTCACAGGATG CA GTC
 ||||| || |||

GAGTGTCTTGT GT CAG
 _ CA
 GAM1904 FLJ20147 3' ATGGGGACTTGCTATGTTG 35131 G
 CAG ATGGCAAGTCCCCGT
 ||| |||||
 GTT TATCGTTCAGGGGTA
 G
 GAM1904 FLJ20154 3' GGCGGCTGTCTTGGA 73306 A AA
 TTC CAGGATGGC GTC
 ||| ||||| |||
 AAG GTTCTGTCTG CGG
 _ G_
 GAM1904 FLJ20300 3' ATGGTTGACGTTGTTTTGTGA 35377 TG AA C_
 TCACAGGA GC GTC CCGT
 ||||| || ||| ||||
 AGTGTTTT TG CAG GGTA
 GT _ TT
 GAM1904 FLJ20340 5' GCGGTTTTCTGCATCTTGTGGA 35459 G AGTCC
 TTCACAGGATG CA CCGT
 ||||| || ||||
 AGGTGTTCTAC GT GGCG
 _ CTTTT
 GAM1904 FLJ20436 3' GGGAGCTGTCTTTGTGAG 35627 _ AAG
 TTCACAG GATGGC TCCC
 ||||| ||||| ||||
 GAGTGTTCTGTCTG AGGG
 T _
 GAM1904 FLJ20487 3' ATGGGGGTTTCAGTCTGTGGA 35708 GA GCA GT
 TTCACAG TG A CCCCCGT
 ||||| || | |||||
 AGGTGTC AC T GGGGTA
 TG _ TG
 GAM1904 FLJ20699 3' GGGGGCTGATTCTGCTGG 35990 _ GGCA
 TCA CAGGAT AGTCCCC
 ||| ||||| |||||
 GGT GTCTTA TCGGGGG
 C G_
 GAM1904 FLJ21742 3' GGGGACCCATGGTCTGTGGA 50815 _ CAA GT
 TTCACAGG ATGG GTCCCC
 ||||| ||||| |||||
 AGGTGTCT TACC CAGGGG
 GG _ T
 GAM1904 FLJ22494 3' ACGTTCTGTGCCGTCCCTTGG 46095 C AGTCCC
 TCA AGGATGGCA CGT
 ||| ||||| |||
 GGT TCCTGCCGT GCA
 _ GTCTT_
 GAM1904 FLJ23091 3' GGGGGTGTATTCCTTGG 46665 C TG AG
 TCA AGGA GCA TCCCC
 ||| ||||| ||| |||||

GGT TCCT TGT GGGGG
_ TA _
GAM1904 FLJ23153 3' ATGAGGTTTTTGTGTTTTTTG 45265 C TG TC _
GA TTCA AGGA GCAAG CC CGT
||||| ||||| |||||
AGGT TTTT TGTTT GG GTA
T GT TT A
GAM1904 FLJ23186 3' GGCACGTGCTATTCTTGAA 61043 C A C
TTCA AGGATGGCA GT CC
||||| ||||| |||||
AAGT TCTTATCGT CA GG
_ _ C
GAM1904 FLJ30678 3' GGACGTATTCTGTGAA 58982 GCAA
TTCACAGGATG GTCC
||||| |||||
AAGTGTCTTAT CAGG
G_
GAM1904 GRIN3A 3' GGAAATGCTGTCTTGTGAG 56784 AG
TTCACAGGATGGCA TCC
||||| |||||
GAGTGTCTGTCTG AGG
AA
GAM1904 GTR2 3' ATGGGAGCTGCTGCTTGTGG 42461 A A TC
TCACAGG TGGCA G CCCGT
||||| ||||| | |||||
GGTGTTC GTCGT C GGGTA
_ _ GA
GAM1904 HSPC065 3' GGGGTCTTTTCATTTTGTGA 27156 C T GT
TCACAGGATGG AAG CCCC
||||| ||||| |||||
AGTGTCTTACT TTC GGGG
_ T T
GAM1904 HSPC177 3' ATGGGTTTTGTTGTGTCTTGTG 33523 _ TC
AA TTCACAGGAT GGCAAG CCCGT
||||| ||||| |||||
AAGTGTCTG TTGTTT GGGTA
TG T_
GAM1904 HSRNAFEV 5' GCGGGGGCGGGGTCCTGGGG 34450 A GGCAA
TTC CAGGAT GTCCCCGT
||| ||||| |||||
GGG GTCCTG CGGGGGCG
_ GGG_
GAM1904 HT008 3' TGGGGAGAGGAATTCTGTGAG 60511 GGCAAG GT
TTCACAGGAT TCCCC
||||| |||||
GAGTGTCTTA AGGGG
AGGAG_ TG
GAM1904 ICB-1 3' ACGGGGAGTAGCTTTGTGGA 17930 GAT AAG
TTCACAG GGC TCCCCGT
||||| ||| |||||

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AGGTGTT TCG AGGGGCA
  ___ ATG
GAM1904 KEAP1 3' GGACAGTTATTTTGTGA 25430 _ AA
TCA CAGGATGGC GTCC
||| ||||| |||
AGT GTTTTATTG CAGG
T A_
GAM1904 KIAA0016 3' GCTTCAACTTGATTATCTTGTG 29308 _ CCCCCT
AA
TTCACAGGATGG CAAGT
||||||| |||
AAGTGTCTATT GTTCA
A ACTTCG
GAM1904 KIAA0062 3' ACGGAAGAGGCCGTTCTATGAA 70784 C AAGTCC
TTCA AGGATGGC CCGT
||| ||||| |||
AAGT TCTTGCCG GGCA
A GAGAA_
GAM1904 KIAA0077 3' ATGGAAGACTGCTGTGTTTGTG 67577 _ A C_
GA
TTCACAGG ATGGCA GTC CCGT
||||| ||||| ||| |||
AGGTGTTT TGTCGT CAG GGTA
G _ AA
GAM1904 KIAA0140 3' GGGGAAGCTGTCCTGGGG 28516 A AAG
TTC CAGGATGGC TCCCC
||| ||||| |||
GGG GTCCTGTCTG AGGGG
_ A_
GAM1904 KIAA0217 3' ATGGGGATTTTTTTTTTGT 67595 TGGC
ACAGGA AAGTCCCCGT
||||| |||||
TGTTTT TTAGGGGTA
TT_
GAM1904 KIAA0255 3' GGGGGATGAGTTTTTTTGTGG 29135 TG AA GT
TCACAGGA GC GTCCCC
||||| || |||||
GGTGT TTTT TG TAGGGG
TT AG GT
GAM1904 KIAA0296 3' GGGAAAGTTGCCTGTGGA 28777 A AAG
TTCACAGG TGGC TCCC
||||| ||| |||
AGGTGTCC GTTG AGGG
_ AA_
GAM1904 KIAA0356 3' GCGGGGGAAGTCCCTGTGGA 66777 ATG AG_
TTCACAGG GCA TCCCCGT
||||| ||| |||||
AGGTGTCC CGT GGGGGCG
_ CAA
GAM1904 KIAA0418 3' ATGGGGTTTCTGTTGTATCTTG 28291 _ AGT_
TGG
TTCACAGGATG GCA CCCCCT
||||||| ||| |||||

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	GGTGTTCTAT TGT GGGGTA	
	GT CTTT	
GAM1904 KIAA0445	5' GCGGTTATCTCCATTTTGTGGA 28639	CAA CC
	TTCACAGGATGG GT CCGT	
	AGGTGTTTTACC TA GGCG	
	TC_ TT	
GAM1904 KIAA0447	3' GCGGGGAGTTGTTGATTTGTGA 72125	A G
G	TTCACAGG TGGCAA TCCCCGT	
	GAGTGTTT GTTGTT AGGGGCG	
	A G	
GAM1904 KIAA0469	3' ATGGGTCCCTCTAGCCTGTGGA 29970	A CAAGTC
	TTCACAGG TGG CCCGT	
	AGGTGTCC ATC GGGTA	
	G TCCCT_	
GAM1904 KIAA0537	3' CGGGTTTAGTCATCCTGTGG 29927	AAGTC T
	TCACAGGATGGC CCCG	
	GGTGTCCCTACTG GGGC	
	ATTT_	
GAM1904 KIAA0574	3' GGCAGCTCTGTTTTGTGGA 69819	CA CC
	TTCACAGGATGG AGT CC	
	AGGTGTTTTGTC TCG GG	
	_ AC	
GAM1904 KIAA0676	5' GTGGTCCGAGCTATACCTGTGG 31148	_ AAGT_ CCGT
A	TTCACAGG ATGGC CC	
	AGGTGTCC TATCG GG	
	A AGCCT TG	
GAM1904 KIAA0705	3' TGGGGGCTTTGGCAGCTATGGA 25485	C GA G _ GT
	TTCA AG TG CAA GTCCCC	
	AGGT TC AC GTT CGGGGG	
	A G_ G T TG	
GAM1904 KIAA0781	3' TGGGGACTGTCAATTTTGTGA 68063	_ A GT
	TCACAGGA TGGCA GTCCCC	
	AGTGTTTT ACTGT CAGGGG	
	T _ TG	
GAM1904 KIAA0934	3' GCGTCGTTTGCCGCCTGTGGA 64885	A TCCC
	TTCACAGG TGGCAAG CGT	
	AGGTGTCC GCCGTTT GCG	
	_ GCT_	
GAM1904 KIAA1012	3' CTTTGACTTGTCATTTTGTGA 30729	_ CCCGT
	TCA CAGGATGGCAAGTC	

AGT GTTTTACTGTTTCAG
 T TTTCA
 GAM1904 KIAA1115 5' GTGGGGCAGCTCTTGTCTTGGGA 30696 A ____ AA CGT
 G TTC CAGGAT GGC GTCCC
 ||| ||||| ||| |||||
 GAG GTTCTG TCG CGGGG
 _ TTC A_ TG
 GAM1904 KIAA1190 3' GCTCCTGCTGTCCTGGGG 71652 A ____
 TTC CAGGATGGCA AGT
 ||| ||||| |||
 GGG GTCCTGTCGT TCG
 _ CC
 GAM1904 KIAA1254 3' GACTTGTTTTCTTGTGAA 70560 TG
 TTCACAGGA GCAAGTC
 ||||| |||||
 AAGTGTTC TGTTCAG
 TT
 GAM1904 KIAA1287 3' ACGGGGGTTTGCCATGTTG 78932 G GT
 CAG ATGGCAA CCCCCT
 ||| ||||| |||||
 GTT TACCGTT GGGGCA
 G TG
 GAM1904 KIAA1328 3' ACGGGGACTTGTCTCACT 62313 _ T
 AG GA GGCAAGTCCCCGT
 || || ||||| |||||
 TC CT CTGTTTCAGGGGCA
 A _
 GAM1904 KIAA1337 3' GTGGACCATGCTGCCTTGTGGA 73059 AT A_ CCGT
 TTCACAGG GGCA GTCC
 ||||| ||| |||
 AGGTGTTT TCGT CAGG
 CG AC TG
 GAM1904 KIAA1463 3' ATGGTTAGATGCTATTCTGTGG 72736 AGTCC
 TCACAGGATGGCA CCGT
 ||||| ||| |||
 GGTGTCTTATCGT GGTA
 AGATT
 GAM1904 KIAA1467 3' GGGTGCTGGTTTCTTGTGAA 72073 T A TC GT
 TTCACAGGA GGC AG CCC
 ||||| ||| |||
 AAGTGTTC TTG TC GGG
 _ G GT T
 GAM1904 KIAA1497 5' ATGGGGATGTGTTCTGAGAA 68113 A GGCAA
 TTC CAGGAT GTCCCCGT
 ||| ||||| |||||
 AAG GTCTTG TAGGGGTA
 A TG____
 GAM1904 KIAA1600 3' TGGGAGATAGTTATTTTGTG 71944 AA _ GT
 CACAGGATGGC GTC CCC
 ||||| ||| |||

		GTGTTTTATTG TAG GGG		
		A_ A TG		
GAM1904 KIAA1602	3'	ACGACTCGCTGTCCTCTTGTGG 65233	___	A CCCGT
		TCACA GGATGGC AGTC		
		GGTGT CCTGTCTG TCAG		
		TCT C CA		
GAM1904 KIAA1671	3'	ATGGGGAGACATTCTGTGG 66269		GCAAG
		TCACAGGATG TCCCCGT		
		GGTGTCTTAC AGGGGTA		
		AG___		
GAM1904 KIAA1822	3'	GCGGGTGTGTGCTGTCCTGGGG 68186	A	A TC
A		TTC CAGGATGGCA G CCCGT		
		AGG GTCCTGTCTGT T GGGCG		
		G G GT		
GAM1904 KIAA1854	3'	GGGAGAGATTGTCTGTGAG 72212	GATG	G_ _
		TTCACAG GCAA TC CCC		
		GAGTGTC TGTT AG GGG		
		___ AG A		
GAM1904 KIAA1855	3'	GGGCAGGTGATTCTGTGG 93956	G	AA
		TCACAGGAT GC GTCC		
		GGTGTCTTA TG CGGG		
		G GA		
GAM1904 KIAA1981	3'	ACGGCCCTGATGCTGGCCTGTG 89708	AT	AGTCC_
AG		TTCACAGG GGCA CCGT		
		GAGTGTC TCCT GGCA		
		GG AGTCCC		
GAM1904 LAIR2	3'	GGCCTCCCGTCTTGTGAA 41479	CA	T
		TTCACAGGATGG AG CC		
		AAGTGTCTGCC TC GG		
		C_ C		
GAM1904 LASP1	3'	ATGGGAGACCTGTTGGCCTGTG 21575	AT	A _
G		TCACAGG GGCA GTC CCCGT		
		GGTGTCC TTGT CAG GGGTA		
		GG C A		
GAM1904 LPAAT-delta	3'	ATGGGGAGGAAGATGTTTTGT 39699	GCAAG_	
		ACAGGATG TCCCCGT		
		TGTTTTGT AGGGGTA		
		AGAAGG		
GAM1904 LRG	3'	GCGGGGGCTCACGCCTGT 54822	A	GCA
		ACAGG TG AGTCCCCGT		

			TGTCC GC TCGGGGGCG		
			— AC—		
GAM1904	MAP2K6	3'	GACTGCTGCCATTTTGGGA 12332	C	—
			TTCA AGGATGGCA AGTC		
			AGGT TTTTACCGT TCAG		
			— CG		
GAM1904	MGC:13379	3'	GTGGGGCAAGTTGTCCTGAGAA 33664	A	TG AA CGT
			TTC CAGGA GC GTCCC		
			AAG GTCCT TG CGGGG		
			A GT AA TG		
GAM1904	MGC10485	3'	GCGGGGGCGGACCTTGTGAG 54624		ATGGCAA
			TTCACAGG GTCCCCGT		
			GAGTGTTT CGGGGGCG		
			CAGG—		
GAM1904	MGC20460	5'	TGGGAAATGTCATTTTTTGG 54908	C	AG_ CGT
			TCA AGGATGGCA TCCC		
			GGT TTTTACTGT AGGG		
			T AAA TA		
GAM1904	MGC2474	3'	GCGGGGACCTGGACCCGCCTGT 43960	A	— A
	GG		TCACAGG TGG CA GTCCCCGT		
			GGTGTCC GCC GT CAGGGGCG		
			— CAG C		
GAM1904	MGC26651	3'	GGCTCTTATCTTGTGGA 58951		CA
			TTCACAGGATGG AGTC		
			AGGTGTTCTATT TCGG		
			C—		
GAM1904	MGC4737	5'	GTGGAGCTGCTGCGTTCTGTGA 49650		— AG CCGT
	A		TTCACAGGATG GCA TCC		
			AAGTGTCTTGC CGT AGG		
			GT CG TG		
GAM1904	MKRN4	3'	GGGACTTGTTTTGTGA 48468		ATG
			TCACAGG GCAAGTCCC		
			AGTGTTT TGTTCAGGG		
			—		
GAM1904	MSP	3'	GTGGCGCCATTGCTGTCCTGGG 50246	A	— C CGT
	A		TTC CAGGATGGCAA GT CC		
			AGG GTCCTGTCGTT CG GG		
			— AC C TG		
GAM1904	MSTP028	3'	GGGGACGTGTGCTTGTGG 50065		ATG A
			TCACAGG GCA GTCCCC		

			GGTGTTC TGT CAGGGG		
			G__ G		
GAM1904 NRF	3'	GTGATT	TACTGTATCTTGTGG 34507	__ C	CCCGT
			TCACAGGAT GG AAGTC		
			GGTGTTC TA TC TTTAG		
			TG A TG		
GAM1904 OKL38	3'	CGGGGACA	ACTTCGTGAG 26290	A	TGGCAA
			TTCAC GGA GTCCCCG		
			GAGTG CTT CAGGGGC		
			_ CAA__		
GAM1904 P66	3'	GGACCAGG	CTGTTTTTGA 40742	C	AA_
			TTCA AGGATGGC GTCC		
			AAGT TTTTGTCTG CAGG		
			_ GAC		
GAM1904 PARG1	3'	GTGGTATT	GTGCTTGTTTTGTG 17870	_ _ C	CGT
AA			TTCACAGGATG GCA AGT CC		
			AAGTGTTTTGT CGT TTA GG		
			T G T TG		
GAM1904 PDZD2	5'	GCGGGGAT	CAAATCCTGGAA 81726	A	GGCAA
			TTC CAGGAT GTCCCCGT		
			AAG GTCCTA TAGGGGCG		
			_ AAC__		
GAM1904 PHF5A	3'	GGCAGCTG	TCCTTGAG 52251	C	AA
			TTCA AGGATGGC GTC		
			GAGT TCCTGTCTG CGG		
			_ A_		
GAM1904 POLR2J2	3'	GCGGGGAC	CTACTGTCCTTTGG 60007	C	CAA
			TCA AGGATGG GTCCCCGT		
			GGT TCCTGTC CAGGGGCG		
			T ATC		
GAM1904 PP1044	3'	ACGGGAGG	GCTGTCCTTGG 41673	C	AAGTC
			TCA AGGATGGC CCCGT		
			GGT TCCTGTCTG GGGCA		
			_ GGA__		
GAM1904 PRO0659	3'	GGGCCCAT	TTTGGGGA 27074	A	CAA
			TTC CAGGATGG GTCC		
			AGG GTTTTACC CGGG		
			G _		
GAM1904 PRRG1	3'	ATGGGGGT	CTTTCTGTGA 8147	T	AAGT
			TCACAGGA GGC CCCCGT		

			AGTGTCTT CTG GGGGTA		
			T _____		
GAM1904	RAB35	3'	GCGGGGTCTCCGTCCTTGG 23416	C	CA T
			TCA AGGATGG AG CCCCCT		
			GGT TCCTGCC TC GGGGCG		
			_____ T		
GAM1904	RAB40C	3'	ATGGCAAGGCATCCTGTGAA 41275		G AAGTCC
			TTCACAGGATG C CCGT		
			AAGTGCCTAC G GGTA		
			_____ GAAC_____		
GAM1904	RBM5	5'	GCGGAGGCGCCATTTTGTG 20505		AA C
			CACAGGATGGC GTC CCGT		
			GTGTTTTACCG CGG GGCG		
			_____ A		
GAM1904	RBPM5	3'	GCGGCTGCAATCTGTCTTGTGG 23432		CAA CC
			TCACAGGATGG GT CCGT		
			GGTGTCTGTC CG GGCG		
			TAA TC		
GAM1904	RNF40	3'	GGGCTTCTGTCCTGTGGA 29365		C
			TTCACAGGATGG AAGTCC		
			AGGTGTCCTGTC TTCGGG		

GAM1904	RRP4	3'	GGGCTCCCATCCTGGAA 27361	A	CA
			TTC CAGGATGG AGTCC		
			AAG GTCCTACC TCGGG		
			_____ C_____		
GAM1904	SCAND2	3'	ACGCTATTTGTTAATTTGTGAA 54412	A	CCC
			TTCACAGG TGGCAAGT CGT		
			AAGTGTTT ATTGTTTA GCA		
			A TC_____		
GAM1904	SCAND2	3'	GTGGGAGCGACGCAGTCCTGTG 54421		G AA_ TC GT
	G		TCACAGGAT GC G CCC		
			GGTGTCTG CG C GGG		
			A CAG GA TG		
GAM1904	SDS3	3'	ATGGGGGTACTTCTGTGG 69743		TG AAGT
			TCACAGGA GC CCCCCT		
			GGTGTCTT TG GGGGTA		
			CA _____		
GAM1904	SDS3	3'	GTGGGACCTCTGCTTTTGTGAA 69752		AT A_ CGT
			TTCACAGG GGCA GTCCC		

			AAGTGTTT TCGT CAGGG		
			___ CTC TG		
GAM1904 SE57-1	3'	ATGACTGCCTGTGTTATTTTGT 48163	_____ CCCGT		
	GGA	TTCACAGGATGGCA AGTC			
		AGGTGTTTTATTGT TCAG			
		GTCCG TA T			
GAM1904 SMT3H2	3'	ATGGGGAAAAATACTGATTCTG 23656	_ CAAG__		
	TGAA	TTCACAGGAT GG TCCCCGT			
		AAGTGTCTTA TC AGGGGTA			
		G ATAAAA			
GAM1904 SULT4A1	3'	GGGAGGACCATTTTGCAGAG 69016	A CAAG		
		TTC CAGGATGG TCCC			
		GAG GTTTTACC AGGG			
		C AGG_			
GAM1904 TDRKH	3'	ATGGGTTCTTTGTCATTCTGT 23422	_ TC		
		ACAGGATGGCAA G CCCGT			
		TGTCTTACTGTT C GGGTA			
		T TT			
GAM1904 UBN1	3'	ACTTGCCTGTCTTGTGAG 34192	_		
		TTCACAGGAT GGCAAGT			
		GAGTGTCTG CCGTTCA			
		T			
GAM1904 URG4	3'	GGGGAAGTTGTCCTGAGGA 35926	A TG AAG		
		TTC CAGGA GC TCCCC			
		AGG GTCCT TG AGGGG			
		A GT A__			
GAM1904 ZAK	3'	GGGGGATCCAACTTGTGAA 34106	A CAA GT		
		TTCACAGG TGG GTCCCC			
		AAGTGTTT ACC TAGGGG			
		A ___ GG			
GAM1904 ZNF220	5'	GGCATTCTGTTTTGTGAA 23159	CAA		
		TTCACAGGATGG GTC			
		AAGTGTTTTGTC CGG			
		TTA			
GAM1904 ZNF323	3'	ATGGAGGGGCTGTTTTTGAG 48819	C AAG _		
		TTCA AGGATGGC TCC CCGT			
		GAGT TTTTGTGCG GGG GGTA			
		_ _ A			
GAM1904 ZNFN1A2	3'	ACCTGGCTTGTTTATTTTGTGG 33216	_ CCCGT		
		TCACAGGATGG CAAGTC			

	GGTGT TTTATT GTTCGG	
	T TCCA	
GAM1904 LOC126382 5'	GCGGGAAATCTGTTTCCTGTGA 76589	T AG C_
A	TTCACAGGA GGCA T CCCGT	
	AAGTGCCT TTGT A GGGCG	
	_ CT AA	
GAM1904 LOC126767 5'	GCGGTTGGCCACCCTGTGAA 75960	A AAGTCC
	TTCACAGG TGGC CCGT	
	AAGTGTCC ACCG GGCG	
	C GTT__	
GAM1904 LOC126906 5'	ATGGGGATACCATTCTGGAA 75962	A CAA
	TTC CAGGATGG GTCCCCGT	
	AAG GTCTTACC TAGGGGTA	
	_ A_	
GAM1904 LOC127702 3'	ATGGGGAAGGCAGTTTGTGAG 75983	ATG AAG
	TTCACAGG GC TCCCCGT	
	GAGTGTTT CG AGGGGTA	
	GA_ GA_	
GAM1904 LOC135932 3'	ATGGGGACTTGACCCTGAGGA 76694	A ATGG
	TTC CAGG CAAGTCCCCGT	
	AGG GTCC GTTCAGGGGTA	
	A CAG_	
GAM1904 LOC137593 5'	GGGACTCTGGTCCTGTGG 75796	GG _
	TCACAGGAT CA AGTCCC	
	GGTGTCTG GT TCAGGG	
	_ C	
GAM1904 LOC138389 5'	TGGGGATATGTCATCTGTGAA 76746	G A GT
	TTCACAG ATGGCA GTCCCC	
	AAGTGTC TACTGT TAGGGG	
	_ A TG	
GAM1904 LOC139390 5'	GGGGGTGTGGTTCTGGGA 76336	A G AG
	TTC CAGGAT GCA TCCCC	
	AGG GTCTTG TGT GGGGG	
	_ G _	
GAM1904 LOC143381 3'	ACGGGGGTAGACTTTGTGG 77058	ATG_ AAGT
	TCACAGG GC CCCCCGT	
	GGTGTTT TG GGGGCA	
	CAGA ____	
GAM1904 LOC144262 5'	ACGTACCTGCCATTCGTGGA 77257	A A CCC
	TTCAC GGATGGCA GT CGT	

AGGTG CTTACCGT CA GCA
 _ C T_
 GAM1904 LOC144373 3' GGGTCCTGGCTGTCCTTGG 77314 C A TC GT
 TCA AGGATGGC AG CCC
 ||| ||||| || |||
 GGT TCCTGTCG TC GGG
 _ G CT T
 GAM1904 LOC145871 5' GGGGAGGGACGTCCTGTGAG 84551 GCAAG GT
 TTCACAGGATG TCCCC
 ||||| ||||
 GAGTGCCTGC AGGGG
 AGGG_ T
 GAM1904 LOC147180 5' ATGGGGATTTGCTCCACTG 85095 GAT
 CAG GGCAAGTCCCCGT
 ||| |||||
 GTC TCGTTTAGGGGTA
 ACC
 GAM1904 LOC148354 3' GGGGGCTGGGGTCTTGATGG 79550 _ GG A GT
 TCA CAGGAT CA GTCCCC
 ||| |||| || ||||
 GGT GTTCTG GT CGGGGG
 A GG _ T
 GAM1904 LOC148753 3' GGATGCAGTCCTGTGAG 85372 G AG
 TTCACAGGAT GCA TCC
 ||||| ||| |||
 GAGTGCCTG CGT AGG
 A _
 GAM1904 LOC148946 5' ATGGCCAGTTTTGCCGTTTTTG 85464 C TCC_
 AA TTCA AGGATGGCAAG CCGT
 ||| ||||| |||
 AAGT TTTTGCCGTTT GGTA
 _ TGACC
 GAM1904 LOC149041 3' ATTTGTTTTTGTTCGTGAA 79870 _
 TTCACAGGAT GGCAAGT
 ||||| |||||
 AAGTGTCTTG TTGTTA
 TTT
 GAM1904 LOC149711 5' ATGGGCTTGGGCTGGTTTGTGG 85838 AT AAGTC
 TCACAGG GGC CCCGT
 ||||| ||| ||||
 GGTGTTT TCG GGGTA
 GG GGTTG
 GAM1904 LOC149992 5' TGGCAAATTGCTGTCCTGTGG 80380 GTCC_ GT
 TCACAGGATGGCAA CC
 ||||| ||| |||
 GGTGTCCTGTCGTT GG
 AAAAC TG
 GAM1904 LOC150084 5' TGGGTCAGATTTGGCCTGTGG 80382 ATGG _ GT
 TCACAGG CAAGTC CCC
 ||||| |||| |||

		GGTGTCC	GTTTAG	GGG		
		G__	ACT	TG		
GAM1904	LOC150245 3'	GGGCCTTGCCCTGTGG	86116	ATG	T	
		TCACAGG	GCAAG	CCC		
		GGTGTCC	CGTTC	GGG		
		__	C			
GAM1904	LOC150271 3'	GCGTAATTGTCATTTTGTGG	86140		GTCCC	
		TCACAGGATGGCAA	CGT			
		GGTGTTTTACTGTT	GCG			
		AAT__				
GAM1904	LOC150343 5'	GCGGGGATCCAGAGTTCTGGGA	80493	A	GGCAA	
		TTC CAGGAT	GTCCCCGT			
		AGG GTCTTG	TAGGGGCG			
		_	AGACC			
GAM1904	LOC150382 3'	GGGACACTGATCTGTGAG	80630	A	CAA	
		TTCACAGG TGG	GTCCC			
		GAGTGTCT GTC	CAGGG			
		A	A__			
GAM1904	LOC150383 3'	GGGACACTGATCTGTGAG	80632	A	CAA	
		TTCACAGG TGG	GTCCC			
		GAGTGTCT GTC	CAGGG			
		A	A__			
GAM1904	LOC152674 5'	GCTTTACCATTTTGTGGA	87002		C_	
		TTCACAGGATGG	AAGT			
		AGGTGTTTTACC	TTCG			
		AT				
GAM1904	LOC153811 3'	ACGGGGGCTCTGAGTTTTG	81821	GG	_	
		CAGGAT CA	AGTCCCCGT			
		GTTTTG GT	TCGGGGGCA			
		A_	C			
GAM1904	LOC155438 3'	ACGGGTTGGGGTTGTCATCCAG	87680	A	G	__
	TGG	TCAC	GGATGGCAA TCC	CCGT		
		GGTG CCTACTGTT	GGG	GGCA		
		A	G	TTG		
GAM1904	LOC158112 5'	GTGGGGAGAATGATGCTATCCT	82607	A	AG__	GT
	GGAG	TTC CAGGATGGCA	TCCCC			
		GAG GTCCTATCGT	AGGGG			
		_	AGTAAG	TG		
GAM1904	LOC158170 5'	ACGGCCAAGGCTGTCTTGGA	82656	A	AAGTCC	
		TTC CAGGATGGC	CCGT			

		AAG GTTCTGTCG	GGCA		
		— GAACC—			
GAM1904	LOC158997 3'	ATGGGGAAAAATACTGATTCTG	82950	— CAAG—	
		TGAA	TTCACAGGAT GG TCCCCGT		
		AAGTGTCTTA TC	AGGGGTA		
		G ATAAAA			
GAM1904	LOC165904 3'	ATGGGGGCTCCCAGCTGCTTGT	83501	A A—	
		GGA	TTCACAGG TGGC AGTCCCCGT		
		AGGTGTTC GTCG	TCGGGGGTA		
		— ACCC			
GAM1904	LOC170394 5'	GCGCACCTGCTGTCCTGGAG	83739	A A CCC	
		TTC CAGGATGGCA GT CGT			
		GAG GTCCTGTCGT CA GCG			
		— C C—			
GAM1904	LOC196023 3'	ATGGGAATGATGTATTTTGTGG	88949	G A_ C	
		A	TTCACAGGATG CA GT CCCGT		
		AGGTGTTTTAT GT TA GGGTA			
		— AG A			
GAM1904	LOC196955 3'	ACGGGGCCATCCAGCCTGTGAA	77859	A CAA T	
		TTCACAGG TGG G CCCCCGT			
		AAGTGTCC ACC C GGGGCA			
		G TAC—			
GAM1904	LOC197335 5'	ACGGGGCGGCTGCGCCTGTGG	89331	AT_ AAGT	
		TCACAGG GGC CCCCCGT			
		GGTGTCC TCG GGGGCA			
		GCG GC—			
GAM1904	LOC197342 5'	GGACACAGCCATCCTGGAA	89371	A AA_	
		TTC CAGGATGGC GTCC			
		AAG GTCCTACCG CAGG			
		— ACA			
GAM1904	LOC199907 3'	GGCACTGCCATCTTTGAG	89831	C A C	
		TTCA AGGATGGCA GT CC			
		GAGT TTCTACCGT CA GG			
		— — C			
GAM1904	LOC200982 3'	ATGGGGACTTGAATGGTGTG	91808	GG GG	
		CACA AT CAAGTCCCCGT			
		GTGT TA GTTCAGGGGTA			
		GG A_			
GAM1904	LOC203052 3'	GGGCAGCCATCCTGGGAA	92077	A AA	
		TTC CAGGATGGC GTCC			

AAG GTCCTACCG CGGG
 G A_
 GAM1904 LOC203054 5' GCGGGCCATCATCCTGCGG 90754 A CAAGTC
 TC CAGGATGG CCCGT
 || ||||| ||||
 GG GTCCTACT GGGCG
 C ACC__
 GAM1904 LOC203274 3' TGGGGATATGTCATCTGTGAA 92103 G A GT
 TTCACAG ATGGCA GTCCCC
 ||||| ||||| |||||
 AAGTGTC TACTGT TAGGGG
 _ A TG
 GAM1904 LOC203636 3' ACGGGACACTTGTCTG 90973 ATG C_
 CAGG GCAAGT CCCGT
 ||| ||||| |||||
 GTCC TGTTC A GGGCA
 _ CA
 GAM1904 LOC204970 3' GTGGGCTCCCTGCCATCCTGGG 90968 A _ CCGT
 A TTC CAGGATGGCA AGTCC
 ||| ||||| |||||
 AGG GTCCTACCGT TCGGG
 _ CCC TG
 GAM1904 LOC206480 5' TGGGGGCTTCAGGGTTTGTGA 92408 _ ATGGC GT
 TCA CAGG AAGTCCCC
 ||| ||| |||||
 AGT GTTT TTCGGGGG
 T GGGAC TG
 GAM1904 LOC219855 3' ATGGGGGCCGGTGCTGTGG 93139 G _ AAGT
 TCACAG AT GGC CCCCCGT
 ||||| || ||| |||||
 GGTGTC TG CCG GGGGTA
 G G _
 GAM1904 LOC220020 5' TGGGTATGAGCTTCCTGTGG 95056 T AA C GT
 TCACAGGA GGC GT CCC
 ||||| ||| || |||
 GGTGTCCT TCG TA GGG
 _ AG T TG
 GAM1904 LOC220758 3' GAGTTGCCATTTTCTGAA 92466 C G
 TTCA AGGATGGCAA TC
 ||| ||||| || ||
 AAGT TTTTACCGTT AG
 C G
 GAM1904 LOC220758 3' GGA CTGTGCCATCTGTGG 92468 G _
 TCACAG ATGGCA AGTCC
 ||||| ||||| |||||
 GGTGTC TACCGT TCAGG
 _ G
 GAM1904 LOC220776 3' GGTCGCTATTCTGTGAG 68932 AAGT
 TTCACAGGATGGC CC
 ||||| ||||| || ||

		GAGTGTCTTATCG	GG		
		CT__			
GAM1904	LOC221042 3'	CACTGGGGCTTGCTATTTTATG	94795	C	C
	AG	TTCA AGGATGGCAAGTCCC	GT		
		GAGT TTTTATCGTTCGGGG	CA		
		A	T CC		
GAM1904	LOC221399 5'	GAGTTTGCTGTCCTTTGAA	95484	C	_
		TTCA AGGATGGCAAG	TC		
		AAGT TCCTGTCGTTT	AG		
		T	G		
GAM1904	LOC221415 5'	GTGGGACACCAGCTATTCTGTG	95500	AA__	CGT
		CACAGGATGGC	GTCCC		
		GTGTCTTATCG	CAGGG		
		ACCA	TG		
GAM1904	LOC221421 3'	GCGGGGGCCTTTTTTGT	93894	T	CAA
		ACAGGA GG	GTCCCCGT		
		TGTTTT TC	CGGGGGCG		
		T	__		
GAM1904	LOC222171 5'	TGGGGGCAAATCTTGAG	94326	A	GGCAA
		TTC CAGGAT	GTCCCCG		
		GAG GTTCTA	CGGGGGT		
		_	AA__		
GAM1904	LOC253502 3'	GCGGGGTCTGCCTGGCCTGTGG	96221	AT_	A T
		TCACAGG	GGCA G CCCCCGT		
		GGTGTCC	CCGT C GGGGCG		
		GGT	_ T		
GAM1904	LOC253815 3'	CGGGGGCAGTCCTGGGG	97343	A	GGCAA
		TTC CAGGAT	GTCCCCG		
		GGG GTCCTG	CGGGGGC		
		_	A__		
GAM1904	LOC255042 3'	TGGGGTGTGGTCTGTGAA	97062	G G	AGT
		TTCACAG AT GCA	CCCCG		
		AAGTGTC TG TGT	GGGGT		
		_	G		
GAM1904	LOC255654 5'	ACGCACAGTGCTATCTGTGAG	98671	G	AGTCCC
		TTCACAG ATGGCA	CGT		
		GAGTGTC TATCGT	GCA		
		_	GACAC_		
GAM1904	LOC256530 3'	GGGGACTCACTTTTGGGA	98623	A	_ GCA
		TTC CAGGA TG	AGTCCCC		

		AGG GTTTT AC TCAGGGG		
		— C —		
GAM1904	LOC256937 3'	GCGCTGATACTGCTATTCTGTG 98914	A_	CC
	AG	TTCACAGGATGGCA GTC CGT		
		GAGTGTCTTATCGT TAG GCG		
		CA TC		
GAM1904	LOC257364 3'	ATGGGGATTCTGGCCTGTG 96642	AT	CA
		CACAGG GG AGTCCCCGT		
		GTGTCC TC TTAGGGGTA		
		GG —		
GAM1904	LOC257458 5'	ACGGGGACTTCCTTGTGCGA 68398	A G T C	
		TC CA GA GG AAGTCCCCGT		
		AG GT TT CC TTCAGGGGCA		
		C G _ _		
GAM1904	LOC51133 3'	GAGGTGCTATGTTTGTGAA 32788	_	AG
		TTCACAGG ATGGCA TC		
		AAGTGTTT TATCGT AG		
		G GG		
GAM1904	LOC51608 3'	ATGGGAGCGGCTGTTTTTGAA 64424	C	AA TC
		TTCA AGGATGGC G CCCGT		
		AAGT TTTTGTCTG C GGGTA		
		_ G_ GA		
GAM1904	LOC54550 5'	GGGAAGCTGTCCTTGGA 78187	C	AAG
		TTCA AGGATGGC TCCC		
		AGGT TCCTGTCTG AGGG		
		_ A_		
GAM1904	LOC57805 3'	ACGGAAGCTGCCATCCTGTGAG 41285	A	CC
		TTCACAGGATGGCA GT CCGT		
		GAGTGTCTTACCGT CA GGCA		
		_ A_		
GAM1904	LOC90342 5'	GCGAGATCTTGGCATCCTGTGA 63012	G _	CC
	G	TTCACAGGATG CAAG TC CGT		
		GAGTGTCTTAC GTTC AG GCG		
		G T A_		
GAM1904	LOC90529 3'	GGGAGATCATCTTGGA 63862	A	CAAG
		TTC CAGGATGG TCCC		
		AAG GTTCTACT AGGG		
		_ AG_		
GAM1904	LOC91115 3'	GCGGGGGCACTCGCTGTGGA 65570	_	TGGCAA
		TTCACAG GA GTCCCCGT		

		AGGTGTC CT CGGGGGCG	
		G CA_____	
GAM1904	LOC91149	3' ATGGGTGACTATTTTGTGAA 65690	GGCA _
		TTCACAGGAT AGTC CCCGT	
		AAGTGTTTTA TCAG GGGTA	
		_____ T	
GAM1904	LOC91960	3' ATGGGGGGCTGCAGGCTTGGAG 68280	A ATG A
		TTC CAGG GCA GTCCCCGT	
		GAG GTTC CGT CGGGGGTA	
		_ GGA _	
GAM1904	LOC92336	3' GGGTTCTGTATCTTGTGGA 69547	G A TC
		TTCACAGGATG CA G CCC	
		AGGTGTTCTAT GT C GGG	
		_ _ TT	
GAM1905	LETM1	3' TGGAATCCCGGAACCCCTCC 25557	T A TATA
		GGAGGGGTT CC GG TA	
		CCTCCCCAA GG CC GT	
		_ C TAAG	
GAM1905	FLJ22393	3' TATCCCTGGCAACCCCTCC 47779	T T
		GGAGGGGTT CCAGG ATA	
		CCTCCCCAA GGTCC TAT	
		C C	
GAM1905	GTR2	3' ATTTGGATGAAAACCCCTTC 42462	_____
		GGAGGGGTT TCCAGGT	
		CTTCCCCAA AGGTTTA	
		AAGT	
GAM1905	LOC222237	3' TTATATACCTCTCCCTCTG 95950	TTTCC
		CGGAGGGG AGGTATATAA	
		GTCTCCCT TCCATATATT	
		C_____	
GAM1906	JJAZ1	3' GTGGTTGAGTAACATCAC 31714	AGC A
		GTGA TACTCAAT CGC	
		CACT ATGAGTTG GTG	
		ACA _	
GAM1906	MUC4	3' GCAGCTGTGCAGCTTCAC 37879	ACTCA C _
		GTGAAGCT ATA GC GC	
		CACTTCGA TGT CG CG	
		CG_____ A	
GAM1906	CECR2	5' TGGCGCGGGCAGCCCCGC 49441	AA A CAATA
		GTG GCT CT CGCGCCA	

		CGC CGA GG GCGCGGT	
		CC C _____	
GAM1906	FLJ10490 5'	GTGGCGCGCACTAGCCCTCGC 36671	A_ CTCAATA
		GTGA GCTA CGCGCCAC	
		CGCT CGAT GCGCGGTG	
		CC CAC_____	
GAM1906	FLJ22457 5'	GCGCGTGGCTTGGCTTCAC 46610	CTCAA
		GTGAAGCTA TACGCGC	
		CACTTCGGT GTGCGCG	
		TCG__	
GAM1906	HSAJ1454 5'	GGCGCGTGCAGCAGCTCCA 34253	A A CAA
		TG AGCT CT TACGCGCC	
		AC TCGA GA GTGCGCGG	
		C C C__	
GAM1906	HT010 5'	GTGGCGCGCACGCGCAGCTCCG 38067	A ACTCAATA
	C	GTG AGCT CGCGCCAC	
		CGC TCGA GCGCGGTG	
		C CGCGCAC_	
GAM1906	KIAA0193 3'	TGCTGCTAAGAGCTTCAC 29319	A CAA C _ C
		GTGAAGCT CT TA GC GC A	
		CACTTCGA GA AT CG CG T	
		_ _ _ T A	
GAM1906	LAGY 3'	TGGCAGGCATTGACAGCTTCAC 51659	AC AC _
		GTGAAGCT TCAAT GC GCCA	
		CACTTCGA AGTTA CG CGGT	
		C_ _ GA	
GAM1906	LAGY 3'	TGGCAGGCATTGACAGCTTCAC 58317	AC AC _
		GTGAAGCT TCAAT GC GCCA	
		CACTTCGA AGTTA CG CGGT	
		C_ _ GA	
GAM1906	mPA-PLA1 3'	GGCTGTTTGAAAGCTTCAC 58359	AC T C
		GTGAAGCT TCAA ACG GCC	
		CACTTCGA AGTT TGT CGG	
		A_ _ _	
GAM1906	NXPH3 3'	GTGGGCTCTCTGTGCAGCCTCA 66346	A ACT ATAC G
	C	GTGA GCT CA GC CCAC	
		CACT CGA GT CG GGTG	
		C CGT CTCT _	
GAM1906	OBSCN 3'	TGGCCAGAGCAGCTTCAC 71193	A AATACGC
		GTGAAGCT CTC GCCA	

			CACTTCGA GAG	CGGT		
			C AC_____			
GAM1906	SDOS	3'	GTGAGGTTTCAAAGTAGCTTCA	51351	CAAT_ G_	
	C		GTGAAGCTACT AC CGC			
			CACTTCGATGA TG GTG			
			AACTT GA			
GAM1906	SNPH	3'	TGGCGCGTACTGAAGCCAC	28910	AA AC A	
			GTG GCT TCA TACGCGCCA			
			CAC CGA AGT ATGCGCGGT			
			— — C			
GAM1906	LOC139422	3'	TGGTTAAAGTAGCTTCAC	76356	CAATACGC	
			GTGAAGCTACT GCCA			
			CACTTCGATGA TGGT			
			AAT_____			
GAM1906	LOC152674	3'	GTGGTTTTCTAAGGCAGCTTCA	87003	A CAATACGC	
	C		GTGAAGCT CT GCCAC			
			CACTTCGA GG TGGTG			
			C AATCTTT_			
GAM1907	ELF3	3'	CCGCTCGAGTGACCTTGA	16680	G TC	
			TC AAGGTCACTCGA TGG			
			AG TTCCAGTGAGCT GCC			
			— C_			
GAM1907	PIAS1	3'	CCCCAGATCGAATGAACTTGG	32932	G G C	
			C AAG TCA TCGATCTGGGG			
			G TTC AGT AGCTAGACCCC			
			G A A			
GAM1907	AGS3	5'	GCCCCAGACCGAGGAATTCTTC	73510	TCA_ A	
	G		CGAAGG CTCG TCTGGGGC			
			GCTTCT GAGC AGACCCCG			
			TAAG C			
GAM1907	CECR6	3'	TGCCCCAGTCACGATGACC	49936	C AT_	
			GGTCA TCG CTGGGGCA			
			CCAGT AGC GACCCCGT			
			— ACT			
GAM1907	FLJ20004	5'	GTCCCTCAAGTGACTTC	34763	G C TCT	
			GAAG TCACT GA GGGGC			
			CTTC AGTGA CT CCCTG			
			— A —			
GAM1907	FLJ23598	5'	TGCCCCAGACCAGGTTCTCTG	96507	A TC CGA	
	A		TCG AGG ACT TCTGGGGCA			

AGT TCC TGG AGACCCCGT
 C T_ ACC
 GAM1907 KIAA0427 3' TGCCCCAGACGCGGGCCT 29394 ACT A
 AGGTC CG TCTGGGGCA
 ||||| || |||||
 TCCGG GC AGACCCCGT
 GC_ _
 GAM1907 KIAA1644 3' CCCGTGAAAGTGACCTTGA 86220 G CGA _
 TC AAGGTCAC T C TGGG
 || ||||| || ||||
 AG TTCCAGTGA AG GCCC
 G A_ T
 GAM1907 MANBAL 5' TGCCCCAGGCACATGACCTTC 42222 CTCGA
 GAAGGTCA TCTGGGGCA
 ||||| |||||
 CTTCCAGT GGACCCCGT
 ACAC_
 GAM1907 LOC137090 5' CCAGATCCGAGTGACCTTGA 76474 G _
 TC AAGGTCAC TCG ATCTGG
 || ||||| |||||
 AG TTCCAGTGAGC TAGACC
 _ C
 GAM1907 LOC143188 5' TGCTGAACAAGTGACCTTC 83796 CGA TGG
 GAAGGTCACT TC GGCA
 ||||| || ||||
 CTTCCAGTGA AG TCGT
 ACA _
 GAM1907 LOC253639 3' TGCTGTTTCAAGTGACCTC 97520 A C TCTGG
 GA GGTCAC TGA GGCA
 || ||||| || ||||
 CT CCAGTGA CT TCGT
 _ A TTG_
 GAM1907 LOC92106 5' GCTTCACCGAGTGACCTTGA 57228 G ATC
 TC AAGGTCAC TCG TGGGGC
 || ||||| |||||
 AG TTCCAGTGAGC ACTTCG
 _ C_
 GAM1908 ADAM20 5' AGCTCCACCAGGACACAGATCC 15101 TAC GA
 GG CTGTGTCCTGG GAGCT
 || ||||| |||||
 CC GACACAGGACC CTCGA
 TA_ AC
 GAM1908 HIP1 3' CTCTCCCAAAGGGCACACC 19253 ACCT _
 GGT GTGTCCT GGGAGAG
 ||| ||||| |||||
 CCA CACGGGA CCCTCTC
 _ AA
 GAM1908 KCNA6 3' TCCAGGACCAAATACCT 11144 CC T
 AGGTA TG GTCCTGGG
 ||||| || |||||

TCCAT AC CAGGACCT
 AA _
 GAM1908 KCNK4 3' CTCTCCCAGCGCAGAGACC 33982 AC G C
 GGT CT TGT CTGGGAGAG
 ||| || ||| |||||
 CCA GA GCG GACCCTCTC
 GA _ C
 GAM1908 LZTS1 3' GCTCTCCCAGTGAACCTCCT 41034 TACCTGTG _
 AGG TC CTGGGAGAGC
 ||| || |||||
 TCC AG GACCCTCTCG
 TCA _ T
 GAM1908 MUCDHL 3' CCTCCCAGGGACCCT 49203 TACCT G A
 AGG GT TCCTGGGAG G
 ||| || ||||| |
 TCC CA GGGACCCTC C
 _ _ C
 GAM1908 MUCDHL 3' CCTCCCAGGGACCCT 88639 TACCT G A
 AGG GT TCCTGGGAG G
 ||| || ||||| |
 TCC CA GGGACCCTC C
 _ _ C
 GAM1908 SERPINH2 3' AGCCCCTGGGACCAGGCACC 8784 A T TG AGA
 GGT CCTG GTCC GG GCT
 ||| ||| ||| || |||
 CCA GGAC CAGG CC CGA
 C _ GT C _
 GAM1908 SOX12 3' CTCTCCCAAGTGGCATAGCCC 23684 TAC _ _
 GG CTGTGTC CT GGGAGAG
 || ||||| || |||||
 CC GATACGG GA CCCTCTC
 C _ T A
 GAM1908 DKFZp762P2111 3' CTCTCCCAGCAGGGTCCT 87631 TA TGTC
 AGG CCTG CTGGGAGAG
 ||| ||| |||||
 TCC GGAC GACCCTCTC
 TG _
 GAM1908 FLJ23510 5' CCAGACACACAAGTACCT 45624 C C_
 AGGTAC TGTGT CTGG
 ||||| ||||| |||
 TCCATG ACACA GACC
 A CA
 GAM1908 KIAA0057 3' CTCTCCCAGCCAGTGGTCCT 25411 T TG TC
 AGG ACC TG CTGGGAGAG
 ||| ||| || |||||
 TCC TGG AC GACCCTCTC
 _ TG C _
 GAM1908 KIAA0084 3' AGCCCTCCCAGGGCCAGGTTCC 68704 T T A
 T
 AGG ACCTG GTCCTGGGAG GCT
 ||| ||||| ||||| |||

TCC TGGAC CGGGACCCTC CGA
 T _ C
 GAM1908 KIAA0872 3' CCCAGGACACAGCACCT 30748 AC
 AGGT CTGTGTCCTGGG
 |||| |||||
 TCCA GACACAGGACCC
 C_
 GAM1908 KIAA0940 3' AGCCCCTGGGTAACACAGGTCC 30530 T _ TG AGA
 T AGG ACCTGTGT CC GG GCT
 ||| ||||| || || |||
 TCC TGGACACA GG CC CGA
 _ AT GT C_
 GAM1908 KIAA1297 3' AGCTCTCCCAGGCCTGAGGGTA 72626 GTGT_
 CC GGTACCT CCTGGGAGAGCT
 ||||| |||||
 CCATGGG GGACCCTCTCGA
 AGTCC
 GAM1908 KIAA1674 3' AGCACGCAAGACACAGGTACC 69328 C GGAGA
 GGTACCTGTGTC TG GCT
 ||||| || |||
 CCATGGACACAG AC CGA
 A GCA_
 GAM1908 MAFB 3' GCCCTGAGACACAGGCCCT 19591 TA CT AGA
 AGG CCTGTGTC GGG GC
 ||| ||||| || ||
 TCC GGACACAG TCC CG
 C_ AG _
 GAM1908 OSBPL5 3' AGCCCTCCCTCCCAGGCACC 73061 A TGTCTT A
 GGT CCTG GGGAG GCT
 ||| ||| ||||| |||
 CCA GGAC CCCTC CGA
 C CCT_ C
 GAM1908 p25 3' CTCTCCCAAATGGCTCAGCCT 23831 TAC T C_
 AGG CTG GTC TGGGAGAG
 ||| ||| ||| |||||
 TCC GAC CGG ACCCTCTC
 _ T TAAA
 GAM1908 LOC147958 5' CTCCCAGGGCACAAACC 88521 ACC
 GGT TGTGTCCTGGGAG
 ||| |||||
 CCA ACACGGGACCCTC
 A_
 GAM1908 LOC148696 5' AGCCCTCCCAGGGATTGCAGTC 85343 TAC _ A
 CT AGG CTGTG TCCTGGGAG GCT
 ||| ||||| ||||| |||
 TCC GACGT GGGACCCTC CGA
 T_ TA C
 GAM1908 LOC149372 5' AGCTCTCCTTCACAGACACCT 80098 AC TCCT
 AGGT CTGTG GGGAGAGCT
 |||| |||| |||||

TCCA GACAC TCCTCTCGA
 CA T___
 GAM1908 LOC220018 5' AGCCCCCTGTGGGCACAGACAC 95026 AC T__ AGA
 C GGT CTGTGTCC GGG GCT
 ||| ||||| ||| |||
 CCA GACACGGG CCC CGA
 CA TGT C__
 GAM1908 LOC222029 5' TCCCAGGGCACAGACACC 95693 AC
 GGT CTGTGTCCTGGGA
 ||| |||||
 CCA GACACGGGACCCT
 CA
 GAM1908 LOC91355 5' AGCCCCCCCAGGCACGGTCCT 66302 T T T AGA
 AGG ACC GTG CCTGGG GCT
 ||| ||| ||| ||||| |||
 TCC TGG CAC GGACCC CGA
 _ _ _ CCC
 GAM1909 FLJ21438 5' CAAAACGCTTCCCCCATCCCA 62190 GAGATTATC
 TGGGA AAGCGTTTTG
 ||||| |||||
 ACCCT TTCGCAAAAC
 ACCCCCC__
 GAM1909 FLJ32334 3' AAAACGCTATTCCTTCCCA 58605 A TTATCA
 TGGGAG GA AGCGTTTT
 ||||| || |||||
 ACCCTT CT TCGCAAAA
 C TA____
 GAM1909 HHLA2 3' CAATGTACTTTGTAATCTCCCC 23953 A C CG T
 CA TGGG GAGATTAT AAG T TTG
 ||||| ||||| ||| | |||
 ACCC CTCTAATG TTC G AAC
 C T ATT
 GAM1910 ADAT1 3' CCAGCAAAGAATGAAGGC 24914 _ C
 GTC CATTCTTTGC GG
 ||| ||||| ||| |||
 CGG GTAAGAAACG CC
 AA A
 GAM1910 M17S2 5' CCGGTAGCGGACGGTCCTT 20910 ATTCT
 AAGGACCGTCC TTGCCGG
 ||||| |||||
 TTCCTGGCAGG GATGGCC
 C____
 GAM1910 ST14 5' CCGGCAGGGACGACGCCT 42042 AC CAT
 AGG CGTC TCTTTGCCGG
 ||| ||| |||||
 TCC GCAG AGGGACGGCC
 _ C__
 GAM1910 HTGN29 5' GCCAACTGTGTGGCGGTCC 39885 _ TC T
 GGACCGTC CAT TT GC
 ||||| ||| || ||

CCTGGCGG GTG AA CG
 T TC C
 GAM1910 PMAIP1 3' GCAAGAATGGAAGACCCTT 41211 ACCG T
 AAGG TCCATTCTT GC
 ||| ||||| ||
 TTCC AGGTAAGAA CG
 CAGA _
 GAM1910 LOC144278 3' GCCAGCAAAGACTGCTCGATGG 77274 _ T C
 TCCT AGGACCGTC CA TCTTTGC GGC
 ||||| || ||||| ||
 TCCTGGTAG GT AGAAACG CCG
 CTC C A
 GAM1910 LOC147976 3' CCGGTGAATGAAGACCCT 79287 ACC CA _ TG
 AGG GTC TTC TT CCGG
 || || ||| ||
 TCC CAG AAG AA GGCC
 _ _ T GT
 GAM1910 LOC254263 5' GCCGGCAGCGGACGCGCC 96367 AC ATTCT
 GG CGTCC TTGCCGGC
 || ||| |||||
 CC GCAGG GACGGCCG
 GC C_
 GAM1911 FMR2 3' CTGTAAAAACAGAAGTCATT 10691 C C
 GATGACTTCTGTTT TT CAG
 ||||| || ||
 TTAAGTGAAGACAAA AA GTC
 A T
 GAM1911 HD 3' ATCTGGGCCAGAAGTCCTC 10906 T TTTCT
 GA GACTTCTG TCCAGAT
 || ||||| |||||
 CT CTGAAGAC GGGTCTA
 C C_
 GAM1911 NFATC1 3' CTGGAGGAGAAGTCATC 21597 TGTT
 GATGACTTC TCTCCAG
 ||||| |||||
 CTAAGTGAAG AGGAGGTC
 _
 GAM1911 PRKY 3' CATCTGGAAGAAACAGGA 12366
 TTCTGTTTCTTCCAGATG
 |||||
 AGGACAAAGAAGGTCTAC
 _
 GAM1911 SFRP4 3' AAGAAAGCAGAAACCATC 13028 AC _
 GATG TTCTGTTT CTT
 ||| ||||| ||
 CTAC AAGACGAA GAA
 CA A
 GAM1911 SLC14A2 3' CATCCTTAAAGAGAAGTCA 24113 G CTTCCA
 TGACTTCT TTT GATG
 ||||| || |||

ACTGAAGA AAA CTAC
 G TTC____
 GAM1911 ESDN 3' TGGCAAAATAGAAATCATC 56065 C CTT
 GATGA TTCTGTTT CCA
 ||||| ||||| ||
 CTA CTACT AAGATAAA GGT
 A AC_
 GAM1911 FLJ10545 3' CATCTGGAAGTTGAAAAATC 36768 GAC TGTTTC
 GAT TTC TTCCAGATG
 ||| ||| |||||
 CTA AAG AAGGTCTAC
 AA_ TTC____
 GAM1911 FLJ23189 3' ATCCAGAAAAGAAGTCA 47527 G TCCA
 TGACTTCT TTTCT GAT
 ||||| ||||| ||
 ACTGAAGA AAAGA CTA
 _ C____
 GAM1911 KIAA0172 5' CATCCAGAAGAGGCGGAAGCCG 65595 A CA
 TC GATG CTTCTGTTTCTTC GATG
 ||||| ||||| ||||| |||||
 CTGC GAAGGCGGAGAAG CTAC
 C AC
 GAM1911 MGC4796 3' CATCTGGAAAAAATGGGG 62160 C
 TTCTGTTT TTCCAGATG
 ||||| |||||
 GGGGTAAA AAGGTCTAC
 A
 GAM1911 PPP4R2 5' GAAGAAACAGAAGCATC 76830 A
 GATG CTTCTGTTTCTTC
 ||||| ||||| |||||
 CTAC GAAGACAAAGAAG
 _
 GAM1911 LOC128153 3' GAAGAACTGAAGCCATC 57917 A T
 GATG CTTC GTTTCTTC
 ||||| ||||| |||||
 CTAC GAAG CAAAGAAG
 C T
 GAM1911 LOC197358 3' ATCCGGACAGGAACCATC 89420 AC TTTCT A
 GATG TTCTG TCC GAT
 ||||| ||||| ||| |||
 CTAC AGGAC AGG CTA
 CA _____ C
 GAM1911 LOC257096 5' GAAGAAACAGAAGCATC 97627 A
 GATG CTTCTGTTTCTTC
 ||||| ||||| ||||| |||||
 CTAC GAAGACAAAGAAG
 _
 GAM1912 ALG6 3' GAACCATGGAACACAGG 26234 _ GA
 CC GTGGT CGTGGTTC
 || ||||| ||||| |||||

			GG CACCA GTACCAAG		
			A AG		
GAM1912 ALOX15	3'	GGTGCCATCACCACGG	8549	CG	T
		CCGTGGTGA TGGT CC			
		GGCACCCT ACCG GG			
		— T			
GAM1912 CHRNE	3'	GGCTGCCGCCACCACGG	5381	AC	TC
		CCGTGGTG GTGGT CC			
		GGCACCAC CGCCG GG			
		— TC			
GAM1912 EFNA1	3'	GGGAACCACTCCCACCAC	16664	AC_	
		GTGGTG GTGGTTCCC			
		CACCAC CACCAAGGG			
		CCT			
GAM1912 EN2	5'	GGGATTTGCCCCACGGTA	9263	TGAC	T_
		TACCGTGG GTGG TCCC			
		ATGGCACC CGCT AGGG			
		C_ TT			
GAM1912 KCNA6	3'	GGGAACCACAGAGCCAGG	11140	G	GAC
		CC TGGT GTGGTTCCC			
		GG ACCG CACCAAGGG			
		— AGA			
GAM1912 PAK1	5'	GGGAGCCCCGCCACGG	11958	ACGT	
		CCGTGGTG GGTTC			
		GGCACCGC CCGAGGG			
		C_			
GAM1912 RALBP1	3'	GGGAACCACACCAGGT	23277	G	GAC
		ACC TGGT GTGGTTCCC			
		TGG ACCA CACCAAGGG			
		— —			
GAM1912 UPK1B	3'	GGAACCTGTGTTATCACAGTA	23702	C	GT_
		TAC GTGGTGAC GGTTC			
		ATG CACTATTG CCAAGG			
		A TGT			
GAM1912 APCL	3'	GGAAACCCAGCCCCACCACGG	20819	AC	— —
		CCGTGGTG GT GGTT CC			
		GGCACCAC CG CCAA GG			
		CC ACC A			
GAM1912 BC008967	3'	GGAAACCACGTTCACAGC	61417	G	— —
		GT GTGA CGTGGTT CC			

		CG CACT GCACCAA GG		
		A T A		
GAM1912	C8orf17	3' GGAATAGTCTGTTACCACGG	39997	TG__
		CCGTGGTGACG GTTCC		
		GGCACCATTGT TAAGG		
		CTGA		
GAM1912	DKFZP434L0117	5' GGGAACCACCGCTCACCGC	43244	_ _
		GTGGTGA CG TGGTTCCC		
		CGCCACT GC ACCAAGGG		
		C C		
GAM1912	FLJ12581	3' GGAAACCACGTGTTCTGGT	46338	T TG _
		ACCG GG ACGTGGTT CC		
		TGGT CT TGCACCAA GG		
		_ TG A		
GAM1912	GMEB2	3' GGGAACCACACTGCAGTG	25665	C TG GAC
		TAC G GT GTGGTTCCC		
		GTG C CA CACCAAGGG		
		A GT _		
GAM1912	HRI	3' GAGTTGGCAGTCATCACGGTA	27739	_ _ GG
		TACCGTGGTGAC G T TTC		
		ATGGCACTACTG C G GAG		
		A G TT		
GAM1912	KBRAS2	3' GGAAGCAGAGTCACCACG	34625	G_ G
		CGTGGTGAC TG TTCC		
		GCACCACTG AC AAGG		
		AG G		
GAM1912	KIAA0280	3' GGAACCACATTCCAGGTG	93306	G TGAC
		TACC TGG GTGGTTCC		
		GTGG ACC CACCAAGG		
		_ TTA_		
GAM1912	KIAA0285	5' GGGACCAGCAGCCACCATGG	29687	AC_ _
		CCGTGGTG G TGGTTCC		
		GGTACCAC C ACCAGGG		
		CGA G		
GAM1912	KIAA1171	3' GGGTCTGGTCACCACGG	89345	G TT
		CCGTGGTGAC TGG CCC		
		GGCACCCTG GTC GGG		
		_ T_		
GAM1912	KIAA1553	3' GGGAACCACATCAGCAGC	93568	_ G C
		G TG TGA GTGGTTCCC		

			C AC ACT CACCAAGGG		
			G G A		
GAM1912	MGC2477	5'	GGCGCCCGCCACCACGG	44308	A T T
			CCGTGGTG CG GGT CC		
			GGCACCAC GC CCG GG		
			C _ C		
GAM1912	PTDSS1	5'	GGGCCGCCGCCACCGCGG	29252	A _
			CCGTGGTG CG TGGTTC		
			GGCGCCAC GC GCCGGG		
			C C		
GAM1912	SEZ6	3'	GGGAACTGCACCAGGGTA	74831	G GAC TG
			TACC TGGT G GTTCCC		
			ATGG ACCA C CAAGGG		
			G _ _ GT		
GAM1912	STHM	3'	GGATGATGTCACCAGGTA	22308	G G
			TACC TGGTGACGT GTTC		
			ATGG ACCACTGTA TAGG		
			_ G		
GAM1912	ZNF297	3'	GGGAACCACAGTTTCACCA	19571	C _ _
			TGGTGA GTGGTTCCC		
			ACCACT CACCAAGGG		
			TTGA		
GAM1912	LOC145317	3'	GGGAACCAACCACACATG	84282	_ ACG
			CGTG GTG TGGTTCCC		
			GTAC CAC ACCAAGGG		
			A CA _		
GAM1912	LOC146517	3'	GGGAACCACATTAGGG	78509	G GAC
			CC TGGT GTGGTTCCC		
			GG ATTA CACCAAGGG		
			G _ _		
GAM1912	LOC148137	3'	GGTGCCCGCCACCACGGT	59110	A T T
			ACCGTGGTG CG GGT CC		
			TGGCACCAC GC CCG GG		
			C _ T		
GAM1912	LOC153688	3'	GGCTTTGTACCCACGGTA	87323	TG_ T
			TACCGTGG ACG GGTT		
			ATGGCACC TGT TCGG		
			CCA T		
GAM1912	LOC219621	5'	GGGAACCACGCCCGAATCGG	93102	TGG A_
			CCG TG CGTGGTTCCC		

GGC GC GCACCAAGGG
TAA CC
GAM1912 LOC221472 3' GGACTGGTGGTCACCATAGTA 93910 CG G__
TAC TGGTGAC TGGTTC
||| ||||| |||||
ATG ACCACTG GTCAGG
AT GTG
GAM1912 LOC222182 5' GGGAAGCTCCTGCTCACCACGG 95858 C TG ____
CCGTGGTGA G G TTCCC
||||||| | | |||||
GGCACCACT C C AAGGG
__GTCTCG
GAM1912 LOC91700 5' GGGCCTCGGTCGCCACGGTA 67575 __T
TACCGTGGTGAC G GGTTTC
||||||| |||||
ATGGCACCGCTG C CCGGG
G T
GAM1913 CCNF 3' ACCTCGGCCTGCATGGGGCACC 10062 CT__ TCA
GGTGCCCCA GGCT AGGT
||||||| ||| |||||
CCACGGGGT CCGG TCCA
ACGT C__
GAM1913 ESRRG 3' ACCTTGGGTTGATGAAACATCA 66987 CCC CT T
A TTGGTG CA GGCT CAAGGT
||||| || ||||| |||||
AACTAC GT TTGG GTTCCA
AAA AG _
GAM1913 FBXL7 3' CCTTGGCATAGAGCACC 25490 CCCA _ TT
GGTGC CTG GC CAAGG
||||| ||| || |||||
CCACG GAT CG GTTCC
A__ A__
GAM1913 NT5M 3' ACCTCAGGCAGCAGGCACCAA 39890 CCA G TCA
TTGGTGCC CTG CT AGGT
||||||| ||| || |||||
AACCACGG GAC GA TCCA
AC_ G C__
GAM1913 PIK3R2 5' ACCAATGGGGCCAGTGGGGGCTC 18506 T A_
CAA TTGG GCCCCTGGCTTCA GGT
||||| ||||| ||||| ||||| ||||| |||||
AACC CGGGGTGACCGGGGT CCA
T AA
GAM1913 POLS 3' ACCCTGAGTTTTTGGAGACCA 23777 C CT T A
TGGTGC CCA GGCT CA GGT
||||| ||| ||||| || |||||
ACCACG GGT TTGA GT CCA
A TT _ C
GAM1913 RAD52 3' CCTTGGGGATGGGACCCAA 12757 TG CACTGG
TTGG CCC CTCAAGG
||||| ||| |||||

			AACC GGG GGGGTTCC		
			CA TA_____		
GAM1913	RAD52	3'	CCTTGGGGATGGGACCCAA 57025	TG	CACTGG
			TTGG CCC CTTCAAGG		
			AACC GGG GGGGTTCC		
			CA TA_____		
GAM1913	RAD52	3'	CCTTGGGGATGGGACCCAA 57043	TG	CACTGG
			TTGG CCC CTTCAAGG		
			AACC GGG GGGGTTCC		
			CA TA_____		
GAM1913	RAD52	3'	CCTTGGGGATGGGACCCAA 57050	TG	CACTGG
			TTGG CCC CTTCAAGG		
			AACC GGG GGGGTTCC		
			CA TA_____		
GAM1913	HIC2	3'	GGAGCCAGCAGGGCGCCAA 65871	CA	
			TTGGTGCCC CTGGCTTC		
			AACCGCGGG GACCGAGG		
			AC		
GAM1913	KIAA1814	3'	GGAGCCAGTGAAGCCCCAA 70881	T	CC
			TTGG GC CACTGGCTTC		
			AACC CG GTGACCGAGG		
			C AA		
GAM1913	RALGPS1A	3'	GGAGCCATGAGGCACCAA 28334	C	C
			TTGGTGCC CA TGGCTTC		
			AACCACGG GT ACCGAGG		
			A _		
GAM1913	TTY7	5'	ACCTTGAAACAGTGGCTAGGGC 50014	_____	GC
			ACCAG TTGGTGCCC CACTG TTCAAGGT		
			GACCACGGG GTGAC AAGTTCCA		
			ATCG A_		
GAM1913	USP20	3'	GAGCACAGCAAGGCACCAA 22900	CCA	_
			TTGGTGCC CTG GCTT		
			AACCACGG GAC CGAG		
			AAC A		
GAM1913	LOC220739	3'	CCCTGAGCTGGGCACCAA 94517	CACT	T A
			TTGGTGCCC GGCT CA GG		
			AACCACGGG TCGA GT CC		
			_____ C		
GAM1913	LOC254107	5'	CCTCAGGCTGGGCACCAA 96040	CACT	CA
			TTGGTGCCC GGCTT AGG		

AACCACGGG TCGGA TCC
 _____ C_
 GAM1914 ADK 5' CGGGAAGCAGTTGCTGTGGTA 22989 TG CGAGG
 TACCACAGC TTGC CCTG
 ||||| ||| |||
 ATGGTGTCTG GACG GGGC
 TT AA____
 GAM1914 ADRBK2 3' CAGGTCTCGACAATTAGCAGTT 18956 _____ C
 GTG CACAGCTGT TG CGAGGCCTG
 ||||| || |||||
 GTGTTGACG AC GCTCTGGAC
 ATTA A
 GAM1914 APM1 3' CAGGTTGAGGTAGTTGATGGTG 17765 _ GTT GA
 TACCA CAGCT GCC GGCCTG
 ||||| ||| |||||
 GTGGT GTTGA TGG TTGGAC
 A ____ AG
 GAM1914 ASIC4 5' CAGGGGCTGACAGCTGTG 38535 _ GAGG
 CACAGCTGTT GCC CCTG
 ||||| ||| |||
 GTGTCGACAG CGG GGAC
 T _____
 GAM1914 BACH2 3' TGGGTCTCCAAATGGCTGGGGT 41791 A GCC
 A TACC CAGCTGTT GAGGCCTG
 ||| ||||| |||||
 ATGG GTCGGTAA CTCTGGGT
 G AC_
 GAM1914 BHLHB3 3' TGGGTCTTTTCGTCAGTTTGGT 48492 C T CC
 G TACCA AGCTG TG GAGGCCTG
 ||||| ||| |||||
 GTGGT TTGAC GC TTCTGGGT
 _ T TT
 GAM1914 BSN 3' TGGGCCTTTGGCACTTGTGGTG 14395 CTGT _
 TACCACAG TGCCGA GGCCTG
 ||||| ||||| |||||
 GTGGTGT ACGGTT CCGGGT
 C____ T
 GAM1914 CACNA2D3 5' GGGCCTCGGCTTTTGGTG 37842 CAGCTGTT
 TACCA GCCGAGGCCT
 |||| |||||
 GTGGT CGGCTCCGGG
 TTT____
 GAM1914 CASP10 3' CAGGAGGCAGAGGCTGTGGTG 53202 G GAGG
 TACCACAGCT TTGCC CCTG
 ||||| ||| |||
 GTGGTGTCTCGG GACGG GGAC
 A A____
 GAM1914 CASP10 3' CAGGAGGCAGAGGCTGTGGTG 53246 G GAGG
 TACCACAGCT TTGCC CCTG
 ||||| ||||| |||

			GTGGTGTCTGG GACGG GGAC	
			A A__	
GAM1914 CERD4	3'	CAGGCTGGTCCAGTGGCTTTGG 24876		C TG CCGA
	TG	TACCA AGC TTG GGCCTG		
		GTGGT TCG GAC TCGGAC		
		T GT CTGG		
GAM1914 COL11A2	5'	TGGGCCGCTGACAGCTGTCGTG 55634		C _ CGA
		TAC ACAGCTGTT GC GGCCTG		
		GTG TGTCGACAG CG CCGGGT		
		C T__		
GAM1914 COX10	3'	AGGCGAGCATGTTGTGGTA 8945		TGT CGAG
		TACCACAGC TGC GCCT		
		ATGGTGTTG ACG CGGA		
		T__ AG__		
GAM1914 CSNK1G3	3'	GGGTTCTGGCAGATGGTGGTGGT 16510		A _ G TG
	A	TACCAC GCTGT TGCCGAG CC		
		ATGGTG TGGTA ACGGCTT GG		
		G G G T		
GAM1914 CUL3	3'	TTTTGGTGAAGCTGTGGTG 14576		G TG
		TACCACAGCT T CCGAGG		
		GTGGTGTCTGA A GGTTTT		
		_GT		
GAM1914 DDX11	3'	AGGCTGTGGCAGCTGTGG 16570		TG CGA G
		CCACAGCTGT C GGCCT		
		GGTGTCTGACG G TCGGA		
		GT__ G		
GAM1914 DDX11	3'	AGGCTGTGGCAGCTGTGG 16571		TG CGA G
		CCACAGCTGT C GGCCT		
		GGTGTCTGACG G TCGGA		
		GT__ G		
GAM1914 DLG3	5'	GGCGGCGGCGGCGGTGGTG 41207		A GAG
		TACCAC GCTGTTGCC GCC		
		GTGGTG CGGCGGCGG CGG		
		G __		
GAM1914 DTNB	3'	CGGGTTTTTCTGAGCTGTG 41863		GTTGCC
		CACAGCT GAGGCCTG		
		GTGTCTGA TTTTGGGC		
		GTCT__		
GAM1914 DUSP1	3'	TGGGTTTCTAAGCAGTTATGGT 16627		C GCC
	G	TACCA AGCTGTT GAGGCCTG		

			GTGGT TTGACGA CTTTGGGT		
			A AT_		
GAM1914	EFNB2	3'	GGGCAGGACTGTTGTGGTA 15845	T	GCCGAG
			TACCACAGC GTT GCCT		
			ATGGTGTTG CAG CGGG		
			T GA_		
GAM1914	FADD	3'	AGGCGGGGTGCTGTGGTG 15123	TGTT	GAG
			TACCACAGC GCC GCCT		
			GTGGTGTCG TGG CGGA		
			_ GG_		
GAM1914	FCMD	3'	CAGGTACAGATAGTTTGTGGTA 23030	_	GCCGAG
			TACCACAG CTGTT GCCTG		
			ATGGTGTT GATAG TGGAC		
			T ACA_		
GAM1914	FZD1	5'	GGCGGCGGCGGCTGCGGTA 14500	A	GAG
			TACC CAGCTGTTGCC GCC		
			ATGG GTCGGCGGCGG CGG		
			C _		
GAM1914	FZD7	3'	CAGGTTTTGGCATCTTTGTG 14502	CTGT	
			CACAG TGCCGAGGCCTG		
			GTGTT ACGGTTTTGGAC		
			TTCT		
GAM1914	GABRE	3'	TAGGCCTTGGTGACTTCCTGGG 18290	A	CT_ TG
			CC CAG GT CCGAGGCCTG		
			GG GTC CA GGTTCGGAT		
			_ CTT GT		
GAM1914	GABRE	3'	TAGGCCTTGGTGACTTCCTGGG 18291	A	CT_ TG
			CC CAG GT CCGAGGCCTG		
			GG GTC CA GGTTCGGAT		
			_ CTT GT		
GAM1914	GAS7	3'	GGGTTCCAGGCAGCTGTG 14669	GCC	G
			CACAGCTGTT GAG CC		
			GTGTCGACGG CTT GG		
			AC_ G		
GAM1914	GPR85	5'	CAGGCTTTGTGGTGTCTGTGGT 39102	C TT	C
	A		TACCACAG TG GC GAGGCCTG		
			ATGGTGTC GT TG TTTCGGAC		
			T GG _		
GAM1914	GRINL1A	3'	TGGGTAAAGCAACAGCTGTG 70072	CGAG	
			CACAGCTGTTGC GCCTG		

			GTGTCGACAACG	TGGGT		
			AAA_			
GAM1914	HOXA3	3'	CAGGCGGCTGCGGCAGCTCTGG	48399	C	CGAG
	TA		TACCA AGCTGTTGC	GCCTG		
			ATGGT TCGACGGCG	CGGAC		
			C	TCGG		
GAM1914	HOXB5	3'	AGGGGCAGCAGTTGAGGTG	10956	A	GAGG
			TACC CAGCTGTTGCC	CCT		
			GTGG GTTGACGACGG	GGA		
			A			
GAM1914	HSD17B1	3'	GGGCGGCGGTAGCAGCTGTGG	6429		AG G
			CCACAGCTGTTGCCG	GCCT		
			GGTGTGACGATGGC	CGGG		
			GG	G		
GAM1914	IDS	5'	CGGGCCCGGGCGGCGGCTGTG	5775		GA
			CACAGCTGTTGCC	GGCCTG		
			GTGTCGGCGGCGG	CCGGGC		
			GC			
GAM1914	ITGB3	3'	CAGGCCTGACTCTCAGCAGCTA	5801	C	CCG__
	TGGTA		TACCA AGCTGTTG	AGGCCTG		
			ATGGT TCGACGAC	TCCGGAC		
			A	TCTCAG		
GAM1914	IVD	3'	AGGTTTTGGTGA	CTGTG	11089	CT TG
			CACAG GT	CCGAGGCCT		
			GTGTC CA	GGTTTTGGA		
			T_	GT		
GAM1914	JRK	3'	GGGCCTTGAGGATGTGGTA	87831	G	GTTGC
			TACCACA CT	CGAGGCCT		
			ATGGTGT GG	GTTCCGGG		
			A	A__		
GAM1914	KCNA6	5'	AGGGAGGAGGTGGCGGCTGTGG	11136		TG GAGG G
			CCACAGCTGT CC	CCT		
			GGTGTGCGCG	GG GGG		
			GT	AGGA AT		
GAM1914	KCNA7	3'	TGGGTCTTGGGTTGTGTGGTTT	49910	C	TG TG__
	GGTA		TACCA AGC T	CCGAGGCCTG		
			ATGGT TTG G	GGTTCTGGGT		
			_	GT TGTTG		
GAM1914	MAP2K2	5'	CGGGCCTCGGCAGCGGTAGCGG	48404		ACA
			CC	GCTGTTGCCGAGGCCTG		

			GG TGGCGACGGCTCCGGGC		
			CGA		
GAM1914	MAP3K12	3'	GGGACACTGGCAGCTGTGG 21943	GTT	AGG_ G
			CCACAGCT GCCG CCT		
			GGTGTCTGA CGGT GGG		
			___ CACA A		
GAM1914	MLC1	3'	CAGGCTGCAGGGACAGTTGGGT 58288	A	G GA_
	G		TACC CAGCTGTT CC GGCCTG		
			GTGG GTTGACAG GG TCGGAC		
			___ _ ACG		
GAM1914	MYO1E	3'	CAGGCCTAGAGAATGGCTGTAG 18438	_	GCCG
	GTG		TACC ACAGCTGTT AGGCCTG		
			GTGG TGTCGGTAA TCCGGAC		
			A GAGA		
GAM1914	NAGA	3'	TGGGACATGTGACAGGCTGTGG 6041	_	TG CGAGG
	TG		TACCACAGC TGT C CCTG		
			GTGGTGTCTG ACA G GGGT		
			G GT TACA_		
GAM1914	NYX	3'	TGGGCTTGAGTGTGTTTGTGGT 42906	CTGT	_ G TG
	A		TACCACAG TGC CGAG CC		
			ATGGTGTT GTG GTTC GG		
			TGT_ A G T		
GAM1914	OGG1	5'	GGCAGGCAGCAGCTGTGG 34159	GAG	
			CCACAGCTGTTGCC GCC		
			GGTGTCTGACGACGG CGG		
			A_		
GAM1914	PKIB	3'	GTCTGGTGGTAAGTGTGGTA 51638	C TT	G
			TACCACAG TG GCC AGGC		
			ATGGTGTC AT TGG TCTG		
			A GG _		
GAM1914	PTPRK	3'	TAGGTAAATAATGGTTTGGTG 12620	C	CCGAG
			TACCA AGCTGTTG GCCTG		
			GTGGT TTGGTAAT TGGAT		
			___ AAA_		
GAM1914	RAB36	3'	CGGGCCAGTGCAGGCACTGTGG 18164	C	_ CGA
	TG		TACCACAG TGT TGC GGCCTG		
			GTGGTGTCTG ACG ACG CCGGGC		
			_ G TGA		
GAM1914	RAB6A	5'	AGGGGCGGCGGCAGCTGTGG 12713	AGG	G
			CCACAGCTGTTGCCG CCT		

			GGTGTCTGACGGCGGC	GGA		
			GG_ G			
GAM1914	RAD1	3'	CGGGAGGCGGAGGTTGTGGTG	12643	G	GAGG
			TACCACAGCT TTGCC	CCTG		
			GTGGTGTGG	GGCGG GGGC		
			A A__			
GAM1914	RASGRP1	5'	GGCAGGCGGCGGCGGTGGTG	20418	A	GAG
			TACCAC GCTGTTGCC	GCC		
			GTGGTG	CGGCGGCGG CGG		
			G A__			
GAM1914	RBL1	3'	CAGGAAGCGGAGGTTGTGGTG	12786	GTTG	AGG
			TACCACAGCT CCG	CCTG		
			GTGGTGTGG	GGC GGAC		
			A__ GAA			
GAM1914	REPS2	5'	AGGAGGCGGTGGCTGTGG	17553	TG	GAGG
			CCACAGC TTGCC	CCT		
			GGTGTCTG	GGCGG GGA		
			GT A__			
GAM1914	REPS2	5'	GGTGGCGGCGGCGGTGGTG	17556	A	GAG
			TACCAC GCTGTTGCC	GCC		
			GTGGTG	CGGCGGCGG TGG		
			G _			
GAM1914	SCA1	3'	CGGGCTTCTTGAGCTGTG	6178	GTTGCC	
			CACAGCT GAGGCCTG			
			GTGTCGA	CTTCGGGC		
			GTT__			
GAM1914	SCN4A	3'	TAGGCCTGTGTGTATAGCTGTG	6205	T _ _	
			CACAGCTGT GC CG	AGGCCTG		
			GTGTCGATA TG GT	TCCGAT		
			_ T G			
GAM1914	SFRP5	5'	GGCGGCGGCGGCTGGGTA	13034	A	GAG
			TACC CAGCTGTTGCC	GCC		
			ATGG	GTCGGCGGCGG CGG		
			- -			
GAM1914	SLC15A1	3'	CAGGTTTAAATGGCTGTG	18637	GCCG	
			CACAGCTGTT	AGGCCTG		
			GTGTCGGTAA	TTTGAC		
			AA__			
GAM1914	SLC1A1	5'	GTGGCGGCGGCAACGGCGGTGG	16057	A	AG TG
	TG		TACCAC GCTGTTGCCG	GCC		

			GTGGTG CGGCAACGGC CGG		
			G GG TGG		
GAM1914	SLC1A4	3'	GGGTGTTAGCACTGTGGTG 13175	CTGT	CG G
			TACCACAG TGC A GCCT		
			GTGGTGTC ACG T TGGG		
			____ AT G		
GAM1914	SLC30A4	5'	GGGAGAGGCGGTGGCTGTGG 26156	TG	GAGG G
			CCACAGC TTGCC CCT		
			GGTGTGC GGCGG GGG		
			GT AGA_ G		
GAM1914	SLC7A4	3'	TGGGCCTTGGCTGGTGCTG 65820	TGTT	
			CAGC GCCGAGGCCTG		
			GTCG CGGTTCCGGGT		
			TGGT		
GAM1914	SLC7A6	3'	TGGGCTCAGAAATGTCTGTGGT 15644	C	GCC G TG
	A		TACCACAG TGTT GAG CC		
			ATGGTGTC GTAA CTC GG		
			T AGA G T		
GAM1914	SYT4	3'	GGTGGTAGCAGCTGAGGTA 63110	A	GAG
			TACC CAGCTGTTGCC GCC		
			ATGG GTCGACGATGG TGG		
			A ____		
GAM1914	WHSC1	3'	CAGGTTAGAAGACGACTGTGGT 24654	C	GCCGA
	G		TACCACAG TGTT GGCCTG		
			GTGGTGTC GCAG TTGGAC		
			A AAGA_		
GAM1914	WHSC1L1	3'	CAGGCAGAAGCAGTTGGTGGTG 35496	_	GCCGAG
			TACCAC AGCTGTT GCCTG		
			GTGGTG TTGACGA CGGAC		
			G AGA_		
GAM1914	YES1	3'	TTGGCAGTGGTTCTGGTA 19547	C	TG
			TACCA AGC TTGCCGA		
			ATGGT TTG GACGGTT		
			C GT		
GAM1914	ALDH9	5'	GGGTATGGCGGCGTGGTG 7346	AGCT	AG
			TACCAC GTTGCCG GCCT		
			GTGGTG CGGCGGT TGGG		
			____ A_		
GAM1914	AP3S2	3'	AGGCTGGAGTGCTGTGGTG 20645	TGTTG	GA
			TACCACAGC CC GGCCT		

GTGGTGTCTG GG TCGGA
 TGA__ __
 GAM1914 AQP10 3' CAGTGCTGGTAATGGCTGGTGG 55393 _ GA _
 TG TACCAC AGCTGTTGCC GGC CTG
 ||||| ||||| || |||
 GTGGTG TCGGTAATGG TCG GAC
 G _ T
 GAM1914 ARHGDIG 3' AGGCAGGAGCAGTGTGGTA 8616 G G GAG
 TACCACA CTGTT CC GCCT
 ||||| |||| || |||
 ATGGTGT GACGA GG CGGA
 _ _ A_
 GAM1914 BZW2 3' CAGGCCACTTTGGTAGTTGTG 26733 GTT _
 CACAGCT GCCGA GGCCTG
 ||||| |||| |||||
 GTGTTGA TGGTT CCGGAC
 _ TCA
 GAM1914 C20orf126 3' CGGGCCTTGGTAGCCACCAGTG 48731 AGCT_
 G CCAC GTTGCCGAGGCCTG
 ||| |||||
 GGTG CGATGGTTCCGGGC
 ACCAC
 GAM1914 C20orf126 3' TGGGTGTGTGGGGCAGTGGCTG 48736 TG GAG_
 TGG CCACAGC TTGCC GCCTG
 ||||| |||| |||||
 GGTGTCG GACGG TGGGT
 GT GGTGTG
 GAM1914 C20orf177 3' CGGGAGGCGGAGGTTGTGGTG 62832 G GAGG
 TACCACAGCT TTGCC CCTG
 ||||| |||| |||
 GTGGTGTTGG GGCGG GGGC
 A A_
 GAM1914 C20orf178 3' TGGGCCCAGACAGACTGTGGTG 75294 _ GCCGA
 TACCACAG CTGTT GGCCTG
 ||||| |||| |||||
 GTGGTGTC GACAG CCGGGT
 A AC_
 GAM1914 CBX5 5' GGCGGTGGTGGCTTGTGGTG 25062 _ TG TG GAG
 TACCACA GC T CC GCC
 ||||| || | || |||
 GTGGTGT CG G GG CGG
 T GT GT _
 GAM1914 CECR6 3' TGGGCTTAGAGTAATAGCTTTG 49937 C CG_
 GTG TACCA AGCTGTTGC AGGCCTG
 ||||| ||||| |||||
 GTGGT TCGATAATG TTCGGGT
 T AGA
 GAM1914 CHL1 3' GGGTTTGTTATCTGTGGTA 22766 C TTGC G
 TACCACAG TG CGAG CC
 ||||| || ||| ||

		ATGGTGTC AT GTTT GG	
		T T___ G	
GAM1914 CHST3	3'	CAGGCAGAAGCAGCTGTGGT 16231	GCCGAG
		ACCACAGCTGTT GCCTG	
		TGGTGTGACGA CGGAC	
		AGA___	
GAM1914 CHST3	3'	CGGGCTTTTATTTATGGCTTGG 16235	C TGCC_
TG		TACCA AGCTGT GAGGCCTG	
		GTGGT TCGGTA TTTCGGGC	
		_ TTTAT	
GAM1914 COVA1	3'	GTGTGGTGGTGGTTGTGGTA 73644	TG TG AG
		TACCACAGC T CCG GC	
		ATGGTGTTG G GGT TG	
		GT GT G_	
GAM1914 CXorf12	3'	CGGGCTTCGGTGTGGAGGGGTG 14487	ACAG TG T
		TACC C T GCCGAGGCCTG	
		GTGG G G TGGCTTCGGGC	
		GGA_ GT _	
GAM1914 D21S2056E	3'	GGGAGGCAGAGGTTGTGGTG 14868	G GAGG
		TACCACAGCT TTGCC CC	
		GTGGTGTGG GACGG GG	
		A AG___	
GAM1914 DKFZP434C128	3'	TGGGTTGTGCTGGCAGCTGTGG 65472	_ CGA
		CCACAGCTGTT GC GGCCTG	
		GGTGTGACGG CG TTGGGT	
		T TG_	
GAM1914 DKFZP434K1772	5'	CAGGCGTCCTGATGGCTGTGG 68333	GCC G
		CCACAGCTGTT GA GCCTG	
		GGTGTGCGTAG CT CGGAC	
		TC_ G	
GAM1914 DKFZP434L1435	3'	GGTCGCAGTGA CTGTGGTG 99685	C GT CGA
		TACCACAG T TGC GGCC	
		GTGGTGTC G ACG CTGG	
		A TG ___	
GAM1914 DKFZp761B0514	3'	CAGGAGCTCTGGCAGCTGTGG 51143	GCC G_
		CCACAGCTGTT GAG CCTG	
		GGTGTGACGG CTC GGAC	
		T_ GA	
GAM1914 DNAJC6	3'	TAGGTTTGTGAGCAGTTGTGGT 29496	GC G
A		TACCACAGCTGTT CGAG CCTG	

ATGGTGTTGACGA GTTT GGAT
 GT _
 GAM1914 EVI5 3' AGGCTGGAGTGCTGTGGTG 20197 TGTTG GA
 TACCACAGC CC GGCCT
 ||||| || ||||
 GTGGTGTCG GG TCGGA
 TGA__ __
 GAM1914 FIGN 3' GGTGGTGATGGTGGTGGTA 36576 A TG GAG
 TACCAC GCTGT CC GCC
 ||||| |||| || |||
 ATGGTG TGGTA GG TGG
 G GT ____
 GAM1914 FLJ10043 3' CAGGAGGTGGAGGTTGTGGTG 36230 G TG GAGG
 TACCACAGCT T CC CCTG
 ||||| || || ||||
 GTGGTGTTGG G GG GGAC
 A GT A ____
 GAM1914 FLJ10466 5' CAGGACCTAGGTGGCGGCGGTG 36629 A TG G _
 GTA TACCAC GCTGT CC AGG CCTG
 ||||| |||| || || ||||
 ATGGTG CGGCG GG TCC GGAC
 G GT A A
 GAM1914 FLJ10477 5' TGGGAGACGGGCGATGGCTGTG 36641 GAGG_
 GT ACCACAGCTGTTGCC CCTG
 ||||| |||| ||||
 TGGTGTCGGTAGCGG GGGT
 GCAGA
 GAM1914 FLJ11370 3' GGGAGGCGGAGGTTGTGGTG 46967 G GAGG
 TACCACAGCT TTGCC CC
 ||||| |||| ||
 GTGGTGTTGG GGCGG GG
 A AG__
 GAM1914 FLJ11827 3' GGTTGTGACATTGTGGTA 47682 C TG CGA
 TACCACAG TGT C GGCC
 ||||| || | ||||
 ATGGTGTT ACA G TTGG
 _ GT ____
 GAM1914 FLJ12122 5' TAGGTCCCCACAGCTGTGG 47096 TGCCGA
 CCACAGCTGT GGCCTG
 ||||| ||||
 GGTGTCGACA CTGGAT
 CCC__
 GAM1914 FLJ12377 5' GGCGGCGGCGGCGGTGGTG 47122 A GAG
 TACCAC GCTGTTGCC GCC
 ||||| ||||| |||
 GTGGTG CGGCGGCGG CGG
 G ____
 GAM1914 FLJ12389 3' TGGGCCGCGAGGTGTGGCACTGT 60903 C _ GA_
 GGTG TACCACAG TGTT GCC GGCCTG
 ||||| |||| || |||||

		GTGGTGTC ACGG TGG CCGGGT	
		_ TG ACG	
GAM1914	FLJ13322	3' GGGAGGCTGCAGTTGTGGTA 45631	T GAGG
		TACCACAGCTGT GCC CC	
		ATGGTGTTGACG CGG GG	
		T AG__	
GAM1914	FLJ13456	3' GGGAGGTGGAGGTTGTGGTG 66557	G TG GAGG
		TACCACAGCT T CC CC	
		GTGGTGTTGG G GG GG	
		A GT AG__	
GAM1914	FLJ13615	5' CGGGTCCAGCTTGGTGGTTGCG 47795	A GTT ____
	GTA	TACC CAGCT GCCGAG GCCTG	
		ATGG GTTGG TGGTTC TGGGC	
		C ____ GACC	
GAM1914	FLJ13848	3' CAGGAGGTGGAGGTTGTGGTG 45818	G TG GAGG
		TACCACAGCT T CC CCTG	
		GTGGTGTTGG G GG GGAC	
		A GT A__	
GAM1914	FLJ13952	3' CGGGAGGCGGAAGTTGTGGTG 46012	G GAGG
		TACCACAGCT TTGCC CCTG	
		GTGGTGTTGA GGCGG GGGC	
		A A__	
GAM1914	FLJ14213	3' AGGCCTTGGCACGGTGCTG 46214	TGT_
		CAGC TGCCGAGGCCT	
		GTCG ACGGTTCCGGA	
		TGGC	
GAM1914	FLJ14251	3' GGGAGGCAGAAGTTGTGGTG 46486	G GAGG
		TACCACAGCT TTGCC CC	
		GTGGTGTTGA GACGG GG	
		A AG__	
GAM1914	FLJ14600	5' TGGGCCTCCAGGCTGTGGTA 52528	GTTGCC
		TACCACAGCT GAGGCCTG	
		ATGGTGTCGG CTCCGGGT	
		AC__	
GAM1914	FLJ20371	3' GGCTGCAATACTGTGGTG 35538	C CGA
		TACCACAG TGTTGC GGCC	
		GTGGTGTC ATAACG TCGG	
		- -	
GAM1914	FLJ20373	3' TGGGCACTCTGGTGGTGTGT 35543	CT TT _ _
	GGTG	TACCACAG G GCC GAG GCCTG	

		GTGGTGT T TGG CTC CGGGT	
		TG GG T A	
GAM1914 FLJ20400	3'	TAGGTAAAAGGGTAGTTGTGG 67105	TTG GAG_
		CCACAGCTG CC GCCTG	
		GGTGTGAT GG TGGAT	
		G_ AAAA	
GAM1914 FLJ21562	3'	AGGGCTGATAGTTGTGGT 47793	GCCG G
		ACCACAGCTGTT AG CCT	
		TGGTGTGATAG TC GGA	
		_____ G	
GAM1914 FYCO1	3'	GGGCCTGCAATGGCTGTG 44775	CG
		CACAGCTGTTGC AGGCCT	
		GTGTCGGTAACG TCCGGG	

GAM1914 H2-ALPHA	5'	TGGGCGCTCAGCAGCTGTGG 73378	GCC _
		CCACAGCTGTT GAG GCCTG	
		GGTGTGACGA CTC CGGGT	
		_____ G	
GAM1914 HCBP6	3'	GGCTGCAACAGCTGTGG 81779	CGA
		CCACAGCTGTTGC GGCC	
		GGTGTGACAACG TCGG	

GAM1914 HEAB	5'	CAGGTGGGAGATGACAGCTTGG 23360	C _ GAG
TG		TACCA AGCTGTTG CC GCCTG	
		GTGGTTCGACAGT GG TGGAC	
		_____ AGA G_	
GAM1914 HSGT1	5'	CAGGCTTCGGCGGCCGGTGG 24389	AGCT
		CCAC GTTGCCGAGGCCTG	
		GGTG CGGCGGCTTCGGAC	
		GC_	
GAM1914 JIK	3'	GGGCTTTGGCAAATGGGTA 33265	ACAGCTG
		TACC TTGCCGAGGCCT	
		ATGG AACGGTTTCGGG	
		GTA_	
GAM1914 KHDRBS1	3'	TAGGTTTTGAAGAGGTTGATGG 22663	_ G GC
TG		TACCA CAGCT TT CGAGGCCTG	
		GTGGT GTTGG GA GTTTTGGAT	
		A A A_	
GAM1914 KIAA0146	3'	GGGTGGTGGTGGTGGTGGTGG 82323	A TG TG GAG G
		TACCAC GC T CC GCCT	

	GTGGTG TG G GG TGGG	
	G GT GT ____ A	
GAM1914 KIAA0217	3' CGGGCGACGGGTAGTGGTGGTG 67600	A TTG AG
	TACCAC GCTG CCG GCCTG	
	GTGGTG TGAT GGC CGGGC	
	G G__ AG	
GAM1914 KIAA0252	3' GGGAGGCGGAGGTTGTGGTG 63459	G GAGG
	TACCACAGCT TTGCC CC	
	GTGGTGTTGG GGCGG GG	
	A AG__	
GAM1914 KIAA0423	5' GCCCGGTGGCAGCTGTGG 89182	TG A
	CCACAGCTGT CCG GGC	
	GGTGTGACG GGC CCG	
	GT _	
GAM1914 KIAA0441	5' CGGGTTGGCTGTGGCTGTGG 29632	TG T AG
	CCACAGC T GCCG GCCTG	
	GGTGTG G CGGT TGGGC	
	GT T _	
GAM1914 KIAA0469	3' TGGGCAGGAGGTGGCTTTGGTG 29999	C TG TG GAG
	TACCA AGC T CC GCCTG	
	GTGGT TCG G GG CGGGT	
	T GT GA A__	
GAM1914 KIAA0544	3' AGGGCTGGTGGCTGGGTG 71457	A GTT G G
	TACC CAGCT GCC AG CCT	
	GTGG GTCGG TGG TC GGA	
	_ _ _ G	
GAM1914 KIAA0552	3' AGGTCTCTGAGCTGGGTG 28987	A GTTGCC
	TACC CAGCT GAGGCCT	
	GTGG GTCGA CTCTGGA	
	_ GT__	
GAM1914 KIAA0563	5' TAGGTAAGAACGGCTGTGG 29889	GCCGAG
	CCACAGCTGTT GCCTG	
	GGTGTGCGCAA TGGAT	
	GAA__	
GAM1914 KIAA0914	3' CAGGGGGCTGGCAGCTGCGGTG 30294	A _ GAGG
	TACC CAGCTGTT GCC CCTG	
	GTGG GTCGACGG CGG GGAC	
	C T G__	
GAM1914 KIAA1010	3' AGTGTTGGTAATGGTTGTG 72538	G CTG
	CACAGCTGTTGCCGA GC	

		GTGTTGGTAATGGTT TG		
		G AC		
GAM1914 KIAA1041	3'	GGGTTTTTTAGTGGTGGTA 30825	A	TTGCC
		TACCAC GCTG GAGGCCT		
		ATGGTG TGAT TTTTGGG		
		G T____		
GAM1914 KIAA1056	3'	TGGGCCACTGGGGGAGCTGTGG 30318	G G	A_
	TG	TACCACAGCT TT CCG GGCCTG		
		GTGGTGTCTGA GG GGT CCGGGT		
		_ G CA		
GAM1914 KIAA1085	5'	CAGTGAGAGTAGCAGTGGTGGT 40733	A	CGAGGC
	A	TACCAC GCTGTTGC CTG		
		ATGGTG TGACGATG GAC		
		G AGAGT_		
GAM1914 KIAA1183	3'	TGGGCACAGCAGCCTGTGGTG 63200	_	CCGAG
		TACCACAG CTGTTG GCCTG		
		GTGGTGTCTGACGAC CCGGT		
		C A____		
GAM1914 KIAA1193	5'	CGGGCTTGCAGACAACAGCAGT 68267	A	CCG__
	GGTG	TACCAC GCTGTTG AGGCCTG		
		GTGGTG CGACAAC TTCGGGC		
		A AGACG		
GAM1914 KIAA1228	3'	CAGGCCTGTGTGTAGCTGTG 65671	GTT	CG
		CACAGCT GC AGGCCTG		
		GTGTCGA TG TCCGGAC		
		TG_ TG		
GAM1914 KIAA1257	3'	TGGTGTGGTGGTGGCTGTGGTG 63426	TG TG	AG TG
		TACCACAGC T CCG GCC		
		GTGGTGTCTG G GGT TGG		
		GT GT G_ T		
GAM1914 KIAA1434	3'	TAGGTCCTTGCATCTGTGGTG 70213	CTGT	C _
		TACCACAG TGC GAGG CCTG		
		GTGGTGTCTG ACG TTCC GGAT		
		T__ _ T		
GAM1914 KIAA1550	3'	AGGCCAGGCAGCTGTGG 67152	GTT	GA
		CCACAGCT GCC GGCCT		
		GGTGTCTGA CGG CCGGA		
		_ A_		
GAM1914 KIAA1550	3'	AGGCCAGGCAGCTGTGG 67153	GTT	GA
		CCACAGCT GCC GGCCT		

		GGTGTCTGA CGG CCGGA	
		___ A_	
GAM1914 KIAA1649	5'	GGGTCTCCTAGCTGTG 51247	TTGCC
		CACAGCTG GAGGCCT	
		GTGTCTGAT CTCTGGG	
		C___	
GAM1914 KIAA1656	3'	GGAGCCAGTAAAGGCTGTGGTG 66374	G CGA _ G
		TACCACAGCT TTGC GGC CT	
		GTGGTGTCTCGG AATG CCG GG	
		A A_ A G	
GAM1914 KIAA1656	3'	GGGTCTCGGTGGGCCTGTG 66382	CTG TG
		CACAG T CCGAGGCCT	
		GTGTC G GGCTCTGGG	
		CG_ GT	
GAM1914 KIAA1877	3'	GGGTGAGGTGGCTGTGGTG 66754	GTT GAG
		TACCACAGCT GCC GCCT	
		GTGGTGTCTCGG TGG TGGG	
		___ AG_	
GAM1914 KIAA1924	3'	TGGGCCTCGGTGGCGAGGTGGT 74063	AGC TG
		ACCAC TGT CCGAGGCCTG	
		TGGTG GCG GGCTCCGGGT	
		GA_ GT	
GAM1914 KIAA1940	5'	CAGGTCATCAGCAGCAGCTGTG 80778	C _
G		CCACAGCTGTTGC GA GGCCTG	
		GGTGTCTGACGACG CT CTGGAC	
		A A	
GAM1914 KR18	3'	CAGGAGGCGGAGGTTGTGGTG 53886	G GAGG
		TACCACAGCT TTGCC CCTG	
		GTGGTGTGGG GGCGG GGAC	
		A A_	
GAM1914 LAT1-3TM	5'	CGGGTATTTAGTACTGTGGTG 49142	CTGT CG _
		TACCACAG TGC AG GCCTG	
		GTGGTGTCT ATG TT TGGGC	
		___ AT A	
GAM1914 MAPK8IP3	3'	CAGGCCCTGTGTGGCTGTGG 54137	GTT _ A
		CCACAGCT GC CG GGCCTG	
		GGTGTCTCGG TG GT CCGGAC	
		___ T C	
GAM1914 MBIP	5'	AAATCTTGGTGGTGGTGGTGGT 33893	A TG TG CCTG
G		TACCAC GC T CCGAGG	

			GTGGTG TG G GGTTC			
			G GT GT AAAC			
GAM1914	MESDC1	5'	TGGCCGCGGCAGCGGCGGTGGT 42903	A	A	TG
	A		TACCAC GCTGTTGCCG GGCC			
			ATGGTG CGGCGACGGC CCGG			
			G G T			
GAM1914	MGC13010	3'	TGGGCTGGACACGGTTGTGG 52063	TG	GA	
			CCACAGCTGT CC GGCCTG			
			GGTGTGGCA GG TCGGGT			
			CA _			
GAM1914	MGC13198	5'	GGGAGGCGGAGGTTGTGGTG 52071	G	GAGG	
			TACCACAGCT TTGCC CC			
			GTGGTGTTGG GGCGG GG			
			A AG_			
GAM1914	MGC14376	3'	CAGGCTTCCTGGATGACAGTTG 52913	A	_ _	
	GGTG		TACC CAGCTGTTG CC GAGGCCTG			
			GTGG GTTGACAGT GG CTTCGGAC			
			_ A TC			
GAM1914	MGC16385	3'	GGGAGGCGGAGGTTGTGGTG 59540	G	GAGG	
			TACCACAGCT TTGCC CC			
			GTGGTGTTGG GGCGG GG			
			A AG_			
GAM1914	MGC21621	3'	GGGACTGGCACTGTGGTG 59441	CTGT	G G	
			TACCACAG TGCC AG CCT			
			GTGGTGTC ACGG TC GGG			
			_ _ A			
GAM1914	MGC3248	3'	GGTGCTGGTGGTTGTGGTG 51650	GTT	AG	
			TACCACAGCT GCCG GCC			
			GTGGTGTTGG TGGT TGG			
			_ CG			
GAM1914	MGC34869	3'	TGGGTTTTGGGTGTTGGCTGGG 58721	A	TTG_	
	TA		TACC CAGCTG CCGAGGCCTG			
			ATGG GTCGGT GGTTTTGGGT			
			_ TGTG			
GAM1914	MGC4368	3'	CAGGCCCGAGGAATGGCTGGGTA 44724	A	G GA	
			TACC CAGCTGTT CC GGCCTG			
			ATGG GTCGGTAA GG CCGGAC			
			_ _ AC			
GAM1914	MGLL	5'	CAGGCTGTCGTGGTTGTGG 24418	TG T	CGA	
			CCACAGC T GC GGCCTG			

		GGTGTTG G TG TCGGAC		
		GT C ____		
GAM1914 OSBPL8	5'	GGCCAGGCGGCGGCTGTAGTG 40847	C	GA
		TAC ACAGCTGTTGCC GGCC		
		GTG TGTCGGCGGCGG CCGG		
		A A_		
GAM1914 P450RAI-2	3'	CAGGCAGCGGGGTGGTGGTTGT 39570	TG TG	__ AG
	GG	CCACAGC T CC G GCCTG		
		GGTGTTG G GG C CGGAC		
		GT GT GG GA		
GAM1914 PRO2214	3'	CAGGTCCATCTATGTTGTGGTA 38169	TGTTGCCGA	
		TACCACAGC GGCCTG		
		ATGGTGTTG CTGGAC		
		TATCTAC__		
GAM1914 PTPRT	3'	TGGGTAAGGCATGGGGTTGTGG 56512	GT_	GAG
	TG	TACCACAGCT TGCC GCCTG		
		GTGGTGTTGG ACGG TGGGT		
		GGT AA_		
GAM1914 RAB14	3'	TAGGCTTTGGTTAATTTGTGG 33337	CTGTT	
		CCACAG GCCGAGGCCTG		
		GGTGTT TGGTTTCGGAT		
		TAAT_		
GAM1914 RALGPS1A	3'	TGGGTCCTTGACAGCTGTG 28339	TGCC	_
		CACAGCTGT GAGG CCTG		
		GTGTCGACG TTCC GGGT		
		____ T		
GAM1914 RDHL	3'	AGGCTTTGCCTGCTTGGTG 60692	C TGTT	C
		TACCA AGC GC GAGGCCT		
		GTGGT TCG CG TTTCGGA		
		_ TC_ _		
GAM1914 RNO2	5'	CGGGAGGCGGAGGTTGTGGTG 53934	G	GAGG
		TACCACAGCT TTGCC CCTG		
		GTGGTGTTGG GGCGG GGGC		
		A A_		
GAM1914 SIMRP7	3'	TGGGCAGAGGCAGCTGTTGTG 93982	T	GAG
		CACAGC GTTGCC GCCTG		
		GTGTTG CGACGG CGGGT		
		T AGA		
GAM1914 SS18L1	3'	CAGGAGACAGAGGTTGTGGTG 65951	G	CCGAGG
		TACCACAGCT TTG CCTG		

		GTGGTGTGG GAC GGAC	
		A AGA__	
GAM1914	TGOLN2	5' CAGACTGTTGTGGCTGTGGTG 64741	TG T CG GC
		TACCACAGC T GC AG CTG	
		GTGGTGTGCG G TG TC GAC	
		GT T __ A_	
GAM1914	TRIM28	5' CGGGTTTCGGCGGCGGCTGAGG 20457	A
		CC CAGCTGTTGCCGAGGCCTG	
		GG GTCGGCGGCGGCTTTGGGC	
		A	
GAM1914	TRIP13	5' CGGGCTGAGGCAGCGGCTGTGG 16178	GA
		CCACAGCTGTTGCC GGCCTG	
		GGTGTGCGCGACGG TCGGGC	
		AG	
GAM1914	VDU1	3' AGGCTGGAGTGCTGTGGTG 31118	TGTTG GA
		TACCACAGC CC GGCCT	
		GTGGTGTGCG GG TCGGA	
		TGA__ __	
GAM1914	WBSCR17	5' CGGGTACAGCTGGGAGCTGTGG 82216	G _ CGAG
	TG	TACCACAGCT TT GC GCCTG	
		GTGGTGTGCGA GG CG TGGGC	
		G T ACA_	
GAM1914	WIT-1	5' CAGGTAACCAACAGCTGTG 32395	CCGAG
		CACAGCTGTTG GCCTG	
		GTGTCGACAAC TGGAC	
		CAA__	
GAM1914	YKT6	3' TGGGTTTTGAACCAGTGTGGTA 22646	G TTGC
		TACCACA CTG CGAGGCCTG	
		ATGGTGT GAC GTTTTGGGT	
		_ CAA_	
GAM1914	LOC112714	5' TGGGCGCTCAGCAGCTGTGG 73247	GCC _
		CCACAGCTGTT GAG GCCTG	
		GGTGTGACGA CTC CGGGT	
		_ G	
GAM1914	LOC118978	5' TGGGTCTGCCACAGCTGTGGT 76506	T_ CG
		ACCACAGCTGT GC AGGCCTG	
		TGGTGTGACA CG TCTGGGT	
		CC _	
GAM1914	LOC132166	3' TGGGTCTCCTACCGTGGCTGT 75539	TG__ CC
	GG	CCACAGC T TG GAGGCCTG	

	GGTGTCTG G AC CTCTGGGT	
	GT CC TC	
GAM1914 LOC132422 5'	CGGGCCTCGCACCGGCTGTGG 76401	T C
	CCACAGCTG TGC GAGGCCTG	
	GGTGTCTGGC ACG CTCCGGGC	
	C _	
GAM1914 LOC134637 3'	CAGGCTGGAATGTAATTGTGGT 75691	GCT CGA__
G	TACCACA GTTGC GGCCTG	
	GTGGTGT TAATG TCGGAC	
	__ TAAGG	
GAM1914 LOC135892 3'	AGGCCTTGGCAGCCAGGG 75758	ACAGCT
	CC GTTGCCGAGGCCT	
	GG CGACGGTTCCGGA	
	GAC__	
GAM1914 LOC139728 5'	CAGGGTGGCAGAGCTGTGGTG 75901	G AGG
	TACCACAGCT TTGCCG CCTG	
	GTGGTGTCTGA GACGGT GGAC	
	_ G__	
GAM1914 LOC143308 5'	GGGTCAGGTGGTTGGGGTG 83836	A GTT GA
	TACC CAGCT GCC GGCCT	
	GTGG GTTGG TGG CTGGG	
	G _ A_	
GAM1914 LOC143916 5'	CAGGCTTTGGCACTGGTGGTA 77139	AGCT T
	TACCAC GT GCCGAGGCCTG	
	ATGGTG CA CGGTTTCGGAC	
	GT__ _	
GAM1914 LOC144245 5'	TGGGTTCTTGGGCAGTGGCTGT 71369	TG _ _
GG	CCACAGC TTGCC GAGG CCTG	
	GGTGTCTG GACGG TTCT GGGT	
	GT G T	
GAM1914 LOC144373 3'	AGGCTGTGGCAGCTGTGG 77310	TG CGA G
	CCACAGCTGT C GGCCT	
	GGTGTCTGACG G TCGGA	
	GT__ G	
GAM1914 LOC144587 5'	GGTGGTGGCAGGTGTGGTG 67591	G TG GAG
	TACCACA CTGT CC GCC	
	GTGGTGT GACG GG TGG	
	G GT __	
GAM1914 LOC144776 3'	CAGGTTTTCTCTCTGGTTGTAG 77486	C GTTGCC
TA	TAC ACAGCT GAGGCCTG	

		ATG TGTGGG	TTTTGGAC		
		A	TCTCTC		
GAM1914	LOC145899 5'	AGGCACCAACAGTTTGGTG	84555	C	CCGAG
		TACCA AGCTGTTG	GCCT		
		GTGGT TTGACAAC	CGGA		
		—	CA—		
GAM1914	LOC146092 5'	CGGAGAAGGTAGCAGCTGTG	84586		GAGG TG
		CACAGCTGTTGCC	CC		
		GTGTCGACGATGG	GG		
		AAGA	C		
GAM1914	LOC146136 5'	TGGGCTTTGGAAGTAGCTGTTG	73321	C	TTG
	TA	TAC ACAGCTG	CCGAGGCCTG		
		ATG TGTTCGAT	GGTTTCGGGT		
		T	GAA		
GAM1914	LOC147071 5'	TAGGTAAGAACGGCTGTGG	73372		GCCGAG
		CCACAGCTGTT	GCCTG		
		GGTGTGCGCAA	TGGAT		
		GAA—			
GAM1914	LOC147400 3'	GCAGCAGTAGCTGTGG	78984		CGAG
		CCACAGCTGTTGC	GC		
		GGTGTGATGACG	CG		
		A—			
GAM1914	LOC149372 5'	GGGTTTCGGCACCGGTGG	80105	ACA	T
		CC	GCTG TGCCGAGGCCT		
		GG	TGGC ACGGCTTTGGG		
		—	C		
GAM1914	LOC149837 5'	TGGGCCTTGGGCTGGCTGTG	85909	—	TG
		CACAGCT GT	CCGAGGCCTG		
		GTGTGCGG CG	GGTTCCGGGT		
		T	—		
GAM1914	LOC150275 5'	CGGGTTTTGGCAGTAGCTGTGG	80522		
		CCACAGCTGTTGCCGAGGCCTG			
		GGTGTGATGACGGTTTTGGGC			
GAM1914	LOC150517 5'	GGAGCGGTGGCGGCTGTGG	80726		TG AGG
		CCACAGCTGT	CCG CC		
		GGTGTGCGCG	GGC GG		
		GT	GA—		
GAM1914	LOC150696 5'	CAGGTTTTGAGAGCTGTGG	59155		G TGC
		CCACAGCT T	CGAGGCCTG		

	GGTGTCTGA A GTTTTGGAC	
	G ____	
GAM1914 LOC151124 5'	GCTGTGGAGCTGTGGTA 86416	GTTG A
	TACCACAGCT CCG GGC	
	ATGGTGTCTGA GGT TCG	
	____ G	
GAM1914 LOC151124 5'	GGGAGGGCGGGGGTTGTGGTG 86417	G GAGG G
	TACCACAGCT TTGCC CCT	
	GTGGTGTGG GGCGG GGG	
	G GA__ A	
GAM1914 LOC151429 5'	CAGGCTGGAAGTGGCTGTGGTG 86527	TG G GA
	TACCACAGC TT CC GGCCTG	
	GTGGTGTCTG GA GG TCGGAC	
	GT A ____	
GAM1914 LOC151556 5'	GGACAAGGGCGACAGTGTGGTG 81081	G GAGG_ TG
	TACCACA CTGTTGCC CC	
	GTGGTGT GACAGCGG GG	
	_ GAACA T	
GAM1914 LOC153243 5'	GGTGGCCTGGGCGGCGGCTGTG 81664	G TG
GTG	TACCACAGCTGTTGCC AGGCC	
	GTGGTGTCTGGCGGCGG TCCGG	
	G TGGG	
GAM1914 LOC158292 5'	GGCACAGCAATATCTGTGGTG 88051	C CGAG
	TACCACAG TGTTGC GCC	
	GTGGTGTCT ATAACG CGG	
	T ACA_	
GAM1914 LOC158332 3'	CAGGTTTTGGCATAGAGTGGTG 82763	AG T
	TACCAC CTGT GCCGAGGCCTG	
	GTGGTG GATA CGGTTTTGGAC	
	A_ _	
GAM1914 LOC158476 5'	GGGTCAGGCAGCTGTTGTG 88196	T GA
	CACAGC GTTGCC GGCCT	
	GTGTTG CGACGG CTGGG	
	T A_	
GAM1914 LOC161635 5'	TGGGCCGGAGCCGACGGCAGTG 98357	A _CGA
GTG	TACCAC GCTGTTG C GGCCTG	
	GTGGTG CGGCAGC G CCGGGT	
	A C AGG	
GAM1914 LOC164278 5'	CGGGCTGTCCTCTGTGGCTGTG 88555	TG TGCCGA_
GTG	TACCACAGC T GGCCTG	

	GTGGTGTCTG G TCGGGC	
	GT TCTCCTG	
GAM1914 LOC196047 5'	GGGCTTTGGTGGCTGCTG 91159	T TG
	CAGC GT CCGAGGCCT	
	GTCG CG GGTTCGGG	
	T GT	
GAM1914 LOC196489 3'	GGTGTGCTGGCTGTGGTG 89077	_ _
	TACCACAGCT GT TGCC	
	GTGGTGTCTGG CG GTGG	
	T T	
GAM1914 LOC197201 3'	CAGGGAGGCAGAGGTTGTGGTG 89269	G GAGG
	TACCACAGCT TTGCC CCTG	
	GTGGTGTGG GACGG GGAC	
	A AG_	
GAM1914 LOC197423 5'	CGGGTATTTAGTACTGTGGTG 78423	CTGT CG _
	TACCACAG TGC AG GCCTG	
	GTGGTGTCT ATG TT TGGGC	
	_____ AT A	
GAM1914 LOC199221 3'	CAGGAGAATGGCGCTGTGGTG 81165	TGTT AGG_
	TACCACAGC GCCG CCTG	
	GTGGTGTCTG CGGT GGAC	
	_____ AAGA	
GAM1914 LOC199906 3'	CGGGTTTATAGTTGGCTGTGG 89851	TTGCCG
	CCACAGCTG AGGCCTG	
	GGTGTCTGGT TTTGGGC	
	TGATA_	
GAM1914 LOC200230 3'	GGAGCAGGTGGTCAGCTGTGGT 90046	_TG GAGG TG
G	TACCACAGCTG T CC CC	
	GTGGTGTCTGAC G GG GG	
	T GT ACGA T	
GAM1914 LOC201173 5'	TAGGTAAGAACGGCTGTGG 88693	GCCGAG
	CCACAGCTGTT GCCTG	
	GGTGTCTGGCAA TGGAT	
	GAA_	
GAM1914 LOC201220 5'	TAGGTAAGAACGGCTGTGG 88726	GCCGAG
	CCACAGCTGTT GCCTG	
	GGTGTCTGGCAA TGGAT	
	GAA_	
GAM1914 LOC219672 5'	GGGTGTGGTGGTGTGGTG 92970	GCTG TG AG
	TACCACA T CCG GCCT	

	GTGGTGT G GGT TGGG ____ GT G_	
GAM1914 LOC219673 3'	CAGGTCAACAGGCAGCTGTGG 94616 CCACAGCTGTT GGCCTG GGTGTGACGG CTGGAC ACAA_	GCCGA
GAM1914 LOC219688 5'	GGTGATGGTGGTGGTGGTGGTG 94642 TACCAC GC T CCG GCC GTGGTG TG G GGT TGG G GT GT AG T	A TG TG AG TG
GAM1914 LOC219688 5'	GGTGGTGGTGGTGGTGGTG 94643 TACCAC GCTGT CC GCC GTGGTG TGGTA GG TGG G GT ____	A TG GAG
GAM1914 LOC221400 3'	AGGTCTCAGTTGATGGTG 93911 TACCA CAGCT GAGGCCT GTGGT GTTGG CTCTGGA A A_____	_ GTTGCC
GAM1914 LOC221421 3'	TGGGTGGAATGGCTGTGG 93897 CCACAGCTGTT CC GCCTG GGTGTGCGTAA GG TGGGT A ____	G GAG
GAM1914 LOC221474 5'	CAGGTATGGGCAGCTGGGGTG 93993 TACC CAGCTGT CCG GCCTG GTGG GTCGACG GGT TGGAC G _ A_	A TG AG
GAM1914 LOC221491 5'	GGGTGGTGGTGGCTGTGGTA 93659 TACCACAGC T CC GCCT ATGGTGTGCG G GG TGGG GT GT ____	TG TG GAG G
GAM1914 LOC221576 3'	TAGGTTTTGGTAACAGCTGTTG 95323 TA TAC ACAGCTGTTGCCGAGGCCTG ATG TGTCGACAATGGTTTTGGAT T	C
GAM1914 LOC222029 5'	GATTCTTGGTGGTGGCTGTGGT 95692 A TACCACAGC T CCGAGG ATGGTGTGCG G GGTTCT GT GT TAGT	TG TG CCTG
GAM1914 LOC222031 3'	GAATCTTGGTGGTGGCTTTGGT 95681 A TACCA AGC T CCGAGG 	C TG TG CCTG

ATGGT TCG G GGTTCT
 T GTGT AAGT
 GAM1914 LOC254746 5' GGGTGAGGTTGTTGTGGTG 96849 TGTT GAG
 TACCACAGC GCC GCCT
 ||||| ||| |||
 GTGGTGTG TGG TGGG
 T__ AG_
 GAM1914 LOC254753 3' TGGGCCTTCCCTGGGCTGTG 97858 GTTGCC
 CACAGCT GAGGCCTG
 ||||| |||||
 GTGTCGG TTCCGGGT
 GTCCC_
 GAM1914 LOC254901 5' CGGGCCTCAGCCCCTGACGCTG 98004 T ____ C
 TGGTG TACCACAGC GTT GC GAGGCCTG
 ||||| || || |||||
 GTGGTGTG CAG CG CTCCGGGC
 _ TCCC A
 GAM1914 LOC255042 3' CAGGAGCCGGAGGTTGTGGTG 97039 GTTG AGG
 TACCACAGCT CCG CCTG
 ||||| ||| |||
 GTGGTGTG GGC GGAC
 A__ CGA
 GAM1914 LOC255167 3' TGGGCCGGCTGAGGTGGCTGCG 98940 A TG ____ GA
 GTA TACC CAGC TT GCC GGCCTG
 ||| ||| || ||| |||||
 ATGG GTCG GG CGG CCGGGT
 C GT AGT __
 GAM1914 LOC255475 5' GGTGGGAGGCAGCTGTGGTG 99461 TG GAG
 TACCACAGCTGT CC GCC
 ||||| || |||
 GTGGTGTGACG GG TGG
 GA G__
 GAM1914 LOC257159 5' CAGGTTGCTGCAGCTGTG 98971 T CGA
 CACAGCTGT GC GGCCTG
 ||||| || |||||
 GTGTCGACG CG TTGGAC
 T ____
 GAM1914 LOC257515 3' TAGGTTTTGGTAACAGCTGTTG 99623 C
 TA TAC ACAGCTGTTGCCGAGGCCTG
 ||| |||||
 ATG TGTCGACAATGGTTTTGGAT
 T
 GAM1914 LOC257572 3' TAGGTTTTGGTAACAGCTGTTG 99743 C
 TA TAC ACAGCTGTTGCCGAGGCCTG
 ||| |||||
 ATG TGTCGACAATGGTTTTGGAT
 T
 GAM1914 LOC63929 3' TGGGAGCATAGCAGCTGTG 42286 CCGAGG
 CACAGCTGTTG CCTG
 ||||| |||

		GTGTCGACGAT GGGT		
		ACGA__		
GAM1914	LOC90019 3'	GGGCCTGGGCAGCTGGGTG 57533	A	GTT G
		TACC CAGCT GCC AGGCCT		
		GTGG GTCGA CGG TCCGGG		
		_ _ _ G		
GAM1914	LOC90019 3'	GGGCCTGGGCAGCTGGGTG 57534	A	GTT G
		TACC CAGCT GCC AGGCCT		
		GTGG GTCGA CGG TCCGGG		
		_ _ _ G		
GAM1914	LOC92148 5'	TGGGTTTTGGTTTCCATTTGGT 68890		CAGCTGTT
	G	TACCA GCCGAGGCCTG		
		GTGGT TGGTTTTGGGT		
		TTACCTT_		
GAM1914	LOC92270 5'	GGGAGGTGGAGGTTGTGGTG 69188		G TG GAGG
		TACCACAGCT T CC CC		
		GTGGTGTGG G GG GG		
		A GT AG__		
GAM1914	LOC93624 3'	GGCTGGCGGTGGTTCTGGTG 73103	C	TG GA
		TACCA AGC TTGCC GGCC		
		GTGGT TTG GGCGG TCGG		
		C GT _		
GAM1915	B3GALT2 3'	CAGCAGGTGTACACATGC 15030	AT	TG
		GCAT TGTAC GCCTGCTG		
		CGTA ACATG TGGACGAC		
		C_ _		
GAM1915	FBN1 3'	CAGCATGTGCAATATGC 65037		TGGCC
		GCATATTGTAC TGCTG		
		CGTATAACGTG ACGAC		
		T_		
GAM1915	GRLF1 3'	CAGCAGGCCAGCTGCAGTG 79256		_
		TATTGTA CTGGCCTGCTG		
		GTGACGT GACCGGACGAC		
		C		
GAM1915	MAPRE1 3'	GCAGCAGGCAGGTGATCATGCT 25591	ATTG	G
	G	CAGCAT TACT GCCTGCTGC		
		GTCGTA GTGG CGGACGACG		
		CTA_ A		
GAM1915	SMURF1 3'	CAGCAGGCCAATGTTCCCTATGT 94044	TTGT	_
		GCATA AC TGGCCTGCTG		

TGTAT TG ACCGGACGAC
 CCT_ TA
 GAM1915 UQCRC1 5' GCCAGGCCAGCACATAGACTG 14015 CA A _
 CAG TATTGT CTGGCCTG C
 ||| ||||| ||||| |
 GTC ATAACA GACCGGAC G
 AG C C
 GAM1915 DKFZP434P211 5' CAGCAAGCCAGTGCTGTGTG 28026 T C
 CATAT GTACTGGC TGCTG
 ||||| ||||| |||||
 GTGTG CGTGACCG ACGAC
 T A
 GAM1915 KIAA0063 3' GCAGCGGTACAGCATGCTG 30259 A GC
 CAGCAT TTGTACTG CTGC
 ||||| ||||| |||||
 GTCGTA GACATGGC GACG
 C _
 GAM1915 KIAA0795 3' CAGCAAGCCAGGTATGGTG 47228 G TGTA C
 CA CATAT CTGGC TGCTG
 || ||||| ||||| |||||
 GT GTATG GACCG ACGAC
 G _ A
 GAM1915 KIAA1817 3' GCAGCAGGCCACATTGCCGTGC 68781 ATT C_
 GCAT GTA TGGCCTGCTGC
 ||||| ||| ||||| |||||
 CGTG CGT ACCGGACGACG
 C_ TAC
 GAM1915 MGC14156 3' GCAACTAGAGTCAATATGCTG 52959 TA_ CC
 CAGCATATTG CTGG TGC
 ||||| ||||| ||||| |||||
 GTCGTATAAC GATC ACG
 TGA A_
 GAM1915 MYH7B 3' GCAGCAGGCCAACACCAACCTG 71057 CATAT AC
 CAG TGT TGGCCTGCTGC
 ||| ||| ||||| |||||
 GTC ACA ACCGGACGACG
 CAACC _
 GAM1915 NEK1 3' CAGCTTCAATCACATATGCTG 97561 AC_ CCT
 GCATATTGT TGG GCTG
 ||||| ||| ||||| |||||
 CGTATAACA ACT CGAC
 CTA T_
 GAM1915 LOC146455 5' GCAACAGGCCAGCAGCCAAAAT 78461 A TA_ C
 G CAT TTG CTGGCCTG TGC
 ||| ||| ||||| ||||| |||||
 GTA AAC GACCGGAC ACG
 A CGAC A
 GAM1915 LOC150174 5' CAGCAAGCCAGTGCTGC 80433 TATT C
 GCA GTACTGGC TGCTG
 ||| ||||| ||||| |||||

		CGT CGTGACCG ACGAC		
		_____ A		
GAM1915	LOC150213 5'	CAGCAAGCCAGTGCTGTGTG 75352	T	C
		CATAT GTACTGGC TGCTG		
		GTGTG CGTGACCG ACGAC		
		T A		
GAM1915	LOC150271 5'	CAGCAAGCTCTGAAGATATGCT 86134	GTACT	C
	G	CAGCATATT GGC TGCTG		
		GTCGTATAG TCG ACGAC		
		AAGTC A		
GAM1915	LOC160646 3'	CAGCAGGCAGAAATGCTG 83108	ATTGTA	G
		CAGCAT CTG CCTGCTG		
		GTCGTA GAC GGACGAC		
		AA_____ _		
GAM1915	LOC164714 5'	AGCAGGCAAGATGCTG 88579	ATTGTA	G
		CAGCAT CT GCCTGCT		
		GTCGTA GA CGGACGA		
		_____ A		
GAM1915	LOC256809 3'	CAGTGTGGAGTCAATATGCT 98130	T GG	_
		AGCATATTG ACT CC TGCTG		
		TCGTATAAC TGA GG GTGAC		
		_ _ T		
GAM1916	EMR1 3'	GAACACCTGGCTACCA 10517	C	CC
		TGGT AGCCAGGTG TTC		
		ACCA TCGGTCCAC AAG		
		- -		
GAM1916	POLS 3'	TGAATTGGCCTGGCTACCA 23783	C	GCC
		TGGT AGCCAGGT TTCA		
		ACCA TCGGTCCG AAGT		
		- GTT		
GAM1916	SLC22A3 3'	AGGGACTAAGCTCCTAGCTGAC 42038	C T CT_	A
	CA	TGGTCAGC AGG GC TC CCT		
		ACCAGTCG TCC CG AG GGA		
		A T AATC _		
GAM1916	ARTN 3'	CAGGTGAAGGGACAACCTGACTA 15610	CCAG	G
		TGGTCAG GT CCTTCACCTG		
		ATCAGTC CA GGAAGTGGAC		
		AA_ G		
GAM1916	ARTN 3'	CAGGTGAAGGGACAACCTGACTA 55108	CCAG	G
		TGGTCAG GT CCTTCACCTG		

		ATCAGTC CA GGAAGTGGAC		
		AA__ G		
GAM1916 ARTN	3'	CAGGTGAAGGGACAACTGACTA 55111	CCAG G	
		TGGTCAG GT CCTTCACCTG		
		ATCAGTC CA GGAAGTGGAC		
		AA__ G		
GAM1916 ARTN	3'	CAGGTGAAGGGACAACTGACTA 55136	CCAG G	
		TGGTCAG GT CCTTCACCTG		
		ATCAGTC CA GGAAGTGGAC		
		AA__ G		
GAM1916 FLJ10211	5'	CAGACAAAGGCACCGAGGCCA 36363	AGCCA CAC	
		TGGTC GGTGCCTT CTG		
		ACCGG CCACGGAA GAC		
		AG__ ACA		
GAM1916 FLJ13089	3'	CAGGCAAAAGCAACATCTGGTT 71427	C__ CA_	
		GACCA TGGTCAGCCAGGTG CTT CCTG		
		ACCAGTTGGTCTAC GAA GGAC		
		AAC AAC		
GAM1916 KIAA1280	5'	GATTAACCTGGCTGACTA 70280	GCCT	
		TGGTCAGCCAGGT TC		
		ATCAGTCGGTCCA AG		
		ATT_		
GAM1916 LRG	3'	CAGGTGAAACTCGGGGCTGTCC 54816	T A__ GCC	
	A	TGG CAGCC G GT TTCACCTG		
		ACC GTCGG C CA AAGTGGAC		
		T GG T ____		
GAM1916 LOC155434	3'	GGAGGCACCCGACTACCA 87691	C CCA	
		TGGT AG GGTGCCTTC		
		ACCA TC CCACGGAGG		
		_ AGC		
GAM1916 LOC196484	5'	CAGGTCACCACCTGGCTGACC 63537	CCTTC	
		GGTCAGCCAGGTG ACCTG		
		CCAGTCGGTCCAC TGGAC		
		CAC__		
GAM1916 LOC256158	5'	AGGCATCCCCCGGCCGACCA 99478	A A__	
		TGGTC GCC GGTGCCT		
		ACCAG CGG CTACGGA		
		C CCCC		
GAM1916 LOC91069	3'	CAGGTCACCACCTGGCTGACC 65400	CCTTC	
		GGTCAGCCAGGTG ACCTG		

		CCAGTCGGTCCAC TGGAC	
		CAC__	
GAM1916	LOC93624	3' CAGGCAAGAGCCGCTGACC 73099	CCA GC CA
		GGTCAG GGT CTT CCTG	
		CCAGTC CCG GAA GGAC	
		TG_ A_ C_	
GAM1917	BAP1	3' TTTCTGGGCTCCAACCCAACA 17399	CA ATCTCA
		TGTT GT AGCCCAGAAA	
		ACAA CA TCGGGTCTTT	
		CC ACC__	
GAM1917	CD8A	3' TCTGAATTTGAGATACAAACA 10097	CA CC
		TGTT GTATCTCAAG CAGA	
		ACAA CATAGAGTTT GTCT	
		A_ AA	
GAM1917	ETF1	3' TCTGCAGAGAGATACTAAGCA 17594	C AAGCC
		TGTT AGTATCTC CAGA	
		ACGA TCATAGAG GTCT	
		A AGAC_	
GAM1917	KTN1	3' TTTCTACTTTGTGAGAAACACT 18376	A_ _ CCC
		GAACA TG TTCAGT TCT CAAG AGAAA	
		ACAAGTCA AGA GTTT TCTTT	
		CAA CT CA_	
GAM1917	MTL5	3' TCTCTAGAGAACTACTGAACA 18200	_ A CCC
		TG TTCAGTA TCTC AG AGA	
		ACAAGTCAT AGAG TC TCT	
		CA A _	
GAM1917	PAX2	3' TCCGGCAGGAACTGAACA 15661	A CAA CA
		TG TTCAGT TCT GCC GA	
		ACAAGTCA AGG CGG CT	
		_ A_ C_	
GAM1917	PAX2	3' TCCGGCAGGAACTGAACA 15668	A CAA CA
		TG TTCAGT TCT GCC GA	
		ACAAGTCA AGG CGG CT	
		_ A_ C_	
GAM1917	PEA15	3' CTGGGCTTGTGAACA 15007	GTATCT
		TG TTCA CAAGCCCAG	
		ACAAGT GTTCGGGTC	

GAM1917	SLC13A3	3' TCTGGGCTCCTGAGCA 61091	TATCTCA
		TG TTCAG AGCCCAGA	

ACGAGTC TCGGGTCT
 C_____
 GAM1917 USP9Y 5' TTTCTGGGCTCAGAGGTG 64737 A_
 TATCTC AGCCCAGAAA
 ||||| |||||
 GTGGAG TCGGGTCTTT
 AC
 GAM1917 AGTRL2 3' TCTGAGGCCAAAGACACTGAGC 18959 A CAA _
 A TGTTCACT TCT GCC CAGA
 ||||| || |||||
 ACGAGTCA AGA CGG GTCT
 C AAC A
 GAM1917 C12orf22 3' TTCTGGGCCACTGGAACA 48713 _ ATCTCAA
 TGTTCACT AGT GCCCAGAA
 ||||| || |||||
 ACAAG TCA CGGGTCTT
 G C_____
 GAM1917 C20orf21 3' TCTCTTGAAAATACTGAA 35573 C_ CCC
 TTCAGTAT TCAAG AGA
 ||||| ||||| ||
 AAGTCATA AGTTC TCT
 AA ____
 GAM1917 D2S448 3' TCTGGGCTCTCTGTAACA 73893 _ TATCTCA
 TGTT CAG AGCCCAGA
 ||||| || |||||
 ACAA GTC TCGGGTCT
 T TC_____
 GAM1917 FLJ12484 3' CTTAGCTTTGAGATACTAAGCA 43173 C _ CC
 TGTT AGTATCTCAA GC AG
 ||||| ||||| || ||
 ACGA TCATAGAGTT CG TC
 A T AT
 GAM1917 FLJ13611 3' TTTCTGTCAAAATACTGAAC 46870 CTCAAGCC
 GTTCAGTAT CAGAAA
 ||||| |||||
 CAAGTCATA GTCTTT
 AACACT____
 GAM1917 FLJ20294 5' CTGGGCCTGGTGTGACA 35354 T G TCAA
 TGT CA TATC GCCCAG
 ||||| |||||
 ACA GT GTGG CGGGTC
 _ _ TC____
 GAM1917 ITGB5 3' TCCGAGCTTGGGATAAAGCA 60217 TCAG CCA
 TGT TATCTCAAGC GA
 ||||| ||||| ||
 ACG ATAGGGTTTCG CT
 AA__ AGC
 GAM1917 KIAA0057 3' TCCAAGCTTGAGAGCTCAGCA 25423 C A CCA
 TGTT AGT TCTCAAGC GA
 ||||| ||||| ||

ACGA TCG AGAGTTCG CT
 C _ AAC
 GAM1917 KIAA0210 5' TTTCTGAGTGAGATACTGAA 29181 AGCC
 TTCAGTATCTCA CAGAAA
 ||||| ||||
 AAGTCATAGAGT GTCTTT
 GA__
 GAM1917 KIAA1317 5' TTCTGGGCTTTCTGAA 87219 TATCTC
 TTCAG AAGCCCAGAA
 |||| |||||
 AAGTC TTCGGGTCTT
 T____
 GAM1917 KPNA6 3' CTAAGCTTGAGATAGGGGGC 25540 AG CC
 GTTC TATCTCAAGC AG
 ||| ||||| ||
 CGGG ATAGAGTTTCG TC
 GG AA
 GAM1917 LHPP 3' TTTCTGGACCCACTGCTGGACA 42368 TCTCAAGC
 TGTTTCAGTA CCAGAAA
 ||||| ||||
 ACAGGTCGT GGTCTTT
 CACCCA__
 GAM1917 MGC29891 3' TCCAGGCTTGAGTGACAGAGCA 58872 A AT CA
 TGTTT GT CTCAAGCC GA
 |||| || ||||| ||
 ACGAG CA GAGTTCGG CT
 A GT AC
 GAM1917 P2RX1 3' TTCAGGTGCAGACACTGAACA 67754 A CAA _ A
 TGTTTCAGT TCT GC CC GAA
 ||||| || || ||
 ACAAGTCA AGA CG GG CTT
 C _ T A
 GAM1917 TCL6 5' TTTGGGCTGAGCACCAAACA 25921 CA AT A
 TGTT GT CTCA GCCCAGA
 ||| || |||||
 ACAA CA GAGT CGGGTTT
 AC C_ _
 GAM1917 TCL6 5' TTTGGGCTGAGCACCAAACA 27773 CA AT A
 TGTT GT CTCA GCCCAGA
 ||| || |||||
 ACAA CA GAGT CGGGTTT
 AC C_ _
 GAM1917 TCL6 5' TTTGGGCTGAGCACCAAACA 40498 CA AT A
 TGTT GT CTCA GCCCAGA
 ||| || |||||
 ACAA CA GAGT CGGGTTT
 AC C_ _
 GAM1917 TCL6 5' TTTGGGCTGAGCACCAAACA 40522 CA AT A
 TGTT GT CTCA GCCCAGA
 ||| || |||||

	ACAA CA GAGT CGGGTTT	
	AC C_ _	
GAM1917 TRAP-1	3' TTCTGAGCCTGCTGGACA 16195	TCTCAA C
	TGTTTCAGTA GC CAGAA	
	ACAGGTCGT CG GTCTT	
	C_____ A	
GAM1917 LOC147184	5' TCTGGGCTTGCCCTGAA 59872	TATCT
	TTCAG CAAGCCCAGA	
	AAGTC GTTCGGGTCT	
	CC_____	
GAM1917 LOC158230	3' TTTGTAAGATGCTGAACA 82703	_____
	TGTTTCAGTATCT CAAG	
	ACAAGTCGTAGA GTTT	
	AT	
GAM1917 LOC200830	3' CTGGGATGATGATACTGAATA 91726	_ AG
	TGTTTCAGTATC TCA CCCAG	
	ATAAGTCATAG AGT GGGTC	
	T A_	
GAM1917 LOC221002	3' TTCTGGGCTGTGACTGAA 93112	ATCTCA
	TTCAGT AGCCCAGAA	
	AAGTCA TCGGGTCTT	
	GTG_____	
GAM1917 LOC221632	3' CTGGGTTACTACTGAACA 95448	TCTCA
	TGTTTCAGTA AGCCCAG	
	ACAAGTCAT TTGGGTC	
	CA_____	
GAM1917 LOC222233	5' CTAGGCTTGAGAATTGA 95904	A C
	TCAGT TCTCAAGCC AG	
	AGTTA AGAGTTCGG TC	
	_ A	
GAM1917 LOC253044	3' TCTGGGCTTTGTCCTGAGACA 98363	_ T CTC
	TGT TCAG AT AAGCCCAGA	
	ACA AGTC TG TTCGGGTCT	
	G C T_	
GAM1917 LOC256032	5' CTGAGCCTGCTGCTGAAC 99360	TCT A C
	GTTCAGTA CA GC CAG	
	CAAGTCGT GT CG GTC	
	C_ C A	
GAM1917 LOC51580	3' TTCTGATAAGTACTGAACA 32431	CTCAAGCC
	TGTTTCAGTAT CAGAA	

ACAAGTCATG GTCTT
 AATA____
 GAM1917 LOC90826 5' TTCTGTAGATACTGAA 64789 CAAGCC
 TTCAGTATCT CAGAA
 ||||| ||||
 AAGTCATAGA GTCTT
 T____
 GAM1918 HMGN1 3' CATGTTGTTTTTTAGTAG 18302 TGTCC
 TTACT AAAAACAACATG
 |||| |||||
 GATGA TTTTGTGTGAC
 T____
 GAM1918 NCOA6 5' ATTGTGTGACCTTGGACAAATA 26829 C AAACA TG
 A TTA TTGTCCAA ACA AT
 || ||||| || ||
 AAT AACAGGTT TGT TA
 A CCAG_ GT
 GAM1918 PKD2 3' CATGTTGTACATGTAA 60716 T CCAA
 TTAC TGT AACAAACATG
 ||| || |||||
 AATG ACA TTGTTGTAC
 T____
 GAM1918 TSPY 3' ATCATGTTGTTCTTTTCGGAGTA 83000 TTG _ _
 A TTAC TCC AAA AACAAACATGAT
 ||| ||| |||||
 AATG AGG TTT TTGTTGTACTA
 _ C C
 GAM1918 FLJ12568 3' ATCATGTTAGTGAGCAGACAA 47139 CAAAA _
 TTGTC AC AACATGAT
 |||| || |||||
 AACAG TG TTGTACTA
 ACGAG A
 GAM1918 TNRC9 3' ATCACTTTGTTTTTAAACAAG 71798 CC CA
 CTTGT AAAAACAAC TGAT
 |||| ||||| |||
 GAACA TTTTGTGTT ACTA
 AA TC
 GAM1918 LOC130355 5' GTTGCATCTCTGGACAAGTAA 75434 AAAA____
 TTACTTGTCCA CAAC
 ||||| |||
 AATGAACAGGT GTTG
 CTCTAC
 GAM1918 LOC145854 3' CATGTTGTTTTTTAGTAG 78006 TGTCC
 TTACT AAAAACAACATG
 |||| |||||
 GATGA TTTTGTGTGAC
 T____
 GAM1919 DLEC1 3' CATCTGGCCCTCCCTTG 24716 A A C
 CAAGG AGGGC GG GTG
 |||| |||| || |||

			GTTCC TCCCG TC TAC			
			C G _			
GAM1919	DLEC1	3'	CATCTGGCCCTCCCTTG	24717	A A C	
			CAAGG AGGGC GG GTG			
			GTTCC TCCCG TC TAC			
			C G _			
GAM1919	PIP5K1A	3'	TATCCCACCCTGCCTTGATA	14520	A CA C	
			TATCAAGG AGGG GG GTG			
			ATAGTTCC TCCC CC TAT			
			G A_ C			
GAM1919	SOX11	3'	ACCCACCCCCCCTTGGTA	13308	AA CA C	
			TATCAAGG GGG GG GT			
			ATGGTTCC CCC CC CA			
			CC A_ _			
GAM1919	CHL1	3'	TGTTACCTTTCCTCAATA	22768	CA CA	
			TAT AGGAAGGG GGCG			
			ATA TCCTTTCC TTGT			
			AC A_			
GAM1919	EPB41L1	3'	CATTCTGCCCTTCCCTGA	71104	A C	
			TCA GGAAGGGCAGG GTG			
			AGT CCTTCCCGTCT TAC			
			C _			
GAM1919	FLJ00060	3'	CATACCCCCTGCCCTCCTCTGA	61741	_ A CGTG	
			TCA AGGA GGGCAGG ATG			
			AGT TCCT CCCGTCC TAC			
			C _ CCCA			
GAM1919	FLJ10898	5'	CACCACAGCCCTTTCTCAATA	60126	CA AGGC	
			TAT AGGAAGGGC GTG			
			ATA TCTTTCCCG CAC			
			AC ACAC			
GAM1919	FLJ22557	3'	ATCATCCCATCCTTAATA	45581	C A CAGGC	
			TAT AAGGA GGG GTGAT			
			ATA TTCCT CCC TACTA			
			A A _			
GAM1919	KIAA0574	3'	CATCCCCTGCCCTCCCCTGA	69808	A A CGT	
			TCA GG AGGGCAGG GATG			
			AGT CC TCCCGTCC CTAC			
			C C C_			
GAM1919	KIAA0632	3'	CACCTCAGAAACCCTTCCTTGA	32071	CA_ C	
			TCAAGGAAGGG GG GTG			

		AGTTCCTTCCC	CT CAC		
		AAAGA C			
GAM1919	KIAA1045	3'	CATCACATGTCCTTCC	71599	GGC
			GGAAGGGCA GTGATG		
			CCTTCCTGT CACTAC		
			A__		
GAM1919	KIAA1354	5'	CAGTGA	CTTCCCTTGATA	61572 A G _
			TATCAAGG AGGGCAG CG TG		
			ATAGTTCC TTCCGTC GT AC		
			C A G		
GAM1919	MGC20460	5'	CACCGCCTCCTACCCTTCTT	54901	C__ _
			AGGAAGGG AGGCG TG		
			TTCTTCCC TCCGC AC		
			ATCC C		
GAM1919	LOC158476	3'	CACGCCCGCCCCCCCCATTGA	88186	_ AA_ A
			TCAA GG GGGC GGC GTG		
			AGTT CC CCCG CCGCAC		
			A CCC C		
GAM1919	LOC90459	3'	CACACCCGCTAATTTTTG	63550	A_ A C
			CAAGGA GGGC GG GTG		
			GTTTTT TCCG CC CAC		
			AA C A		
GAM1920	EGLN3	3'	ACCTGGATTTTCTGCCTCA	42208	A ATAA A
			TGGG CAGAAA ATCTA GT		
			ACTC GTCTTT TAGGT CA		
			C _ _ C		
GAM1920	EGLN3	3'	ACCTGGATTTTCTGCCTCA	54046	A ATAA A
			TGGG CAGAAA ATCTA GT		
			ACTC GTCTTT TAGGT CA		
			C _ _ C		
GAM1920	FGF2	3'	AACTTAGATTCATTTCTTC	10609	C ATA
			GA AGAAA AATCTAAGTT		
			CT TCTTT TTAGATTCAA		
			_ AC_		
GAM1920	MMP19	3'	ACTTAGATTTGGCCCCCA	11615	ACAGAAAA
			TGGG TAAATCTAAGT		
			ACCC GTTTAGATTCA		
			CCG_____		
GAM1920	MMP19	3'	ACTTAGATTTGGCCCCCA	43300	ACAGAAAA
			TGGG TAAATCTAAGT		

		ACCC	GTTTAGATTCA		
		CCG_____			
GAM1920	MMP19	3'	ACTTAGATTTGGCCCCCA	43308	ACAGAAAA
			TGGG TAAATCTAAGT		
			ACCC GTTTAGATTCA		
			CCG_____		
GAM1920	MMP19	3'	ACTTAGATTTGGCCCCCA	43312	ACAGAAAA
			TGGG TAAATCTAAGT		
			ACCC GTTTAGATTCA		
			CCG_____		
GAM1920	FLJ23309	3'	TGGGCCTATTTTCTATCCC	46594	C AA
			GGGA AGAAAATA TCTA		
			CCCT TCTTTTAT GGGT		
			A CC		
GAM1920	HNRPAB	3'	AACTTTCTATTGCCTGTCCCA	49207	AA AATCT
			TGGGACAG AATA AAGTT		
			ACCCTGTC TTAT TTCAA		
			CG CT__		
GAM1920	KIAA0152	3'	TGGATCTACACTCTGTCCCA	28983	AAA A
			TGGGACAGA TA ATCTA		
			ACCCTGTCT AT TAGGT		
			CAC C		
GAM1920	MEGF10	3'	AACTTAAATCTGGACTGTTCCA	51603	AAAA A C
			TGGGACAG TA AT TAAGTT		
			ACCTTGTC GT TA ATTCAA		
			AG__ C A		
GAM1920	NCOA2	3'	AACTTAGATCTCTCCTCCC	22570	C_ AAATAA
			GGGA AGA ATCTAAGTT		
			CCCT TCT TAGATTCAA		
			CC C_____		
GAM1920	LOC149506	3'	AACTTAGGTGATTCTCCTGCCT	85618	A AAAATAA
	CA		TGGG CAG ATCTAAGTT		
			ACTC GTC TGGATTCAA		
			C CTCTTAG		
GAM1920	LOC150935	3'	GGAACCATTTTCTGTCCCA	80830	AAA
			TGGGACAGAAAAT TCT		
			ACCCTGTCTTTTA AGG		
			CCA		
GAM1921	ARHC	5'	GCTCCCACCCCTCTCCCAGCT	18972	AA AT _
			AGCTG GAGAG GTGG AGT		

			TCGAC CTCTC CACC TCG		
			CC CC C		
GAM1921	EP300	5'	TCCGCATCCCTCTCCAGC 9289	A A	
			GCTG AGAG GATGTGGA		
			CGAC TCTC CTACGCCT		
			C C		
GAM1921	GNAS	3'	GAAACCCCCTTTTCCCTTCAGC 33916	A TGT A	
	T		AGCTGAAG GAGA GG GTTTC		
			TCGACTTC CTTT CC CAAAG		
			C TCC _		
GAM1921	GNAS	3'	GAAACCCCCTTTTCCCTTCAGC 6711	A TGT A	
	T		AGCTGAAG GAGA GG GTTTC		
			TCGACTTC CTTT CC CAAAG		
			C TCC _		
GAM1921	GNAS	3'	GAAACCCCCTTTTCCCTTCAGC 55383	A TGT A	
	T		AGCTGAAG GAGA GG GTTTC		
			TCGACTTC CTTT CC CAAAG		
			C TCC _		
GAM1921	GNAS	3'	GAAACCCCCTTTTCCCTTCAGC 55387	A TGT A	
	T		AGCTGAAG GAGA GG GTTTC		
			TCGACTTC CTTT CC CAAAG		
			C TCC _		
GAM1921	HPS1	3'	AAACTCCAATCCCCTGAGC 5761	GA AGA G	
			GCT AG GAT TGGAGTTT		
			CGA TC CTA ACCTCAA		
			G_ CC_ _		
GAM1921	IRTA2	3'	TCCACACGTCTCTCCAAC 49233	C A GA	
			AG TG AGAGA TGTGGA		
			TC AC TCTCT ACACCT		
			A C GC		
GAM1921	MAPK14	3'	GATATCACCTCTCTTCAGC 58127	AT A	
			GCTGAAGAGAG GTGG GTT		
			CGACTTCTCTC CACT TAG		
			_ A		
GAM1921	MAPK14	3'	GATATCACCTCTCTTCAGC 58133	AT A	
			GCTGAAGAGAG GTGG GTT		
			CGACTTCTCTC CACT TAG		
			_ A		
GAM1921	MAPK14	3'	GATATCACCTCTCTTCAGC 8979	AT A	
			GCTGAAGAGAG GTGG GTT		

			CGACTTCTCTC CACT TAG		
			— A		
GAM1921	PLAC1	5'	AAAGGCCACCCCTCTTCAGTT 41719	AGAT	AG
			AGCTGAAGAG GTGG TTT		
			TTGACTTCTC CACC AAA		
			CC__ GG		
GAM1921	TNFSF4	3'	AAGCTTACATCTTCCTCAGC 13908	A AG	G
			GCTGA G AGATGTG AGTTT		
			CGACT C TCTACAT TCGAA		
			_CT _		
GAM1921	C5orf7	3'	AAATGTATATCTCTCCAGCT 64596	AA	GA
			AGCTG GAGAGATGTG GTTT		
			TCGAC CTCTCTATAT TAAA		
			_ G_		
GAM1921	CNNM3	3'	GCTCCACACCTCCCCACAGC 34809	AAGA	A
			GCTG GAG TGTGGAGT		
			CGAC CTC ACACCTCG		
			ACCC C		
GAM1921	DKFZP586M1120	5'	AAACTCTGCTGCTTTCCCCAGC 49272	AA	AT TG
	T		AGCTG GAGAG G GAGTTT		
			TCGAC CTTTC C CTCAAA		
			CC GT GT		
GAM1921	HEMK	3'	GCCTACATCTCCCCTCAGC 32958	AGA	A
			GCTGA GAGATGTGG GT		
			CGACT CTCTACATC CG		
			CCC _		
GAM1921	ITM3	3'	GAAATTCCATCCCCCTCAGCT 48889	AGAGAGAT	
			AGCTGA GTGGAGTTTC		
			TCGACT TACCTTAAAG		
			CCCC__		
GAM1921	KIAA0923	3'	AAACTCTTAAGCTCTTTCAGT 26704	ATGT	
			GCTGAAGAGAG GGAGTTT		
			TGACTTCTCTC TCTCAA		
			GAAT		
GAM1921	KIAA1872	3'	GAAACCCAGCATCCTTTTCAGC 63610	A _	A
	T		AGCTGAAGAG GATG TGG GTTTC		
			TCGACTTTTC CTAC ACC CAAAG		
			_ G _		
GAM1921	MGC2198	3'	CCACATCTCCCCTCCACT 57981	C A A_	
			AG TG AG GAGATGTGG		

			TC AC TC CTCTACACC		
			_ C CC		
GAM1921	MGC2780	5'	GAAACTCTCTGAGCTCTCCTCG 48287	T A	ATGT_
	C		GC GA GAGAG GGAGTTTC		
			CG CT CTCTC TCTCAAAG		
			_ C GAGTC		
GAM1921	MIDORI	3'	GAATTTACATCCCCTCTCA 74214	A A_	
			TGA GAG GATGTGGAGTTT		
			ACT CTC CTACACTTTAAG		
			_ CC		
GAM1921	LOC142941	5'	CCACATCTTCCTTCAGCT 83764	AG	
			AGCTGAAG AGATGTGG		
			TCGACTTC TCTACACC		
			CT		
GAM1921	LOC147077	3'	AAACTTCTGATTTCTCTTCAGC 78843		GT
	T		AGCTGAAGAGAGAT GGAGTTT		
			TCGACTTCTCTTTA CTTCAA		
			GT		
GAM1921	LOC152078	3'	AAACTCCACATCCATTTGCAGC 81283	A GA	
	T		AGCTG AGA GATGTGGAGTTT		
			TCGAC TTT CTACACCTCAA		
			G AC		
GAM1921	LOC201617	5'	CCAGAGTTTCTCTCCAAC 91823	C A	G_
			AG TG AGAGAGAT TGG		
			TC AC TCTCTTTG ACC		
			A C AG		
GAM1921	LOC51205	5'	AAACTCCCAGGGACTCTTCGCT 33465	T	AGA_ T
			AGC GAAGAG TG GGAGTTT		
			TCG CTTCTC AC CCTCAA		
			_ AGGG _		
GAM1922	GNAS	3'	CAACGACTGCCGTGACATCATT 33914		
	CA		TGAATGATGTCACGGCAGTCGTTG		
			ACTTACTACAGTGCCGTCAGCAAC		
GAM1922	HIC2	3'	CAACGACTGATCTCTCCATTCA 65860		ATGTCACGG
			TGAATG CAGTCGTTG		
			ACTTAC GTCAGCAAC		
			CTCTCTA__		
GAM1922	MGC13114	3'	CTGCCGTGGCACCCTCA 51392	A A	
			TGA TG TGTCACGGCAG		

ACT AC ACGGTGCCGTC
 C C
 GAM1922 MGC19556 5' CTGCCGTGACACCCTTCA 54339 TGA
 TGAA TGTCACGGCAG
 ||| |||||
 ACTT ACAGTGCCGTC
 CCC
 GAM1922 NY-BR-1 5' CAACGACTCCTACATCGTCCA 54849 A CAC C
 TG ATGATGT GG AGTCGTTG
 || ||||| || |||||
 AC TGCTACA CC TCAGCAAC
 C T__ _
 GAM1923 CHRNA2 3' TGGAGATGAGCCCAAAGTGC 7432 GTAG AC C
 GCA TG GC CATCTCCA
 ||| || || |||||
 CGT AC CG GTAGAGGT
 GAA_ C_ A
 GAM1923 GNAS 3' TGGAGATGGGCGTCACTACTGC 33919
 TA TAGCAGTAGTGACGCCCATCTCCA
 |||||
 ATCGTCATCACTGCGGGTAGAGGT

 GAM1923 MYCL2 3' GAGATGGGGTTTCACCAC 19376 A C _
 GT GTGA GCCC ATCTC
 || ||| ||| |||||
 CA CACT TGGG TAGAG
 C T G
 GAM1923 PLAG1 3' GAAATGACACAGAACTATTGCT 12148 GACGCC_ C
 A TAGCAGTAGT CAT TC
 ||||| ||| ||
 ATCGTTATCA GTA AG
 AGACACA A
 GAM1923 CCR1 3' GAAATGGGGGAACTACTGCTG 8926 GACG C
 TAGCAGTAGT CCCAT TC
 ||||| ||||| ||
 GTCGTCATCA GGGTA AG
 AGG_ A
 GAM1923 FLJ12960 3' GAGATGGGGTTTCACCGT 45297 A AGT G
 GC GT GAC CCCATCTC
 || || || |||||
 TG CA TTG GGGTAGAG
 C CT_ _
 GAM1923 GG2-1 3' GAGATGGAGCACTGCTG 27576 ACGC C
 CAGTAGTG CCATCT C
 ||||| ||||| |
 GTCGTCAC GGTA G
 GA_ A
 GAM1923 KIAA1297 3' AGATGGGCGGCAGCTGCT 72625 A GA
 AGCAGT GT CGCCCATCT
 ||||| || |||||

		TCGTCTCG CG GCGGGTAGA	
		A _	
GAM1923 KIAA1449	3'	GAGACAGGGTTCCCTCACTGCT 40839	_ T C A_
	A	TAGCAGT AG GA GCCC TCTC	
		ATCGTCA TC CT TGGG AGAG	
		C C _ AC	
GAM1923 KIAA1643	3'	TGGAGATGACACACCTACTGCT 65158	_ ACGCC
		AGCAGTAG TG CATCTCCA	
		TCGTCATC AC GTAGAGGT	
		C ACA_	
GAM1923 KIAA1755	3'	GAGATGGGGCCTCACTAC 62016	C _
		GTAGTGA GCCC ATCTC	
		CATCACT CGGG TAGAG	
		C G	
GAM1923 KIAA1978	3'	GAGATGGGCTTTCTCTGC 74892	T T C
		GCAG AG GA GCCCATCTC	
		CGTC TC TT CGGGTAGAG	
		_ T _	
GAM1923 MGC5149	3'	GAGATGGGGTTTCACCAC 72757	A C _
		GT GTGA GCCC ATCTC	
		CA CACT TGGG TAGAG	
		C T G	
GAM1923 PRO1580	5'	AGATAGTTACTACTGCTA 38124	GCCC
		TAGCAGTAGTGAC ATCT	
		ATCGTCATCATTG TAGA	
		A_	
GAM1923 RPIA	3'	GAAATGCTTGCCAGTACTGC 58591	G A CC C
		GCAGTA TG CG CAT TC	
		CGTCAT AC GT GTA AG	
		G C TC A	
GAM1923 TGIF2	3'	GGAGACAAGCATGGTGCTGCTG 41753	G GAC CCA
		TAGCAGTA T GC TCTCC	
		GTCGTCGT G CG AGAGG	
		G TA_ AAC	
GAM1923 LOC126327	3'	TGGAGACAGAAAGCCACTGCTG 74986	AC CCA_
		CAGTAGTG GC TCTCCA	
		GTCGTCAC CG AGAGGT	
		_ AAAGAC	
GAM1923 LOC126731	3'	ATGAGTGTCAGCACTACTACTG 59835	C _ C
		TAG AGTAGT GACGC CAT	

		GTC TCATCA CTGTG GTA	
		A CGA A	
GAM1923	LOC149117 3'	TGGAAATAAGTTGTGTTACTAC 85509	CC__ C
		GTAGTGACGC AT TCCA	
		CATCATTGTG TA AGGT	
		TTGAA A	
GAM1923	LOC149483 3'	TGGAGATGAGCATCTGAACATG 80189	_ AGT C C
	C	GCA GT GA GC CATCTCCA	
		CGT CA CT CG GTAGAGGT	
		A AGT A A	
GAM1923	LOC149832 5'	GAGATGGGATTGTCAGCCAC 85863	A_ _
		GT G TGACG CCCATCTC	
		CA C ACTGT GGGTAGAG	
		C G TA	
GAM1923	LOC89985 3'	TGGAGATGGGCACCACTGC 61675	AC
		GTAGTG GCCCATCTCCA	
		CGTCAC CGGGTAGAGGT	
		CA	
GAM1924	FLJ11000 3'	AACGCTGCCACCCTCCACTTC 37524	AATTC_
		GAAGTG GGCAGCGTT	
		CTTCAC CCGTCGCAA	
		CTCCCA	
GAM1924	KIAA1058 3'	GAGCGTCTTACCGAATTCCCTT 83138	T CA__
	CA	TGAAG GAATTCGG GCGTTC	
		ACTTC CTTAAGCC TGCGAG	
		C ATTC	
GAM1924	PLAGL2 3'	GTACCCGAACTCACTTCA 70963	A CA
		TGAAGTGA TTCGG GC	
		ACTTCACT AAGCC TG	
		C CA	
GAM1925	ADCY6 5'	CCTGACCTTGTGATCTACCTGC 40947	C
	C	GGCAGG AGATCACAAGGTCAGG	
		CCGTCC TCTAGTGTTCCAGTCC	
		A	
GAM1925	ALDH1B1 3'	CCTGACCTCAGGTGATCCACC 7320	CA A__
		GG GATCAC AGGTCAGG	
		CC CTAGTG TCCAGTCC	
		AC GAC	
GAM1925	APAF1 3'	CTTGACCTCATGATCTACCCGC 25971	A C CA
	CT	AGGC GG AGATCA AGGTCAGG	

			TCCG CC TCTAGT TCCAGTTC		
			C A AC		
GAM1925	APM1	3'	CCTGACCTTGTGATCTGCCCCG 17777	A	
	CT		AGGC GGCAGATCACAAGGTCAGG		
			TCCG CCGTCTAGTGTTCCAGTCC		
			C		
GAM1925	APM1	3'	CCTGACTTTGTGATCCACCCG 17778	A CA	
	CT		AGGC GG GATCACAAGGTCAGG		
			TCCG CC CTAGTGTTTCAGTCC		
			C AC		
GAM1925	APOL1	3'	CCTGACCTCTTGATCTGCCCCAC 14734	CA CA	
	CT		AGG GGCAGATCA AGGTCAGG		
			TCC CCGTCTAGT TCCAGTCC		
			AC TC		
GAM1925	APPL	3'	CCTGACCTCATGATCCGCCCG 24946	A A CA	
	CT		AGGC GGC GATCA AGGTCAGG		
			TCCG CCG CTAGT TCCAGTCC		
			C C AC		
GAM1925	AQP6	3'	CCTGAGGCGATCTGCCCCACCT 54998	CA ACAAGG	
			AGG GGCAGATC TCAGG		
			TCC CCGTCTAG AGTCC		
			AC CGG__		
GAM1925	AQP6	3'	CCTGAGGCGATCTGCCCCACCT 54999	CA ACAAGG	
			AGG GGCAGATC TCAGG		
			TCC CCGTCTAG AGTCC		
			AC CGG__		
GAM1925	ATP8B2	3'	CCTGACCTCCTGACCTGCCCCAC 65831	CA A CA	
	CT		AGG GGCAG TCA AGGTCAGG		
			TCC CCGTC AGT TCCAGTCC		
			AC C CC		
GAM1925	AXL	3'	CCTGACCTCAAGTGATCTGCCC 41882	CA A__	
	ACCT		AGG GGCAGATCAC AGGTCAGG		
			TCC CCGTCTAGTG TCCAGTCC		
			AC AAC		
GAM1925	BAZ2B	5'	CCTGACCTTGTGATCCACCTCC 26520	C CA	
	T		AGG AGG GATCACAAGGTCAGG		
			TCC TCC CTAGTGTTCCAGTCC		
			_ AC		
GAM1925	C7	3'	CCTGACCTCAGGTAATCCGTCT 6984	A C A__	
	GCCT		AGGCAGGC GAT AC AGGTCAGG		

			TCCGTCTG CTA TG TCCAGTCC		
			C A GAC		
GAM1925	CAMLG	3'	CCTCAGGTGATCTGCCCCACCT 9998	CA	A__
			AGG GGCAGATCAC AGG		
			TCC CCGTCTAGTG TCC		
			AC GAC		
GAM1925	CASP2	3'	CCTGACCTCATGATCCACCCAC 8707	CA CA	CA
	CT		AGG GG GATCA AGGTCAGG		
			TCC CC CTAGT TCCAGTCC		
			AC AC AC		
GAM1925	CASP2	3'	CCTGACCTCATGATCCACCCAC 53325	CA CA	CA
	CT		AGG GG GATCA AGGTCAGG		
			TCC CC CTAGT TCCAGTCC		
			AC AC AC		
GAM1925	CASP2	3'	CCTGACCTCATGATCCACCCAC 53326	CA CA	CA
	CT		AGG GG GATCA AGGTCAGG		
			TCC CC CTAGT TCCAGTCC		
			AC AC AC		
GAM1925	CASP2	3'	CCTGACCTCATGATCCACCCAC 53326	CA CA	CA
	CT		AGG GG GATCA AGGTCAGG		
			TCC CC CTAGT TCCAGTCC		
			AC AC AC		
GAM1925	CASP8	3'	CCTGACCTCGTGATCCACCCAC 8750	CA CA	A
	CT		AGG GG GATCAC AGGTCAGG		
			TCC CC CTAGTG TCCAGTCC		
			AC AC C		
GAM1925	CBFA2T2	3'	CGACCCCATCTGCCTCCT 18710	C	CACAA A
			AGG AGGCAGAT GGTC G		
			TCC TCCGTCTA CCAG C		
			_ CC__ C		
GAM1925	CLECSF12	3'	CCTGACCTCAAGTGATCTGCCT 77208		A__
	GCCT		AGGCAGGCAGATCAC AGGTCAGG		
			TCCGTCCGTCTAGTG TCCAGTCC		
			AAC		
GAM1925	CNGA1	5'	CCTGATCTCAAGTGATCTGCCC 60238	CA	A__
	ACCT		AGG GGCAGATCAC AGGTCAGG		
			TCC CCGTCTAGTG TCTAGTCC		
			AC AAC		
GAM1925	CR1	3'	CCTGACCTCGTGATCCACCCGC 6942	A CA	A
	CT		AGGC GG GATCAC AGGTCAGG		
			TCCG CC CTAGTG TCCAGTCC		
			C AC C		
GAM1925	CYP1A2	3'	CCTGACCTCAAGTGATCTGCCC 7511	A	A__
	GCCT		AGGC GGCAGATCAC AGGTCAGG		

			TCCG CCGTCTAGTG	TCCAGTCC	
			C	AAC	
GAM1925	CYP1A2	3'	CTTGACCTCGTGATCCACCCGC	69658	A CA A
	CT		AGGC GG GATCAC AGGTCAGG		
			TCCG CC CTAGTG TCCAGTTC		
			C AC	C	
GAM1925	DFFB	3'	CCTGACCTCAGGTGATCCGCC	88766	A A__
			GGC GATCAC AGGTCAGG		
			CCG CTAGTG TCCAGTCC		
			C	GAC	
GAM1925	DFFB	3'	CCTGACCTCAGGTGATCTGCCC	88767	A A__
	GCCT		AGGC GGCAGATCAC AGGTCAGG		
			TCCG CCGTCTAGTG TCCAGTCC		
			C	GAC	
GAM1925	DNASE1L1	5'	CCTGACCTCGTATCCACCCGCC	23016	A CA C A
	T		AGGC GG GAT AC AGGTCAGG		
			TCCG CC CTA TG TCCAGTCC		
			C AC	_ C	
GAM1925	DSC3	3'	CCTGACCTCGTGATCCGCCTGC	10436	A A
	CT		AGGCAGGC GATCAC AGGTCAGG		
			TCCGTCCG CTAGTG TCCAGTCC		
			C	C	
GAM1925	DSC3	3'	CCTGACCTCGTGATCCGCCTGC	44618	A A
	CT		AGGCAGGC GATCAC AGGTCAGG		
			TCCGTCCG CTAGTG TCCAGTCC		
			C	C	
GAM1925	DSCR3	3'	CCTGACCTCGTGACCCACCCGC	21308	A CAGA A
	CT		AGGC GG TCAC AGGTCAGG		
			TCCG CC AGTG TCCAGTCC		
			C ACCC	C	
GAM1925	EIF2C1	3'	CTGCCTGCCTGCCTGCCT	25190	ATCACA T
			AGGCAGGCAG AGG CAG		
			TCCGTCCGTC TCC GTC		
			CG_____		
GAM1925	EIF2C1	3'	CTGCCTGCCTGCCTGCCT	25191	ATCACA T
			AGGCAGGCAG AGG CAG		
			TCCGTCCGTC TCC GTC		
			CG_____		
GAM1925	EIF2C1	3'	CTGCCTGCCTGCCTGCCT	25192	ATCACA T
			AGGCAGGCAG AGG CAG		

			TCCGTCCGTC	TCC GTC		
			CG_____			
GAM1925	EIF2C1	3'	CTGCCTGCCTGCCTGCCT	25193	ATCACA	T
			AGGCAGGCAG	AGG CAG		
			TCCGTCCGTC	TCC GTC		
			CG_____			
GAM1925	FANCF	3'	CCTGACCTTGTGATCCGTCCGC	42979	A	A
	CT		AGGC GGC GATCACAAGGTCAGG			
			TCCG CTG CTAGTGTTCAGTCC			
			C C			
GAM1925	FCGR2A	3'	CCTCTAGCGATCTGCCCCGCCT	80027	A	ACA__
			AGGC GGCAGATC	AGG		
			TCCG CCGTCTAG	TCC		
			C CGATC			
GAM1925	FEZ1	3'	CCTGACCTGGTGATTTGCCCGC	18783	A	A
	CT		AGGC GGCAGATCAC AGGTCAGG			
			TCCG CCGTTTAGTG TCCAGTCC			
			C G			
GAM1925	FGF5	3'	CCTGACCTCATGATCTGCCCCAC	53657	CA	CA
	CT		AGG GGCAGATCA AGGTCAGG			
			TCC CCGTCTAGT TCCAGTCC			
			AC AC			
GAM1925	FGF5	3'	CCTGACCTCATGATCTGCCCCAC	53658	CA	CA
	CT		AGG GGCAGATCA AGGTCAGG			
			TCC CCGTCTAGT TCCAGTCC			
			AC AC			
GAM1925	FUT1	3'	CCTGACCTCGTGATCTGCCCCAC	5588	CA	A
	CT		AGG GGCAGATCAC AGGTCAGG			
			TCC CCGTCTAGTG TCCAGTCC			
			AC C			
GAM1925	FUT1	3'	CCTGACCTTGTGCATCCACCTGT	5589	CA	C
	CT		AGGCAGG GAT ACAAGGTCAGG			
			TCTGTCC CTA TGTTCCAGTCC			
			AC C			
GAM1925	G6PC	3'	CCTGACCTCAAGTGATCCACCT	5657	CA	A__
			AGG GATCAC AGGTCAGG			
			TCC CTAGTG TCCAGTCC			
			AC AAC			
GAM1925	GHR	3'	CCTGACCTCGTGATCCACCCGA	5697	GCA CA	A
	CT		AG GG GATCAC AGGTCAGG			

			TC CC CTAGTG TCCAGTCC			
			AGC AC C			
GAM1925	GM2A	3'	CTTGACCTCGTGATCCGTCCAC 68380	CA	A	A
	CT		AGG GGC GATCAC AGGTCAGG			
			TCC CTG CTAGTG TCCAGTTC			
			AC C C			
GAM1925	GNE	3'	CCTGACCTCAGGTGATCCGCC 19666	A	A__	
			GGC GATCAC AGGTCAGG			
			CCG CTAGTG TCCAGTCC			
			C GAC			
GAM1925	GPR81	3'	CCTGACCTCAGGTGATCCGCCT 51746	A	A__	
	GCCT		AGGCAGGC GATCAC AGGTCAGG			
			TCCGTCCG CTAGTG TCCAGTCC			
			C GAC			
GAM1925	GPR81	3'	CCTGACTTGTGATCCGCCTGCC 51747	A	G	
	T		AGGCAGGC GATCACAAG TCAGG			
			TCCGTCCG CTAGTGTTT AGTCC			
			C _			
GAM1925	GRAF	3'	CCTGACCTCAAGTGATCTGCCC 31233	CA	A__	
	ACTT		AGG GGCAGATCAC AGGTCAGG			
			TTC CCGTCTAGTG TCCAGTCC			
			AC AAC			
GAM1925	HCS	3'	CCTGACCTCGTGATCCACCCAC 38975	CA CA	A	
	CT		AGG GG GATCAC AGGTCAGG			
			TCC CC CTAGTG TCCAGTCC			
			AC AC C			
GAM1925	HLCS	5'	CCTGACCTCGTGATCCACCTGT 6411	CA	A	
	CT		AGGCAGG GATCAC AGGTCAGG			
			TCTGTCC CTAGTG TCCAGTCC			
			AC C			
GAM1925	HTR1D	3'	CTTGACCTCGTGATCCGCCCGC 7843	A A	A	
	CT		AGGC GGC GATCAC AGGTCAGG			
			TCCG CCG CTAGTG TCCAGTTC			
			C C C			
GAM1925	HUNK	3'	CCTGGGCTCCAACGATCTGCCC 28184	CA	ACA__ G	
	ACCT		AGG GGCAGATC AG TCAGG			
			TCC CCGTCTAG TC GGTCC			
			AC CAACC G			
GAM1925	HYAL4	5'	CCTGACCTCAAGTGATCTGCCT 25367	A__		
	GCCT		AGGCAGGCAGATCAC AGGTCAGG			

			TCCGTCCGTCTAGTG	TCCAGTCC		
			AAC			
GAM1925	IFNAR2	3'	CCTGACCTCAAGTGATCTGCCC	7898	CA	A__
		TCCT	AGG GGCAGATCAC	AGGTCAGG		
			TCC CCGTCTAGTG	TCCAGTCC		
			TC	AAC		
GAM1925	IGF1	3'	CCTGACCTTGTGATTTGCCCGC	7069	A	
		CT	AGGC GGCAGATCACAAGGTCAGG			
			TCCG CCGTTTAGTGTTCCAGTCC			
			C			
GAM1925	INMT	3'	CCTGACCTGGTGATCCACCCAC	23213	CA CA	A
		CT	AGG GG GATCAC	AGGTCAGG		
			TCC CC CTAGTG	TCCAGTCC		
			AC AC	G		
GAM1925	KCNQ3	5'	CTGACCCCCCTGCCTGGCCT	16926	_	ATCACAA
			AGGC AGGCAG	GGTCAG		
			TCCG TCCGTC	CCAGTC		
			G	CC_____		
GAM1925	KMO	3'	CCTCATGTGATCTGCCACCT	14841	CA	__
			AGG GGCAGATCACA	AGG		
			TCC CCGTCTAGTGT	TCC		
			AC	AC		
GAM1925	MAK	3'	CCTGACCTCAGGTGATCCACCT	20945	CA	A__
			AGG GATCAC	AGGTCAGG		
			TCC CTAGTG	TCCAGTCC		
			AC	GAC		
GAM1925	MICB	3'	CCTGACCTCAGGTGATCTGCCT	21021		A__
		GCCT	AGGCAGGCAGATCAC	AGGTCAGG		
			TCCGTCCGTCTAGTG	TCCAGTCC		
			GAC			
GAM1925	MPL	3'	CTCGTGATCCGCCTGCCT	19351	A	A
			AGGCAGGC	GATCAC AG		
			TCCGTCCG CTAGTG	TC		
			C	C		
GAM1925	MTR	3'	CCCGACCTCGTGATCTGCCAC	6016	CA	A A
		CT	AGG GGCAGATCAC	AGGTC GG		
			TCC CCGTCTAGTG	TCCAG CC		
			AC	C C		
GAM1925	MYCL2	3'	CCTGACCTAGGTGATCCA	19374	GCA	A_
		CT	AGGCAG	GATCAC	AGGTCAGG	

			TCCGTC CTAGTG TCCAGTCC		
			AC_ GA		
GAM1925 NDRG3	3'	CCTGACCTCAGGTGATCCACCT 42764	CA A__		
		AGG GATCAC AGGTCAGG			
		TCC CTAGTG TCCAGTCC			
		AC GAC			
GAM1925 NONO	3'	CCTGACCTCGTGATCTACCCAC 82887	CA C A		
CT		AGG GG AGATCAC AGGTCAGG			
		TCC CC TCTAGTG TCCAGTCC			
		AC A C			
GAM1925 NQO1	3'	CCTGACCTCAGGTGATCCGCCT 8046	A A__		
		AGGC GATCAC AGGTCAGG			
		TCCG CTAGTG TCCAGTCC			
		C GAC			
GAM1925 PCDHA9	3'	CCTGACCTCATGATCCTCCCGC 49838	A CA CA		
CT		AGGC GG GATCA AGGTCAGG			
		TCCG CC CTAGT TCCAGTCC			
		C TC AC			
GAM1925 PCDHA9	3'	CCTGACCTTGTGATGCTCCAC 49839	CA C _		
CT		AGG GG AG ATCACAAGGTCAGG			
		TCC CC TC TAGTGTTCCAGTCC			
		AC _ G			
GAM1925 PIGR	3'	CCTCAAGTGATCTGCCGCCT 72993	A A__		
		AGGC GGCAGATCAC AGG			
		TCCG CCGTCTAGTG TCC			
		— AAC			
GAM1925 PIGR	3'	CCTGACCTCGTGATCCGCCTGC 72994	A A		
CT		AGGCAGGC GATCAC AGGTCAGG			
		TCCGTCCG CTAGTG TCCAGTCC			
		C C			
GAM1925 PIK3C2B	3'	CTCGTGATCTGCCTGCCT 12096	A		
		AGGCAGGCAGATCAC AG			
		TCCGTCCGTCTAGTG TC			
		C			
GAM1925 PIK3C2B	3'	CTTGACCTCGTGATCTGCCTGC 12097	A		
CT		AGGCAGGCAGATCAC AGGTCAGG			
		TCCGTCCGTCTAGTG TCCAGTTC			
		C			
GAM1925 PIK3CD	3'	CCTGACCTCAGGTGATCCACC 18488	CA A__		
		GG GATCAC AGGTCAGG			

			CC CTAGTG TCCAGTCC		
			AC GAC		
GAM1925	PMCHL1	3'	CCTGACCTCGTGATCCACCTGC 49914	CA	A
	CT		AGGCAGG GATCAC AGGTCAGG		
			TCCGTCC CTAGTG TCCAGTCC		
			AC C		
GAM1925	POU2AF1	3'	CCTGACCTTGTGATCCGCGCGC 21740	AG	A
	CT		AGGC GC GATCACAAGGTCAGG		
			TCCG CG CTAGTGTTCCAGTCC		
			CG C		
GAM1925	PRKWNK3	3'	CCTAACCTTGTGATCCGCCCTC 62230	CA	A C
	CT		AGG GGC GATCACAAGGT AGG		
			TCC CCG CTAGTGTTCCA TCC		
			TC C A		
GAM1925	PTGIS	3'	CCTGACCTCGTGATTTGCCTGC 8204	A	
	CT		AGGCAGGCAGATCAC AGGTCAGG		
			TCCGTCCGTTTAGTG TCCAGTCC		
			C		
GAM1925	PTGIS	3'	CCTGAGCTCGTGATCTGCCCGC 8205	A	A G
	CT		AGGC GGCAGATCAC AG TCAGG		
			TCCG CCGTCTAGTG TC AGTCC		
			C C G		
GAM1925	RAB36	3'	CTGACCTCGTGATCTGCCCGCC 18167	A	A
	T		AGGC GGCAGATCAC AGGTCAG		
			TCCG CCGTCTAGTG TCCAGTC		
			C C		
GAM1925	RHD	3'	CCTCATGATCAGCCTGCCT 32822	A	CA
			AGGCAGGC GATCA AGG		
			TCCGTCCG CTAGT TCC		
			A AC		
GAM1925	RHD	3'	CCTCATGATCAGCCTGCCT 32823	A	CA
			AGGCAGGC GATCA AGG		
			TCCGTCCG CTAGT TCC		
			A AC		
GAM1925	RHD	3'	CCTGACCTCAAGTGATCTGCCC 32824	A	A__
	GCCT		AGGC GGCAGATCAC AGGTCAGG		
			TCCG CCGTCTAGTG TCCAGTCC		
			C AAC		
GAM1925	RHD	3'	CCTGACCTCAAGTGATCTGCCC 32825	A	A__
	GCCT		AGGC GGCAGATCAC AGGTCAGG		

			TCCG CCGTCTAGTG TCCAGTCC		
			C AAC		
GAM1925	RPP30	3'	CCTGACCTCATATTCCACCCGC 22195	A CA	TCACA
	CT		AGGC GG GA AGGTCAGG		
			TCCG CC CT TCCAGTCC		
			C AC TATAC		
GAM1925	SCML2	3'	CCTGACCTCAGGTGATCCGCC 21423	A	A__
			GGC GATCAC AGGTCAGG		
			CCG CTAGTG TCCAGTCC		
			C GAC		
GAM1925	SEDL	3'	CCTGACCTCAGTTGATCCACC 28090	CA	CA__
			GG GATCA AGGTCAGG		
			CC CTAGT TCCAGTCC		
			AC TGAC		
GAM1925	SEDL	3'	CCTGACCTCGTGATCCACCCAC 28091	CA CA	A
	CT		AGG GG GATCAC AGGTCAGG		
			TCC CC CTAGTG TCCAGTCC		
			AC AC C		
GAM1925	SEDL	3'	CCTGACCTCGTGATCTGCCCGC 28092	A	A
	CT		AGGC GGCAGATCAC AGGTCAGG		
			TCCG CCGTCTAGTG TCCAGTCC		
			C C		
GAM1925	SEDL	3'	CTCGTGATCTGCCCGCCT 28095	A	A
			AGGC GGCAGATCAC AG		
			TCCG CCGTCTAGTG TC		
			C C		
GAM1925	SERPINB9	3'	CCTGACCTCGTGATCCACCCGC 16016	A CA	A
	CT		AGGC GG GATCAC AGGTCAGG		
			TCCG CC CTAGTG TCCAGTCC		
			C AC C		
GAM1925	SH3BP2	3'	CCTGACCTCAACTGATCCGCC 13061	A	CA__
			GGC GATCA AGGTCAGG		
			CCG CTAGT TCCAGTCC		
			C CAAC		
GAM1925	SH3BP2	3'	CCTGACCTCAGGTGATCTGCCC 13062	CA	A__
	ACCT		AGG GGCAGATCAC AGGTCAGG		
			TCC CCGTCTAGTG TCCAGTCC		
			AC GAC		
GAM1925	SH3GL3	5'	CCTGACCTCGTGATCCGCCTGC 13107	A	A
	CT		AGGCAGGC GATCAC AGGTCAGG		

			TCCGTCCG CTAGTG TCCAGTCC		
			C C		
GAM1925 SHOX	3'	CCTGACCTCAGGTGATCTGCCC 6569	A A__		
	GCCT	AGGC GGCAGATCAC AGGTCAGG			
		TCCG CCGTCTAGTG TCCAGTCC			
		C GAC			
GAM1925 SLA2	3'	CCTGACCTCAGGTGATCCACC 50887	CA A__		
		GG GATCAC AGGTCAGG			
		CC CTAGTG TCCAGTCC			
		AC GAC			
GAM1925 SLC24A1	3'	CCTGAAGTCGTGATCTGCCCCG 17562	A AAGG		
	CT	AGGC GGCAGATCAC TCAGG			
		TCCG CCGTCTAGTG AGTCC			
		C CTGA			
GAM1925 SMAC	5'	CCTGACCTCAAGTGATCCACC 57997	CA A__		
		GG GATCAC AGGTCAGG			
		CC CTAGTG TCCAGTCC			
		AC AAC			
GAM1925 SULT2B1	5'	CCTGACCTCAGGTGATCCACC 17222	CA A__		
		GG GATCAC AGGTCAGG			
		CC CTAGTG TCCAGTCC			
		AC GAC			
GAM1925 TAPBP	3'	CCTGACCTCAGGTGATCTGCCC 13558	CA A__		
	ACCT	AGG GGCAGATCAC AGGTCAGG			
		TCC CCGTCTAGTG TCCAGTCC			
		AC GAC			
GAM1925 TAPBP	3'	CCTGACCTTGTGATCTGCCCCG 13559	A		
	CT	AGGC GGCAGATCACAAGGTCAGG			
		TCCG CCGTCTAGTGTTCCAGTCC			
		C			
GAM1925 TERF1	3'	CCTGACTTCATGATCCACCCAC 34392	CA CA CA		
	CT	AGG GG GATCA AGGTCAGG			
		TCC CC CTAGT TTCAGTCC			
		AC AC AC			
GAM1925 TERF2	3'	CCTGACCTCGTGATCCACCCAA 20150	GCA CA A		
	CT	AG GG GATCAC AGGTCAGG			
		TC CC CTAGTG TCCAGTCC			
		AAC AC C			
GAM1925 TES	3'	CCTGACCTCAGATGATCCGCCT 72462	A CA__		
	GCCT	AGGCAGGC GATCA AGGTCAGG			

			TCCGTCCG CTAGT TCCAGTCC		
			C AGAC		
GAM1925	TIM3	3'	CCTGACCTCATGATTTGCCTGC 52354	CA	
	CT		AGGCAGGCAGATCA AGGTCAGG		
			TCCGTCCGTTTAGT TCCAGTCC		
			AC		
GAM1925	TLR5	5'	CCTGACCTTATAGTTGCCAGC 13785	A_	ATCAC
	T		GGC GGCAG AAGGTCAGG		
			TCG CCGTT TTCCAGTCC		
			AC GATA_		
GAM1925	TNFRSF10B	3'	CCTGACCTCAGGTGATCCACCT 15223	CA	A__
			AGG GATCAC AGGTCAGG		
			TCC CTAGTG TCCAGTCC		
			AC GAC		
GAM1925	TP53BP2	5'	CCTGACCTTGTGATCCGCCTGC 19460	A	
	CT		AGGCAGGC GATCACAAGGTCAGG		
			TCCGTCCG CTAGTGTTCCAGTCC		
			C		
GAM1925	TPMT	3'	CCTGACCTCAGGTGATCTACC 6309	C	A__
			GG AGATCAC AGGTCAGG		
			CC TCTAGTG TCCAGTCC		
			A GAC		
GAM1925	TRAF5	3'	CCTGACCTCAAGTGATCTGCCC 17271	A	A__
	GCCT		AGGC GGCAGATCAC AGGTCAGG		
			TCCG CCGTCTAGTG TCCAGTCC		
			C AAC		
GAM1925	TRPM6	3'	CCTGACCTCAGATGATCCACCT 35031	CA	CA__
			AGG GATCA AGGTCAGG		
			TCC CTAGT TCCAGTCC		
			AC AGAC		
GAM1925	TRPV1	3'	CCTCAGGTGATCTGCCCCGCCT 55666	A	A__
			AGGC GGCAGATCAC AGG		
			TCCG CCGTCTAGTG TCC		
			C GAC		
GAM1925	TRPV1	3'	CCTCAGGTGATCTGCCCCGCCT 55667	A	A__
			AGGC GGCAGATCAC AGG		
			TCCG CCGTCTAGTG TCC		
			C GAC		
GAM1925	TRPV1	3'	CCTGACCTCAGGTGATCCGCC 55668	A	A__
			GGC GATCAC AGGTCAGG		

			CCG CTAGTG TCCAGTCC		
			C GAC		
GAM1925 TUFT1	3'	CCTGACCTCAGGTGATCCACC 39672	CA A__		
		GG GATCAC AGGTCAGG			
		CC CTAGTG TCCAGTCC			
		AC GAC			
GAM1925 UGDH	3'	CCTGACCTTGTGAACCAACCCGT 13995	A CAGA		
CT		AGGC GG TCACAAGGTCAGG			
		TCTG CC AGTGTTCCAGTCC			
		C ACCA			
GAM1925 VHL	3'	CCTGACCTCAGGTGATCCGCC 6847	A A__		
		GGC GATCAC AGGTCAGG			
		CCG CTAGTG TCCAGTCC			
		C GAC			
GAM1925 VHL	3'	CCTGACCTTGTGATCCACCCAC 6848	CA CA		
CT		AGG GG GATCACAAGGTCAGG			
		TCC CC CTAGTGTTCCAGTCC			
		AC AC			
GAM1925 VIPR2	3'	CCTGACCTCGTGATGGGCCCGC 14062	A AG A		
CT		AGGC GGC ATCAC AGGTCAGG			
		TCCG CCG TAGTG TCCAGTCC			
		C GG C			
GAM1925 WHSC1	3'	CCTGACCTCGTGATCCACCCGC 24665	A CA A		
CT		AGGC GG GATCAC AGGTCAGG			
		TCCG CC CTAGTG TCCAGTCC			
		C AC C			
GAM1925 WHSC1	5'	CCTGACCTTGTGATCCGCTCGC 24666	AG A		
CT		AGGC GC GATCACAAGGTCAGG			
		TCCG CG CTAGTGTTCCAGTCC			
		CT C			
GAM1925 XRCC2	3'	CCTGACCTCAAGTGATCCACC 19498	CA A__		
		GG GATCAC AGGTCAGG			
		CC CTAGTG TCCAGTCC			
		AC AAC			
GAM1925 YES1	3'	CCTGACCTTGTGATCTGCCCGC 19534	A		
CT		AGGC GGCAGATCACAAGGTCAGG			
		TCCG CCGTCTAGTGTTCCAGTCC			
		C			
GAM1925 ZNF264	3'	CCTGACCTTGTGATCCGCCAAC 14207	CA A		
CT		AGG GGC GATCACAAGGTCAGG			

TCC CCG CTAGTGTTCAGTCC
 AA C
 GAM1925 ZNF264 3' CTTGACCTCATGATCCACCCGC 14213 A CA CA
 CT AGGC GG GATCA AGGTCAGG
 |||| || |||| ||||
 TCCG CC CTAGT TCCAGTTC
 C AC AC
 GAM1925 AAK1 3' CCTGACCTCAGGTGATCCGCCT 30519 A A__
 GCCT AGGCAGGC GATCAC AGGTCAGG
 |||| |||| ||||
 TCCGTCCG CTAGTG TCCAGTCC
 C GAC
 GAM1925 AIF1 5' CCCAACCCCACTTCCTCTGCCT 17924 TCACAA__ CA
 GCC GGCAGGCAGA GGT GG
 |||| || || ||
 CCGTCCGTCT CCA CC
 CCTTCACC AC
 GAM1925 ARHF 3' CCTGACCTCGTGATCCACCCGC 39264 A CA A
 CT AGGC GG GATCAC AGGTCAGG
 |||| || |||| ||||
 TCCG CC CTAGTG TCCAGTCC
 C AC C
 GAM1925 ARHGAP11A 3' CCTGACCTTGTGATCCGCCCGC 29447 A A
 CT AGGC GGC GATCACAAGGTCAGG
 |||| || |||| |||| ||||
 TCCG CCG CTAGTGTTCAGTCC
 C C
 GAM1925 ARHGAP5 5' CCCAACCTCAGGTGATCCGCCT 77598 A A__ CA
 GCCT AGGCAGGC GATCAC AGGT GG
 |||| |||| || ||
 TCCGTCCG CTAGTG TCCA CC
 C GAC AC
 GAM1925 ASE-1 3' CCTGACCTCCTGATGCGCCTGC 24974 AG CA
 CT AGGCAGGC ATCA AGGTCAGG
 |||| || || || ||||
 TCCGTCCG TAGT TCCAGTCC
 CG CC
 GAM1925 ASE-1 3' CCTGACCTCGTGATCCACCTGC 24975 CA A
 CT AGGCAGG GATCAC AGGTCAGG
 |||| || || || ||||
 TCCGTCC CTAGTG TCCAGTCC
 AC C
 GAM1925 ASE-1 3' CTCGTGATCCACCTGCCT 24978 CA A
 AGGCAGG GATCAC AG
 |||| || || ||
 TCCGTCC CTAGTG TC
 AC C
 GAM1925 ATP1B4 3' CCTGACCTCAAGTGATCCGCCT 24841 A A__
 GCCT AGGCAGGC GATCAC AGGTCAGG
 |||| || || || ||||

TCCGTCCG CTAGTG TCCAGTCC
 C AAC
 GAM1925 ATP6V0A1 3' CCCGACCTTGTGCAGCCCCCT 18985 CA AGAT A
 AGG GGC CACAAGGTC GG
 ||| ||| ||||| ||
 TCC CCG GTGTTCCAG CC
 CC AC__ C
 GAM1925 BA108L7.2 3' CCTGACCTCAGGTGATCCACCT 49071 CA A__
 AGG GATCAC AGGTCAGG
 ||| ||||| |||||
 TCC CTAGTG TCCAGTCC
 AC GAC
 GAM1925 BAG5 3' CCTGACCTCGTGATCCGCCCGC 18036 A A A
 CT AGGC GGC GATCAC AGGTCAGG
 ||||| ||| ||||| |||||
 TCCG CCG CTAGTG TCCAGTCC
 C C C
 GAM1925 BCL2L1 5' CCGGGGGCTGCACCTGCCTGCC 57591 ATCACA G A_
 T AGGCAGGCAG AG TC GG
 ||||| || || ||
 TCCGTCCGTC TC GG CC
 CACG__ G GG
 GAM1925 BTN3A1 3' CTTGACCTCATGATCCACCCAC 23892 CA CA CA
 CT AGG GG GATCA AGGTCAGG
 ||| || ||||| |||||
 TCC CC CTAGT TCCAGTTC
 AC AC AC
 GAM1925 C11orf11 3' CTACCTGCCCTGCCTGCCT 94876 ATCACA C
 AGGCAGGCAG AGGT AG
 ||||| || || ||
 TCCGTCCGTC TCCA TC
 CCG__ _
 GAM1925 C13orf1 3' CCTGACCTCATGATCCACCTCC 40361 C CA CA
 CT AGG AGG GATCA AGGTCAGG
 ||| ||| ||||| |||||
 TCC TCC CTAGT TCCAGTCC
 C AC AC
 GAM1925 C21orf25 3' CCTGACCTCAGGTGATCCACC 64289 CA A__
 GG GATCAC AGGTCAGG
 || ||||| |||||
 CC CTAGTG TCCAGTCC
 AC GAC
 GAM1925 C6orf5 3' CCTGACCTTGTGATCCGCCAC 31985 CA A
 CT AGG GGC GATCACAAGGTCAGG
 ||| ||| ||||| |||||
 TCC CCG CTAGTGTTCCAGTCC
 AC C
 GAM1925 C9orf5 3' CTGACCTTGCAGTCTCCT 50107 C CA
 AGG AGAT CAAGGTCAG
 ||| ||| |||||

TCC TCTG GTTCCAGTC
 _ AC
 GAM1925 C9orf9 3' CCTGACCTCAACTGGTCCACC 39015 CA CA__
 GG GATCA AGGTCAGG
 || |||| |||||
 CC CTGGT TCCAGTCC
 AC CAAC
 GAM1925 C9orf9 3' CCTGACCTCATGATCTACCCTC 39016 _ C_ CA
 GT GC AGG AGATCA AGGTCAGG
 || || |||| |||||
 TG TCC TCTAGT TCCAGTCC
 C CA AC
 GAM1925 CDC14B 3' CCTGACCTCAAGTGATCTGCCT 14775 A__
 GCCT AGGCAGGCAGATCAC AGGTCAGG
 ||||| |||||
 TCCGTCCGTCTAGTG TCCAGTCC
 AAC
 GAM1925 DCOHM 3' CCTGACCTCAAGCGACCTGCCT 50517 A ACA__
 GCCT AGGCAGGCAG TC AGGTCAGG
 ||||| || |||||
 TCCGTCCGTCTAGTG TCCAGTCC
 C CGAAC
 GAM1925 DJ726C3.2 5' CCTCTGCATCTGCCTGCCT 48208 _ CA
 AGGCAGGCAGAT CA AGG
 ||||| || |||
 TCCGTCCGTCTA GT TCC
 C C_
 GAM1925 DKFZp434A2417 3' CCCAACCTCAGGTGATCTGCCT 66676 A__ CA
 GCCT AGGCAGGCAGATCAC AGGT GG
 ||||| || ||| ||
 TCCGTCCGTCTAGTG TCCA CC
 GAC AC
 GAM1925 DKFZP434C212 3' CCTGACCTCGTGATCCACCCGC 69484 A CA A
 CT AGGC GG GATCAC AGGTCAGG
 ||| || |||| |||||
 TCCG CC CTAGTG TCCAGTCC
 C AC C
 GAM1925 DKFZp434N2435 5' CCTGAATGTGATCTACCCACT 98088 CA C AGG _
 GG GG AGATCACA TCA GG
 || || |||| || |||
 TC CC TCTAGTGT AGT CC
 AC A A__ A
 GAM1925 DKFZP564G092 5' CCTGACCTCAAGTAATCTGCC 32157 C A__
 GGCAGAT AC AGGTCAGG
 ||||| || |||||
 CCGTCTA TG TCCAGTCC
 A AAC
 GAM1925 DKFZP727G051 3' CCTGGCAGAATGCCCTGCCTGC 70005 AT CAAG
 CT AGGCAGGCAG CA GTCAGG
 ||||| || |||||

TCCGTCCGTC GT CGGTCC
 CC AAGA
 GAM1925 DKFZp761N1114 3' CCTGACCTCATGATCTGCCCGT 79780 A CA
 CT AGGC GGCAGATCA AGGTCAGG
 ||| ||||| |||||
 TCTG CCGTCTAGT TCCAGTCC
 C AC
 GAM1925 DSCR6 3' CCTGACCTCAGGTGATCCACC 39064 CA A__
 GG GATCAC AGGTCAGG
 || ||||| |||||
 CC CTAGTG TCCAGTCC
 AC GAC
 GAM1925 EZFIT 3' CTGACCTCATGACCTCCC 41378 C CAGA CA
 GG AGG TCA AGGTCAG
 || ||| ||| |||||
 CC TCC AGT TCCAGTC
 C ____ AC
 GAM1925 FBP17 3' CCTGACCTCAGGTGATCCGCC 73148 A A__
 GGC GATCAC AGGTCAGG
 ||| ||||| |||||
 CCG CTAGTG TCCAGTCC
 C GAC
 GAM1925 FER1L4 3' CCTGACCTCAAGTGATCCACC 48118 CA A__
 GG GATCAC AGGTCAGG
 || ||||| |||||
 CC CTAGTG TCCAGTCC
 AC AAC
 GAM1925 FLJ00060 5' CCTGACCTCATGATCCGCCCGC 61745 A A CA
 CT AGGC GGC GATCA AGGTCAGG
 |||| ||| ||||| |||||
 TCCG CCG CTAGT TCCAGTCC
 C C AC
 GAM1925 FLJ10081 3' CCTGAGGTGTGATCTGTCCACC 36289 CA AGG
 T AGG GGCAGATCACA TCAGG
 ||| ||||| ||||| |||||
 TCC CTGTCTAGTGT AGTCC
 AC GG_
 GAM1925 FLJ10535 3' CCTAAAGTGATCTGCCCGCCT 36744 A A__
 AGGC GGCAGATCAC AGG
 |||| ||||| |||
 TCCG CCGTCTAGTG TCC
 C AAA
 GAM1925 FLJ10535 3' CTTGACCTTGTGATCCACCCAC 36746 CA CA
 CT AGG GG GATCACAAGGTCAGG
 ||| || ||||| ||||| |||||
 TCC CC CTAGTGTTCCAGTTC
 AC AC
 GAM1925 FLJ10901 3' CCTGACCTCAAGTGATCCACCT 37359 CA A__
 AGG GATCAC AGGTCAGG
 ||| ||||| |||||

TCC CTAGTG TCCAGTCC
 AC AAC
 GAM1925 FLJ10956 3' CCTGAGCTCAAGTGATCTGCCC 37465 CA A__ G
 ATCT AGG GGCAGATCAC AG TCAGG
 ||| ||||| |||||
 TCT CCGTCTAGTG TC AGTCC
 AC AAC G
 GAM1925 FLJ12787 3' CCTGACCTCAAGTGATCTACCT 50691 C A__
 AGG AGATCAC AGGTCAGG
 ||| ||||| |||||
 TCC TCTAGTG TCCAGTCC
 A AAC
 GAM1925 FLJ12876 3' CCTGACCTCGTGATCCGCCCGC 43089 A A A
 CT AGGC GGC GATCAC AGGTCAGG
 ||| ||| ||||| |||||
 TCCG CCG CTAGTG TCCAGTCC
 C C C
 GAM1925 FLJ12876 3' CTCGTGATCCGCCCGCCT 43090 A A A
 AGGC GGC GATCAC AG
 ||| ||| ||||| ||
 TCCG CCG CTAGTG TC
 C C C
 GAM1925 FLJ12903 3' CCTGACCTCAGGTGATCTGCCC 43067 CA A__
 ACCT AGG GGCAGATCAC AGGTCAGG
 ||| ||||| |||||
 TCC CCGTCTAGTG TCCAGTCC
 AC GAC
 GAM1925 FLJ13193 3' CCTAATGATCTGCCACCT 50719 CA CA
 AGG GGCAGATCA AGG
 ||| ||||| |||
 TCC CCGTCTAGT TCC
 AC AA
 GAM1925 FLJ14442 3' CCTCGTGATCCACCTGCTT 52380 CA A
 AGGCAGG GATCAC AGG
 ||||| ||||| |||
 TTCGTCC CTAGTG TCC
 AC C
 GAM1925 FLJ14681 5' CCGGATTCGGACCCGCTGCCT 52594 AGA ACAA A
 AGGCAGGC TC GGTC GG
 ||||| || ||| ||
 TCCGTCCG AG TTAG CC
 CCC GC__ G
 GAM1925 FLJ14957 3' CCTGACCTCAGGTGATCCACCT 52815 CA A__
 AGG GATCAC AGGTCAGG
 ||| ||||| |||||
 TCC CTAGTG TCCAGTCC
 AC GAC
 GAM1925 FLJ20136 3' CCTGACCTTGTGATCCGCATGC 35095 G A
 CT AGGCA GC GATCACAAGGTCAGG
 ||||| || ||||| |||||

TCCGT CG CTAGTGTTCAGTCC
 A C
 GAM1925 FLJ20320 3' CCTCAGGTGATCTGCTTGCCT 35422 A__
 AGGCAGGCAGATCAC AGG
 ||||| ||||| |||||
 TCCGTTCGTCTAGTG TCC
 GAC
 GAM1925 FLJ20344 3' CCTGACCTCAAGTGATCCGCCT 35480 A A__
 GCCT AGGCAGGC GATCAC AGGTCAGG
 ||||| ||||| |||||
 TCCGTCCG CTAGTG TCCAGTCC
 C AAC
 GAM1925 FLJ20452 3' CCTGACCTCAGGTGATCCACC 35645 CA A__
 GG GATCAC AGGTCAGG
 || ||||| |||||
 CC CTAGTG TCCAGTCC
 AC GAC
 GAM1925 FLJ20511 3' CCTGACCTCGTGATCTGCCCTC 35769 CA A
 CT AGG GGCAGATCAC AGGTCAGG
 ||| ||||| |||||
 TCC CCGTCTAGTG TCCAGTCC
 TC C
 GAM1925 FLJ20511 3' CCTGGACCTGCCTGCCT 35771 A A AG
 AGGCAGGCAG TC CA G
 ||||| || || |
 TCCGTCCGTC AG GT C
 C _ CT
 GAM1925 FLJ20700 3' CCTGACCTCATGATCTGCCCGC 36006 A CA
 CT AGGC GGCAGATCA AGGTCAGG
 ||| ||||| |||||
 TCCG CCGTCTAGT TCCAGTCC
 C AC
 GAM1925 FLJ21302 3' CCTGACCTCATGATCTACCCGC 43508 A C CA
 CT AGGC GG AGATCA AGGTCAGG
 ||| || ||||| |||||
 TCCG CC TCTAGT TCCAGTCC
 C A AC
 GAM1925 FLJ22167 5' CCTGACCTCGTGATCCGCCCGC 44866 A A A
 CT AGGC GGC GATCAC AGGTCAGG
 ||| || ||||| |||||
 TCCG CCG CTAGTG TCCAGTCC
 C C C
 GAM1925 FLJ22329 3' CCTGACCTCAAGTGATCTGCCC 45398 A A__
 GCCT AGGC GGCAGATCAC AGGTCAGG
 ||| ||||| |||||
 TCCG CCGTCTAGTG TCCAGTCC
 C AAC
 GAM1925 FLJ22794 3' CCTGACCTCGTGATCCACCTGC 93241 CA A
 CT AGGCAGG GATCAC AGGTCAGG
 ||||| ||||| |||||

			TCCGTCC CTAGTG TCCAGTCC		
			AC C		
GAM1925	FLJ22865	5'	CCTGACCTGGCCCGCCCGCCT 47785	A	AGATCACA
			AGGC GGC AGGTCAGG		
			TCCG CCG TCCAGTCC		
			C CCCGG__		
GAM1925	FLJ23024	3'	CCTCAAGTGATTTGCCTGCCT 46840	A__	
			AGGCAGGCAGATCAC AGG		
			TCCGTCCGTTTAGTG TCC		
			AAC		
GAM1925	FLJ23519	3'	CCTGACCTCGTGATCCGCCTGC 50947	A	A
	CT		AGGCAGGC GATCAC AGGTCAGG		
			TCCGTCCG CTAGTG TCCAGTCC		
			C C		
GAM1925	FLJ23556	3'	CCTGACCTTGTGATCCTCCCGC 46436	A	CA
	CT		AGGC GG GATCACAAGGTCAGG		
			TCCG CC CTAGTGTTCCAGTCC		
			C TC		
GAM1925	FLJ32356	3'	CCTGGCTCTGTGCCTGCCTGCC 59018	AT	AG
	T		AGGCAGGCAG CACA GTCAGG		
			TCCGTCCGTC GTGT CGGTCC		
			C_ CT		
GAM1925	GGA2	3'	CCTGACCTCAGGTGATCCGCCT 57661	A	A__
	GCCT		AGGCAGGC GATCAC AGGTCAGG		
			TCCGTCCG CTAGTG TCCAGTCC		
			C GAC		
GAM1925	GGA2	3'	CCTGACCTCAGGTGATCCGCCT 31163	A	A__
	GCCT		AGGCAGGC GATCAC AGGTCAGG		
			TCCGTCCG CTAGTG TCCAGTCC		
			C GAC		
GAM1925	GNG4	3'	CCTGACCTCGTGATCCACCCGC 16844	A	CA A
	CT		AGGC GG GATCAC AGGTCAGG		
			TCCG CC CTAGTG TCCAGTCC		
			C AC C		
GAM1925	GOLGA3	3'	CCTGACCTCAAGTGATCTGCCC 20887	CA	A__
	ATCT		AGG GGCAGATCAC AGGTCAGG		
			TCT CCGTCTAGTG TCCAGTCC		
			AC AAC		
GAM1925	GREB1	3'	CCTCAGGTGATCTGCCACCT 28563	CA	A__
			AGG GGCAGATCAC AGG		

			TCC CCGTCTAGTG TCC			
			AC GAC			
GAM1925	GREB1	3'	CCTGACCTCGTGATCCGCCCGC 28564	A A A		
	CT		AGGC GGC GATCAC AGGTCAGG			
			TCCG CCG CTAGTG TCCAGTCC			
			C C C			
GAM1925	GTF2E1	3'	CCTGACCTCATGATCCACCCGC 19797	A CA CA		
	CT		AGGC GG GATCA AGGTCAGG			
			TCCG CC CTAGT TCCAGTCC			
			C AC AC			
GAM1925	HSMPP8	3'	CCTGACCTCAGGTGATCCGCC 95130	A A__		
			GGC GATCAC AGGTCAGG			
			CCG CTAGTG TCCAGTCC			
			C GAC			
GAM1925	HSNOV1	3'	CCCGACCTCAAGTGATCTGCCT 34433	A__ A		
	GCC		GGCAGGCAGATCAC AGGTC GG			
			CCGTCCGTCTAGTG TCCAG CC			
			AAC C			
GAM1925	HSNOV1	3'	CCTGAGCTAAAGCGATCTGCC 34434	CA ACA__ G		
	ACCT		AGG GGCAGATC AG TCAGG			
			TCC CCGTCTAG TC AGTCC			
			AC CGAAA G			
GAM1925	HSPC065	3'	CCTGACCTCATGATCCACCCGC 27148	A CA CA		
	CT		AGGC GG GATCA AGGTCAGG			
			TCCG CC CTAGT TCCAGTCC			
			C AC AC			
GAM1925	HSU79274	5'	CCGGGGTTCGCGGATCTGCCCGC 26146	A ACAA GT A_		
	C		GGC GGCAGATC G C GG			
			CCG CCGTCTAG C G CC			
			C GCG_ TG GG			
GAM1925	HT002	3'	CCTGACCTCGTGATCCGCCAC 26788	CA A A		
	CT		AGG GGC GATCAC AGGTCAGG			
			TCC CCG CTAGTG TCCAGTCC			
			AC C C			
GAM1925	ICK	3'	CCTGACCTCGTGATCCACCCTC 33684	C CA_ A		
	CT		AGG AGG GATCAC AGGTCAGG			
			TCC TCC CTAGTG TCCAGTCC			
			_ CAC C			
GAM1925	JAM1	3'	CCTGACCTCTTGATCCGCCTGC 34223	A CA		
	CT		AGGCAGGC GATCA AGGTCAGG			

			TCCGTCCG CTAGT TCCAGTCC		
			C TC		
GAM1925	JAM1	3'	CCTGACCTCTTGATCCGCCTGC 34224	A	CA
	CT		AGGCAGGC GATCA AGGTCAGG		
			TCCGTCCG CTAGT TCCAGTCC		
			C TC		
GAM1925	JM11	3'	CTCGTGATCTGCCCCGCT 54356	A	A
			AGGC GGCAGATCAC AG		
			TCCG CCGTCTAGTG TC		
			C C		
GAM1925	JM11	3'	CTTGACCTCGTGATCTGCCCCG 54358	A	A
	CT		AGGC GGCAGATCAC AGGTCAGG		
			TCCG CCGTCTAGTG TCCAGTTC		
			C C		
GAM1925	KCNT1	3'	CCCAACCCTGTGCCACCTCCTG 62487	C AT__	A CA
	CCT		AGGCAGG AG CACA GGT GG		
			TCCGTCC TC GTGT CCA CC		
			_ CACC C AC		
GAM1925	KIAA0022	3'	CCTGACCTCAAGTGATCCACC 30279	CA	A__
			GG GATCAC AGGTCAGG		
			CC CTAGTG TCCAGTCC		
			AC AAC		
GAM1925	KIAA0063	3'	CCCGACCTCAAGTGATCTGCCC 30256	A	A__ A
	GCCT		AGGC GGCAGATCAC AGGTC GG		
			TCCG CCGTCTAGTG TCCAG CC		
			C AAC C		
GAM1925	KIAA0087	3'	CCTGACCTTGTGGTCCACCCGC 29342	A	CA
	CT		AGGC GG GATCACAAGGTCAGG		
			TCCG CC CTGGTGTTCAGTCC		
			C AC		
GAM1925	KIAA0161	3'	CCTGACCTCAGGTGATCTGCCC 29197	CA	A__
	ACCT		AGG GGCAGATCAC AGGTCAGG		
			TCC CCGTCTAGTG TCCAGTCC		
			AC GAC		
GAM1925	KIAA0186	3'	CCTGACCTCAAGTGACCCACCT 41105	CA CAGA	A__
			AGG GG TCAC AGGTCAGG		
			TCC CC AGTG TCCAGTCC		
			AC ____ AAC		
GAM1925	KIAA0205	3'	CCTGACCTCAGGTGATCTGCCC 30208	CA	A__
	ACCT		AGG GGCAGATCAC AGGTCAGG		

TCC CCGTCTAGTG TCCAGTCC
 AC GAC
 GAM1925 KIAA0210 5' CCTCAAGTAATCCGCCTGCCT 29154 A C A__
 AGGCAGGC GAT AC AGG
 ||||| ||| || |||
 TCCGTCCG CTA TG TCC
 C A AAC
 GAM1925 KIAA0355 3' CTGCCTGCCTGCCTGCCT 28706 ATCACA T
 AGGCAGGCAG AGG CAG
 ||||| ||| |||
 TCCGTCCGTC TCC GTC
 CG_____
 GAM1925 KIAA0391 3' CCTGACCTCAGGTGATCCACC 28604 CA A__
 GG GATCAC AGGTCAGG
 || ||||| |||||
 CC CTAGTG TCCAGTCC
 AC GAC
 GAM1925 KIAA0426 3' CCTGACCTTGTGATCTGCCCAC 28924 CA
 CT AGG GGCAGATCACAAGGTCAGG
 ||| |||||
 TCC CCGTCTAGTGTTCCAGTCC
 AC
 GAM1925 KIAA0426 3' CTTGTGATCTGCCCACCT 28925 CA
 AGG GGCAGATCACAAG
 ||| |||||
 TCC CCGTCTAGTGTTCC
 AC
 GAM1925 KIAA0435 5' CCTGACTTCAAATGCTCTGCCT 29659 T CA__
 GCCT AGGCAGGCAGA CA AGGTCAGG
 ||||| || |||||
 TCCGTCCGTCT GT TTCAGTCC
 C AAAC
 GAM1925 KIAA0459 3' CCTGACCTTGTGATCTGCCCCG 61648 A
 CT AGGC GGCAGATCACAAGGTCAGG
 ||| |||||
 TCCG CCGTCTAGTGTTCCAGTCC
 C
 GAM1925 KIAA0469 3' CCTGACCTTGTGATCTGCCTGG 29978 G
 CT AG CAGGCAGATCACAAGGTCAGG
 || |||||
 TC GTCCGTCTAGTGTTCCAGTCC
 G
 GAM1925 KIAA0472 5' CCTGACCTCAAACGATCTGCCC 72347 CA ACA__
 ACC GG GGCAGATC AGGTCAGG
 || ||||| |||||
 CC CCGTCTAG TCCAGTCC
 AC CAAAC
 GAM1925 KIAA0513 5' CCTGACCTCAGGTGAGCCACC 29026 CA AGA A__
 GG GGC TCAC AGGTCAGG
 || ||| ||| |||||

CC CCG AGTG TCCAGTCC
 A_ _ GAC
 GAM1925 KIAA0527 3' CCTGACCTCAAGTGATCTGCCC 97494 CA A_
 TCCT AGG GGCAGATCAC AGGTCAGG
 ||| ||||| |||||
 TCC CCGTCTAGTG TCCAGTCC
 TC AAC
 GAM1925 KIAA0555 3' CCTGACCTCAAGTGATCTGCCT 60739 A_
 GCCT AGGCAGGCAGATCAC AGGTCAGG
 ||||| |||||
 TCCGTCCGTCTAGTG TCCAGTCC
 AAC
 GAM1925 KIAA0557 3' CCCGACCTTGTGATCCACCCAC 78549 CA CA A
 CT AGG GG GATCACAAGGTC GG
 ||| || ||||| ||
 TCC CC CTAGTGTTCCAG CC
 AC AC C
 GAM1925 KIAA0561 3' CCTGACCTCATGATTTGCCTGC 66471 CA
 CT AGGCAGGCAGATCA AGGTCAGG
 ||||| |||||
 TCCGTCCGTTTAGT TCCAGTCC
 AC
 GAM1925 KIAA0562 3' CCTGACCTTGTGATCCACCCAC 28820 CA CA
 CT AGG GG GATCACAAGGTCAGG
 ||| || ||||| |||||
 TCC CC CTAGTGTTCCAGTCC
 AC AC
 GAM1925 KIAA0594 3' CCTGACCTTGTGATCCACCCGC 65510 A CA
 CT AGGC GG GATCACAAGGTCAGG
 |||| || ||||| |||||
 TCCG CC CTAGTGTTCCAGTCC
 C AC
 GAM1925 KIAA0682 3' CCTGACCTCAAGTGATCCACCT 30019 CA A_
 AGG GATCAC AGGTCAGG
 ||| |||| |||||
 TCC CTAGTG TCCAGTCC
 AC AAC
 GAM1925 KIAA0737 3' CCTGACCTCATGATCCGCCCGC 29806 A A CA
 CT AGGC GGC GATCA AGGTCAGG
 |||| |||| |||||
 TCCG CCG CTAGT TCCAGTCC
 C C AC
 GAM1925 KIAA0759 3' CTGACCTTTTCCCTGCCT 67886 C TCACA
 AGGCAGG AGA AGGTCAG
 ||||| || |||||
 TCCGTCC TTT TCCAGTC
 C _
 GAM1925 KIAA0831 5' CCTAACCTCTTGATCTGCCCTC 30631 CA CA C
 CT AGG GGCAGATCA AGGT AGG
 ||| ||||| |||||

TCC CCGTCTAGT TCCA TCC
 TC TC A
 GAM1925 KIAA0841 3' CCTGACCTCAAGTGATCTGCCT 71894 A__
 GCCT AGGCAGGCAGATCAC AGGTCAGG
 ||||| |||||
 TCCGTCCGTCTAGTG TCCAGTCC
 AAC
 GAM1925 KIAA0861 3' CCTGACCTCGTGATCCCCCTGC 90345 CA A
 CT AGGCAGG GATCAC AGGTCAGG
 ||||| ||||| |||||
 TCCGTCC CTAGTG TCCAGTCC
 CC C
 GAM1925 KIAA0924 3' CCTGACCTTGTGATCCGCCAC 30360 CA A
 CT AGG GGC GATCACAAGGTCAGG
 ||| ||| ||||| |||||
 TCC CCG CTAGTGTTCCAGTCC
 AC C
 GAM1925 KIAA0961 3' CCTGACCTCAGGTGATCCACCT 30399 CA A__
 AGG GATCAC AGGTCAGG
 ||| ||||| |||||
 TCC CTAGTG TCCAGTCC
 AC GAC
 GAM1925 KIAA1026 3' CCTGACCTCAGGCGATCTGCCC 71736 CA ACA__
 ACCT AGG GGCAGATC AGGTCAGG
 ||| ||||| |||||
 TCC CCGTCTAG TCCAGTCC
 AC CGGAC
 GAM1925 KIAA1040 3' CCTGACCTCAGGTGATCTGCCC 72685 A A__
 GCCT AGGC GGCAGATCAC AGGTCAGG
 ||||| ||||| |||||
 TCCG CCGTCTAGTG TCCAGTCC
 C GAC
 GAM1925 KIAA1115 5' CCTCAAGTGATATGCCTGCCT 30689 G A__
 AGGCAGGCA ATCAC AGG
 ||||| ||||| |||
 TCCGTCCGT TAGTG TCC
 A AAC
 GAM1925 KIAA1128 3' CCTGACCTCAAGTGATCCACC 69000 CA A__
 GG GATCAC AGGTCAGG
 || ||||| |||||
 CC CTAGTG TCCAGTCC
 AC AAC
 GAM1925 KIAA1143 3' CCTGACCTCATGATCCACCTGC 69237 CA CA
 CT AGGCAGG GATCA AGGTCAGG
 ||||| ||||| |||||
 TCCGTCC CTAGT TCCAGTCC
 AC AC
 GAM1925 KIAA1170 3' CCTGACCTCAGGTGATCCGCC 70414 A A__
 GGC GATCAC AGGTCAGG
 ||| ||||| |||||

CCG CTAGTG TCCAGTCC
 C GAC
 GAM1925 KIAA1198 3' CCTGACCTCAGGTAATCCACCT 64023 CA CAG ACA
 AGG GG ATC AGGTCAGG
 ||| || ||| |||||
 TCC CC TGG TCCAGTCC
 A_ TAA AC_
 GAM1925 KIAA1198 3' CCTGACCTCAGGTGATCTGCCT 64024 A__
 GCCT AGGCAGGCAGATCAC AGGTCAGG
 ||||| |||||
 TCCGTCCGTCTAGTG TCCAGTCC
 GAC
 GAM1925 KIAA1198 3' CCTGACCTCGTGATCCGCCCTC 64025 CA A A
 CT AGG GGC GATCAC AGGTCAGG
 ||| ||| ||||| |||||
 TCC CCG CTAGTG TCCAGTCC
 TC C C
 GAM1925 KIAA1198 3' CCTGACCTTGTGATCCACCCAC 64026 CA CA
 CT AGG GG GATCACAAGGTCAGG
 ||| || ||||| |||||
 TCC CC CTAGTGTTCCAGTCC
 AC AC
 GAM1925 KIAA1198 3' CCTGACCTTGTGATCTGCCTGC 64027
 CT AGGCAGGCAGATCACAAGGTCAGG
 ||||| ||||| |||||
 TCCGTCCGTCTAGTGTTCCAGTCC
 GAM1925 KIAA1200 3' CCTGACCTCAGGTGATCTGCCC 63036 CA A__
 ACTT AGG GGCAGATCAC AGGTCAGG
 ||| ||||| |||||
 TTC CCGTCTAGTG TCCAGTCC
 AC GAC
 GAM1925 KIAA1209 3' CCTGATCTCATGATCCGTCTGC 61403 A CA
 CT AGGCAGGC GATCA AGGTCAGG
 ||||| ||||| |||||
 TCCGTCTG CTAGT TCTAGTCC
 C AC
 GAM1925 KIAA1210 3' CCTGACCTCGTGATCCGCCCGC 98069 A A A
 CT AGGC GGC GATCAC AGGTCAGG
 |||| ||| ||||| |||||
 TCCG CCG CTAGTG TCCAGTCC
 C C C
 GAM1925 KIAA1257 3' CCCGACTTCAGGTGATCCGCCT 63399 A AA__ A
 GCCT AGGCAGGC GATCAC GGTC GG
 ||||| ||||| ||| ||
 TCCGTCCG CTAGTG TCAG CC
 C GACT C
 GAM1925 KIAA1257 3' CCTGACCTCGTGATTGTCT 63400 A A
 AGGCAG TCAC AGGTCAGG
 ||||| ||||| |||||

TCTGTT AGTG TCCAGTCC
 _ C
 GAM1925 KIAA1287 3' CCTCAGGTGATCTGCCCCACCT 78935 CA A__
 AGG GGCAGATCAC AGG
 ||| ||||| |||
 TCC CCGTCTAGTG TCC
 AC GAC
 GAM1925 KIAA1320 5' CCTGACCTCAAGTGATCTACC 69837 C A__
 GG AGATCAC AGGTCAGG
 || ||||| |||||
 CC TCTAGTG TCCAGTCC
 A AAC
 GAM1925 KIAA1328 5' CCTCGTGATATGCCACCT 62320 CA G A
 AGG GGCA ATCAC AGG
 ||| ||| ||||| |||
 TCC CCGT TAGTG TCC
 AC A C
 GAM1925 KIAA1443 3' CCTGACCTCATGATCCGCCAC 64570 CA A CA
 CT AGG GGC GATCA AGGTCAGG
 ||| ||| ||||| |||||
 TCC CCG CTAGT TCCAGTCC
 AC C AC
 GAM1925 KIAA1465 3' CCTCAGGTGATCCATCTGCCT 61490 CA A__
 AGGCAGG GATCAC AGG
 ||||| ||||| |||
 TCCGTCT CTAGTG TCC
 AC GAC
 GAM1925 KIAA1467 3' CCTGACCTCAGATAATCCACCT 72064 CA CAG ACA
 AGG GG ATC AGGTCAGG
 ||| || ||| |||||
 TCC CC TAG TCCAGTCC
 A_ TAA AC_
 GAM1925 KIAA1508 3' CCTGACCTCAGGTAATCCACCT 62546 CA CAG ACA
 AGG GG ATC AGGTCAGG
 ||| || ||| |||||
 TCC CC TGG TCCAGTCC
 A_ TAA AC_
 GAM1925 KIAA1530 3' CTTGACCTCGTGATCCACCCAC 68558 CA CA A
 CT AGG GG GATCAC AGGTCAGG
 ||| || ||||| |||||
 TCC CC CTAGTG TCCAGTTC
 AC AC C
 GAM1925 KIAA1571 3' CCTGACCTTGTGGTCCACCCGC 61614 A CA
 CT AGGC GG GATCACAAGGTCAGG
 ||||| || ||||| |||||
 TCCG CC CTGGTGTTCAGTCC
 C AC
 GAM1925 KIAA1615 3' CCTGACCTTGTGATCCCCCTGC 69274 CA
 CT AGGCAGG GATCACAAGGTCAGG
 ||||| ||||| ||||| |||||

TCCGTCC CTAGTGTTCAGTCC
 CC
 GAM1925 KIAA1617 3' CCCAACCTCAAGTGATCTGCCC 93072 A A__ CA
 GCCT AGGC GGCAGATCAC AGGT GG
 |||| ||||| ||| ||
 TCCG CCGTCTAGTG TCCA CC
 C AAC AC
 GAM1925 KIAA1649 3' CCTGACCTCGGGTGGTCTGCCT 51230 A__
 GCCT AGGCAGGCAGATCAC AGGTCAGG
 ||||| |||||
 TCCGTCCGTCTGGTG TCCAGTCC
 GGC
 GAM1925 KIAA1668 3' CCTGACCTTGTGATCCACCCAC 67064 CA CA
 CT AGG GG GATCACAAGGTCAGG
 ||| || |||||
 TCC CC CTAGTGTTCAGTCC
 AC AC
 GAM1925 KIAA1712 3' CCTGACCTCAGGTGATCTGCCT 68153 A__
 GTCT AGGCAGGCAGATCAC AGGTCAGG
 ||||| |||||
 TCTGTCCGTCTAGTG TCCAGTCC
 GAC
 GAM1925 KIAA1719 3' CCCAGTGAGCGCCCTGCCTGCC 68729 A____ AA
 T AGGCAGGCAG TCAC GG
 ||||| ||| ||
 TCCGTCCGTC AGTG CC
 CCGCG AC
 GAM1925 KIAA1737 3' CCTGACCTCAGTTGATCCGCCT 67939 A CA__
 GCCT AGGCAGGC GATCA AGGTCAGG
 ||||| ||||| |||||
 TCCGTCCG CTAGT TCCAGTCC
 C TGAC
 GAM1925 KIAA1814 3' CCAAGTGCCCTGCCTGCCT 70875 AT AA
 AGGCAGGCAG CAC GG
 ||||| ||| ||
 TCCGTCCGTC GTG CC
 CC AA
 GAM1925 KIAA1877 3' CCTGACCTTGTGATCTGCCTGC 66745
 CT AGGCAGGCAGATCACAAGGTCAGG
 ||||| ||||| |||||
 TCCGTCCGTCTAGTGTTCAGTCC
 GAM1925 KIAA1922 5' CCTGACCTCAGGTGATCCGCCT 73992 A A__
 GCCT AGGCAGGC GATCAC AGGTCAGG
 ||||| ||||| |||||
 TCCGTCCG CTAGTG TCCAGTCC
 C GAC
 GAM1925 KIAA1975 5' CCTGACCTCGTGATCCGCCCGC 74419 A A A
 CT AGGC GGC GATCAC AGGTCAGG
 ||| || ||||| |||||

			TCCG CCG CTAGTG TCCAGTCC		
			C C C		
GAM1925	KLHL6	3'	CCTGACCTTGATCTGCCCCG 56169	A	
	CT		AGGC GGCAGATCACAAGGTCAGG		
			TCCG CCGTCTAGTGTTCCAGTCC		
			C		
GAM1925	MAIL	3'	CCTGAGCTCATGCCATCTGCCT 49472	___	CA G
	GCCT		AGGCAGGCAGAT CA AG TCAGG		
			TCCGTCCGTCTA GT TC AGTCC		
			CC AC G		
GAM1925	MEF-2	3'	CCTGACCTCGTGATCCACCCGC 65020	A CA	A
	CT		AGGC GG GATCAC AGGTCAGG		
			TCCG CC CTAGTG TCCAGTCC		
			C AC C		
GAM1925	MGC21738	3'	CCTGACCTCAAGTGATCCGCCT 59575	A	A__
	GCCT		AGGCAGGC GATCAC AGGTCAGG		
			TCCGTCCG CTAGTG TCCAGTCC		
			C AAC		
GAM1925	MGC2477	5'	CCTGACCTCGTGATCCGCC 44298	A	A
			GGC GATCAC AGGTCAGG		
			CCG CTAGTG TCCAGTCC		
			C C		
GAM1925	MGC4766	5'	CCTGACCTCGTGATCCGCCTGC 49556	A	A
	CT		AGGCAGGC GATCAC AGGTCAGG		
			TCCGTCCG CTAGTG TCCAGTCC		
			C C		
GAM1925	MGC4766	5'	CTCGTGATCCGCCTGCCT 49557	A	A
			AGGCAGGC GATCAC AG		
			TCCGTCCG CTAGTG TC		
			C C		
GAM1925	MKRN4	3'	CCTGACCTCAGGTGATCCACCT 48458	CA	A__
			AGG GATCAC AGGTCAGG		
			TCC CTAGTG TCCAGTCC		
			AC GAC		
GAM1925	MLZE	5'	CCTGACCTCGGGATCCACCGGC 49450	A CA	ACA
	CT		AGGC GG GATC AGGTCAGG		
			TCCG CC CTAG TCCAGTCC		
			G AC GGC		
GAM1925	moblak	3'	CCTGACCTTGATCCACCAGC 56394	A CA	
	CT		AGGC GG GATCACAAGGTCAGG		

			TCCG CC CTAGTGTTCAGTCC			
			A AC			
GAM1925	MRPS27	3'	CCTGACCTCAAGTGATCTGCCC 31327	A	A__	
	GCCT		AGGC GGCAGATCAC AGGTCAGG			
			TCCG CCGTCTAGTG TCCAGTCC			
			C AAC			
GAM1925	MYO5C	3'	CTTGACCTCGTGATCCGCCAC 38718	CA	A	A
	CT		AGG GGC GATCAC AGGTCAGG			
			TCC CCG CTAGTG TCCAGTTC			
			AC C C			
GAM1925	NDUFC2	3'	CTTGACCTTGTGATCCACCTGC 17028	CA		
	CT		AGGCAGG GATCACAAGGTCAGG			
			TCCGTCC CTAGTGTTCAGTTC			
			AC			
GAM1925	NDUFC2	3'	CTTGTGATCCACCTGCCT 17030	CA		
			AGGCAGG GATCACAAG			
			TCCGTCC CTAGTGTTT			
			AC			
GAM1925	NINJ2	3'	CCTGACCTCAGGTGATCTGCCC 33720	A	A__	
	GTCT		AGGC GGCAGATCAC AGGTCAGG			
			TCTG CCGTCTAGTG TCCAGTCC			
			C GAC			
GAM1925	NXN	3'	CCTGACCTCAGGTGATCCACC 42672	CA	A__	
			GG GATCAC AGGTCAGG			
			CC CTAGTG TCCAGTCC			
			AC GAC			
GAM1925	OCT11	3'	CCTGACCTCCTGATCCACCCAC 27587	CA	CA	CA
	CT		AGG GG GATCA AGGTCAGG			
			TCC CC CTAGT TCCAGTCC			
			AC AC CC			
GAM1925	OR51E2	3'	CCTGACCTTGTGATCCACCCGC 48508	A	CA	
	CT		AGGC GG GATCACAAGGTCAGG			
			TCCG CC CTAGTGTTCAGTCC			
			C AC			
GAM1925	OSBPL2	3'	CCCGACCTCAAGTAGTCTGCCT 58482	C	A__	A
	GCCT		AGGCAGGCAGAT AC AGGTC GG			
			TCCGTCCGTCTG TG TCCAG CC			
			A AAC C			
GAM1925	PASK	5'	CCTCAGGTGATCTGCCCCGCCT 31407	A	A__	
			AGGC GGCAGATCAC AGG			

			TCCG CCGTCTAGTG	TCC		
			C	GAC		
GAM1925	PIP3-E	3'	CCTGACCTCAGGTGATCTGCCT	67350	A__	
		GCCT	AGGCAGGCAGATCAC	AGGTCAGG		
			TCCGTCCGTCTAGTG	TCCAGTCC		
			GAC			
GAM1925	PP2447	5'	CCTGACCTCGTGATCCGCCTGC	48098	A	A
		CT	AGGCAGGC	GATCAC	AGGTCAGG	
			TCCGTCCG	CTAGTG	TCCAGTCC	
			C	C		
GAM1925	PRO0365	5'	CCTGACCTCAAGTGATCTGCCC	26980	A	A__
		GCCT	AGGC	GGCAGATCAC	AGGTCAGG	
			TCCG	CCGTCTAGTG	TCCAGTCC	
			C	AAC		
GAM1925	PRO0365	5'	CCTGACCTCATGATCCACCTGC	26981	CA	CA
		CT	AGGCAGG	GATCA	AGGTCAGG	
			TCCGTCC	CTAGT	TCCAGTCC	
			AC	AC		
GAM1925	PSTPIP2	3'	CCTGACCTCAGGTGATCCACCT	44652	CA	A__
			AGG	GATCAC	AGGTCAGG	
			TCC	CTAGTG	TCCAGTCC	
			AC	GAC		
GAM1925	QKI	3'	CTGACCATGCCTGCCTGCT	66045	ATCA	A
			GGCAGGCAG	CA	GGTCAG	
			TCGTCCGTC	GT	CCAGTC	
			C__	A		
GAM1925	RAB21	3'	CCTGACCTTGTGATCCGCCCGC	31087	A	A
		CT	AGGC	GGC	GATCACAAGGTCAGG	
			TCCG	CCG	CTAGTGTTCCAGTCC	
			C	C		
GAM1925	RAB33B	3'	CTTGACCTCATGATCCACCCGC	49325	A	CA
		CT	AGGC	GG	GATCA	AGGTCAGG
			TCCG	CC	CTAGT	TCCAGTTC
			C	AC	AC	
GAM1925	RAP140	3'	CCTGACCTCATGATCTGCCTGC	31513	CA	
		CT	AGGCAGGCAGATCA	AGGTCAGG		
			TCCGTCCGTCTAGT	TCCAGTCC		
			AC			
GAM1925	RASSF2	3'	CCTGACCTCGTGATCCACCCGC	29094	A	CA
		CT	AGGC	GG	GATCAC	AGGTCAGG

TCCG CC CTAGTG TCCAGTCC
 C AC C
 GAM1925 RNF8 3' CCTGACCTTAAGTGATCCACCT 15564 CA ____
 AGG GATCAC AAGGTCAGG
 ||| ||||| |||||
 TCC CTAGTG TTCCAGTCC
 AC AA
 GAM1925 Rpo1-2 3' CCTGACCTCAAGTGATCCACC 39218 CA A__
 GG GATCAC AGGTCAGG
 || ||||| |||||
 CC CTAGTG TCCAGTCC
 AC AAC
 GAM1925 Rpo1-2 3' CCTGACCTCAAGTGATCCACC 39219 CA A__
 GG GATCAC AGGTCAGG
 || ||||| |||||
 CC CTAGTG TCCAGTCC
 AC AAC
 GAM1925 SCAMP-4 3' CCTGACCTCAAGTGATCCACC 55344 CA A__
 GG GATCAC AGGTCAGG
 || ||||| |||||
 CC CTAGTG TCCAGTCC
 AC AAC
 GAM1925 SCYA22 3' CCTGACCTCAAGTGATCCACCT 92588 CA A__
 AGG GATCAC AGGTCAGG
 ||| ||||| |||||
 TCC CTAGTG TCCAGTCC
 AC AAC
 GAM1925 SERF1B 3' CCTGACCTCGTGATTACCCGC 43694 A CA A
 CT AGGC GG GATCAC AGGTCAGG
 |||| || ||||| |||||
 TCCG CC TTAGTG TCCAGTCC
 C AC C
 GAM1925 SFXN2 3' CCTGACCTCAGGTGATCCGCC 74374 A A__
 GGC GATCAC AGGTCAGG
 ||| ||||| |||||
 CCG CTAGTG TCCAGTCC
 C GAC
 GAM1925 SIRPB1 3' CCAGGTCATCTGCCTGCC 21360 C AA
 GGCAGGCAGAT AC GG
 ||||| || ||
 CCGTCCGTCTA TG CC
 C GA
 GAM1925 SLC19A3 3' CCTGACTTCAGGTGATCTGTCT 48242 AA__
 GCCT AGGCAGGCAGATCAC GGTCAGG
 ||||| |||||
 TCCGTCTGTCTAGTG TCAGTCC
 GACT
 GAM1925 SLC6A14 3' CCCGACCTCAAGTGATCTGTCT 24306 C A__ A
 ACCT AGG AGGCAGATCAC AGGTC GG
 ||| ||||| ||||| ||||| ||

TCC TCTGTCTAGTG TCCAG CC
 A AAC C
 GAM1925 SS-56 3' CCTGACCTCATGATCCGCCCTC 60348 CA A CA
 CT AGG GGC GATCA AGGTCAGG
 ||| ||| ||||| |||||
 TCC CCG CTAGT TCCAGTCC
 TC C AC
 GAM1925 SSH2 3' CCCAGTGCCTGCCTGCCT 62890 AT AA
 AGGCAGGCAG CAC GG
 ||||| ||| ||
 TCCGTCCGTC GTG CC
 C_ AC
 GAM1925 STAF65(gamma) 3' CCTGACCTCAAGTGATCTGCCC 30066 A A__
 GCCT AGGC GGCAGATCAC AGGTCAGG
 ||| ||||| |||||
 TCCG CCGTCTAGTG TCCAGTCC
 C AAC
 GAM1925 STRBP 5' CCTGAACGCAAGTGATCCGCCT 37817 A AAGG__
 GCCT AGGCAGGC GATCAC TCAGG
 ||||| ||||| |||||
 TCCGTCCG CTAGTG AGTCC
 C AACGCA
 GAM1925 TCL6 3' CCTGACCTCGTGATCCGCCTAC 40469 C A A
 CT AGG AGGC GATCAC AGGTCAGG
 ||| ||| ||||| |||||
 TCC TCCG CTAGTG TCCAGTCC
 A C C
 GAM1925 TGIF2 3' CCTGACCTCGTGAGCCACC 41747 CA AGA A
 GG GGC TCAC AGGTCAGG
 || ||| ||| |||||
 CC CCG AGTG TCCAGTCC
 A_ _ C
 GAM1925 THEA 3' CCTGACTTCAAGTGATCTGCCC 66885 A A__
 GCCT AGGC GGCAGATCAC AGGTCAGG
 ||| ||||| |||||
 TCCG CCGTCTAGTG TTCAGTCC
 C AAC
 GAM1925 TU12B1-TY 3' CCTGACCTCAGATAATCTGCC 33843 CAG ACA
 GGCAGG ATC AGGTCAGG
 ||||| ||| |||||
 CCGTCT TAG TCCAGTCC
 AA_ AC_
 GAM1925 TU12B1-TY 3' CCTGACCTTGGGTAATCCACCT 33844 CA CAG A
 AGG GG ATC CAAGGTCAGG
 ||| || ||| |||||
 TCC CC TGG GTTCCAGTCC
 A_ TAA _
 GAM1925 TUCAN 3' CCTGACCTCATGATCCACCCGC 30971 A CA CA
 CT AGGC GG GATCA AGGTCAGG
 |||| || ||||| |||||

		TCCG CC CTAGT TCCAGTCC		
		C AC AC		
GAM1925 TUSP	3'	CCTGACCTCAGGTGATCCGCC 40022	A	A__
		GGC GATCAC AGGTCAGG		
		CCG CTAGTG TCCAGTCC		
		C GAC		
GAM1925 UBF-fl	3'	CCTCAAGTGATCTGCCTGCCT 52621		A__
		AGGCAGGCAGATCAC AGG		
		TCCGTCCGTCTAGTG TCC		
		AAC		
GAM1925 UBF-fl	3'	CCTGACCTCAAGTGATCCACC 52623	CA	A__
		GG GATCAC AGGTCAGG		
		CC CTAGTG TCCAGTCC		
		AC AAC		
GAM1925 VDU1	3'	CCTGACCTCAGGTGATCCACC 31122	CA	A__
		GG GATCAC AGGTCAGG		
		CC CTAGTG TCCAGTCC		
		AC GAC		
GAM1925 WBSCR23	3'	CCTGACCTCAGGTGATCCACCT 47430	CA	A__
		AGG GATCAC AGGTCAGG		
		TCC CTAGTG TCCAGTCC		
		AC GAC		
GAM1925 LOC112687	3'	CCTGACCTCATGTAATCCACC 73231	CA C	__
		GG GATACA AGGTCAGG		
		CC CTA TGT TCCAGTCC		
		AC A AC		
GAM1925 LOC113523	5'	CCTGACCTCGTGATTCACCCAC 73418	CA CA	A
CT		AGG GG GATCAC AGGTCAGG		
		TCC CC TTAGTG TCCAGTCC		
		AC AC C		
GAM1925 LOC115648	3'	CCTGACCTCAGGTGATCCACC 60018	CA	A__
		GG GATCAC AGGTCAGG		
		CC CTAGTG TCCAGTCC		
		AC GAC		
GAM1925 LOC120114	3'	CCTGACCTCGTAATCCACCTGC 76044	CA C A	
C		GGCAGG GAT AC AGGTCAGG		
		CCGTCC CTA TG TCCAGTCC		
		AC A C		
GAM1925 LOC120224	5'	CCTGACCTCAGGTGATCTGCCT 57886		A__
GCCT		AGGCAGGCAGATCAC AGGTCAGG		

TCCGTCCGTCTAGTG TCCAGTCC
 GAC
 GAM1925 LOC122773 3' CCTGACCTTTTCGACACTTACC 74635 C CA__ TCAC
 T AGG AGG GA AAGGTCAGG
 ||| ||| || |||||
 TCC TTC CT TTCCAGTCC
 A ACAG T__
 GAM1925 LOC126661 3' CCTCAAGTGATCTGCCCCGCCT 75054 A A__
 AGGC GGCAGATCAC AGG
 |||| ||||| |||
 TCCG CCGTCTAGTG TCC
 C AAC
 GAM1925 LOC126669 3' CCTGACCTCAAATGATCCACC 75931 CA CA__
 GG GATCA AGGTCAGG
 || |||| |||||
 CC CTAGT TCCAGTCC
 AC AAAC
 GAM1925 LOC126917 3' CCTGGGTCCGGCCTGCCTGCCT 75087 AT ACAA __
 AGGCAGGCAG C GG TCAGG
 ||||| || || |||||
 TCCGTCCGTC G CC GGTCC
 CG__ TG
 GAM1925 LOC126917 3' CTGCCTGCCTGCCTGCCT 75091 ATCACA T
 AGGCAGGCAG AGG CAG
 ||||| ||| |||
 TCCGTCCGTC TCC GTC
 CG__ _
 GAM1925 LOC126917 3' CTGCCTGCCTGCCTGCCT 75092 ATCACA T
 AGGCAGGCAG AGG CAG
 ||||| ||| |||
 TCCGTCCGTC TCC GTC
 CG__ _
 GAM1925 LOC128077 3' CCTGACCTCGTGATCCACCTGC 75213 CA A
 CT AGGCAGG GATCAC AGGTCAGG
 ||||| ||||| |||||
 TCCGTCC CTAGTG TCCAGTCC
 AC C
 GAM1925 LOC130813 3' CCCAACTTCAGGTGATCCGCCT 76268 A AA__ CA
 GCCT AGGCAGGC GATCAC GGT GG
 ||||| ||||| ||| ||
 TCCGTCCG CTAGTG TCA CC
 C GACT AC
 GAM1925 LOC132625 3' CCTGACCTCCAGTGATCTGCCC 76439 CA A__
 ACCT AGG GGCAGATCAC AGGTCAGG
 || ||||| |||||
 TCC CCGTCTAGTG TCCAGTCC
 AC ACC
 GAM1925 LOC133686 3' CCTGACCTTGTGATCTGCCTGC 75616
 CT AGGCAGGCAGATCACAAGGTCAGG
 ||||| ||||| ||||| |||||

TCCGTCCGTCTAGTGTTCCAGTCC

GAM1925 LOC135818 3' CCTGACCTCAGGTGATCTGCCC 75746 CA A__
ACCT AGG GGCAGATCAC AGGTCAGG

||| ||||| |||||
TCC CCGTCTAGTG TCCAGTCC
AC GAC

GAM1925 LOC142820 5' CCTGAGCTCAAGTGGTCTGCCT 76912 A__ G
GCCT AGGCAGGCAGATCAC AG TCAGG

||||||| || |||||
TCCGTCCGTCTGGTG TC AGTCC
AAC G

GAM1925 LOC144871 3' CCTGACCTTGTGATCTGCCCCG 84124 A
CT AGGC GGCAGATCACAAGGTCAGG

||| |||||||||
TCCG CCGTCTAGTGTTCCAGTCC
C

GAM1925 LOC144871 3' CTTGTGATCTGCCCCGCT 84125 A
AGGC GGCAGATCACAAG

||| |||||||
TCCG CCGTCTAGTGTTTC
C

GAM1925 LOC145009 3' CCTGACCTCGTGATCCACCCG 60972 A CA A
CT AGGC GG GATCAC AGGTCAGG

||| || ||||| |||||
TCCG CC CTAGTG TCCAGTCC
C AC C

GAM1925 LOC146050 3' CCCGACCTCAGGTGATCTGCCT 78112 A__ A
GCCT AGGCAGGCAGATCAC AGGTC GG

||||||| |||||
TCCGTCCGTCTAGTG TCCAG CC
GAC C

GAM1925 LOC146050 3' TTGACCTCATGATCTGCCTGCC 78129 CA
T AGGCAGGCAGATCA AGGTCAG

||||||| |||||
TCCGTCCGTCTAGT TCCAGTT
AC

GAM1925 LOC146138 3' CCTGACCTGCTTTCCTGCC 84590 C TCACA
GGCAGG AGA AGGTCAGG

||||| || |||||
CCGTCC TTT TCCAGTCC
_ CG__

GAM1925 LOC146229 3' CCTGACCTCAAGTGATCCACC 78275 CA A__
GG GATCAC AGGTCAGG

|| ||||| |||||
CC CTAGTG TCCAGTCC
AC AAC

GAM1925 LOC146229 3' CCTGACCTCAGGTGATCCACC 78276 CA A__
GG GATCAC AGGTCAGG

|| ||||| |||||

		CC CTAGTG TCCAGTCC		
		AC GAC		
GAM1925	LOC146346 5'	CCTGACCTCATGATGTGCCAC 78393	CA G CA	
	TT	AGG GGCA ATCA AGGTCAGG		
		TTC CCGT TAGT TCCAGTCC		
		AC G AC		
GAM1925	LOC146429 5'	CCTGACCTCATGATCCGCCTGC 84662	A CA	
	CT	AGGCAGGC GATCA AGGTCAGG		
		TCCGTCCG CTAGT TCCAGTCC		
		C AC		
GAM1925	LOC146429 5'	CTCATGATCCGCCTGCCT 84664	A CA	
		AGGCAGGC GATCA AG		
		TCCGTCCG CTAGT TC		
		C AC		
GAM1925	LOC146603 5'	CCTGACCTCATGATCCGCCTGC 78594	A CA	
	CT	AGGCAGGC GATCA AGGTCAGG		
		TCCGTCCG CTAGT TCCAGTCC		
		C AC		
GAM1925	LOC146784 5'	CCTGACCTCATGATCTGCCTGC 78710	CA	
	CT	AGGCAGGCAGATCA AGGTCAGG		
		TCCGTCCGTCTAGT TCCAGTCC		
		AC		
GAM1925	LOC146901 3'	CCTGACCTCAGGTGATCCACC 84898	CA A__	
		GG GATCAC AGGTCAGG		
		CC CTAGTG TCCAGTCC		
		AC GAC		
GAM1925	LOC146909 3'	CCTGACCTCAGGTGATCCGCCT 78766	A A__	
	GCCT	AGGCAGGC GATCAC AGGTCAGG		
		TCCGTCCG CTAGTG TCCAGTCC		
		C GAC		
GAM1925	LOC146909 3'	CTGACCTCATGATCCACCCGCC 78770	A CA CA	
	T	AGGC GG GATCA AGGTCAG		
		TCCG CC CTAGT TCCAGTC		
		C AC AC		
GAM1925	LOC146952 5'	CCTGACCTCAGATGATCTACC 84926	C CA__	
		GG AGATCA AGGTCAGG		
		CC TCTAGT TCCAGTCC		
		A AGAC		
GAM1925	LOC147063 5'	CCTAAGACCTGACCTGCCT 85017	_ A ACA	
		AGGCAGG CAG TC AGG		

TCCGTCC GTC AG TCC
 A C AA_
 GAM1925 LOC147080 5' CCTGACCTTGTGATCCGCCCGC 85032 A A
 CT AGGC GGC GATCACAAGGTCAGG
 |||| ||| ||||||||||||
 TCCG CCG CTAGTGTTCCAGTCC
 C C
 GAM1925 LOC147276 3' CCTGACCTCAAGTGATCCACCT 78956 CA A_
 AGG GATCAC AGGTCAGG
 ||| ||||| |||||||
 TCC CTAGTG TCCAGTCC
 AC AAC
 GAM1925 LOC147429 3' CCTGACCTTGTGATCCGCCCGC 78995 A A
 C GGC GGC GATCACAAGGTCAGG
 ||| ||| ||||||||||||
 CCG CCG CTAGTGTTCCAGTCC
 C C
 GAM1925 LOC147694 3' CCTGACCTTGTGATCTGCCTGC 79095
 CT AGGCAGGCAGATCACAAGGTCAGG
 ||||||||||||||||
 TCCGTCCGTCTAGTGTTCCAGTCC

 GAM1925 LOC147694 3' CTTGTGATCTGCCTGCCT 79096
 AGGCAGGCAGATCACAAG
 ||||||||||||
 TCCGTCCGTCTAGTGTTCC

 GAM1925 LOC147817 3' CCTCAAGTGATCTGCTCACCT 79173 CA A_
 AGG GGCAGATCAC AGG
 ||| ||||||| |||
 TCC TCGTCTAGTG TCC
 AC AAC
 GAM1925 LOC147817 3' CCTGACCTTATAATCCGCCAC 79174 CA A CAC
 CT AGG GGC GAT AAGGTCAGG
 ||| ||| ||| |||||||
 TCC CCG CTA TTCCAGTCC
 AC C ATA
 GAM1925 LOC147990 3' CCTGACCTTGTGATCTGCCTGT 85219
 CT AGGCAGGCAGATCACAAGGTCAGG
 ||||||||||||||||
 TCTGTCCGTCTAGTGTTCCAGTCC

 GAM1925 LOC148137 3' CCTGACCTCGTGATCCACCCGC 59096 A CA A
 CT AGGC GG GATCAC AGGTCAGG
 |||| || ||||| |||||||
 TCCG CC CTAGTG TCCAGTCC
 C AC C
 GAM1925 LOC148147 3' CCTGACCTTCTGATCTGCCTGC 79394 C
 CT AGGCAGGCAGATCA AAGGTCAGG
 ||||||||||| |||||||

TCCGTCCGTCTAGT TTCCAGTCC
 C
 GAM1925 LOC148195 3' CCTGACCTCAGGTGAGCCGCCT 85279 AGA A__
 GCCT AGGCAGGC TCAC AGGTCAGG
 ||||| ||| |||||
 TCCGTCCG AGTG TCCAGTCC
 CCG GAC
 GAM1925 LOC148918 5' CCTGACCTCAGGTGATCCACC 79823 CA A__
 GG GATCAC AGGTCAGG
 || ||||| |||||
 CC CTAGTG TCCAGTCC
 AC GAC
 GAM1925 LOC149171 5' CCTCAGGTGATCTGCCCCACCT 79966 CA A__
 AGG GGCAGATCAC AGG
 ||| ||||| |||
 TCC CCGTCTAGTG TCC
 AC GAC
 GAM1925 LOC149692 3' CCTGACCTCAGGTGATCCACC 85731 CA A__
 GG GATCAC AGGTCAGG
 || ||||| |||||
 CC CTAGTG TCCAGTCC
 AC GAC
 GAM1925 LOC149692 3' CCTGACCTCAGGTGATCTGCCT 85732 A__
 GCCT AGGCAGGCAGATCAC AGGTCAGG
 ||||| |||||
 TCCGTCCGTCTAGTG TCCAGTCC
 GAC
 GAM1925 LOC149711 3' CCTGACCTCAGGTGATCCACC 85849 CA A__
 GG GATCAC AGGTCAGG
 || ||||| |||||
 CC CTAGTG TCCAGTCC
 AC GAC
 GAM1925 LOC149821 5' CCTGACCTCGTGATGCACCTGC 85930 CAG A
 CT AGGCAGG ATCAC AGGTCAGG
 ||||| ||||| |||||
 TCCGTCC TAGTG TCCAGTCC
 ACG C
 GAM1925 LOC150282 5' CCTGACCTCAGGTGATCCACCT 80541 CA A__
 AGG GATCAC AGGTCAGG
 ||| ||||| |||||
 TCC CTAGTG TCCAGTCC
 AC GAC
 GAM1925 LOC150397 3' CCTGACCTCAGGTGATCCGCCT 80660 A A__
 GCCT AGGCAGGC GATCAC AGGTCAGG
 ||||| ||||| |||||
 TCCGTCCG CTAGTG TCCAGTCC
 C GAC
 GAM1925 LOC150630 5' CCTGACCTCGTGATCCGCCCGC 86297 A A A
 CT AGGC GGC GATCAC AGGTCAGG
 ||| ||| ||||| |||||

		TCCG CCG CTAGTG TCCAGTCC		
		C C C		
GAM1925	LOC150960 3'	CCTGACCTCAGGTGATCCACC 80874	CA	A__
		GG GATCAC AGGTCAGG		
		CC CTAGTG TCCAGTCC		
		AC GAC		
GAM1925	LOC151057 3'	CCTGACCTTGTGATCTGCCCAC 86386	CA	
	CT	AGG GGCAGATCACAAGGTCAGG		
		TCC CCGTCTAGTGTTCCAGTCC		
		AC		
GAM1925	LOC151201 3'	CCTCGTGATTTGCCCGCCT 86472	A	A
		AGGC GGCAGATCAC AGG		
		TCCG CCGTTTAGTG TCC		
		C C		
GAM1925	LOC151475 5'	CCTGACCTTAGGTGATCTGCCC 86592	CA	__
	ACTT	AGG GGCAGATCAC AAGGTCAGG		
		TTC CCGTCTAGTG TTCCAGTCC		
		AC GA		
GAM1925	LOC151979 5'	CCTGACCTCATGATCTGCCCAC 81247	CA	CA
	CT	AGG GGCAGATCA AGGTCAGG		
		TCC CCGTCTAGT TCCAGTCC		
		AC AC		
GAM1925	LOC152137 3'	CCTGACCTCAAGTGATCCACCT 81313	CA	A__
		AGG GATCAC AGGTCAGG		
		TCC CTAGTG TCCAGTCC		
		AC AAC		
GAM1925	LOC152343 3'	CTGACCTTGTGATCCACCCACC 81425	CA	CA
	T	AGG GG GATCACAAGGTCAG		
		TCC CC CTAGTGTTCCAGTC		
		AC AC		
GAM1925	LOC152445 3'	CCTGACCTCGTGATCCACCTGC 86944	CA	A
	CT	AGGCAGG GATCAC AGGTCAGG		
		TCCGTCC CTAGTG TCCAGTCC		
		AC C		
GAM1925	LOC152719 5'	CCTGACCTCGTGATCCGCCCGC 87021	A	A A
	CT	AGGC GGC GATCAC AGGTCAGG		
		TCCG CCG CTAGTG TCCAGTCC		
		C C C		
GAM1925	LOC152719 5'	CCTGACCTCGTGATCCGCCCGC 87022	A	A A
	CT	AGGC GGC GATCAC AGGTCAGG		

TCCG CCG CTAGTG TCCAGTCC
 C C C
 GAM1925 LOC153077 3' CCTGACCTCAGGTGATCCACCT 87120 CA A__
 AGG GATCAC AGGTCAGG
 ||| ||||| |||||
 TCC CTAGTG TCCAGTCC
 AC GAC
 GAM1925 LOC153811 3' CCTGACCTCAAATGATCCACCT 81831 CA CA__
 AGG GATCA AGGTCAGG
 ||| ||||| |||||
 TCC CTAGT TCCAGTCC
 AC AAAC
 GAM1925 LOC153883 5' CCTGACCTCAAGTGATCCACC 81893 CA A__
 GG GATCAC AGGTCAGG
 || ||||| |||||
 CC CTAGTG TCCAGTCC
 AC AAC
 GAM1925 LOC154282 5' CTTGACCTTGTGATCCACCTGC 87403 CA
 CT AGGCAGG GATCACAAGGTCAGG
 ||||| |||||
 TCCGTCC CTAGTGTTCCAGTTC
 AC
 GAM1925 LOC154877 3' CCTGACCTTACGTGATCCACC 87542 CA __
 GG GATCAC AAGGTCAGG
 || ||||| |||||
 CC CTAGTG TTCCAGTCC
 AC CA
 GAM1925 LOC154877 5' CCTGAGCTCAGGTGATCTGCCC 87544 CA A__ G
 ACCT AGG GGCAGATCAC AG TCAGG
 ||| ||||| |||||
 TCC CCGTCTAGTG TC AGTCC
 AC GAC G
 GAM1925 LOC157247 5' CCTGACCTCAGGTGATCCACC 82293 CA A__
 GG GATCAC AGGTCAGG
 || ||||| |||||
 CC CTAGTG TCCAGTCC
 AC GAC
 GAM1925 LOC157621 3' CTGAGTGGATCTGCCTGCC 87789 A AGG
 GGCAGGCAGATC CA TCAG
 ||||| || |||||
 CCGTCCGTCTAG GT AGTC
 _ G__
 GAM1925 LOC157858 5' CCTGACCTCTGGTGATCTGCCC 87886 CA A__
 ACTT AGG GGCAGATCAC AGGTCAGG
 ||| ||||| |||||
 TTC CCGTCTAGTG TCCAGTCC
 AC GTC
 GAM1925 LOC158056 5' CTGGGACTGTGGTCTGCCCACC 82590 CA A G_
 GG GGCAGATCACA G TCAG
 || ||||| |||||

CC CCGTCTGGTGT C GGTC
 AC _AG
 GAM1925 LOC158310 5' CCTGACCTTAAGTGATCCACC 88079 CA _
 GG GATCAC AAGGTCAGG
 || ||||| |||||
 CC CTAGTG TTCCAGTCC
 AC AA
 GAM1925 LOC158476 3' CCTGATCTGAAGTGATCTGCCT 88192 A_
 GCCT AGGCAGGCAGATCAC AGGTCAGG
 ||||| |||||
 TCCGTCCGTCTAGTG TCTAGTCC
 AAG
 GAM1925 LOC158549 5' CCTGACCTGGTGATCCACCTGC 88219 CA A
 CT AGGCAGG GATCAC AGGTCAGG
 ||||| ||||| |||||
 TCCGTCC CTAGTG TCCAGTCC
 AC G
 GAM1925 LOC158668 3' CCTGACTTCATGATCCACCCAC 69897 CA CA CA
 CT AGG GG GATCA AGGTCAGG
 ||| || ||||| |||||
 TCC CC CTAGT TTCAGTCC
 AC AC AC
 GAM1925 LOC158865 5' CCTGACCTCAAGTGATGTGCCT 88306 G A_
 GCCT AGGCAGGCA ATCAC AGGTCAGG
 ||||| ||||| |||||
 TCCGTCCGT TAGTG TCCAGTCC
 G AAC
 GAM1925 LOC169611 3' CCTGACCTCAGGTGATCCACCT 83644 CA A_
 AGG GATCAC AGGTCAGG
 ||| ||||| |||||
 TCC CTAGTG TCCAGTCC
 AC GAC
 GAM1925 LOC169611 3' CCTGACCTTAGGTGATCCGCC 83645 A _
 GGC GATCAC AAGGTCAGG
 ||| ||||| |||||
 CCG CTAGTG TTCCAGTCC
 C GA
 GAM1925 LOC170082 5' CCTGACCTCGTGATCTGCCTGC 83442 A
 CT AGGCAGGCAGATCAC AGGTCAGG
 ||||| ||||| |||||
 TCCGTCCGTCTAGTG TCCAGTCC
 C
 GAM1925 LOC196264 3' CCTGACCTCGTGATCCACCTGC 88983 CA A
 CT AGGCAGG GATCAC AGGTCAGG
 ||||| ||||| |||||
 TCCGTCC CTAGTG TCCAGTCC
 AC C
 GAM1925 LOC196411 3' CCTGACCTCGTGATTGGCCAC 89044 CA A A
 CT AGG GGC GATCAC AGGTCAGG
 ||| ||| ||||| |||||

TCC CCG TTAGTG TCCAGTCC
 AC G C
 GAM1925 LOC197358 3' CCTGACCTCAAGTGATCCACC 89428 CA A__
 GG GATCAC AGGTCAGG
 || ||||| |||||
 CC CTAGTG TCCAGTCC
 AC AAC
 GAM1925 LOC199725 5' CCTGACCTCGTGATCGACCTTC 91415 C CA A
 CT AGG AGG GATCAC AGGTCAGG
 ||| ||| ||||| |||||
 TCC TCC CTAGTG TCCAGTCC
 T AG C
 GAM1925 LOC199775 5' CCCGACCTCTGGTGATCTGCCC 89723 A A__ A
 GCCT AGGC GGCAGATCAC AGGTC GG
 |||| ||||| ||||| ||
 TCCG CCGTCTAGTG TCCAG CC
 C GTC C
 GAM1925 LOC199786 3' CCTGACCTCATGATCCGCCAC 89748 CA A CA
 CT AGG GGC GATCA AGGTCAGG
 ||| ||| ||||| |||||
 TCC CCG CTAGT TCCAGTCC
 AC C AC
 GAM1925 LOC199786 3' CCTTAAGTGATCTGCCCCCT 89749 CA _
 AGG GGCAGATCAC AAGG
 ||| ||||| ||||| |||||
 TCC CCGTCTAGTG TTCC
 CC AA
 GAM1925 LOC200014 3' CCTGACCTCATGATCCACCCAC 89928 CA CA CA
 CT AGG GG GATCA AGGTCAGG
 ||| || ||||| |||||
 TCC CC CTAGT TCCAGTCC
 AC AC AC
 GAM1925 LOC200107 3' TCGGGTGATCTGCCTGCCT 89991 AA
 AGGCAGGCAGATCAC GG
 ||||| ||||| ||||| ||
 TCCGTCCGTCTAGTG CT
 GG
 GAM1925 LOC200310 3' CCTGACCTCGTGATCTACCCGC 66324 A C A
 CT AGGC GG AGATCAC AGGTCAGG
 |||| || ||||| |||||
 TCCG CC TCTAGTG TCCAGTCC
 C A C
 GAM1925 LOC200314 3' CCTGACCTCAGGTGATCCACC 91598 CA A__
 GG GATCAC AGGTCAGG
 || ||||| |||||
 CC CTAGTG TCCAGTCC
 AC GAC
 GAM1925 LOC200316 5' CCTGACCTCGTGATCCGCCCGC 90177 A A A
 CT AGGC GGC GATCAC AGGTCAGG
 |||| ||| ||||| |||||

		TCCG CCG CTAGTG TCCAGTCC		
		C C C		
GAM1925	LOC200845 5'	CCTGACCTGGTGATCCTCCTGC 90314	CA	A
	CT	AGGCAGG GATCAC AGGTCAGG		
		TCCGTCC CTAGTG TCCAGTCC		
		TC G		
GAM1925	LOC201294 3'	CTTGACCTCCTGATCCACCCAC 89582	CA CA	CA
	CT	AGG GG GATCA AGGTCAGG		
		TCC CC CTAGT TCCAGTTC		
		AC AC CC		
GAM1925	LOC201626 3'	CCTGACCTCAGGTGATCCACC 90430	CA	A__
		GG GATCAC AGGTCAGG		
		CC CTAGTG TCCAGTCC		
		AC GAC		
GAM1925	LOC202868 5'	CTGCCTGCCTGCCTGCCT 92002	ATCACA	T
		AGGCAGGCAG AGG CAG		
		TCCGTCCGTC TCC GTC		
		CG__ _		
GAM1925	LOC202934 3'	CCTGACCTCGTGATCTACCGGC 92036	A C	A
	CT	AGGC GG AGATCAC AGGTCAGG		
		TCCG CC TCTAGTG TCCAGTCC		
		G A C		
GAM1925	LOC203197 3'	CCTGACCTCAGGTGATCCACC 90809	CA	A__
		GG GATCAC AGGTCAGG		
		CC CTAGTG TCCAGTCC		
		AC GAC		
GAM1925	LOC203339 3'	CCTGCCCTTGTGATCCACCCAC 92210	CA CA	T
	CT	AGG GG GATCACAAGG CAGG		
		TCC CC CTAGTGTTCC GTCC		
		AC AC C		
GAM1925	LOC203350 3'	CCTGACCTTGTGATCCACCTGC 92233	CA	
	CT	AGGCAGG GATCACAAGGTCAGG		
		TCCGTCC CTAGTGTTCCAGTCC		
		AC		
GAM1925	LOC203350 3'	CTTGTGATCCACCTGCCT 92239	CA	
		AGGCAGG GATCACAAG		
		TCCGTCC CTAGTGTTCC		
		AC		
GAM1925	LOC203369 3'	CCTGACCTCGTGATCCGCCCGC 90883	A A	A
	CT	AGGC GGC GATCAC AGGTCAGG		

		TCCG CCG CTAGTG TCCAGTCC			
		C C C			
GAM1925	LOC203369 3'	CTCGTGATCCGCCGCCT	90886	A A A	
		AGGC GGC GATCAC AG			
		TCCG CCG CTAGTG TC			
		C C C			
GAM1925	LOC205251 5'	CCTGACCTCAAGTGATCTGCCT	92356	C	A__
	ACCT	AGG AGGCAGATCAC	AGGTCAGG		
		TCC TCCGTCTAGTG	TCCAGTCC		
		A AAC			
GAM1925	LOC219445 5'	CTTGACCTTGTGATCTGCCTGC	93203		
	CT	AGGCAGGCAGATCACAAGGTCAGG			
		TCCGTCCGTCTAGTGTTCCAGTTC			
GAM1925	LOC219673 5'	CCTGACCTCAAGTAATCCACCT	94622	CA C A__	
		AGG GAT AC	AGGTCAGG		
		TCC CTA TG	TCCAGTCC		
		AC A AAC			
GAM1925	LOC219731 5'	CCTGAGCTCAAGTGATCCGCCT	94700	A	A__ G
	GCCT	AGGCAGGC GATCAC	AG TCAGG		
		TCCGTCCG CTAGTG	TC AGTCC		
		C AAC G			
GAM1925	LOC219894 3'	CCTGACCTCATGATCTGCCTGC	94904		CA
	CT	AGGCAGGCAGATCA	AGGTCAGG		
		TCCGTCCGTCTAGT	TCCAGTCC		
		AC			
GAM1925	LOC220074 3'	CCTGACCTCAGGTGATCTGCCC	59971	CA	A__
	ACCT	AGG GGCAGATCAC	AGGTCAGG		
		TCC CCGTCTAGTG	TCCAGTCC		
		AC GAC			
GAM1925	LOC220074 3'	CCTGACCTTGTGATCCACCAC	59972	CA CA	
	CT	AGG GG GATCACAAGGTCAGG			
		TCC CC CTAGTGTTCCAGTCC			
		AC AC			
GAM1925	LOC221271 3'	CCTGATCTCAAGTGATCTGCCC	93508	CA	A__
	ACCT	AGG GGCAGATCAC	AGGTCAGG		
		TCC CCGTCTAGTG	TCTAGTCC		
		AC AAC			
GAM1925	LOC221964 3'	CCTGACCTCAGGTGATCCACC	95603	CA	A__
		GG GATCAC	AGGTCAGG		

		CC CTAGTG TCCAGTCC		
		AC GAC		
GAM1925	LOC222031 3'	CCTGACCTCAGGTGATCCACC 95676	CA	A__
		GG GATCAC AGGTCAGG		
		CC CTAGTG TCCAGTCC		
		AC GAC		
GAM1925	LOC222057 3'	CCAGGCCACGAATCTGCCTGCC 94349		CACAA A
	T	AGGCAGGCAGAT GGTC GG		
		TCCGTCCGTCTA CCGG CC		
		AGCA_ A		
GAM1925	LOC222068 3'	CCTGACCTCAGTTGATCCACCT 94273	CA	CA__
		AGG GATCA AGGTCAGG		
		TCC CTAGT TCCAGTCC		
		AC TGAC		
GAM1925	LOC245771 5'	CCTGACCTCAAGTGATCCACCT 94472	CA	A__
		AGG GATCAC AGGTCAGG		
		TCC CTAGTG TCCAGTCC		
		AC AAC		
GAM1925	LOC253842 5'	CCTGACCTCGTGATCCGCCTGC 99236	A	A
	CT	AGGCAGGC GATCAC AGGTCAGG		
		TCCGTCCG CTAGTG TCCAGTCC		
		C C		
GAM1925	LOC253981 3'	CCTGACCTCGTGATCCACCCGC 97534	A CA	A
	CT	AGGC GG GATCAC AGGTCAGG		
		TCCG CC CTAGTG TCCAGTCC		
		C AC C		
GAM1925	LOC254018 5'	CCTGACCTCGTGATCCGCCCGC 98738	A A	A
	CT	AGGC GGC GATCAC AGGTCAGG		
		TCCG CCG CTAGTG TCCAGTCC		
		C C C		
GAM1925	LOC254249 5'	CCTGACCTCGTGATCTGCACC 97181	CAG	A
		GG GCAGATCAC AGGTCAGG		
		CC CGTCTAGTG TCCAGTCC		
		A__ C		
GAM1925	LOC254295 5'	CCTGACCTCGTGATCCGCGCGC 97890	AG A	A
	CT	AGGC GC GATCAC AGGTCAGG		
		TCCG CG CTAGTG TCCAGTCC		
		CG C C		
GAM1925	LOC254351 5'	CCTGACCTCGGGTGATCCACC 96686	CA	A__
		GG GATCAC AGGTCAGG		

	CC CTAGTG TCCAGTCC		
	AC GGC		
GAM1925 LOC254532 5'	CCTGACCTCAAGTGATCCACC 98452	CA	A__
	GG GATCAC AGGTCAGG		
	CC CTAGTG TCCAGTCC		
	AC AAC		
GAM1925 LOC254672 3'	CCTGTGATCCACCTGCCT 96292	CA	A
	AGGCAGG GATCACA GG		
	TCCGTCC CTAGTGT CC		
	AC _		
GAM1925 LOC255065 5'	CCTCAAGTAATCCACCTGGCCT 98369	_ CA	C A__
	AGGC AGG GAT AC AGG		
	TCCG TCC CTA TG TCC		
	G AC A AAC		
GAM1925 LOC255465 3'	CCTGACCTCGTGATCTACCCGC 99110	A C	A
CT	AGGC GG AGATCAC AGGTCAGG		
	TCCG CC TCTAGTG TCCAGTCC		
	C A C		
GAM1925 LOC256306 3'	CCTGACCTCAAATGATCCGCC 98513	A	CA__
	GGC GATCA AGGTCAGG		
	CCG CTAGT TCCAGTCC		
	C AAAC		
GAM1925 LOC256790 5'	CCCAGCTTAGTGTTCCACCTGC 96491	CA T A	CA
CT	AGGCAGG GA CAC AGGT GG		
	TCCGTCC CT GTG TTCG CC		
	AC T A AC		
GAM1925 LOC257127 5'	CCTGACCTCAGGTGATCCGCCT 98495	A	A__
GCCT	AGGCAGGC GATCAC AGGTCAGG		
	TCCGTCCG CTAGTG TCCAGTCC		
	C GAC		
GAM1925 LOC257465 3'	CCTGACCTTGGTGATCCACCCG 82493	A CA	_
CC	GGC GG GATCAC AAGGTCAGG		
	CCG CC CTAGTG TTCCAGTCC		
	C AC G		
GAM1925 LOC257486 3'	CTTGACCTCGTGATCCGCCCGC 69770	A A	A
CT	AGGC GGC GATCAC AGGTCAGG		
	TCCG CCG CTAGTG TCCAGTTC		
	C C C		
GAM1925 LOC51159 5'	CCTGACCTCGTGATCTGCCTGC 33029	A	
CT	AGGCAGGCAGATCAC AGGTCAGG		

			TCCGTCCGTCTAGTG TCCAGTCC			
			C			
GAM1925	LOC51200	3'	CCCAACCTCAGGTGATCTGCCC 33434 CA A__ CA			
		TCCT	AGG GGCAGATCAC AGGT GG			
			TCC CCGTCTAGTG TCCA CC			
			TC GAC AC			
GAM1925	LOC51219	5'	CCCGACCTCAGGTGATCTGCCC 33542 CA A__ A			
		ACCT	AGG GGCAGATCAC AGGTC GG			
			TCC CCGTCTAGTG TCCAG CC			
			AC GAC C			
GAM1925	LOC51696	3'	CCTGACCTTGTGATCTGCCTGC 33081			
		CT	AGGCAGGCAGATCACAAGGTCAGG			
			TCCGTCCGTCTAGTGTTCCAGTCC			
GAM1925	LOC56181	5'	CCTGACCTCGTGATCCGCCAC 97272 CA A A			
		CT	AGG GGC GATCAC AGGTCAGG			
			TCC CCG CTAGTG TCCAGTCC			
			AC C C			
GAM1925	LOC57107	3'	CCTGACCTCAGGTGATCCGCCT 40185 A A__			
		GCCT	AGGCAGGC GATCAC AGGTCAGG			
			TCCGTCCG CTAGTG TCCAGTCC			
			C GAC			
GAM1925	LOC81034	3'	CCTGACCTTGTGATCCGCCTGC 48589 A			
		CT	AGGCAGGC GATCACAAGGTCAGG			
			TCCGTCCG CTAGTGTTCCAGTCC			
			C			
GAM1925	LOC81034	3'	CTTGTGATCCGCCTGCCT 48591 A			
			AGGCAGGC GATCACAAG			
			TCCGTCCG CTAGTGTTCC			
			C			
GAM1925	LOC89932	3'	CCTCAGATGATCTGCCCCGCCT 61454 A CA__			
			AGGC GGCAGATCA AGG			
			TCCG CCGTCTAGT TCC			
			C AGAC			
GAM1925	LOC90288	3'	CCTGACTTCATGATCCGCCCTC 62783 CA A CA			
		CT	AGG GGC GATCA AGGTCAGG			
			TCC CCG CTAGT TTCAGTCC			
			TC C AC			
GAM1925	LOC90459	3'	CCTGACCTCAAGTGATTGCCC 63553 CA A__			
		ACCT	AGG GGCAGATCAC AGGTCAGG			

TCC CCGTTTAGTG TCCAGTCC
 AC AAC
 GAM1925 LOC90485 3' CCTAACATCAGGCGATCTGCCT 63695 ACAAG__ C
 GCCT AGGCAGGCAGATC GT AGG
 ||||| || ||
 TCCGTCCGTCTAG CA TCC
 CGGACTA A
 GAM1925 LOC90485 3' CCTGACTTCGTTATCCACCCGC 63696 A CA C A
 CT AGGC GG GAT AC AGGTCAGG
 ||| || ||| || |||||
 TCCG CC CTA TG TTCAGTCC
 C AC T C
 GAM1925 LOC90591 3' CCTGACCTCAGGTGATCCACCT 64161 CA A__
 AGG GATCAC AGGTCAGG
 || |||| |||||
 TCC CTAGTG TCCAGTCC
 AC GAC
 GAM1925 LOC90591 3' CCTGACCTCGTGATCTGCCCGC 64162 A A
 CT AGGC GGCAGATCAC AGGTCAGG
 ||| ||||| |||||
 TCCG CCGTCTAGTG TCCAGTCC
 C C
 GAM1925 LOC91115 3' CCTGACCTCAGATGGTCCACC 65557 CA AG ACA
 GG GGC ATC AGGTCAGG
 || ||| || |||||
 CC CTG TAG TCCAGTCC
 AC G_ AC_
 GAM1925 LOC91115 3' CCTGACCTTGTGATCCGCCCAC 65558 CA A
 CT AGG GGC GATCACAAGGTCAGG
 ||| || ||||| |||||
 TCC CCG CTAGTGTTCCAGTCC
 AC C
 GAM1925 LOC91291 5' CCTGACGCCAGGTGATCTGCCC 66087 CA AAG__
 ACCT AGG GGCAGATCAC GTCAGG
 ||| ||||| |||||
 TCC CCGTCTAGTG CAGTCC
 AC GACCG
 GAM1925 LOC91373 3' CCTGACCTCGTGATCCACCCAC 66411 CA CA A
 CT AGG GG GATCAC AGGTCAGG
 ||| || ||||| |||||
 TCC CC CTAGTG TCCAGTCC
 AC AC C
 GAM1925 LOC91561 5' CCTGACCTCAGGTGATCTGCCC 67042 A A__
 GCC GGC GGCAGATCAC AGGTCAGG
 ||| ||||| |||||
 CCG CCGTCTAGTG TCCAGTCC
 C GAC
 GAM1925 LOC92148 5' CCTGACCTTGTGATCCTCCCGC 68875 A CA
 CT AGGC GG GATCACAAGGTCAGG
 ||| || ||||| |||||

TCCG CC CTAGTGTTCAGTCC
 C TC
 GAM1925 LOC92689 3' CCTGACCTCGTGATCTGCCCCG 70772 A A
 CT AGGC GGCAGATCAC AGGTCAGG
 ||| ||||| |||||
 TCCG CCGTCTAGTG TCCAGTCC
 C C
 GAM1925 LOC92876 5' CCTGACCTCAGGTGATCCACCT 71347 CA A__
 AGG GATCAC AGGTCAGG
 || |||| |||||
 TCC CTAGTG TCCAGTCC
 AC GAC
 GAM1925 LOC93349 3' CCTGACCTCATGAGCCGCCCG 57266 A AGA CA
 CT AGGC GGC TCA AGGTCAGG
 ||| || || |||||
 TCCG CCG AGT TCCAGTCC
 C CCG AC
 GAM1926 AEGL1 3' CATCCTGATACATCCTGAAGT 8531 CAC GTGCT_
 ACTTCAGG ATG GATG
 ||||| || |||
 TGAAGTCC TAC CTAC
 ____ ATAGTC
 GAM1926 ATP10C 3' CATCAGCACACGTGCCAAGGA 44666 A_ A
 G CTTT GGCAC TGGTGCTGATG
 ||| |||| |||||
 GAGG CCGTG ACCACGACTAC
 AA C
 GAM1926 BIN1 3' CACCATGCTTGCCTGAAG 58450 ____
 CTTT CAGGCA CATGGTG
 ||||| |||||
 GAAGTCCGT GTACCAC
 TC
 GAM1926 BIN1 3' CACCATGCTTGCCTGAAG 16288 ____
 CTTT CAGGCA CATGGTG
 ||||| |||||
 GAAGTCCGT GTACCAC
 TC
 GAM1926 CEP2 3' CATGGACACATCCTGAAGT 23243 CACATG _ G
 ACTTCAGG GTG CT ATG
 ||||| || |||
 TGAAGTCC CAC GG TAC
 TA____ A _
 GAM1926 FCMD 3' CATCAGCACCAACCTGCT 23031 CA_
 GGCA TGGTGCTGATG
 ||| |||||
 TCGT ACCACGACTAC
 CCA
 GAM1926 GLP1R 3' CATCAGCACCATGGAGGC 10793 A_
 GC CATGGTGCTGATG
 || |||||

		CG GTACCACGACTAC	
		GAG	
GAM1926 KCNK10	5'	CACCAGACTTAACCCGCCTGAA 41267	ACAT__ G A
	G	CTTCAGGC GGT CTG TG	
		GAAGTCCG TCA GAC AC	
		CCCAAT _ C	
GAM1926 MCC	3'	CACCAGGACTGTGCCTGAA 11481	TG G A
		TTCAGGCACA GT CTG TG	
		AAGTCCGTGT CA GAC AC	
		_ G C	
GAM1926 SMAC	5'	CACCAACACCCTGCCTGAGG 58017	CAT C A
		CTTCAGGCA GGTG TG TG	
		GGAGTCCGT CCAC AC AC	
		C__ A C	
GAM1926 TRIM9	3'	CACCACTGCCACATTCTGAA 54828	CACA T __ A
	GT	ACTTCAGG TGG GC TG TG	
		TGAAGTCC ACC CG AC AC	
		TTAC _ TC C	
GAM1926 ZFH1B	3'	TCATGCACGTGCCTGA 29607	ATG _
		TCAGGCAC GTGC TGA	
		AGTCCGTG CACG ACT	
		_ T	
GAM1926 CYP2A7	5'	AGTCCATATGCCTGGAGT 7538	C T
		ACTTCAGGCA ATGG GCT	
		TGAGGTCCGT TACC TGA	
		A _	
GAM1926 CYP2A7	5'	AGTCCATATGCCTGGAGT 48351	C T
		ACTTCAGGCA ATGG GCT	
		TGAGGTCCGT TACC TGA	
		A _	
GAM1926 DKFZp434B1222	5'	CATCTACATGTGCCAGAGT 34550	CA GTGCT
		ACTT GGCACATG GATG	
		TGAG CCGTGTAC CTAC	
		AC AT__	
GAM1926 FLJ32452	3'	AGCACCATATGCCTGCAG 58631	T C
		CT CAGGCA ATGGTGCT	
		GA GTCCGT TACCACGA	
		C A	
GAM1926 GRIN3A	3'	CATCAACATTGCTTGAA 56778	CATG C
		TTCAGGCA GTG TGATG	

		AAGTTCGT TAC ACTAC	
		_____ A	
GAM1926 KIAA0342	5'	CAGTTGTCACGTGCCTGAA 71139	A GT_
		TTCAGGCAC TG G CTG	
		AAGTCCGTG AC T GAC	
		C TG T	
GAM1926 KIAA1016	5'	CATCAGCACACGGAGG 93382	AGGCACA
		CTTC TGGTGCTGATG	
		GGAG ACCACGACTAC	
		GC_____	
GAM1926 LENE	3'	CATCAAGACTCCTGAAG 38476	CACAT GC
		CTTCAGG GGT TGATG	
		GAAGTCC TCA ACTAC	
		_____ GA	
GAM1926 OSBPL11	3'	TCAGCCATTGTGCCTGAA 43208	TGGT
		TTCAGGCACA GCTGA	
		AAGTCCGTGT CGACT	
		TAC_	
GAM1926 PCAF	3'	TCACCAAGCAGTGTGCCTAAAG 15287	C GG GA_
		CTT AGGCACAT TGCT TGA	
		GAA TCCGTGTG ACGA ACT	
		A _ ACC	
GAM1926 RAI17	3'	CACCAGTGCAGCCTGAAGT 92899	A_ _
		ACTTCAGGC CA TGGTG	
		TGAAGTCCG GT ACCAC	
		AC G	
GAM1926 SYT13	3'	CACCAGCATCACCAAAGT 95097	CA CACA A
		ACTT GG TGGTGCTG TG	
		TGAA CC ACTACGAC AC	
		A_ _ C	
GAM1926 TACTILE	3'	TCATCTCCAAACGCCTGAAG 20594	ACA TGCT
		CTTCAGGC TGG GATGA	
		GAAGTCCG ACC CTACT	
		CAA T_	
GAM1926 LOC126364	5'	TCAGTGCCACGTGCCTGAA 76199	A TG
		TTCAGGCAC TGG CTGA	
		AAGTCCGTG ACC GACT	
		C GT	
GAM1926 LOC128954	5'	CATCAGCACCTCCCCAAG 76301	CA CACAT
		CTT GG GGTGCTGATG	

GAA CC CCACGACTAC
 CC CT____
 GAM1926 LOC149685 5' CACACATGCGCCATGAAGT 80295 _ A _
 ACTTCA GGC CATG GTG
 ||||| ||| ||| |||
 TGAAGT CCG GTAC CAC
 A C A
 GAM1926 LOC152286 3' CATAGATTCACTGCCTGAA 86804 CA TG A
 TTCAGGCA TGG CTG TG
 ||||| ||| ||| ||
 AAGTCCGT ACT GAT AC
 C_ TA _
 GAM1926 LOC152674 3' CAGCATTTACCATGTACCCGA 87000 A C ____
 TC GG ACATGGT GCTG
 || || ||||| |||
 AG CC TGTACCA CGAC
 C A TTTA
 GAM1926 LOC222484 3' CATCAATGGGCACGACCTGAAG 96001 CACATG ____
 T ACTTCAGG GTGCT GATG
 ||||| ||| |||
 TGAAGTCC CACGG CTAC
 AG____ GTAA
 GAM1926 LOC253634 5' TCACGACATGTGCCCAAGGT 98418 CA G C
 ACTT GGCACATG TG TGA
 ||| ||||| || |||
 TGGA CCGTGTAC GC ACT
 AC A _
 GAM1927 CHRNA2 3' TGGAGATGAGCCCAAAGTGC 7432 GTAG AC C
 GCA TG GC CATCTCCA
 ||| || || |||||
 CGT AC CG GTAGAGGT
 GAA_ C_ A
 GAM1927 GNAS 3' TGGAGATGGGCGTCACTACTGC 33919
 TA TAGCAGTAGTGACGCCCATCTCCA
 ||||| ||||| ||||| |||||
 ATCGTCATCACTGCGGGTAGAGGT
 GAM1927 MYCL2 3' GAGATGGGGTTTCACCAC 19376 A C _
 GT GTGA GCCC ATCTC
 || ||| ||| |||||
 CA CACT TGGG TAGAG
 C T G
 GAM1927 PLAG1 3' GAAATGACACAGAACTATTGCT 12148 GACGCC_ C
 A TAGCAGTAGT CAT TC
 ||||| ||| ||
 ATCGTTATCA GTA AG
 AGACACA A
 GAM1927 CCR1 3' GAAATGGGGGAAGTACTGCTG 8926 GACG C
 TAGCAGTAGT CCCAT TC
 ||||| ||| ||| ||

		CGTCAT AC GT GTA AG	
		G C TC A	
GAM1927	TGIF2	3' GGAGACAAGCATGGTGCTGCTG 41753	G GAC CCA
		TAGCAGTA T GC TCTCC	
		GTCGTCGT G CG AGAGG	
		G TA_ AAC	
GAM1927	LOC126327	3' TGGAGACAGAAAGCCACTGCTG 74986	AC CCA__
		CAGTAGTG GC TCTCCA	
		GTCGTCAC CG AGAGGT	
		__ AAAGAC	
GAM1927	LOC126731	3' ATGAGTGTGAGCACTACTACTG 59835	C __ C
		TAG AGTAGT GACGC CAT	
		GTC TCATCA CTGTG GTA	
		A CGA A	
GAM1927	LOC149117	3' TGGAAATAAGTTGTGTTACTAC 85509	CC__ C
		GTAGTGACGC AT TCCA	
		CATCATTGTG TA AGGT	
		TTGAA A	
GAM1927	LOC149483	3' TGGAGATGAGCATCTGAACATG 80189	_ AGT C C
	C	GCA GT GA GC CATCTCCA	
		CGT CA CT CG GTAGAGGT	
		A AGT A A	
GAM1927	LOC149832	5' GAGATGGGATTGTCAGCCAC 85863	A_ _
		GT G TGACG CCCATCTC	
		CA C ACTGT GGGTAGAG	
		C G TA	
GAM1927	LOC89985	3' TGGAGATGGGCACCACTGC 61675	AC
		GTAGTG GCCCATCTCCA	
		CGTCAC CGGGTAGAGGT	
		CA	
GAM1928	ABCA3	3' CGGGCACCGTCCACAGCATCT 8444	CCAATA TA
		AGATGCTG AC TGCCCG	
		TCTACGAC TG ACGGGC	
		ACCC_ CC	
GAM1928	DAPP1	3' AGTTCATTGGCAGAATCT 27677	G _
		AGAT CTGCCAAT AACT	
		TCTA GACGGTTA TTGA	
		A C	
GAM1928	RRM2	3' GTAATGTTTCATTAACAGCATCT 8288	CC _ TA
		AGATGCTG AAT AAC TGC	

		TCTACGAC TTA TTG ATG		
		AA C TA		
GAM1928 WHSC1	5'	CGGGCTTCCACGGCAGCATCT 56705		AATAACTAT
		AGATGCTGCC GCCCG		
		TCTACGACGG CGGGC		
		CACCTT__		
GAM1928 FLJ12150	3'	CGGGCATGGCCTGGCAGCTCT 45682	T	ATAA
		AGA GCTGCCA CTATGCCCG		
		TCT CGACGGT GGTACGGGC		
		_ CC__		
GAM1928 FLJ13491	3'	CGGGTGGGCCACCAGTAGCATC 45216		CAATAACTA
	T	AGATGCTGC TGCCCG		
		TCTACGATG GTGGGC		
		ACCACCGG_		
GAM1928 FLJ20619	3'	CACAGTGAGGTAGCATCT 35890		AATA A
		AGATGCTGCC ACT TG		
		TCTACGATGG TGA AC		
		AG__ C		
GAM1928 HS6ST	3'	AGTTCCTTTGCCAGCAGCATCT 62726		__ T__
		AGATGCTGC CAA AACT		
		TCTACGACG GTT TTGA		
		ACC TCC		
GAM1928 KIAA0339	3'	GGGCATTGGCAGCAGCT 71967	A	ATAACT
		AG TGCTGCCA ATGCCC		
		TC ACGACGGT TACGGG		
		G _____		
GAM1928 KIAA1377	3'	GGCATGGTGGCATGCACCT 67759	A _	ATAA
		AG TGC TGCC ACTATGCC		
		TC ACG ACGG TGGTACGG		
		C T _____		
GAM1928 P114-RHO-GEF	3'	GGCGTCGGCAGCATCT 31673		AATAACT
		AGATGCTGCC ATGCC		
		TCTACGACGG TGCGG		
		C_____		
GAM1928 SHAPY	3'	CGGGCATAGCCTGGAAGC 57908	G	ATAA
		GCT CCA CTATGCCCG		
		CGA GGT GATACGGGC		
		A CC__		
GAM1928 LOC115051	3'	AGTTCCTTTGCCAGCAGCATCT 60674		__ T__
		AGATGCTGC CAA AACT		

TCTACGACG GTT TTGA
 ACC TCC
 GAM1928 LOC152627 5' AGTTTATTGGCAGCATTT 81502 _
 AGATGCTGCCAATAA CT
 |||||
 TTTACGACGGTTATT GA
 T
 GAM1928 LOC152804 3' GGCATGGTGGCAGGCACCT 87084 A _ AATA
 AG TGC TGCC ACTATGCC
 || ||| |||||
 TC ACG ACGG TGGTACGG
 C G _
 GAM1928 LOC203083 5' GGCATGGTGGCAGGCACCT 92093 A _ AATA
 AG TGC TGCC ACTATGCC
 || ||| |||||
 TC ACG ACGG TGGTACGG
 C C _
 GAM1928 LOC221795 5' GGCATGGTGGCAGGCACCT 94077 A _ AATA
 AG TGC TGCC ACTATGCC
 || ||| |||||
 TC ACG ACGG TGGTACGG
 C C _
 GAM1928 LOC254176 5' GGCATGGTGGCAGGCACCT 99174 A _ AATA
 AG TGC TGCC ACTATGCC
 || ||| |||||
 TC ACG ACGG TGGTACGG
 C C _
 GAM1929 SCAMP1 3' GCTAAATAAATATTCTCC 18013 T C
 GGA AATATT ATTTAGC
 ||| ||||| |||||
 CCT TTATAA TAAATCG
 C A
 GAM1929 SCAMP1 3' GCTAAATAAATATTCTCC 54501 T C
 GGA AATATT ATTTAGC
 ||| ||||| |||||
 CCT TTATAA TAAATCG
 C A
 GAM1929 NX-17 3' TGAATATCAGCCCCTAATA 40706 ATA_
 TATTAGGG ATATTCA
 ||||| |||||
 ATAATCCC TATAAGT
 CGAC
 GAM1929 LOC161589 3' GCTAAATGAATATTATCCCTAA 83159
 TA TATTAGGGATAATATTCATTTAGC
 |||||
 ATAATCCCTATTATAAGTAAATCG
 GAM1930 AMACR 3' TTGTATGCATGGAAACATGGA 69103 ATC G
 TCCAT TCCATGCATG CGG
 ||||| ||||| |||

		AGGTA AGGTACGTAT GTT	
		CAA _	
GAM1930 BCL2L11	3'	TCGCCCAGAGATATGGA 57615	CA CAT G
		TCCATATCTC TG GGCG A	
		AGGTATAGAG AC CCGC T	
		_ _ G	
GAM1930 BCL2L11	3'	TCGCCCAGAGATATGGA 57616	CA CAT G
		TCCATATCTC TG GGCG A	
		AGGTATAGAG AC CCGC T	
		_ _ G	
GAM1930 FGFR2	5'	CGTCCACATGGAGATATGGA 5559	CA _
		TCCATATCTCCATG TGG CG	
		AGGTATAGAGGTAC ACC GC	
		_ T	
GAM1930 FGFR2	5'	CGTCCACATGGAGATATGGA 43633	CA _
		TCCATATCTCCATG TGG CG	
		AGGTATAGAGGTAC ACC GC	
		_ T	
GAM1930 FGFR2	5'	CGTCCACATGGAGATATGGA 43638	CA _
		TCCATATCTCCATG TGG CG	
		AGGTATAGAGGTAC ACC GC	
		_ T	
GAM1930 FGFR2	5'	CGTCCACATGGAGATATGGA 43642	CA _
		TCCATATCTCCATG TGG CG	
		AGGTATAGAGGTAC ACC GC	
		_ T	
GAM1930 FGFR2	5'	CGTCCACATGGAGATATGGA 43652	CA _
		TCCATATCTCCATG TGG CG	
		AGGTATAGAGGTAC ACC GC	
		_ T	
GAM1930 FGFR2	5'	CGTCCACATGGAGATATGGA 43665	CA _
		TCCATATCTCCATG TGG CG	
		AGGTATAGAGGTAC ACC GC	
		_ T	
GAM1930 FGFR2	5'	CGTCCACATGGAGATATGGA 43674	CA _
		TCCATATCTCCATG TGG CG	
		AGGTATAGAGGTAC ACC GC	
		_ T	
GAM1930 FGFR2	5'	CGTCCACATGGAGATATGGA 43678	CA _
		TCCATATCTCCATG TGG CG	

AGGTATAGAGGTAC ACC GC
 — T
 GAM1930 FGFR2 5' CGTCCACATGGAGATATGGA 43763 CA _
 TCCATATCTCCATG TGG CG
 ||||| ||||| |||||
 AGGTATAGAGGTAC ACC GC
 — T
 GAM1930 FGFR2 5' CGTCCACATGGAGATATGGA 43767 CA _
 TCCATATCTCCATG TGG CG
 ||||| ||||| |||||
 AGGTATAGAGGTAC ACC GC
 — T
 GAM1930 FGFR2 5' CGTCCACATGGAGATATGGA 43771 CA _
 TCCATATCTCCATG TGG CG
 ||||| ||||| |||||
 AGGTATAGAGGTAC ACC GC
 — T
 GAM1930 MAP3K14 3' ATCCGCCACGTGAAGAGA 15541 CA A
 TCTC TGC TGGCGGAT
 |||| |||||
 AGAG GTG ACCGCCTA
 AA C
 GAM1930 KIAA0819 3' CCCCAGCATCACAGGAGACATG 64330 A ____ A C
 GA TCCAT TCTCC ATGC TGG GG
 |||| |||| |||| ||||
 AGGTA AGAGG TACG ACC CC
 C ACAC _ _
 GAM1930 PORIMIN 3' CATACATGGAGTATGGA 54702 T C
 TCCATA CTCCATG ATG
 |||| ||||| |||||
 AGGTAT GAGGTAC TAC
 — A
 GAM1930 RDC1 3' CCGGCACGGGATATGGA 72832 T A A
 TCCATATC CC TGC TGG
 ||||| || |||||
 AGGTATAG GG ACG GCC
 — C _
 GAM1930 VEZATIN 3' ATCCGCCACAACAGACAATG 34656 A_ CCA CA
 CAT TCT TG TGGCGGAT
 ||| ||| || |||||
 GTA AGA AC ACCGCCTA
 AC CA_ _
 GAM1930 LOC147645 5' ATCCGCTGGTGGCAGAGACACG 79065 ATA CA AT__
 G CC TCTC TGC GGCGGAT
 || |||| || |||||
 GG AGAG ACG TCGCCTA
 CAC _ GTGG
 GAM1930 LOC199775 3' TTGCTGCATCAGAGATATG 89726 C_ TG
 CATATCTC ATGCA GCGG
 ||||| |||| ||||

		GTATAGAG TACGT CGTT		
		AC _		
GAM1930	LOC51279	3' CCGCTATTAGAGTATGGA	33752	T CATGC
		TCCATA CTC ATGGCGG		
		AGGTAT GAG TATCGCC		
		_ AT_		
GAM1931	CDH12	3' CTTATCATTAAAGTGGTGTA	15777	CCCAA GA
		TACACCACT GAA ATAAG		
		ATGTGGTGA TTT TATTC		
		AA_ AC		
GAM1931	GOCAP1	3' ATTGTTCTTGGGAGCAGTGTA	43007	CA G
		TACAC CTCCCAAGAA AAT		
		ATGTG GAGGGTTCTT TTA		
		AC G		
GAM1931	DKFZp434N2435	5' CTTATTACTGTGGGGTGGT	98090	T AGAAG
		ACCAC CCCA AATAAG		
		TGGTG GGGT TTATTC		
		_ GTCA_		
GAM1931	DKFZP564I122	3' CTTATTCTTCTCCCTCATGTGT	63877	CACTCCCA
	A	TACAC AGAAGAATAAG		
		ATGTG TCTTCTTATTC		
		TACTCCC_		
GAM1931	FLJ21791	3' CTTATTTGCAGAAAGTGGTGTA	62126	CCCAAGAA
		TACACCACT GAATAAG		
		ATGTGGTGA TTTATTC		
		AGACG_		
GAM1931	HMP19	3' CTTATTCTTTGTTAGGAAAATG	88860	CCAC CAA_
	TA	TACA TCC GAAGAATAAG		
		ATGT AGG TTTCTTATTC		
		AAA_ ATTG		
GAM1931	KIAA1719	3' TCTGTCTTGGGAGTGGTGTA	68742	_
		TACACCACTCCCAAGA AGA		
		ATGTGGTGAGGGTTCT TCT		
		G		
GAM1931	KIAA1853	3' TTTTCTTGGAAGCAGTG	69929	CA C
		CAC CT CCAAGAAGAA		
		GTG GA GGTTCTTTTT		
		AC A		
GAM1931	KIAA1877	3' CTTATTCTTCTGCCATGAGT	66748	CCA_
		ACTC AGAAGAATAAG		

		TGAG TCTTCTTATTC		
		TACCG		
GAM1931 KIAA1906	3'	CTTATTCTTCTTGACTTTTGG	73571	CTCC_
		CCA CAAGAAGAATAAG		
		GGT GTTCTTCTTATTC		
		TTTCA		
GAM1931 OSBPL11	3'	CTTAATTTCCCAAGAGTGGTG	43206	CCAA AA
		CACCACTC GAAG TAAG		
		GTGGTGAG CTTT ATTC		
		AACC A_		
GAM1931 YME1L1	3'	TCATTCTTGATGTGGTGTA	58438	TCC _
		TACACCAC CAAGAA GA		
		ATGTGGTG GTTCTT CT		
		TA_ A		
GAM1931 ZNF262	3'	CTTATTTTGTGGGAGT	18723	A
		ACTCCCAAG AGAATAAG		
		TGAGGGTTT TTTTATTC		
		G		
GAM1931 LOC91960	3'	TGTGGCTTGGAACGTGGTGTA	68294	TC_ AAGA
		TACACCAC CCAAG ATA		
		ATGTGGTG GGTTT TGT		
		CAA GG__		
GAM1932 SCAMP1	3'	GCTAAATAAATATTCTCC	18013	T C
		GGA AATATT ATTTAGC		
		CCT TTATAA TAAATCG		
		C A		
GAM1932 SCAMP1	3'	GCTAAATAAATATTCTCC	54501	T C
		GGA AATATT ATTTAGC		
		CCT TTATAA TAAATCG		
		C A		
GAM1932 NX-17	3'	TGAATATCAGCCCCTAATA	40706	ATA_
		TATTAGGG ATATTCA		
		ATAATCCC TATAAGT		
		CGAC		
GAM1932 LOC161589	3'	GCTAAATGAATATTATCCCTAA	83159	
	TA	TATTAGGGATAATATTCATTTAGC		
		ATAATCCCTATTATAAGTAAATCG		
GAM1933 FLJ20321	3'	TAACGGTGACTTTGTATTGTCA	35431	C_____
	TG	CATGGCAA GTCACCGTT A		

			GTACTGTT	CAGTGGCAA	T	
			ATGTTT	—		
GAM1933	SDCCAG33	3'	AATGGTGAAGTTGCCATG	20524	G	
			CATGGCAAC	TCACCGTT		
			GTACCGTTG	AGTGGTAA		
			A			
GAM1933	SERF2	5'	GACTGTGCTACGTTGCCA	20491	—	C
			TGGCAACGT	CAC GTT		
			ACCGTTGCA	GTG CAG		
			TC	T		
GAM1933	TP53INP1	3'	AACAGGTGATAGTTGCCATG	53865	—	—
			CATGGCAAC	GTCACC GTT		
			GTACCGTTG	TAGTGG CAA		
			A	A		
GAM1933	LOC144766	3'	AACGGTCCATGAGTTGCCAT	77477	G	—
			ATGGCAAC	TC ACCGTT		
			TACCGTTG	AG TGGCAA		
			—	TACC		
GAM1933	LOC153810	5'	AACGGTCACTCTTGCTATG	81813	C	—
			CATGGCAA	GT ACCGTT		
			GTATCGTT	CA TGGCAA		
			CT	C		
GAM1934	AAT1	3'	GGCAATCTGCCCATCCTGTG	81333	A	TCA
			CACAGGATGGG	CAG CC		
			GTGTCCTACCC	GTC GG		
			—	TAAC		
GAM1934	ABCF1	3'	GGTGACCACCTTATTGTGAG	8449	GAT	ACA
			TTCACAG	GGG GTCACC		
			GAGTGTT	TCC CAGTGG		
			AT	AC		
GAM1934	AGL	3'	TGACTGTCCTTGAGAG	5255	A	GGAT
			TTC CA	GGGACAGTCA		
			GAG GT	TCCTGTCAGT		
			A	—		
GAM1934	AGL	3'	TGACTGTCCTTGAGAG	7200	A	GGAT
			TTC CA	GGGACAGTCA		
			GAG GT	TCCTGTCAGT		
			A	—		
GAM1934	AGL	3'	TGACTGTCCTTGAGAG	7203	A	GGAT
			TTC CA	GGGACAGTCA		

			GAG GT TCCTGTCAGT		
			A ____		
GAM1934	AGL	3'	TGACTGTCCTTGAGAG 7206	A	GGAT
			TTC CA GGGACAGTCA		
			GAG GT TCCTGTCAGT		
			A ____		
GAM1934	AGL	3'	TGACTGTCCTTGAGAG 7209	A	GGAT
			TTC CA GGGACAGTCA		
			GAG GT TCCTGTCAGT		
			A ____		
GAM1934	AGL	3'	TGACTGTCCTTGAGAG 7218	A	GGAT
			TTC CA GGGACAGTCA		
			GAG GT TCCTGTCAGT		
			A ____		
GAM1934	AMD1	3'	TGACTGTCCCAGAATGAGAA 9685	A	GGA
			TTC CA TGGGACAGTCA		
			AAG GT ACCCTGTCAGT		
			A AAG		
GAM1934	ATRN	3'	TGACCAGTCTTGTCCTGAGAA 58446	A	TG A_
			TTC CAGGA GGAC GTCA		
			AAG GTCCT TCTG CAGT		
			A GT AC		
GAM1934	CHAT	5'	GACGCCCATCCTGGAA 40968	A	ACA
			TTC CAGGATGGG GTC		
			AAG GTCCTACCC CAG		
			— G_		
GAM1934	CHAT	5'	GACGCCCATCCTGGAA 40972	A	ACA
			TTC CAGGATGGG GTC		
			AAG GTCCTACCC CAG		
			— G_		
GAM1934	CTBP2	5'	GACAGCCCATCGTGTGAA 9003	G	ACA
			TTCACA GATGGG GTC		
			AAGTGT CTACCC CAG		
			G GA_		
GAM1934	DNMT3L	5'	GGCCCCATCCTCTGAA 26289	C	ACA
			TTCA AGGATGGG GTC		
			AAGT TCCTACCC CGG		
			C ____		
GAM1934	DUSP1	3'	GTACTGTACTATCCTGT 16626	G	C
			ACAGGATGG ACAGT AC		

			TGTCCTATC TGTC		
			A _		
GAM1934	ENAM	3'	GGTGA	CTGTCTAGGATGCTG 49929	G G__
			CAG AT	GGACAGTCACC	
			GTC TA	TCTGTCAGTGG	
			G GGA		
GAM1934	ENC1	3'	GACCAT	TCTCACCTGTGAA 14647	A CA_
			TTCACAGG	TGGGA GTC	
			AAGTGTCC	ACTCT CAG	
			C TAC		
GAM1934	EPHB2	3'	GACTCCCTCCTGTGAA	16698	T CA
			TTCACAGGA	GGA GTC	
			AAGTGTCCCT	CCCT CAG	
			- -		
GAM1934	GATA3	3'	GACCCCATCTGTGAA	10770	G ACA
			TTCACAG	ATGGG GTC	
			AAGTGTC	TACCC CAG	
			- -		
GAM1934	GTF2I	3'	GTGACTGTGGGTCTGGAA	53382	A ATGGG
			TTC CAGG	ACAGTCAC	
			AAG GTCT	TGTCAGTG	
			- GGG_		
GAM1934	GTF2I	3'	GTGACTGTGGGTCTGGAA	53384	A ATGGG
			TTC CAGG	ACAGTCAC	
			AAG GTCT	TGTCAGTG	
			- GGG_		
GAM1934	LMO2	5'	GGTGA	CTGTCCTTGAGCGCGGA 19939	ACAGGAT
			TTC	GGGACAGTCACC	
			AGG	TCCTGTCAGTGG	
			CGCGAGT		
GAM1934	MID1	5'	GACAAACCCCCATCCTGGGAA	53902	A ACA__
			TTC CAGGATGGG	GTC	
			AAG GTCCTACCC	CAG	
			G CCAA		
GAM1934	NPR2L	3'	TGATCATCATCTGTGAA	22601	G GACA
			TTCACAG	ATGG GTCA	
			AAGTGTC	TACT TAGT	
			- AC_		
GAM1934	PDGFRB	5'	GGTGA	CTGTCCAGAGCCTGGAA 66583	A ATG_
			TTC CAGG	GGACAGTCACC	

			AAG GTCC	CCTGTCAGTGG		
			—	GAGA		
GAM1934	SLC10A1	3'	GTGACTGTAAACTCTATGAA	13201	C	ATGGG
			TTCA AGG	ACAGTCAC		
			AAGT TCT	TGTCAGTG		
			A	CAAA—		
GAM1934	THRA	3'	GGTCACCTCCCATCCCGT	13754	A	CA C
			AC GGATGGGA	GT ACC		
			TG CCTACCCT	CA TGG		
			C	C_ C		
GAM1934	TYK2	3'	GACCCACCTCTGTGAA	60563	_ A	ACA
			TTACACAG G	TGGG GTC		
			AAGTGTG C	ACCC CAG		
			T C	—		
GAM1934	AFAP	3'	GATGTCCATCCTTGAA	41607	C	G G
			TTCA AGGATGG	ACA TC		
			AAGT TCCTACC	TGT AG		
			—	—		
GAM1934	BP75	5'	GACTTCCCCATCCTGTGGA	25041		AC
			TTACACAGGATGGG	AGTC		
			AGGTGTCCTACCC	TCAG		
			CT			
GAM1934	DDM36	3'	GGCCCTTCCCACCCTGTGAG	40927	A	CA_
			TTACACAGG	TGGGA GTC		
			GAGTGTCC	ACCCT CGG		
			C	TCC		
GAM1934	FLJ10260	5'	GGCCTGCTCCCACCCTGTGGA	36413	A	_ _
			TTACACAGG	TGGGA CAG TC		
			AGGTGTCC	ACCCT GTC GG		
			C	C C		
GAM1934	FLJ10292	3'	GATTCCCATCCATGAA	36431	CA	CA
			TTCA GGATGGGA	GTC		
			AAGT CCTACCCT	TAG		
			A_	—		
GAM1934	FLJ12132	3'	GGTAACTGTCCCGGGCTG	47104	GA	C
			CAG TGGGACAGT	ACC		
			GTC GCCCTGTCA	TGG		
			GG	A		
GAM1934	FLJ14564	3'	GGTGCCAGCCCACCTGTGAA	77014	A	ACA T
			TTACACAGG	TGGG G CACC		

AAGTGTCC ACCC C GTGG
 _ GAC _
 GAM1934 FLJ21839 3' GACTCCCCATCCTGGAA 41834 A AC
 TTC CAGGATGGG AGTC
 ||| ||||| |||
 AAG GTCCTACCC TCAG
 _ C_
 GAM1934 FLJ22477 3' GTGACTGTGGCCTTGAA 45677 C ATGGG
 TTCA AGG ACAGTCAC
 ||| ||| |||||
 AAGT TCC TGTCAGTG
 _ GG_
 GAM1934 HYPH 3' GTAACCATCTTGTAGTACCTGT 96570 ____ TG CA C
 GAA TTCACAGG A GGA GT AC
 ||||| | ||| |||
 AAGTGTCC T TCT CA TG
 ATGA GT AC A
 GAM1934 KIAA0676 5' GGCGCCCATCCTGGGAA 31145 A ACA
 TTC CAGGATGGG GTC
 ||| ||||| |||
 AAG GTCCTACCC CGG
 G G_
 GAM1934 KIAA1266 3' GGTGACTGCAGATTCTGGAA 66701 A GGGA
 TTC CAGGAT CAGTCACC
 ||| ||||| |||||
 AAG GTCTTA GTCAGTGG
 _ GAC_
 GAM1934 KIAA1719 5' GGTGACTATATTCGGTCTGTGA 68734 GA AC_
 A TTCACAG TGGG AGTCACC
 ||||| ||| |||||
 AAGTGTC GCTT TCAGTGG
 TG ATA
 GAM1934 KIAA1870 3' ATTTTCCCATCTGTGAA 52897 G C
 TTCACAG ATGGGA AGT
 ||||| ||||| |||
 AAGTGTC TACCCT TTA
 _ T
 GAM1934 KRTAP4-2 3' GATATGATCCACCTGTGAA 53520 A A _
 TTCACAGG TGGG CA GTC
 ||||| ||| ||| |||
 AAGTGTCC ACCT GT TAG
 _ A A
 GAM1934 MFN2 5' GATGCCTACCCTGTGAA 30225 A A G
 TTCACAGG TGGG CA TC
 ||||| ||| ||| |||
 AAGTGTCC ATCC GT AG
 C _ _
 GAM1934 MGC10870 5' GGTGACTGGCACCTATGA 51180 C A GGA
 TCA AGG TG CAGTCACC
 ||| ||| ||| |||||

AGT TCC AC GTCAGTGG
 A _ G__
 GAM1934 MGC29761 3' ACTGCATCACCTCCTGTGA 58974 T _ _
 TCACAGGA GG GA CAGT
 ||||| || || ||||
 AGTGTCTCT CC CT GTCA
 _ A AC
 GAM1934 MKRN4 3' GATCGAGACCATCCTGTGAA 48465 GACA_
 TTCACAGGATGG GTC
 ||||| ||||| ||||
 AAGTGTCTCTACC TAG
 AGAGC
 GAM1934 OAZ3 3' GACACTTTCCATCCTAGGAA 32975 AC CA_
 TTC AGGATGGGA GTC
 || ||||| ||||| ||||
 AAG TCCTACCTT CAG
 GA TCA
 GAM1934 P66 3' ACTGCCCCATCCTTGAA 40735 C A
 TTCA AGGATGGG CAGT
 |||| ||||| ||||| ||||
 AAGT TCCTACCC GTCA
 _ C
 GAM1934 RAI17 3' GTGACTGTGGAGCCTGAGAA 92907 A ATGGG
 TTC CAGG ACAGTCAC
 || |||| ||||| ||||| |||||
 AAG GTCC TGTCAGTG
 A GAGG_
 GAM1934 RRP4 3' GGCTCCCATCCTGGAA 27358 A CA
 TTC CAGGATGGGA GTC
 || ||||| ||||| ||||| |||||
 AAG GTCCTACCCT CGG
 _ _
 GAM1934 SPRY4 3' TGA CTGTACACCTTGAA 49034 C ATGG
 TTCA AGG GACAGTCA
 |||| |||| ||||| ||||| |||||
 AAGT TCC CTGTCTAGT
 _ A__
 GAM1934 TIMM22 3' GTGAAATCCCATCCATGAA 78913 CA CAG
 TTCA GGATGGGA TCAC
 |||| ||||| ||||| ||||| |||||
 AAGT CCTACCCT AGTG
 A_ AA_
 GAM1934 LOC124045 3' GGCCACCCACCCCTGTGAG 76543 A ACA
 TTCACAGG TGGG GTC
 ||||| ||||| ||||| ||||| |||||
 GAGTGTCC ACCC CGG
 C CAC
 GAM1934 LOC124045 3' GGCCACCCACCCCTGTGAG 76544 A ACA_
 TTCACAGG TGGG GTC
 ||||| ||||| ||||| ||||| |||||

	GAGTGTCC ACCC CGG		
	C CACC		
GAM1934 LOC124045 3'	GGCCCCACCCACCCCTGTGAG 76545	A	ACA_
	TTCACAGG TGGG GTC		
	GAGTGTCC ACCC CGG		
	C CACC		
GAM1934 LOC124045 3'	GGCCCGCCCCACCCCTGTGAG 76546	A	ACA_
	TTCACAGG TGGG GTC		
	GAGTGTCC ACCC CGG		
	C CGCC		
GAM1934 LOC124045 3'	GGCCCGCCCCACCCCTGTGAG 76547	A	ACA_
	TTCACAGG TGGG GTC		
	GAGTGTCC ACCC CGG		
	C CGCC		
GAM1934 LOC124045 3'	GGCCTGCCACCCCTGTGAG 76548	A	A _
	TTCACAGG TGGG CAG TC		
	GAGTGTCC ACCC GTC GG		
	C _ C		
GAM1934 LOC124045 3'	GGTTGCCACCCCTGTGAG 76550	A	A GT
	TTCACAGG TGGG CA C		
	GAGTGTCC ACCC GT G		
	C C TG		
GAM1934 LOC136345 3'	GGTGACTGGGAGGCCTTGAA 76715	C	ATGGGA
	TTCA AGG CAGTCACC		
	AAGT TCC GTCAGTGG		
	_ GGAGG_		
GAM1934 LOC151808 5'	GACTTTCCCATCCTATGAG 86685	C	C
	TTCA AGGATGGGA AGTC		
	GAGT TCCTACCCT TCAG		
	A T		
GAM1934 LOC155032 5'	GGTGACTGGGAGGCCTTGAA 87596	C	ATGGGA
	TTCA AGG CAGTCACC		
	AAGT TCC GTCAGTGG		
	_ GGAGG_		
GAM1934 LOC157931 3'	GGCGTGAGTCCATCCTGGGAA 87943	A	ACA__
	TTC CAGGATGGG GTC		
	AAG GTCCTACCT CGG		
	G GAGTG		
GAM1934 LOC221410 3'	GATACAGAACCATCCTGTGAA 93696		GACA__
	TTCACAGGATGG GTC		

AAGTGTCTACC TAG
 AAGACA
 GAM1934 LOC221421 3' GTAAGTGTGAGCGTCCTGT 93895 ____ A C
 ACAGGATG GG CAGT AC
 ||||| || ||| ||
 TGTCTGC TC GTCA TG
 GAG _ A
 GAM1934 LOC221474 3' ACAGTCTCCATCTTGTGAA 93983 _ A
 TTCACAGGATGG GAC GT
 ||||| ||| ||
 AAGTGTCTACC CTG CA
 T A
 GAM1934 LOC253517 3' GGCCACCCACCCTGTGAG 96809 A ACA_
 TTCACAGG TGGG GTC
 ||||| ||| ||
 GAGTGTCC ACCC CGG
 C CACC
 GAM1935 HRH1 3' CTCAAACATGTTTAGAGTGGA 7819 A TGG
 TCCA TCTGA GCATGTTTGAG
 ||| ||| |||||
 AGGT AGATT TGTACAACTC
 G ____
 GAM1935 TRIM37 3' CTCAAATTTGTCATCAG 31625 G T
 CTGATGG CA GTTTGAG
 ||||| || |||||
 GACTACT GT TAACTC
 _ T
 GAM1935 HTMP10 3' CTCAAAAAAGCCATCAGATCTG 53758 CA G ATG
 A TC ATCTGATGG C TTTGAG
 || ||||| | |||||
 AG TAGACTACC G AAACTC
 TC _ AAA
 GAM1935 PAK2 5' CTCAAATATCACCAAACCTAGA 67140 A__ GC
 TCTG TGG ATGTTTGAG
 ||| ||| |||||
 AGAT ACC TATAAACTC
 CAA AC
 GAM1935 SEMA6A 3' CTCGAGTACCCACCAGA 40818 A CA
 TCTG TGGG TGTTTGAG
 ||| ||| |||||
 AGAC ACCC ATGAGCTC
 C ____
 GAM1935 TTY7 3' TCAAACATGCAGGCTGGA 50019 AT GATGG
 TCCA CT GCATGTTTGA
 ||| || |||||
 AGGT GA CGTACAACT
 CG ____
 GAM1935 LOC144766 3' CTCAAACATGAGAAGACTGGG 77481 A GATGGG
 TCCA TCT CATGTTTGAG
 ||| ||| |||||

		GGGT AGA GTACAAACTC		
		C AGA__		
GAM1935	LOC201685 5'	TAAACACCCATCAGATGGA	91845	A CA
		TCCA TCTGATGGG TGTTTG		
		AGGT AGACTACCC ACAAAT		
		— —		
GAM1935	LOC221596 5'	CTCAAACAAAACTCAGATT	93623	TG GCA
		AATCTGA G TGTTTGAG		
		TTAGACT C ACAAACCTC		
		__AAA		
GAM1935	LOC93622 3'	CTCTGCAGACCATCAGAT	57729	GCA TT
		ATCTGATGG TGT GAG		
		TAGACTACC ACG CTC		
		AG_ T_		
GAM1936	BCAT1 3'	AGAAAACAAAGAGGCATACT	66782	C AAT
		AG ATGCCTCTT TTTTCT		
		TC TACGGAGAA AAAAGA		
		A AC_		
GAM1936	ETF1 3'	AGAAAAATTAAATTGCTGC	17587	T CTC
		GCA GC TTAATTTTTCT		
		CGT CG AATTAAAAAGA		
		_ TTA		
GAM1936	EXTL2 5'	AGAAGGATAGATGCACGCTA	9325	A C TA
		TAGC TGC TCT ATTTTTCT		
		ATCG ACG AGA TAGGAAGA		
		C T _		
GAM1936	FOX1 3'	AGAAAAATTAAGTTAGGGCA	16777	__
		TGCCT CTTAATTTTTCT		
		ACGGG GAATTAAAAAGA		
		ATT		
GAM1936	FZD3 3'	AGAAAAATGCTGGAACATGCT	34257	CC TA_
		AGCATG TCT ATTTTTCT		
		TCGTAC AGG TAAAAAGA		
		A_ TCG		
GAM1936	RRM2B 3'	AAAAATTAAGAGTGTGTT	68429	C
		AGCATGC TCTTAATTTTT		
		TTGTGTG AGAATTAAAAA		
		—		
GAM1936	ZNF132 3'	AGAAAAATTACCTCCATGCT	14286	CCTCT
		AGCATG TAATTTTTCT		

			TCGTAC ATTA AAAAGA		
			CTCC_		
GAM1936	BAP29	3'	AGAAAAATATAAGCATGTTA	61331	CTCTTA
			TAGCATGC ATTTTCT		
			ATTGTACG TAAAAAGA		
			AATA_		
GAM1936	FAM8A1	3'	AGAAAAATCTGGCATACTG	33197	C TCTTA
			TAG ATGCC ATTTTCT		
			GTC TACGG TAAAAAGA		
			A TC_		
GAM1936	FLJ10648	3'	AGAAAAATTAGTTCCATGC	36888	CCT
			GCATG CTTAATTTTCT		
			CGTAC GGATTAAAAAGA		
			CTT		
GAM1936	FLJ10970	3'	AGAAAAATCAAGATAGGCCTG	37476	T _ A
			CA GCC TCTT ATTTTCT		
			GT CGG AGAA TAAAAAGA		
			C AT C		
GAM1936	FLJ14735	3'	AAAAACTGATGAGGCATGC	52663	_ A
			GCATGCCTC TTA TTTT		
			CGTACGGAG AGT AAAAA		
			T C		
GAM1936	KIAA0830	3'	AGAAAAATAGCGGAGGCA	70266	TA_
			TGCCTCT ATTTTCT		
			ACGGAGG TAAAAAGA		
			CGA		
GAM1936	KIAA0907	3'	AGAAAAATTAAGCTGGGCA	30862	_
			TGCCT CTTAATTTTCT		
			ACGGG GAATTAAAAAGA		
			TC		
GAM1936	KIAA1348	3'	AGAAACTTTGAGCCATGCTA	69116	CCT TT
			TAGCATG CTAA TTTCT		
			ATCGTAC GAGTT AAAGA		
			C_ TC		
GAM1936	PLAGL2	3'	AGAAATGAAAGGCATGC	70952	C ATT
			GCATGCCT TTA TTTCT		
			CGTACGGA AGT AAAGA		
			A _		
GAM1936	RNF2	3'	AGAAAAATTAAATTGGTAGT	24256	A TC_
			GC TGCC TTAATTTTCT		

		TG ATGG AATTAAAAAGA		
		— TTA		
GAM1936	LOC143146 3'	AGAAAATGGCCGAGGCATGCTA 60763	TTAAT	
		TAGCATGCCTC TTTTCT		
		ATCGTACGGAG AAAAGA		
		CCGGT		
GAM1936	LOC146059 3'	AGAAAAGTCCAGAGATGC 78082	GC TA	
		GCAT CTCT ATTTTTCT		
		CGTA GAGA TGAAAAGA		
		— CC		
GAM1936	LOC151391 3'	AGAAAGATCAAAGCATGC 86511	CTC A	
		GCATGC TT ATTTTTCT		
		CGTACG AA TAGAAAGA		
		A_ C		
GAM1936	LOC157507 5'	AAAGAAGAGGAGGCAACTA 82374	CA AA	
		TAG TGCCTCTT TTTT		
		ATC ACGGAGGA AGAAA		
		A_ GA		
GAM1936	LOC158434 3'	AAAAATTACAAGGCATGC 88156	CT	
		GCATGCCT TAATTTT		
		CGTACGGA ATTA AAAA		
		AC		
GAM1936	LOC220020 5'	AGAAAACAGGTGAAGGCATGC 95043	_ TTAAT	
		GCATGCCT C TTTTCT		
		CGTACGGA G AAAAGA		
		A TGGAC		
GAM1936	LOC221979 3'	AGAGTGCAGAAGGCATGC 94216	_ TA	
		GCATGCCT CT ATTTT		
		CGTACGGA GA TGAGA		
		A CG		
GAM1936	LOC92078 3'	AGAAATCCGAAGAGGCAGCTA 68588	A AATT	
		TAGC TGCCTCTT TTTCT		
		ATCG ACGGAGAA AAAGA		
		— GCCT		
GAM1936	LOC92080 5'	AGAAAAATCAAGACCATGTTA 68617	CC A	
		TAGCATG TCTT ATTTTTCT		
		ATTGTAC AGAA TAAAAAGA		
		C_ C		
GAM1937	DDEF1 3'	CTCAGTGTGAGGGCACATGTGA 60305	C C G G	
	A	TTCAC TG GCT TG ACACTGAG		

			AAGTG AC CGG AC TGTGACTC		
			T A G _		
GAM1937	EPM2A	5'	CCCAGCGCCACAGGTGGA 20234	_____	T
			TTCACCT GCGCTG GG		
			AGGTGGA CGCGAC CC		
			CACC _		
GAM1937	MAPK14	3'	CTCACCATCCACAGCAAGATGA 58126	C GC	CAC
	A		TTCA CT GCTGTGGA TGAG		
			AAGT GA CGACACCT ACTC		
			A A_ ACC		
GAM1937	MAPK14	3'	CTCACCATCCACAGCAAGATGA 58132	C GC	CAC
	A		TTCA CT GCTGTGGA TGAG		
			AAGT GA CGACACCT ACTC		
			A A_ ACC		
GAM1937	MAPK14	3'	CTCACCATCCACAGCAAGATGA 8977	C GC	CAC
	A		TTCA CT GCTGTGGA TGAG		
			AAGT GA CGACACCT ACTC		
			A A_ ACC		
GAM1937	FLJ20967	5'	AGTGCCAGCACAGGTGGA 42205	C GT A	
			TTCACCTG GCT GG CACT		
			AGGTGGAC CGA CC GTGA		
			A _ _		
GAM1937	KIAA1069	3'	CTCAGCACCCACCCCTGCAGTG 68530	C CT_	ACA
	AA		TTCAC TGCG GTGG CTGAG		
			AAGTG ACGT CACC GACTC		
			_ CCC CAC		
GAM1937	KIAA1145	3'	CTCAGTGTCCACAGCAGTCAG 66238	_ _	
			CTG C GCTGTGGACACTGAG		
			GAC G CGACACCTGTGACTC		
			T A		
GAM1937	KIAA1719	3'	TCAGTGTCCACAAATCAG 68735	CGC	
			CTG TGTGGACACTGA		
			GAC ACACCTGTGACT		
			TAA		
GAM1937	KIAA1795	3'	CAGTGTCCACATTAATGAA 72613	CCTGCGC	
			TTCA TGTGGACACTG		
			AAGT ACACCTGTGAC		
			AATT_		
GAM1937	KIAA1912	3'	CTCAATGTCCACAACAG 73758	CGC	C
			CTG TGTGGACA TGAG		

GAC ACACCTGT ACTC
 A__ A
 GAM1937 Kv6.3 3' CTCAGTGGGCCACACAG 56853 CGC A_
 CTG TGTGG CACTGAG
 ||| |||| |||||
 GAC ACACC GTGACTC
 ____ GG
 GAM1937 LHFPL2 3' CTCAGTGTCTTACAAGT 70496 GC ____
 GC TGT GGACACTGAG
 || ||| |||||
 TG ACA CCTGTGACTC
 A_ TT
 GAM1937 MGC11386 3' CTCAGCATCCACAGTAGC 53063 _ CA
 GC GCTGTGGA CTGAG
 || ||||| ||||
 CG TGACACCT GACTC
 A AC
 GAM1937 OS4 3' CAGTGTCTTAGCCAGG 20384 C T
 CCTG GCTG GGACACTG
 ||| ||| |||||
 GGAC CGAT CCTGTGAC
 - -
 GAM1937 LOC152674 5' CTCAATTATGTCAGCCACAGGT 87001 C_ TGGACAC
 GAA TTCACCTG GCTG TGAG
 ||||| ||| |||
 AAGTGGAC CGAC ACTC
 AC TGTATTA
 GAM1937 LOC51716 3' CAGTTTCACAGCCAGG 33260 C C
 CCTG GCTGTGGA ACTG
 ||| ||||| |||
 GGAC CGACACTT TGAC
 - -
 GAM1938 ABR 3' CAGCCCCAGCCTCACCACCGC 8451 _ T T
 GTGGTG TGA G CTGGGGCTG
 ||||| ||| | |||||
 CGCCAC ACT C GACCCCGAC
 C C_
 GAM1938 ABR 3' CAGCCCCAGCCTCACCACCGC 41994 _ T T
 GTGGTG TGA G CTGGGGCTG
 ||||| ||| | |||||
 CGCCAC ACT C GACCCCGAC
 C C_
 GAM1938 GA 5' GCCCCAGCCCCACCCA 26088 T TGATGT
 TGGGTGG G CTGGGGC
 ||||| | |||||
 ACCCACC C GACCCCG
 C ____
 GAM1938 COTL1 3' CAGCCCCCGCCACACCACC 89292 A TCT
 GGGTGGTGTG TG GGGGCTG
 ||||| || |||||

CCCACCACAC GC CCCCAC
 C ____
 GAM1938 DKFZP434J193 3' CCCCAGGCCACCCCA 71560 T TGAT
 TGGG GGTG GTCTGGGG
 |||| ||| |||||
 ACCC CCAC CGGACCCC
 - - - -
 GAM1938 DKFZP727G051 3' CCCCACACGGCCACACCACC 70004 A_ C
 GGTGGTGTG TGT TGGGG
 ||||| ||| ||||
 CCACCACAC GCA ACCCC
 CG C
 GAM1938 FLJ23074 3' GCCCAAACCCACCTA 47503 TGTGAT C
 TGGGTGG GT TGGGGC
 ||||| || |||||
 ATCCACC CA ACCCCG
 - - - - A
 GAM1938 PTRF 3' CAGCCTCTCCCCACACCACCA 64234 ATGTCT
 TGGGTGGTGTG GGGGCTG
 ||||| ||| |||||
 ACCCACCACAC CTCCGAC
 CCCT__
 GAM1938 RAI17 3' CAGCCCACCCACCACCACCA 92902 _ ATGTCTG
 TGGGTGGTGTG TG GGGCTG
 ||||| || |||||
 ACCCACCAC AC CCGAC
 C CCA____
 GAM1938 SEC14L1 3' CAGACACACCCACACCACCA 13004 A____
 TGGGTGGTGTG TGTCTG
 ||||| ||| |||||
 ACCCACCACAC ACAGAC
 CCAC
 GAM1938 UBE4B 3' CCCCAGGCCACCCA 21285 TGTGAT
 TGGGTGG GTCTGGGG
 ||||| |||||
 ACCCACC CGGACCCC
 - - - -
 GAM1938 LOC136345 3' CAGCCCCATCCTACCCACCCA 76710 T ATGTC
 TGGGTGG GTG TGGGGCTG
 ||||| ||| |||||
 ACCCACC CAT ACCCCGAC
 C CCT__
 GAM1938 LOC155032 5' CAGCCCCATCCTACCCACCCA 87591 T ATGTC
 TGGGTGG GTG TGGGGCTG
 ||||| ||| |||||
 ACCCACC CAT ACCCCGAC
 C CCT__
 GAM1938 LOC222129 3' CAGCCATCCACACCACCA 95727 _ T
 TGGGTGGTGTG ATG CTG
 ||||| ||| |||

		ACCCACCACAC TAC GAC	
		C C	
GAM1938	LOC90785	3' CAGCCCCAGAGAGGGACCCCCA 64710	T GTGATG
		TGGG GGT TCTGGGGCTG	
		ACCC CCA AGACCCCGAC	
		_ GGGAG_	
GAM1939	GNAS	3' CAACGACTGCCGTGACATCATT 33914	
	CA	TGAATGATGTACGGCAGTCGTTG	
		ACTTACTACAGTGCCGTCAGCAAC	
GAM1939	HIC2	3' CAACGACTGATCTCTCCATTCA 65860	ATGTCACGG
		TGAATG CAGTCGTTG	
		ACTTAC GTCAGCAAC	
		CTCTCTA_	
GAM1939	MGC13114	3' CTGCCGTGGCACCCTCA 51392	A A
		TGA TG TGTCACGGCAG	
		ACT AC ACGGTGCCGTC	
		C C	
GAM1939	MGC19556	5' CTGCCGTGACACCCTTCA 54339	TGA
		TGAA TGTCACGGCAG	
		ACTT ACAGTGCCGTC	
		CCC	
GAM1939	NY-BR-1	5' CAACGACTCCTACATCGTCCA 54849	A CAC C
		TG ATGATGT GG AGTCGTTG	
		AC TGCTACA CC TCAGCAAC	
		C T_ _	
GAM1940	ARHGEF12	3' CCCAAGGATCAACTGCT 31647	CTGTGA
		AGCAGT GATCCTTGGG	
		TCGTCA CTAGGAACCC	
		A_	
GAM1940	BMP4	3' CCCACACACTACACAGACTGCT 56463	_ ATCCT
	T	AAGCAGTCTGTG AG TGGG	
		TTCGTCAGACAC TC ACCC	
		A ACAC_	
GAM1940	BMP4	3' CCCACACACTACACAGACTGCT 56466	_ ATCCT
	T	AAGCAGTCTGTG AG TGGG	
		TTCGTCAGACAC TC ACCC	
		A ACAC_	
GAM1940	BMP4	3' CCCACACACTACACAGACTGCT 8661	_ ATCCT
	T	AAGCAGTCTGTG AG TGGG	

TTCGTCAGACAC TC ACCC
 A ACAC_
 GAM1940 LNK 3' CCCACGTCCAGACTGCTT 19636 TGA CCT
 AAGCAGTCTG GAT TGGG
 ||||| ||| |||
 TTCGTCAGAC CTG ACCC
 ____ C_
 GAM1940 PODXL 3' CCCAAGGTCAGAGCCACTT 19414 CAT G GAT
 AAG G CT TGA CCTTGGG
 ||| ||| ||| |||||
 TTC C GA ACT GGAACCC
 AC _ G ____
 GAM1940 SHANK2 3' GCTCTCCACCTCGCAGACTGCT 25530 ATCCTT
 AGCAGTCTGTGAG GGGC
 ||||| |||
 TCGTCAGACGCTC CTCG
 CACCT_
 GAM1940 SLC9A1 3' GCCTGTCCCCTCACAGACTCTT 70926 C ATCCT
 AAG AGTCTGTGAG TGGGC
 ||| ||||| |||
 TTC TCAGACACTC GTCCG
 ____ CCCT_
 GAM1940 DKFZP564O0423 3' CCCAAGGACCACACCAAGTGC 93346 GTC_ AGA
 GCA TGTG TCCTTGGG
 ||| ||| |||||
 CGT ACAC AGGAACCC
 GACC C_
 GAM1940 DKFZP586A011 3' CCCAAGTAAAGACTGCTT 31840 GTGAGATC
 AAGCAGTCT CTTGGG
 ||||| |||||
 TTCGTCAGA GAACCC
 AAT____
 GAM1940 FLJ20232 5' CCCTTCCCACAGACTCCT 39183 C A TCCTT
 AG AGTCTGTG GA GGG
 || ||||| || |||
 TC TCAGACAC CT CCC
 C C T____
 GAM1940 FLJ22329 3' CCAGGCCTCACAGACT 45395 ATC
 AGTCTGTGAG CTTGG
 ||||| |||||
 TCAGACACTC GGACC
 C_
 GAM1940 LNIR 3' CCCATCCCAGTACTGCTT 48870 T A TCCT
 AAGCAGTC GTG GA TGGG
 ||||| ||| || |||
 TTCGTCAG CAC CT ACCC
 T C ____
 GAM1940 NDRG4 3' AGGAACCCACAGACTGTCC 40376 A AGA_
 A GCAGTCTGTG TCCT
 | ||||| |||

			C TGTCAGACAC	AGGA		
			C	CCCA		
GAM1940	NDRG4	3'	AGGAACCCCACAGACTGTCC	43575	A	AGA_
			A GCAGTCTGTG	TCCT		
			C TGTCAGACAC	AGGA		
			C	CCCA		
GAM1940	P450RAI-2	3'	GCCCATACCACACAGACTGCT	39574		AGATCCT
			AGCAGTCTGTG	TGGGC		
			TCGTCAGACAC	ACCCG		
			ACCAT_			
GAM1940	TBL1Y	5'	GCCGGGCCTCACAGGCTGC	53861		AT TTG
			GCAGTCTGTGAG	CC GGC		
			CGTCGGACACTC	GG CCG		
			CG	_		
GAM1940	TBL1Y	5'	GCCGGGCCTCACAGGCTGC	56952		AT TTG
			GCAGTCTGTGAG	CC GGC		
			CGTCGGACACTC	GG CCG		
			CG	_		
GAM1940	TBL1Y	5'	GCCGGGCCTCACAGGCTGC	56955		AT TTG
			GCAGTCTGTGAG	CC GGC		
			CGTCGGACACTC	GG CCG		
			CG	_		
GAM1940	UHRF1	3'	GCCATCCCCCACCAGACTGCTT	26124		_ AGATCCTTG
			AAGCAGTCTG	TG GGC		
			TTCGTCAGAC	AC CCG		
			C	CCCCTA_		
GAM1940	LOC149421	5'	GCCCAGCAGCTCACAGAC	80146		ATCC
			GTCTGTGAG	TTGGGC		
			CAGACACTC	GACCCG		
			GAC_			
GAM1940	LOC151457	5'	CATTCATCTCACAGCCACTT	81046	CA T	CCT
			AAG G	CTGTGAGAT TG		
			TTC C	GACACTCTA AC		
			AC_	CTT		
GAM1940	LOC151458	5'	CATTCATCTCACAGCCACTT	81047	CA T	CCT
			AAG G	CTGTGAGAT TG		
			TTC C	GACACTCTA AC		
			AC_	CTT		
GAM1941	CREBL2	3'	GAAGCAAATATTTAGCTTCCA	8967	TAC TT T	
			TGGA	CT AT TTTGCTTC		

			ACCT GA TA AAACGAAG		
			TC_ TT T		
GAM1941	GAN	3'	AAGCAAAAACAAAAAGCTATC 42117	C A__	
			CAGA TCTGGATA CTTT TTTTGGCTT		
			AGACCTAT GAAA AAAAACGAA		
			C AAAC		
GAM1941	LAMC1	3'	GAAGCAAATTAAACATCCTGA 11265	T ACC TT	
			TC GGAT TTTA TTTGCTTC		
			AG CCTA AAAT AAACGAAG		
			T C_ T_		
GAM1941	MPP5	5'	AAAATAAGGATTTCCAGA 42746	TAC	
			TCTGGA CTTTATTTT		
			AGACCT GGAATAAAA		
			TTA		
GAM1941	OXTR	3'	GAAATAAATGTATCCAGA 8077	C	
			TCTGGATAC TTTATTTT		
			AGACCTATG AAATAAAG		
			T		
GAM1941	AKAP5	5'	AAGCAAAAATTTATCCA 17953	CCTTT	
			TGGATA ATTTTGGCTT		
			ACCTAT TAAAAACGAA		
			T__		
GAM1941	CCR6	3'	AAGCAAAGGAGTGGTTACCCAG 16434	AT_ TTTA	
	A		TCTGG ACC TTTTGGCTT		
			AGACC TGG GGAAACGAA		
			CAT TGA_		
GAM1941	CCR6	3'	AAGCAAAGGAGTGGTTACCCAG 49391	AT_ TTTA	
	A		TCTGG ACC TTTTGGCTT		
			AGACC TGG GGAAACGAA		
			CAT TGA_		
GAM1941	CRA	3'	GAAACAGAAATTAAAGACACCAG 22936	ATAC T C	
	A		TCTGG CTTTA TTTTG TTC		
			AGACC GAAAT AAGAC AAG		
			ACA_ T A		
GAM1941	Cyt19	3'	AAGCAGGAAAGGCATCAGA 73309	G A TAT	
			TCTG AT CCTT TTTTGGCTT		
			AGAC TA GGAA AGGACGAA		
			_ C _		
GAM1941	FLJ11577	3'	GAAGCAAAAATAAAAATGATC 47958	ACC_	
			GAT TTTATTTTGGCTTC		

			CTA AAATAAAAACGAAG		
			GTAA		
GAM1941	FLJ32468	5'	GAAGATGCTTAAAGAGCATCCA	59709	AC_ TTTTGTG
			GA TCTGGAT CTTTA CTTC		
			AGACCTA GAAAT GAAG		
			CGA TCGTA_		
GAM1941	GNG3	3'	AAGAATAAAGTCATCCAGA	25204	AC
			TCTGGAT CTTTATTTTT		
			AGACCTA GAAATAAGAA		
			CT		
GAM1941	KIAA0534	5'	GAAGCAAATATAGTATC	71931	CTT T
			GATAC TAT TTTGCTTC		
			CTATG ATA AAACGAAG		
			___ T		
GAM1941	MMP28	3'	AAGCAAAAAAGGGTCCCAGA	53091	AT AT
			TCTGG ACCTTT TTTTGCTT		
			AGACC TGGGAA AAAACGAA		
			C_ _		
GAM1941	MMP28	3'	AAGCAAAAAAGGGTCCCAGA	44441	AT AT
			TCTGG ACCTTT TTTTGCTT		
			AGACC TGGGAA AAAACGAA		
			C_ _		
GAM1941	PDE10A	3'	GGACAAAAATTATCCAGA	22844	CCTTT _
			TCTGGATA ATTTTGT CT		
			AGACCTAT TAAAAAC GG		
			___ A		
GAM1941	SPUF	3'	CAAAAATAAAGGTCCCA	26244	AT
			TGG ACCTTTATTTTTG		
			ACC TGGAAATAAAAAC		
			C_		
GAM1941	UBE4B	3'	GAAGCAAAAACAAAAGTA	21286	C A
			TAC TTT TTTTGTCTTC		
			ATG AAA AAAAACGAAG		
			A C		
GAM1941	WDR9	3'	AAGCAAAAACCTACCCAGA	39082	A CCTTTA
			TCTGG TA TTTTGTCTT		
			AGACC AT AAAAACGAA		
			C C_		
GAM1941	LOC120856	3'	AAAATTAAGGTATCACA	74471	_ T
			TG GATACCTTTA TTTT		

		AC CTATGGAAAT AAAA	
		A T	
GAM1941	LOC142779 3'	GAAGCAAATTAAAGACACCCAA 76906	_ ATAC TT
	GA	TCT GG CTTTA TTTGCTTC	
		AGA CC GAAAT AAACGAAG	
		A CACA T_	
GAM1941	LOC151643 3'	AAGCAAAGTGGGTCCCAGA 81135	AT TTAT
		TCTGG ACCT TTTTGCTT	
		AGACC TGGG GAAACGAA	
		C_ T__	
GAM1941	LOC153883 3'	AAGCAAATAGTCGTATCAGA 81883	G CT T
		TCTG ATAC TTATTTT GCTT	
		AGAC TATG GATAAAA CGAA	
		_ CT _	
GAM1941	LOC163131 5'	AAGCAGATGGTATCCAGA 83322	TTTATT
		TCTGGATACC TTTGCTT	
		AGACCTATGG AGACGAA	
		T_____	
GAM1941	LOC169933 5'	GAAGATAAAGGCATCAGA 83432	G A
		TCTG AT CCTTTATTTT	
		AGAC TA GGAAATAGAAG	
		_ C	
GAM1941	LOC91263 5'	CAAAAATAAAGGGAAAAGA 65997	GGATA
		TCT CCTTTATTTTG	
		AGA GGAAATAAAAAC	
		AAAG_	
GAM1941	LOC91263 5'	GAAGCAAAAATATCTTTCA 65999	TACCTT
		TGGA TATTTTGGCTTC	
		ACTT ATAAAAACGAAG	
		TCT__	
GAM1942	BTG4 3'	CTTGGAAGGCACTGCCTTGGGC 34588	___ A_
		GCCCAAGGCA TC CCAAG	
		CGGGTTCCGT GG GGTTC	
		CAC AA	
GAM1942	CEP2 5'	TAATCTTTTTTAATTCCTTGGG 23248	CATCACC_
	C	GCCCAAGG AAGATTA	
		CGGGTTCC TTCTAAT	
		TTAATTTT	
GAM1942	DBH 3'	CTTAGGGAGTGTGCCTTGGGC 7626	CA__ _
		GCCCAAGGCAT CC AAG	

		CGGGTTCCGTG GG TTC	
		TGAG A	
GAM1942 EDAR	3'	TAGTTGTGCCACCTTGGGC 42531	CAT CAA
		GCCCAAGG CAC GATTA	
		CGGGTTCC GTG TTGAT	
		ACC ____	
GAM1942 FGFR1	3'	TTAATCAAATGCTTTGG 43877	CACCAA
		CCAAGGCAT GATTAA	
		GGTTTCGTA CTAATT	
		AA ____	
GAM1942 FGFR1	3'	TTAATCAAATGCTTTGG 43882	CACCAA
		CCAAGGCAT GATTAA	
		GGTTTCGTA CTAATT	
		AA ____	
GAM1942 IFNAR2	3'	AGTCGGTGAGCCTTGGGC 7896	A AA
		GCCCAAGGC TCACC GATT	
		CGGGTTCCG AGTGG CTGA	
		— —	
GAM1942 LAMP2	3'	TAACCTTGAAGTATGCCTTG 11278	C _ A
		CAAGGCAT AC CAAG TTA	
		GTTCCGTA TG GTTC AAT	
		_ AA C	
GAM1942 MYO1D	3'	TTTGGATGGTGCCTTGGGC 72252	_
		GCCCAAGGCATCA CCAAG	
		CGGGTTCCGTGGT GGTTT	
		A	
GAM1942 NPTX1	3'	TAACCTTGATAGAAGAACCTTG 11842	CA__ AC_ A
GGT		GCCCAAGG TC CAAG TTA	
		TGGGTTCC AG GTTC AAT	
		AAGA ATA C	
GAM1942 SHANK2	3'	TTTAATTGAAGATGTCTTGAGC 25537	C ACCAA
		GC CAAGGCATC GATTAAA	
		CG GTTCTGTAG TTAATTT	
		A AAG__	
GAM1942 SOX9	3'	TTAATCTTAATTACTGCTGTGG 6234	CAA TCACC_
C		GCC GGCA AAGATTAA	
		CGG TCGT TTCTAATT	
		TG_ CATTAA	
GAM1942 ARF4	3'	TTAACCTTGGTGGGGTTTGG 83709	G AT A
		CCAAG C CACCAAG TTAA	

GGTTT G GTGGTTC AATT
_ GG _ C
GAM1942 FLJ22167 5' CTCGGCGAGCCTGGTGGTGC 44868 _ _ A A A
GC CCA AGGC TC CC AG
|| ||| |||| || ||
CG GGT TCCG AG GG TC
T GG _ C C
GAM1942 KIAA1858 3' TGAGGTGGTGGTGGTCTTTG 67726 AGA
CAAGGCATCACCA TTA
||||||| |||
GTTTCGTAGTGGT AGT
GG_
GAM1942 KIAA1908 5' TTTAATCTCGTTTCGGGCCTCGG 73803 A ATCACCA
G CCC AGGC AGATTAAA
||| ||| |||||
GGG TCCG TCTAATTT
C GGCTTGC
GAM1942 MAGE-E1 3' TTTGGCGATGCCTGGGC 48678 A A
GCCCCA GGCATC CCAAG
||||| ||||| |||||
CGGGT CCGTAG GGTTT
_ C
GAM1942 MGC5466 3' TAATCCCATGATGCCTGG 73438 A CCAA
CCA GGCATCA GATTA
||| ||||| |||||
GGT CCGTAGT CTAAT
_ ACC_
GAM1942 RAB14 3' TTTAATTTGGTGATATCTTAAG 33338 CC GC A
C GC AAG ATCACCA GATTAAA
|| ||| ||||| |||||
CG TTC TAGTGGT TTAATTT
AA TA _
GAM1942 SDCCAG28 5' TAATCCTCCTGCCTTTGGGC 22808 _ TCACCAA
GCCCAA GGCA GATTA
||||| ||||| |||||
CGGGTT CCGT CTAAT
T CCTC_
GAM1942 LOC144571 3' TTTAATCTTGGTATTCTATTGG 84082 GGCATC
G CCCAA ACCAAGATTAAA
||||| ||||| |||||
GGGTT TGGTTCTAATTT
ATCTTA
GAM1942 LOC146556 3' AATCTTGGAAGCCCTGAGT 78535 C A ATCA
GC CA GGC CCAAGATT
|| ||| ||||| |||||
TG GT CCG GGTCTAA
A C AA_
GAM1942 LOC147991 3' TTTAATCTTAGTGATAGTTGTG 79304 AG _ C
GG CCCA GC ATCAC AAGATTAAA
|||| || ||||| ||||| |||||

GGGT TG TAGTG TTCTAATTT
GT A A
GAM1942 LOC158572 3' TAATCCTGGTGGTGGCTGGC 82851 CA G A
GCC AG CATCACCA GATTA
||| || ||||| |||||
CGG TC GTGGTGGT CTAAT
_ G C
GAM1942 LOC158714 5' TTGATCAGTGATGCCT 82870 CAA
AGGCATCAC GATTAA
||||||| |||||
TCCGTAGTG CTAGTT
A_
GAM1942 LOC200420 3' TAATCTGTGCCTTGAGT 59929 C CACCA
GC CAAGGCAT AGATTA
|| ||||| |||||
TG GTTCCGTG TCTAAT
A _
GAM1942 LOC220763 5' TAATGCTTCTGATGCCTTGG 73736 CC _
CCAAGGCATCA AAG ATTA
||||||| ||| |||||
GGTCCGTAGT TTC TAAT
C_ G
GAM1943 IHPK1 3' CTCTCAGCCAGGCTCCTCA 97462 T TG_ A
TGA GGAGCCTG GA AG
||| ||||| |||
ACT CCTCGGAC CT TC
_ CGA C
GAM1943 C1orf24 3' CATGTCTTTGAGGGATCC 54784 G GTGG
GGA CCT AAAGACATG
||| ||| |||||
CCT GGG TTTCTGTAC
A AG_
GAM1943 DDX34 3' CGTGGGACCACAGGCTGCACCA 28669 A G AAAGA
TG TG AGCCTGTGG CATG
|| || ||||| |||||
AC AC TCGGACACC GTGC
C G AGG_
GAM1943 FKBP5 3' ATGTCTCCCCAGTTCCACA 15930 A CTG AA
TG TGGAGC TGG AGACAT
|| ||||| ||| |||||
AC ACCTTG ACC TCTGTA
_ _ CC
GAM1943 FLJ10036 3' CGTGGAGTTCACAGGCTCATCA 96626 G AAGA
TGATG AGCCTGTGGA CATG
||||| ||||| |||||
ACTAC TCGGACACTT GTGC
_ GAG_
GAM1943 FLJ10352 3' CATGCCTTTCCACGGATTCCCT 50470 T GC A
CA TGA GGA CTGTGGAAAG CATG
||| ||| ||||| |||||

ACT CCT GGCACCTTTC GTAC
 C TA C
 GAM1943 FLJ13263 3' CTTTCTATTCTCAATCA 47812 G CCT
 TGAT GAG GTGGAAAG
 |||| || |||||
 ACTA CTC TATCTTTC
 A T__
 GAM1943 HEMK 3' CATGTCTTTCCCTATCCA 32951 GCCTGT
 TGGA GGAAAGACATG
 ||| |||||
 ACCT CCTTTCTGTAC
 ATC__
 GAM1943 MGC19595 3' CATGTCCTCCACTGTCCCCCAT 54181 A__ CT AA
 TA TGATGG GC GTGGA GACATG
 |||| || |||| ||||
 ATTACC TG CACCT CTGTAC
 CCC T_ C_
 GAM1943 LOC145815 3' CATGTCTCCCCAACTCCACA 84517 A CCTG AA
 TG TGGAG TGG AGACATG
 || |||| || |||||
 AC ACCTC ACC TCTGTAC
 _ A__ CC
 GAM1943 LOC219988 3' CATGCTGTAACCCAGGCTCCA 93260 A T AA__ A
 CCA TG TGGAGCCTG GG AG CATG
 || ||||| || || ||||
 AC ACCTCGGAC CC TC GTAC
 C C AATG _
 GAM1943 LOC257476 3' CTCTCAGCCAGGCTCCTCA 61921 T TG_ A
 TGA GGAGCCTG GA AG
 || ||||| || ||
 ACT CCTCGGAC CT TC
 _ CGA C
 GAM1944 CDH12 3' CTTATCATTTAAAGTGGTGTA 15777 CCCAA GA
 TACACCACT GAA ATAAG
 ||||| || ||||
 ATGTGGTGA TTT TATTC
 AA__ AC
 GAM1944 GOCAP1 3' ATTGTTCTTGGGAGCAGTGTA 43007 CA G
 TACAC CTCCCAAGAA AAT
 |||| ||||| ||||
 ATGTG GAGGGTTCTT TTA
 AC G
 GAM1944 DKFZp434N2435 5' CTTATTACTGTGGGGTGGT 98090 T AGAAG
 ACCAC CCCA AATAAG
 |||| |||| ||||
 TGGTG GGGT TTATTC
 _ GTCA_
 GAM1944 DKFZP564I122 3' CTTATTCTTCTCCCTCATGTGT 63877 CACTCCCA
 A TACAC AGAAGAATAAG
 |||| |||||

		ATGTG	TCTTCTTATTC		
		TACTCCC_			
GAM1944	FLJ21791	3'	CTTATTTGCAGAAAGTGGTGTA 62126	CCCAAGAA	
			TACACCACT GAATAAG		
			ATGTGGTGA TTTATTC		
			AGACG__		
GAM1944	HMP19	3'	CTTATTCTTTGTTAGGAAAATG 88860	CCAC CAA_	
	TA		TACA TCC GAAGAATAAG		
			ATGT AGG TTTCTTATTC		
			AAA_ ATTG		
GAM1944	KIAA1579	3'	TACTCTTAGTGGTGTA 37154	CCCAAG A	
			TACACCACT AAGA TA		
			ATGTGGTGA TTCT AT		
			_____ C		
GAM1944	KIAA1719	3'	TCTGTCTTGGGAGTGGTGTA 68742	_	
			TACACCACTCCCAAGA AGA		
			ATGTGGTGAGGGTTCT TCT		
			G		
GAM1944	KIAA1853	3'	TTTTTCTTGAAGCAGTG 69929	CA C	
			CAC CT CCAAGAAGAA		
			GTG GA GGTTCTTTTT		
			AC A		
GAM1944	KIAA1877	3'	CTTATTCTTCTGCCATGAGT 66748	CCA_	
			ACTC AGAAGAATAAG		
			TGAG TCTTCTTATTC		
			TACCG		
GAM1944	KIAA1906	3'	CTTATTCTTCTTGACTTTTGG 73571	CTCC_	
			CCA CAAGAAGAATAAG		
			GGT GTTCTTCTTATTC		
			TTTCA		
GAM1944	OSBPL11	3'	CTTAATTTCCCAAGAGTGGTG 43206	CCAA AA	
			CACCACTC GAAG TAAG		
			GTGGTGAG CTTT ATTC		
			AACC A_		
GAM1944	YME1L1	3'	TCATTCTTGATGTGGTGTA 58438	TCC _	
			TACACCAC CAAGAA GA		
			ATGTGGTG GTTCTT CT		
			TA_ A		
GAM1944	YME1L1	3'	TCATTCTTGATGTGGTGTA 27323	TCC _	
			TACACCAC CAAGAA GA		

		ATGTGGTG GTTCTT CT	
		TA_ A	
GAM1944	ZNF262	3' CTTATTTTGTGGGAGT 18723	A
		ACTCCCAAG AGAATAAG	
		TGAGGGTTT TTTTATTC	
		G	
GAM1944	LOC91960	3' TGTGGCTTGGAACGTGGTGTA 68294	TC_ AAGA
		TACACCAC CCAAG ATA	
		ATGTGGTG GGTTT TGT	
		CAA GG_	
GAM1945	ALDH1A3	3' AGGATTTTCACAGTGAGAAAGTT 7335	CTAC C_
		AACTTTCTCAT GTGG CCT	
		TTGAAAGAGTG CACT GGA	
		A_ TTA	
GAM1945	ART1	5' GGCCTAGATGAGGAA 16302	CGT
		TTTCTCATCTA GGCC	
		AAGGAGTAGAT CCGG	
		—	
GAM1945	ATP10C	3' GAGGTACCAAAAAAGAAAGTT 44667	CATCTACG C_
		AACTTTCT TGG CCTC	
		TTGAAAGA ACC GGAG	
		AAAA_ AT	
GAM1945	CASP8	3' AGGGCCATGTTTCAAGAAA 54109	CATCT
		TTTCT ACGTGGCCCT	
		AAAGA TGTACCGGGA	
		ACTT_	
GAM1945	CDH23	3' CCACGTGGACAAGAAAGT 42354	CA
		AACTTTCT TCTACGTGG	
		TGAAAGA AGGTGCACC	
		AC	
GAM1945	CR1	3' AGAGCTTGGAATGCAGAAAG 6937	_ CTACGT C
	TT	AACTTTCT CAT GGC CT	
		TTGAAAGA GTA TCG GA	
		C AAAGGT A	
GAM1945	DLG5	5' GAGGTACAGTGAGAAAGT 83815	CTACG GC
		AACTTTCTCAT TG CCTC	
		TGAAAGAGTG AC GGAG	
		_ AT	
GAM1945	EIF2AK3	5' GAGAGCCAACGCGCGGAAAGTT 17900	CATCTA _ C
		AACTTTCT CGT GGC CTC	

		TTGAAAGG	GCA CCG GAG		
		CGC__	A A		
GAM1945 F2RL3	3'	GAGACACACAGAGAAGAAAG	15515	CA AC GCC	
		CTTTCT TCT GTG CTC			
		GAAAGA AGA CAC GAG			
		AG _	ACA		
GAM1945 IHPK3	5'	GGCCAAGAAGGAGAAAGTT	55097	A_ ACG	
		AACTTTCTC TCT TGGCC			
		TTGAAAGAG AGA ACCGG			
		GA _			
GAM1945 KCNN3	5'	GAGGACCACCTCCTGAGAGAGT	11185	TCTAC C	
T		AACTTTCTCA GTGG CCTC			
		TTGAGAGAGT CACC GGAG			
		CCTC_	A		
GAM1945 NFRKB	5'	AGGATCAAATGGAAAGTT	21605	T CTACG GC	
		AACTTTC CAT TG CCT			
		TTGAAAG GTA AC GGA			
		_ A_	TA		
GAM1945 NORE1	3'	AGGGTGTTTATGAAATGAGAAA	49523	CTA _	
		TTTCTCAT CGTG GCCCT			
		AAAGAGTA GTAT TGGGA			
		AA_	TTG		
GAM1945 BCCIP	3'	AGAGCCATGTGAGAAG	55272	ATCT C	
		TTTCTC ACGTGGC CT			
		GAAGAG TGTACCG GA			
		_	A		
GAM1945 C21orf42	3'	CCAGCAGAAGAGAAAGTT	55227	A ACG	
		AACTTTCTC TCT TGG			
		TTGAAAGAG AGA ACC			
		A CG_			
GAM1945 DKFZP434F0318	3'	GAAGGCAAAGGATGAGAAA	48756	ACGTG C	
		TTTCTCATCT GCC TC			
		AAAGAGTAGG CGG AG			
		AAA_	A		
GAM1945 DKFZp547D155	3'	GAGAACCCCCAGATGAGAAA	70948	ACGT CC	
		TTTCTCATCT GG CTC			
		AAAGAGTAGA CC GAG			
		CCC_	AA		
GAM1945 FLJ10450	5'	GAGGGAACGCAGGTGAGAAAG	36601	A GG	
		CTTTCTCATCT CGT CCCTC			

	GAAAGAGTGGG GCA GGGAG	
	C A_	
GAM1945 FLJ10546	5' GAGAGTGACAGTGAGAAAGTT 60181	CTAC G C
	AACTTTCTCAT GT GC CTC	
	TTGAAAGAGTG CA TG GAG	
	A_ G A	
GAM1945 FLJ13310	3' AGAGCTAGTGTGAGAAAGTT 47806	CT G C
	AACTTTCTCAT AC TGGC CT	
	TTGAAAGAGTG TG ATCG GA	
	_ _ A	
GAM1945 FLJ14686	5' GAGGAGCTCAAAAGAGAAAGTT 52599	ATCTACG _ _
	AACTTTCTC TG GC CCTC	
	TTGAAAGAG AC CG GGAG	
	AAA_ T A	
GAM1945 FLJ20190	3' GAGGACCTGTGAAAGAAAGTT 35207	CA T T C
	AACTTTCT TC ACG GG CCTC	
	TTGAAAGA AG TGT CC GGAG	
	A_ _ _ A	
GAM1945 GDF11	3' TTGCAGATGAGAAGGTT 20560	AC TG
	AACTTTCTCATCT G G	
	TTGGAAGAGTAGA C T	
	_ GT	
GAM1945 KIAA0635	3' AGAACTATGATGAGAAAG 28409	TAC CC
	CTTTCTCATC GTGG CT	
	GAAAGAGTAG TATC GA	
	_ AA	
GAM1945 KIAA1958	5' AGAATATGAAGATGAGAA 82770	A GCC
	TTCTCATCT CGTG CT	
	AAGAGTAGA GTAT GA	
	A AA_	
GAM1945 MGC12335	3' AGGACCTAGATGAGAAGTT 52201	T CGT C
	AACTT CTCATCTA GG CCT	
	TTGAA GAGTAGAT CC GGA	
	_ _ A	
GAM1945 MGC15435	3' GAGGGTGCGTGGAATGAGAAA 51396	_ G
G	CTTTCTCA TCTACGTG CCCTC	
	GAAAGAGT AGGTGCGT GGGAG	
	AA _	
GAM1945 PRKCBP1	5' GAGAACAGCCCAGAAAAGAAAG 25750	CA ACGT C_
TT	AACTTTCT TCT GGC CTC	

		TTGAAAGA AGA CCG GAG	
		AA C___ ACAA	
GAM1945 PRO0149	3'	GGGGACCCAGAGAGAAAGT 26942	A ACGT _
		ACTTTCTC TCT GG CCCT	
		TGAAAGAG AGA CC GGGG	
		_ C___ A	
GAM1945 PRO1430	3'	AGGTGCAGAGAAGAAAGTT 38356	CA ACGTG _
		AACTTTCT TCT GC CCT	
		TTGAAAGA AGA CG GGA	
		AG _____ T	
GAM1945 RASD2	3'	AGGCCAGATGAGAAAG 27459	ACGT C
		CTTTCTCATCT GGCC T	
		GAAAGAGTAGA CCGG A	
		_____ A	
GAM1945 SAC2	3'	CCACAGTAAGAAAGTT 30725	CATC _
		AACTTTCT TAC GTGG	
		TTGAAAGA ATG CACC	
		_____ A	
GAM1945 TSGA14	3'	GAGGGCCTCTCATGGGAAAG 38667	CTACGT
		CTTTCTCAT GGCCCTC	
		GAAAGGGTA CCGGGAG	
		CTCT__	
GAM1945 TUBGCP3	3'	AGGAGTGATGAGAAAGTT 21981	TACGTG _
		AACTTTCTCATC GC CCT	
		TTGAAAGAGTAG TG GGA	
		_____ A	
GAM1945 LOC115273	3'	GAGGCTTTTCTACAGAAAAGAAA 73752	CA AC C___
	GTT	AACTTTCT TCT GTGG CCTC	
		TTGAAAGA AGA CATC GGAG	
		AA _ TTTC	
GAM1945 LOC115442	3'	AGAGCAGATGCAAGAAAGTT 73054	_ ACGTG C
		AACTTTCT CATCT GC CT	
		TTGAAAGA GTAGA CG GA	
		AC _____ A	
GAM1945 LOC115939	3'	GGCTGGGTGACGAGAAA 74033	A T G
		TTTCTC TC AC TGGCC	
		AAAGAG AG TG GTCGG	
		C _ G	
GAM1945 LOC122786	3'	AGGGCCATTTTAAAGACAGTT 74619	T CATCTAC
		AACT TCT GTGGCCCT	

	TTGA AGA TACCGGGA C ATTTT__	
GAM1945 LOC145951 3'	GGCCTCTGTAAGAAAAAGTT 78035 AACTTT TC TACG GGCC TTGAAA AG ATGT CCGG A A__ CT	C ATC T_
GAM1945 LOC147229 5'	GAGGGTTCCGAAATGAGAAA 78921 TTTCTCAT CG GCCCTC AAAGAGTA GC TGGGAG AA_ CT	CTA TG
GAM1945 LOC157349 5'	CACATAAATGAGAAAGTT 82328 AACTTTCTCAT TA GTG TTGAAAGAGTA AT CAC A A	C C
GAM1945 LOC197201 3'	AGGAACAGATGGGAAAGTT 89264 AACTTTCTCATCT G CCT TTGAAAGGGTAGA C GGA __ AA	ACGT GC
GAM1945 LOC199786 3'	GAGGGAGCAGATGAGGAA 89755 TTTCTCATCT GT CCCTC AAGGAGTAGA CG GGGAG __ A_	AC GG
GAM1945 LOC221760 3'	AGGATACCACAGATGAGAAA 95426 TTTCTCATCT GTGG CCT AAAGAGTAGA CACC GGA __ ATA	AC C__
GAM1945 LOC222070 5'	GAGACAGGTCAGATGGGAAA 95815 TTTCTCATCT AC TG CTC AAAGGGTAGA TG AC GAG C G A__	_ G GCC
GAM1945 LOC222681 3'	AGGACAGCCAATGAGAAG 94420 TTTCTCAT TGGC CCT GAAGAGTA ACCG GGA __ ACA	CTACG __
GAM1945 LOC222681 3'	AGGACAGCCAATGAGAAG 94421 TTTCTCAT TGGC CCT GAAGAGTA ACCG GGA __ ACA	CTACG __
GAM1945 LOC222681 3'	AGGACAGCCAATGAGAAG 94422 TTTCTCAT TGGC CCT 	CTACG __

	GAAGAGTA ACCG GGA	
	_____ ACA	
GAM1945 LOC222681 3'	AGGACAGCCAATGAGAAG 94423	CTACG ____
	TTTCTCAT TGGC CCT	
	GAAGAGTA ACCG GGA	
	_____ ACA	
GAM1945 LOC222681 3'	AGGACCCCATTTGCCAATGAGA 94424	C__ C C__
AA	TTTCTCAT TA GTGG CCT	
	AAAGAGTA GT TACC GGA	
	ACC T CCA	
GAM1945 LOC222681 3'	AGGACCCCATTTGCCAATGAGA 94425	C__ C C__
AA	TTTCTCAT TA GTGG CCT	
	AAAGAGTA GT TACC GGA	
	ACC T CCA	
GAM1945 LOC222681 3'	AGGACAGCCAATGAGAAG 94419	CTACG ____
	TTTCTCAT TGGC CCT	
	GAAGAGTA ACCG GGA	
	_____ ACA	
GAM1945 LOC222701 5'	AGGATTCTGTTAATGAGAAA 94430	CT TG C
	TTTCTCAT ACG G CCT	
	AAAGAGTA TGT T GGA	
	AT CT A	
GAM1945 LOC254251 3'	GGTTAGAAAAGAAAGTT 97598	CA CGTG
	AAC TTTCT TCTA GCC	
	TTGAAAGA AGAT TGG	
	AA _____	
GAM1945 LOC255000 3'	GAGAATCTCAATGATGAGAAAAG 98632	TACGT CC
T	ACTTTCTCATC GG CTC	
	TGAAAGAGTAG CT GAG	
	TAACT AA	
GAM1945 LOC257507 3'	AGGACAGCCAATGAGAAG 99606	CTACG ____
	TTTCTCAT TGGC CCT	
	GAAGAGTA ACCG GGA	
	_____ ACA	
GAM1945 LOC257507 3'	AGGACAGCCAATGAGAAG 99607	CTACG ____
	TTTCTCAT TGGC CCT	
	GAAGAGTA ACCG GGA	
	_____ ACA	
GAM1945 LOC257507 3'	AGGACAGCCAATGAGAAG 99608	CTACG ____
	TTTCTCAT TGGC CCT	

	GAAGAGTA ACCG GGA	
	_____ ACA	
GAM1945 LOC257507 3'	AGGACAGCCAATGAGAAG 99609	CTACG ____
	TTTCTCAT TGGC CCT	
	GAAGAGTA ACCG GGA	
	_____ ACA	
GAM1945 LOC257507 3'	AGGACAGCCAATGAGAAG 99610	CTACG ____
	TTTCTCAT TGGC CCT	
	GAAGAGTA ACCG GGA	
	_____ ACA	
GAM1945 LOC257507 3'	AGGACCCCATTTGCCAATGAGA 99611	C__ C C__
AA	TTTCTCAT TA GTGG CCT	
	AAAGAGTA GT TACC GGA	
	ACC T CCA	
GAM1945 LOC257507 3'	AGGACCCCATTTGCCAATGAGA 99612	C__ C C__
AA	TTTCTCAT TA GTGG CCT	
	AAAGAGTA GT TACC GGA	
	ACC T CCA	
GAM1945 LOC257625 3'	AGGACAGCCAATGAGAAG 99726	CTACG ____
	TTTCTCAT TGGC CCT	
	GAAGAGTA ACCG GGA	
	_____ ACA	
GAM1945 LOC257625 3'	AGGACAGCCAATGAGAAG 99727	CTACG ____
	TTTCTCAT TGGC CCT	
	GAAGAGTA ACCG GGA	
	_____ ACA	
GAM1945 LOC257625 3'	AGGACAGCCAATGAGAAG 99728	CTACG ____
	TTTCTCAT TGGC CCT	
	GAAGAGTA ACCG GGA	
	_____ ACA	
GAM1945 LOC257625 3'	AGGACAGCCAATGAGAAG 99729	CTACG ____
	TTTCTCAT TGGC CCT	
	GAAGAGTA ACCG GGA	
	_____ ACA	
GAM1945 LOC257625 3'	AGGACAGCCAATGAGAAG 99730	CTACG ____
	TTTCTCAT TGGC CCT	
	GAAGAGTA ACCG GGA	
	_____ ACA	
GAM1945 LOC257625 3'	AGGACCCCATTTGCCAATGAGA 99731	C__ C C__
AA	TTTCTCAT TA GTGG CCT	

		AAAGAGTA GT TACC GGA	
		ACC T CCA	
GAM1945	LOC257625 3'	AGGACCCCATTGCCAATGAGA 99732	C__ C C__
	AA	TTTCTCAT TA GTGG CCT	
		AAAGAGTA GT TACC GGA	
		ACC T CCA	
GAM1945	LOC89919 5'	GAGGGCTACAGGATGAGAAA 61375	AC
		TTTCTCATCT GTGGCCCTC	
		AAAGAGTAGG CATCGGGAG	
		A_	
GAM1945	LOC90594 5'	GAGTGTCACAGAAGAGAAAGT 64217	A AC C
		ACTTTCTC TCT GTGGC CTC	
		TGAAAGAG AGA CACTG GAG	
		A _ T	
GAM1945	LOC92078 3'	GAGAAGCAGAAATGAGAAGGTT 68602	CTACGTG C_
		AACTTTCTCAT GC CTC	
		TTGGAAGAGTA CG GAG	
		AAGA__ AA	
GAM1946	ALDOA 5'	CTCAACCACACTCCGTCCACGG 5264	AGC GA A
		CTGTGGAC AG TG TTGAG	
		GGCACCTG TC AC AACTC	
		CC_ AC C	
GAM1946	BIRC7 5'	TATCCCTGCTGTCCCCAGG 42465	T _
		CCTG GGACAGCAGG ATG	
		GGAC CCTGTCGTCC TAT	
		C C	
GAM1946	BIRC7 5'	TATCCCTGCTGTCCCCAGG 58442	T _
		CCTG GGACAGCAGG ATG	
		GGAC CCTGTCGTCC TAT	
		C C	
GAM1946	CARKL 3'	CAATCACCCAGGAAAGCTGTCC 26098	A_____ A
	ACAG	CTGTGGACAGC GG TGATTG	
		GACACCTGTCG CC ACTAAC	
		AAAGGA C	
GAM1946	DMBT1 3'	CTCAGACCCCACTGTCCACCGG 16608	T CA ATGA
		CC GTGGACAG GG TTGAG	
		GG CACCTGTC CC GACTC	
		C AC CA__	
GAM1946	GPR4 5'	TCCTTCCTGCCGTCCACAG 60584	A T_
		CTGTGGAC GCAGGA GA	

GACACCTG CGTCCT CT
 C TC
 GAM1946 LFG 3' CGACACTCCTGCTGTCCACTGG 77233 T _ A
 CC GTGGACAGCAGGA TG TTG
 || ||||| || ||
 GG CACCTGTCGTCCT AC AGC
 T C _
 GAM1946 MAP3K7IP1 3' CAGCAGACCCTGCTGTCCCA 21489 T A_ A
 TG GGACAGCAGG TG TTG
 || ||||| || ||
 AC CCTGTCGTCC AC GAC
 _ CAG _
 GAM1946 PLOD3 3' CTCCTCCGCCACAGG 8432 ACA A T TT
 CCTGTGG GC GGA GA G
 ||||| || || ||
 GGACACC CG CCT CT C
 _ _ C _
 GAM1946 PML 3' CTCAACCATCCTGCCAATGCCC 53811 T A _ A
 AG CTG GG CA GCAGGATG TTGAG
 ||| || ||||| |||||
 GAC CC GT CGTCCTAC AACTC
 _ _ AAC C
 GAM1946 PML 3' CTCAACCATCCTGCCAATGCCC 53817 T A _ A
 AG CTG GG CA GCAGGATG TTGAG
 ||| || ||||| |||||
 GAC CC GT CGTCCTAC AACTC
 _ _ AAC C
 GAM1946 SELL 3' TCAACCCCCAGCCACAGG 7230 ACA A ATGA
 CCTGTGG GC GG TTGA
 ||||| || || ||
 GGACACC CG CC AACT
 _ _ A CCC_
 GAM1946 SLC25A14 5' CAAGATCCTGCTACCCAGAGG 15533 G AC GA
 CCT TGG AGCAGGAT TTG
 ||| || ||||| ||
 GGA ACC TCGTCCTA AAC
 G CA G_
 GAM1946 SLC25A14 5' CAAGATCCTGCTACCCAGAGG 43334 G AC GA
 CCT TGG AGCAGGAT TTG
 ||| || ||||| ||
 GGA ACC TCGTCCTA AAC
 G CA G_
 GAM1946 CXYorf1 5' TTGTCCCTGTGTCCACAGG 82926 G _ TG
 CCTGTGGACA CAGG A A
 ||||| ||| |
 GGACACCTGT GTCC T T
 _ C GT
 GAM1946 FLJ32356 3' CAAGCCCTGCTCTCCACAGG 59016 C ATGA
 CCTGTGGA AGCAGG TTG
 ||||| ||||| ||

			GGACACCT TCGTCC AAC		
			C CG__		
GAM1946	KIAA0513	3'	CAGCTGCGTCCACAGG 29020	A	GA
			CCTGTGGAC GCAG TG		
			GGACACCTG CGTC AC		
			_ G_		
GAM1946	KIAA1026	3'	CGCCTGCTGCCCCGAGG 71737	A	A
			CCTGTGG CAGCAGG TG		
			GGACGCC GTCGTCC GC		
			C _		
GAM1946	KIAA1679	3'	TCTCCTACTGTACACAGG 70716	G	C T
			CCTGTG ACAG AGGA GA		
			GGACAC TGTC TCCT CT		
			A A _		
GAM1946	PSK-1	3'	CAGCATCCTGCCGCCCA 25752	T	ACA A
			TG GG GCAGGATG TTG		
			AC CC CGTCCTAC GAC		
			_ GC_ _		
GAM1946	SLC38A5	5'	GTTCCCCTGCTGTCCCCAGG 54311	T	AT
			CCTG GGACAGCAGG GAT		
			GGAC CCTGTCGTCC TTG		
			C CC		
GAM1946	TPC2	3'	CAACAACCGTCTACAG 58193	AGCA	A A
			CTGTGGAC GG TG TTG		
			GACATCTG CC AC AAC		
			_ _ A _		
GAM1946	LOC148932	3'	CTCACAGCACAGCTATCCACAG 79848	C	AGGA AT_
	G		CCTGTGGA AGC TG TGAG		
			GGACACCT TCG AC ACTC		
			A AC_ GAC		
GAM1946	LOC150481	3'	CAAATGTCCATCCACAGG 80695	CAGCA	A
			CCTGTGGA GGATG TTG		
			GGACACCT CCTGT AAC		
			A_ _ A		
GAM1946	LOC158191	3'	CAAATGTCCATCCACAGG 82666	CAGCA	A
			CCTGTGGA GGATG TTG		
			GGACACCT CCTGT AAC		
			A_ _ A		
GAM1946	LOC196528	3'	CTCACCTCCTGCTGTCCCCA 89105	T	TGAT
			TG GGACAGCAGGA TGAG		

		AC CCTGTCGTCCT ACTC		
		C CC__		
GAM1946	LOC200093	5' TTGTCCCTGTGTCCACAGG 63782	G	_ TG
		CCTGTGGACA CAGG A A		
		GGACACCTGT GTCC T T		
		_ C GT		
GAM1946	LOC90631	3' CGAGCCCTGCTGTCCACA 64392	ATGA	
		TGTGGACAGCAGG TTG		
		ACACCTGTCGTCC AGC		
		CG__		
GAM1946	LOC91040	5' TTGTCCCTGTGTCCACAGG 65358	G	_ TG
		CCTGTGGACA CAGG A A		
		GGACACCTGT GTCC T T		
		_ C GT		
GAM1947	DISC1	3' GACTGTGTATCCTCAATCA 38508	AT_	
		TGATTGAGGATGCA TC		
		ACTAACTCCTATGT AG		
		GTC		
GAM1947	PPARGC1	3' GACTTCAAATTGCATCTAGAAT 26080	GA	C
	TA	TGATT GGATGCAATT GAAGTC		
		ATTAA TCTACGTAA CTTCAG		
		GA A		
GAM1947	LOC124989	5' GAACACATCCTCAATCA 74845	CAA	
		TGATTGAGGATG TTC		
		ACTAACTCCTAC AAG		
		AC_		
GAM1947	LOC135398	3' ACTTGGGCATCCTCAAT 76466	AATT G	
		ATTGAGGATGC C AAGT		
		TAACTCCTACG G TTCA		
		___ G		
GAM1947	LOC257054	3' GACCCCAAGGGCATCCTCAA 97373	AA CGAA	
		TTGAGGATGC TT GTC		
		AACTCCTACG AA CAG		
		GG CCC_		
GAM1948	AQP6	3' GGCCCCAGGCCCCAGC 55008	A	CTC
		GCTG GGCCTGGG GCC		
		CGAC CCGGACCC CGG		
		C _		
GAM1948	GCK	5' CCCAAGCGCCCAGCAATG 5682	A _ _	
		CATTGCTG GGC CT GGG		

		GTAACGAC CCG GA CCC	
		_ C A	
GAM1948	GGT1	5' TGTCCCCAGGCCTCAGCAA 26439	CT
		TTGCTGAGGCCTGGG CG	
		AACGACTCCGGACCC GT	
		CT	
GAM1948	GNAT1	3' GACGCACAGACTCAGCAAT 5721	GC G _
		ATTGCTGAG CTG GC TC	
		TAACGACTC GAC CG AG	
		A_ A C	
GAM1948	HAS3	3' AGGCAAGCGTGTTCCTCAGCA 19231	CCT G C
		TGCTGAGG G GCT GCCT	
		ACGACTCT T CGA CGGA	
		TG_ G A	
GAM1948	P23	3' AGGCGAGCCCTCCCCAGCA 22751	A CCT
		TGCTG GG GGGCTCGCCT	
		ACGAC CC CCCGAGCGGA	
		_ CT_	
GAM1948	SF1	3' AGGCAGACAGCCTCAGCAA 17339	C GG C
		TTGCTGAGGC TG CT GCCT	
		AACGACTCCG AC GA CGGA	
		_ A_ _	
GAM1948	SYN3	3' GTCGCCTAGTCAGACCTCAGCA 14482	C _____ CTCG
	AT	ATTGCTGAGG CTG GG C	
		TAACGACTCC GAC CC G	
		A TGA__T GCTC	
GAM1948	SYN3	3' GTCGCCTAGTCAGACCTCAGCA 56904	C _____ CTCG
	AT	ATTGCTGAGG CTG GG C	
		TAACGACTCC GAC CC G	
		A TGA__T GCTC	
GAM1948	SYN3	3' GTCGCCTAGTCAGACCTCAGCA 56906	C _____ CTCG
	AT	ATTGCTGAGG CTG GG C	
		TAACGACTCC GAC CC G	
		A TGA__T GCTC	
GAM1948	WNT5A	3' CTCAGAAGCATCAGCAATG 14120	G _
		CATTGCTGA GC CTGGG	
		GTAACGACT CG GACTC	
		A AA	
GAM1948	ARGBP2	5' AGGCAAGCTTTCCCTGCAAT 14589	TG CCT C
		ATTGC AGG GGGCT GCCT	

			TAACG TCC TTCGA CGGA		
			___ CT_ A		
GAM1948	ATP9B	3'	AGGCAAGCCCAGGGCACAG 78971	AG _	C
			CTG GCC TGGGCT GCCT		
			GAC CGG ACCCGA CGGA		
			A_ G A		
GAM1948	ATP9B	3'	AGGCAAGCCCAGGGCACAG 78972	AG _	C
			CTG GCC TGGGCT GCCT		
			GAC CGG ACCCGA CGGA		
			A_ G A		
GAM1948	ATP9B	3'	AGGCAAGCCCAGGGCACAG 78973	AG _	C
			CTG GCC TGGGCT GCCT		
			GAC CGG ACCCGA CGGA		
			A_ G A		
GAM1948	ATP9B	3'	AGGCGAGCCCAGGGCACAG 78974	AG _	
			CTG GCC TGGGCTCGCCT		
			GAC CGG ACCCGAGCGGA		
			A_ G		
GAM1948	CALN1	3'	AGGCAAACCCAGTGGTTTCAGA 49659	G _	CTC
	AATG		CATT CTGAGGCC TGGG GCCT		
			GTAA GACTTTGG ACCC CGGA		
			A TG AAA		
GAM1948	CNR2	3'	GCGAGCCTCCAGGCCAGCAAT 10234	A _	
	G		CATTGCTG GGCCTGG GCTCGC		
			GTAACGAC CCGGACC CGAGCG		
			_ TC		
GAM1948	DKFZp434A171	3'	GGCTCGCCTAAACATAACCTCA 71342	CCT_____	CTCG
	GCAAT		ATTGCTGAGG GGG CC		
			TAACGACTCC TCC GG		
			AATACAAA_ GCTC		
GAM1948	DKFZp762L0311	3'	GTCGCCTAGACGGGCTTCAACA 38672	C _____	CTCG
	ATG		CATTG TGAGGCCTG GG C		
			GTAAC ACTTCGGGC CC G		
			A AGA__T GCTC		
GAM1948	FLJ12076	3'	AGCACCTGTGCCCTCAGCAATG 48020	_CT_ _	
			CATTGCTGAGG C GG GCT		
			GTAACGACTCC G CC CGA		
			C TGT A		
GAM1948	FLJ20297	3'	AGGCAGGTGGGCCCCAGCAA 35369	A GG TC	
			TTGCTG GGCCT GC GCCT		

	AACGAC CCGGG TG CGGA		
	C _ GA		
GAM1948 FLJ20297 3'	AGGCAGGTGGGCCCCAGCAA 36076	A	GG TC
	TTGCTG GGCCT GC GCCT		
	AACGAC CCGGG TG CGGA		
	C _ GA		
GAM1948 KIAA1069 3'	AGTTCCAAACCCCAGCAATG 68525	A	CC _
	CATTGCTG GG TGGG CT		
	GTAACGAC CC ACCT GA		
	C AA T		
GAM1948 KIAA1272 3'	AGGCCTCACACAGGCCTCAGAA 70731	G	GGCTC_
ATG	CATT CTGAGGCCTG GCCT		
	GTAA GACTCCGGAC CGGA		
	A AACTC		
GAM1948 MGC:5244 3'	GGCCGGACCTCAGCAAT 49151	_	TG
	ATTGCTGAGG CC GGCT		
	TAACGACTCC GG CCGG		
	A _		
GAM1948 LOC149194 3'	GCAAGCCCAGGTTGCCAGT 79984	A_	C
	GCTG GGCCTGGGCT GC		
	TGAC TTGGACCCGA CG		
	CG A		
GAM1948 LOC150207 3'	GGCCGGACCTCAGCAAT 80596	_	TG
	ATTGCTGAGG CC GGCT		
	TAACGACTCC GG CCGG		
	A _		
GAM1948 LOC158281 3'	AGGCGAGCCCTCCCCAGCA 82734	A	CCT
	TGCTG GG GGGCTCGCCT		
	ACGAC CC CCCGAGCGGA		
	_ CT_		
GAM1948 LOC163479 5'	AGGCATATTCAAACCTCAGCAA 83021	GCC	CTC
	TTGCTGAG TGGG GCCT		
	AACGACTC ACTT CGGA		
	AAA ATA		
GAM1948 LOC220020 5'	GATCCAGACCTCACCAATG 95045	C	C C
	CATTG TGAGG CTGGG TC		
	GTAAC ACTCC GACCT AG		
	C A _		
GAM1948 LOC256286 3'	GGCCGGACCTCAGCAAT 96895	_	TG
	ATTGCTGAGG CC GGCT		

		TAACGACTCC GG CCGG		
		A _		
GAM1948	LOC91632	3' AGCCGGACCTCAGCAAT 67314	_ TG	
		ATTGCTGAGG CC GGCT		
		TAACGACTCC GG CCGA		
		A _		
GAM1948	LOC93538	5' AGACGAGAACCTGCCTCAGCAA 72952	CT G_ C	
		TTGCTGAGGC GG CTCG CT		
		AACGACTCCG CC GAGC GA		
		T_ AA A		
GAM1949	CRYPTIC	3' GCTGAAGCACTGGGTGAA 51692	ACATT T	
		TTCACCCA TGCTTT GC		
		AAGTGGGT ACGAAG CG		
		C_ T		
GAM1949	CRYPTIC	3' GCTGAAGCACTGGGTGAA 71314	ACATT T	
		TTCACCCA TGCTTT GC		
		AAGTGGGT ACGAAG CG		
		C_ T		
GAM1949	DISC1	3' AGCAAAAGCACAAATATGTGAA 38500	CCAACATT	
		TTCAC TGCTTTTGCT		
		AAGTG ACGAAAACGA		
		TATAAC_		
GAM1949	NUDT2	3' AGCAAAAATCTTGGCTGGGTGG 8597	A_ TTTGC	
	A	TTCACCCA CA TTTTGCT		
		AGGTGGGT GT AAAACGA		
		CG TCTA_		
GAM1949	ATP1B4	3' CAAAAGCAACATTGGGT 24837	CAT	
		ACCCAA TTGCTTTTG		
		TGGGTT AACGAAAAC		
		AC_		
GAM1949	BC022889	3' AGCAAAAGCAAAGGAGCGTGGG 84625	A ACA_	
	GAA	TTC CCCA TTTGCTTTTGCT		
		AAG GGGT AAACGAAAACGA		
		_ GCGAGG		
GAM1949	CBX3	3' AGCTTTTCTAAATGTTGGGGGA 24407	A CTTTT	
	A	TTC CCCAACATTTG GCT		
		AAG GGGTTGTAAAT CGA		
		G CTTTT		
GAM1949	CBX3	3' AGCTTTTCTAAATGTTGGGGGA 33897	A CTTTT	
	A	TTC CCCAACATTTG GCT		

		AAG GGGTTGTAAAT	CGA	
		G	CTTTT	
GAM1949	CHCR	3' AGCAAAAGTCAGTCAGGGTGAA	37823	AAC T
		TTCACCC	ATT GCTTTTGCT	
		AAGTGGG	TGA TGAAAACGA	
		AC_	C	
GAM1949	CHL1	3' AGCAAAAGTCTTAGGTGAA	22764	CAACATTT
		TTCACC	GCTTTTGCT	
		AAGTGG	TGAAAACGA	
		ATTC	_____	
GAM1949	FLJ21432	3' AGCAAAAGACTCAGTGGATGAA	44938	C ACATTTG
		TTCA CCA	CTTTTGCT	
		AAGT GGT	GAAAACGA	
		A	GA CTCA_	
GAM1949	FLJ22202	3' GCAAAAAGCTGGGCGAG	46499	A ACATTT _
		TTC CCCA	GCTTTT GC	
		GAG GGGT	CGAAAA CG	
		C	_____ A	
GAM1949	HERPUD1	3' AGCAAAAGCAGAAACGTGAA	28692	CCAACA
		TTCAC	TTTGCTTTTGCT	
		AAGTG	AGACGAAAACGA	
		CAA	_____	
GAM1949	KIAA1710	3' AGGGGACAAATGCTGGTGAA	63175	CAA _
		TTCACC	CATTTG CTTT	
		AAGTGG	GTAAAC GGGGA	
		TC_	A	
GAM1949	KIAA1958	3' AGCAAAAACAAGTGAAGGAAGA	82772	AC AA C
	A	TTC CC	CATTTG TTTTGCT	
		AAG GG	GTGAAC AAAACGA	
		AA AA	A	
GAM1949	MGC4266	3' AGCAAAACTGTTAGGTGAG	52041	C _
		TTCACC	AACA TTTGCT	
		GAGTGG	TTGT AAACGA	
		A	CA	
GAM1949	LOC147632	5' CAAAAGTAAGGTGTTAATGAA	57468	CCC _
		TTCA	AACAT TTGCTTTG	
		AAGT	TTGTG AATGAAAAC	
		AA_	G	
GAM1949	LOC164200	5' AGGC AAAAATTAGGTGAA	83389	C CA
		TTCACC	AA TTTGCTT	

		AAGTGG TT AAACGGA		
		A AA		
GAM1949	LOC253389 3'	CAAAAGTATTGGGTGAG 97645	CATT	
		TTCACCCAA TGCTTTTG		
		GAGTGGGTT ATGAAAAC		

GAM1949	LOC90509 5'	CAAAAGCAAACACTGTTG 63790	_____	
		CAACA TTTGCTTTTG		
		GTTGT AAACGAAAAC		
		CAC		
GAM1950	NPHS2 3'	GCACGAAGTCACAATGCA 28279	A GTGG	
		TGCATTGT ACTT TGTGC		
		ACGTAACA TGAA GCACG		
		C _____		
GAM1950	SCGB2A2 3'	TACTACAAACTACAAGACAA 11573	CA AC	
		TTG TTGTA TTGTGGTG		
		AAC AACAT AACATCAT		
		AG CA		
GAM1950	XBP1 3'	TGCAATTAAAAGGTACAATGCA 18679	A G G	
	A	TTGCATTGTA CTT TGGT TGCA		
		AACGTAACAT GAA ATTA ACGT		
		G A _		
GAM1950	IL14 5'	CACACCCCCATCCCCAATGCAA 97162	TAACT T_	
		TTGCATTG TG GGTGTG		
		AACGTAAC AC CCACAC		
		CCCT_ CC		
GAM1950	KIAA0329 3'	TGCACACCACAACACACAACAC 29942	CA AAC	
	A	TG TTGT TTGTGGTGTGCA		
		AC AACA AACACCACACGT		
		AC CAC		
GAM1950	KIAA1972 3'	CACACAGTCAGTACTACAAGCA 93412	A _ TGTG	
	A	TTGC TTGTA ACT GTGTG		
		AACG AACAT TGA CACAC		
		_ CA CTGA		
GAM1950	MGC14844 3'	CACACTGATAGTCACAAGCAA 51340	A A TGT	
		TTGC TTGT ACT GGTGTG		
		AACG AACA TGA TCACAC		
		_ C TAG		
GAM1950	UNC5D 3'	TGCACAGTATGTTACAATACAA 56011	C TT G	
		TTG ATTGTAAC GTG TGTGCA		

		AAC TAACATTG TAT ACACGT	
		A _ G	
GAM1950	LOC145978 3'	TACCAGAGTTACAATGCAA 78053	G
		TTGCATTGTA ACTT TGGTG	
		AACGTAACATTGAG ACCAT	
		-	
GAM1950	LOC154421 3'	CACTGGATCAACCCACAATGCA 87419	AAC TGGT_
	A	TTGCATTGT TTG GTG	
		AACGTAACA AAC CAC	
		CCC TAGGT	
GAM1951	CDH12 3'	CTTATCATTTAAAGTGGTGTA 15777	CCCAA GA
		TACACCACT GAA ATAAG	
		ATGTGGTGA TTT TATTC	
		AA_ AC	
GAM1951	GOCAP1 3'	ATTGTTCTTGGGAGCAGTGTA 43007	CA G
		TACAC CTCCCAAGAA AAT	
		ATGTG GAGGGTTCTT TTA	
		AC G	
GAM1951	DKFZp434N2435 5'	CTTATTACTGTGGGGTGGT 98090	T AGAAG
		ACCAC CCCA AATAAG	
		TGGTG GGGT TTATTC	
		_ GTCA_	
GAM1951	DKFZP564I122 3'	CTTATTCTTCTCCCTCATGTGT 63877	CACTCCCA
	A	TACAC AGAAGAATAAG	
		ATGTG TCTTCTTATTC	
		TACTCCC_	
GAM1951	FLJ21791 3'	CTTATTTGCAGAAAGTGGTGTA 62126	CCCAAGAA
		TACACCACT GAATAAG	
		ATGTGGTGA TTTATTC	
		AGACG_	
GAM1951	HMP19 3'	CTTATTCTTTGTTAGGAAAATG 88860	CCAC CAA_
	TA	TACA TCC GAAGAATAAG	
		ATGT AGG TTTCTTATTC	
		AAA_ ATTG	
GAM1951	KIAA1579 3'	TACTCTTAGTGGTGTA 37154	CCCAAG A
		TACACCACT AAGA TA	
		ATGTGGTGA TTCT AT	
		_ C	
GAM1951	KIAA1719 3'	TCTGTCTTGGGAGTGGTGTA 68742	_
		TACACCACTCCCAAGA AGA	

			ATGTGGTGAGGGTTCT TCT		
			G		
GAM1951	KIAA1853	3'	TTTTTCTTGGAAGCAGTG 69929	CA C	
			CAC CT CCAAGAAGAA		
			GTG GA GGTTCTTTT		
			AC A		
GAM1951	KIAA1877	3'	CTTATTCTTCTGCCATGAGT 66748	CCA__	
			ACTC AGAAGAATAAG		
			TGAG TCTTCTTATTC		
			TACCG		
GAM1951	KIAA1906	3'	CTTATTCTTCTTGACTTTTGG 73571	CTCC_	
			CCA CAAGAAGAATAAG		
			GGT GTTCTTCTTATTC		
			TTTCA		
GAM1951	OSBPL11	3'	CTTAATTTCCCAAGAGTGGTG 43206	CCAA AA	
			CACCACTC GAAG TAAG		
			GTGGTGAG CTTT ATTC		
			AACC A_		
GAM1951	YME1L1	3'	TCATTCTTGATGTGGTGTA 58438	TCC _	
			TACACCAC CAAGAA GA		
			ATGTGGTG GTTCTT CT		
			TA_ A		
GAM1951	YME1L1	3'	TCATTCTTGATGTGGTGTA 27323	TCC _	
			TACACCAC CAAGAA GA		
			ATGTGGTG GTTCTT CT		
			TA_ A		
GAM1951	ZNF262	3'	CTTATTTTGTGTTGGGAGT 18723	A	
			ACTCCCAAG AGAATAAG		
			TGAGGGTTT TTTTATTC		
			G		
GAM1951	LOC91960	3'	TGTGGCTTGGAACGTGGTGTA 68294	TC_ AAGA	
			TACACCAC CCAAG ATA		
			ATGTGGTG GGTTT TGT		
			CAA GG_		
GAM1952	FLJ22332	5'	GGAAAGAAAACATCACA 45637	G A _____	
			TGTG AT TAGTTTTT CC		
			ACAC TA ATCAAAAG GG		
			_ C AAA_		
GAM1953	AMACR	3'	TTGTATGCATGGAAACATGGA 69103	ATC G	
			TCCAT TCCATGCATG CGG		

		AGGTA AGGTACGTAT GTT	
		CAA _	
GAM1953 BCL2L11	3'	TCGCCCAGAGATATGGA 57615	CA CAT G
		TCCATATCTC TG GGCG A	
		AGGTATAGAG AC CCGC T	
		_ _ G	
GAM1953 BCL2L11	3'	TCGCCCAGAGATATGGA 57616	CA CAT G
		TCCATATCTC TG GGCG A	
		AGGTATAGAG AC CCGC T	
		_ _ G	
GAM1953 FGFR2	5'	CGTCCACATGGAGATATGGA 5559	CA _
		TCCATATCTCCATG TGG CG	
		AGGTATAGAGGTAC ACC GC	
		_ T	
GAM1953 FGFR2	5'	CGTCCACATGGAGATATGGA 43633	CA _
		TCCATATCTCCATG TGG CG	
		AGGTATAGAGGTAC ACC GC	
		_ T	
GAM1953 FGFR2	5'	CGTCCACATGGAGATATGGA 43638	CA _
		TCCATATCTCCATG TGG CG	
		AGGTATAGAGGTAC ACC GC	
		_ T	
GAM1953 FGFR2	5'	CGTCCACATGGAGATATGGA 43642	CA _
		TCCATATCTCCATG TGG CG	
		AGGTATAGAGGTAC ACC GC	
		_ T	
GAM1953 FGFR2	5'	CGTCCACATGGAGATATGGA 43652	CA _
		TCCATATCTCCATG TGG CG	
		AGGTATAGAGGTAC ACC GC	
		_ T	
GAM1953 FGFR2	5'	CGTCCACATGGAGATATGGA 43665	CA _
		TCCATATCTCCATG TGG CG	
		AGGTATAGAGGTAC ACC GC	
		_ T	
GAM1953 FGFR2	5'	CGTCCACATGGAGATATGGA 43674	CA _
		TCCATATCTCCATG TGG CG	
		AGGTATAGAGGTAC ACC GC	
		_ T	
GAM1953 FGFR2	5'	CGTCCACATGGAGATATGGA 43678	CA _
		TCCATATCTCCATG TGG CG	

AGGTATAGAGGTAC ACC GC
 — T
 GAM1953 FGFR2 5' CGTCCACATGGAGATATGGA 43763 CA _
 TCCATATCTCCATG TGG CG
 ||||| ||||| |||||
 AGGTATAGAGGTAC ACC GC
 — T
 GAM1953 FGFR2 5' CGTCCACATGGAGATATGGA 43767 CA _
 TCCATATCTCCATG TGG CG
 ||||| ||||| |||||
 AGGTATAGAGGTAC ACC GC
 — T
 GAM1953 FGFR2 5' CGTCCACATGGAGATATGGA 43771 CA _
 TCCATATCTCCATG TGG CG
 ||||| ||||| |||||
 AGGTATAGAGGTAC ACC GC
 — T
 GAM1953 MAP3K14 3' ATCCGCCACGTGAAGAGA 15541 CA A
 TCTC TGC TGGCGGAT
 ||||| ||||| |||||
 AGAG GTG ACCGCCTA
 AA C
 GAM1953 KIAA0819 3' CCCCAGCATCACAGGAGACATG 64330 A ____ A C
 GA TCCAT TCTCC ATGC TGG GG
 ||||| ||||| ||||| |||||
 AGGTA AGAGG TACG ACC CC
 C ACAC _ _
 GAM1953 PORIMIN 3' CATACATGGAGTATGGA 54702 T C
 TCCATA CTCCATG ATG
 ||||| ||||| |||||
 AGGTAT GAGGTAC TAC
 _ A
 GAM1953 RDC1 3' CCGGCACGGGATATGGA 72832 T A A
 TCCATATC CC TGC TGG
 ||||| ||||| ||||| |||||
 AGGTATAG GG ACG GCC
 _ C _
 GAM1953 VEZATIN 3' ATCCGCCACAACAGACAATG 34656 A_ CCA CA
 CAT TCT TG TGGCGGAT
 ||||| ||||| ||||| |||||
 GTA AGA AC ACCGCCTA
 AC CA_ _
 GAM1953 LOC147645 5' ATCCGCTGGTGGCAGAGACACG 79065 ATA CA AT__
 G CC TCTC TGC GCGCGGAT
 ||||| ||||| ||||| |||||
 GG AGAG ACG TCGCCTA
 CAC _ GTGG
 GAM1953 LOC199775 3' TTGCTGCATCAGAGATATG 89726 C_ TG
 CATATCTC ATGCA GCGG
 ||||| ||||| |||||

		GTATAGAG TACGT CGTT		
		AC _		
GAM1953	LOC51279	3' CCGCTATTAGAGTATGGA 33752	T	CATGC
		TCCATA CTC ATGGCGG		
		AGGTAT GAG TATCGCC		
		_ AT__		
GAM1954	ACVR1	5' AGCAGTCCTTCCCCCCTCGCC 8472	A A	T_ _
		GG GA GGGGG GGG TGCT		
		CC CT CCCCC CCT ACGA		
		G C TT G		
GAM1954	ADRA2A	5' AGCACCTTCGGCTGCCTCC 7288	A_	GG T
		GGAG AG GG GGGTGCT		
		CCTC TC CT CCCACGA		
		CG GG T		
GAM1954	ALPPL2	3' AGCACCCACCTGAGTTCC 69423	AAGG	
		GGAG GGGTGGGTGCT		
		CCTT TCCACCCACGA		
		GAG_		
GAM1954	ANPEP	3' AGCACCTCCCAGCCCCTGCCC 8564	AGA	G _
		GG AGGGG TGGG TGCT		
		CC TCCCC ACCC ACGA		
		CG_ G TCC		
GAM1954	APBA2	3' AGCCGTCACCCCTGCCTCC 19738	AA	GT
		GGAG GGGGGTGG GCT		
		CCTC TCCCCACT CGA		
		CG GC		
GAM1954	ARHGDIB	3' AGCACCTGTCCCTCCTCC 8613	A	GT
		GGAG AGGGG GGGTGCT		
		CCTC TCCCT CCCACGA		
		C GT		
GAM1954	AXIN1	3' GGTGACCCCCCCCCATCC 61541	GAA	T _
		GGA GGGGG GGGT GCT		
		CCT CCCCC CCCA TGG		
		AC_ _ G		
GAM1954	AXL	5' AGCACCAGGGTCCCCTTCCC 41876	A	TG__
		GG GAAGGGGG GGTGCT		
		CC CTTCCCCT CCACGA		
		_ GGA		
GAM1954	C5R1	3' TAGCACCTCCCACCCCCACC 9976	AGAA	_____
	CC	GG GGGGGT GGGTGCT	A	

			CC CCCCCA CCCACGA T		
			CCAC CCCT _		
GAM1954	CA14	3'	AGCAGATGTCCTCCTTCCC 25056	A	_ GG
			GG GAAGGGGG TG TGCT		
			CC CTCCTCC GT ACGA		
			_ T AG		
GAM1954	CALM3	3'	AGCACCTCCCGCTTCTCC 19000	G	T
			GGAGAAG GGG GGGTGCT		
			CCTCTTC CCC TCCACGA		
			G _		
GAM1954	CCT3	3'	AGCAGAGTCTCCCCTTTTCC 69401	T	G _
			GGAGAAGGGGG GG TGCT		
			CCTTTTCCCCT CT ACGA		
			_ GAG		
GAM1954	CD3E	3'	AGCCTGATCCCCCGCTCC 7418	AA	G T
			GGAG GGGGGT GG GCT		
			CCTC CCCCTA TC CGA		
			GC G _		
GAM1954	CD79A	3'	AGTGTCACCCCTCCTCC 10120	A	G TG
			GGAG AGGGGGTG G CT		
			CCTC TCCCCAC T GA		
			C _ GT		
GAM1954	CDH23	3'	AGCACCCATCCACCGTCCC 54515	A	A _
			GG GA GG GGGTGGTGCT		
			CC CT CC CCTACCCACGA		
			_ G A		
GAM1954	CLN6	3'	AGCTCTGTCCCCTGCTCC 35834	A	TG T
			GGAG AGGGGG GG GCT		
			CCTC TCCCC TC CGA		
			G TG T		
GAM1954	CNTN2	3'	AGCTCTCCCGCCTTCTCC 18657	G	T T
			GGAGAAGG GG GGG GCT		
			CCTCTTCC CC CTC CGA		
			G _ T		
GAM1954	COL4A4	3'	AGCATCTCACTCCCCTCC 5403	AA	_
			GGAG GGGGGT GGTGCT		
			CCTC CCCTCAC CTACGA		
			_ T		
GAM1954	COMP	5'	AGCACCCAGCTCCCCGCC 5413	AGAA	_
			GG GGGGG TGGTGCT		

			CC CCCTC ACCCACGA		
			GC__ G		
GAM1954	CREB1	3'	CACCTGCCTCCACTTCTCC 16492	__	TG
			GGAGAAG GG GG GGTG		
			CCTCTTC CC CC CCAC		
			A T GT		
GAM1954	CRY1	5'	AGCGCCCCCGCCTTCTCC 15807	G	T
			GGAGAAGG GG GGGTGCT		
			CCTCTTCC CC CCCGCGA		
			G _		
GAM1954	CSF1R	3'	AGCCCTCACCCCCCGCCTCC 19049	AA_	T
			GGAG GGGGGTGGG GCT		
			CCTC CCCCCACTC CGA		
			CGC C		
GAM1954	CYBB	3'	CACCCACCCCTTATTTTCC 76844	__	
			GGAGAA GGGGGTGGGTG		
			CCTTTT TCCCCACCCAC		
			AT		
GAM1954	CYP1B1	5'	AGCGAGGCACCCTTCTCC 5445	G	GGG
			GGAGAAGGG GT TGCT		
			CCTCTTCCC CG GCGA		
			A GA_		
GAM1954	DCN	5'	AGCACCTACCCCTCCTCC 56868	A	
			GGAG AGGGGGTGGGTGCT		
			CCTC TCCCCATCCACGA		
			C		
GAM1954	DLG5	5'	AGCACCA GTGCGCCCTCTCC 83808	A	G G__
			GGAGA GGG GT GGTGCT		
			CCTCT CCC CG CCACGA		
			_ G TGA		
GAM1954	DMRT1	3'	AGCCCCACCCCATCCTCC 41981	AAG	T
			GGAG GGGGTGGG GCT		
			CCTC CCCCACCC CGA		
			CTA _		
GAM1954	DRPLA	3'	AGCACCCCCACCCTCCCC 10425	A A _	T
			GG GA GGG GG GGGTGCT		
			CC CT CCC CC CCCACGA		
			C _ A _		
GAM1954	EBI3	3'	AGCACCTGGGTCCTCGCC 20439	A A	GG
			GG GA GGG TGGTGCT		

			CC CT CCT GTCCACGA		
			G _ GG		
GAM1954	EPHA8	3'	AGCACCCAGCCCACCCCTTCC 40428	AA _ _	
			GGAG GG GGG TGGGTGCT		
			CCTT CC CCC ACCCACGA		
			CC A G		
GAM1954	EPS15	3'	AGCACCCAAGCTTCTGCC 10531	_ GGGG	
			GG AGAAG TGGGTGCT		
			CC TCTTC ACCCACGA		
			G GA__		
GAM1954	F2RL3	3'	AGCACTCACTCCCCACTCC 15492	AA	
			GGAG GGGGGTGGGTGCT		
			CCTC CCCTCACTCACGA		
			AC		
GAM1954	FACL3	3'	AGCACCTTATCCTTTCTCC 16738	GT	
			GGAGAAGGGG GGGTGCT		
			CCTCTTTCCT TCCACGA		
			AT		
GAM1954	FKBP2	3'	AGCATACCCACACCTTCTCC 16773	G ____	
			GGAGAAGG GGTGGG TGCT		
			CCTCTTCC CCACCC ACGA		
			A CAT		
GAM1954	GAS7	3'	CAAGTCAGCCCCTTCTACC 20843	_ G G_	
			GG AGAAGGGG TGG TG		
			CC TCTTCCCC ACT AC		
			A G GA		
GAM1954	GATA2	3'	AGCCTGCACCCTCTTCTCC 10767	_ T	
			GGAGAAGGGGGTG GG GCT		
			CCTCTTCTCCAC TC CGA		
			G _		
GAM1954	GBF1	3'	AGCCCTGGGCCACCTCCTCC 16092	A G _ T	
			GGAG AGG GGT GGG GCT		
			CCTC TCC CCG TCC CGA		
			C A GG _		
GAM1954	GFAP	3'	AGCTGCTCCCCTCCCTCC 10775	AA T _	
			GGAG GGGGG GGGT GCT		
			CCTC CTCCC CTCG CGA		
			C_ _ T		
GAM1954	GNL1	5'	GGTCCACGCCCCCTCTCC 93673	A _ TG	
			GGAGA GGGG GTGGG C		

			CCTCT CCCC CACCT G		
			C G GT		
GAM1954	GZMM	5'	AGCACCCACACTGGGTCTC 19212	AGG _	
			GAGA GG GTGGGTGCT		
			CTCT TC CACCCACGA		
			GGG A		
GAM1954	HCN2	3'	AGCACCCCGCCTCCCTCC 8651	AA _	
			GGAG GGGGGTGGG TGCT		
			CCTC CCTCCGCCC ACGA		
			__ C		
GAM1954	HCN4	3'	AGCAGGCCCCCTCTCTCC 19683	_ GGG	
			GGAGA AGGGGGT TGCT		
			CCTCT TCCCCG ACGA		
			C G__		
GAM1954	HHLA1	5'	AGCACCTTGAGACCCCACTCC 20335	AA ____	
			GGAG GGGGGT GGGTGCT		
			CCTC CCCCCA TCCACGA		
			A_ GAGT		
GAM1954	HLCS	3'	AGCATGGTCGCCCTTGCCC 6405	AGA _	
			GG AGGGGGTGG GTGCT		
			CC TTCCCCGCT TACGA		
			CG_ GG		
GAM1954	HNRPD1	5'	AGCCCCCGCCCCTCCTCC 19598	AA T	
			GGAG GGGGGTGGG GCT		
			CCTC TCCCCGCCC CGA		
			C_ C		
GAM1954	HNRPD1	3'	AGCGTCACCCTCTTCTCC 19599	G GT	
			GGAGAAGGGGGT G GCT		
			CCTCTTCTCCCA C CGA		
			_ TG		
GAM1954	HSPB2	3'	AGCACCCAGCAAATCCCTCTCT 9522	A ____	
			GGAGA GGGG G TGGGTGCT		
			TCTCT CCCT C ACCCACGA		
			_ AAA G		
GAM1954	HSPG2	3'	AGCACCCCCACCCACCTCC 19838	AA _ T	
			GGAG GGG GG GGGTGCT		
			CCTC CCC CC CCCACGA		
			CA A _		
GAM1954	IGFBP4	3'	AGCTCTGCCTCCCTCTCC 9550	A TG T	
			GGAGA GGGGG GG GCT		

			CCTCT CCTCC CT CGA		
			C GT _		
GAM1954	INSR	3'	GCTCATCCCCCTCTCTCC 71539	_	_
			GGAGA AGGGGG TGGGT		
			CCTCT TCCCCC ACTCG		
			C T		
GAM1954	IRAK1	3'	AGCACCCACCTCCAACCTC 9607	AA_	
			GAG GGGGGTGGGTGCT		
			CTC CCTCCACCCACGA		
			CAA		
GAM1954	ITGA2B	3'	AGCTGGGCTACCCCCCTCC 6460	AA	GT__
			GGAG GGGGGTGG GCT		
			CCTC CCCCCATC CGA		
			C_ GGGT		
GAM1954	KCNJ10	3'	AGCACCCATCCTCCACTCC 11152	AA	
			GGAG GGGGGTGGGTGCT		
			CCTC CTCCTACCCACGA		
			AC		
GAM1954	LGALS3BP	3'	CACCCCAGCTTCCTCTTCC 69857	GA	__
			GGA AGGGGGT GGGTG		
			CCT TCCTTCG CCCAC		
			TC AC		
GAM1954	LY64	3'	AGCACACACACCCCGCCC 19948	AGAA	_ _
			GG GGGG GTG GGTGCT		
			CC CCCC CAC CCACGA		
			CG_ A A		
GAM1954	MAPK1	3'	AGTGGTTCCTCCCTCTCC 12295	A	TG G
			GGAGA GGGGG G TGCT		
			CCTCT CCCTC T GTGA		
			_ CT G		
GAM1954	MARK1	5'	AGCGGCTCCCCCTCCTCT 38468	A	T G
			GGAG AGGGGG GG TGCT		
			TCTC TCCCCC TC GCGA		
			C _ G		
GAM1954	MCC	3'	AGCACTCACTCTCCCCCTCC 11480	AA	_
			GGAG GGGG GTGGGTGCT		
			CCTC CCTC CACTCACGA		
			CC T		
GAM1954	MN1	3'	AGCTCCCCCACCCCCTCC 11648	GAA	T__
			GGA GGGGGTGGG GCT		

CCT CCCCCACCC CGA
 _____ CCT
 GAM1954 MSF 3' AGCACCTGGACCCCCTGCCC 89463 AGA ____
 GG AGGGGGT GGGTGCT
 || ||||| |||||
 CC TCCCCCA TCCACGA
 CG_ GG
 GAM1954 MYO1A 3' AGCACTAATCCCCCTCTGCC 19386 _ A TG_
 GG AGA GGGGG GGTGCT
 || ||| ||||| |||||
 CC TCT CCCCC TCACGA
 G _ TAA
 GAM1954 NDST1 5' AGCACCCCCGGGCCTGTCC 9525 GA G__ T
 GGA AGG GG GGGTGCT
 ||| ||| || |||||
 CCT TCC CC CCCACGA
 G_ GGG _
 GAM1954 NFIA 3' AGCACCCCTTTGCTTCCC 70883 A G T
 GG GAAG GGG GGGTGCT
 || ||||| ||| |||||
 CC CTTC TTT CCCACGA
 _ G C
 GAM1954 NINJ1 3' AGCACCAGCGTCCCTGCCTCC 15975 A_ _ G
 GGAG AGGGG GT GGTGCT
 |||| ||||| || |||||
 CCTC TCCCT CG CCACGA
 CG G A
 GAM1954 NTE 3' GGTCACCCCCTCCCTCC 22950 AA T _
 GGAG GGGGG GGGTG CT
 |||| ||||| ||||| ||
 CCTC CCTCC CCCAC GG
 _ _ T
 GAM1954 OFD1 5' AGCACCTTTGTTCCTCCC 14607 A A GT_
 GG GA GGGG GGGTGCT
 || || |||| |||||
 CC CT CCTT TCCACGA
 _ _ GTT
 GAM1954 OGDH 3' GCCCCACCCACCCCTCC 92750 AA _ T
 GGAG GG GGGTG GG GC
 |||| || ||||| ||
 CCTC CC CCCACCC CG
 C_ A _
 GAM1954 PCDHGA1 3' AGCACCTACCCCTTCCCC 38833 A G
 GG GAAGGGG TGGGTGCT
 || ||||| |||||
 CC CTTCCCC ATCCACGA
 C _
 GAM1954 PCDHGA10 3' AGCACCTACCCCTTCCCC 50309 A G
 GG GAAGGGG TGGGTGCT
 || ||||| |||||

				CC CTTCCCC ATCCACGA			
				C _			
GAM1954	PCDHGA11	3'	AGCACCTACCCCTTCCCC	38840	A	G	
			GG GAAGGGG TGGGTGCT				
			CC CTTCCCC ATCCACGA				
			C _				
GAM1954	PCDHGA12	3'	AGCACCTACCCCTTCCCC	50316	A	G	
			GG GAAGGGG TGGGTGCT				
			CC CTTCCCC ATCCACGA				
			C _				
GAM1954	PCDHGA2	3'	AGCACCTACCCCTTCCCC	38847	A	G	
			GG GAAGGGG TGGGTGCT				
			CC CTTCCCC ATCCACGA				
			C _				
GAM1954	PCDHGA3	3'	AGCACCTACCCCTTCCCC	50092	A	G	
			GG GAAGGGG TGGGTGCT				
			CC CTTCCCC ATCCACGA				
			C _				
GAM1954	PCDHGA4	3'	AGCACCTACCCCTTCCCC	38855	A	G	
			GG GAAGGGG TGGGTGCT				
			CC CTTCCCC ATCCACGA				
			C _				
GAM1954	PCDHGA5	3'	AGCACCTACCCCTTCCCC	50290	A	G	
			GG GAAGGGG TGGGTGCT				
			CC CTTCCCC ATCCACGA				
			C _				
GAM1954	PCDHGA6	3'	AGCACCTACCCCTTCCCC	38863	A	G	
			GG GAAGGGG TGGGTGCT				
			CC CTTCCCC ATCCACGA				
			C _				
GAM1954	PCDHGA7	3'	AGCACCTACCCCTTCCCC	50297	A	G	
			GG GAAGGGG TGGGTGCT				
			CC CTTCCCC ATCCACGA				
			C _				
GAM1954	PCDHGA8	3'	AGCACCTACCCCTTCCCC	26598	A	G	
			GG GAAGGGG TGGGTGCT				
			CC CTTCCCC ATCCACGA				
			C _				
GAM1954	PCDHGA9	3'	AGCACCTACCCCTTCCCC	50304	A	G	
			GG GAAGGGG TGGGTGCT				

				CC CTTCCCC ATCCACGA			
				C _			
GAM1954	PCDHGB1	3'	AGCACCTACCCCTTCCCC	38872	A	G	
			GG GAAGGGG TGGGTGCT				
			CC CTTCCCC ATCCACGA				
			C _				
GAM1954	PCDHGB2	3'	AGCACCTACCCCTTCCCC	50322	A	G	
			GG GAAGGGG TGGGTGCT				
			CC CTTCCCC ATCCACGA				
			C _				
GAM1954	PCDHGB3	3'	AGCACCTACCCCTTCCCC	38880	A	G	
			GG GAAGGGG TGGGTGCT				
			CC CTTCCCC ATCCACGA				
			C _				
GAM1954	PCDHGB4	3'	AGCACCTACCCCTTCCCC	14964	A	G	
			GG GAAGGGG TGGGTGCT				
			CC CTTCCCC ATCCACGA				
			C _				
GAM1954	PCDHGB5	3'	AGCACCTACCCCTTCCCC	38887	A	G	
			GG GAAGGGG TGGGTGCT				
			CC CTTCCCC ATCCACGA				
			C _				
GAM1954	PCDHGB6	3'	AGCACCTACCCCTTCCCC	50333	A	G	
			GG GAAGGGG TGGGTGCT				
			CC CTTCCCC ATCCACGA				
			C _				
GAM1954	PCDHGB7	3'	AGCACCTACCCCTTCCCC	38896	A	G	
			GG GAAGGGG TGGGTGCT				
			CC CTTCCCC ATCCACGA				
			C _				
GAM1954	PCDHGC3	3'	AGCACCTACCCCTTCCCC	51526	A	G	
			GG GAAGGGG TGGGTGCT				
			CC CTTCCCC ATCCACGA				
			C _				
GAM1954	PCDHGC4	3'	AGCACCTACCCCTTCCCC	38902	A	G	
			GG GAAGGGG TGGGTGCT				
			CC CTTCCCC ATCCACGA				
			C _				
GAM1954	PCDHGC5	3'	AGCACCTACCCCTTCCCC	51553	A	G	
			GG GAAGGGG TGGGTGCT				

				CC CTTCCCC ATCCACGA		
				C _		
GAM1954	PFKFB4	3'	GGCTGCCGCCCCCTCTCC	17086	A	GT
			GGAGA GGGGGTGG GCT			
			CCTCT CCCCCGCC CGG			
			_ GT			
GAM1954	PIK3CG	3'	ACACTACTTGCCTTATCC	12114	G	_ _
			GGA AAGG GGGTGG GT			
			CCT TTCC TTCATC CA			
			A G A			
GAM1954	PIK3R3	3'	CACTTTCACCTCCCTCTCC	61704	A	_
			GGAGA GGGGGTG GGTG			
			CCTCT CCCTCAC TCAC			
			_ TT			
GAM1954	PLA2G2D	3'	AGGGCTCACTCCCTCCTCC	25707	A	G
			GGAG AGGGGGTGGGT CT			
			CCTC TCCCTCACTCG GA			
			C G			
GAM1954	PNOC	5'	AGCACCTGCTTCCTGCTCC	21718	A	TG
			GGAG AGGGGG GGTGCT			
			CCTC TCCTTC CCACGA			
			G GT			
GAM1954	POU3F2	3'	AGCGCGGGGCTCCCCCTCC	20025	AA	GG_
			GGAG GGGGGT GTGCT			
			CCTC CCCTCG CGCGA			
			C_ GGG			
GAM1954	PPP1R12B	3'	AGCACCACTGCCTGCTCC	50343	A	G G
			GGAG AGG GGTGG TGCT			
			CCTC TCC TCACC ACGA			
			G G _			
GAM1954	PPP2R5A	5'	AGCACCCCGCGCCTCTCC	21793	AG	G _
			GGAGA GG GTGGG TGCT			
			CCTCT CC CGCCC ACGA			
			_ G C			
GAM1954	PPP2R5C	3'	CACCGTGTCTCCTTCTCT	12248	GT	_
			GGAGAAGGGG G GGTG			
			TCTCTTCCTC T CCAC			
			TG G			
GAM1954	PPT1	3'	AGCACCCACTTTGTCTCC	62444	AG	
			GGAGA GGGGTGGGTGCT			

			CCTCT TTTCACCCACGA		
			G_		
GAM1954	PRKACA	3'	AGCTGCTCCCCCTCATCC 12265	GA	TG _
			GGA AGGGGG GGT GCT		
			CCT TCCCCC TCG CGA		
			AC _ T		
GAM1954	PSCD4	3'	AGCACCTGGAGACCCACCTCC 26322	AA	GG__
			GGAG GGG TGGGTGCT		
			CCTC CCC GTCCACGA		
			CA AGAG		
GAM1954	PSD	5'	AGCAGGCCCCCCCATCTCC 12430	A	T G_
			GGAGA GGGGG GG TGCT		
			CCTCT CCCCC CC ACGA		
			A _ GG		
GAM1954	PTMS	3'	AGCTGCCCCCTCCCCTCC 12561	AA	T _
			GGAG GGGGG GGGT GCT		
			CCTC CTCCC CCCG CGA		
			CC _ T		
GAM1954	PTPN18	3'	AGCACCTGAGCCTCCCTC 27647	AA	_
			GAG GGGGGT GGGTGCT		
			CTC CCTCCG TCCACGA		
			_ AG		
GAM1954	PTPRA	5'	AGCAGGTACCCCTTCTCC 55946	G	GG
			GGAGAAGGGG TG TGCT		
			CCTCTTCCCC AT ACGA		
			_ GG		
GAM1954	PUM1	3'	AGGATTACTCCCTCCTCC 28645	A	G G
			GGAG AGGGGGTGG T CT		
			CCTC TCCCTCATT A GA		
			C _ G		
GAM1954	RAB26	5'	AGCACCCCCGCTGCCTCC 27598	AA	G T
			GGAG GG GG GGGTGCT		
			CCTC TC CC CCCACGA		
			CG G _		
GAM1954	RAB26	3'	AGCCTTGTCCTTCCTCC 27599	A	TG T
			GGAG AGGGGG GG GCT		
			CCTC TTCCCT TC CGA		
			C GT _		
GAM1954	SDC1	3'	AGCCATGCGCCCCCTCCGCC 12985	AGA	G _
			GG AGGGGGTG GTG CT		

			CC TCCCCCGC TAC GA		
			GCC G C		
GAM1954	SF3B4	3'	AGCACCCCCACTCCATTCCC 20719	A G	___
			GG GAA GGGGT GGGTGCT		
			CC CTT CCTCA CCCACGA		
			_ A CC		
GAM1954	SH3BP2	3'	AGCACCCAAGTGCCCTCCC 13048	A A	GG___
			GG GA GGG TGGGTGCT		
			CC CT CCC ACCCACGA		
			_ _ GTGA		
GAM1954	SHC1	3'	ACCTGATGCCCTTCCCC 13119	A	_ _
			GG GAAGGGG GT GGGT		
			CC CTTCCCC TA TCCA		
			C G G		
GAM1954	SLC12A4	3'	AGCACCCACCTGCCAGCC 18625	AGAA	_
			GG GG GGGTGGGTGCT		
			CC CC TCCACCCACGA		
			GA_ G		
GAM1954	SLC2A4	3'	AGCACTTTAACCCTCTCT 8306	A	GGT
			GGAGA GGG GGGTGCT		
			TCTCT CCC TTCACGA		
			_ AAT		
GAM1954	SLC30A4	5'	AGCACGACCCCCACTCTCC 26155	AG	GG
			GGAGA GGGGT GTGCT		
			CCTCT CCCCACACGA		
			CA G_		
GAM1954	SLIT3	5'	AGCACCGAGCTCGCCCCTCC 13235	AA	_ G_
			GGAG GG GGGT GGTGCT		
			CCTC CC CTCG CCACGA		
			C_ G AG		
GAM1954	SMAC	3'	AGCACACTGCCCTGTCTCC 57993	AG	TG_
			GGAGA GGGG G GTGCT		
			CCTCT TCCC C CACGA		
			G_ GT A		
GAM1954	SMARCD1	3'	AGCTTTCGCTCCTTCTCC 58183	G	T
			GGAGAAGGGG TGGG GCT		
			CCTCTTCCTC GCTT CGA		
			_ T		
GAM1954	STX1A	3'	AGGGCTACCTCCTCCTCC 17206	A	G G
			GGAG AGGGGGTGG T CT		

			CCTC TCCTCCATC G GA		
			C _ G		
GAM1954	SULT2B1	5'	AGCACCCACCTCCCTACTCTCC 17220	__	_
			GGAGA AGGG GGTGGGTGCT		
			CCTCT TCCC CCACCCACGA		
			CA T		
GAM1954	SUOX	5'	AGCACCCATCCCTCCTACC 6602	_	AA
			GG AG GGGGGTGGGTGCT		
			CC TC TCCCTACCCACGA		
			A C_		
GAM1954	TCF3	3'	AGCACCCAGGCCTCTCTCC 71271	AG	GG
			GGAGA GG TGGGTGCT		
			CCTCT CC ACCCACGA		
			CT GG		
GAM1954	TNC	5'	AGCACCCAGCCAAACCCACCTC 10976	AA	__ _
	C		GGAG GGG GG TGGGTGCT		
			CCTC CCC CC ACCCACGA		
			CA AAA G		
GAM1954	TRIM9	3'	AGCAGGCTCCCATTCTCC 31441	_	GGG
			GGAGAA GGGGGT TGCT		
			CCTCTT CCCTCG ACGA		
			A G__		
GAM1954	TTC3	5'	AGCACCAATCCCCCTTGCCC 13879	AG	TG_
			GG AAGGGGG GGTGCT		
			CC TTCCCCC CCACGA		
			CG TAA		
GAM1954	WNT5A	3'	AGCACTCAGCCCCGCTCC 14114	AA	G
			GGAG GGGG TGGGTGCT		
			CCTC CCCC ACTCACGA		
			G_ G		
GAM1954	ZNF148	5'	AGCAAAAGTTCTCCCCCTCC 42015	AA	T ____
			GGAG GGGGG GGG TGCT		
			CCTC CCCCC CTT ACGA		
			_ T GAAA		
GAM1954	ZNF26	3'	AGCACCCCTGTTTTCTCT 73336	G	T
			GGAGAAGG GG GGGTGCT		
			TCTCTTTT TC CCCACGA		
			G _		
GAM1954	AP1M2	3'	AGCACCCGCCCCTTCCTC 19723	A	
			GAG AGGGGGTGGGTGCT		

		CTC TTCCCCGCCCACGA		
		C		
GAM1954	AP3S2	3' AGCAGGGCTGCCTCTTCTCC 20643	G TG G__	
		GGAGAAGGG G G TGCT		
		CCTCTTCTC C C ACGA		
		_ GT GGG		
GAM1954	APR-3	5' AGCGGCTCCCCCTTCTCC 55481	T G	
		GGAGAAGGGGG GG TGCT		
		CCTCTTCCCC TC GCGA		
		_ G		
GAM1954	ARHGEF9	5' AGCACCCCGTCCCCATCCCC 31480	A A GT _	
		GG GA GGGG GGG TGCT		
		CC CT CCCC CCC ACGA		
		C A TG C		
GAM1954	ATP9B	3' AGCACCTTCTGCCCTTCCC 78970	A _ T	
		GG GAAGGG GG GGGTGCT		
		CC CTTCCC TC TCCACGA		
		_ G T		
GAM1954	B3GAT3	3' AGCATGCTGACCCCTTC 25203	G _	
		GAAGGGGGT GGT GCT		
		CTTCCCCCA TCG CGA		
		G TA		
GAM1954	BPESC1	5' AGCACCTGGGTTCTCTCC 41767	A GG	
		GGAGA GGG TGGGTGCT		
		CCTCT CTT GTCCACGA		
		_ GG		
GAM1954	BTF3	3' AGCACTAATGACCCTTGCTCC 97639	_ GGTG_	
		GGAG AAGGG GGTGCT		
		CCTC TTCCC TCACGA		
		G AGTAA		
GAM1954	C20orf102	3' AGCCTCGCCTCCCTCCTCC 55507	A _ T	
		GGAG AGGG GGTGGG GCT		
		CCTC TCCC CCGCTC CGA		
		C T _		
GAM1954	C20orf150	3' AGCACCCACCTGGCCCTCCTCC 66004	A _	
		GGAG AGGG GGTGGGTGCT		
		CCTC TCCC CCACCCACGA		
		C GGT		
GAM1954	C20orf164	5' AGCAAATACACCCCTTCCTC 80294	GA GG__	
		G GAAGGGGGTG TGCT		

			C CTTCCCCAC ACGA			
			TC ATAA			
GAM1954	C20orf28	3'	AGCAGTCACCCCTCCCTCC 31843	AA		G
			GGAG GGGGGTGG TGCT			
			CCTC TCCCCACT ACGA			
			CC G			
GAM1954	C20orf44	3'	AGCTTTGGTCCCCCTTCCC 37307	A		_G T
			GG GAAGGGGG T GG GCT			
			CC CTTCCCCC G TT CGA			
			_ T G T			
GAM1954	C22orf20	3'	AGCATGATCCCACTTCCC 48191	A		_ GG
			GG GAAG GGGGT GTGCT			
			CC CTTC CCCTA TACGA			
			_ A G_			
GAM1954	C4.4A	3'	AGCACTGCCTCCCCTACTCC 27703	A		_TG
			GGAG AGGGG G GGTGCT			
			CCTC TCCCC C TCACGA			
			A TCG			
GAM1954	C6orf28	5'	AGCACCTGCTGTCTTCCC 41291	A		G _
			GG GAAGG GGT GGGTGCT			
			CC CTTCT TCG CCCACGA			
			_ G T			
GAM1954	CABP5	5'	AGCTCCACCCACCCCTCC 39560	AAG_		T
			GGAG GGGGTGGG GCT			
			CCTC CCCCACCT CGA			
			CCCA _			
GAM1954	CBCIP2	3'	CACCTTTCCCCTCTTCTCC 52652			_ T_
			GGAGAAG GGGG GGGTG			
			CCTCTTC CCCC TCCAC			
			T TT			
GAM1954	CD84-H1	3'	AGCACCCAGAGAATCCTTCCTC 54223	GA		GG__
			G GAAGGG TGGGTGCT			
			C CTTCT ACCCACGA			
			TC AAGAG			
GAM1954	CILP	5'	AGCACCCACATCTACCTCT 14613	AA		GG
			GGAG GG GTGGGTGCT			
			TCTC TC CACCCACGA			
			CA TA			
GAM1954	DCNP1	3'	AGTCTGACCCCTCTCTCC 56455	AG		G T
			GGAGA GGGGT GG GCT			

CCTCT CCCCA TC TGA
 CT G _
 GAM1954 DDM36 3' AGCACCAGTGCCCTTCTCC 40914 G TG
 GGAGAAGGG G GGTGCT
 ||||| | |||||
 CCTCTTCCC T CCACGA
 G GA
 GAM1954 dJ55C23.6 3' AGCAGGTCAGCCTCCTTCCC 54508 A G _
 GG GAAGGGGGT GG TGCT
 || ||||| || |||||
 CC CTCCTCCG CT ACGA
 _ A GG
 GAM1954 DKFZP434J1813 5' ACCTACACCGCCCTCTCC 62435 A _ _
 GGAGA GG GG GTGGGT
 |||| || || |||||
 CCTCT CC CC CATCCA
 C G A
 GAM1954 DKFZP434L0117 3' AGCTGCTTACCCCCTCACC 43238 A A _
 GG GA GGGGGTGGGT GCT
 || || ||||| |||||
 CC CT CCCCCATTCTG CGA
 A _ T
 GAM1954 DKFZp434M0331 3' AGCACCTGCCTCCCTCTCT 34658 A _
 GGAGA GGGGGT GGGTGCT
 |||| |||| |||||
 TCTCT CCTCCG CCCACGA
 C T
 GAM1954 DKFZP434N014 3' AGACATCCCCCTCCATCC 61226 GAA T _
 GGA GGGGG GGGTG CT
 || |||| |||| |||||
 CCT TCCCC CCTAC GA
 ACC _ A
 GAM1954 DKFZp547I094 5' AGCATCTTCCCATCCTCC 50552 AAG T
 GGAG GGGG GGGTGCT
 |||| |||| |||||
 CCTC CCCT TCTACGA
 CTA _
 GAM1954 DKFZp564A176 3' AGCACCTCCTACCCTGCTCC 50971 A _ TG
 GGAG AGGG GG GGTGCT
 |||| |||| || |||||
 CCTC TCCC TC CCACGA
 G A CT
 GAM1954 DKFZP564C1940 5' AGCATCTTTGCCCCCCTCTCC 26741 A _
 GGAGA GGGGGT GGGTGCT
 |||| |||| |||||
 CCTCT CCCCCG TCTACGA
 C TT
 GAM1954 DKFZP564D0478 3' AGCACCTGTCCCCTCCTCC 50441 A GT_
 GGAG AGGGG GGGTGCT
 |||| |||| |||||

CCTC TCCCC CCCACGA
 C TGT
 GAM1954 DKFZP564K1964 5' AGCACCTGCCATCCTCTTCC 32069 GA _ TG
 GGA AGGG GG GGTGCT
 ||| |||| || |||||
 CCT TCCT CC CCACGA
 TC A GT
 GAM1954 DKFZP564O1664 3' AGCACCCCTGCCTTCCTC 48664 GA G T
 G GAAGG GG GGGTGCT
 | |||| || |||||
 C CTTCC TC CCCACGA
 TC G _
 GAM1954 DKFZP566N034 3' AGCAGACCCACCTCCTCC 80941 GAA _
 GGA GGGGGTGGGT GCT
 ||| ||||| |||
 CCT CCTCCACCCA CGA
 _ GA
 GAM1954 DKFZP727M111 5' AGCTTTGGTCCCTTCTCC 32054 G GG T
 GGAGAAGGGG T G GCT
 ||||| |||
 CCTCTTCCCT G T CGA
 G TT _
 GAM1954 DKFZp761B0514 3' AGCACCATCCTCTCCTCC 51142 A G
 GGAG AGGGGGTGG TGCT
 ||| ||||| |||
 CCTC TCTCCTACC ACGA
 C _
 GAM1954 DKFZp761D0614 3' AGCACTTTATCATTCTCC 88943 G GGT
 GGAGAA GG GGGTGCT
 |||| || |||||
 CCTCTT CT TTCACGA
 A AT_
 GAM1954 DLGAP1 3' AGCATCTGTCCCCTCCTCC 17641 A TG
 GGAG AGGGGG GGTGCT
 ||| |||| |||||
 CCTC TCCCCT CTACGA
 C GT
 GAM1954 DNAJA3 3' AGCAGAACCCCCATTCCC 61097 A _ GGG
 GG GAA GGGGGT TGCT
 || ||| ||||| |||
 CC CTT CCCCCA ACGA
 _ A AG_
 GAM1954 DOK4 3' TAGCACCCCTGCTGCCCCCCTC 36663 A _ _
 TC GAGA GGGGGT GGGTGCT A
 ||| |||| ||||| |
 CTCT CCCCCG CCCACGA T
 C TCGTC _
 GAM1954 EFA6R 3' AGCACCCCTTCCCTTTCC 31631 A T
 GGAGA GGGGG GGGTGCT
 |||| |||| |||||

			CCTTT CCCTT CCCACGA		
			— C		
GAM1954	EHM2	3'	AGCACCTCTTCCTCTTC	39416	A T
			GGAGA GGGGG GGGTGCT		
			CTTCT CCTTC CCCACGA		
			— T		
GAM1954	FLJ10724	3'	AGTCTTGTCCACCCTCTCC	37037	A _ TG T
			GGAGA GG GGG GG GCT		
			CCTCT CC CCT TC TGA		
			C A GT _		
GAM1954	FLJ10759	5'	AGCACCCCCTCCCTTCTCC	37118	T
			GGAGAAGGGGG GGGTGCT		
			CCTCTCCCTC CCCACGA		
			C		
GAM1954	FLJ11004	3'	AGCACGTTGTCTTCCTCC	37529	AA TG _
			GGAG GGGGG G GTGCT		
			CCTC CTTCT T CACGA		
			— GT G		
GAM1954	FLJ11280	5'	AGCACTAACGGCCCTTGCC	37785	AG G_ G
			GG AAGGG GT GGTGCT		
			CC TTCCC CA TCACGA		
			G_ GG A		
GAM1954	FLJ11413	3'	AGATGTCCCCTCCTCTCC	44953	A T GT _
			GGAGA GGGGG GG G CT		
			CCTCT CCTCC CC T GA		
			— _ TG A		
GAM1954	FLJ11722	3'	AGCAGACCCACCTCTCC	46989	AGGG _
			GGAGA GGTGGG TGCT		
			CCTCT CCACCC ACGA		
			— CAG		
GAM1954	FLJ11773	5'	ACCGTGTGCCCCCTCTCC	41932	A _
			GGAGA GGGGGTG GGT		
			CCTCT CCCCCGT CCA		
			— GTG		
GAM1954	FLJ12448	3'	AGCCCCACCTCCCTCTCC	43474	A T
			GGAGA GGGGGTG GGT		
			CCTCT CCTCCACCC CGA		
			C _		
GAM1954	FLJ12650	3'	AGCATCCTGCCCCCCTGTCC	44816	GAA _
			GGA GGGGGT GGGTGCT		

			CCT CCCCCG CCTACGA		
			GTC T		
GAM1954	FLJ13114	3'	AGCAGTCCCCCACCTCC 44894	AA	T G
			GGAG GGGGG GG TGCT		
			CCTC CCCCC TC ACGA		
			CA _ G		
GAM1954	FLJ13855	3'	AGCACCTTTCTCCCCTCC 43843	AA	T_
			GGAG GGGGG GGGTGCT		
			CCTC CCCTC TCCACGA		
			_ TT		
GAM1954	FLJ13855	3'	AGCACCTGAGCACCTTTCTCC 43842		G _
			GGAGAAGGG GT GGGTGCT		
			CCTCTTTCC CG TCCACGA		
			A AG		
GAM1954	FLJ14437	3'	AGCATGCTCCCCTGCTCC 51797	A	_ GG
			GGAG AGGGG GT GTGCT		
			CCTC TCCCC CG TACGA		
			G T _		
GAM1954	FLJ14708	3'	AGCAATATTACTCCCTCCC 52604	A A	GG_
			GG GA GGGGGTG TGCT		
			CC CT CCCTCAT ACGA		
			_ _ TATA		
GAM1954	FLJ14708	3'	AGCACGCCTGCCTCCCTCTCC 52605	A	_ _
			GGAGA GGGGGT GG GTGCT		
			CCTCT CCTCCG CC CACGA		
			C T G		
GAM1954	FLJ20195	3'	AGCGCGCCCCCACCTCTCC 35211	A	_ T _
			GGAGA GG GGG GG GTGCT		
			CCTCT CC CCC CC CGCGA		
			_ A _ G		
GAM1954	FLJ20559	3'	AGCAAGTTGCTCCCTCTCC 35831	A	TG G_
			GGAGA GGGGG G TGCT		
			CCTCT CCCTC T ACGA		
			_ GT GA		
GAM1954	FLJ21687	3'	AGCACTCGGCCCATCCCC 46288	A A	G
			GG GA GGGG TGGGTGCT		
			CC CT CCCC GCTCACGA		
			C A G		
GAM1954	FLJ21736	3'	AGCACGGCAGCCCGCCTCTCC 46776	A	_ GG_
			GGAGA GG GGGT GTGCT		

			CCTCT CC CCCG CACGA		
			_ G ACGG		
GAM1954	FLJ21777	5'	AGCACCCCCGACCCGCCTCC 50832	AA	_ T
			GGAG GGG GG GGGTGCT		
			CCTC CCC CC CCCACGA		
			CG AG _		
GAM1954	FLJ22386	3'	AGCACCCAGGAGCTTGTCTCC 45041	AG	GG__
			GGAGA GG TGGGTGCT		
			CCTCT TC ACCCACGA		
			GT GAGG		
GAM1954	FLJ23462	3'	AGCACCTGGTTCCTTTCTCC 46220	GG	_
			GGAGAAGGG T GGGTGCT		
			CCTCTTTCC G TCCACGA		
			TT G		
GAM1954	FLJ23590	5'	AGCACCCGCTTCCTCACC 45362	A A	
			GG GA GGGGGTGGGTGCT		
			CC CT CCTTCGCCCACGA		
			A _		
GAM1954	FLJ31300	3'	AGCCATTCTCCCCTTTCCC 58925	A	T _
			GG GAAGGGGG GGGTG CT		
			CC CTTTCCCC CTTAC GA		
			_ T C		
GAM1954	FLJ31300	3'	AGTCTGGCACCCCTTCCC 58926	A	_ G T
			GG GAAGGGG GT GG GCT		
			CC CTTCCCC CG TC TGA		
			_ A G _		
GAM1954	GAL3ST2	3'	AGCGCTGGGCCACCCTCTCC 53481	A	_ G_
			GGAGA GGG GGT GGTGCT		
			CCTCT CCC CCG TCGCGA		
			_ A GG		
GAM1954	H105E3	3'	AGCCAGTCACTCCTTCCC 32488	A	G G _
			GG GAAGGGG TGG TG CT		
			CC CTTCTC ACT AC GA		
			_ _ G C		
GAM1954	HARS2	3'	AGCAGAGCTACCCTTTCC 55863	AAG	G__
			GGAG GGGGTGG TGCT		
			CCTT TCCCATC ACGA		
			_ GAG		
GAM1954	HEYL	3'	GCTCCCACCCTCCTCC 28130	AA	T
			GGAG GGGGGTGGG GC		

			CCTC CTCCCACCC CG		
			___ T		
GAM1954	HHLA3	3'	AGCACCTTGTGACCCCGCCC 23949	AGAA	___
			GG GGGGGT GGGTGCT		
			CC CCCCCA TCCACGA		
			CG___ GTGT		
GAM1954	HSPBP1	5'	AGCGGTGACCACCTTCTCC 25356	G	GGG
			GGAGAAGG GGT TGCT		
			CCTCTTCC CCA GCGA		
			A GTG		
GAM1954	HSPC023	3'	CATCCACCCCCTACCTCC 26756	A_	_
			GGAG AGGGGGTGGG TG		
			CCTC TCCCCACCC AC		
			CA T		
GAM1954	IRF7	5'	AGCCCGGCCACCTCTCC 9621	A _	G T
			GGAGA GG GGGT GG GCT		
			CCTCT CC CCG CC CGA		
			C A G _		
GAM1954	JAM1	3'	AGCTATGTGCCCCATCCTCC 58564	AAG	G _
			GGAG GGGGTG GT GCT		
			CCTC CCGGT TA CGA		
			CTA G T		
GAM1954	KIAA0040	3'	AGCAAAGTGCCTTTCTCC 28487	G	GGG
			GGAGAAGGG GT TGCT		
			CCTCTTCC TG ACGA		
			G AA_		
GAM1954	KIAA0121	3'	AGCGTTTCTATCCCCTCCCC 73044	A A	___
			GG GA GGGGGTGGG TGCT		
			CC CT CCCCTATCT GCGA		
			C _ TT		
GAM1954	KIAA0218	3'	AGCACAACCATCTCCTCTCC 29290	A	___
			GGAGA GGGGGTGG GTGCT		
			CCTCT CCTCTACC CACGA		
			_ AA		
GAM1954	KIAA0240	3'	AGCAGTCCTCCCCCTACCC 94034	AGA	T _
			GG AGGGGG GGG TGCT		
			CC TCCCCC CCT ACGA		
			CA_ T G		
GAM1954	KIAA0256	5'	AGCTGCCACCGCCTCCTCC 65047	A G	GT
			GGAG AGG GGTGG GCT		

			CCTC TCC CCACC CGA		
			C G GT		
GAM1954	KIAA0284	3'	AGCACCCCTACTCACCTGTCC 63800	GA	__ _
			GGA AGGG G GT GGGTGCT		
			CCT TCCC C CA CCCACGA		
			G_ A T T		
GAM1954	KIAA0427	5'	AGCCTCGTCCCTCCCTTCCC 29372	A	__ T
			GG GAAGGGGG TGGG GCT		
			CC CTTCCCTC GCTC CGA		
			__ CCT __		
GAM1954	KIAA0433	5'	CACCTCACCCCTGCCTCC 31500	AA	_
			GGAG GGGGGTG GGTG		
			CCTC TCCCCAC CCAC		
			CG T		
GAM1954	KIAA0481	3'	AGCATCCCCACCCACCCCTCC 72319	AAG_	__
			GGAG GGGGTGGG TGCT		
			CCTC CCCCACCC ACGA		
			CCCA CT		
GAM1954	KIAA0515	3'	AGCGTCTACCTCCTCCTCC 64541	A	GT
			GGAG AGGGGGTGG GCT		
			CCTC TCCTCCATC CGA		
			C TG		
GAM1954	KIAA0564	3'	AGCAAATGTCCTCTTCTCC 66789	GT GG	
			GGAGAAGGGG G TGCT		
			CCTCTTCTCC T ACGA		
			TG AA		
GAM1954	KIAA0618	3'	AGCAGTTCACCCCATCCCC 29841	A AG	_
			GG GA GGGGTGGG TGCT		
			CC CT CCCCACTT ACGA		
			C A_ G		
GAM1954	KIAA0668	3'	AGCACCCCGCCGCTTCCCC 67117	A G GT	
			GG GAAG GG GGGTGCT		
			CC CTTC CC CCCACGA		
			C G GC		
GAM1954	KIAA0676	3'	AGCAGTTACCCCTTATCC 31142	G	G
			GGA AAGGGGGTGG TGCT		
			CCT TTCCCCCATT ACGA		
			A G		
GAM1954	KIAA0843	3'	AGCACCTCCTGACCCTTCCC 30794	A	__ TG
			GG GAAGGG GG GGTGCT		

CC CTTCCC TC CCACGA
 _ AG CT
 GAM1954 KIAA0914 3' AGCATGCAGCCCTTCTGCC 30290 _ G G G
 GG AGAAGG G TG GTGCT
 || ||||| | || |||||
 CC TCTTCC C AC TACGA
 G _ G G
 GAM1954 KIAA0939 3' AGCACCCAGTGCTCCCTCCTCT 62707 A ____
 GGAG AGGGGGT GGGTGCT
 |||| ||||| |||||
 TCTC TCCCTCG CCCACGA
 C TGA
 GAM1954 KIAA0978 3' AGCACTCTTGCCTTCCCC 70988 A G T
 GG GAAGG GG GGGTGCT
 || |||| | |||||
 CC CTTCC TT CTCACGA
 C G _
 GAM1954 KIAA1023 3' AGCCTGGCCCCTGTCTCC 34672 A G T
 GGAGA GGGGGT GG GCT
 |||| ||||| || |||
 CCTCT TCCCCG TC CGA
 G G _
 GAM1954 KIAA1037 3' AGCACCTCGCTCCTCTCC 31134 A GT_
 GGAGA GGGG GGGTGCT
 |||| ||| |||||
 CCTCT CCTC CCCACGA
 _ GCT
 GAM1954 KIAA1056 3' AGTTTTCCCTCCCTTCCC 30310 A T T_
 GG GAAGGGGG GGG GCT
 || ||||| ||| |||
 CC CTTCCCTC CCT TGA
 _ _ TT
 GAM1954 KIAA1096 3' ACTGATGTCCCCTTCTTC 69058 _ G
 GGAGAAGGGG GT GGT
 ||||| || |||
 CTTCTTCCCC TA TCA
 TG G
 GAM1954 KIAA1196 3' AGCACCCCCAGCTACCTCC 62145 AA G_ T
 GGAG GG GG GGGTGCT
 |||| || || |||||
 CCTC TC CC CCCACGA
 CA GA _
 GAM1954 KIAA1196 3' TAGCACCCACCCTCCCCATTTC 62154 AA ____
 C GGAG GGGGGTGGGTGCT A
 ||| ||||| ||||| |
 CCTT CTCCCACCCACGA T
 ACCCC _
 GAM1954 KIAA1364 3' TAGCACCCATGGAGGCCCACT 64357 AG ____
 CTCC GGAGA GGGGT GGGTGCT A
 |||| |||| ||||| |

CCTCT CCCC G CCCACGA T
 CA GAGGTA _
 GAM1954 KIAA1391 3' AGCAGGGGACTCCCTTTCC 67850 A GGG
 GGAGA GGGGGT TGCT
 ||||| ||||| ||||
 CCTTT CCCTCA ACGA
 C GGG
 GAM1954 KIAA1511 3' AGCATTGGCCCTGTCTCC 70725 AG G
 GGAGA GGGGT GGTGCT
 ||||| ||||| |||||
 CCTCT TCCCG TTACGA
 G_ G
 GAM1954 KIAA1668 3' AGCACTTCCGCCCTCACC 67058 A AG _
 GG GA GGGGTGG GTGCT
 || || ||||| ||||
 CC CT CCCC GCC CACGA
 A _ TT
 GAM1954 KIAA1870 5' AGCACCCACAAACCTCCC 50577 A A GG_
 GG GA GG GTGGGTGCT
 || || || |||||
 CC CT CC CACCCACGA
 _ _ AAA
 GAM1954 KIAA1870 5' AGCACCCGGCCCCTACCTCC 50578 A_ G
 GGAG AGGGG TGGGTGCT
 |||| ||||| |||||
 CCTC TCCCC GCCCAGCA
 CA G
 GAM1954 KIAA1870 5' AGCACCTGCCGTCCCCACTCC 50579 AA _ TG
 GGAG GGG GG GGTGCT
 |||| || || |||||
 CCTC CCC CC CCACGA
 AC TG GT
 GAM1954 KIAA1883 3' GGCTGGGGCCCTCCCCCTCC 73810 GAA T _
 GGA GGGGG GGGT GCT
 || ||||| |||| ||||
 CCT CCCCC CCG CGG
 _ T GGT
 GAM1954 KIAA1893 3' AGCACCTCACCTCCCACCCC 73585 AGAA _
 GG GGGGGT GGGTGCT
 || ||||| |||||
 CC CCTCCA CCCACGA
 CCAC CT
 GAM1954 KIAA1910 3' AGCACCCACCCTCTTACC 73713 AG
 GG AAGGGGGTGGGTGCT
 || ||||| |||||
 CC TTCTCCCACCCACGA
 A_
 GAM1954 KIAA1910 3' AGTGCCACCCACCCTCC 73714 AA _ TG
 GGAG GG GGGTGGG CT
 |||| || ||||| ||

CCTC CC CCCACCC GA
 _ A GT
 GAM1954 KIAA1938 3' AGCCTTGCCCCCTTCATCC 93815 _ TG T
 GGA GAAGGGGG GG GCT
 ||| ||||| || |||
 CCT CTTCCCCC TC CGA
 A GT _
 GAM1954 KIAA1938 3' AGTTGTCTCCCCTTCTCC 93817 T GT
 GGAGAAGGGGG GG GCT
 ||||| || |||
 CCTCTTCCCCT CT TGA
 _ GT
 GAM1954 LIP8 5' AGTCTTCCTCCCTTCTCC 89523 TG T
 GGAGAAGGGGG GG GCT
 ||||| || |||
 CCTCTTCCCTC TC TGA
 CT _
 GAM1954 MAD4 3' AGCACCAGCTCCCTGCCC 22270 AGA G
 GG AGGGGGT GGTGCT
 || ||||| |||||
 CC TCCCTCG CCACGA
 CG_ A
 GAM1954 MGC10986 5' AGCGGGTGCCGCTTCTCC 48324 G G GG
 GGAGAAG GG TG TGCT
 ||||| || || |||
 CCTCTTC CC GT GCGA
 G _ GG
 GAM1954 MGC11115 3' AGCCTGGCACCCCCACTCC 51203 AA _ T
 GGAG GGGGGTG GG GCT
 ||| ||||| || |||
 CCTC CCCCCAC TC CGA
 A_ GG _
 GAM1954 MGC12837 3' AGCATCATCCCCTCCATCC 52168 GA_ G
 GGA AGGGGGTG TGCT
 || ||||| |||||
 CCT TCCCCTACT ACGA
 ACC _
 GAM1954 MGC15429 3' CACCCACTTCCCCACCTCC 52209 AA _
 GGAG GGGG GTGGGTG
 ||| ||| |||||
 CCTC CCCC CACCCAC
 CA TT
 GAM1954 MGC15437 5' AGCCCGACTCCCTCCTCC 52841 A G T
 GGAG AGGGGGT GG GCT
 ||| ||||| || |||
 CCTC TCCCTCA CC CGA
 C G _
 GAM1954 MGC17347 5' AGCACCTCCCCCGCCTCC 57172 AA T
 GGAG GGGGG GGGTGCT
 ||| ||||| |||||

CCTC CCCCC TCCACGA
 CG _
 GAM1954 MGC20460 5' AGCACCCGACCCACCCATCC 54900 GAA _ _
 GGA GG GG GTGGGTGCT
 ||| ||| |||||
 CCT CC CC CGCCCACGA
 AC_ A A
 GAM1954 MGC2594 3' AGCACCCCGCCCGCCCGCCTCC 44126 AA_ _ _
 GGAG GG GGGTGGG TGCT
 |||| || ||||| ||||
 CCTC CC CCCGCCC ACGA
 CGC G C
 GAM1954 MGC26954 3' AGCACCCAGACGCCCTCTC 59491 A G _
 GAGA GGG GT GGGTGCT
 |||| ||| || |||||
 CTCT CCC CA CCCACGA
 _ G GA
 GAM1954 MGC4606 3' GCCTGGGCCCTCCTTCCC 44793 A _ _
 GG GAAGG GGGT GGGT
 || ||||| |||| ||||
 CC CTTCC CCCG TCCG
 _ T GG
 GAM1954 moblak 3' CACCCACACCTCTGTCTCC 56386 _ _
 GGAGA AGGGG GTGGGTG
 ||||| ||||| |||||
 CCTCT TCTCC CACCCAC
 G A
 GAM1954 MOV10 3' AGCCATTCCACCCCTCCCC 40933 A A T_
 GG GA GGGGGTGGG GCT
 || || ||||| |||| |||
 CC CT CCCCCACCT CGA
 C _ TAC
 GAM1954 MRPL9 3' AGCACCCCTGATCTCACTCC 49476 AA GT_
 GGAG GGGG GGGTGCT
 |||| |||| |||||
 CCTC CTCT CCCACGA
 A_ AGT
 GAM1954 NEUROG3 3' AGCACTTGTTCTTCTGC 41001 G G TG
 G AGAAGGG G GGTGCT
 | ||||| | |||||
 C TCTTCCT T TCACGA
 G _ GT
 GAM1954 nexilin 3' AGCTCCCCTCCCCTCTCC 58624 A T T
 GGAGA GGGGG GGG GCT
 ||||| ||||| ||| |||
 CCTCT CCCCT CCC CGA
 _ C T
 GAM1954 NKD2 3' AGCCCCCACCCCCACCTCC 53592 AA_ T
 GGAG GGGGGTGGG GCT
 |||| ||||| |||| |||

			CCTC CCCCCACCC CGA		
			CAC C		
GAM1954	NPTXR	3'	AGCACTGAGTCCCCCTCC 27424	AA	TG__
			GGAG GGGGG GGTGCT		
			CCTC CCCCC TCACGA		
			__ TGAG		
GAM1954	NPTXR	3'	AGCCTTGCCCCTTTCTCC 27426		TG T
			GGAGAAGGGGG GG GCT		
			CCTCTTTCCCC TC CGA		
			GT _		
GAM1954	OBTP	3'	AGCCCCTACCCCCACCTCC 34661	AA	T
			GGAG GGGGGTGGG GCT		
			CCTC CCCCCATCC CGA		
			CA C		
GAM1954	OS4	3'	AGCATGTGCCACCCCCTTTCC 20379	A	__
			GGAGA GGGGGTGG GTGCT		
			CCTTT CCCCCACC TACGA		
			_ GTG		
GAM1954	PHF5A	3'	AGCTTGCCACCCCCTCCTCT 52249	A	GT_
			GGAG AGGGGGTGG GCT		
			TCTC TCCCCCACC CGA		
			C GTT		
GAM1954	PHYHIP	3'	AGCTGTCCCTCCTTCTCC 29286		T GT
			GGAGAAGGGGG GG GCT		
			CCTCTTCCTCC CT CGA		
			_ GT		
GAM1954	PIGQ	3'	AGTCGCTGACCCCCGTCCC 16102	A A	G _
			GG GA GGGGGT GGTG CT		
			CC CT CCCCCA TCGC GA		
			_ G G T		
GAM1954	PISD	5'	AGCCTCGCCCCGCCCTCC 27542	AAG	T
			GGAG GGGGTGGG GCT		
			CCTC CCCCCGCTC CGA		
			CCG _		
GAM1954	PLEKHA4	5'	AGCACCACACCGTCCTCT 40879	AA_	GG
			GGAG GG GTGGGTGCT		
			TCTC CC CACCACGA		
			CTG A_		
GAM1954	PP1057	3'	AGCCGTGTACCCCCCTCTCC 49251	A	GT__
			GGAGA GGGGGTGG GCT		

			CCTCT CCCCCACT CGA		
			C GTGC		
GAM1954	PRKRI	5'	AGCGCTTCCACCTCCCCCTCC 21827	AA	___
			GGAG GGGGGTGG GTGCT		
			CCTC CCTCCACC CGCGA		
			CC TT		
GAM1954	PSK	5'	GGTTGTCACCCCTCCCC 32880	A A	GT
			GG GA GGGGGTGG GCT		
			CC CT CCCCCACT TGG		
			C _ GT		
GAM1954	PSMA6	3'	AGCCTCTCCCACTCCTCC 70741	A G T T	
			GGAG AG GGG GGG GCT		
			CCTC TC CCC CTC CGA		
			C A T _		
GAM1954	PTPN3	3'	CACCTCTCTGCCCTCCCTCC 12584	AA	_____
			GGAG GGGGGT GGGTG		
			CCTC CTCCCG TCCAC		
			C_ TCTC		
GAM1954	RAB11B	3'	AGCGCCACCCGCTCCTCC 74333	A G	
			GGAG AG GGGTGGGTGCT		
			CCTC TC CCCACCCGCGA		
			C G		
GAM1954	RAB1B	3'	AGCACCTCCTCCCTTTCCC 49114	AG	TG
			GG AAGGGGG GGTGCT		
			CC TTCCCTC CCACGA		
			CT CT		
GAM1954	RAB40C	3'	AGCCATTGGCCGCTCCTCC 41274	AA G G	_
			GGAG GG GGT GGTG CT		
			CCTC TC CCG TTAC GA		
			C_ G G C		
GAM1954	RASGRP4	3'	AGCCCTGTGCCCCCTCTTC 54743	A	___ T
			GGAGA GGGGGT GGG GCT		
			CTTCT CCCCCG TCC CGA		
			C TG _		
GAM1954	RIL	3'	AGCACTTTATTCTCCTCC 14883	AA	_
			GGAG GGGGGTGG GTGCT		
			CCTC CTCTTATT CACGA		
			_ T		
GAM1954	RIP60	3'	CACCGCAGCCCTCCTTC 26359	A G	_
			GGAG AGGGG TG GGTG		

CTTC TCCCC AC CCAC
 C G G
 GAM1954 RNPS1 3' AGCACACTTTTCCCTTCCC 55484 A T _
 GG GAAGGGGG GG GTGCT
 || ||||| || ||||
 CC CTTCCCTT TC CACGA
 _ T A
 GAM1954 SARS 3' TAGCACCCATTTCATCCCCCTGC 22514 AGA _ _
 CCC GG AGGGGG TGGGTGCT A
 || ||||| ||||| |
 CC TCCCC ACCCACGA T
 CCG TACTT _
 GAM1954 SCAMP5 3' AGCCCCACCCCCACCCTCC 58051 AA_ T
 GGAG GGGGGTGGG GCT
 ||| ||||| |||
 CCTC CCCCCACCC CGA
 CCA C
 GAM1954 SCRG1 5' AGCACCTCCTCTCTTCTCC 24414 TG
 GGAGAAGGGGG GGTGCT
 ||||| |||||
 CCTCTTCTCTC CCACGA
 CT
 GAM1954 SES2 3' AGCACCCCACTCTCCTGCCTCC 49589 A_ _ _
 GGAG AGGGG GTGGG TGCT
 ||| |||| |||| ||||
 CCTC TCCTC CACCC ACGA
 CG T C
 GAM1954 SHANK3 3' AGCACCTGTCTCCTCTTCC 66098 GA GT_
 GGA AGGGG GGGTGCT
 ||| |||| |||||
 CCT TCCTC CCCACGA
 TC TGT
 GAM1954 SLC26A10 5' AGCACCTAACCCTCCTC 56837 A G
 GAG AGGGG TGGGTGCT
 ||| |||| |||||
 CTC TCCCC ATCCACGA
 C A
 GAM1954 SP192 5' AGCTCTTTCCTTCCCC 41615 A T T
 GG GAAGGGGG GGG GCT
 || ||||| ||| |||
 CC CTTCCCT TCT CGA
 C T _
 GAM1954 STK25 3' AGCTCTGCCTCCTCCTCC 22092 A TG T
 GGAG AGGGGG GG GCT
 ||| ||||| || |||
 CCTC TCCTCC CT CGA
 C GT _
 GAM1954 STMN3 3' AGCATCCCCCACTTCTCC 32461 G T
 GGAGAAG GGG GGGTGCT
 ||||| ||| |||||

CCTCTTC CCC CCTACGA
 A _
 GAM1954 STRN3 5' AGCGCGGGGCCACCCTCTCC 28136 A _ GG_
 GGAGA GGG GGT GTGCT
 ||||| ||| ||| |||||
 CCTCT CCC CCG CGCGA
 _ A GGG
 GAM1954 SYNGR4 5' AGCACCCCTGGCTCCCACCTCC 25863 AA _
 GGAG GGGGGT GGGTGCT
 |||| ||||| |||||
 CCTC CCCTCG CCCACGA
 CA GT
 GAM1954 TAO1 5' GGTTGTCACCCCCTCCCC 17719 A A GT
 GG GA GGGGGTGG GCT
 || || ||||| |||
 CC CT CCCCCACT TGG
 C _ GT
 GAM1954 TLOC1 5' GGTTTCACCGCCCCCTCC 13775 AA G T
 GGAG GG GGTGGG GCT
 |||| || ||||| |||
 CCTC CC CCACCT TGG
 CC G T
 GAM1954 TM4-B 5' AGCATTGGCGCCCCTTCCTC 25888 GA _ G
 G GAAGGGG GT GGTGCT
 | ||||| || |||||
 C CTCCCC CG TTACGA
 TC G G
 GAM1954 TOLLIP 3' AGCACCCGTGTCGCCCCCTCCC 39191 A A _
 GG GA GGGGGT GGGTGCT
 || || ||||| |||||
 CC CT CCCCCG CCCACGA
 _ _ CTGTG
 GAM1954 TOR2A 3' AGCACAAAGTCCCCTCCCC 56181 A A GG_
 GG GA GGGGGT GTGCT
 || || ||||| |||||
 CC CT CCCCTG CACGA
 C _ AAA
 GAM1954 TRIM29 3' AGCACAGCCACCCATCTCC 25004 A _ GG
 GGAGA GGG GGT GTGCT
 ||||| ||| ||| |||||
 CCTCT CCC CCG CACGA
 A A A_
 GAM1954 TU3A 3' AGCACCCAGCCCTCCTGCTCC 24175 A _ _
 GGAG AGG GGG TGGGTGCT
 |||| ||| ||| |||||
 CCTC TCC CCC ACCCACGA
 G T G
 GAM1954 YAP1 5' AGCCGTCGCCGCTTCTCC 21457 G G GT
 GGAGAAG GG TGG GCT
 ||||| || ||| |||

			CCTCTTC CC GCT CGA		
			G _ GC		
GAM1954	YARS	3'	AGCATCTTCCCCCTTCTTC 14852	T_	
			GGAGAAGGGGG GGGTGCT		
			CTTCTTCCCC TCTACGA		
			CT		
GAM1954	ZAP3	5'	AGCACTGCTTCCTACTCC 77733	A	TG G
			GGAG AGGGGG G TGCT		
			CCTC TCCTTC C ACGA		
			A GT_		
GAM1954	ZNF213	3'	AGCACTAACGCCCTGCTCC 65696	A	G G
			GGAG AGGG GT GGTGCT		
			CCTC TCCC CA TCACGA		
			G G A		
GAM1954	LOC115399	3'	AGCACCTGGTCCCTTCACC 73811	A	G
			GG GAAGGGG TGGGTGCT		
			CC CTTCCCT GTCCACGA		
			A G		
GAM1954	LOC115574	3'	AGCACCAGCTGTCCACCTCC 73846	AA	_ G
			GGAG GGG GGT GGTGCT		
			CCTC CCC TCG CCACGA		
			CA TG A		
GAM1954	LOC118976	5'	GGTTCGACGCCCTCCTCC 74389	A	G G T
			GGAG AGGG GT GG GCT		
			CCTC TCCC CA CT TGG		
			C G G _		
GAM1954	LOC120939	3'	GGCCTGACCCCTGCTCC 76766	A	G T
			GGAG AGGGGGT GG GCT		
			CCTC TCCCCA TC CGG		
			G G _		
GAM1954	LOC121133	5'	AGCACTTCCACCCCTCCTCT 76509	A	_
			GGAG AGGGGGTGG GTGCT		
			TCTC TCCCCACC CACGA		
			C TT		
GAM1954	LOC124045	3'	AGCCACCGCCCCCTTCTCC 76535		GT
			GGAGAAGGGGGTGG GCT		
			CCTCTTCCCCCGCC CGA		
			AC		
GAM1954	LOC124045	3'	AGCCGCGCCCCCTTCTCC 76536		GT
			GGAGAAGGGGGTGG GCT		

	CCTCTTCCCCCGCC CGA		
	GC		
GAM1954 LOC124045 3'	GCCGTGGCCCCCTTCTCC 76538	G__	
	GGAGAAGGGGGT GGT		
	CCTCTTCCCCCG CCG		
	GTG		
GAM1954 LOC124045 3'	GCCGTGGCCCCCTTCTCC 76539	G__	
	GGAGAAGGGGGT GGT		
	CCTCTTCCCCCG CCG		
	GTG		
GAM1954 LOC124045 3'	GCCGTGGCCCCCTTCTCC 76540	G__	
	GGAGAAGGGGGT GGT		
	CCTCTTCCCCCG CCG		
	GTG		
GAM1954 LOC124460 3'	AGTGGGTCCCCCCTACC 76555	AGA T __	
	GG AGGGGG GGG TGCT		
	CC TCCCC CCT GTGA		
	A__ _ GG		
GAM1954 LOC127702 3'	AGCACTCTTCCCTTTCTCC 75982	T	
	GGAGAAGGGGG GGGTGCT		
	CCTCTTCCCT CTCACGA		
	T		
GAM1954 LOC130497 3'	AGCTCCACCTCCTCCTCC 75445	A T	
	GGAG AGGGGGTGGG GCT		
	CCTC TCCTCCACCC CGA		
	C T		
GAM1954 LOC130617 5'	AGCACTCGTCGCTTCTCC 57937	G G GT	
	GGAGAA G G GGGTGCT		
	CCTCTT C C CTCACGA		
	_ G TG		
GAM1954 LOC143308 5'	AGCACCTCTCCTACTCC 83832	A T	
	GGAG AGGGGG GGGTGCT		
	CCTC TCCTCT CCCACGA		
	A _		
GAM1954 LOC144501 3'	CACCCGCATCCCTTCCTCC 84026	_ _	
	GGAG AAGGGG GTGGGTG		
	CCTC TTCCCT CGCCCAC		
	C A		
GAM1954 LOC145231 3'	AGTGCCACCCACCTCCTCC 84239	A _ GT	
	GGAG AGG GGGTG GCT		

CCTC TCC CCCACC CGA
 C A GT
 GAM1954 LOC145581 3' AGCACCCTTCTCCTCTC 77792 A TG_
 GAGA GGGGG GGTGCT
 ||| ||| |||
 CTCT CCTCT CCACGA
 _ TCA
 GAM1954 LOC145652 3' AGCACCCATTGTTTTCCC 84404 A G
 GG GAAGG GGTGGGTGCT
 || ||| |||||
 CC CTTTT TTACCCACGA
 _ G
 GAM1954 LOC145717 3' AGATTCCCACCCCCCTCC 67369 AA TG_
 GGAG GGGGGTGGG CT
 ||| ||||| ||
 CCTC CCCCCACCC GA
 _ TTA
 GAM1954 LOC146669 3' AGCACCATGTCCCTTCCC 78657 A GTG
 GG GAAGGGG GGTGCT
 || ||||| |||
 CC CTTCCCT CCACGA
 _ GTA
 GAM1954 LOC146958 5' AGCCTTTCTCCCCTTCCC 84939 A _TG T
 GG GAAGGGG G GG GCT
 || ||||| | |||
 CC CTTCCCC C TC CGA
 _ TTT _
 GAM1954 LOC147160 5' AGCACCTCGGCCTCCTTC 85065 _
 GAAGGGGGT GGGTGCT
 ||||| |||||
 CTTCTCCG TCCACGA
 GC
 GAM1954 LOC148029 5' AGCACCCAGATGCTCCTTCCTC 79318 GA G__
 G GAAGGGG TGGGTGCT
 | ||||| |||||
 C CTTCTC ACCCACGA
 TC GTAG
 GAM1954 LOC148183 5' CACACACACCCCTCTGCC 85261 _ A _ G
 GG AGA GGGG GTG GTG
 || ||| ||| ||| |||
 CC TCT CCCC CAC CAC
 G _ A A
 GAM1954 LOC148397 5' AGCACCCAGCGCCTCCTCC 79556 AA G_
 GGAG GGG G TGGGTGCT
 ||| ||| | |||||
 CCTC TCC C ACCCACGA
 C_ G G
 GAM1954 LOC148525 3' AGCACCTATCCCTTTTCC 79624 G
 GGAGAAGGGG TGGGTGCT
 ||||| |||||

CCTTTTCCCT ATCCACGA

GAM1954 LOC148764 5' AGCCCCACCCACCTTCTCC 79732 _ T
GGAGAAGG GGGTGGG GCT
||||| ||||| ||
CCTCTTCC CCCACCC CGA

A _

GAM1954 LOC149461 3' AGCACCCACCCTGCAATCT 80199 GAAG
GGA GGGGTGGGTGCT
|| |||||
TCT TCCCACCCACGA

AACG

GAM1954 LOC149506 5' AGCATCCCCACCCCTCTCC 85623 AG _
GGAGA GGGGTGGG TGCT
|||| ||||| ||
CCTCT CCCCACCC ACGA

_ CT

GAM1954 LOC150157 5' AGCACCTACGCCTTCCCC 86021 A G G
GG GAAG G GTGGGTGCT
|| ||| | |||||
CC CTTC C CATCCACGA

C _ G

GAM1954 LOC150951 5' AGCCTTCACCCACCCCTCC 86341 AAG T
GGAG GGGGTGGG GCT
|||| ||||| ||
CCTC CCCCATT CGA

CCA C

GAM1954 LOC151278 5' AGCCGGTTCACCTCCTTCTCC 81010 GG _
GGAGAAGGGGGTG T GCT
||||||| | ||
CCTCTCCTCCAC G CGA

TT GC

GAM1954 LOC151556 5' AGCACCAGCTCCCTTCTCC 81074 G
GGAGAAGGGGGT GGTGCT
||||||| |||||
CCTCTCCCTCG CCACGA

A

GAM1954 LOC153027 3' AGCACACTTTTCCCTTCCC 68028 A T _
GG GAAGGGGG GG GTGCT
|| ||||| || |||||
CC CTTCCCTT TC CACGA

_ T A

GAM1954 LOC153592 3' ACCCGGTGCCTCCTCCTCC 87245 A _
GGAG AGGGGGT GGGT
|||| ||||| ||
CCTC TCCTCCG CCCA

C TGG

GAM1954 LOC153770 3' AGCAAGATAACTCCTCCTCC 81812 A G GG_
GGAG AGGGG TG TGCT
|||| |||| || |||||

	CCTC TCCTC AT ACGA		
	C A AGA		
GAM1954 LOC153810 5'	AGCATTGTGCCCCTGCCC	81814	AGAA _
	GG GGGGGTG GGTGCT		
	CC TCCCCGT TTACGA		
	CG_ G		
GAM1954 LOC155179 3'	AGCCTGGCCCCTGTCTCC	82221	A G T
	GGAGA GGGGGT GG GCT		
	CCTCT TCCCCG TC CGA		
	G G _		
GAM1954 LOC157349 3'	AGCCACTGACCCCCTCTCC	82327	A G _
	GGAGA GGGGGT GGTG CT		
	CCTCT CCCCCA TCAC GA		
	_ G C		
GAM1954 LOC158308 5'	AGCAAGCGCACCTCTCC	88064	A G GG
	GGAGA GGG GTG TGCT		
	CCTCT CCC CGC ACGA		
	_ A GA		
GAM1954 LOC158434 5'	AGCCGCCTGACCCACTCCTCC	88158	A _ GT _
	GGAG AG GGG GGGTG CT		
	CCTC TC CCC TCCGC GA		
	C A AG C		
GAM1954 LOC160376 5'	AGCACCTGGTTCTTCTCT	88437	GGT
	GGAGAAGGG GGGTGCT		
	TCTCTTCTT TCCACGA		
	GG_		
GAM1954 LOC162333 5'	AGCACCGCTTCCACCTCC	88486	AA G
	GGAG GGGGGTGG TGCT		
	CCTC CCTTCGCC ACGA		
	CA _		
GAM1954 LOC195977 3'	AGCACCATGTCTTCTCT	88930	G _
	GGAGAAGGG GTG GGTGCT		
	TCTCTTCCT TAC CCACGA		
	G A		
GAM1954 LOC196500 3'	CACCCACCCACCTCGTTTCC	89081	_ _
	GGAGA AGG GGGTGGGTG		
	CCTTT TCC CCCACCCAC		
	GC A		
GAM1954 LOC196890 5'	AGCACCTACACCTTCCCC	91223	A GG
	GG GAAGG GTGGGTGCT		

		CC CTTCC CATCCACGA		
		C A_		
GAM1954	LOC199986 5'	AGCCTCCCTCCCCTCTCC	91504	A T T_
		GGAGA GGGGG GGG GCT		
		CCTCT CCCCT CCC CGA		
		_ _ TC		
GAM1954	LOC200010 3'	AGCACCTTTGCTCCCCCTTATC	91524	G T_____
	C	GGA AAGGGGG GGGTGCT		
		CCT TTCCCCC TCCACGA		
		A TCGTT		
GAM1954	LOC200225 5'	AGCTCTTCCCCACCTCCTCC	91572	A _ TG T
		GGAG AGG GGG GG GCT		
		CCTC TCC CCC TC CGA		
		C A CT T		
GAM1954	LOC200473 5'	AGCAATGCTGCCTTCTCC	91644	G GG
		GGAGAAGG GGTG TGCT		
		CCTCTTCC TCGT ACGA		
		G A_		
GAM1954	LOC200734 3'	AGTTTCCCTCCCTTCTCC	90271	T T
		GGAGAAGGGGG GGG GCT		
		CCTCTTCCCTC CCT TGA		
		_ T		
GAM1954	LOC201324 5'	AGCACCTTCTGCCCTTCCC	69096	A _ T
		GG GAAGGG GG GGGTGCT		
		CC CTTCCC TC TCCACGA		
		_ G T		
GAM1954	LOC202050 5'	AGTCATCCCCTCTTCTCC	90625	TG _
		GGAGAAGGGGG GGTG CT		
		CCTCTTCTCCC CTAC GA		
		_ T		
GAM1954	LOC203232 5'	AGCAATTTTCTCCTTCTCC	71913	TGGG
		GGAGAAGGGGG TGCT		
		CCTCTTCCTCT ACGA		
		TTTA		
GAM1954	LOC221751 5'	AGCACTTTATTCCCTCTCC	93674	A _
		GGAGA GGGGGTG GTGCT		
		CCTCT CCCTTATT CACGA		
		_ T		
GAM1954	LOC253842 5'	AGCCTTTCCCTCCCTCTCC	99233	A _ TG T
		GGAGA GG GGG GG GCT		

	CCTCT CC CCC TC CGA		
	C T TT _		
GAM1954 LOC253985 5'	AGCACTTCATCCTTCTTC 98239	GGT	
	GGAGAAGGG GGGTGCT		
	CTTCTTCCT TTCACGA		
	AC_		
GAM1954 LOC254263 3'	AGTCTGCCCTCCCCTCTCC 96365	A T _	
	GGAGA GGGGG GGGT GCT		
	CCTCT CCCCT CCCG TGA		
	_ _ TC		
GAM1954 LOC254531 3'	AGCCTCTCACCCCTCCTCC 96659	A T_	
	GGAG AGGGGGTGGG GCT		
	CCTC TCCCCCACTC CGA		
	C TC		
GAM1954 LOC254873 3'	AGCACTTTAACCTCTCT 96210	A GGT	
	GGAGA GGG GGGTGCT		
	TCTCT CCC TTCACGA		
	_ AAT		
GAM1954 LOC254946 3'	AGCATAGGGACCCCTTCTCC 97757	GTGG_	
	GGAGAAGGGG GTGCT		
	CCTCTTCCCC TACGA		
	AGGGA		
GAM1954 LOC255518 5'	AGCACCCGCCAGCCACCTCC 98651	AA G_	
	GGAG GG GGTGGGTGCT		
	CCTC CC CCGCCACGA		
	CA GA		
GAM1954 LOC256369 3'	AGCATGGATCTCTTCTCC 96609	GTGG	
	GGAGAAGGGG GTGCT		
	CCTCTTCTCT TACGA		
	AGG_		
GAM1954 LOC256901 3'	AGCACCACTTCCCCCTTCTCC 98419	TG__	
	GGAGAAGGGGG GGTGCT		
	CCTCTTCCCC CCACGA		
	TTCA		
GAM1954 LOC257541 5'	GGTCCACGCCCCCTCTCC 99598	A _ TG	
	GGAGA GGGG GTGGG C		
	CCTCT CCCC CACCT G		
	C G GT		
GAM1954 LOC56270 3'	AGCACCCACCACCTGCCGCC 39502	AGAA _	
	GG GGG GGTGGGTGCT		

CC TCC CCACCCACGA
 GCCG A
 GAM1954 LOC57115 3' CACCTTTTGCCCTCCTCC 40207 AA ____
 GGAG GGGGGT GGGTG
 ||| ||||| |||||
 CCTC CTCCCG TCCAC
 ____ TTT
 GAM1954 LOC57406 3' AGCATCTGCTCCCATCCCC 40713 A A TG
 GG GA GGGGG GGTGCT
 || || ||||| |||||
 CC CT CCCTC CTACGA
 C A GT
 GAM1954 LOC90010 5' AGCTGCTCACCCCCTTTCCC 61720 AG _
 GG AAGGGGGTGGGT GCT
 || ||||| ||||| |||||
 CC TTCCCCCACTCG CGA
 CT T
 GAM1954 LOC90019 3' AGCACCACTGCCCTTGTCC 57521 G GTG__
 GGA AAGGGG GGTGCT
 ||| ||||| |||||
 CCT TTCCCC CCACGA
 G GTCCA
 GAM1954 LOC90139 3' AGCACCCAATGTCCTCCC 56263 A A G _
 GG GA GGG GT GGGTGCT
 || || || || |||||
 CC CT CCT TA CCCACGA
 _ _ G A
 GAM1954 LOC91464 5' AGCACCCAGGGACCCCCTTTCC 66709 A ____
 GGAGA GGGGGT GGGTGCT
 ||||| ||||| |||||
 CCTTT CCCCCA CCCACGA
 _ GGGA
 GAM1954 LOC91632 5' AGCACCCCACCCCTCCCC 67313 A A GT
 GG GA GGGG GGGTGCT
 || || || || |||||
 CC CT CCCC CCCACGA
 C _ AC
 GAM1954 LOC92078 5' AGCACCTTCTGGCCTGCTCC 68589 A _ T
 GGAG AGG GGG GGGTGCT
 |||| || || |||||
 CCTC TCC TCT CCCACGA
 G GG T
 GAM1954 LOC92249 3' AGCTGGTACCCCCTCTCC 69105 A GGT
 GGAGA GGGGGTG GCT
 ||||| ||||| |||||
 CCTCT CCCCCAT CGA
 _ GGT
 GAM1954 LOC92661 3' CACCCAGCCTCCTGCTCC 70620 A _
 GGAG AGGGGG TGGGTG
 |||| ||||| |||||

CCTC TCCTCC ACCCAC
 G G
 GAM1955 ALOX12 3' AAGGCAGCCACAGACAACATGG 7350 C ATTA ____
 CCGTGTTG CT GC CCTT
 ||||| || || |||
 GGTACAAC GA CG GGAA
 A CAC_ AC
 GAM1955 ITCH 3' GCCTGGGCAACATAGGGA 49755 CG TTA
 TCCC TGTTGCCTA GC
 ||| ||||| ||
 AGGG ACAACGGGT CG
 AT C_
 GAM1955 FLJ21276 3' AAGGGAGCTGGCAACACCAGGA 45256 CC TATTAG
 TCC GTGTTGCC CCCTT
 || ||||| |||
 AGG CACAACGG GGGAA
 AC TCGA_
 GAM1955 GT650 3' TGATAGGCACACGAGGA 54555 C T
 TCC CGTGT GCCTATTA
 ||| ||| |||||
 AGG GCACA CGGATAGT
 A _
 GAM1955 KIAA1036 3' AAGGGCTGGGGGGCTACACAAG 30482 CC T A
 GA TCC GTGT GCCT TTAGCCCTT
 ||| ||| ||| |||||
 AGG CACA CGGG GGTCGGGAA
 AA T G
 GAM1955 KIAA1364 3' AGGACGGGCACACGGGGA 64342 T ATTAGC
 TCCCCGTGT GCCT CCT
 ||||| ||| |||
 AGGGGCACA CGGG GGA
 _ CA____
 GAM1955 MGC10999 3' GCCTAGGCAACATAGGGA 51197 CG TTA
 TCCC TGTTGCCTA GC
 ||| ||||| ||
 AGGG ACAACGGAT CG
 AT C_
 GAM1955 POLR3F 5' GGCTGCGACACGAGGA 60619 C CTATT
 TCC CGTGTTGC AGCC
 || ||||| |||
 AGG GCACAGCG TCGG
 A _____
 GAM1955 LOC253019 3' GAGGGCTGAGCAACTCAGG 97109 GT_ CTA
 CC GTTGC TTAGCCCTT
 || ||| |||||
 GG CAACG AGTCGGGAG
 ACT ____
 GAM1956 APOC1 3' GCCATGTGGCCCCAGGTGCCAC 9702 ATC G A
 GTGG CC TGG GCCACATGGC
 ||| || ||| |||||

CACC GG ACC CGGTGTACCG
 GT_ _ C
 GAM1956 EGFL5 5' CCATGTGACTGTAGTCCAC 87910 CCCG G C
 GTGGAT TG AG CACATGG
 ||||| || |||||
 CACCTG AT TC GTGTACC
 _ _ G A
 GAM1956 RFX2 3' CCATGTGGGAGGGACCCA 7155 A GTGGAG
 TGG TCCC CCACATGG
 ||| ||| |||||
 ACC AGGG GGTGTACC
 C AG_ _
 GAM1956 TBXA2R 5' CCATGTGAGAAGGATCCAC 8350 CGTGGAGC
 GTGGATCC CACATGG
 ||||| |||||
 CACCTAGG GTGTACC
 AAGA_ _
 GAM1956 XK 3' CCATATGGAATAGGGATCCAC 41155 GTGGAG C
 GTGGATCCC CCA ATGG
 ||||| ||| |||
 CACCTAGGG GGT TACC
 ATAA_ _ A
 GAM1956 FRAT1 3' CCATGTGGCCACAATCCAC 19688 CCCG GA
 GTGGAT TG GCCACATGG
 ||||| || |||||
 CACCTA AC CGGTGTACC
 _ _ AC
 GAM1956 LOC147118 5' CCATGGCACCTCTCCACGGGGT 85062 A_ _ _ ACAT
 CCAC GTGGATCCCGTGG GCC GG
 ||||| ||| ||
 CACCTGGGGCACC CGG CC
 TCTCCA_ _ TAC
 GAM1956 LOC205095 3' GCCACGCAACGAGGGGGCCAC 92385 AT G_ GA CACA
 GTGG CCC TG GC TGGC
 ||| ||| || |||
 CACC GGG GC CG ACCG
 CG GA AA C_ _
 GAM1957 CRLF1 3' TGAGTTGCCTAGAACCCCTGC 17642 AGCG CT CTA
 GCAG TC GGCA ACTCA
 ||| || ||| |||
 CGTC AG CCGT TGAGT
 CCCA AT _ _
 GAM1957 DPEP1 3' AGATGCCAGGAGCCCTGC 16618 A G _
 GCAG GC TCCTGGCA CT
 ||| || ||||| ||
 CGTC CG AGGACCGT GA
 C _ A
 GAM1957 SLC25A12 3' TGAATTAGTGTCTAGACTCTG 14920 CGTCCT C
 C GCAGAG GGCATAA TCA
 ||||| ||||| |||

			CGTCTC	TTGTGATT	AGT		
			AGATC_	A			
GAM1957	TBXA2R	5'	TGAACCA	GTGCCAGCCTGCCCT	8369	A TC	AAC
	GT		GCAG	GCG CTGGCACT	TCA		
			TGTC	CGT GACCGTGA	AGT		
			C	CC	CCA		
GAM1957	ADAR3	3'	GAGTTAGCGCCGACTCTT	38634	C CT	A	
			GAG	GTC GGC CTA	ACTC		
			TTC	CAG CCG GATTGAG			
			T	_	C		
GAM1957	ARH2	5'	AGGCCAGGACGCTCCGC	57373	A	A	
			GC	GAGCGTCCTGGC	CT		
			CG	CTCGCAGGACCG	GA		
			C	_			
GAM1957	GMPPB	5'	GAGTCAGTGCCAGAGCCTC	97449	C TC	A	
			GAG	G CTGGCACT	ACTC		
			CTC	C GACCGTGA	TGAG		
			_	GA	C		
GAM1957	KIAA0275	3'	TGAGACGGGCCAGGACGCCAG	29335	AGA	A AA	
	C		GC	GCGTCCTGGC	CT CTCA		
			CG	CGCAGGACCG	GG GAGT		
			ACC	_	CA		
GAM1957	LOC200812	5'	TGAGCTCCACATCCAGGATGCC	90305	A	CACTAA_	
	CTGC		GCAG	GCGTCCTGG	CTCA		
			CGTC	CGTAGGACC	GAGT		
			C	TACACCTC			
GAM1957	LOC222169	5'	TGAGCGGCGGCCAGGCCGCTCT	95731	T	ACTAA	
	GC		GCAGAGCG	CCTGGC	CTCA		
			CGTCTCGC	GGACCG	GAGT		
			C	GCGGC			
GAM1958	DEC1	3'	GAACCTTACCTCCCCACAATA	34276	AACC_	A	
	CA		TGTGTTGTGG	TGAG	TTC		
			ACATAACACC	ATTC	AAG		
			CCCTCC	C			
GAM1958	EBAG9	3'	AGAAATCTCAGCTCCACAACCC	16156	T	AC	C
	A		TG	GTTGTGGA	CTGAGATT	CT	
			AC	CAACACCT	GA	CTCTAA	GA
			C	C_	A		
GAM1958	LGALS3BP	3'	TCCAGACTCCACAACAC	69861	AC	A	
			GTGTTGTGGA	CTG	GA		

			CACAACACCT GAC CT		
			CA _		
GAM1958	MMP19	5'	AGAAATCTCAGGTCAGAGGCAC 43309	GTG A	C
			GTGTT GA CCTGAGATT CT		
			CACGG CT GGA CTCTAA GA		
			AGA _ A		
GAM1958	MMP19	5'	AGAAATCTCAGGTCAGAGGCAC 11616	GTG A	C
			GTGTT GA CCTGAGATT CT		
			CACGG CT GGA CTCTAA GA		
			AGA _ A		
GAM1958	NFIC	3'	AGGAATCCCAGGGGGCAGCACA 20011	GGAA A	
			TGTGTTGT CCTG GATTCCT		
			ACACGACG GGAC CTAAGGA		
			GG_ C		
GAM1958	CYP3A7	5'	GGAAAGCTCCACACACACA 7545	_ AC GAGA	
			TGTGT TGTGGA CT TTCC		
			ACACA ACACCT GA AAGG		
			C C_ _		
GAM1958	FLJ21007	5'	GAATCTCAGGCTGCACCA 48647	T TG AA	
			TG TG G CCTGAGATTC		
			AC AC C GGA CTCTAAG		
			C GT _		
GAM1958	FLJ22477	3'	GGAATCTCAGATCTCAA 45676	T AC	
			TTG GGA CTGAGATTCC		
			AAC TCT GACTCTAAGG		
			_ A_		
GAM1958	KIAA0872	3'	AATCTCAGGCCGGGCAC 30732	G AA	
			GTGTT TGG CCTGAGATT		
			CACGG GCC GGA CTCTAA		
			_ _		
GAM1958	MAGEB1	3'	GAACCTCACACAACATA 11427	GAACC A	
			TGTGTTGTG TGAG TTC		
			ATACAACAC ACTC AAG		
			_ _ C		
GAM1958	MGC12538	3'	CTGAGCTCCATAACACA 52203	AC G	
			TGTGTTGTGGA CT AG		
			ACACAATACCT GA TC		
			C_ G		
GAM1958	MRPL35	3'	AGGAATCTCAAGTGGGACAAAC 34017	G GGA C	
	A		TGT TTGT AC TGAGATTCCT		

		ACA AACA TG ACTCTAAGGA		
		_ GGG A		
GAM1958	LOC145945 5'	AGGAATCTCAAAAACAAACAAA 84562	G	GGAACC_
	CA	TGT TTGT TGAGATTCCT		
		ACA AACA ACTCTAAGGA		
		_ AACAAAA		
GAM1958	LOC157697 5'	AGAAATCTCAGCGACAGCACA 82461	GGAAC	C
		TGTGTTGT CTGAGATT CT		
		ACACGACA GACTCTAA GA		
		GC_ A		
GAM1958	LOC169436 5'	AGGAATCTCAAACCCTCCAACA 83616	TG AACC	
	T	GTGTTG G TGAGATTCCT		
		TACAAC C ACTCTAAGGA		
		CT CCAA		
GAM1958	LOC57406 3'	CTCAGGTTCCACACACA 40714	T	
		TGTGT GTGGAACCTGAG		
		ACACA CACCTTGGA		
		CTC		
GAM1958	LOC92360 3'	TGGGAAATTCCACA	ACTCA 69627	T _
		TG GTTGTGGAA CCTG		
		AC CAACACCTT GGGT		
		T AAA		
GAM1959	ELF3 3'	TGACCTTGACCTTGACCAA 16685	T	GAT AAA
		TTGGT CAAGG GG GTCA		
		AACCA GTTCC TC CAGT		
		_ AGT _		
GAM1959	JAK2 3'	TGACCTTCATTCTGAGACCAA 18318	CAA	AA
		TTGGT GGGATGGA GTCA		
		AACCAG TCTTACTT CAGT		
		AG_ C_		
GAM1959	SLC10A2 5'	ACTCTCTGTCTTGACCAA 6590	CAA	A
		TTGGT GGGATGGA AGT		
		AACCAG TTCTGTCT TCA		
		_ C		
GAM1959	FLJ10803 3'	GTGACTTTCAGTTAAAGCCAA 37205	CAAGG	G
		TTGGT GAT GAAAGTCAC		
		AACCGA TTG CTTTCAGTG		
		AA_ A		
GAM1959	KIAA1958 5'	GTGACTTTGAACCCCAAACC 82788	CAA	ATGG
		GGTT GGG AAAGTCAC		

CCAA CCC TTTCAGTG
 A__ CAAG
 GAM1959 MARCKS 3' ACTTTCCACCCTGCCCA 11411 TTCA A
 TGG AGGG TGGAAAGT
 ||| |||| |||||
 ACC TCCC ACCTTTCA
 CG__ _
 GAM1959 TUB 5' GTGGGACCATCCCTTAAACC 13898 C AAAG
 GGTT AAGGGATGG TCAC
 |||| ||||| ||||
 CCAA TTCCCTACC GGTG
 A AG__
 GAM1959 LOC80298 3' ACTTTTACCTTGAACCA 48062 GATG
 TGGTTCAAGG GAAAGT
 ||||| |||||
 ACCAAGTTCC TTTTCA
 A__
 GAM1960 ACCN2 3' CTGCTCCTCCTATCCCATTGCC 39625 __ _ A A
 CTCT AGAGGGCAA GGA AGGAG GA CAG
 ||||| || |||| || ||||
 TCTCCCGTT CCT TCCTC CT GTC
 AC A _ C
 GAM1960 ACN 3' CTGTCCTGCAGCCCTTGCCTCT 31068 G A__ G
 AGAGG CAAGG AGGA AG
 |||| |||| |||| ||
 TCTCC GTTCC TCCT TC
 _ CGACG G
 GAM1960 AMN 3' CTCCCCTTCCTTTCCCCCT 48920 A C A
 AG GGG AAGGAAGG GAG
 || |||| ||||| ||||
 TC CCC TTCCTTCC CTC
 C T C
 GAM1960 ARHGEF1 3' TCTCTCCCTCCTGCCCTCT 17482 A A
 AGAGGGCA GGA GGAGAGA
 ||||| || |||||
 TCTCCCGT CCT CCTCTCT
 _ C
 GAM1960 AXUD1 3' CTCCACTTCCTGCCCTCT 53441 A GA
 AGAGGGCA GGAAG GAG
 ||||| |||| ||||
 TCTCCCGT CCTTC CTC
 _ AC
 GAM1960 B4GALT5 3' TTTTCCTCCCCCGCCCTT 17695 AA A
 GAGGGC GG AGGAGAG
 ||||| || |||||
 TTCCCG CC TCCTTTT
 CC C
 GAM1960 C1orf6 3' CTGTCAATCCTTACCCTCT 39695 C AG G
 AGAGGG AAGGA GA AG
 ||||| |||| || ||

		TCTCCC TTCCT CT TC		
		A AA G		
GAM1960	CCKBR	3' CTGCCCTCTCCTTCCTTACCC 7415	C	AA
		GGG AAGGAAGGAGAG CAG		
		CCC TTCCTTCCTCTC GTC		
		A CC		
GAM1960	CD3E	3' TCCCTCCTCCCTGCCTTCT 7421	A A A	
		AGAGGGCA GGA GGAG GA		
		TCTTCCGT CCT CCTC CT		
		C _ C		
GAM1960	CHP	5' TTCCCTCCCTCCTTCCCTC 24324	C	A A
		GAGGG AAGGA GGAG GAA		
		CTCCC TTCCT CCTC CTT		
		_ C C		
GAM1960	CHST1	3' CTGCCCCCTCCTGCCCGCCCTT 14698	AA A	AGAA
		GAGGGC GG AGGAG CAG		
		TTCCCG CC TCCTC GTC		
		C_ G CCCC		
GAM1960	CLN6	3' CTGTCCTGTCACTGCCCTCT 35837	AG _	G
		AGAGGGCA GA AGGA AG		
		TCTCCCGT CT TCCT TC		
		CA G G		
GAM1960	CMRF35	3' CTCCCTCCCGGGCTGCTCTCT 22906	A_____	A
		AGAGGGCA GGA GGAG		
		TCTCTCGT CCT CCTC		
		CGGGC C		
GAM1960	CNP	3' CTGGGGTGCCCTCCACTGCCCT 53620	A_	A AGAGAA
	CT	AGAGGGCA GGA GG CAG		
		TCTCCCGT CCT CC GTC		
		CA C GTGGG_		
GAM1960	COL4A6	3' CTCTGCCCTTGCCCTC 54438	AA _	
		GAGGGCAAGG GG AGAG		
		CTCCCGTTCC CC TCTC		
		_ G		
GAM1960	CRABP2	3' CTGCCCCCTCCGTCCCACCCCC 10294	CAA_	A AGAA
	TC	GAGGG GGA GGAG CAG		
		CTCCC CCT CCTC GTC		
		CCAC G CCCC		
GAM1960	CSK	5' CTGGCGGTCCCTCCTCCCCTCT 16506	CA	A GAGAA
		AGAGGG AGGA GGA CAG		

			TCTCCC TCCT CCT GTC		
			C_ C GGCG_		
GAM1960 CTNS	3'	TGCCTCTCTCCTACCTC	18223	GCA AG AA	
		GAGG AGGA GAGAG CA			
		CTCC TCCT CTCTC GT			
		A_ _ CC			
GAM1960 DDX3	5'	CTCTCCTCCCCTTCCCTCT	9054	C A_	
		AGAGGG AAGG AGGAGAG			
		TCTCCC TTCC TCCTCTC			
		_ CC			
GAM1960 DDX3	5'	CTCTTTTCCCTCCCTCT	9055	CA A	
		AGAGGG AGG AGGAGAG			
		TCTCCC TCC TTTTCTC			
		_ C			
GAM1960 DDX3 TC	5'	CTGTTCTCTCCTCCTTCCCC	43991	C _A	
		GAGGG AAG G AGGAGAGAACAG			
		CTCCC TTC C TCCTCTCTTGTC			
		C T C			
GAM1960 DFFB	3'	TTCTCCTTCCTCAGCCTC	88791	GCA	
		GAGG AGGAAGGAGAG			
		CTCC TCCTTCCTCTT			
		GAC			
GAM1960 DKC1	3'	CTACTTGTTCCCTGTGCCCTCT	9077	_ G _	
		AGAGGGCA AGGAA GAG AG			
		TCTCCCGT TCCTT TTC TC			
		G G A			
GAM1960 DNA2L	3'	CTATCCTCCCTTACTATCCTC	92949	C_ A G	
		GAGGG AAGG AGGA AG			
		CTCCT TTCC TCCT TC			
		ATCA C A			
GAM1960 DTNA	5'	CTGCTCTCTCCTTCAGAACCCC	9141	CAAG_ A	
		GGG GAAGGAGAGA CAG			
		CCC CTCCTCTCT GTC			
		CAAGA C			
GAM1960 EBI3	3'	TCTCTCCTTTACCTTT	20440	CAAG	
		GAGGG GAAGGAGAGA			
		TTTCC TTCCTCTCT			
		A_			
GAM1960 FGD1	5'	GTTCTCTCTTCCCTCCCCTC	16753	CA A	
		GAGGG AGG AGGAGAGAAC			

			CTCCC TCC TTCTCTCTTG			
			C_ C			
GAM1960	FMR2	3'	TTCTTTCTCCTTCCCTCT	10705	C A	
			AGAGGG AAGGA GGAGAGAA			
			TCTCCC TTCCT CCTTTCTT			
			— —			
GAM1960	FRAT2	3'	TGCTCTCTTCTGGCCCTC	24903	AAGGA A	
			GAGGGC AGGAGAGA CA			
			CTCCCG TCTTCTCT GT			
			G_____ C			
GAM1960	FZD7	3'	CTCTCCTCCCCTGCCCCCT	14503	A A A	
			AG GGGCA GG AGGAGAG			
			TC CCCGT CC TCCTCTC			
			C C C			
GAM1960	GARP	3'	CTGCTCTGGACTTGCCCTCT	19780	GAA _	
			AGAGGGCAAG GGAG AG			
			TCTCCCGTTC TCTC TC			
			AGG G			
GAM1960	GARP	3'	TGTCTCTCCTCTCTCCC	19789	CA GA A	
			GGG AG AGGAGAGA CA			
			CCC TC TCCTCTCT GT			
			__ TC C			
GAM1960	GPR44	3'	TGTTCCAGCCTGCCCTCT	17704	A AA GAGA	
			AGAGGGCA GG GGA ACA			
			TCTCCCGT CC CCT TGT			
			_ GA _____			
GAM1960	GSTA4	3'	CTGTTCTCTTATCCTTATCCCC	9497	A GC AG	
	T		AG GG AAGGA GAGAGAACAG			
			TC CC TTCCT TTCTCTTGTC			
			C TA A_			
GAM1960	HHIP	5'	TGTCCTCTCCTTTTCTTC	42756	CAAG A	
			GAGGG GAAGGAGAG ACA			
			CTTCT TTCCTCTC TGT			
			_____ C			
GAM1960	HMG20A	3'	CTTCCCTTCCCTTCCCCCT	37065	A C AG	
			AG GGG AAGGAAGG AG			
			TC CCC TTCCTTCC TC			
			_ C CT			
GAM1960	HOXB3	3'	CTGGAGCTCCTTCCCTTCCCCC	10953	A CAA AGAA	
	T		AG GGG GGAAGGAG CAG			

			TC CCC CCTTCCTC GTC			
			C TTC GAG_			
GAM1960	HOXB5	3'	TCTCTCCCTTACCCATCT 10960 _ C AAG			
			AGA GGG AAGG GAGAGA			
			TCT CCC TTCC CTCTCT			
			A A _			
GAM1960	HS2ST1	3'	TTCTCTCTCCCTGCCCTC 25331 A AG			
			GAGGGCA GGA GAGAGAA			
			CTCCCGT CCT CTCTCTT			
			C _			
GAM1960	IKBB	3'	CTGCTCTCCAAAGGCCCTGCTC 63904 A A AA_ AA			
	CCT		AG GGGCA GG GGAGAG CAG			
			TC CTCGT CC CCTCTC GTC			
			C C GGAAA _			
GAM1960	INHBC	3'	TGAGCTCCCCTGCCCTCT 19860 A AA AGAA			
			AGAGGGCA GG GGAG CA			
			TCTCCCGT CC CCTC GT			
			_ _ GA_			
GAM1960	IRS1	5'	CTCTCGCCCTTGCCCT 19877 A AAG			
			AG GGGCAAGG GAGAG			
			TC CCTGTTCC CTCTC			
			C CG_			
GAM1960	KIAA0857	3'	CTATTGCTGCCTGCCCTCT 67253 A A G _			
			AGAGGGCA GG AG AG AG			
			TCTCCCGT CC TC TT TC			
			_ G G A			
GAM1960	KLK5	5'	CTGTCCCCTCCTTGCCCT 25785 A_ G			
			AGGGCAAGGA GGA AG			
			TCCCGTTCCT CCT TC			
			CC G			
GAM1960	KRT15	3'	CTATTCCCCCTCTGCCTCTC 11232 _ _ AA _			
			GAG GGCA AGG GGAG AG			
			CTC CCGT TCC CCTT TC			
			T C C_ A			
GAM1960	KRT15	3'	TGCCTCTCCCCACCTTCT 11234 CAA AA AA			
			AGAGGG GG GGAGAG CA			
			TCTTCC CC CCTCTC GT			
			A_ _ C_			
GAM1960	KRT5	5'	CTGTTCTCTCCAGCACCTC 6462 _ AAGGAA			
			GAGG GC GGAGAGAACAG			

			CTCC CG	CCTCTCTTGTC		
			A A			
GAM1960	KRT6B	3'	CTGCTCTCTTTGCCTTCT	19899		_ G
			AGAGGGCAAGGA AG AG			
			TCTTCCGTTTCT TC TC			
			C G			
GAM1960	LRAT	5'	CTGTCCTCCTTTGCCTTC	60730	A	G
			GAGGGCAAGG AGGA AG			
			CTTCCGTTTC TCCT TC			
			C G			
GAM1960	LZTR1	3'	CTGCCCTGCCTTGCCCCCT	23169	A	A AG
			AG GGGCAAGG AGG AG			
			TC CCCGTTCC TCC TC			
			_ G CG			
GAM1960	MKI67	3'	CTTTGCCCCCTGTCCTCT	11596	A AA	_
			AGAGGGCA GG GG AGAG			
			TCTCCTGT CC CC TTTC			
			C _ G			
GAM1960	MN1	3'	TGTCTGTTTCCTTCCCCCT	11660	CAA	GA_
			AGGG GGAAGGAGA ACA			
			TCCC CCTTCCTTT TGT			
			_ GTC			
GAM1960	MTA1L1	3'	CTTTCCTTCCCTCCCCTC	17632	CAA	
			GAGGG GGAAGGAGAG			
			CTCCC CCTTCCTTTC			
			CTC			
GAM1960	MTMR8	3'	GTTCTCTCCTTGTGCCCTT	31915	AGG	
			GAGGGCA AAGGAGAGAAC			
			TTCCCGT TTCCTCTCTTG			
			G_			
GAM1960	MUC3B	3'	TCCCATCTCCTGCCCTCT	95925	A A_ A	
			AGAGGGCA GGA GG GA			
			TCTCCCGT CCT CC CT			
			_ CTA _			
GAM1960	MYD88	3'	CTGTTCTCTCCCTCTCTCCTTC	11732	CAA A	
			GAGGG GGA GGAGAGAACAG			
			CTTCC TCT CCTCTCTTGTC			
			TC_ C			
GAM1960	NCOR2	3'	CTGTGTCCTCCCTCCCTC	21958	CA A GAGA	
			GAGGG AGG AGGA ACAG			

			CTCCC TCC TCCT TGTC		
			__ C G__		
GAM1960	NGFR	3'	CTCAACCCTCCCTCAGCCCT 11792	A	A_ A A__
			AG GGGC AGG AGG GAG		
			TC CCCG TCC TCC CTC		
			_ AC C CAA		
GAM1960	NGFR	3'	CTCCCCTCCTTGCCCTCCT 11793	AG	A A
			AG GGCAAGGA GG GAG		
			TC CCGTTCCT CC CTC		
			CT C _		
GAM1960	NHLH1	3'	CTGCCCTGTGACCCTTGCCCTCT 20016	G	A__ AG
			AGAGG CAAGG AGG AG		
			TCTCC GTTCC TCC TC		
			_ CAGTG CG		
GAM1960	NKX2H	5'	CTGCCCCCGCCTCCTTCCCCTC 27631	C	A AGAGAA
			GAGGG AAGGA GG CAG		
			CTCCC TTCCT CC GTC		
			C _ GCCCCC		
GAM1960	NPHS2	3'	CTGTCCTCATTCCCTGCCCTT 28277	A	G A A
			GAGGGCA GGAA GAG GA CAG		
			TTCCCGT CCTT CTC CT GTC		
			C A _ _		
GAM1960	NUCB1	3'	CTGTCCTCCGAGGGGCTTGCCCT 21642	GAA__	A A
	TCT		AGAGGGCAAG GGAG GA CAG		
			TCTTCCGTTC CCTC CT GTC		
			GGGGAG _ _		
GAM1960	OAS2	3'	TTCCTCCTTCCCTTGCCCTTCT 11870	_	A
			AGAGGGCAAGG AAGGAG GAA		
			TCTTCCGTTCC TTCCTC CTT		
			C _		
GAM1960	OAS3	3'	TGTTCTCTCTGCCCTCT 21659	AGGAAG	_
			AGAGGGCA GAGAGAA CA		
			TCTCCCGT CTCTCTT GT		
			_____ T		
GAM1960	OTOF	3'	CTGTCTTCCCACCCCTGCCCCC 17831	A	A AA AG A
	T		AG GGGCA GG GG AGA CAG		
			TC CCCGT CC CC TCT GTC		
			C C CA CT _		
GAM1960	PAFAH1B1	5'	CTCCCCCTCCTTCCCTC 6473	C	A A_
			GAGGG AAGGA GG GAG		

			CTCCC TTCCT CC CTC				
			— C CC				
GAM1960	PAFAH1B1	3'	TGTCTCCCGTTCGCCTCT	6480	G AA	A A	A
			AGAGG C GGA GG GAGA CA				
			TCTCC G CTT CC CTCT GT				
			— — G — C				
GAM1960	PFKL	5'	CTGCCCTCTCCTTGCCCTGCC	12058	A —		AA
			GGCA GG AAGGAGAG CAG				
			CCGT CC TTCCTCTC GTC				
			C G CC				
GAM1960	PIK3R2	3'	TTCTCCAGATCTCCCTCT	18518	CAA	A —	
			AGAGGG GGA GGAGAG				
			TCTCCC TCT CCTCTT				
			— — AGA				
GAM1960	PLA2G2D	3'	TTGTCCTTCCTCACCCCCT	25725	A CA		G
			AG GGG AGGAAGGA AG				
			TC CCC TCCTTCCT TT				
			C AC G				
GAM1960	PMX1	5'	CTCTCCTTCCCTCCCTCT	23564	CAA		
			AGAGGG GGAAGGAGAG				
			TCTCCC CCTTCCTCTC				
			TC —				
GAM1960	PPP2R5B	3'	CTGTGTACTTCCTTGTCCTCCCT	21797	A		GAGAGA
			AG GGGCAAGGAAG ACAG				
			TC CCTGTTCTTC TGTC				
			C ATG —				
GAM1960	PRKACB	5'	CTTCCCTTCCCTGACCCCT	12275	A — A		AG
			AG GGG CA GGAAGG AG				
			TC CCC GT CCTTCC TC				
			— A C CT				
GAM1960	PTK2B	3'	CTCTCTTCCTGCCCCTCT	15905	CA		G
			AGAGGG AGGAAG AGAG				
			TCTCCC TCCTTC TCTC				
			CG —				
GAM1960	PTPN7	5'	CTGTTTCCTCCCTTGCTTCT	55462	A		GAG
			AGAGGGCAAGG AGGA AACAG				
			TCTTCCGTTCC TCCT TTGTC				
			C —				
GAM1960	RABGGTB	5'	TGCTCTCTCCTTTCCT	17155	CAAG		A
			AGGG GAAGGAGAGA CA				

TCCC TTTCTCTCT GT
____ C
GAM1960 RBP5 3' TCTCTCCTGTCCATTTGACCTC 49802 G _ _
T AGAGG CAA GGA AGGAGAGA
||||| ||| ||| |||||
TCTCC GTT CCT TCCTCTCT
A TA G
GAM1960 SEPN1 3' GTTCTCTCCCCACCCCT 66980 CAA AA
AGGG GG GGAGAGAAC
|||| | |||||
TCCC CC CCTCTCTTG
CCA _
GAM1960 SFRP5 3' TGTGCCTTGCTTGCCCTCT 13036 G AGAGA
AGAGGGCAAG AAGG ACA
||||||| ||| |||
TCTCCCGTTC TTCC TGT
G G____
GAM1960 SFRS2IP 3' CTGTATCCTTCCTTCCCCTC 17539 C GAGA
GAGGG AAGGAAGGA ACAG
||||| ||||| |||
CTCCC TTCCTTCCT TGTC
C A____
GAM1960 SIX3 3' CTCCCTCTCCTTCCCCTC 19441 C _ A
GAGGG AAGGA AGG GAG
||||| ||||| ||| |||
CTCCC TTCCT TCC CTC
C C _
GAM1960 SIX3 5' CTGCTCCCCCCTCCTTTCCTTC 19442 C A A_ AA
T AGAGGG AAGGA GG GAG CAG
||||| ||||| || ||| |||
TCTTCC TTCCT CC CTC GTC
T C CC _
GAM1960 SLC28A1 3' CTGTTCTCCCCCGGGAACCATC 16155 _ GCAA_ AA A
T AGA GG GG GG GAGAACAG
||| || || || |||||
TCT CC CC CC CTCTTGTC
A AAGGG _ _
GAM1960 SLC7A8 3' TCTCTCCTTCCTCCCCCTTT 25306 CA
AGAGGG AGGAAGGAGAGA
||||| |||||
TTTCCC TCCTTCCTCTCT
CC
GAM1960 SON 3' TTCCCTTCTCCTTCCCCTCT 57988 C A A
AGAGGG AAGGA GGAG GAA
||||| ||||| ||| |||
TCTCCC TTCCT CTTC CTT
C _ C
GAM1960 SOX13 3' CTGTCCTTTGCCCCCTGTGCCC 20281 _ AA _ A
TCT AGAGGGCA AGG GG AGAG ACAG
||||||| ||| || ||| |||

			TCTCCCGT TCC CC TTTC TGTC		
			G C_ G C		
GAM1960	SREBF2	3'	TCTCTCCTTTTGTCTCC 17191	AG	G
			G GGCAAG AAGGAGAGA		
			C TCGTTT TTCCTCTCT		
			CT _		
GAM1960	TBXA2R	3'	CTCCCTTCCTCGGCCCT 8353	A A_ A	
			AG GGGC AGGAAGG GAG		
			TC CCG TCCTTCC CTC		
			_ GC _		
GAM1960	TEM5	3'	CTTTCCTCCCTGCCCTCT 52299	A A	
			AGAGGGCA GGA GGAGAG		
			TCTCCCGT CCT CCTTTC		
			C _		
GAM1960	TERT	3'	CTGCCCTCCTTTGCCTTC 13681	A AG	
			GAGGGCAAGG AGG AG		
			CTTCCGTTTC TCC TC		
			C CG		
GAM1960	TERT	3'	TTGTTACCCCTCGCCCTGCC 13683	A A_ AGA	
	TC		GAGGGCA GG AGG GAACAG		
			CTCCCGT CC TCC CTTGTT		
			C GC CCA		
GAM1960	TGFA	3'	CTGCTCAGGAGACCCCTGCCCT 13708	A AAG_____	
	CT		AGAGGGCA GG GAG AG		
			TCTCCCGT CC CTC TC		
			C CAGAGGA G		
GAM1960	TNF	3'	CTGTCCCATGTAGCCCCCTGG 92708	G A AA AGA_____	
	CCTCT		AGAGG CA GG GG GAACAG		
			TCTCC GT CC CC CTTGTC		
			G C _ GATGTACC		
GAM1960	TPS1	3'	CTGTCCTAAGCCCCCTGCTCTC 61104	A AA AG_ A	
	T		AGAGGGCA GG GG AG ACAG		
			TCTCTCGT CC CC TC TGTC		
			C _ GAA C		
GAM1960	TPSB1	3'	CTGTCCTAAGCCCCCTGCTCTC 13837	A AA AG_ A	
	T		AGAGGGCA GG GG AG ACAG		
			TCTCTCGT CC CC TC TGTC		
			C _ GAA C		
GAM1960	USP5	3'	TGTGCCTCCCCTCCCCCT 14449	CAA A A A_	
			AGGG GGA GG GAG ACA		

TCCC CCT CC CTC TGT
___ C _ CG
GAM1960 XYLB 3' TCTCTCCTCTCCCCCT 18832 CAA _
AGGG GGA AGGAGAGA
|||| ||| |||||
TCCC CCT TCCTCTCT
___ C
GAM1960 XYLB 3' TTCTCTCCTTTCACCATCT 18833 G CAA
AGA GG GGAAGGAGAGAA
||| || |||||
TCT CC CTTTCCTCTCTT
A A__
GAM1960 ZAP70 3' CTGCCTGGCCCCCTGTCCTCT 71374 A AA AG AA
AGAGGGCA GG GG AG CAG
||||| || || |||
TCTCCTGT CC CC TC GTC
C __ GG C_
GAM1960 ZNF264 5' CTCTCCTCCCCCGCCCTT 14209 AA A
GAGGGC GG AGGAGAG
||||| || |||||
TTCCCG CC TCCTCTC
CC C
GAM1960 ZNF289 3' CTCTTCCCCTTGCCCCT 65929 A AA
AG GGGCAAGG GGAGAG
|| ||||| |||||
TC CCCGTTCC CTTCTC
_ C_
GAM1960 A 5' TCTCCTCCCCTGCCCTCT 27339 A A
AGAGGGCA GG AGGAGA
||||| || |||||
TCTCCCGT CC TCCTCT
C C
GAM1960 AF9Q34 3' TTCTCTCCCCAGCCCCCT 51727 A AA AA
AG GGC GG GGAGAGAA
|| ||| || |||||
TC CCCG CC CCTCTCTT
C A_ _
GAM1960 AGMAT 3' CTCCCATGCCTGTCCTCT 45740 A AA_ A
AGAGGGCA GG GG GAG
||||| || |||
TCTCCTGT CC CC CTC
_ GTA _
GAM1960 BCAN 3' CTGCCCTCTCCCTGGCAGCCAT 41970 G AAGGAA AA
CT AGA GGC GGAGAG CAG
||| || ||||| |||
TCT CCG CCTCTC GTC
A ACGGTC CC
GAM1960 C11orf11 5' CTCTCCTTCCTTCTGCGCCC 94877 _
GGGC AAGGAAGGAGAG
|||| |||||

CCGG TTCCTTCCTCTC
 CGTC
 GAM1960 C20orf39 5' CTTCTCTTCCCTGCCCTC 46575 A GA
 GAGGGCA GGAAG GAG
 ||||| |||| ||
 CTCCCGT CCTTC TTC
 C TC
 GAM1960 CAMKK1 3' CTCCTCTTCTTGGCCCTC 51153 A GA
 GAGGGC AGGAAG GAG
 ||||| |||| ||
 CTCCCG TTCTTC CTC
 G TC
 GAM1960 CAT56 3' CTGTTCCCCAGTATTGCCCTC 48278 GGAA AGA
 GAGGGCAA GG GAACAG
 ||||| || |||||
 CTCCCGTT CC CTTGTC
 ATGA C__
 GAM1960 CHIT1 3' CTGCTCTCAGCCTTGCCTTC 14411 AAG AA
 GAGGGCAAGG GAGAG CAG
 ||||| |||| ||
 CTTCCGTTCC CTCTC GTC
 GA_ _
 GAM1960 CHRAC1 3' CTGTTCTCTCTTCTCCTGCC 34334 A A _ _
 CCT AG GGGCA GGA AGGAGAG AACAG
 || |||| || ||||| ||||
 TC CCCGT CCT TTCTCTC TTGTC
 C _ C C
 GAM1960 CKAP4 3' TGTATCTCCCTTCCCTCT 23349 C AAG GA
 AGAGGG AAGG GAGA ACA
 ||||| |||| |||| ||
 TCTCCC TTCC CTCT TGT
 _ _ _ A_
 GAM1960 CLSTN1 3' CTGTTCTCTCCTCTCTCCTC 30788 GCA GA
 GAGG AG AGGAGAGAACAG
 |||| || ||||| |||||
 CTCC TC TCCTCTCTTGTC
 _ _ TC
 GAM1960 CPLX1 3' TGCTCGCCCTGTGCCCTCT 22825 A AA A AA
 AGAGGGCA GG GG GAG CA
 ||||| || || |||| ||
 TCTCCCGT TC CC CTC GT
 G _ G _
 GAM1960 CYP4F11 5' CTGCCCATCCTTGCCCCT 41319 A A AG
 AG GGGCAAGGA GG AG
 || ||||| || ||
 TC CCCGTTCCCT CC TC
 _ A CG
 GAM1960 DDA3 3' CTAACCTCCCTGCCCTCT 51950 A A AG
 AGAGGGCA GGA GG AG
 ||||| |||| || ||

TCTCCCGT CCT CC TC
 C _ AA
 GAM1960 DGKD 3' TCTCTCCTCCCGCTCCTC 60112 _ AA A
 GAGG GC GGA GGAGAGA
 |||| || ||| |||||
 CTCC CG CCT CCTCTCT
 T C_ _
 GAM1960 DKFZP434J037 5' CTGATTCCCCTGCCGCCCT 48947 AA A A AA
 AGGGC GG AGG GAG CAG
 |||| || ||| ||| |||
 TCCCG CC TCC CTT GTC
 _ G C A_
 GAM1960 DKFZP434N178 5' CTCCGGGATCCTTGCCCTCT 72400 G A__
 AGAGG CAAGGA GGAG
 |||| ||||| |||
 TCTCC GTTCCT CCTC
 _ AGGG
 GAM1960 DKFZP564B1162 5' GTTATTTTCCTCCCCTCT 49352 CAAG A _
 AGAGGG GA GGAGAG AAC
 ||||| || ||||| |||
 TCTCCC CT CCTTTT TTG
 _ _ A
 GAM1960 DKFZP564O0823 3' CTGTTCTCCCCTCCAGGCCACC 60256 AG AA A A
 T AG GGC GGA GG GAGAACAG
 || ||| ||| || |||||
 TC CCG CCT CC CTCTTGTC
 CA GA C _
 GAM1960 DKFZP564O1664 5' CTGCTCAGCTCCCCTCTGCCCC 48666 A _ AA A_ A
 CT AG GGGCA AGG GGAG GA CAG
 || ||||| ||| ||| || |||
 TC CCCGT TCC CCTC CT GTC
 C C _ GA C
 GAM1960 DKFZP566B183 3' CTACTTTCCTTTCCCTCT 31942 C _
 AGAGGG AAGGAAGG AG
 ||||| ||||| ||| |||
 TCTCCC TTCCTTTC TC
 T A
 GAM1960 DKFZP566D1346 5' TTCCCCCCTTGCCCCT 48738 A AA A
 AG GGGCAAGG GG GAG
 || ||||| || |||
 TC CCCGTTCC CC CTT
 _ CC _
 GAM1960 DKFZP566I1024 3' TTCTCTCCCCCTTTCTCCCT 70654 C__ AA
 AGGG AAGG GGAGAGAA
 ||| ||| |||||
 TCCC TTCC CCTCTCTT
 TCT C_
 GAM1960 DKFZP727G051 3' CTGTTCTCTGGCCTCACCCCCT 70008 CAA A_ _
 C GAGGG GG AGG AGAGAACAG
 |||| || ||| |||||

CTCCC CC TCC TCTCTTGTC
 ____ AC GG
 GAM1960 DKFZP761G1913 3' CTGCCTCCCCTGCCCTTT 49694 A A _
 AGAGGGCA GG AGG AG
 ||||| || ||| ||
 TTTCCCGT CC TCC TC
 C C G
 GAM1960 EFNA5 5' CTTTCCTTTCTCGCCCCCT 10487 A A
 AG GGGC AGGAAGGAGAG
 || ||| |||||
 TC CCG TCTTTCCTTTC
 C C
 GAM1960 ELF4 3' CTCTTCTTTCTCCCTGCCCCCT 9230 A _
 AG GGGCA AGGAAGGAGAG
 || ||| |||||
 TC CCGT TCTTCTTCTC
 C CCC
 GAM1960 ELF4 3' CTGCTTCCCCCTTCCCTCT 9231 C AA _
 AGAGGG AAGG GGAG AG
 ||||| ||| ||| ||
 TCTCCC TTCC CTTC TC
 _ CC G
 GAM1960 ENDO180 3' CTGCTCCCTCTCGCCCCCT 21265 A AA A _
 AG GGGC GGA GGAG AG
 || ||| ||| ||| ||
 TC CCG TCT CCTC TC
 _ C_ C G
 GAM1960 EZF-2 3' TTCCTCTCTCCCTGCCCTTT 37681 A AG A
 AGAGGGCA GGA GAG GAA
 ||||| ||| ||| |||
 TTTCCCGT CCT CTC CTT
 C CT _
 GAM1960 FEM-2 3' CTGCCCTCCCCTTCCCTCCC 28313 CA A AA
 GGG AGGAAGG GAG CAG
 ||| ||||| ||| |||
 CCC TCCTTCC CTC GTC
 _ C CC
 GAM1960 FLJ10079 3' CTGCAGCCTTCCTTGCCCTT 60833 AGAGAA
 GAGGGCAAGGAAGG CAG
 ||||| ||| |||
 TTCCCGTTCCTTCC GTC
 GAC__
 GAM1960 FLJ10142 3' CTGCCTTGCCCTTCCTTCCCTC 36320 C A_ AA
 GAGGG AAGGAAGG GAG CAG
 ||||| ||||| ||| |||
 CTCCC TTCCTTCC TTC GTC
 _ CG C_
 GAM1960 FLJ10307 3' CTGTCCTCTAGAATTCTTCCTT 36476 C _ A
 CCCTC GAGGG AAGGAAGG AGAG ACAG
 ||||| ||||| ||| |||

CTCCC TTCCTTCT TCTC TGTC
 _ TAAGA C
 GAM1960 FLJ10330 5' CTCCCCCCCCTCCTTCCCTC 36506 C A__ A
 GAGGG AAGGA GG GAG
 ||||| ||||| || ||||
 CTCCC TTCCT CC CTC
 _ CCCC C
 GAM1960 FLJ10342 5' CTCTTCACCCCTTCCCTC 36514 C AA_
 GAGGG AAGG GGAGAG
 ||||| ||||| |||||
 CTCCC TTCC CTTCTC
 _ CCA
 GAM1960 FLJ10922 3' CTGTTCTTTGCCCTACGCCCT 37401 A AA AA _
 AG GGGC GG GG AGAGAACAG
 || |||| || || |||||
 TC CCG TC CC TTTCTTGTC
 _ CA _ G
 GAM1960 FLJ11565 3' CTGTTCTCTTTTCTCTCCCTC 45411 CA GA
 GAGGG AG AGGAGAGAACAG
 ||||| || |||||
 CTCCC TC TTTTCTCTTGTC
 _ TC
 GAM1960 FLJ11715 5' CTGCTCTCTCCTTTCCCTTT 44978 CAA A
 AGAGGG GGAAGGAGAGA CAG
 ||||| ||||| ||||| |||||
 TTTCCC CTTTCCTCTCT GTC
 _ C
 GAM1960 FLJ11939 5' TGTCCCCTCCTTTCCTGCT 45497 A AGA
 GGCA GGAAGGAG ACA
 ||||| ||||| |||||
 TCGT CTTTCCTC TGT
 C CCC
 GAM1960 FLJ12783 3' TTCCCTCCTTCCCCGCTCCCT 49493 A AA A
 AG GGGC GGAAGGAG GAA
 || |||| ||||| |||||
 TC CTCG CCTTCCTC CTT
 C CC C
 GAM1960 FLJ13158 3' CTGTTTTTCTCTCCCCGCCC 46650 AA AA _
 GGGC GG GGAGAGA ACAG
 ||||| || ||||| |||||
 CCGG CC CCTCTCT TGTC
 _ C_ TTT
 GAM1960 FLJ13881 3' CTCTCCTTCCCTACCCTCT 45640 CAA
 AGAGGG GGAAGGAGAG
 ||||| |||||
 TCTCCC CCTTCCTCTC
 ATC
 GAM1960 FLJ13881 3' CTCTCCTTCCCTACCCTCT 45641 CAA
 AGAGGG GGAAGGAGAG
 ||||| |||||

TCTCCC CCTTCCTCTC
 ATC
 GAM1960 FLJ14251 3' CTGTTGGTGACTCCTTCCCCGG 46483 AA_ AG____
 CCC GGGC GGAAGGAG AACAG
 ||| ||||| ||||
 CCGC CCTTCCTC TTGTC
 GCC AGTGG
 GAM1960 FLJ14442 3' TTTTCCCCCTCCTCCCCTC 52394 CA A A
 GAGGG AGGA GG GAGAA
 |||| ||| || ||||
 CTCCC TCCT CC CTTTT
 C_ C C
 GAM1960 FLJ14721 3' CTGTTTCCTCCTTCCCCTACCC 52641 CAA_ A
 GGG GGAAGGAG GAACAG
 || ||||| |||||
 CCC CCTTCCTC CTTGTC
 ATCC _
 GAM1960 FLJ20113 3' CTTTTCTTCCCCGCCCCCT 35056 A AA
 AG GGGC GGAAGGAGAG
 || ||| |||||
 TC CCGC CCTTCTTTTC
 C CC
 GAM1960 FLJ20123 5' CTCCTTCTCCTTTGCCCTCT 35070 ____
 AGAGGGCAA GGAAGGAG
 ||||| |||||
 TCTCCCGTT TCTTCCTC
 TCC
 GAM1960 FLJ20373 3' TGTTGTCCCCCACCCTTT 35544 CAA AA A G
 AGAGGG GG GG GA AACA
 |||| || || ||||
 TTTCCC CC CC CT TTGT
 A_ C_ _ G
 GAM1960 FLJ20626 3' CTGCTCTCTCTCTTCTTGCCCC 35902 A AG A
 T AG GGGCAAGGA GAGAGA CAG
 || ||||| ||||| |||
 TC CCGTTCTT CTCTCT GTC
 _ CT C
 GAM1960 FLJ20671 3' TTCTCTTCCTTACCCCT 35948 A C G
 AG GGG AAGGAAG AGAG
 || ||| ||||| |||
 TC CCC TTCCTTC TCTT
 C A _
 GAM1960 FLJ22471 3' CTGCTTCTCTTGCCCTCT 47860 _ G
 AGAGGGCAAG GAAG AG
 ||||| ||| ||
 TCTCCCGTTC CTTC TC
 T G
 GAM1960 FLJ22477 3' TTTGTCACTCCCTGCCCTCT 45680 A AG G
 AGAGGGCA GGA GA AGA
 ||||| ||| || |||

TCTCCCGT CCT CT TTT
 C CA G
 GAM1960 FLJ22679 3' CTGCCCCTCTTCCCCTACCCCT 35178 CA AA AA_
 AGGG AGG GGAGAG CAG
 |||| ||| ||||| |||
 TCCC TCC CTTCTC GTC
 CA C_ CCC
 GAM1960 FLJ22679 3' CTGCCCCTCTTCCCCTACCCCT 35179 CA AA AA_
 AGGG AGG GGAGAG CAG
 |||| ||| ||||| |||
 TCCC TCC CTTCTC GTC
 CA C_ CCC
 GAM1960 FLJ23322 3' TCCCTTCTGTCTCCCTGCCCTC 90216 A ____ A
 T AGAGGGCA GGA AGGAG GA
 ||||| ||| |||| |||
 TCTCCCGT CCT TCTTC CT
 C CTG C
 GAM1960 HEMK 3' TCCCCTCCCTTGCTCCT 32963 A A A
 AG GGGCAAGG AGG GA
 || ||||| ||| |||
 TC CTCGTTCC TCC CT
 _ C C
 GAM1960 HIF3A 3' TGTGCCTCCCTTACCCCCC 42656 CAA _ A A_
 GGG GG AAGG GAG ACA
 ||| || ||| ||| |||
 CCC CC TTCC CTC TGT
 C_ A _ CG
 GAM1960 HSA243666 3' TTCTTTCCCCTCCCCTACCCCT 34558 CAA__ A_
 T GAGGG GGA GGAGAGAA
 |||| ||| |||||
 TTCCC CCT CCTTTCTT
 CATCC CC
 GAM1960 ITM3 3' CTGCTCTCTGGCCCTCCTCCTT 48888 A C _ _ A
 CCCCCT AG GGG AAGGA AGG AGAGA CAG
 || ||| |||| ||| ||||| |||
 TC CCC TTCCT TCC TCTCT GTC
 _ C CC CGG C
 GAM1960 KIAA0064 3' CTACCTTTCTTGTCCCCT 29236 A AG
 AG GGGCAAGGAAGG AG
 || ||||| ||||| |||
 TC CCTGTTCTTTTC TC
 C CA
 GAM1960 KIAA0255 3' TTCTCTCCCTGCCCTCT 29139 AGGAA
 AGAGGGCA GGAGAGAA
 ||||| |||||
 TCTCCCGT CCTCTCTT
 C____
 GAM1960 KIAA0257 3' CTGCAGCTCCCCTCCCCACCCT 71371 CAA A A AA_
 C GAGGG GGA GG GAG CAG
 |||| ||| ||| ||| |||

CTCCC CCT CC CTC GTC
 ACC C _ GAC
 GAM1960 KIAA0295 3' CTGTTCTCCCCTCCTATCTTT 68664 CA A A
 GAGGG AGGA GG GAGAACAG
 |||| ||| || |||||
 TTTCT TCCT CC CTCTTGTC
 A_ C _
 GAM1960 KIAA0450 5' CTGCCCTTGGCTTGCCCTC 28352 G_ AG
 GAGGGCAAG AAGG AG
 ||||| ||| ||
 CTCCCGTTC TTCC TC
 GG CG
 GAM1960 KIAA0514 5' CTCCCTCCCTTTCTCTCT 28745 C A A
 AGAGGG AAGG AGG GAG
 |||| ||| ||| |||
 TCTCTC TTCC TCC CTC
 T C _
 GAM1960 KIAA0826 3' CTGTCCTCTGTTTTTCTTACCC 83526 C _ A
 TC GAGGG AAGGAAGG AGAG ACAG
 |||| ||||| ||| |||
 CTCCC TTCTTTTT TCTC TGTC
 A G C
 GAM1960 KIAA0844 3' CTGTCTTCCCCTCCTTCCCTC 30892 C A AG A
 GAGGG AAGGA GG AGA CAG
 |||| ||| || ||| |||
 CTCCC TTCCT CC TCT GTC
 _ C CT _
 GAM1960 KIAA0918 3' TTCTCTCCTCCCCTCCCCTC 73523 CAA A
 GAGGG GG AGGAGAGAA
 |||| || |||||
 CTCCC CC TCCTCTCTT
 CTC C
 GAM1960 KIAA0953 3' CTGTTCTCCAGCGCCCGGCCCC 67325 A AA AAGGA
 T AG GGGC GG GAGAACAG
 || ||| || |||||
 TC CCCG CC CTCTTGTC
 _ GC GCGAC
 GAM1960 KIAA1029 3' CTGTTCTCTCATTGTCACTGCC 24428 AG AG__
 CTCT AGAGGGCA GA GAGAGAACAG
 ||||| || |||||
 TCTCCCGT CT CTCTCTTGTC
 CA GTTA
 GAM1960 KIAA1068 3' CTTTCCTCCCCTGCTCTCT 31686 A A
 AGAGGGCA GG AGGAGAG
 ||||| || |||||
 TCTCTCGT CC TCCTTTC
 C C
 GAM1960 KIAA1089 3' TCCTCCTTTTCAGCCCCCT 69433 A AA A
 AG GGGC GGAAGGAG GA
 || ||| ||||| ||

		TC CCCG CTTTCCTC CT		
		C A _ _		
GAM1960 KIAA1128	3'	CTGCTCCCTCCTTCTCTC 69003	C A _	
		GAGGG AAGGA GGAG AG		
		CTCTC TTCCT CCTC TC		
		_ C G		
GAM1960 KIAA1160	3'	TTCTCAGCCTTCCTTCCCTCT 40764	C A _	
		AGAGGG AAGGAAGG GAGAA		
		TCTCCC TTCCTTCC CTCTT		
		_ GA		
GAM1960 KIAA1388	3'	CTGCTCTATCCCCTGCCCTCT 95228	A AA G A	
		AGAGGGCA GG GGA AGA CAG		
		TCTCCCGT CC CCT TCT GTC		
		_ _ A C		
GAM1960 KIAA1656	3'	CTGCCCTCCCTTCCCTGCCTCT 66367	G A A AA	
		AGAGG CA GGAAGG GAG CAG		
		TCTCC GT CCTTCC CTC GTC		
		_ C _ CC		
GAM1960 KIAA1750	3'	TGTTCTTCCCTACCTTCT 68814	C A AG	
		GG AAGG AGG AGAACA		
		TC TTCC TCC TCTTGT		
		_ A CT		
GAM1960 KIAA1762	3'	CTCTCCCTCCTAACCCTCT 64531	CA A	
		AGAGGG AGGA GGAGAG		
		TCTCCC TCCT CCTCTC		
		AA C		
GAM1960 KIAA1819	5'	TTCTTTCTCCCCACCCTCT 70257	CAA AA	
		AGAGGG GG GGAGAGAA		
		TCTCCC CC TCTTTCTT		
		A _ CC		
GAM1960 KIAA1828	5'	CTTTCCTCCCTCCCTCT 74205	CAA A	
		AGAGGG GGA GGAGAG		
		TCTCCC CCT CCTTTC		
		TC _ C		
GAM1960 KIAA1831	3'	TCCCTCCTTCCCTCCCTCT 64526	CA A	
		AGAGGG AGGAAGGAG GA		
		TCTCCC TCCTTCCTC CT		
		C _ C		
GAM1960 KIAA1855	3'	CTGCCTCCCCTTCCTCGCCCT 93953	A A AA	
		AGGGC AGGAAGG GAG CAG		

TCCCG TCCTTCC CTC GTC
 C C C_
 GAM1960 KIAA1908 5' TGTTCCTCCTGCTGCTCTC 73802 AGGAA A
 GAGGGCA GG GAGAACA
 ||||| || |||||
 CTCTCGT TC CTCTTGT
 CG__ _
 GAM1960 LASP1 3' CTGTTCTCTCCCCTCACATCCT 21578 CA__ AA
 C GAGGG AGG GGAGAGAACAG
 |||| ||| |||||
 CTCCT TCC CCTCTCTTGTC
 ACAC __
 GAM1960 MAP2K5 5' TTCCCTTGTTTTACCCCTCT 12330 C__ G A
 AGAGGG AAG AAGG GAG
 ||||| ||| ||| |||
 TCTCCC TTT TTCC CTT
 ACT G _
 GAM1960 MGC13138 3' TTCTCCTTCCTCAGCCTC 54165 GCA
 GAGG AGGAAGGAGAG
 ||| |||||
 CTCC TCCTTCCTCTT
 GAC
 GAM1960 MGC14839 3' TTTTCTCCCCTGGCCTCT 55588 G A AA
 AGAGG CA GG GGAGAGAA
 |||| || || |||||
 TCTCC GT CC CCTCTTTT
 G _ _
 GAM1960 MGC15482 3' CTGTTGCTCCCCCCCACACTCT 52854 GGCAA AA AG
 AGAG GG GGAG AACAG
 ||| || ||| |||||
 TCTC CC CCTC TTGTC
 ACAC_ CC G_
 GAM1960 MGC2668 3' CTGTCCCCCTTGCCTGCCTTCT 61194 A _ AGA A
 AGAGGGCA GG AAGG GA CAG
 ||||| || ||| || |||
 TCTTCCGT CC TTCC CT GTC
 _ G CC_ _
 GAM1960 MGC3035 5' CTGTCTTCCTCGTCCCTC 44399 _A AG
 GAGGG C AGGAAGG AG
 |||| | ||||| ||
 CTCCC G TCCTTCT TC
 T C G_
 GAM1960 MGC4796 3' TTGTCTCCTTCCCACCCTC 62170 CAA G
 GAGGG GGAAGGAGA AA
 |||| ||||| ||
 CTCCC CCTTCCTCT TT
 AC_ G
 GAM1960 NCUBE1 3' CTGTTATCACCACCCCTGCCC 32605 A AA_ A G
 TCT AGAGGGCA GG GG GA AACAG
 ||||| || || |||||

		TCTCCCGT CC CC CT TTGTC	
		C CCA A A	
GAM1960 NEDD5	5'	CTGCCCTCCCGCGACCGCCTCT 16603	_ AA AA_ A AA
CT		AGAG GGC GG GG GAG CAG	
		TCTC CCG CC CC CTC GTC	
		T _ AGCG _ CC	
GAM1960 NFASC	3'	TCATTCCTCCCCTGCCCTTT 70861	A A A
		AGAGGGCA GG AGGAG GA	
		TTTCCCGT CC TCCTT CT	
		C C A	
GAM1960 OCIA	5'	TTTTCTCCCTCCCTGCCCCCT 35658	A A A
		AG GGGCA GGA GGAGAGAA	
		TC CCCGT CCT CCTCTTTT	
		C C C	
GAM1960 P450RAI-2	3'	CTCTCCCCCTTTGCCCTC 39572	AA
		GAGGGCAAGG GGAGAG	
		CTCCCGTTTC CCTCTC	
		CC	
GAM1960 PAK6	3'	TGCTGTCTCCTTGTCTC 39811	AG G AA
		GAGGGCAAGGA GA AG CA	
		CTCCTGTTCT CT TC GT	
		_ G _	
GAM1960 PFTK1	3'	TCACTCCCTCCCTCCCTCT 25690	CAA A A
		AGAGGG GGA GGAG GA	
		TCTCCC CCT CCTC CT	
		TC_ C A	
GAM1960 PHRET1	5'	CTGTGCGCTCCCTCCTTGCCCT 41351	A AGA
		GGGCAAGGA GGAG ACAG	
		TCCGTTCTCCT CCTC TGTC	
		C GCG	
GAM1960 PLAGL2	3'	TCTCTCCACCTGCCCTCT 70964	A AA
		AGAGGGCA GG GGAGAGA	
		TCTCCCGT CC CCTCTCT	
		_ A_	
GAM1960 PLSCR4	5'	TCTCCCTTCCCTGCCTCCT 40133	AG A A
		AG GGCA GGAAGG GAGA	
		TC CCGT CCTTCC CTCT	
		CT C _	
GAM1960 POFUT1	3'	CTGTTCTCCCGCCGTCCTC 70976	AA AA A
		GAGGGC GG GG GAGAACAG	

CTCCTG CC CC CTCTTGTC
 _ GA _
 GAM1960 PPP1R1A 3' CTTCTTGCCCTGCCCTCT 23094 A _
 AGAGGGCA GG AAGGAG
 ||||| || |||||
 TCTCCCGT CC TTCTTC
 C G
 GAM1960 QSCN6 3' TTCCCTCCCCTCCCACCCCTT 12572 CAA A_ A
 GAGGG GGA GGAG GAA
 |||| || |||| ||
 TTCCC CCT CCTC CTT
 CAC CC C
 GAM1960 RAB3IL1 3' CTCCCTTCCTTTCCCCCT 26366 A C A
 AG GGG AAGGAAGG GAG
 || || ||||| ||
 TC CCC TTCCTTCC CTC
 C T _
 GAM1960 RHOBTB2 3' CTGCAGGCTCCCTTCCTTACCC 61598 C A AA_
 TC GAGGG AAGGAAGG GAG CAG
 |||| ||||| || ||
 CTCCC TTCCTTCC CTC GTC
 A _ GGAC
 GAM1960 RNF2 5' TCGCTCCTTCCCGCCCTC 24258 AA A
 GAGGGC GGAAGGAG GA
 |||| ||||| ||
 CTCCCG CCTTCCTC CT
 C_ G
 GAM1960 RPS6KA4 3' CTGTTCTCCCCTGAGGCCC 15454 AAGGA A
 GGGC AGG GAGAACAG
 |||| || |||||
 CCGG TCC CTCTTGTC
 GAG_ C
 GAM1960 SAE1 3' CTGTATTCCCTGTCCCCT 19727 CAA GA A A
 AGGG G AGG GAG ACAG
 |||| | || || ||||
 TCCC C TCC CTT TGTC
 _ TG _ A
 GAM1960 SCAM-1 3' CTGCCCTCTTTGCCTTCT 20503 A _
 AGAGGGCAAGGA GG AG
 ||||| || ||
 TCTTCCGTTTCT CC TC
 C G
 GAM1960 SCYA22 3' CTGTCCTGTCCTTGCCCCT 92592 A _ G
 AG GGGCAAGGA AGGA AG
 || ||||| || ||
 TC CCGTTCCT TCCT TC
 _ G G
 GAM1960 SCYA22 3' TTCCACTTTCCTGCCTCCT 92616 AG A AGA
 AG GGCA GGAAGG GAA
 || |||| |||| ||

		TC CCGT CCTTTC CTT		
		CT C AC_		
GAM1960	SDCCAG43	3' CTGCCCTCTCTCCTGCCC	70894	A AG AA
		GGGCA GGA GAGAG CAG		
		CCCGT CCT CTCTC GTC		
		_ _ CC		
GAM1960	SDCCAG43	3' TGCCCTCACCTGTCCCCCT	70898	CAA _ A AA
		AGGG GGA AGG GAG CA		
		TCCC CCT TCC CTC GT		
		_ _ G A CC		
GAM1960	SDS3	3' CTGTATTTCTTCTCTGCCCTC	69746	AG AGA
		GAGGGCA GAAGGAG ACAG		
		CTCCCGT CTTCTTT TGTC		
		CT A_		
GAM1960	SEC24C	3' CTGTTCCCTCATTCTACCCTCT	18195	CAA G A
		AGAGGG GGAA GAG GAACAG		
		TCTCCC TCTT CTC CTTGTC		
		A_ A C		
GAM1960	SEMA7A	3' TCTGTCCAGCCCTGTCCTCT	14612	A AA G
		AGAGGGCA GG GGA AGA		
		TCTCCTGT CC CCT TCT		
		C GA G		
GAM1960	SP2	3' CTGTTCCCTGTATTGTCCTC	13330	GGA AGA
		GAGGGCAA AGG GAACAG		
		CTCCTGTT TCC CTTGTC		
		ATG _		
GAM1960	SPRY1	3' CTGCCCTCTCCTTCTTTCTCCT	65632	C AA
		AGGG AAGGAAGGAGAG CAG		
		TCCT TTTCTTCCTCTC GTC		
		C CC		
GAM1960	SSH-3	3' CTCCCTGCACCTCCTGTCCTCT	35791	A _ _ _ A
		AGAGGGCA GGA AGG GAG		
		TCTCCTGT CCT TCC CTC		
		_ CCACG _		
GAM1960	STK17A	3' TGTTCCTCTCTCACACTCT	17669	GGCAAG AG
		AGAG GA GAGAGAACA		
		TCTC CT CTCTCTTGT		
		ACA_ _		
GAM1960	STMN3	3' CTGGCCCCTCCTGTGCCCTCT	32466	_ A_ AG
		AGAGGGCA AGGA GG AG		

TCTCCCGT TCCT CC TC
 G CC GG
 GAM1960 STX12 5' TTAGCTCCTTCCCCGCCCTT 66954 AA AG
 GAGGGC GGAAGGAG AA
 ||||| ||||| ||
 TTCCCG CCTTCCTC TT
 CC GA
 GAM1960 SYT12 3' CTGACTCCCCCCTGCCCTCT 96381 A AA AGAA
 AGAGGGCA GG GGAG CAG
 ||||| || ||| |||
 TCTCCCGT CC CCTC GTC
 C CC A__
 GAM1960 TIGD5 3' TCTCTCCTCCCCTCCCCT 52772 CA A_
 AGGG AGG AGGAGAGA
 ||| || |||||
 TCCC TCC TCCTCTCT
 CC CC
 GAM1960 TOB2 3' TCCTCTATCTATCCCTCT 33243 CAA A A
 AGAGGG GGA GGAG GA
 ||||| ||| ||| ||
 TCTCCC TCT TCTC CT
 TA_ A _
 GAM1960 ZDHHC7 3' CTGTGCGGCCCTTCGTTGCCCT 35321 G AGAGA
 C GAGGGCAA GAAGG ACAG
 ||||| |||| |||
 CTCCCGTT CTTCC TGTC
 G CGGCG
 GAM1960 ZFP91 3' CTGTTCTCCCTCTGTTGCTC 54875 _ A A
 GGGCAA GGA GG GAGAACAG
 ||||| ||| || |||||
 CTCGTT TCT CC CTCTTGTC
 G _ _
 GAM1960 ZFP91 3' TCCCCTGTTCTCCCTCT 54879 CA _ A
 AGAGGG AGGA AGG GA
 ||||| |||| ||| ||
 TCTCCC TCTT TCC CT
 _ G C
 GAM1960 LOC126122 3' TGTCCCTCCTTTCCCCC 74907 CAA A A
 GGG GGAAGGAG GA CA
 ||| ||||| ||| ||
 CCC CTTTCCTC CT GT
 C__ C G
 GAM1960 LOC126964 3' CTCCCTGCTGTGCTCTCT 75114 A A A
 AGAGGGCA GG AGG GAG
 ||||| || ||| |||
 TCTCTCGT TC TCC CTC
 G G _
 GAM1960 LOC127002 5' CTGTCCTTCCCTTCCCTCT 75125 CAA G
 AGAGGG GGAAGGA AG
 ||||| ||||| ||

TCTCCC CCTTCCT TC
TTC G
GAM1960 LOC127544 3' TTCCCCTCCCCTCCCCTC 75169 CA AA A_
GAGGG AGG GGAG GAA
||||| ||| ||||| |||
CTCCC TCC CCTC CTT
C_ _ CC
GAM1960 LOC128954 5' TCTCTCCTCTTACTCCCT 76307 CA_ A
AGGG AGGA GGAGAGA
||||| ||||| |||||
TCCC TTCT CCTCTCT
TCA _
GAM1960 LOC138389 5' TTTCTCCCTCCCTCCCTCT 76748 CAA A
AGAGGG GGA GGAGAGA
||||| ||| |||||
TCTCCC CCT CCTCTTT
TC_ C
GAM1960 LOC144519 5' CTGCTCCCCCTTTGCCTTCT 77371 AA _
AGAGGGCAAGG GGAG AG
||||||| ||| ||
TCTTCCGTTTC CCTC TC
CC G
GAM1960 LOC145809 3' CTGCTCCCTGATTCCCCCTTGT 84495 A AA A____ A
CCCCT AG GGGCAAGG GGAG GA CAG
|| ||||| ||| || |||
TC CCTGTTCC CCTT CT GTC
C C_ AGTCC C
GAM1960 LOC146287 5' CTGCGTTTCCTTTCCCACCCTCT 84631 CAA A AA
AGAGGG GGAAGG GAG CAG
||||| ||||| ||| |||
TCTCCC CCTTTC CTT GTC
AC_ _ GC
GAM1960 LOC146669 3' TCATTCCTTCCCCACCCCT 78665 A CAA A
AG GGG GGAAGGAG GA
|| ||| ||||| ||
TC CCC CCTTCCTT CT
_ ACC A
GAM1960 LOC147639 5' CTGTTCTCACCTTGGCCCCCT 79010 A A AA A
AG GGGC AGG GG GAGAACAG
|| ||| ||| || |||||
TC CCCG TTC CC CTCTTGTC
_ G _ A
GAM1960 LOC148894 5' CTA CTCCCTCCTGTTCTC 85420 CA A _
GAGGG AGGA GGAG AG
||||| ||| ||||| ||
CTCCT TCCT CCTC TC
TG C A
GAM1960 LOC148930 3' CTGCCTATTCCCTGCCCCCT 79843 A A _ _
AG GGGCA GGA AGG AG
|| ||||| ||| ||| ||

	TC CCCGT CCT TCC TC		
	— C TA G		
GAM1960 LOC149670 5'	CTGCCACTCCTTCCTCACCCCTC 80303	CA	AGAA
	GAGGG AGGAAGGAG CAG		
	CTCCC TCCTTCCTC GTC		
	AC ACC_		
GAM1960 LOC149950 3'	CTATTCTGTTCCCTTGCCCT 80368	—	—
	AGGGCAAGGAA GGAG AG		
	TCCCGTTCCTT TCTT TC		
	G A		
GAM1960 LOC150135 3'	TTCCCTCCTTCCCTCCCCTCT 80396	CAA	A
	AGAGGG GGAAGGAG GAA		
	TCTCCC CCTTCCTC CTT		
	CTC C		
GAM1960 LOC150170 5'	TGTTCTCCCATCACACCCT 80416	CAAG	A A
	AGGG GA GG GAGAACA		
	TCCC CT CC CTCTTGT		
	ACA_ A _		
GAM1960 LOC150175 5'	TGTTCTCCCATCACACCCT 80455	CAAG	A A
	AGGG GA GG GAGAACA		
	TCCC CT CC CTCTTGT		
	ACA_ A _		
GAM1960 LOC150215 5'	TGTTCTCCCATCACACCCT 80458	CAAG	A A
	AGGG GA GG GAGAACA		
	TCCC CT CC CTCTTGT		
	ACA_ A _		
GAM1960 LOC150218 5'	TGTTCTCCCATCACACCCT 80527	CAAG	A A
	AGGG GA GG GAGAACA		
	TCCC CT CC CTCTTGT		
	ACA_ A _		
GAM1960 LOC150295 3'	GTGGCTCCTTCCTTGCCC 86156	AGA	
	GGGCAAGGAAGGAG AC		
	CCCGTTCCTTCCTC TG		
	GG_		
GAM1960 LOC151429 3'	CTTTCCCCCACTGCCCTCT 86537	A_	AA
	AGAGGGCA GG GGAGAG		
	TCTCCCGT CC CCTTTC		
	CA C_		
GAM1960 LOC151470 3'	CTCCTTCCCTGTGTCTTTT 81056	A__	
	AGAGGGCA GGAAGGAG		

TTTTCTGT CCTTCCTC
 GTC
 GAM1960 LOC152220 3' TTCTTCCCTCCTTTCCCCCT 86772 A C A AG
 AG GGG AAGGA GG AGAA
 || ||| ||||| || ||||
 TC CCC TTCCT CC TCTT
 C T _ CT
 GAM1960 LOC152762 3' TTTCTCCTCCCCCGCCCCCT 81540 A AA A
 AG GGGC GG AGGAGAGA
 || |||| || |||||
 TC CCGG CC TCCTCTTT
 _ CC C
 GAM1960 LOC153232 5' CTCCTTACCCTGCCCCCT 87182 A A _
 AG GGGCA GG AAGGAG
 || |||| || |||||
 TC CCGT CC TTCCTC
 C C A
 GAM1960 LOC157586 5' CTTTCCCTCCGCGCCCTC 82399 AA A
 GAGGGC GGA GGAGAG
 ||||| ||| |||||
 CTCCCG CCT CCTTTC
 CG C
 GAM1960 LOC158046 3' CTGTTCTCCCCCGCACC 59903 _ AA AA A
 GG GC GG GG GAGAACAG
 || || || || |||||
 CC CG CC CC CTCTTGTC
 A _ C _ _
 GAM1960 LOC158056 5' CTGTCCCAATACCCTCCTTGCT 82591 A A AGAGA_
 CCCT AG GGGCAAGGA GG ACAG
 || ||||| || ||||
 TC CTCGTTCCCT CC TGTC
 C C ATAACCC
 GAM1960 LOC158125 5' CTGCCCTCTGCTGCCTTCT 82617 A_ A _
 AGAGGGCA GGA GG AG
 ||||| ||| || ||
 TCTTCCGT TCT CC TC
 CG C G
 GAM1960 LOC158549 3' CTACTCCCTCCTTTTCCTTC 88221 C A _
 GAGGG AAGGA GGAG AG
 |||| |||| |||| ||
 CTTCC TTCCT CCTC TC
 T C A
 GAM1960 LOC158549 5' TTCTCCTTCCTCAGCCTC 88233 GCA
 GAGG AGGAAGGAGAG
 ||| |||||
 CTCC TCCTTCCTCTT
 GAC
 GAM1960 LOC159090 5' CTGTCCTCCTCCCTCCCCTCTG 82961 A_ A _ A
 CCCTCT AGAGGGCA GGA GGAG AG ACAG
 ||||| ||| |||| || ||||

	TCTCCCGT CCT CTC TC TGTC	
	CTCC C C C	
GAM1960 LOC161489 5'	CTGTGGCCCTTCCTTGCCTTC 88454	AGAGA
	GAGGGCAAGGAAGG ACAG	
	CTTCCGTTCTTCC TGTC	
	CGG__	
GAM1960 LOC168742 5'	CTGTTCTCCACACTTACTCTCT 83595	C GAA GA
	AGAGGG AAG GGAGA ACAG	
	TCTCTC TTC CCTCT TGTC	
	A ACA _	
GAM1960 LOC196500 3'	CTGTCCCCTCCTTTCTCCCTC 89083	CA _ AGA
	GAGGG AGGAA GGAG ACAG	
	CTCCC TCCTT CCTC TGTC	
	_ T CCC	
GAM1960 LOC197342 3'	CTCTCACCTTGCCCTCT 89364	AAG
	AGAGGGCAAGG GAGAG	
	TCTCCCGTTCC CTCTC	
	CA_	
GAM1960 LOC201283 3'	GTGAGCCTTCCTTACTCTCT 61053	C AGAGA
	AGAGGG AAGGAAGG AC	
	TCTCTC TTCCTTCC TG	
	A GAG__	
GAM1960 LOC202460 5'	TGTTTCATCCCCTCCCTCT 90684	CA AA GA
	AGAGGG AGG GGA GAACA	
	TCTCCC TCC CCT CTTGT	
	_ _ A_	
GAM1960 LOC203068 5'	CTTTCCCTCCGCGCCCTC 90755	AA A
	GAGGGC GGA GGAGAG	
	CTCCCG CCT CCTTTC	
	CG C	
GAM1960 LOC219654 3'	CTCCCTTTCCTTCCCCTCT 92931	C A
	AGAGGG AAGGAAGG GAG	
	TCTCCC TTCCTTTC CTC	
	C C	
GAM1960 LOC219700 5'	CTGTCCTCCCCACCCACCTC 94651	CAA AA A A
	GAGGG GG GG GAG ACAG	
	CTCCC CC CC CTC TGTC	
	AC_ CA C C	
GAM1960 LOC219731 3'	CTGTCCTCCTTGCCTTCT 94705	A G
	AGAGGGCAAGGA GGA AG	

TCTTCCGTTTCCT CCT TC
 _ G
 GAM1960 LOC219843 5' TGTTCTCTATCAGCCTCT 93138 GCAAG AGG
 AGAGG GA AGAGAACA
 |||| || |||||
 TCTCC CT TCTCTTGT
 GA__ A__
 GAM1960 LOC220980 5' TGTTCTCTGCCACCCACCT 94775 CAA AA _
 GGG GG GG AGAGAACA
 || | || |||||
 TCC CC CC TCTCTTGT
 A__ CA G
 GAM1960 LOC221466 3' CTGTTCCCCATTTGCCTCTCT 95314 _ GAA AGA
 AGAG GGCAAG GG GAACAG
 |||| || || |||||
 TCTC CCGTTT CC CTTGTC
 T AC_ _
 GAM1960 LOC221935 3' TCCCTCCCTCCTTCCCTC 94208 C A A
 GAGGG AAGGA GGAG GA
 |||| || || || ||
 CTCCC TTCCT CCTC CT
 _ C C
 GAM1960 LOC221975 5' CTACTGCTCCCTCCCTCT 94189 CA A G _
 AGAGGG AGG AG AG AG
 |||| || || || ||
 TCTCCC TCC TC TC TC
 _ C G A
 GAM1960 LOC221975 5' CTGCTCCCTCCCTCTCTTGCCT 94191 G _ A A A
 CT AGAGG CAAG GA GGAG GA CAG
 |||| || || || || ||
 TCTCC GTTC CT CCTC CT GTC
 _ T C C C
 GAM1960 LOC253891 3' CTGCCTCTCTTCCTTCCCCC 96066 CAA _ A_
 GGG GGAAGGA GAGA CAG
 || ||||| || ||
 CCC CCTTCCT CTCT GTC
 _ T CC
 GAM1960 LOC254182 3' CTGCATCCCTCCCTTGCTCCCT 97747 A A A GAA
 AG GGGCAAGG AGG GA CAG
 || ||||| || || ||
 TC CTCGTTCC TCC CT GTC
 C C _ AC_
 GAM1960 LOC254302 3' TCTCTCCTCCCTCTGGCTCT 97903 A__ A
 AGGGC AGG AGGAGAGA
 |||| || |||||
 TCTCG TCC TCCTCTCT
 GTC C
 GAM1960 LOC254532 5' GTCCTCCCCTCCCCTTCCCTT 98458 C A_ A A
 GAGGG AAGG AGG GAG AC
 |||| || || || ||

TTCCC TTCC TCC CTC TG
 _ CC C C
 GAM1960 LOC254874 3' TCTCTCCTCCCTCTGGCTCT 97901 A__ A
 AGGGC AGG AGGAGAGA
 |||| | |||||
 TCTCG TCC TCCTCTCT
 GTC C
 GAM1960 LOC255147 3' TGTTTCCTCCTTCCCCCT 97410 CAA AG
 AGGG GGAAGGAG AACA
 ||| ||||| |||
 TCCC CCTTCCTC TTGT
 ____ CT
 GAM1960 LOC257438 3' CTGTCCTCTAGAATTCTTCCTC 95593 CA ____ A
 CCCTC GAGGG AGGAAGG AGAG ACAG
 |||| ||||| ||| |||
 CTCCC TCCTTCT TCTC TGTC
 C_ TAAGA C
 GAM1960 LOC257551 3' CTGTTCCCATGTAGCCCCCTGG 99557 G A AA AGA____
 CCTCT AGAGG CA GG GG GAACAG
 |||| || || |||||
 TCTCC GT CC CC CTTGTC
 G C _ GATGTACC
 GAM1960 LOC257601 3' CTGTTCCCATGTAGCCCCCTGG 99651 G A AA AGA____
 CCTCT AGAGG CA GG GG GAACAG
 |||| || || |||||
 TCTCC GT CC CC CTTGTC
 G C _ GATGTACC
 GAM1960 LOC51308 3' CTGCTCCTATGACCTTGCTCCC 33965 A A__ _
 T AG GGGCAAGG AGGAG AG
 || ||||| |||||
 TC CTCGTTCC TCCTC TC
 C AGTA G
 GAM1960 LOC64116 5' CTGTCCCCCTTTGTCCTCT 42460 AA G
 AGAGGGCAAGG GGA AG
 ||||| ||| ||
 TCTCCTGTTTC CCT TC
 CC G
 GAM1960 LOC64744 3' TCCTCTTTTCCTACCTCT 62443 GCAA A
 AGAGG GGAAGGAG GA
 |||| ||||| ||
 TCTCC CTTTTCTC CT
 ATC_ _
 GAM1960 LOC90139 3' CTGCTCTCTTCTCTCCCCTCT 56268 CAA GA A
 AGAGGG G AGGAGAGA CAG
 |||| | ||||| |||
 TCTCCC C TCTTCTCT GTC
 ____ TC C
 GAM1960 LOC90288 3' TTCCCTCCCCTGACCTCT 62806 GCA AA A
 AGAGG AGG GGAG GAA
 |||| || |||| |||

		TCTCC TCC CCTC CTT		
		AG_ _ C		
GAM1960	LOC90499 3'	TTCTGCCCTTCCTTTCCCTC 63747	C	AG
		GAGGG AAGGAAGG AGAA		
		CTCCC TTCCTTCC TCTT		
		T CG		
GAM1960	LOC91445 3'	CTGTTCTCTTTCCCTTCCCCTC 61169	C	AG
		GAGGG AAGGA GAGAGAACAG		
		CTCCC TTCCT TTCTCTTGTC		
		C _		
GAM1960	LOC91663 3'	GTTCCCTCTCCAACCTCT 57224	GCAA	AG A
		AGAGG GGA GAG GAAC		
		TCTCC CCT CTC CTTG		
		AA_ _ C		
GAM1960	LOC92299 5'	TTCTCTCCTCCCCCTCCCTC 69377	CAA	A
		GAGGG GG AGGAGAGAA		
		CTCCC CC TCCTCTCTT		
		TCC C		
GAM1960	LOC92973 3'	CTGTTCCCTCCCCTCCCCTTC 71590	CA	AA A
		GAGGG AGG GGAG GAACAG		
		CTTCC TCC CCTC CTTGTC		
		CC _ C		
GAM1961	AEGL1 3'	CATCCTGATACATCCTGAAGT 8530	CAC	CT_
		ACTTCAGG ATGTG GATG		
		TGAAGTCC TACAT CTAC		
		_ AGTC		
GAM1961	CR2 3'	CTTATGAGATGCCTGAAG 10291	CATGTG	G
		CTTCAGGCA CT ATGAG		
		GAAGTCCGT GA TATTC		
		A_ G		
GAM1961	MAPK9 3'	CTCACCTCCGTGGGCCTGAA 12316	A	TGCTGA
		TTCAGGC CATG TGAG		
		AAGTCCG GTGC ACTC		
		G CTCC_		
GAM1961	MAPK9 3'	CTCACCTCCGTGGGCCTGAA 58176	A	TGCTGA
		TTCAGGC CATG TGAG		
		AAGTCCG GTGC ACTC		
		G CTCC_		
GAM1961	MAPK9 3'	CTCACCTCCGTGGGCCTGAA 58179	A	TGCTGA
		TTCAGGC CATG TGAG		

			AAGTCCG GTGC	ACTC		
			G CTCC__			
GAM1961	MAPK9	3'	CTCACCTCCGTGGGCCTGAA	58182	A	TGCTGA
			TTCAGGC CATG	TGAG		
			AAGTCCG GTGC	ACTC		
			G CTCC__			
GAM1961	NXF5	3'	TCAGTGCATTGCCTGAA	53692	C	TG
			TTCAGGCA ATG	CTGA		
			AAGTCCGT TAC	GACT		
			_ GT			
GAM1961	RPS6KA5	3'	TCAGCATATGCCTGAG	17652	CA	
			TTCAGGCA TGTGCTGA			
			GAGTCCGT ATACGACT			

GAM1961	SLC38A2	3'	CTCATCAGGCATAATGTCT	39114	CA	_
			AGGCA TGTGC TGATGAG			
			TCTGT ATACG ACTACTC			
			A_ G			
GAM1961	AEBP1	3'	CATCAGCACATGGAAG	8519	AGGCA	
			CTTC CATGTGCTGATG			
			GAAG GTACACGACTAC			

GAM1961	CABP2	3'	CACCAGCATGTTTCCTTGAAG	33476	CAC	A
			CTTCAGG ATGTGCTG TG			
			GAAGTTC TGTACGAC AC			
			CT_ C			
GAM1961	CABP2	3'	CACCAGCATGTTTCCTTGAAG	49127	CAC	A
			CTTCAGG ATGTGCTG TG			
			GAAGTTC TGTACGAC AC			
			CT_ C			
GAM1961	FLJ21432	3'	CTCACCAGGTTGGCGCCTGAA	44942	A_	TGTG A
			TTCAGGC CA CTG TGAG			
			AAGTCCG GT GAC ACTC			
			CG TG_ C			
GAM1961	GREAT	3'	CTCACCCACATGCCTGAA	56373	CA	CTGA
			TTCAGGCA TGTG TGAG			
			AAGTCCGT ACAC ACTC			
			_ CCC_			
GAM1961	KIAA0513	3'	CATCCATGTGCCAAAGT	29021	CA	TGCT
			ACTT GGCACATG GATG			

			TGAA CCGTGTAC CTAC		
			A_ _ _ _		
GAM1961	MDN1	3'	CAAAGCATGTACCTGAAGT 63357	C	GC
			ACTTCAGG ACATGT TG		
			TGAAGTCC TGTACG AC		
			A AA		
GAM1961	MGC10540	3'	CACACATGCGCCTGCAG 51357	T A C	
			CT CAGGC CATGTG TG		
			GA GTCCG GTACAC AC		
			C C _		
GAM1961	MRPL10	3'	CTCATCAGGTTACCCAGAAGT 59832	A CACAT _	
			ACTTC GG GTG CTGATGAG		
			TGAAG CC CAT GACTACTC		
			A _ _ _ TG		
GAM1961	PCAF	3'	CTCACCAAGCAGTGTGCCTAAA 15285	C G GA_	
	G		CTT AGGCACAT TGCT TGAG		
			GAA TCCGTGTG ACGA ACTC		
			A _ _ ACC		
GAM1961	RAI17	3'	CACCAGTGCAGCCTGAAGT 92898	ACA TG A	
			ACTTCAGGC TG CTG TG		
			TGAAGTCCG AC GAC AC		
			_ _ GT C		
GAM1961	RRP46	3'	CTCACCCCCTACAGCCTGAAG 39759	ACA CTGA_	
			CTTCAGGC TGTG TGAG		
			GAAGTCCG ACAT ACTC		
			_ _ CCCCC		
GAM1961	LOC123876	5'	TCATCTTTATGCCTGGA 74719	CATG CT	
			TTCAGGCA TG GATGA		
			AGGTCCGT AT CTA CT		
			_ _ TT		
GAM1961	LOC146515	3'	CACATACACCATGCCTGAAG 78517	CA_ C A	
			CTTCAGGCA TGTG TG TG		
			GAAGTCCGT ACAT AC AC		
			ACC _ _		
GAM1961	LOC153910	5'	CTCATCAGCACGTGTCTACAGT 81906	TC AT	
			ACT AGGCAC GTGCTGATGAG		
			TGA TCTGTG CACGACTACTC		
			CA _		
GAM1961	LOC201799	3'	CTCACCAAGCACATCTGAATGAG 90490	GG C A	
	G		CTTCA CA ATGTGCTG TGAG		

		GGAGT GT TACACGAC ACTC	
		AA C C	
GAM1961	LOC203392 5'	CAGCGAACTGTGCCTGAAGT 90909	TG_
		ACTTCAGGCACA TGCTG	
		TGAAGTCCGTGT GCGAC	
		CAA	
GAM1961	LOC220071 5'	TCATCAGGTCACCGAAGT 95082	A CACA TG
		ACTTC GG TG CTGATGA	
		TGAAG CC AC GACTACT	
		_ _ _ TG	
GAM1961	LOC253634 5'	TCACGACATGTGCCCAAGGT 98417	CA GC
		ACTT GGCACATGT TGA	
		TGGA CCGTGTACA ACT	
		AC GC	
GAM1962	CDH12 3'	CTTATCATTTAAAGTGGTGTA 15777	CCCAA GA
		TACACCACT GAA ATAAG	
		ATGTGGTGA TTT TATTC	
		AA_ AC	
GAM1962	GOCAP1 3'	ATTGTTCTTGGGAGCAGTGTA 43007	CA G
		TACAC CTCCCAAGAA AAT	
		ATGTG GAGGGTTCTT TTA	
		AC G	
GAM1962	DKFZp434N2435 5'	CTTATTACTGTGGGGTGGT 98090	T AGAAG
		ACCAC CCCA AATAAG	
		TGGTG GGGT TTATTC	
		_ GTCA_	
GAM1962	DKFZP564I122 3'	CTTATTCTTCTCCCTCATGTGT 63877	CACTCCCA
	A	TACAC AGAAGAATAAG	
		ATGTG TCTTCTTATTC	
		TACTCCC_	
GAM1962	FLJ21791 3'	CTTATTTGCAGAAAGTGGTGTA 62126	CCCAAGAA
		TACACCACT GAATAAG	
		ATGTGGTGA TTTATTC	
		AGACG_	
GAM1962	HMP19 3'	CTTATTCTTTGTTAGGAAAATG 88860	CCAC CAA_
	TA	TACA TCC GAAGAATAAG	
		ATGT AGG TTTCTTATTC	
		AAA_ ATTG	
GAM1962	KIAA1719 3'	TCTGTCTTGGGAGTGGTGTA 68742	_
		TACACCACTCCCAAGA AGA	

ATGTGGTGAGGGTTCT TCT
 G
 GAM1962 KIAA1853 3' TTTTCTTGGAAGCAGTG 69929 CA C
 CAC CT CCAAGAAGAA
 ||| || |||||
 GTG GA GGTTCTTTT
 AC A
 GAM1962 KIAA1877 3' CTTATTCTTCTGCCATGAGT 66748 CCA__
 ACTC AGAAGAATAAG
 ||| |||||
 TGAG TCTTCTTATTC
 TACCG
 GAM1962 KIAA1906 3' CTTATTCTTCTTGACTTTTGG 73571 CTCC_
 CCA CAAGAAGAATAAG
 ||| |||||
 GGT GTTCTTCTTATTC
 TTTCA
 GAM1962 OSBPL11 3' CTTAATTTCCCAAGAGTGGTG 43206 CCAA AA
 CACCACTC GAAG TAAG
 ||||| ||| |||
 GTGGTGAG CTTT ATTC
 AACC A_
 GAM1962 YME1L1 3' TCATTCTTGATGTGGTGTA 58438 TCC _
 TACACCAC CAAGAA GA
 ||||| |||||
 ATGTGGTG GTTCTT CT
 TA_ A
 GAM1962 ZNF262 3' CTTATTTTGTGTTGGGAGT 18723 A
 ACTCCCAAG AGAATAAG
 ||||| |||||
 TGAGGGTTT TTTTATTC
 G
 GAM1962 LOC91960 3' TGTGGCTTGGAACGTGGTGTA 68294 TC_ AAGA
 TACACCAC CCAAG ATA
 ||||| |||||
 ATGTGGTG GGTTT TGT
 CAA GG_
 GAM1963 BMP1 3' CTGAATACCCCAATGGCT 21530 _ C
 AGCCATTGGG AT CAG
 ||||| |||
 TCGGTAACCC TA GTC
 CA A
 GAM1963 ISGF3G 3' GATGAGGGTCCCATGGC 21407 T AGA
 GCCAT GGGATCC CATC
 ||||| |||||
 CGGTA CCCTGGG GTAG
 _ A_
 GAM1963 NR5A2 5' TCTGATGTGTCCTTCCCAAGGC 15118 A TCCAG
 GCC TTGGGA ACATCAGA
 ||| ||||| |||||

CGG AACCTT TGTAGTCT
 _ TCCTG
 GAM1963 PKD2 3' TCTGATGTCTGTGGGACTAA 60720 GA _
 TTGG TC CAGACATCAGA
 |||| || |||||
 AATC GG GTCTGTAGTCT
 AG T
 GAM1963 SLA 3' CTGATGTCTGCAGCCATGGCT 23112 TG ATC
 AGCCAT GG CAGACATCAG
 ||||| || |||||
 TCGGTA CC GTCTGTAGTC
 _ GAC
 GAM1963 SPINT2 5' CTGATCGCGAGACCCCAACGGC 63849 A A CAGAC
 T AGCC TTGGG TC ATCAG
 |||| ||| ||||
 TCGG AACCC AG TAGTC
 C C AGCGC
 GAM1963 DKFZP434G1411 3' CTGATGTCTAAATTGCAGTG 93731 G CC
 CATTG GAT AGACATCAG
 |||| ||| |||||
 GTGAC TTA TCTGTAGTC
 G AA
 GAM1963 DKFZp434G179 3' TCTGATGTCTTCAAACAAACAG 80893 CA_ GGATCC
 CT AGC TTG AGACATCAGA
 ||| ||| |||||
 TCG AAC TCTGTAGTCT
 ACA AAAC_
 GAM1963 DUSP9 3' TCGTTGCACTGGATCCAGTGG 9158 A_ TCA
 CT AGCCATTGGGATCCAG CA GA
 ||||| ||| ||
 TCGGTGACCCTAGGTC GT CT
 AC TG_
 GAM1963 FLJ10111 3' GATGAGGGTCCCAGTGGC 36302 T AGA
 GCCAT GGGATCC CATC
 |||| ||||| ||||
 CGGTA CCCTGGG GTAG
 _ A_
 GAM1963 FLJ21135 5' ATGGCCCGGATCCCGACGGC 46347 A AGA_
 GCC TTGGGATCC CAT
 ||| ||||| |||
 CGG AGCCCTAGG GTA
 C CCG
 GAM1963 FLJ21865 3' TGTCTGGACCCACGGC 43115 AT A
 GCC TGGG TCCAGACA
 ||| ||| |||||
 CGG ACCC AGGTCTGT
 C_ C
 GAM1963 KIAA0542 5' GTCAGGCCCGATGGCT 66666 AT A
 AGCCATTGGG CC GAC
 ||||| ||| |||

TCGGTAGCCC GG CTG
 — A
 GAM1963 KIAA0644 3' CTAATGCCTGGATCTGTG 29725 TG A C
 CAT GGATCCAG CAT AG
 ||| ||||| ||| ||
 GTG TCTAGGTC GTA TC
 — C A
 GAM1963 MIG2 3' CTAATGCCTGGACTGGC 72858 TTGG A A C
 GCCA G TCCAG CAT AG
 ||| | |||| ||| ||
 CGGT C AGGTC GTA TC
 — — C A
 GAM1963 LOC126767 3' CTGATGTCCAGAGGACGTGGT 75959 T GGA CA
 GCCAT G TC GACATCAG
 |||| | || |||||
 TGGTG C AG CTGTAGTC
 _ AGG AC
 GAM1963 LOC146562 5' TCTGATGCCCCGCGGTAGCCAAT 58256 _ GAT AGA_
 GAGCT AGC CATTGG CC CATCAGA
 ||| ||||| || |||||
 TCG GTAACC GG GTAGTCT
 A GAT CGCCC
 GAM1963 LOC146957 3' CTGATTTTGACCCCAAGTGGC 78814 ATC C
 GCCATTGGG CAGA ATCAG
 ||||| ||| |||||
 CGGTGACCC GTTT TAGTC
 CA_ _
 GAM1963 LOC220980 5' TCTGATGTCTATTGTGAATTGG 94774 _ G CC
 CT AGCCA TTG GAT AGACATCAGA
 |||| ||| ||| |||||
 TCGGT AGT TTA TCTGTAGTCT
 TA G _
 GAM1963 LOC221486 3' TCTGATGTCCATTTGTCCCAAT 92662 C CCA_
 AGCT AGC ATTGGGAT GACATCAGA
 ||| ||||| |||||
 TCG TAACCCTG CTGTAGTCT
 A TTTAC
 GAM1963 LOC221496 3' TCTGATGTCTGGATGATCGGC 93644 _ GGG
 GCC ATT ATCCAGACATCAGA
 ||| ||| |||||
 CGG TAG TAGGTCTGTAGTCT
 C _
 GAM1963 LOC91050 3' CTGAGACTAGATCCCAAAGCT 65374 CA C ACA
 AGC TTGGGATC AG TCAG
 ||| ||||| || |||
 TCG AACCCTAG TC AGTC
 A_ A AG_
 GAM1964 ADCY1 5' ACGACAATGTGAGCATC 94336 AG
 GATGCTCACAT GTTGT
 ||||| |||||

			CTACGAGTGTA CAGCA		
			A_		
GAM1964	C8orf1	3'	ATAGCATGATGTGAGCATC 16343		AG_
			GATGCTCACAT GTTGT		
			CTACGAGTGTA CGATA		
			GTA		
GAM1964	CDH12	3'	ATAGCTATGTGGCATCA 15776	T	G
			TGATGC CACATAG TTGT		
			ACTACG GTGTATC GATA		
			- -		
GAM1964	HIP1	3'	ACAAACTTGTGAGCATCA 19242	T	G
			TGATGCTCACA AG TTGT		
			ACTACGAGTGT TC AACA		
			- A		
GAM1964	DKFZp547l224	5'	ATGGCCTATGTGAGATCA 39948	G	TG
			TGAT CTCACATAGGT T		
			ACTA GAGTGTATCCG A		
			- GT		
GAM1964	DKFZp761P1010	3'	GGCACAAATAAGCTCA 37943	T	CACA GG
			TGA GCT TA TTGTGCC		
			ACT CGA AT AACACGG		
			- ____ A_		
GAM1964	FLJ13114	3'	ACAGGCCAGGTGAGCATCA 44889	ATA	_
			TGATGCTCAC GGT TGT		
			ACTACGAGTG CCG ACA		
			GA_ G		
GAM1964	FLJ23024	3'	TGGCACAACTCAGCTCA 46851	T	CACAT
			TGA GCT AGGTTGTGCCA		
			ACT CGA TCCAACACGGT		
			- C ____		
GAM1964	HNK-1ST	5'	ACAGCAAGGAAATGTGAGCCCC 17946	AT	AG ____
	A		TG GCTCACAT GTTGT		
			AC CGAGTGTA CGACA		
			CC AAGGAA		
GAM1964	KIAA0459	3'	ACAATCATGTGAGCTCA 61639	T	A
			TGA GCTCACAT GGTGT		
			ACT CGAGTGTA CTAACA		
			- -		
GAM1964	KIAA1466	3'	ATAACCTATGAAACATCA 72405	CTCA	
			TGATG CATAGGTTGT		

		ACTAC GTATCCAATA		
		AAA_		
GAM1964	KIAA1954	5' ACAGCTTACTGAGCATCA	78220	CA
		TGATGCTCA TAGGTTGT		
		ACTACGAGT ATTCGACA		
		C_		
GAM1964	PACSIN2	3' ATGGCACAGATTGATGCGCACC	24296	A T _ TAGG
	A	TG TGC CA CA TTGTGCCAT		
		AC ACG GT GT GACACGGTA		
		C C A TA_		
GAM1964	PARVA	3' GGCCCATGTGAGCATCA	37183	A TTGT
		TGATGCTCACAT GG GCC		
		ACTACGAGTGTA CC CGG		
		- - - - -		
GAM1964	RoXaN	3' GCACACATGTGAGCACA	47292	A AGGT
		TG TGCTCACAT TGTGC		
		AC ACGAGTGTA ACACG		
		- C_		
GAM1964	LOC148638	3' ATGGCCATGTGAGCACA	79665	A A TG
		TG TGCTCACAT GGT T		
		AC ACGAGTGTA CCG A		
		- - - GT		
GAM1964	LOC148696	5' GGCCAGCATTGAGCATCA	85348	CATAG T
		TGATGCTCA GTTG GCC		
		ACTACGAGT CGAC CGG		
		TA_ -		
GAM1964	LOC200609	5' ATAACACTGTGCAATCATCA	91658	CTCA _
		TGATG CATAG GTTGT		
		ACTAC GTGTC CAATA		
		TAAC A		
GAM1964	LOC203235	3' ATGACACAACCTGAGAGGCACC	92097	A CACA C
	A	TG TGCT TAGGTTGTG CAT		
		AC ACGG GTCCAACAC GTA		
		C AGA_ A		
GAM1964	LOC219667	3' GCCAGCCTATGCAACATCA	92948	CTCA T
		TGATG CATAGGTTG GC		
		ACTAC GTATCCGAC CG		
		AAC_ -		
GAM1964	LOC220514	3' ATGGCACAGATTGATGCGCACC	61072	A T _ TAGG
	A	TG TGC CA CA TTGTGCCAT		

AC ACG GT GT GACACGGTA
 C C A TA__
 GAM1964 LOC221463 3' GGCATGGCACGTGAGCAGCA 93706 A ATAG TG
 TG TGCTCAC GT TGCC
 || ||||| || ||||
 AC ACGAGTG CG ACGG
 G CA__ GT
 GAM1965 RBM8A 3' TATTAGAACTGGTTCCC 18812 CAATT
 GGGA TCAGTTCTAATA
 |||| |||||
 CCCT GGTCAAGATTAT
 T____
 GAM1965 PELI1 5' ATTATTGGGCAAATGTCCCA 40626 A CA T
 TGGGACA TTT GT CTAATAAT
 ||||| ||| || |||||
 ACCCTGT AAA CG GGTTATTA
 A _ _
 GAM1965 PTK9 3' AGAACTGAAATCATTCCA 12554 CA
 TGGGA ATTTCAAGTTCT
 |||| |||||
 ACCTT TAAAGTCAAGA
 AC
 GAM1965 LOC131870 3' TATCAGAAGGGAATTGACCCA 75511 A AG A
 TGGG CAATTC TTCT ATA
 |||| ||||| |||||
 ACCC GTTAAGG AAGA TAT
 A G_ C
 GAM1965 LOC145842 5' TATTAGAAATTGTTCCCA 77996 _ TCAGT
 TGGGA CAATT TCTAATA
 |||| |||| |||||
 ACCCT GTTAA AGATTAT
 T _____
 GAM1966 FLRT3 3' TTGTAGTATAAGCACAGG 26122 ACAC CCGC
 CCTG TGC TACTACAA
 |||| ||| |||||
 GGAC ACG ATGATGTT
 _____ AAT_
 GAM1966 MAN2A2 3' CTTGGTCAGAGTGGGCAGTGCC 21509 A ACTA_
 AGG CCTG CACTGCCCGCT CAAG
 |||| ||||| |||||
 GGAC GTGACGGGTGA GTTC
 C GACTG
 GAM1966 T 3' TGCAGTAGCGGTGCTGTCCCAG 13509 AC T _ A
 CTG AC GC CCGCTACT CA
 ||| ||| ||||| ||
 GAC TG CG GGCGATGA GT
 CC T T C
 GAM1966 WTAP 3' TGTAGTAGTTTCAGTGTTAG 18141 CCC
 CTGACACTG GCTACTACA
 ||||| |||||

			GATTGTGAC	TGATGATGT			
			TT_				
GAM1966	FLJ20507	3'	TGTAGGGCAGTGCCAGG	35754	A	GCTAC	
			CCTG CACTGCCC	TACA			
			GGAC GTGACGGG	ATGT			
			C				
GAM1966	FLJ20507	3'	TGTAGGGCAGTGCCAGG	60855	A	GCTAC	
			CCTG CACTGCCC	TACA			
			GGAC GTGACGGG	ATGT			
			C				
GAM1966	GMPPA	5'	CTTGCAGTAGCGGGCGGCAG	72648	ACA	A	
			CTG CTGCCCCGCTACT CAAG				
			GAC GCGGGCGATGA GTTC				
			C				
GAM1966	KIAA0379	5'	CTTGTAGTGAGGAAGCAGTTCA	68715	C	GC	
			GG CCTGA ACTGC CC TACTACAAG				
			GGACT TGACG GG GTGATGTTC				
			AA A_				
GAM1966	KIAA0964	3'	AGCCCTGGGCAGTGTGAGG	30444			
			CCTGACACTGCCC GCT				
			GGACTGTGACGGG CGA				
			TCC				
GAM1966	MVD	3'	CTTGCTGTGGGGCAGTGCAGG	11717	A	GC TA	
			CCTG CACTGCCC TAC CAAG				
			GGAC GTGACGGG GTG GTTC				
			TC				
GAM1966	ST7L	3'	GTAGTAGCAGGCAGTTC	35340	C	C	
			GA ACTGCC GCTACTAC				
			CT TGACGG CGATGATG				
			A				
GAM1966	ST7L	3'	GTAGTAGCAGGCAGTTC	57817	C	C	
			GA ACTGCC GCTACTAC				
			CT TGACGG CGATGATG				
			A				
GAM1966	ST7L	3'	GTAGTAGCAGGCAGTTC	58285	C	C	
			GA ACTGCC GCTACTAC				
			CT TGACGG CGATGATG				
			A				
GAM1966	WDR13	3'	GGCAGCGGGCAGCTCCAGG	35843	ACA	A	
			CCTG CTGCCCCGCT CT				

			GGAC GACGGGCGA GG		
			CTC C		
GAM1966	LOC145980	5'	AGTGCCGGGCAGTTCAGG 84579	C	C
			CCTGA ACTGCCCCG TACT		
			GGA CT TGACGGGC GTGA		
			— C		
GAM1966	LOC148397	3'	AGTGCCAGGCAGTGT CAGG 79558		C_ T
			CCTGACACTGCC GC ACT		
			GGA CT GTGACGG CG TGA		
			AC —		
GAM1966	LOC150605	5'	TGTTTCTGGGCAGTGCAGG 86264	A	CTACT
			CCTG CACTGCCCCG ACA		
			GGAC GTGACGGGT TGT		
			— CTT—		
GAM1966	LOC162333	5'	TAGTAGTGGGCAACATCA 88501	CAC	
			TGA TGCCCCGCTACTA		
			ACT ACGGGTGATGAT		
			ACA		
GAM1966	LOC199907	3'	TGTACATGGGCAGTATCAG 89832	C	CTAC
			CTGA ACTGCCCCG TACA		
			GACT TGACGGGT ATGT		
			A AC—		
GAM1966	LOC203246	3'	TTGTAGTAGACAGCCAGG 90840	ACACT	CCG
			CCTG GC CTACTACAA		
			GGAC CG GATGATGTT		
			— ACA		
GAM1966	LOC220753	3'	CTTGTAGAGGTGGGCAGTCCAG 94533	AC	A
			CTG ACTGCCCCGCT CTACAAG		
			GAC TGACGGGTGG GATGTTC		
			C_ A		
GAM1967	EML1	3'	GAATTGTCCTAAAAGGACAGA 60449	CTAC	GGT
			TCTGTCCTT AGGA GTTC		
			AGACAGGAA TCCT TAAG		
			AA_ GGT		
GAM1967	EPHB2	3'	AACACTTTCAGAAAAACA 34342	CC	ACA
			TGT TTCT GGAGGTGTT		
			ACA AAGA CTTTCACAA		
			AA —		
GAM1967	EPHB2	3'	AACACTTTCAGAAAAACA 16695	CC	ACA
			TGT TTCT GGAGGTGTT		

		ACA AAGA CTTTCACAA	
		AA ____	
GAM1967	GYS1	3' GAATCCGCCTGCAGAGGACAGA 89783	T A A T
		TCTGTCCT CT CAGG GG GTTC	
		AGACAGGA GA GTCC CC TAAG	
		_ C G _	
GAM1967	HAO2	3' AAGATCTCAAAAGGACAGA 33701	CTACAG G
		TCTGTCCTT GAGGT TT	
		AGACAGGAA CTCTA AA	
		AA____ G	
GAM1967	LAIR1	3' ACTTCCTGAGAAGGACAGA 41661	A
		TCTGTCCTTCT CAGGAGGT	
		AGACAGGAAGA GTCCTTCA	
		-	
GAM1967	NID	3' ACCCCTACACAAGGACAGA 11804	CTAC A
		TCTGTCCTT AGG GGT	
		AGACAGGAA TCC CCA	
		CACA _	
GAM1967	NUP98	3' GAACTATCCACAGAAGGAAGA 33325	G ACA GGT
		TCT TCCTTCT GGA GTTC	
		AGA AGGAAGA CCT CAAG	
		_ CA_ AT_	
GAM1967	PMM2	3' AACACCTCCTGGAACGA 72555	C TA
		TC TTC CAGGAGGTGTT	
		AG AAG GTCCTCCACAA	
		C _	
GAM1967	TACC1	3' GAACTGCTCTACAGAAGGACA 21873	ACA GT
		TGTCCTTCT GGAG GTTC	
		ACAGGAAGA TCTC CAAG	
		CA_ GT	
GAM1967	THBD	3' AACACCTCCCAGGAGACAG 6273	C ACA
		CTGTC TTCT GGAGGTGTT	
		GACAG AGGA CCTCCACAA	
		_ C_	
GAM1967	KIAA1735	5' GAACAGAACAGAAGGGACAGA 89005	_ ACAGGAGG
		TCTGTCC TTCT TGTTT	
		AGACAGG AAGA ACAAG	
		G CAAG____	
GAM1967	KIAA1977	5' TCCCGTAAAAGGGACAGA 74768	C_ A
		TCTGTCCTT TAC GGA	

			AGACAGGGA ATG CCT		
			AA C		
GAM1967 NR4A3	3'	AGCAGCTCCTGTAGAAAGCA	23717	CC	G
		TGT TTCTACAGGAG TGTT			
		ACG AAGATGTCCTC ACGA			
		A_ G			
GAM1967 PANK	3'	AACAGCCTCCCAAAGGACAGA	57158	CTACA	_
		TCTGTCCTT GGAGG TGTT			
		AGACAGGAA CCTCC ACAA			
		AAC_ G			
GAM1967 PYPAF4	3'	AACACCTGCAAAGGACAGG	79274	CTACAGG	
		TCTGTCCTT AGGTGTT			
		GGACAGGAA TCCACAA			
		ACG_			
GAM1967 SSH2	3'	GAACACCTTTATCAAAGGCA	62891	T CTACA	
		TG CCTT GGAGGTGTTT			
		AC GGAA TTTCCACAAG			
		_ ACTA_			
GAM1967 TU12B1-TY	3'	AACCTTTTCCTGTAAAAGGCCAG	33815	T C T	
A		TCTG CCTT TACAGGAGG GTT			
		AGAC GGAA ATGTCCTTT CAA			
		C A T			
GAM1967 LOC113523	3'	GATACTTCTTATAGAAAAACA	73424	CC C	
		TGT TTCTA AGGAGGTGTT			
		ACA AAGAT TTCTTCATAG			
		AA A			
GAM1967 LOC146517	3'	AACAAAGTAAATAGGACAGA	78503	TC_ AGGAGG	
		TCTGTCCT TAC TGTT			
		AGACAGGA ATG ACAA			
		TAA AA_			
GAM1967 LOC148696	5'	GGCACAGCAGGACAGA	85347	T ACAGGAG	
		TCTGTCCT CT GTGTT			
		AGACAGGA GA CACGG			
		C _			
GAM1967 LOC153163	3'	AATACCTCCTAAGAAGGACA	81654	AC	
		TGTCCTTCT AGGAGGTGTT			
		ACAGGAAGA TCCTCCATAA			
		A_			
GAM1967 LOC221456	5'	GAACAGTTACAAAAGGACAG	95292	CTACAGG G	
		CTGTCCTT AG TGTTT			

		GACAGGAA	TT ACAAG		
		ACA	G		
GAM1967	LOC221935 3'	ACAACTTGTAGGAAGACAGA	94197	C	AG
		TCTGTC TTCTACAGG	GT		
		AGACAG AGGATGTTC	CA		
		A	AA		
GAM1967	LOC253596 5'	AACATCTACGAAGAACAGA	97229	C	TACAGG
		TCTGT CTTC	AGGTGTT		
		AGACA GAAG	TCTACAA		
		A	CA		
GAM1967	LOC256310 5'	AACACCTTCTCAGAAGAACCGA	98095	T C	AC
		TC GT CTTCT	AGGAGGTGTT		
		AG CA GAAGA	TCTTCCACAA		
		C A	C		
GAM1968	KIAA1069 3'	TGACCTACATTCAACTGCAA	68535		C
		TTGCAGTTGAA	GT GTCG		
		AACGTCAACTT	CA CAGT		
		A	TC		
GAM1968	NICN1 3'	TGGCGACTTCATCTGCAA	51261	T	
		TTGCAG TGAAGTCGTCG			
		AACGTC ACTTCAGCGGT			
		T			
GAM1968	TEX27 3'	GCTGAACACCTGCAACTGCAA	41952	A TC	CG
		TTGCAGTTG	AG GT TAGC		
		AACGTCAAC	TC CA GTCG		
		G	CA A		
GAM1968	LOC142948 3'	TGGCCACCGGCCCAACTGCAG	83782	AA	TC A
		TTGCAGTTG	GTCG GT GCCA		
		GACGTCAAC	CGGC CA CGGT		
		C	C		
GAM1968	LOC146488 5'	GCTACAACCGCTTCAACAACAA	71359	CA	C C
		TTG GTTGAAGT	GT GTAGC		
		AAC CAACTTCG	CA CATCG		
		AA	C A		
GAM1968	LOC147080 3'	TGCACAACCTTCAGCCACAA	85053	CA	C C
		TTG GTTGAAGT	GT GTA		
		AAC CGACTTCA	CA CGT		
		AC	A		
GAM1968	LOC152845 5'	GCGGTGACCTCAGCTGCAA	60958	A	GT
		TTGCAGTTGA	GTC CGT		

		AACGTCGACT CAG GCG		
		C TG		
GAM1968	LOC203052	3' ACCACCATTTCAACTGCA 92073	C C	
		TGCAGTTGAAGT GT GT		
		ACGTCAACTTTA CA CA		
		C C		
GAM1968	LOC204084	5' GGCCAGACCTCCAACTGCAG 91000	A TC GTA	
		TTGCAGTTG AG GTC GCC		
		GACGTCAAC TC CAG CGG		
		C _ AC_		
GAM1969	EMR1	3' GAACACCTGGCTACCA 10517 C CC		
		TGGT AGCCAGGTG TTC		
		ACCA TCGGTCCAC AAG		
		- -		
GAM1969	POLS	3' TGAATTGGCCTGGCTACCA 23783 C GCC		
		TGGT AGCCAGGT TTCA		
		ACCA TCGGTCCG AAGT		
		- GTT		
GAM1969	SLC22A3	3' AGGGACTAAGCTCCTAGCTGAC 42038 C T CT_ A		
	CA	TGGTCAGC AGG GC TC CCT		
		ACCAGTCG TCC CG AG GGA		
		A T AATC _		
GAM1969	ARTN	3' CAGGTGAAGGGACAACTGACTA 15610 CCAG G		
		TGGTCAG GT CCTTCACCTG		
		ATCAGTC CA GGAAGTGGAC		
		AA_ G		
GAM1969	ARTN	3' CAGGTGAAGGGACAACTGACTA 55108 CCAG G		
		TGGTCAG GT CCTTCACCTG		
		ATCAGTC CA GGAAGTGGAC		
		AA_ G		
GAM1969	ARTN	3' CAGGTGAAGGGACAACTGACTA 55111 CCAG G		
		TGGTCAG GT CCTTCACCTG		
		ATCAGTC CA GGAAGTGGAC		
		AA_ G		
GAM1969	ARTN	3' CAGGTGAAGGGACAACTGACTA 55136 CCAG G		
		TGGTCAG GT CCTTCACCTG		
		ATCAGTC CA GGAAGTGGAC		
		AA_ G		
GAM1969	FLJ10211	5' CAGACAAAGGCACCGAGGCCA 36363 AGCCA CAC		
		TGGTC GGTGCCTT CTG		

ACCGG CCACGGAA GAC
 AG__ ACA
 GAM1969 FLJ13089 3' CAGGCAAAAGCAACATCTGGTT 71427 C__ CA_
 GACCA TGGTCAGCCAGGTG CTT CCTG
 ||||| ||| ||||
 ACCAGTTGGTCTAC GAA GGAC
 AAC AAC
 GAM1969 KIAA1280 5' GATTAACCTGGCTGACTA 70280 GCCT
 TGGTCAGCCAGGT TC
 ||||| ||
 ATCAGTCGGTCCA AG
 ATT_
 GAM1969 LRG 3' CAGGTGAAACTCGGGGCTGTCC 54816 T A__ GCC
 A TGG CAGCC G GT TTCACCTG
 ||| ||| | || |||||
 ACC GTCGG C CA AAGTGGAC
 T GG T __
 GAM1969 LOC155434 3' GGAGGCACCCGACTACCA 87691 C CCA
 TGGT AG GGTGCCTTC
 ||| || |||||
 ACCA TC CCACGGAGG
 _ AGC
 GAM1969 LOC196484 5' CAGGTCACCACCTGGCTGACC 63537 CCTTC
 GGTCAGCCAGGTG ACCTG
 ||||| ||||
 CCAGTCGGTCCAC TGGAC
 CAC__
 GAM1969 LOC256158 5' AGGCATCCCCCGGCCGACCA 99478 A A__
 TGGTC GCC GGTGCCT
 |||| | |||||
 ACCAG CGG CTACGGA
 C CCCC
 GAM1969 LOC91069 3' CAGGTCACCACCTGGCTGACC 65400 CCTTC
 GGTCAGCCAGGTG ACCTG
 ||||| ||||
 CCAGTCGGTCCAC TGGAC
 CAC__
 GAM1969 LOC93624 3' CAGGCAAGAGCCGTCTGACC 73099 CCA GC CA
 GGTCAG GGT CTT CCTG
 |||| | ||| ||||
 CCAGTC CCG GAA GGAC
 TG_ A_ C_
 GAM1970 B3GALT2 3' CAGCAGGTGTACACATGC 15030 AT TG
 GCAT TGTAC GCCTGCTG
 ||| |||| |||||
 CGTA ACATG TGGACGAC
 C_ _
 GAM1970 FBN1 3' CAGCATGTGCAATATGC 65037 TGGCC
 GCATATTGTAC TGCTG
 ||||| ||||

CGTATAACGTG ACGAC
T____
GAM1970 GRLF1 3' CAGCAGGCCAGCTGCAGTG 79256 _
TATTGTA CTGGCCTGCTG
||||| |||||
GTGACGT GACCGGACGAC
C
GAM1970 MAPRE1 3' GCAGCAGGCAGGTGATCATGCT 25591 ATTG G
G CAGCAT TACT GCCTGCTGC
||||| ||| |||||
GTCGTA GTGG CGGACGACG
CTA_ A
GAM1970 SMURF1 3' CAGCAGGCCAATGTTCTATGT 94044 TTGT _
GCATA AC TGGCCTGCTG
||||| || |||||
TGTAT TG ACCGGACGAC
CCT_ TA
GAM1970 UQCRC1 5' GCCAGGCCAGCACAACTAGACTG 14015 CA A _
CAG TATTGT CTGGCCTG C
||| ||||| ||||| |
GTC ATAACA GACCGGAC G
AG C C
GAM1970 DKFZP434P211 5' CAGCAAGCCAGTGCTGTGTG 28026 T C
CATAT GACTGGC TGCTG
||||| ||||| |||||
GTGTG CGTGACCG ACGAC
T A
GAM1970 KIAA0063 3' GCAGCGGTACAGCATGCTG 30259 A GC
CAGCAT TTGTA CTGC
||||| ||||| |||||
GTCGTA GACATGGC GACG
C _
GAM1970 KIAA0795 3' CAGCAAGCCAGGTATGGTG 47228 G TGTA C
CA CATAT CTGGC TGCTG
|| ||||| ||||| |||||
GT GTATG GACCG ACGAC
G _ A
GAM1970 KIAA1817 3' GCAGCAGGCCACATTGCCGTGC 68781 ATT C_
GCAT GTA TGGCCTGCTGC
||||| ||| |||||
CGTG CGT ACCGGACGACG
C_ TAC
GAM1970 MGC14156 3' GCAACTAGAGTCAATATGCTG 52959 TA_ CC
CAGCATATTG CTGG TGC
||||||| ||| |||
GTCGTATAAC GATC ACG
TGA A_
GAM1970 MYH7B 3' GCAGCAGGCCAACACCAACCTG 71057 CATAT AC
CAG TGT TGGCCTGCTGC
||| ||| |||||

GTC ACA ACCGGACGACG
 CAACC ____
 GAM1970 NEK1 3' CAGCTTCAATCACAAATATGC 97561 AC_ CCT
 GCATATTGT TGG GCTG
 ||||| ||| ||||
 CGTATAACA ACT CGAC
 CTA T____
 GAM1970 LOC146455 5' GCAACAGGCCAGCAGCCAAAAT 78461 A TA__ C
 G CAT TTG CTGGCCTG TGC
 ||| ||| ||||| |||
 GTA AAC GACCGGAC ACG
 A CGAC A
 GAM1970 LOC150174 5' CAGCAAGCCAGTGCTGC 80433 TATT C
 GCA GTACTGGC TGCTG
 ||| ||||| |||||
 CGT CGTGACCG ACGAC
 ____ A
 GAM1970 LOC150213 5' CAGCAAGCCAGTGCTGTGTG 75352 T C
 CATAT GTACTGGC TGCTG
 |||| ||||| |||||
 GTGTG CGTGACCG ACGAC
 T A
 GAM1970 LOC150271 5' CAGCAAGCTCTGAAGATATGCT 86134 GTACT C
 G CAGCATATT GGC TGCTG
 ||||| ||| |||||
 GTCGTATAG TCG ACGAC
 AAGTC A
 GAM1970 LOC160646 3' CAGCAGGCAGAAATGCTG 83108 ATTGTA G
 CAGCAT CTG CCTGCTG
 ||||| ||| |||||
 GTCGTA GAC GGACGAC
 AA_____
 GAM1970 LOC164714 5' AGCAGGCAAGATGCTG 88579 ATTGTA G
 CAGCAT CT GCCTGCT
 ||||| || |||||
 GTCGTA GA CGGACGA
 ____ A
 GAM1970 LOC256809 3' CAGTGTGGAGTCAATATGCT 98130 T GG _
 AGCATATTG ACT CC TGCTG
 ||||| ||| || |||||
 TCGTATAAC TGA GG GTGAC
 _ _ T
 GAM1971 AES 3' CCACCTGGTCCTCTCCCA 8523 T _ C
 TGGGA AGGATT GG GG
 |||| ||||| || ||
 ACCCT TCCTGG CC CC
 C T A
 GAM1971 BLu 5' CCGCAACTGTCCTGTCCCA 32473 TG____
 TGGGATAGGAT GCGG
 ||||| ||||| |||||

ACCCTGTCCTG CGCC
 TCAA
 GAM1971 DKFZp547D155 3' CCGCCAGGGCCTATCCCA 70945 A_
 TGGGATAGG TTGGCGG
 ||||| |||||
 ACCCTATCC GACCGCC
 GG
 GAM1971 KIAA0564 3' GCCACCAAAATGCTCCTATCC 66793 ____ C ____
 GGATAGGA TTGG GG C
 ||||| ||| || |
 CCTATCCT AACC CC G
 CGTAA A ____
 GAM1971 LOC146481 5' CCACCATATCGTGTCCCA 78485 G _ C
 TGGGATA GAT TGG GG
 ||||| ||| ||| ||
 ACCCTGT CTA ACC CC
 G T A
 GAM1971 LOC222183 5' CCGCAAGCGTCCTATTCCA 95826 TG____
 TGGGATAGGAT GCGG
 ||||| ||| |||
 ACCTTATCCTG CGCC
 CGAA
 GAM1972 ALDH3B2 3' CTGGAAAATACAGTGCCCTGCC 7342 A GACC C
 T AG CAGGGTAC AT TTCCAG
 || ||||| || |||||
 TC GTCCCGTG TA AAGGTC
 C ACA_ A
 GAM1972 BID 3' CTGGAAGATAGCTGTGACTTCT 8653 C GG ACC
 AGA AG TACG ATCTTCCAG
 ||| || ||| |||||
 TCT TC GTGT TAGAAGGTC
 _ A_ CGA
 GAM1972 DPP6 3' GGGACATCACACCCTGTCT 56321 AC CCATC
 AGACAGGGT GA TTCC
 ||||| || |||
 TCTGTCCCA CT AGGG
 CA AC____
 GAM1972 LTB4R 5' CTGGAAGATGGCCCTCTTCCC 7463 TAC ____
 GGG GA CCATCTTCCAG
 ||| || |||||
 CCC CT GGTAGAAGGTC
 TT_ CCC
 GAM1972 SIGLEC5 3' CTGGAGGAGCCACAGCCTGTCT 15148 GTACGACCA
 AGACAGG TCTTCCAG
 ||||| |||||
 TCTGTCC AGGAGGTC
 GACACCG____
 GAM1972 TGFA 3' CTGGAAGACAGGGCCCCGGCT 13709 ACA ACGA A_
 AG GGGT CC TCTTCCAG
 || ||| || |||||

TC CCCG GG AGAAGGTC
 GGC ____ AC
 GAM1972 C2F 3' CTGGAAGATGATCTTTCTG 22005 TAC C
 CAGGG GA CATCTTCCAG
 |||| || |||||
 GTCTT CT GTAGAAGGTC
 T__ A
 GAM1972 CARD9 5' CTGGAAGACCCTCAGCCTGCCT 54476 A GTAC CCA
 AG CAGG GA TCTTCCAG
 || |||| || |||||
 TC GTCC CT AGAAGGTC
 C GA__ CCC
 GAM1972 CARD9 5' CTGGAAGACCCTCAGCCTGCCT 54477 A GTAC CCA
 AG CAGG GA TCTTCCAG
 || |||| || |||||
 TC GTCC CT AGAAGGTC
 C GA__ CCC
 GAM1972 CYorf15B 5' TGGAAGATTAAGCCTATCT 51796 CA ACGACC
 AGA GGGT ATCTTCCA
 ||| |||| |||||
 TCT TCCG TAGAAGGT
 A_ AAT__
 GAM1972 DKFZP434G156 5' CTGGAAGACATGTCCCCTTCT 70337 C TAC CA_
 AGA AGGG GAC TCTTCCAG
 ||| |||| || |||||
 TCT TCCC CTG AGAAGGTC
 _ __ TAC
 GAM1972 FLJ12229 3' GAGCAGGCCGTACCCTGCT 46405 A A AT
 AG CAGGGTACG CC CTT
 || ||||| || |||
 TC GTCCCATGC GG GAG
 _ C AC
 GAM1972 FLJ13639 3' GGAGGATGGCCGCACCCCTTC 45553 CA A A
 GA GGGT CG CCATCTTCC
 || |||| || |||||
 CT CCCA GC GGTAGGAGG
 TC C C
 GAM1972 FLJ22378 3' CTGGGGCCTGCCGCATCCTGTC 47595 A AC TC
 GACAGGGT CG CA TTCCAG
 ||||| || || |||||
 CTGTCCTA GC GT GGGGTC
 C C_ CC
 GAM1972 KCND1 3' CTGGAAATGGACCCCGCAACCC 18343 A_ A__ C
 TGTC GACAGGGT CG CCAT TTCCAG
 ||||| || ||| |||||
 CTGTCCCA GC GGTA AAGGTC
 AC CCCA _
 GAM1972 KIAA0169 5' CTGGAAGACGGCGCTTCCCTGC 73181 A TA_ A A
 T AG CAGGG CG CC TCTTCCAG
 || |||| || || |||||

TC GTCCC GC GG AGAAGGTC
 _ TTC _ C
 GAM1972 KIAA0557 3' CTGGAAGACAGAGTGAGATCCT 78558 ACG CA__
 GTCT AGACAGGGT AC TCTTCCAG
 ||||| || |||||
 TCTGTCCTA TG AGAAGGTC
 GAG AGAC
 GAM1972 KIAA1560 3' TGGAAGACAAGTGCCTTCT 64854 CA GACCA
 AGA GGGTAC TCTTCCA
 || |||| |||||
 TCT TCCGTG AGAAGGT
 _ AAC_
 GAM1972 MDN1 3' CTGGGAGGAGGTCATACCC 63358 C AT
 GGGTA GACC CTTCCAG
 |||| || |||||
 CCCAT CTGG GAGGGTC
 A AG
 GAM1972 MGC9753 5' CTGGAAGATGACAGCCTGT 54191 GTACGAC
 ACAGG CATCTTCCAG
 |||| |||||
 TGTCC GTAGAAGGTC
 GACA_
 GAM1972 NEIL1 5' CTGGGGGTGCCGACCCTGTC 45152 A AC T
 GACAGGGT CG CATCT CCAG
 ||||| || |||| ||||
 CTGTCCCA GC GTGGG GGTC
 _ C _
 GAM1972 ORCTL4 3' GAGATTGGACCCATACCCTGTC 17834 CGA__ _
 T AGACAGGGTA CCA TCTT
 ||||| || ||||
 TCTGTCCCAT GGT AGAG
 ACCCA T
 GAM1972 PRDM12 3' GAAGATGGTCACTTTAACCTT 41511 AC____
 AGGGT GACCATCTTC
 |||| |||||
 TTCCA CTGGTAGAAG
 ATTTCA
 GAM1972 SGK2 5' CTGGGAGGGGGCCACACCCTG 33251 ACGA A
 CAGGGT CC TCTTCCAG
 |||| || |||||
 GTCCCA GG GGAGGGTC
 CACC _
 GAM1972 SIMRP7 3' CTGGGCAGCCTCACCCTGTCT 93973 AC CCAT _
 AGACAGGGT GA CT TCCAG
 ||||| || || ||||
 TCTGTCCCA CT GA GGGTC
 _ CC _ C
 GAM1972 SNX11 3' TGGCTATCCTACCCTGTCT 26177 C ____
 AGACAGGGTA GA CCA
 ||||| || |||

		TCTGTCCCAT CT GGT	
		C ATC	
GAM1972	SPINT1	3' CTGGAGGCCCAACCCTGTC 63333	ACGACCAT
		GACAGGGT CTTCCAG	
		CTGTCCCA GGAGGTC	
		ACCC_	
GAM1972	LOC115817	5' AAGACAGTCAGCCTTGTC 57409	AC CA
		GACAGGGT GAC TCTT	
		CTGTTCCG CTG AGAA	
		A_ AC	
GAM1972	LOC146146	5' CTGGATGTCTGACCGTGCCCTG 78167	AC TCT_
	TC	GACAGGGTACG CA TCCAG	
		CTGTCCCGTGC GT AGGTC	
		CA CTGT	
GAM1972	LOC154386	3' GAAGATGTCGTCCCTGTCT 81988	T C
		AGACAGGG ACGAC ATCTTC	
		TCTGTCCC TGCTG TAGAAG	
		- -	
GAM1972	LOC196320	5' CTGGAAGATGGCACCCCTTC 89011	C ACGA
		GA AGGGT CCATCTTCCAG	
		CT TCCA GGTAGAAGGTC	
		- C_	
GAM1972	LOC202781	3' CTGGACGATATAGCCAGACCCT 91971	ACGACC_ T
	GTCT	AGACAGGGT ATC TCCAG	
		TCTGTCCCA TAG AGGTC	
		GACCGATA C	
GAM1972	LOC220729	3' CTGGAGGAAGCACACCCTGTC 72050	ACGACCA
		GACAGGGT TCTTCCAG	
		CTGTCCCA AGGAGGTC	
		CACGA_	
GAM1972	LOC255144	5' TGGAAGGGAACACCTGCCT 96769	A _ ACGA AT
		AG CAGG GT CC CTTCCA	
		TC GTCC CA GG GAAGGT	
		C A A_ _	
GAM1973	ADCY8	5' CACCGCTCCTCCACCTGCATC 8498	_ CT_
		GATGCAGGTG AG CGGTG	
		CTACGTCCAC TC GCCAC	
		C CTC	
GAM1973	AIM1	3' TGTCTCCTATCCACCTGCATC 93473	AGCTC T_
		GATGCAGGTG GG GACA	

			CTACGTCCAC	CC	CTGT		
			CTAT_	TC			
GAM1973	ALDH3B2	3'	TCACCAAGACACGCCTGCATGT	7344	G	AG_	C
	A		TA ATGCAGGTG	CT GGTGA			
			AT TACGTCCGC	GA CCACT			
			G	ACA A			
GAM1973	ITGA6	3'	CACCTACACTCACCTGCACTA	5785	A	CTC_	
			TAG TGCAGGTGAG	GGTG			
			ATC ACGTCCACTC	CCAC			
			_	ACAT			
GAM1973	LYAAT1	3'	TGCCATCGCTCACCTGTACCTA	55310	A	TC	A
			TAG TGCAGGTGAGC	GGTG CA			
			ATC ATGTCCACTCG	CTAC GT			
			C	_ C			
GAM1973	APACD	5'	GTCACCGAGAGCTCAGCA	20521	AGG	_	
			TGC TGAGCTC	GGTGAC			
			ACG ACTCGAG	CCACTG			
			_	AG			
GAM1973	CABYR	3'	TCACCGCCACCTGCACCTG	25173	A	A TC	
			TAG TGCAGGTG GC	GGTGA			
			GTC ACGTCCAC CG	CCACT			
			C	_ _			
GAM1973	FLJ12056	3'	CACCGTGGCCCTCCCCTGCATC	46818		T _ _	
	TA		TAGATGCAGG GA	GCT CGGTG			
			ATCTACGTCC CT	CGG GCCAC			
			C CC	T			
GAM1973	FLJ14103	3'	TGCCAGGGCTCAACTCACCTGC	97939		_____	_
	ATC		GATGCAGGTGA	GCTC GGTG			
			CTACGTCCACT	CGGG CCGT			
			CAACT	A			
GAM1973	FLJ21478	3'	TGTCACCAAGGGGCTCAC	45198		_____	
			GTGAGCTC	GGTGACA			
			CACTCGGG	CCACTGT			
			GAA				
GAM1973	FLJ22746	3'	TATGGGTGCCCACCTGCACCTG	45920	A	A _ G	
			TAG TGCAGGTG GC	TC GTG			
			GTC ACGTCCAC CG	GG TAT			
			C	C T G			
GAM1973	FLJ23420	5'	TACGGACTTACCTGCATCTA	47543		C G	
			TAGATGCAGGTGAG	TC GTG			

		ATCTACGTCCATTC AG CAT		
		_ G		
GAM1973	KIAA0978	3' TGCACCGAGCAAACGCATCT 71000	AG GA	A
		AGATGC GT GCTCGGTG CA		
		TCTACG CA CGAGCCAC GT		
		_ AA C		
GAM1973	KIAA1061	3' TGCCAAGCCACCTGCATC 71725	A C	
		GATGCAGGTG GCT GGTG		
		CTACGTCCAC CGA CCGT		
		_ A		
GAM1973	KIAA1887	3' TGCCAGCCACCTGCACCTG 77278	A A C	
		TAG TGCAGGTG GCT GGTG		
		GTC ACGTCCAC CGA CCGT		
		C _ _		
GAM1973	TEB4	3' TCACCAACTGTACTGCATCT 61286	GTG CTC	
		AGATGCAG AG GGTGA		
		TCTACGTC TC CCACT		
		ATG AA_		
GAM1973	WIRE	3' TGTCTCCCAGCTCACCTCCAT 78908	C C T_	
	CTA	TAGATG AGGTGAGCT GG GACA		
		ATCTAC TCCACTCGA CC CTGT		
		C C TC		
GAM1973	LOC138307	3' CACCAGGTCACCTGCACCTG 75839	A G C	
		TAG TGCAGGTGA CT GGTG		
		GTC ACGTCCACT GA CCAC		
		C G _		
GAM1973	LOC138399	5' CACCAGCCACCCGCACCT 75848	A A A C	
		AG TGC GGTG GCT GGTG		
		TC ACG CCAC CGA CCAC		
		C C _ _		
GAM1973	LOC147160	5' CACCCAGGCCACCTGCA 85067	A C_	
		TGCAGGTG GCT GGTG		
		ACGTCCAC CGG CCAC		
		C AC		
GAM1973	LOC149535	3' CTGGGTCACCTGCATCTA 80218	G	
		TAGATGCAGGTGA CTCGG		
		ATCTACGTCCACT GGGTC		
		_		
GAM1973	LOC151176	5' CGCCTGCTCATCTGCATC 86441	TC	
		GATGCAGGTGAGC GGTG		

		CTACGTCTACTCG CCGC		
		T_		
GAM1973	LOC196812 3'	TGCCAAGTTTTCACTACATCTA 91129	CA	_ C
		TAGATG GGTGA GCT GGTG		
		ATCTAC TCACT TGA CCGT		
		A_ TT A		
GAM1973	LOC219653 3'	TGTCACCCCTGCACCTGCACCT 92924	A	AGCTC
	G	TAG TGCAGGTG GGTGACA		
		GTC ACGTCCAC CCACTGT		
		C GTCC_		
GAM1973	LOC253769 5'	TCACAGATGCCACCTGCA 99021	A	_ G
		TGCAGGTG GC TC GTGA		
		ACGTCCAC CG AG CACT		
		_ T A		
GAM1973	LOC256949 3'	CGTCTGGCTCACTACACCTA 96982	A CA	C GT
		TAG TG GGTGAGCT G G		
		ATC AC TCACTCGG C C		
		C A_ T TG		
GAM1973	LOC90957 3'	TGCTACTCACCTGCTTCTA 65092	T	CTC
		TAGA GCAGGTGAG GGTG		
		ATCT CGTCCACTC TCGT		
		T A_		
GAM1973	LOC91301 5'	TCACCGAGTCACGGATCTA 66152	GCAG	G
		TAGAT GTGA CTCGGTGA		
		ATCTA CACT GAGCCACT		
		GG_ _		
GAM1974	ANPEP 3'	TGGCACCTCCCAGCCCCT 8567	G	G
		AGGGG TGGGAGGTGT CA		
		TCCCC ACCCTCCACG GT		
		G A		
GAM1974	ATP2B2 5'	CTCGGCCACCCCCACCCCC 9849	A	T ATA
		GGGGGTGGG GGTG GC AG		
		CCCCACCC CCAC CG TC		
		_ _ GC_		
GAM1974	BACH2 3'	CACCTTCCTCCCACCCACC 41776	_	T_
		GG GGGTGGGAGG GTG		
		CC CCCACCCTCC CAC		
		A TTC		
GAM1974	C18orf2 3'	CACATCCCGCCCACCCCC 49459	A_	
		GGGGGTGGG GGTGTG		

		CCCCCACCC CTACAC		
		GCC		
GAM1974 CST3	3'	ATCTTATGCACACCTCCACCCC 5433		_____
	CCT	AGGGGGTGGGAGGTGTGCATAAGA T		
		TCCCCCACCCCTCCACACGTATTCT A		
GAM1974 DNM1	3'	GCATCCCTCCCACCCCCT 16613	TG	_
		AGGGGGTGGGAGG TG C		
		TCCCCCACCCCTCC AC G		
		CT C		
GAM1974 EGFL4	3'	CACCACCTCCACCACCCCCT 62452	__	_
		AGGGGGTGGG GAGGTG TG		
		TCCCCCACCC CTCCAC AC		
		AC C		
GAM1974 FUS1	3'	CTTACAGTAACCCCCACCCCTT 24405	A G A	_
		AGGGGGTGGG GGT TGC TAAG		
		TTCCCCACCC CCA ATG ATTC		
		_ _ AC		
GAM1974 KPNB1	5'	CACCCGACCCCCAACCCCC 11217	_ A	_____
		GGGGGT GGG GGT GTG		
		CCCCCA CCC CCA CAC		
		A _ GCC		
GAM1974 LTBR	3'	GCAGACCCACCCACCCCCT 11373	A_ G	
		AGGGGGTGGG GGT TGC		
		TCCCCCACCC CCA ACG		
		AC G		
GAM1974 MEIS1	3'	ATGCAACAACCACCACCT 11533	G GAG G	
		AGG GGTGG GT TGCAT		
		TCC CCACC CA ACGTA		
		A AA_ _		
GAM1974 MSX2	3'	TCTATCTCTCCCCCGCCCC 66173	A TGTGC A	
		GGGGGTGGG GG ATA GA		
		CCCCCGCCC CC TAT CT		
		_ TCTC_ C		
GAM1974 NPTX1	3'	CTCATGCACACGAAGCAGCCCC 11833	G GGAG A	
	T	AGGGG TG GTGTGCAT AG		
		TCCCC AC CACACGTA TC		
		G GAAG C		
GAM1974 PLP2	3'	GCAGACCAACTCCCACCCCCT 12175	__ G	
		AGGGGGTGGGA GGT TGC		

TCCCCCACCT CCA ACG
 CAA G
 GAM1974 PPP2R4 3' CTTGTCCTCCCACCTCCCT 61180 _ TGTGC
 AGGG GGTGGGAGG ATAAG
 ||| ||||| ||||
 TCCC CCACCCTCC TGTTC
 T _
 GAM1974 TBX6 3' CTTGATTTCACTCCCACCCCC 55812 G TGCA
 GGGGGTGGGAG TG TAAG
 ||||| || ||||
 CCCCCACCCTC AC GTTC
 _ TTTA
 GAM1974 TCF7L2 3' TCTTAATTTGCCCCCACCCTCC 48442 A TGCA
 GGGGGTGGG GGTG TAAGA
 ||||| || ||||
 CCCCCACCC CCGT ATTCT
 C TTA_
 GAM1974 TNFRSF6 3' TCTTATTTTCCCCCACCCTCC 5268 A TGTGC
 GGGGGTGGG GG ATAAGA
 ||||| || ||||
 CCCCCACCC CC TATTCT
 _ TTTT_
 GAM1974 TNFSF12 3' TCTTACAACCTCCCCACCGCCC 15084 _ A T GCA
 GGG GGTGGG GG GT TAAGA
 || ||||| || ||||
 CCC CCACCC CC CA ATTCT
 G _ T AC_
 GAM1974 TP53 3' TGCAGCCTCCCACCCCC 6808 GTG
 GGGGGTGGGAGGT CA
 ||||| || ||||
 CCCCCACCCTCCG GT
 ACA
 GAM1974 UCP3 3' ATGCAGCCTCTTCCCCACCCCC 13980 _ G
 GGGGGTGGG AGGT TGCAT
 ||||| || ||||
 CCCCCACCC TCCG ACGTA
 CTC _
 GAM1974 ABT1 3' TCTTAGAGCCCCCTCCCCCT 26306 T A T GCA
 AGGGGG GGG GG GT TAAGA
 ||||| || || ||||
 TCCCCC CCC CC CG ATTCT
 T _ _ AG_
 GAM1974 CAMTA2 3' CACGCCTTGCTCCCACACCCT 61881 _ _
 AGGGG GTGGGA GGTGTG
 ||||| |||| ||||
 TCCCC CACCCT CCGCAC
 A CGTT
 GAM1974 CCR1 3' TCTTCCATCACCTCCCCCCCC 8931 T _ CAT
 GGGGG GGGAGGTG TG AAGA
 ||||| ||||| || ||||

		CCCCC CCCTCCAC AC TTCT	
		_ T C_	
GAM1974 COP9	3'	TCTTTTCACCCCCACCTCCT 22965	A T CAT
		AGGGGGTGGG GG GTG AAGA	
		TCCTCCACCC CC CAC TTCT	
		_ _ TT_	
GAM1974 DKFZP727M111	3'	TCTTACCTAACTCCCAACCCCT 32063	G GTGTGCA
		AGGGG TGGGAG TAAGA	
		TCCCC ACCCTC ATTCT	
		A AATCC_	
GAM1974 DMWD	3'	GCGCCACCCTCCACCCCC 61551	GA _
		GGGGGTGG GGTG TGC	
		CCCCCACC CCAC GCG	
		TC C	
GAM1974 FLJ00058	5'	CACCCCTCTCCCACCCTC 79506	T_
		GGGGGTGGGAGG GTG	
		CTCCCACCCTCT CAC	
		CCC	
GAM1974 FLJ20625	3'	CATCTCTACCCCACCCCT 35897	_____
		AGGGGGTGGG AGGTG	
		TCCCCCACC TCTAC	
		CATC	
GAM1974 FLJ21736	3'	TGACCCTCCCCCACCCTC 46788	_____ T G
		GGGGGT GGGAGG GT CA	
		CCCCCA CCCTCC CA GT	
		CCC _ _	
GAM1974 HTR3A	3'	TACACCCTTGTCACCCCC 7879	_____
		GGGGGTGGGA GGTGTG	
		CCCCCACCCT CCACAT	
		GTTC	
GAM1974 IKKE	3'	TACGCCTTCCCACTCCCT 26595	_
		AGGGGGTGGGA GGTGTG	
		TCCCTCACCT CCGCAT	
		T	
GAM1974 KCND1	5'	CTTCAACACCCCACCCCC 18344	AG GCAT
		GGGGGTGGG GTGT AAG	
		CCCCCACC CACA TTC	
		_ ACT_	
GAM1974 KIAA0757	3'	GCTGGACTCCCCACCCCT 21258	AG G _
		AGGGGGTGGG GT T GC	

	TCCCCCACCC CA G CG	
	CT G T	
GAM1974 KIAA1402 5'	CACGCCTCCGCCCCGCCCCCT 66991	_____
	AGGGGGTGGG AGGTGTG	
	TCCCCCGCCC TCCGCAC	
	CGCC	
GAM1974 KIAA1553 3'	TATACCTGGCCACCCCCT 93570	G_
	AGGGGGTGG AGGTGTG	
	TCCCCCACC TCCATAT	
	GG	
GAM1974 KIAA1822 3'	GCATCCCCCCCCACCCCCT 68185	A TG
	AGGGGGTGGG GG TGC	
	TCCCCCACCC CC ACG	
	C CT	
GAM1974 LR8 5'	CACACCTCGACCCCTCACCCCC 26700	_____
T	AGGGGGTGG GAGGTGTG	
	TCCCCCACT CTCCACAC	
	CCCCAG	
GAM1974 MGC10986 3'	TGTAACCTTCCACCCCCT 48329	G
	AGGGGGTGGGAGGT TGCA	
	TCCCCCACCTTCCA ATGT	
	—	
GAM1974 MGC15476 3'	CTATGACCCCCACTCCCT 59609	A GTG A
	AGGGGGTGGG GGT CAT AG	
	TCCCTCACCC CCA GTA TC	
	— —	
GAM1974 P450RAI-2 3'	TATGCCACGGTTCCCACCCTC 39578	G _
	GGGGGTGGGAG TGTG CATA	
	CTCCCACCCTT GCAC GTAT	
	G C	
GAM1974 PARVB 3'	CACGCCTGCCCCACCCCCT 26189	—
	AGGGGGTGGG AGGTGTG	
	TCCCCCACCC TCCGCAC	
	CG	
GAM1974 PLA2G6 3'	CACACTGGCCCAGCCCCT 67087	G A_
	AGGGG TGGG GGTGTG	
	TCCCC ACCC TCACAC	
	G GG	
GAM1974 PLSCR3 3'	ATGCACTCTCTCCCACCCCCT 40151	_ T
	AGGGGGTGGGAG G GTGCAT	

		TCCCCCACCCTC C CACGTA		
		T T		
GAM1974	SDS3	3' ATGCCCTGCCTACCCCT 69742	_	TGT
		AGGGGGTGGG AGG GCAT		
		TCCCCCATCC TCC CGTA		
		G ____		
GAM1974	STRAIT11499	3' TCTATGGCACCCCCACCCC 41432	A	G A
		GGGGTGGG GGTGT CATA GA		
		CCCCACCC CCACG GTAT CT		
		— —		
GAM1974	XPO5	3' CACAAGCCCTCCCACCCCC 92872	—	
		GGGGGTGGGAGG TGTG		
		CCCCCACCCTCC ACAC		
		CGA		
GAM1974	LOC144473	3' CTTATTTCCACCCCCACCCCC 83995	A	TGC
		GGGGGTGGG GGTG ATAAG		
		CCCCCACCC CCAC TATTC		
		C CTT		
GAM1974	LOC149876	3' TGCTGCCCCCACCACCCT 80352	_	A T
		AGGG GGTGGG GGTG GCA		
		TCCC CCACCC CCGT CGT		
		A C _		
GAM1974	LOC170396	3' CTATGTTTTGTCCCACTCCC 83729	GGTGT	A
		GGGGGTGGGA GCAT AG		
		CCCTCACCT TGTA TC		
		GTTT_ C		
GAM1974	LOC200014	3' CATCTTCCCCCACCCT 89925	—	
		AGGGGGTGGG AGGTG		
		TCCCCCACC TCTAC		
		CCT		
GAM1974	LOC95633	3' CACCTTGGCCCCCACCCT 60557	A	—
		AGGGGGTGGG GGT GTG		
		TCCCCCACC CCG CAC		
		_ GTTC		
GAM1975	CDKN1A	3' GAAGTAAACAGATGGCACTTTG 55268	—	CTCGCC
		CAAGGTGC TCTG TACTTC		
		GTTTCACG AGAC ATGAAG		
		GT AA_		
GAM1975	PPOX	5' GGCAAGCAGAGCACCTCA 6129	A	C
		C AGGTGCTCTGCT GCC		

A TCCACGAGACGA CGG
 C A
 GAM1975 SIRT5 3' AAGTAGCAAAGAGCACC 25294 GCTC C
 GGTGCTCT GC TACTT
 ||||| || ||||
 CCACGAGA CG ATGAA
 AA__ _
 GAM1975 WDR1 3' AAGTAAGTATAAAGCACC 34404 C__ CGCC
 GGTGCT TGCT TACTT
 |||| ||| ||||
 CCACGA ATGA ATGAA
 AAT ____
 GAM1975 WDR1 3' AAGTAAGTATAAAGCACC 18844 C__ CGCC
 GGTGCT TGCT TACTT
 |||| ||| ||||
 CCACGA ATGA ATGAA
 AAT ____
 GAM1975 C20orf44 3' GAAGCACGTGCTGCAGAGCCAC 37310 _ T_ CTA
 CTTG CAAGGTG CTCTGC CGC CTTC
 ||||| ||||| || ||||
 GTTCCAC GAGACG GTG GAAG
 C TC CAC
 GAM1975 FLJ10769 3' AAGTAAACAGGCACCTTG 37141 T CTCGCC
 CAAGGTGC CTG TACTT
 ||||| || ||||
 GTTCCACG GAC ATGAA
 _ AA____
 GAM1975 KIAA0716 3' GAAGTGTGAAAAAAGCACCTTG 28836 CTGC CT
 CAAGGTGCT TCGC ACTTC
 ||||| ||| ||||
 GTTCCACGA AGTG TGAAG
 AAAA ____
 GAM1975 KIAA1950 3' AGGTGCCGGCAGAGCACCTTG 94177 A ____
 CA GGTGCTCTGCT CGCCT
 || ||||| ||||
 GT CCACGAGACGG GTGGA
 C CC
 GAM1975 MGC26684 3' GAAGTAGGCAAACGTTGCCCT 58612 T TC CTC_
 T AAGG GC TG GCCTACTTC
 ||| || || |||||
 TTCC CG GC CGGATGAAG
 _ TT AAAA
 GAM1975 NTSR2 3' AAGCAGGTGAGCAACCTCA 25631 A GCTC A
 C AGGT TGCTCGCCT CTT
 | ||| ||||| |||
 A TCCA ACGAGTGGA GAA
 C ____ C
 GAM1975 SDCCAG8 5' GAAGCAGGCGGGCGCTCC 89994 T TCT A
 GG GC GCTCGCCT CTTC
 || || ||||| ||||

		CC CG CGGGCGGA GAAG		
		T _ C		
GAM1975	LOC127262 3'	AAGTTGCAGAGCAGCCT	76590	_ TCGCCT
		AGG TGCTCTGC ACTT		
		TCC ACGAGACG TGAA		
		G T _		
GAM1975	LOC152190 5'	AAGATGGAACAGACACCTCA	70234	A C CTCG TA
		C AGGTG TCTG CC CTT		
		A TCCAC AGAC GG GAA		
		C _ AA _ TA		
GAM1975	LOC253890 3'	TAGTGTTCCAGAGCACTTTG	97385	CTC _
		CAAGGTGCTCTG GC CTA		
		GTTTCACGAGAC TG GAT		
		CCT T		
GAM1975	LOC90625 3'	GAAGCAGGCGGGCAACACC	64379	CTC A
		GGTG TGCTCGCCT CTTC		
		CCAC ACGGGCGGA GAAG		
		A _ C		
GAM1976	ACADM 3'	GAATACTGTCAACTTGACAGTA	5233	C TCA
		TGCTG TT TTGACAGTATTC		
		ATGAC AG AACTGTCATAAG		
		_ TTC		
GAM1976	GPR85 3'	ACTAGATAATGAAAGTAGCAG	39101	AC _
		CTGCTGCTTTCATTG AGT		
		GACGATGAAAGTAAT TCA		
		AGA		
GAM1976	RAD54B 3'	AATCTCTCAAAGGCAGCAG	57061	CAT C T
		CTGCTGCTTT TGA AG ATT		
		GACGACGGAA ACT TC TAA		
		_ C _		
GAM1976	AMOT 3'	GAATACCTTTGGGAAGCAGCAG	56543	ATTGACA
		CTGCTGCTTTC GTATTC		
		GACGACGAAGG CATAAG		
		GTTTC _		
GAM1976	ATP9A 3'	GAACACTTTTCCTGAAAGCA	62737	TT C A
		TGCTTTCA GA AGT TTC		
		ACGAAAGT TT TCA AAG		
		CC T C		
GAM1976	FLJ32978 3'	AATACCAAGCAAGCAGCA	58885	TCA ACA
		TGCTGCTT TTG GTATT		

ACGACGAA AAC CATAA
 CG_ ____
 GAM1976 LOC133177 5' GAATATCAAAGAAAGCAGCA 76451 A CAG
 TGCTGCTTTC TTGA TATTC
 ||||| ||| ||||
 ACGACGAAAG AACT ATAAG
 A ____
 GAM1976 LOC144465 3' ATACTAGAAGCAGCAG 77340 CATTGAC
 CTGCTGCTTT AGTAT
 ||||| ||| ||||
 GACGACGAAG TCATA
 A_____
 GAM1976 LOC147057 3' GAACACTGAGATAAAGCAGCAG 84984 C GA A
 CTGCTGCTTT ATT CAGT TTC
 ||||| ||| ||| |||
 GACGACGAAA TAG GTCA AAG
 _ A_ C
 GAM1976 LOC149912 3' GAATGAAGCAATGAAAGAGCA 85880 G ACAG
 TGCT CTTTCATTG TATTC
 ||| ||||| ||||
 ACGA GAAAGTAAC GTAAG
 _ GAA_
 GAM1976 LOC220038 5' AATACTGTCCTAAAACAG 93373 C CATT
 CTG TTT GACAGTATT
 ||| ||| |||||
 GAC AAA CTGTCATAA
 A TC_
 GAM1976 LOC221496 3' GAATAGAAAACAAGAGCAGCAG 93638 CA GACAG
 CTGCTGCTTT TT TATTC
 ||||| || |||||
 GACGACGAGA AA ATAAG
 AC AAG_
 GAM1976 LOC222346 5' AACACTATCTCAGCAGTAG 94380 TTCATT C A
 CTGCTGCT GA AGT TT
 ||||| || ||| ||
 GATGACGA CT TCA AA
 CT____ A C
 GAM1976 LOC93538 3' ACTACTCAATGAAAACAGC 72951 C C_
 GCTG TTTTATTGA AGT
 ||| ||||| |||
 CGAC AAAGTAACT TCA
 A CA
 GAM1977 SELE 3' ATCAAAACTCTCCTACACTT 6552 TGCCG
 AAGTGTGGGAG TTGAT
 ||||| ||| ||||
 TTCACATCCTC AACTA
 TCAA_
 GAM1977 SLC21A2 3' ATTGGTTGCACTCCCAAACCTT 20079 TG_ CG TG
 T AAAG TGGGAGTGC T AT
 ||| ||||| ||| ||

		TTTC ACCCTCACG G TA		
		CAA TT GT		
GAM1977	FLJ10898	5' ATCAACAAGCACACATTTT 60124	GGGA	C_
		AAAGTGT GTGC GTTGAT		
		TTTTACA CACG CAACTA		
		____ AA		
GAM1977	FLJ22002	3' ATCAATTTCCACTCCCACAC 46192	CC_	
		GTGTGGGAGTG GTTGAT		
		CACACCCTCAC TAACTA		
		CTT		
GAM1977	FLJ23189	3' ATCAACAATAACCACACTT 47526	GA	GCC
		AAGTGTGG GT GTTGAT		
		TTCACACC TA CAACTA		
		AA A_		
GAM1977	SMARCF1	3' ATCAACGGGATGCCACATTTCA 58223	A	GA G
		A AAGTGTGG GT CCGTTGAT		
		A TTTACACC TA GGCAACTA		
		C G_ G		
GAM1977	SMARCF1	3' ATCAACGGGATGCCACATTTCA 21182	A	GA G
		A AAGTGTGG GT CCGTTGAT		
		A TTTACACC TA GGCAACTA		
		C G_ G		
GAM1977	SMARCF1	3' ATCAACGGGATGCCACATTTCA 38039	A	GA G
		A AAGTGTGG GT CCGTTGAT		
		A TTTACACC TA GGCAACTA		
		C G_ G		
GAM1977	SMARCF1	3' ATCAACGGGATGCCACATTTCA 38040	A	GA G
		A AAGTGTGG GT CCGTTGAT		
		A TTTACACC TA GGCAACTA		
		C G_ G		
GAM1977	LOC129011	3' CAACAACACTTTTATCACTTTT 75365	_	CC
		AAAAGTG TGGGAGTG GTTG		
		TTTTCAC ATTTTCAC CAAC		
		T AA		
GAM1977	LOC256529	5' ATCAACAGAATTCCACAAC TTT 99428	_	GTGCC
		AAAGT GTGGGA GTTGAT		
		TTTCA CACCTT CAACTA		
		A AAGA_		
GAM1978	ADAMTS8	3' GGTGACTGGGTCCCTTG GCC 23855	GGCA	
		GGTCAAGGGAT AGTCACC		

CCGGTTCCCTG TCAGTGG
 GG__
 GAM1978 CLDN5 3' GTGACTTGGCCTGGACC 13817 A GATGG
 GGTC AGG CAAGTCAC
 ||| ||| |||||
 CCAG TCC GTTCAGTG
 G G__
 GAM1978 CLPS 3' GGCTGGCCACCTCCTTGACC 10215 _A A
 GGTC AAGG G TGGC AGTC
 ||||| | ||| |||
 CCAGTTCC C ACCG TCGG
 T C G
 GAM1978 COL7A1 3' GACCCGCCCTTGACC 5411 A CAA
 GGTC AAGG TGG GTC
 ||||| ||| |||
 CCAGTTCCC GCC CAG
 C __
 GAM1978 ELF3 3' GTGACCTTGACCTTGACC 16684 GAT CAA
 GGTC AAGG GG GTCAC
 ||||| || |||||
 CCAGTTCC TC CAGTG
 AGT __
 GAM1978 MAP2K2 3' GGTGACCTGCCACCGTCCCTG 48406 T A ____ A
 TCC GG CA GGGAT GGCA GTCACC
 || ||||| ||| |||||
 CC GT CCCTG CCGT CAGTGG
 T _ CCAC C
 GAM1978 NF1 3' GTGACCCCTTCCCTGTCC 6048 T A T CAA
 GG CA GGA GG GTCAC
 || ||||| || |||||
 CC GT CCCT CC CAGTG
 T _ T C__
 GAM1978 WHSC1L1 5' GGCGACCCCGTCCCTCGGCC 35503 A CAA A
 GGTC AGGGATGG GTC CC
 ||| ||||| ||| ||
 CCGG TCCCTGCC CAG GG
 C CC_ C
 GAM1978 WHSC1L1 5' GGCGACCCCGTCCCTCGGCC 43781 A CAA A
 GGTC AGGGATGG GTC CC
 ||| ||||| ||| ||
 CCGG TCCCTGCC CAG GG
 C CC_ C
 GAM1978 ZNF22 3' GCATGACATCCTTGACC 93106 G G A
 GGTC AAGG ATG CA GT
 ||||| ||| |||
 CCAGTTCC TAC GT CG
 _ A A
 GAM1978 ALOX15B 3' GATGACATCCCTTTGACC 8553 _ GCAA
 GGTC AA GGGATG GTC
 ||||| ||||| |||

CCAGTT CCCTAC TAG
 T AG__
 GAM1978 ARTS-1 3' TGA CTGTTTATTCTCTTGACC 33607 TGGCA_
 GGTCAAGGGA AGTCA
 ||||| ||||
 CCAGTTCTCT TCAGT
 TATTTG
 GAM1978 C11orf14 3' GTGACTTGCTGTGGACC 40600 AAGGG
 GGTC ATGGCAAGTCAC
 ||| |||||
 CCAG TGTCGTTTCAGTG
 G____
 GAM1978 C16orf5 3' GGCGACCTCTGGCCCTGGCC 26354 A AT CAA A
 GGTCA GGG GG GTC CC
 |||| || || ||
 CCGGT CCC TC CAG GG
 _ GG TC_ C
 GAM1978 C2F 3' GATGTCACATCCTTTGACC 22007 GCAA
 GGTCAAGGGATG GTC
 ||||| ||
 CCAGTTTCCTAC TAG
 ACTG
 GAM1978 C6orf32 3' GTGTGCCCATCCCTCAACC 32406 CA _ AGT
 GGT AGGGATGG CA CAC
 || ||||| || ||
 CCA TCCCTACC GT GTG
 AC C ____
 GAM1978 COL4A3BP 5' GCTTCGCCATCCCCGACC 20341 AA _
 GGTC GGGATGGC AAGT
 ||| ||||| |||
 CCAG CCCTACCG TTCG
 CC C
 GAM1978 DCOHM 3' GACCTGCCTGCCTTGACC 50521 GAT A
 GGTCAAGG GGCA GTC
 ||||| ||| ||
 CCGGTTCC CCGT CAG
 GT_ C
 GAM1978 DKFZp434D177 5' GGTGACCCAGGCTCTCACC 51070 CA A_ CAA
 GGT AGGG TGG GTCACC
 || ||| || |||||
 CCA TCTC ACC CAGTGG
 C_ GG ____
 GAM1978 DKFZp434D177 5' GGTGACCCGGGCTCTCACC 80251 CA A_ CAA
 GGT AGGG TGG GTCACC
 || ||| || |||||
 CCA TCTC GCC CAGTGG
 C_ GG ____
 GAM1978 DKFZP564B1162 5' GGTAACCTATCCCTAAGCC 49351 CA GCA C
 GGT AGGGATG AGT ACC
 || ||||| || |||

CCG TCCCTAT TCA TGG
 AA A
 GAM1978 EFA6R 3' GTGAGTCATCCCTTGACT 31640 AAG
 GGTCAAGGGATGGC TCAC
 ||||| |||
 TCAGTTCCTACTG AGTG

 GAM1978 FLJ10242 5' GGTGACTTGCAGACACCTAAC 36393 CA GATG_
 GT AGG GCAAGTCACC
 || ||| |||||
 CA TCC CGTTCAGTGG
 A_ ACAGA
 GAM1978 FLJ14124 3' GACTCCATCCCTCAACT 46357 CA CA
 GGT AGGGATGG AGTC
 ||| ||||| |||
 TCA TCCCTACC TCAG
 AC
 GAM1978 FLJ21791 3' GATCCATCCCTTGAGC 62128 G CAA
 G TCAAGGGATGG GTC
 | ||||| |||
 C AGTTCCTACC TAG
 G
 GAM1978 FLJ22672 3' GGCCCCATCCCTGACC 46598 A CAA
 GGTCA GGGATGG GTC
 |||| ||||| |||
 CCAGT CCCTACC CGG
 _ C_
 GAM1978 FLJ23153 3' GTGAAATGACCCCTTGACT 45270 ATGG AG
 GGTCAAGGG CA TCAC
 ||||| || |||
 TCAGTTCCC GT AGTG
 CA_ AA
 GAM1978 FLJ23233 5' GGCGACTCACGCTGTTCTCGCC 45518 CAA A_ A
 GGT GGGATGGC AGTC CC
 ||| ||||| ||| ||
 CCG TCTTGTCG TCAG GG
 C_ CAC C
 GAM1978 KCND1 3' GACCTGCCATCCCCAGGCC 18347 AA A
 GGTC GGGATGGCA GTC
 |||| ||||| |||
 CCGG CCCTACCGT CAG
 AC C
 GAM1978 KIAA0040 3' TGACTTGCCATCTGCC 28497 CAAG
 GGT GGATGGCAAGTCA
 ||| |||||
 CCG TCTACCGTTCAGT

 GAM1978 KIAA0182 3' ACGTAGCTCATCCCTTACC 72495 C _ AA_
 GGT AAGGGATG GC GT
 ||| ||||| || ||

CCA TTCCCTAC CG CA
 _ T ATG
 GAM1978 KIAA0293 3' GTGTTGGTCATCCCATGACC 61239 A AAGT
 GGTCA GGGATGGC CAC
 ||||| ||||| ||
 CCAGT CCCTACTG GTG
 A GTT_
 GAM1978 KIAA0417 3' GGTGACCCCATACCTTGCC 71761 T G CAA
 GG CAAGG ATGG GTCACC
 || ||||| ||||| |||||
 CC GTTCC TACC CAGTGG
 _ A C_
 GAM1978 KIAA0453 3' GCTACCCAGTCCCTTGACC 69608 _ CA
 GGTC AAGGGA TGG AGT
 ||||| ||||| ||||| |||||
 CCAGTTCCT ACC TCG
 G CA
 GAM1978 KIAA0939 3' GTGACCTTTTGTCTTTTACC 62721 C TG CAA
 GGT AAGGGA G GTCAC
 ||||| ||||| | |||||
 CCA TTTCCT T CAGTG
 _ GT TTC
 GAM1978 KIAA1163 3' GATGACCGATCCCTTTAACC 79650 C_ _ CAA
 GGT AAGGGAT GG GTC
 ||||| ||||| || |||||
 CCA TTCCCTA CC TAG
 AT G AG_
 GAM1978 KIAA1193 3' GACTCGACCATCCCTCACC 68271 CA CA_
 GGT AGGGATGG AGTC
 ||||| ||||| ||||| |||||
 CCA TCCCTACC TCAG
 C_ AGC
 GAM1978 KIAA1500 3' GACATCCATCCCTGACC 64809 A CAA
 GGTCA GGGATGG GTC
 ||||| ||||| ||||| |||||
 CCAGT CCCTACC CAG
 _ TA_
 GAM1978 KIAA1671 3' GGTGACCTTTGCCCCTTGCC 66287 ATG _
 GGTCAAGGG GCAA GTCACC
 ||||| ||||| ||||| |||||
 CCGGTTCCC CGTT CAGTGG
 _ TC
 GAM1978 KIAA1724 3' GGTGACTTCATGCCCCAGCC 67620 CAA _ CA
 GGT GGG ATGG AGTCACC
 ||||| ||||| ||||| |||||
 CCG CCC TACT TCAGTGG
 AC_ G _
 GAM1978 KIAA1776 3' GTGACTTGCCACATTTGCC 51611 T GGA
 GG CAAG TGGCAAGTCAC
 ||||| ||||| ||||| |||||

			CC GTTT ACCGTTCAAGTG		
			— AC—		
GAM1978	KRTAP1-5	3'	ACTGTTTCATCCCTTGACC 50072	CA	
			GGTCAAGGGATGG AGT		
			CCAGTTCCCTACT TCA		
			TG		
GAM1978	MAFB	3'	GGCTTAGCCATCCCTGACC 19593	A	—
			GGTCA GGGATGGC AAGTC		
			CCAGT CCCTACCG TTCGG		
			— A		
GAM1978	NXPH3	3'	GGCTTGCCACCCCCCACC 66344	CAA	A
			GGT GGG TGGCAAGTC		
			CCA CCC ACCGTTTCGG		
			CC_ C		
GAM1978	PLSCR4	3'	TGGCTTCTATCCCTAACC 40135	CA	C
			GGT AGGGATGG AAGTCA		
			CCA TCCCTATC TTCGGT		
			A_ _		
GAM1978	RAP140	5'	GATTCCATCTCTTGACC 31518	CA	
			GGTCAAGGGATGG AGTC		
			CCAGTTCTCTACC TTAG		
			—		
GAM1978	RASD2	3'	GTGACTCCCTCCTTGACC 27466	AT	CA
			GGTCAAGGG GG AGTCAC		
			CCGGTTCCT CC TCAGTG		
			— C_		
GAM1978	SLC12A5	5'	GGCGCAGCCATCCCCGGACC 40771	AA	AA_
			GGTC GGGATGGC GTC		
			CCAG CCCTACCG CGG		
			GC ACG		
GAM1978	SLC26A9	3'	GACAGTCCCCCTTGACC 54716	AT	AA
			GGTCAAGGG GGC GTC		
			CCAGTTCCC CTG CAG		
			C_ A_		
GAM1978	SLC26A9	3'	GACAGTCCCCCTTGACC 57008	AT	AA
			GGTCAAGGG GGC GTC		
			CCAGTTCCC CTG CAG		
			C_ A_		
GAM1978	SSR3	3'	ACTTGTTTCCTTGATC 24027	TG	
			GGTCAAGGGA GCAAGT		

CTAGTTCCTT TGTTC A

GAM1978 TBLR1 3' T G A C T G T C C C T G A C C 45431 A G G C A
G G T C A G G G A T A G T C A
||||| ||||| |||||
C C A G T C C C T G T C A G T

GAM1978 LOC112609 3' G A C A G C C A T C C C C T G C C 73199 T A A A
G G C A G G G A T G G C G T C
|| || ||||| ||||| |||||
C C G T C C C T A C C G C A G

GAM1978 LOC114926 3' G T G A C T T G A C C T T G C C 57389 T G A T G G
G G C A A G G C A A G T C A C
|| ||||| ||||| |||||
C C G T T C C G T T C A G T G

GAM1978 LOC115297 3' T G A C T T A G A A C C A T C C T T G A C C 73263 G C
G G T C A A G G A T G G A A G T C A
||||||| ||||| |||||
C C A G T T C C T A C C T T C A G T
A A G A

GAM1978 LOC121344 5' G G C G C C T C A T C C C T T C A C C 74502 C C A A
G G T A A G G G A T G G G T C
||| ||||| ||||| |||||
C C A T T C C C T A C T C G G
C C C G

GAM1978 LOC126364 5' G T G A T T C T C C T T G A C C 76198 T G G C A A
G G T C A A G G G A G T C A C
||||||| || |||||
C C A G T T C C C T T A G T G
T

GAM1978 LOC130074 3' G T G A C C C A T G A A C T T G C C 76631 T G G C A A
G G C A A G A T G G G T C A C
|| ||||| ||||| |||||
C C G T T C T A C C C A G T G
A A G

GAM1978 LOC131583 3' G A C A A C C T C C C T G T C C C T T G C C 76380 T C A A
G G C A A G G G A T G G G T C
|| ||||| ||||| |||||
C C G T T C C C T G T C C A G
C C T C C A A

GAM1978 LOC143384 5' G T G A C T C A C A G C T C C C G C C 77064 C A A G C A
G G T G G G A T G A G T C A C
||| ||||| || |||||
C C G C C C T A C T C A G T G
C G A C

GAM1978 LOC145231 3' G G C T T G T C C A T C C C T T G A C 84254
G T C A A G G G A T G G C A A G T C
||||||| ||||| |||||

		CAGTTCCTACC GTTCGG		
		T		
GAM1978	LOC148137 3'	GGCCTGCCCATCCCTGACC 59106	A	_ A
		GGTCA GGGATGG CA GTC		
		CCAGT CCCTACC GT CGG		
		_ C C		
GAM1978	LOC162048 5'	GGTGAAGACGCCCTTGACC 83202	A	GCAAG
		GGTCAAGGG TG TCACC		
		CCAGTTCCC GC AGTGG		
		_ AGA_		
GAM1978	LOC220469 3'	GTGACTCATTCTCCTGTCC 76893	T A_	GCA
		GG CA GGGATG AGTCAC		
		CC GT TCTTAC TCAGTG		
		T CC _		
GAM1978	LOC221466 5'	GGCCCTTCCATCCCTTGTC 95316	T	CAA_
		GG CAAGGGATGG GTC		
		CC GTTCCCTACC CGG		
		T TTCC		
GAM1978	LOC221491 5'	GGCATGCCCCCTTGACC 93658	AT	A
		GGTCAAGGG GGCA GTC		
		CCAGTTCCC CCGT CGG		
		_ A		
GAM1978	LOC222865 3'	GGTTACCACCCCTTGACC 94449	AT	CAA C
		GGTCAAGGG GG GT ACC		
		CCAGTTCCC CC CA TGG		
		_ AC_ T		
GAM1978	LOC254105 3'	GTGACCCAGACCTCTGACC 96421	_	GA CAA
		GGTCA AGG TGG GTCAC		
		CCAGT TCC ACC CAGTG		
		C AG _		
GAM1978	LOC256364 5'	GGTGACCCGCCCGCCTTGGCC 96448	GAT	AA
		GGTCAAGG GGC GTCACC		
		CCGGTTCC CCG CAGTGG		
		GC_ CC		
GAM1978	LOC257441 5'	GGTGACCCGGGCTCTCACC 97302	CA	A_ CAA
		GGT AGGG TGG GTCACC		
		CCA TCTC GCC CAGTGG		
		C_ GG _		
GAM1978	LOC56965 3'	GACTCCATCCCCTGACT 39924	A	CA
		GGTCA GGGATGG AGTC		

TCAGT CCCTACC TCAG
 C _
 GAM1978 LOC56965 3' GACTCCATCCCCTGACT 39931 A CA
 GGTCA GGGATGG AGTC
 ||||| ||||| |||
 TCAGT CCCTACC TCAG
 C _
 GAM1978 LOC91301 5' GGTGAACGCCATCCCCCACC 66151 CAA AAG
 GGT GGGATGGC TCACC
 || ||||| |||||
 CCA CCCTACCG AGTGG
 CC_ CA_
 GAM1978 LOC92736 5' GACGCTCGCCGTCCCCTGACC 70941 A AA_
 GGTCA GGGATGGC GTC
 ||||| ||||| |||
 CCAGT CCCTGCCG CAG
 C CTCG
 GAM1979 ABCC1 3' CTCTTTTCTTTCCCTCTC 39604 AT TC
 GAGA GG GGAAAAGAG
 ||| || |||||
 CTCT CC TCTTTTCTC
 C_ TT
 GAM1979 ACCN2 3' TCTCTGAGAACCATTCTCCCA 39632 A _GGAAA
 TG GGAGAATGGT C AGAGA
 || ||||| || |||||
 AC CCTCTTACCA G TCTCT
 _ A AG_
 GAM1979 ADAM19 3' TCTCTCTTCCCTTCCCCTCTC 53848 AT TC A
 GAGA GG GGAA AGAGA
 ||| || ||| |||||
 CTCT CC CCTT TCTCT
 CC TT C
 GAM1979 ADCY8 5' CTCCTCCGGCTGCCTCCCCA 8499 A AAT AAA
 TG GGAG GGTCCGA GAG
 || ||| ||||| |||
 AC CCTC TCGGCCT CTC
 C CG_ C_
 GAM1979 ADRBK1 3' CTCCCCTCCCGTCTACTCA 9666 G A TC AAAA
 TGAG AGA TGG GG GAG
 ||||| ||| || |||
 ACTC TCT GCC CC CTC
 A _ CT C_
 GAM1979 B4GALT5 3' CTCCTCTCCCCTTTCTCTCA 17686 AT TC AAA
 TGAGGAGA GG GGA GAG
 ||||| || ||| |||
 ACTCCTTT CC CCT CTC
 _ _ CTC
 GAM1979 BAK1 3' CTCCCTTCCTCTCTCCTTA 93626 AT TC AAAA
 TGAGGAGA GG GG GAG
 ||||| || || |||

ATTCCTCT CC CC CTC
 CT TT ____
 GAM1979 CHC1 3' CTCTTTTCCTTCCTCCTC 8862 GAAT TC
 GAGGA GG GGAAAAGAG
 |||| | |||||
 CTCCT CC CCTTTTCTC
 ____ TT
 GAM1979 CKTSF1B1 3' CTCCTTTTCCTCCTCCTCA 26294 AAT TC A
 TGAGGAG GG GGAAA GAG
 ||||| | |||| |
 ACTCCTC CC CCTTT CTC
 CT_ T_ C
 GAM1979 DDX3 5' CTCTTTTCCCTCCCTCTCCTC 9056 AT TC
 GAGGAGA GG GGAAAAGAG
 ||||| | |||||
 CTCCTCT CC CCTTTTCTC
 C_ TC
 GAM1979 DLX4 3' CTCTCTCCCTTTCTCCTC 10419 T TC AAA
 GAGGAGAA GG GGA GAG
 ||||| | || |
 CTCCTCTT CC TCT CTC
 T C_ ____
 GAM1979 EN2 3' CTCCTTCCTTCCTCCTCCTC 9257 AAT TC AA
 GAGGAG GG GGAA GAG
 |||| | || |
 CTCCTC CC CCTT CTC
 CT_ TT C_
 GAM1979 FABP6 5' CTCAGCACCAACCCATTCTCCTC 9344 TC AAAA
 A TGAGGAGAATGG GG GAG
 ||||| || |
 ACTCCTCTTACC CC CTC
 CA ACGA
 GAM1979 FHL1 3' TCTCCTTCCGTCTTTTCTCCCA 9362 A T T AA
 TG GGAGAA GG CGGAA GAGA
 || |||| | |||| |
 AC CCTCTT TC GCCTT CTCT
 _ T T C_
 GAM1979 GPR61 3' CTCCCTGATCTCTCTCCTCA 79660 AT AAAA
 TGAGGAGA GGTCGG GAG
 ||||| |||| |
 ACTCCTCT CTAGTC CTC
 CT C_
 GAM1979 GPR86 3' CTCCCCTCCAAACACCTTCTCA 43903 AA GTC AAA
 TGAGGAG TG GGA GAG
 ||||| | || |
 ACTCTTC AC CCT CTC
 C_ AAA CCC
 GAM1979 HAS3 3' TCTTTGAGACCATCCATTCTCC 57603 TC AAA_
 TCA TGAGGAGAATGG GG AGAGA
 ||||| || ||||

ACTCCTCTTACC CC TTTCT
 TA AGAG
 GAM1979 HD 3' TTCTCTCTTTTCTTCTCA 10919 T TC
 TGAGGAGAA GG GGAA
 ||||| || |||
 ACTCTTCTT TC TCTT
 T TC
 GAM1979 HMGA2 5' CTCTCCTCCTCCTCCTCCCTC 14455 A AT TC AA
 GAGG GA GG GGA AGAG
 ||| || || ||| |||
 CTCC CT TC CCT TCTC
 C CC CT CC
 GAM1979 KLF8 5' TTTCGACCCCCCTCCTCA 24375 AAT_
 TGAGGAG GGTCGGAA
 ||||| |||||
 ACTCCTC CCAGCTTT
 CCCC
 GAM1979 KMO 3' CTCCTTTCCGCTTCTCCTC 14842 AT T A
 GAGGAGA GG CGGAAA GAG
 ||||| || ||||| |||
 CTCCTCT TC GCCTTT CTC
 — — C
 GAM1979 LFG 3' CTCTCCTCCGGGCCCTCA 77235 AGAAT _ AA
 TGAGG GGTC GGA AGAG
 |||| ||| || |||
 ACTCC CCGG CCT TCTC
 ——— G CC
 GAM1979 LRAT 5' CTCCTTTGCCTTCCTCTCTCCT 60729 AT TC _ A
 CA TGAGGAGA GG GG AAA GAG
 ||||| || || ||| |||
 ACTCCTCT CC CC TTT CTC
 CT TT G C
 GAM1979 MEF2D 3' TCCCTTCTCAGGCTATTCCC 20988 A G A A
 GG GAATGGTC GA AAG GA
 || ||||| || ||| ||
 CC CTTATCGG CT TTC CT
 — A C C
 GAM1979 MYO1D 3' TCTCCTTCCACTTATTTCTCCTCA 72250 AT C AA
 TGAGGAGA GGT GGAA GAGA
 ||||| || ||| |||
 ACTCCTTT TCA CCTT CTCT
 AT _ C_
 GAM1979 NFIA 5' CTCTCTCCCTCTTTCTCCTC 70885 T TC AA
 GAGGAGAA GG GGA AGAG
 ||||| || || |||
 CTCCTCTT TC CCT TCTC
 _ TC C_
 GAM1979 NR3C1 3' CTCCCATTCTGACCACCCTTCT 5729 AA AA_
 CA TGAGGAG TGGTCGGAA GAG
 ||||| ||||| |||

		ACTCTTC ACCAGTCTT CTC	
		CC ACC	
GAM1979	OVOL1	5' TCTCTTCTCCACCAAGCCTC 17073	AGAA C A
		GAGG TGGT GGA AAGAGA	
		CTCC ACCA CCT TTCTCT	
		GA__ _ C	
GAM1979	PIGR	3' CTCCCTCCCGTCCTTCCCCTC 72996	A T T AAAA
		GAGG GAA GG CGG GAG	
		CTCC CTT CC GCC CTC	
		C _ T CTCC	
GAM1979	PLXNA2	3' TCTCCCTTCCTTCTTTTCTCCC 48004	A T TC AA
	A	TG GGAGAA GG GGAA GAGA	
		AC CCTCTT TC CCTT CTCT	
		_ T TT CC	
GAM1979	PRKACB	3' CTCCTTTTATATCCTCCTC 12273	AAT CG A
		GAGGAG GGT GAAA GAG	
		CTCCTC CTA TTTT CTC	
		__ TA C	
GAM1979	PSEN1	5' TCCCTCTCAGATTCTTCTCA 24622	__ TC
		TGAGGAGAAT GG GGA	
		ACTCTTCTTA TC CCT	
		GAC TC	
GAM1979	PTK2B	3' CTCTTTTCTTACTCCTCCTC 15906	AAT C
		GAGGAG GGT GGAAAAGAG	
		CTCCTC TCA TCTTTTCTC	
		C__ T	
GAM1979	RAB5B	3' CTCTTTTCTCCTCTCCCCA 12708	A AT TC
		TG GGAGA GG GGAAAAGAG	
		AC CCTCT CC TCTTTTCTC	
		C _ _	
GAM1979	RABIF	3' TCTCTTCCCTGGCATTCTCC 12731	G AA
		GGAGAATG TCGG AAGAGA	
		CCTCTTAC GGTC TTCTCT	
		_ CC	
GAM1979	RBM8A	3' TCTCCTCTTGGAGCATTCTCCC 18813	A G G AAA
	A	TG GGAGAATG TC GA GAGA	
		AC CCTCTTAC AG TT CTCT	
		_ G G CTC	
GAM1979	RGS5	3' CTCTTTTATACCTTCCTCA 14623	AAT CGG
		TGAGGAG GGT AAAAGAG	

ACTCCTT CCA TTTTCTC
 ____ TA_
 GAM1979 RTN3 5' TCTCTTTTCACCCTTCTCCCA 74332 A T CG
 TG GGAGAA GGT GAAAAGAGA
 || ||||| ||| |||||
 AC CCTCTT CCA CTTTCTCT
 _ C _
 GAM1979 SHB 5' TCTCTCCCGGCCGCATTCTCCT 13118 ____ AAA
 C GAGGAGAAAT GGTCGG AGAGA
 ||||| ||||| |||||
 CTCCTCTTA CCGGCC TCTCT
 CG C_
 GAM1979 SMCX 3' TCCCTTCCCCTGACTGTTCCAC 16089 A A_ AA_ A
 CCA TG GG GAATGGTCGG AAG GA
 || || ||||| ||| ||
 AC CC CTTGTCAGTC TTC CT
 _ AC CCC C
 GAM1979 SOX4 3' CTCTTTTCCCCTTGCCCCCTC 13305 AGAAT_ TC
 GAGG GG GGAAAAGAG
 ||| || |||||
 CTCC CC CCTTTTCTC
 CCGTT _
 GAM1979 SPARC 3' CTCCTTTTCTTCACCCTCC 13345 AAT C_ _
 GGAG GGT GGAAAAG AG
 ||| || ||||| ||
 CCTC CCA TCTTTTC TC
 ____ CT C
 GAM1979 SPON1 3' CTCTTTTCAAGTCTCCTCA 63119 ATGGTCG
 TGAGGAGA GAAAAGAG
 ||||| |||||
 ACTCCTCT CTTTCTC
 GAA____
 GAM1979 TCF7L2 5' CTCCTCCCTCTTTTCCCCTC 48440 A T TC AAA
 GAGG GAA GG GGA GAG
 ||| ||| || ||| |||
 CTCC CTT TC CCT CTC
 C T TC C_
 GAM1979 TNFSF5 3' CTCCCCCAGTCTCTCTTCTCA 5368 AT TC AAAA
 TGAGGAGA GG GG GAG
 ||||| || || |||
 ACTCTTCT CT CC CTC
 CT GA CC_
 GAM1979 UBE2L3 3' CTCCTCCAGTCCTTCTCCTCA 13964 T TC AAA
 TGAGGAGAA GG GGA GAG
 ||||| || ||| |||
 ACTCCTCTT CT CCT CTC
 C GA C_
 GAM1979 UBQLN2 3' CTCCCTCCTACTTCCCTCA 26492 A AT C AAA
 TGAGG GA GGT GGA GAG
 |||| || ||| ||| |||

ACTCC CT TCA CCT CTC
 _ _ T CC_
 GAM1979 XPNPEP2 3' CTCCCAGCCCTCTCCTCA 14142 AT C AAAA
 TGAGGAGA GGT GG GAG
 ||||| ||| ||
 ACTCCTCT CCG CC CTC
 C_ A ____
 GAM1979 ACTR3 3' CTCTCCACCCCTTCCCCCA 20366 A A T TC AAA
 TG GG GAA GG GGA GAG
 || ||||| ||| ||
 AC CC CTT CC CCT CTC
 C C C CA ____
 GAM1979 AGPAT1 3' CTCTCCCCACTTATTCTCCTC 22172 _ C AAA
 GAGGAGAATG GT GG AGAG
 ||||| ||| ||
 CTCCTCTTAT CA CC TCTC
 T C C_
 GAM1979 AGPAT1 3' CTCTTCCTTGTCTCCCCTCTCC 22175 A AT TC____ AA
 CCA TG GGAGA GG GGA AGAG
 || |||| || ||| ||
 AC CCTCT CC CCT TCTC
 C CC TCTGTT ____
 GAM1979 AP3S2 3' CTCAGGTGCCATTCTCCCA 20649 A CGGAAAA
 TG GGAGAATGGT GAG
 || ||||| ||
 AC CCTCTTACCG CTC
 _ TGGA____
 GAM1979 BCL2L12 5' CTCTTTTCTCTTTCTCCTC 57643 ATGGTC
 GAGGAGA GGAAAAGAG
 ||||| |||||
 CTCCTTT CTTTTCTC
 CT____
 GAM1979 BRPF3 3' CTCCTTCCTTCTTTCTCTTCA 93929 T TC AA
 TGAGGAGAA GG GGAA GAG
 ||||| || ||| ||
 ACTTCTCTT TC CCTT CTC
 _ TT C_
 GAM1979 C1orf34 3' TCTCTCTCTGCAACACTCTCCT 61324 A GT_ AA
 CA TGAGGAGA TG CGGA AGAGA
 ||||| || ||| ||||
 ACTCCTCT AC GTCT TCTCT
 C AAC C_
 GAM1979 C20orf110 3' CTCTTTTCATTTTCTCCCA 80362 A TGGTCG
 TG GGAGAA GAAAAGAG
 || |||| |||||
 AC CCTCTT CTTTTCTC
 _ TTA____
 GAM1979 CX46.6 3' CTTCTCCTCAGCCTTCTCCTTA 40313 T C_ A
 TGAGGAGAA GGT GGA AAG
 ||||| || ||| ||

ATTCCTCTT CCG CCT TTC
 _ ACT C
 GAM1979 DC-TM4F2 3' CTCTCCTCCAGCATTCTCCTC 48900 GTC AA
 GAGGAGAATG GGA AGAG
 ||||| ||| |||
 CTCCTCTTAC CCT TCTC
 GA_ CC
 GAM1979 DKFZP586B2420 3' CTCTGTGACCTCTCTCCTCA 75489 AT GAAA
 TGAGGAGA GGTCTG AGAG
 ||||| |||| |||
 ACTCCTCT CCAGT TCTC
 CT G__
 GAM1979 DPCR1 3' TCTCCTCCCACCTTCACCCCA 55998 A A T C AAA
 TG GG GAA GGT GGA GAGA
 || || || || || |||
 AC CC CTT CCA CCT CTCT
 C A _ C C__
 GAM1979 DUSP14 3' CTCTCCACTCTCTTCTCA 23817 AT C AAA
 TGAGGAGA GGT GGA GAG
 ||||| || ||| |||
 ACTCTTCT TCA CCT CTC
 C_ _ __
 GAM1979 EDG1 3' TTCCCTTCATACCCCTCCTCA 60054 A__ TC
 TGAGGAG ATGG GGAA
 ||||| ||| |||
 ACTCCTC TACT CCTT
 CCCA TC
 GAM1979 FADS2 3' TCTCCTCTCCTTTTTCTCTTCA 16219 TGGTC AAA
 TGAGGAGAA GGA GAGA
 ||||| || |||
 ACTTCTCTT CCT CTCT
 TTT__ CTC
 GAM1979 FLJ10251 3' CTCTCTTCCCCTCCCTCA 36411 A AT TC A
 TGAGG GA GG GGAA AGAG
 |||| || || ||| |||
 ACTCC CT CC CCTT TCTC
 _ _ _ C
 GAM1979 FLJ10898 3' TCTCTTTTCTCTTCTCTCCA 60139 A AT TC
 TG GGAGA GG GGAAAAGAGA
 || |||| || |||||
 AC CCTCT TC CCTTTTCTCT
 _ CT T_
 GAM1979 FLJ11362 3' TCTCCTCCCACCTCCTCCCTCA 41965 A AT_ C AAA
 TGAGG GA GGT GGA GAGA
 |||| || || ||| |||
 ACTCC CT CCA CCT CTCT
 _ CCT C C__
 GAM1979 FLJ11565 3' TCTCTTTTCTCTCCCTCCCTCA 45412 A AT TC
 TGAGG GA GG GGAAAAGAGA
 |||| || || |||||

ACTCC CT CC TCTTTTCTCT
 _ C_ TC
 GAM1979 FLJ13782 3' TTCCGATCCATTCCCCTC 46706 A _
 GAGG GAATGG TCGGAA
 |||| |||| ||||
 CTCC CTTACC AGCCTT
 C T
 GAM1979 FLJ22679 3' TCTCTTTCTCTCTCTCCTCA 50910 AT TC GA
 TGAGGAGA GG G AAAGAGA
 ||||| || | |||||
 ACTCCTCT CT C TTTCTCT
 CT _ TC
 GAM1979 FLJ22679 3' CTCCTTCCCTTTGGCTCTCTCC 35177 AT _ _ AA
 TCA TGAGGAGA GGTC GGAA GAG
 ||||| ||| ||| |||
 ACTCCTCT TCGG CCTT CTC
 C_ TTTC C_
 GAM1979 FLJ31300 3' TCTCCTCCCCAGCAGCCATTCT 58934 C_ _ AAAA
 CC GGAGAATGGT GG GAGA
 ||||| || |||
 CCTCTTACCG CC CTCT
 ACGA CCTC
 GAM1979 GAL3ST-4 3' CTCCTCCACCCTCCACTCA 45276 GA AT C AAA
 TGAG GA GGT GGA GAG
 ||| || ||| ||| |||
 ACTC CT CCA CCT CTC
 AC C_ _ C_
 GAM1979 HEMK 3' TCTCCCCTCAGCCTCTCCTCA 32965 AT CG AAA
 TGAGGAGA GGT GA GAGA
 ||||| ||| || |||
 ACTCCTCT CCG CT CTCT
 _ A_ CCC
 GAM1979 KIAA0280 3' TCCCTTTTCTTTTGCCCTTCCC 93310 A T C_ _ A
 GG GAA GGT GGAAAAG GA
 || ||| ||| ||||| ||
 CC CTT CCG TCTTTTC CT
 _ C TTT C
 GAM1979 KIAA0295 3' TCTCTTTTCCTCTACCTTCCTC 68674 AA TC
 A TGAGGAG TGG GGAAAAGAGA
 ||||| ||| ||||| |||
 ACTCCTT ATC CCTTTTCTCT
 CC T_
 GAM1979 KIAA0296 3' CTCCTTCCCCCAGCCTCATCA 28772 G AA TC AA
 TGA GAG TGG GGAA GAG
 ||| ||| ||| ||| |||
 ACT CTC ACC CCTT CTC
 A CG C_ C_
 GAM1979 KIAA0321 3' CTCTTTTCCTTCCTTCCC 63050 A T TC
 GG GAA GG GGAAAAGAG
 || ||| || ||||| |||

CC CTT CC CCTTTTCTC
 _ _ TT
 GAM1979 KIAA0435 3' TCCTTTTCTTTATTTCTCA 29665 A TC A
 TGAGGAGA TGG GGAAAAG GA
 ||||| || ||||| ||
 ACTCCTTT ATT TCTTTTC CT
 _ _ C
 GAM1979 KIAA0451 3' CTCTCTCCCTTCTCTTCTCA 29772 AT TC AA
 TGAGGAGA GG GGA AGAG
 ||||| || || ||||
 ACTCTTCT TC CCT TCTC
 CT _ C_
 GAM1979 KIAA0451 3' TCCCTTTCCCTTGCCTTCTCC 29782 T C_ A A
 TC GAGGAGAA GGT GG AAAG GA
 ||||| || || ||||
 CTCCTCTT CCG CC TTTC CT
 _ TTC C C
 GAM1979 KIAA0903 3' CTCTCCTCTGCTTTCTCA 71911 AAT T AA
 TGAGGAG GG CGGA AGAG
 ||||| || || ||||
 ACTCCTT TC GTCT TCTC
 _ _ CC
 GAM1979 KIAA1030 3' TCTCTCTCCCTTTTTTCTCCT 94986 TG TC AAA
 C GAGGAGAA G GG AGAGA
 ||||| | || ||||
 CTCCTCTT T CC TCTCT
 TT TT CTC
 GAM1979 KIAA1130 3' CTCCCTTCACTCAGTCTCCTCA 63089 A TCG AA
 TGAGGAGA TGG GAA GAG
 ||||| || || ||||
 ACTCCTCT ACT CTT CTC
 G CA_ CC
 GAM1979 KIAA1183 3' CTCTTCCTGTCCTCCGCA 63192 A AAT TC AA
 TG GGAG GG GGA AGAG
 || |||| || || ||||
 AC CCTC CT CCT TCTC
 G _ GT _
 GAM1979 KIAA1271 3' CTCTGGTCTCCATTCTCTTCA 70136 TC AA
 TGAGGAGAATGG GGA AGAG
 ||||| || || ||||
 ACTTCTCTTACC TCT TCTC
 _ GG
 GAM1979 KIAA1384 5' TCTCTTTTCTCCCTCTCCTACA 65180 _ AT TC
 TG AGGAGA GG GGAAAAGAGA
 || |||| || |||||
 AC TCCTCT CC TCTTTTCTCT
 A _ C_
 GAM1979 KIAA1511 3' CTCCTCTATTCTCTCTCA 70727 G TC AAA
 TGAG AGAATGG GGA GAG
 ||| ||||| || |||

ACTC TCTTACT TCT CTC
 _ TA C_
 GAM1979 KIAA1536 3' CTCTCCTCGCATCTCCTCA 40877 A GTC AAA
 TGAGGAGA TG GGA GAG
 ||||| || ||| |||
 ACTCCTCT AC CCT CTC
 _ GCT _
 GAM1979 KIAA1819 5' CTCTTTTACTAACTCCCCTC 70251 A A_ CG
 GAGG GA TGGT GAAAAGAG
 ||| || ||| |||||
 CTCC CT ATCA TTTTCTC
 C CA _
 GAM1979 LAP1B 5' CTCCTCCCCCTTCTCCTC 65192 T TC AAA
 GAGGAGAA GG GGA GAG
 ||||| || ||| |||
 CTCCTCTT CC CCT CTC
 _ C_ C_
 GAM1979 LIP8 3' TCTCTCCTCTTTGTTCTCTCA 89528 G TG TC AA
 TGAG AGAA G GGA AGAGA
 ||| ||| | ||| |||||
 ACTC TCTT T TCT TCTCT
 _ GT_ CC
 GAM1979 MAB21L2 3' CTTTTCCTTCTTTCCCCCT 22240 A_ T TC
 AGG GAA GG GGAAAAG
 ||| ||| || |||||
 TCC CTT TC CCTTTTC
 CC _ TT
 GAM1979 MGC15882 3' CTCTTCTCCCTTCTCCTC 52883 TGGTC A
 GAGGAGAA GGA AAGAG
 ||||| ||| |||||
 CTCCTCTT CCT TTCTC
 C_ C
 GAM1979 MGC26766 3' TCTCTTTTCTAAACCCTCCTT 59470 AAT C_
 A TGAGGAG GGT GGAAAAGAGA
 ||||| ||| |||||
 ATTCCTC CCA CTTTTTCTCT
 _ AAT
 GAM1979 MGC3035 5' CTCCCCTTCCATTCTCCCA 44397 A TC AAAA
 TG GGAGAATGG GG GAG
 || ||||| || |||
 AC CCTCTTACC CC CTC
 _ TT C_
 GAM1979 PAK6 3' CTCCTCTCAGTATTCTCTCCA 39808 AG GTC AAA
 TG GAGAATG GGA GAG
 || ||||| ||| |||
 AC CTCTTAT TCT CTC
 CT GAC C_
 GAM1979 PSK 3' TCTCTTTTCACCCACCTTCCTC 32883 AA TCG
 A TGAGGAG TGG GAAAAGAGA
 ||||| ||| |||||

ACTCCTT ACC CTTTCTCT
 CC CA_
 GAM1979 SLC34A1 3' TCCAAGATACCATCTCCTCA 13208 A C____
 TGAGGAGA TGGT GGA
 ||||| ||| ||
 ACTCCTCT ACCA CCT
 _ TAGAA
 GAM1979 ULK2 3' CTCTCCTCTTCCTCTCCCA 28686 A AT TC AA
 TG GGAGA GG GGA AGAG
 || |||| || ||| ||||
 AC CCTCT CC TCT TCTC
 _ _ T_ CC
 GAM1979 LOC127733 3' ATCTCCCTTCCAGCTGTTCCAT 75182 AG TC____ AA ____
 TCTCTCCA TG GAGAATGG GGAA GAGA T
 || ||||| ||| ||| |
 AC CTCTTACC CCTT CTCT A
 CT TTGTCGA CC ____
 GAM1979 LOC130644 3' CTCTTCCCTATCTCCCCTC 76252 A _ TC AA
 GAGG GA ATGG GGA AGAG
 ||| || ||| ||| ||||
 CTCC CT TATC CCT TCTC
 C C _ _
 GAM1979 LOC131034 5' CTCTTTTCTCAGTACCCTCCTC 56420 AAT C____
 GAGGAG GGT GGAAAAGAG
 ||||| ||| |||||
 CTCCTC CCA TCTTTTCTC
 _ TGAC
 GAM1979 LOC135763 3' TCCCTTCTCCTGGTCTCTCCTC 57563 AT GT_ A A
 A TGAGGAGA G C GGA AAG GA
 ||||| | ||| ||| ||
 ACTCCTCT C G CCT TTC CT
 _ TG T C C
 GAM1979 LOC139770 5' TCTCTCCCCGCCCTCTCCTC 75907 AT T AAA
 GAGGAGA GG CGG AGAGA
 ||||| || ||| |||||
 CTCCTCT CC GCC TCTCT
 CC _ CC_
 GAM1979 LOC143943 5' TCTCTCTCAGCCACTGCTCCTC 83922 AA_ C AAA
 A TGAGGAG TGGT GG AGAGA
 ||||| ||||| || |||||
 ACTCCTC ACCG CT TCTCT
 GTC A C_
 GAM1979 LOC145813 5' CTCCTCCAACATTCTCCCA 84506 A GTC AAA
 TG GGAGAATG GGA GAG
 || ||||| ||| |||
 AC CCTCTTAC CCT CTC
 _ AA_ C_
 GAM1979 LOC147007 3' TCTCTTTTCTTCCCCTCC 84970 AAT TC
 GGAG GG GGAAAAGAGA
 ||| || |||||

CCTC CC TCTTTTCTCT
 ____ CT
 GAM1979 LOC150051 3' CTCCTTCTTCTTAACCCTCTCC 85953 A AT C_ _ _
 CA TG GGAGA GGT GGAA AAG AG
 || |||| || |||| ||
 AC CCTCT CCA TCTT TTC TC
 _ C_ AT C C
 GAM1979 LOC152905 5' TCTCTTTTCACCCTTCTCCCA 61096 A T CG
 TG GGAGAA GGT GAAAAGAGA
 || |||| || |||||
 AC CCTCTT CCA CTTTCTCT
 _ C _
 GAM1979 LOC154834 3' TCTCTCCAGCTCATTTTCCCCA 87498 A _ C AAA
 TG GGAGAATG GT GGA GAGA
 || ||||| || || ||
 AC CCTTTTAC CG CCT CTCT
 C T A _
 GAM1979 LOC200316 3' CTCCTCCCCGCTCTCCCA 90178 A A TC AAA
 TG GGAGA TGG GGA GAG
 || |||| || || ||
 AC CCTCT GCC CCT CTC
 _ C _ C_
 GAM1979 LOC220827 3' TCTCTTTTCCCCACCCTGCCCT 92882 _ AA TC
 CA TGAGG AG TGG GGAAAAGAGA
 |||| || || |||||
 ACTCC TC ACC CCTTTTCTCT
 CG CC _
 GAM1979 LOC221308 5' CTCTCTCCCAGCACTTTCTCCT 94406 TG_ C AAA
 C GAGGAGAA GT GG AGAG
 ||||| || || ||
 CTCCTCTT CG CC TCTC
 TCA A CTC
 GAM1979 LOC254428 3' TTCCCTCCACCTCTCCTTA 97202 A_ TC
 TGAGGAGA TGG GGAA
 ||||| || ||
 ATTCCTCT ACC CCTT
 CC TC
 GAM1979 LOC257459 3' CTCCCCTCCTTTCTCCTC 91529 T TC AAAA
 GAGGAGAA GG GG GAG
 ||||| || || ||
 CTCCTCTT CC CC CTC
 T TC _
 GAM1979 LOC257464 3' TCTCTCCTTTTGGCCTCCCC 91247 A AT A_
 GG GA GGTCGGAA AGAGA
 || || ||||| ||||
 CC CT CCGGTTTT TCTCT
 C _ CC
 GAM1979 LOC51028 3' CTCTTTTAATTTCTCCCCA 32692 A TGGTCGG
 TG GGAGAA AAAAGAG
 || |||| |||||

		AC CCTCTT	TTTTCTC		
		C	TAA_____		
GAM1979	LOC51094	3'	CTCTCCTCCAACCATTTT	32596	C AA
			AGAATGGT GGA AGAG		
			TTTTACCA CCT TCTC		
			A CC		
GAM1979	LOC51312	5'	TCTCTTTTTACTCTGCTCA	33995	G ATGGTCG
			TGAG AGA GAAAAGAGA		
			ACTC TCT TTTTTCTCT		
			G CA_____		
GAM1979	LOC55971	5'	TCTCCTCCCCGTCCCTTCTCCT	38734	T T AAAA
	C		GAGGAGAA GG CGG GAGA		
			CTCCTCTT CC GCC CTCT		
			C T CCTC		
GAM1979	LOC90750	3'	CTTTTCTGGATTTTTCCCCA	64628	A TGG
			TG GGAGAA TCGGAAAAG		
			AC CCTTTT GGTCTTTTC		
			C TA_		
GAM1980	ATP8A2	3'	GTTCCACTGCAGACTCAG	95158	_A_
			CTG G TGCAGTGGAAC		
			GAC C ACGTCACCTTG		
			T AG		
GAM1980	CTLA4	3'	TTTTTTGCTATCCAGCTA	19057	_ TG
			TAGCTGGAT GCAG GA		
			ATCGACCTA CGTT TT		
			T TT		
GAM1980	CYBB	3'	CCCTGTGTTATCCAGTTA	76845	___ T
			TAGCTGGAT GCAG GG		
			ATTGACCTA TGTC CC		
			TTG _		
GAM1980	NCAM2	3'	TTCCGGATGTTCTAGCTA	17005	T G_
			TAGCTGGA GCA TGGAA		
			ATCGATCT TGT GCCTT		
			_ AG		
GAM1980	P2RY6	3'	TCCATGCATATCCAGCTG	16000	___ G
			TAGCTGGA TGCA TGGA		
			GTCGACCT ACGT ACCT		
			AT _		
GAM1980	RNASE1	5'	TCCAATGCATCATTGAGCT	64603	___
			AGCTG GATGCAGTGGA		

		TCGAC CTACGTCACCT		
		TTA		
GAM1980	SLC24A1	5' GTTCCCTGCTGTCCAGCT 17565	_	T
		AGCTGGAT GCAG GGAAC		
		TCGACCTG CGTC CCTTG		
		T _		
GAM1980	ARPC5	3' GTTCCACTAATATGGCT 20360	G	GC
		AGCTG AT AGTGGAAC		
		TCGGT TA TCACCTTG		
		A A_		
GAM1980	BANP	5' CCCTGGCATCACCCAGCTG 66801	___	_ T
		TAGCTGG ATGC AG GG		
		GTCGACC TACG TC CC		
		CAC G _		
GAM1980	BIRC8	5' TCCACCGCGTGGTTTCCAGCTG 54040	_____	A
		TAGCTGGA TGC GTGGA		
		GTCGACCT GCG CACCT		
		TTGGT C		
GAM1980	CDH24	3' TCCACTGGCCTCCAGCTG 96606	T	_
		TAGCTGGA GC AGTGGA		
		GTCGACCT CG TCACCT		
		C G		
GAM1980	DNAJA2	3' GTTCTCAGCAATCCAGCTG 60489	_	AGT
		TAGCTGGAT GC GGAAC		
		GTCGACCTA CG TCTTG		
		A AC_		
GAM1980	FLJ10520	3' TTCCAGTTATCCAGTTA 36714		CAG
		TAGCTGGATG TGGAA		
		ATTGACCTAT ACCTT		
		TG_		
GAM1980	FLJ10847	3' TTCTCTGCACATCCAGCTG 37304	___	T
		TAGCTGGA TGCAG GGA		
		GTCGACCT ACGTC CTT		
		AC T		
GAM1980	HSPC228	3' GTTCCACATTTGCATCTA 33650	___	
		TGGATGCA GTGGAAC		
		ATCTACGT CACCTTG		
		TTA		
GAM1980	KIAA0864	3' GTTCCACTGATGCAGCT 63942	G	G
		AGCTG AT CAGTGGAAC		

	TCGAC TA GTCACCTTG	
	G _	
GAM1980 KIAA1522 3'	GTTCCACTGGGGGCAGCTA 65609	GATG
	TAGCTG CAGTGGAAC	
	ATCGAC GTCACCTTG	
	GGGG	
GAM1980 MGC11034 3'	GTTCCCTTGTCTAGCTA 49575	T T
	TAGCTGGA GCAG GGAAC	
	ATCGATCT TGTT CCTTG	
	_ C	
GAM1980 NKD1 3'	TCCACTAATATTTAGCTA 53590	C_
	TAGCTGGATG AGTGGA	
	ATCGATTTAT TCACCT	
	AA	
GAM1980 SEPT3 3'	GTTCCCAGTGTCCAGTTA 39405	AGT
	TAGCTGGATGC GGAAC	
	ATTGACCTGTG CCTTG	
	AC_	
GAM1980 LOC143465 5'	TTCCAGTGGAATCCAGTTA 83880	G_ G
	TAGCTGGAT CA TGGAA	
	ATTGACCTA GT ACCTT	
	AG G	
GAM1980 LOC147077 5'	GTTCCACTCATCCAAGT 78853	C C
	TAG TGGATG AGTGGAAC	
	GTC ACCTAC TCACCTTG	
	A _	
GAM1980 LOC151473 3'	TTCAGTGCTATCCAGTTA 81051	_ G
	TAGCTGGAT GCA TGGAA	
	ATTGACCTA CGT ACTT	
	T G	
GAM1980 LOC154992 5'	TCCCTGTAATTCAGCTA 82142	_ T
	TAGCTGGA TGCAG GGA	
	ATCGACCT ATGTC CCT	
	TA _	
GAM1980 LOC157273 5'	TCCAGGGCAGCATCCAGCTG 87726	A _
	TAGCTGGATGC GT GGA	
	GTCGACCTACG CG CCT	
	A GGA	
GAM1980 LOC157556 5'	GTTCCACTCCTCCAGCT 87784	TGC
	AGCTGGA AGTGGAAC	

TCGACCT TCACCTTG
CC_
GAM1980 LOC161403 5' GTTCCAAGTGGCATCATCTA 83147 CTG _
TAG GATGC AGTGGAA
||| ||||| |||||
ATC CTACG TCACCTTG
TA_ G
GAM1980 LOC219972 3' TTCCAATTTTCCAGCTG 93282 TGC
TAGCTGGA AGTGGAA
||||||| |||||
GTCGACCT TCACCTT
TTT
GAM1980 LOC254975 5' GTTCCAGGCGTCCAGTTA 98755 AG
TAGCTGGATGC TGGAAC
||||||| |||||
ATTGACCTGCG ACCTTG
G_
GAM1981 ATF7 3' TCCCAGCCCCGAGCCTCATA 23404 _ TAGA CC
TATGAGGC CC GCT GGGA
||||||| || ||| |||||
ATACTCCG GG CGA CCCT
A CCC_ _
GAM1981 CREBBP 5' CCCGCCGGTCCCGGGCCCCA 16495 A TA G C_
TG GGCC GA CT CGGG
|| ||||| || ||| |||||
AC CCGGG CT GG GCCC
C CC _ CC
GAM1981 EGLN2 5' TTGGGGCTCCAGAACCTC 54926 CC A
GAGG CT GAGCTCCGG
|||| || |||||
CTCC GA CTCGGGGTT
AA C
GAM1981 GNA11 5' CCCAGTGAAGTCTGGGCCTCA 10810 T C C_
TGAGGCC AGAG TC GGG
||||||| ||||| || |||
ACTCCGGG TCTC AG CCC
_ _ TGA
GAM1981 LATS2 3' GTCCCGGAGCCGGTGCCCTCA 28135 _ TAGA
TGAGG C CC GCTCCGGGAC
||||| || |||||
ACTCC G GG CGAGGCCCTG
C T C_
GAM1981 NLGN3 3' GTCTCTCTGGCTCTAGGACC 39121 C CC_
GG CCTAGAGCT GGGAC
|| ||||| |||||
CC GGATCTCGG CTCTG
A TCT
GAM1981 NOTCH1 5' GTCCCGGAGCCCCAAGTGCTT 92138 C AGA_
AGGC CT GCTCCGGGAC
|||| || |||||

TTCG GA CGAGGCCCTG
 T ACCC
 GAM1981 PCDH1 3' CCCATTCCAGGGCCTCA 51575 A CTCC
 TGAGGCCCT GAG GGG
 ||||| ||| |||
 ACTCCGGGA CTT CCC
 C A__
 GAM1981 PML 3' TCCCAGAGGGGCCTCAT 53805 TAGAG C
 ATGAGGCC CTC GGGA
 ||||| ||| |||
 TACTCCGGG GAG CCCT
 ____ A
 GAM1981 RBBP9 3' TCCGGAGTCTAGAGCCCCA 70699 A C G
 TG GGC CTAGA CTCCGGG
 || ||| |||| |||||
 AC CCG GATCT GAGGCCT
 C A _
 GAM1981 UBQLN1 5' CCGAGCTCCGGGGCCCCA 26473 A TA C
 TG GGCC GAGCTC GG
 || |||| ||||| ||
 AC CCGGG CTCGAG CC
 C GC _
 GAM1981 ARTN 5' CCCGGGCCTGGAGCCCCA 15612 A C A T
 TG GGC CTAG GC CCGGG
 || ||| |||| || |||||
 AC CCG GGTC CG GGCCC
 C A _ _
 GAM1981 CNTNAP1 3' CCCAAAGGAGAAGCCTCATG 14641 CCTAGAG ____
 TATGAGGC CTCC GGG
 ||||| ||| |||
 GTACTCCG GAGG CCC
 AA ____ AAA
 GAM1981 FLJ10898 5' CCCCAAGCCAGGCACAGCCTCA 60130 ____ AGA CC
 TA TATGAGGC CCT GCT GGG
 ||||| ||| ||| |||
 ATACTCCG GGA CGA CCC
 ACAC C__ AC
 GAM1981 KIAA1977 5' CGAAGGCTCAGGGCCTCA 74765 A C_
 TGAGGCCCT GAGCT CG
 ||||| |||| ||
 ACTCCGGGA CTCGG GC
 _ AA
 GAM1981 P24B 3' TCCTGCTCTAGGGCCCCTCA 24774 ____ TCC
 TGA GGCCCTAGAGC GGGA
 || ||||| ||||| |||
 ACT CCGGGATCTCG TCCT
 CC ____
 GAM1981 LOC146669 3' GTCTTTCTCCAGGGGCCTCA 78664 A_ CTCC
 TGAGGCCCT GAG GGGAC
 ||||| ||| |||||

ACTCCGGGG CTC TTCTG
 AC T____
 GAM1981 LOC170127 5' CCCGGAGCCCCAGGGGCCCA 83456 A AGA_
 TG GGCCCT GCTCCGGG
 || ||||| |||||
 AC CCGGGG CGAGGCCC
 _ ACCC
 GAM1981 LOC256812 5' CCCGGAGCCCCCTGGGCCCCA 99406 A TAGA_
 TG GGCCC GCTCCGGG
 || ||||| |||||
 AC CCGGG CGAGGCCC
 C TCCCC
 GAM1981 LOC90408 5' CCCCTCTCCGAGGCCTCATA 63342 CTA CTCC
 TATGAGGCC GAG GGG
 ||||| ||| |||
 ATACTCCGG CTC CCC
 AGC TC____
 GAM1982 ARHGEF12 3' CCAAATGGTTACATTGTGCTGC 31646 TCGC ____
 TA TAGCAGCACA TGACT TGG
 ||||| |||| |||
 ATCGTCGTGT ATTGG ACC
 TAC_ TAA
 GAM1982 GPRK6 3' AGCCTTCAGCACTGTGCTGC 10864 TC CTT
 GCAGCACA GCTGA GGCT
 ||||| |||| |||
 CGTCGTGT CGACT CCGA
 CA T____
 GAM1982 HTR4 3' GCAACAGTATGCTGCTA 7884 CATC AC G
 TAGCAGCA GCTG TTG C
 ||||| |||| ||| |
 ATCGTCGT TGAC AAC G
 A____ _ A
 GAM1982 NGFR 3' AGCCAAGTCAGCTTTGC 11786 CATC
 GCA GCTGACTTGGCT
 || |||||
 CGT CGACTGAACCGA
 TT____
 GAM1982 ZNFN2A1 5' CCAAATCAACGTTGCTGCTA 61392 CAT C C
 TAGCAGCA CG TGA TTGG
 ||||| || ||| |||
 ATCGTCGT GC ACT AACC
 T_ A A
 GAM1982 FLJ20038 5' CCAAGTCAGAACTGCGATGC 34862 _ CATCG
 GCA GCA CTGACTTGG
 ||| ||| |||||
 CGT CGT GACTGAACC
 AG CAA____
 GAM1982 KIAA0247 3' CCATCAGCCATGTGCTGCTA 29066 C CT
 TAGCAGCACAT GCTGA TGG
 ||||| |||| |||

ATCGTCGTGTA CGACT ACC
 C ____
 GAM1982 KIAA1726 3' CCAGAGTCATATGCTGCTA 67829 CATCGC _
 TAGCAGCA TGACT TGG
 ||||| |||||
 ATCGTCGT ACTGA ACC
 AT____ G
 GAM1982 PRO1598 5' CAGGAGCATGTGCTGC 38128 C GA
 GCAGCACAT GCT CTTG
 ||||| |||||
 CGTCGTGTA CGA GGAC
 - -
 GAM1982 LOC158237 5' CCAAGTCAGAAATGCGATGC 61082 GCA CG
 GCA CAT CTGACTTGG
 ||| ||| |||||
 CGT GTA GACTGAACC
 AGC AA
 GAM1982 LOC58525 3' AGCCAGGCAGGGCGATGTCTGC 79341 C GA_
 GCAG ACATCGCT CTTGGCT
 ||| ||||| |||||
 CGTC TGTAGCGG GGACCGA
 GAC
 -
 GAM1982 LOC92912 3' AGCCAAGTCAACATCAGGCTAC 71405 C ACATCGC
 TG TAG AGC TGACTTGGCT
 ||| ||| |||||
 GTC TCG ACTGAACCGA
 A GACTACA
 GAM1983 HRH1 3' AAATGTGCCCTTTTGGCCGG 7812 A A TCA
 CC GGCCAAAA GGC ACATTT
 || ||||| ||| |||||
 GG CCGGTTTT CCG TGTA
 C ____
 GAM1983 POLD2 5' TTGAACCTCCTTGGCCTGG 21721 AA C
 CCAGGCCAA AGG TCAA
 ||||| ||| |||||
 GGTCCGGTT TCC AGTT
 CC A
 GAM1983 SCN7A 3' AAATGTTGAAAGCCTAAGCC 12947 CAAAA _
 GGC AGGC TCAACATTT
 ||| ||| |||||
 CCG TCCG AGTTGTAAA
 AA__ AA
 GAM1983 SHANK2 3' GTTGAACCTTCTTCTTTGGCCTC 25531 C _ C_
 A C AGGCCAAA AAGG TCAAC
 | ||||| ||| |||||
 A TCCGGTTT TTCT AGTTG
 C C TCA
 GAM1983 SIAT8E 3' TGAGCCTCCTGGCCTGG 60552 AAA
 CCAGGCCA AGGCTCA
 ||||| |||||

			GGTCCGGT TCCGAGT		
			CC_		
GAM1983	SLC7A8	3'	GAGCCCTTCCTGGCCTGG 25304	AA	_
			CCAGGCCA AAGG CTC		
			GGTCCGGT TTCC GAG		
			CC C		
GAM1983	TFAP2C	3'	TGGGAACCCCTCCTGGCCTGG 13687	AAA	_____
			CCAGGCCA AGG CTCA		
			GGTCCGGT TCC GGGT		
			CC_ CCAA		
GAM1983	TRPM2	3'	GAGCCTTGCTGGCCTGG 13864	AA_	
			CCAGGCCA AAGGCTC		
			GGTCCGGT TTCCGAG		
			CCG		
GAM1983	FLJ13189	3'	TTGAACCTTTTTTGCCTGG 46498	C	C
			CCAGGC AAAAAGG TCAA		
			GGTCCG TTTTTC AGTT		
			T A		
GAM1983	FLJ20208	3'	AAATGCAGGCTTTTTAGCC 35240	C	G CAA
			GGC AAAAAG CT CATTT		
			CCG TTTTTC GA GTAAA		
			A G C_		
GAM1983	FLJ22944	3'	AAATGTTGGGATTTGAACCC 47866	CCAA	GG
			GG AAA CTCAACATTT		
			CC TTT GGGTTGTAAA		
			CAAG A_		
GAM1983	HPRP8BP	3'	AAATGTTGGATGTCCAGGCT 60060	AAAAA	_____
			GGCC GGC TCAACATTT		
			TCGG CTG GGTGTAAA		
			AC_ TA		
GAM1983	KIAA0872	3'	AAATGTTAAGCCTTTTGTATT 30731	GCCA	C
	G		CAG AAAAGGCT AACATTT		
			GTT TTTTCCGA TTGTAAA		
			ATTG A		
GAM1983	KIAA1843	3'	AAATGTTGACTGAACCTGACCT 62880	C AAAA_	C
	G		CAGG CA GG TCAACATTT		
			GTCC GT TC AGTTGTAAA		
			A CCAAG _		
GAM1983	KIAA1975	3'	AAATGTTGATTTTCTGACC 74407	C A	C
			GG CA AAAGG TCAACATTT		

			CC GT TTTT AGTTGTAA		
			A C _		
GAM1983	MRIP2	3'	AAATGTTGATTTTCTGACC 56789	C A C	
			GG CA AAAGG TCAACATTT		
			CC GT TTTT AGTTGTAA		
			A C _		
GAM1983	SLC26A10	5'	TTGAACCCCTTTGGCCTG 56851	AA C	
			CAGGCCAAA GG TCAA		
			GTCCGGTTT CC AGTT		
			CC A		
GAM1983	THEG	3'	TGAGCTTTTGGCCTGG 33892	G	
			CCAGGCCAAAAAG CTCA		
			GGTCCGGTTTTTC GAGT		
			_		
GAM1983	LOC118704	3'	AAATGTTGATTTTCTGACC 74359	C A C	
			GG CA AAAGG TCAACATTT		
			CC GT TTTT AGTTGTAA		
			A C _		
GAM1983	LOC118706	3'	AAATGTTGATTTTCTGACC 74361	C A C	
			GG CA AAAGG TCAACATTT		
			CC GT TTTT AGTTGTAA		
			A C _		
GAM1983	LOC123036	3'	AAATGTTTGCAGTTTTGGCT 74645	AG TC	
			GGCCAAA GC AACATTT		
			TCGGTTTT CG TTGTAA		
			GA T_		
GAM1983	LOC123624	3'	AAATGTTGGGCTTCTGTGCCT 76134	_ AAA	
			AGGC CA AGGCTCAACATTT		
			TCCG GT TTCGGGTTGTAA		
			T C_		
GAM1983	LOC128338	3'	AAATATTGAGCCTTTTAATAG 75250	AGGCC C	
	G		CC AAAAAGGCTCAA ATTT		
			GG TTTTCCGAGTT TAAA		
			ATAA_ A		
GAM1983	LOC143158	3'	AAATGTTGATTTTCTGACC 76997	C A C	
			GG CA AAAGG TCAACATTT		
			CC GT TTTT AGTTGTAA		
			A C _		
GAM1983	LOC195979	3'	AAATGTTGATTTTCTGACC 88928	C A C	
			GG CA AAAGG TCAACATTT		

CC GT TTTTT AGTTGTAAA
 A C _
 GAM1983 LOC219672 5' AATGGTGCTTTTTGGCTGG 92963 G G TCAA
 CCAG CCAAAAAG C CATT
 ||| ||||| | |||
 GGTC GGTTTTTC G GTAA
 _ _TG_
 GAM1983 LOC220466 3' AAATGTTGATTTTTCTGACC 74398 C A C
 GG CA AAAGG TCAACATT
 || || |||| |||||
 CC GT TTTTT AGTTGTAAA
 A C _
 GAM1983 LOC254105 3' AGGTGTGGCCCCCTTGGCCTGG 96416 AAA CA
 CCAGGCCAA GGCT ACATT
 ||||| ||| |||||
 GGTCCGGTT CCGG TGTGGA
 CCC _
 GAM1983 LOC255319 3' AAATGTTGATTTTTCTGACC 96152 C A C
 GG CA AAAGG TCAACATT
 || || |||| |||||
 CC GT TTTTT AGTTGTAAA
 A C _
 GAM1983 LOC91300 5' GTTGAGCTTTTCTGGCCCGG 96238 A A
 CC GGCCA AAAGGCTCAAC
 || |||| |||||
 GG CCGGT TTTTCGAGTTG
 C C
 GAM1983 LOC91300 5' GTTGAGCTTTTCTGGCCCGG 96239 A A
 CC GGCCA AAAGGCTCAAC
 || |||| |||||
 GG CCGGT TTTTCGAGTTG
 C C
 GAM1983 LOC91660 5' AAATGTTTATCTTCTTTTTGGC 67399 CTC_
 TT AGGCCAAAAAGG AACATT
 ||||| |||||
 TTCGGTTTTTCT TTGTAAA
 TCTAT
 GAM1984 CSNK1G2 3' TGAGGGGGCCGCGCCTGGCTCA 8991 _ CCAC A
 TGAGC AGGT CGGCCCT CA
 |||| ||| ||||| ||
 ACTCG TCCG GCCGGGGA GT
 G C_ C
 GAM1984 DRIL1 5' AGGGGGCCGCCCCCGCCGCCA 19076 A A CCAC_
 TG GC GGT CGGCCCT
 || ||| |||||
 AC CG CCG GCCGGGGA
 C _ CCCC
 GAM1984 HDAC4 5' TGCAGAAGCCAGCGGACGCCTC 21255 _ ACC CC A
 TGTTCAT TGAGCAG GTCC GGC CT CA
 ||||| ||| ||| |||

ACTTGTC CAGG CCG GA GT
 TCCG CGA AA C
 GAM1984 WNT11 3' AGGAGCGAGGACTCTGCTCA 17323 _ ACCG C
 TGAGCAG GTCC GC CCT
 ||||| ||| ||||
 ACTCGTC CAGG CG GGA
 T AG_ A
 GAM1984 B3GNT7 3' AGAGGCCGGTGGGCTCCCT 71676 CA C
 AG GGTCCACCGGCC CT
 || ||||| ||||| ||
 TC TCGGGTGGCCGG GA
 CC A
 GAM1984 CBX6 3' GGCCGGTGGGCCCCGCCCA 27421 A A
 TG GC GGTCCACCGGCC
 || || ||||| |||||
 AC CG CCGGGTGGCCGG
 C C
 GAM1984 CDW52 3' TGTAGGGGCCAAGCAGTGCCCA 10164 A G_ CCACC
 TG GCA GT GGCCCCTACA
 || ||| || ||||| |||||
 AC CGT CG CCGGGGATGT
 C GA AA_
 GAM1984 FLJ21415 5' GTAGGGGCCATGCCGCCCG 45689 A A CCACC
 TG GC GGT GGCCCCTAC
 || ||| || ||||| |||||
 GC CG CCG CCGGGGATG
 C _ TA_
 GAM1984 HSPC009 3' TGTAGAAATTGAATCCTGCTCA 26699 TCCAC CCC
 TGAGCAGG CGG CTACA
 ||||| ||| |||||
 ACTCGTCC GTT GATGT
 TAA_ AAA
 GAM1984 KIAA0556 3' TAGGGGCCTCTCTCCTCTCA 69652 C TCCACC
 TGAG AGG GGCCCCTA
 ||||| ||| |||||
 ACTC TCC CCGGGGAT
 _ TCTCT_
 GAM1984 PP1628 3' AGCTTCCGATAGGACCTGCCCA 48072 A AC_ CCC
 TG GCAGGTCC CGG CT
 || ||||| ||| ||
 AC CGTCCAGG GCC GA
 C ATA TTC
 GAM1984 LOC221968 3' AGGATGCTAGACCTGCTC 94141 CACC C_
 GAGCAGGTC GGC CCT
 ||||| ||| |||
 CTCGTCCAG TCG GGA
 A_ TA
 GAM1984 LOC256861 3' GCCAAAATGGGGACCTGTCA 98600 G A _____
 TGA CAGGTCC CC GGC
 ||| ||||| || |||

			ACT GTCCAGG GG CCG		
			— — TAAAA		
GAM1985	ATP2B3	3'	CGTGGACGAGAACGAGGA 41972	A C	
			TCTTC TTC CGTCCATG		
			AGGAG AAG GCAGGTGC		
			C A		
GAM1985	KAL1	3'	GCATGGAGAAAAATGAAGA 5836	CCCG	
			TCTTCATT TCCATGC		
			AGAAGTAA AGGTACG		
			AAG_		
GAM1985	WRN	5'	CTCGGCAGCGCGGGAATAAAG 6892	C CCA	
			CTT ATTCCCGT TGCCGAG		
			GAA TAAGGGCG ACGGCTC		
			A CG_		
GAM1985	AD-020	3'	GGGGACGGGGATGAAGA 39715	ATG	
			TCTTCATTCCCGTCC CC		
			AGAAGTAGGGGCAGG GG		
			—		
GAM1985	AD-020	3'	GGGGACGGGGATGAAGA 60093	ATG	
			TCTTCATTCCCGTCC CC		
			AGAAGTAGGGGCAGG GG		
			—		
GAM1985	FLJ10769	3'	CTGGGAAGACGGAAATGAAGA 37144	C CATG G	
			TCTTCATT CCGTC CC AG		
			AGAAGTAA GGCAG GG TC		
			A AA_ G		
GAM1985	FLJ12661	5'	GTAGGAACAGAGAATGAAGA 47856	CCG_ A	
			TCTTCATTC TCC TGC		
			AGAAGTAAG AGG ATG		
			AGACA _		
GAM1985	FLJ13852	3'	GGAGATGGGAATAAAGA 43840	C CATG	
			TCTT ATTCCCGTC CC		
			AGAA TAAGGGTAG GG		
			A A_		
GAM1985	FLJ21615	3'	CTTGGAAGAAAAATGAAGA 50809	CCCG CATG	
			TCTTCATT TC CCGAG		
			AGAAGTAA AG GGTTC		
			AA_ AAA_		
GAM1985	FLJ22501	5'	CGGCATGGAGGATGAGGA 45704	CCG	
			TCTTCATTC TCCATGCCG		

AGGAGTAGG AGGTACGGC

GAM1985 FLJ32894 3' CTCAACATGAAGATGATGAGGA 58995 TCC _ CC
TCTTCAT CGTC CATG GAG
||||| ||| ||| |||
AGGAGTA GTAG GTAC CTC

_ AA AA
GAM1985 HTCD37 3' CTCGGCATGGATCTTGAA 68299 TTCCC
TTCA GTCCATGCCGAG
||| |||||
AAGT TAGGTACGGCTC

TC_
GAM1985 ITPK1 3' CTCGGCATGACACCATGGAGA 27230 TCCC C
TCTTCAT GTC ATGCCGAG
||||| ||| |||||
AGAGGTA CAG TACGGCTC
CCA_ _

GAM1985 KIAA0495 5' CGACAATGGGCGGGAAAAAGA 63262 CA GC_
TCTT TTCCCGTCCAT CG
||| ||||| ||
AGAA AAGGGCGGGTA GC
A_ ACA

GAM1985 KIAA0971 3' GCTCAGCATAAAGTCATGAGAA 30672 _ C CC_ C _
GTGAAGA TCTTCATT C CGT ATGC GAG C
||||| | ||| ||| |
AGAAGTGA G GTA TACG CTC G
A A CTGAAA A _

GAM1985 KIAA1210 3' TCGGCTGAGGATGAAGA 98085 C TCCAT
TCTTCATT C G GCCGA
||||| || |||
AGAAGTAGG GT CGGCT
A _

GAM1985 KIAA1671 3' CTCAAGGATATCAGACAGGAAT 66276 C C_ _ _
GAA TTCATTCC GTC ATG CC GAG
||||| ||| ||| |||
AAGTAAGG CAG TAT GG CTC
A AC A AA

GAM1985 MRPS6 3' GCATGGACGAGAAGGAAGA 51644 A C
TCTTC TTC CGTCCATGC
||||| ||| |||||
AGAAG AAG GCAGGTACG
G A

GAM1985 N4BP3 3' CATGGAAAGAATGAAGA 66844 CCG
TCTTCATT C TCCATG
||||| |||||
AGAAGTAAG AGGTAC
AA_

GAM1985 P66 3' CTCAGCAGAGAAGAATGAGGA 40738 CCG CA C
TCTTCATT C TC TGC GAG
||||| || ||| |||

		AGGAGTAAG AG ACG CTC	
		A__ AG A	
GAM1985 SDS3	3'	CTCAGCCTTGAAATGGAGA 69744	CCCG T_ C
		TCTTCATT TCCA GC GAG	
		AGAGGTAA AGGT CG CTC	
		_____ TC A	
GAM1985 WWP1	3'	CTCAAGGCTTACAGAATGAAGA 81259	CC CCAT _
		TCTTCATTG GT GCC GAG	
		AGAAGTAAG CA CGG CTC	
		A_ TT__ AA	
GAM1985 LOC129446	3'	GTTTGAAGTGAATGAAGA 76617	C C T
		TCTTCATTCC GT CA GC	
		AGAAGTAAGG CA GT TG	
		T A T	
GAM1985 LOC145919	3'	GCTCAACATGAAGACAACGAGG 78028	C C _____ CC _
		ATGAAGA TCTTCATTG CGT CATG GAG C	
		AGAAGTAGG GCA GTAC CTC G	
		A ACAGAA AA _	
GAM1985 LOC147072	5'	GCGTGAGGAAAATGAAGA 61048	CCCG _
		TCTTCATT TC CATGC	
		AGAAGTAA GG GTGCG	
		AA__ A	
GAM1985 LOC149935	3'	CTCAGCAATTGGGATGAAGA 60934	T TCCA C
		TCTTCAT CCCG TGC GAG	
		AGAAGTA GGGT ACG CTC	
		_ TA__ A	
GAM1985 LOC152274	5'	CGGCACACAATGAGGA 81340	CCC CCA
		TCTTCATT GT TGCCG	
		AGGAGTAA CA ACGGC	
		_____ C_	
GAM1985 LOC221560	3'	CTCAACATGGACAAGGTGGGGG 95412	CCC CC
		TCTTCATT GTCCATG GAG	
		GGGGGTGG CAGGTAC CTC	
		AA_ AA	
GAM1985 LOC257486	3'	TCGGCTGAGGATGAAGA 69784	C TCCAT
		TCTTCATTG CG GCCGA	
		AGAAGTAGG GT CGGCT	
		A _____	
GAM1985 LOC257535	3'	CTCAACATGGACAAGGTGGGGG 99618	CCC CC
		TCTTCATT GTCCATG GAG	

		GGGGGTGG CAGGTAC CTC		
		AA_ AA		
GAM1985	LOC257595 3'	CTCAACATGGACAAGGTGGGGG 99799	CCC	CC
		TCTTCATT GTCCATG GAG		
		GGGGGTGG CAGGTAC CTC		
		AA_ AA		
GAM1985	LOC57107 3'	TGGCATGCAATGAAGA 40196	CCCGTC	
		TCTTCATT CATGCCG		
		AGAAGTAA GTACGGT		
		C_____		
GAM1986	ADAM17 3'	GTCATTTGAGGATCTCA 41846	CA	_
		TGGGATCCTCA GGTG C		
		ACTCTAGGAGT TTAC G		
		_____ T		
GAM1986	AICDA 3'	GGCACCTGTAATCCCA 40696	CCTC	
		TGGGAT ACAGGTGCC		
		ACCCTA TGTCCACGG		
		A_____		
GAM1986	ATM 3'	GGCACCTGTAATCCCA 57134	CCTC	
		TGGGAT ACAGGTGCC		
		ACCCTA TGTCCACGG		
		A_____		
GAM1986	ATM 3'	GGCACCTGTAGTCCCA 5297	CCTC	
		TGGGAT ACAGGTGCC		
		ACCCTG TGTCCACGG		
		A_____		
GAM1986	ATP2B3 3'	GGCATTTGCAAGGACCCA 41973	A CA	
		TGGG TCCT CAGGTGCC		
		ACCC AGGA GTTTACGG		
		_____ AC		
GAM1986	BRCA1 3'	GGCACCTGTGGTGACCCG 24505	A C	
		TGGG TC TCACAGGTGCC		
		GCCC AG GGTGTCCACGG		
		_____ T		
GAM1986	BRCA1 3'	GGCACCTGTGGTGACCCG 24569	A C	
		TGGG TC TCACAGGTGCC		
		GCCC AG GGTGTCCACGG		
		_____ T		
GAM1986	CARKL 3'	GGCATCCCTGTAGGGATCCCA 26106	TC	_____
		TGGGATCC ACAGG TGCC		

			ACCCTAGG TGTCC ACGG	
			GA CT	
GAM1986	CBFA2T2	3'	GGCACCTGCTGAGCCA 18713	GATC _
			TGG CTCA CAGGTGCC	
			ACC GAGT GTCCACGG	
			_____ C	
GAM1986	CD28	3'	GGCACCTGTAATCCCA 21554	CCTC
			TGGGAT ACAGGTGCC	
			ACCCTA TGTCCACGG	
			A_____	
GAM1986	CDH1	5'	GCACCTGTGAGCTTGCG 16404	G TC
			TG GA CTCACAGGTGC	
			GC TT GAGTGTCCACG	
			G C_	
GAM1986	CYLN2	5'	GCACCTATCGCGGGGATCCC 14091	AC_____
			GGGATCCTC AGGTGC	
			CCCTAGGGG TCCACG	
			CGCTA	
GAM1986	DDOST	3'	GGCACCTGTAGTCCCA 19064	CCTC
			TGGGAT ACAGGTGCC	
			ACCCTG TGTCCACGG	
			A_____	
GAM1986	DGKI	5'	GGCACCTGTTGTCCCA 17528	CCTC
			TGGGAT ACAGGTGCC	
			ACCCTG TGTCCACGG	
			T_____	
GAM1986	F2R	3'	GGCACCTGTAGTCCCA 10571	CCTC
			TGGGAT ACAGGTGCC	
			ACCCTG TGTCCACGG	
			A_____	
GAM1986	FGFR1	3'	GGCACCTGTAGTCCCA 43876	CCTC
			TGGGAT ACAGGTGCC	
			ACCCTG TGTCCACGG	
			A_____	
GAM1986	FGFR1	3'	GGCACCTGTAGTCCCA 43881	CCTC
			TGGGAT ACAGGTGCC	
			ACCCTG TGTCCACGG	
			A_____	
GAM1986	FOXEO	3'	GGCACCTGTGCGACCT 25163	A CT
			GGG TC CACAGGTGCC	

			TCC AG GTGTCCACGG		
			_ C_		
GAM1986	GRLF1	3'	GGCACCTGCTGCGACCCA	79261	A CT _
			TGGG TC CA CAGGTGCC		
			ACCC AG GT GTCCACGG		
			_ C_ C		
GAM1986	H2AFO	3'	GGCACCTGTGAACTCA	96246	ATCC
			TGGG TCACAGGTGCC		
			ACTC AGTGTCCACGG		
			A__		
GAM1986	H2AFO	3'	GGCACCTGTGAACTCA	14512	ATCC
			TGGG TCACAGGTGCC		
			ACTC AGTGTCCACGG		
			A__		
GAM1986	HCS	3'	GGCACCTGTAGTCTCA	38985	CCTC
			TGGGAT ACAGGTGCC		
			ACTCTG TGTCCACGG		
			A__		
GAM1986	IFIT4	3'	GGCACCTGTAGTCCCA	71494	CCTC
			TGGGAT ACAGGTGCC		
			ACCCTG TGTCCACGG		
			A__		
GAM1986	KAI1	3'	GGCACCTGTAGTCCCA	11126	CCTC
			TGGGAT ACAGGTGCC		
			ACCCTG TGTCCACGG		
			A__		
GAM1986	KCNA7	3'	GGCACCTGTAGTCCCA	49902	CCTC
			TGGGAT ACAGGTGCC		
			ACCCTG TGTCCACGG		
			A__		
GAM1986	LDLR	3'	GGCACCTGTAGTCCCA	6739	CCTC
			TGGGAT ACAGGTGCC		
			ACCCTG TGTCCACGG		
			A__		
GAM1986	MAPK12	5'	GGCACCTGGGACATCCC	12937	CC A
			GGGAT TC CAGGTGCC		
			CCCTA GG GTCCACGG		
			CA _		
GAM1986	NGB	5'	CGGCACCCGAGCCCTGAGGGTC	41462	CA_____
	CCA		TGGGATCCTCA	GGTGCC	G

			ACCCTGGGAGT	CCACGG	C
			CCCGAGC	_____	
GAM1986	NLGN3	5'	GGCACCTGTAGGTGTCCC	39120	_ C
			GGGAT CCT ACAGGTGCC		
			CCCTG GGA TGTCCACGG		
			T _		
GAM1986	PAICS	3'	GGCACCTGTAATCCCA	22264	CCTC
			TGGGAT ACAGGTGCC		
			ACCCTA TGTCCACGG		
			A_____		
GAM1986	PKD2	3'	GGTTCTTCACAGGATCCCA	33615	CAC T
			TGGGATCCT AGG GCC		
			ACCCTAGGA TTC TGG		
			CAC T		
GAM1986	RAB7L1	3'	GGCACCTGTAATCCCA	15409	CCTC
			TGGGAT ACAGGTGCC		
			ACCCTA TGTCCACGG		
			A_____		
GAM1986	RFC2	3'	GGCACCTGTAATCCCA	12845	CCTC
			TGGGAT ACAGGTGCC		
			ACCCTA TGTCCACGG		
			A_____		
GAM1986	ZNF24	3'	GGTCACCTGTGAGGTTCCCA	23708	T _
			TGGGA CCTCACAGGTG CC		
			ACCCT GGAGTGTCCAC GG		
			T T		
GAM1986	ZNF36	3'	GGCACCTGTAATCCCA	95583	CCTC
			TGGGAT ACAGGTGCC		
			ACCCTA TGTCCACGG		
			A_____		
GAM1986	ACTR1A	3'	GGCACCTGCTGGTTCCA	63652	T TCA
			TGGGA CC CAGGTGCC		
			ACCTT GG GTCCACGG		
			_ TC_		
GAM1986	AKAP11	3'	GGCACCTGTAATCCCA	58462	CCTC
			TGGGAT ACAGGTGCC		
			ACCCTA TGTCCACGG		
			A_____		
GAM1986	Apg4B	3'	GGCACCTGTGAGAGCCT	26183	ATC
			GGG CTCACAGGTGCC		

			TCC GAGTGTCCACGG		
			GA_		
GAM1986	BIVM	3'	GGCACCTGTAGTCCTA	35159	CCTC
			TGGGAT ACAGGTGCC		
			ATCCTG TGTCCACGG		
			A__		
GAM1986	BTN3A2	3'	GGCACCTGTAGTCCCA	23878	CCTC
			TGGGAT ACAGGTGCC		
			ACCCTG TGTCCACGG		
			A__		
GAM1986	C8orf2	3'	GGCACCTGTAATCCCA	24154	CCTC
			TGGGAT ACAGGTGCC		
			ACCCTA TGTCCACGG		
			A__		
GAM1986	C8orf6	5'	GCGATGGAGGATCCCA	90783	A GG
			TGGGATCCTC CA TGC		
			ACCCTAGGAG GT GCG		
			_ A_		
GAM1986	CDT1	3'	GGCACCTGTCGTCCCA	78163	CCTC
			TGGGAT ACAGGTGCC		
			ACCCTG TGTCCACGG		
			C__		
GAM1986	CLONE24922	3'	GGCACTTGTAATCCCA	32250	CCTC
			TGGGAT ACAGGTGCC		
			ACCCTA TGTTACGG		
			A__		
GAM1986	CPR2	3'	GGCACCTGTAATCCCA	48836	CCTC
			TGGGAT ACAGGTGCC		
			ACCCTA TGTCCACGG		
			A__		
GAM1986	CRA	3'	GGTATCTGGGACCCCA	22937	A TCA
			TGGG TCC CAGGTGCC		
			ACCC AGG GTCTATGG		
			C _		
GAM1986	DEPP	3'	GGCATGGTCAGGGTCCCA	23807	C AG
			TGGGATCCT AC GTGCC		
			ACCCTGGGA TG TACGG		
			C G_		
GAM1986	DKFZP434A043	3'	GGCACCTGCGAGCATCCCA	31821	C A
			TGGGAT CTC CAGGTGCC		

	ACCCTA GAG GTCCACGG		
	C C		
GAM1986 DKFZP547L112 5'	GGCACCGGAGGATCCC	67132	ACA
	GGGATCCTC GGTGCC		
	CCCTAGGAG CCACGG		
	G__		
GAM1986 DKFZP564M182 3'	GGCACCTGTAATCCCA	78637	CCTC
	TGGGAT ACAGGTGCC		
	ACCCTA TGTCCACGG		
	A__		
GAM1986 DKFZP564O043 3'	GGCACCATGGCAGGATTCCA	94092	CA _
	TGGGATCCT CA GGTGCC		
	ACCTTAGGA GT CCACGG		
	CG A		
GAM1986 DKFZp761J1523 3'	GCAGTGACAGGATCCCA	51150	_ AGG
	TGGGATCC TCAC TGC		
	ACCCTAGG AGTG ACG		
	AC ____		
GAM1986 ERAP140 3'	GGCACCTGTAATCCCA	75704	CCTC
	TGGGAT ACAGGTGCC		
	ACCCTA TGTCCACGG		
	A__		
GAM1986 FBXO6 5'	GGCCCGGGGGATCCCA	37995	ACA T
	TGGGATCCTC GG GCC		
	ACCCTAGGGG CC CGG		
	G__ _		
GAM1986 FLJ10613 3'	GGCACCTGTAATCCCA	39339	CCTC
	TGGGAT ACAGGTGCC		
	ACCCTA TGTCCACGG		
	A__		
GAM1986 FLJ11106 3'	GGCACCTGTAGTCCCA	37624	CCTC
	TGGGAT ACAGGTGCC		
	ACCCTG TGTCCACGG		
	A__		
GAM1986 FLJ12687 3'	GGCACCTGTAATCCCA	46752	CCTC
	TGGGAT ACAGGTGCC		
	ACCCTA TGTCCACGG		
	A__		
GAM1986 FLJ13456 3'	GGCACCTGTAATCCCA	66552	CCTC
	TGGGAT ACAGGTGCC		

ACCCTA TGTCCACGG
 A____
 GAM1986 FLJ13769 3' GGCACCTGTGCCTGTAGTCCCA 47258 CCT____
 TGGGAT CACAGGTGCC
 ||||| |||||
 ACCCTG GTGTCCACGG
 ATGTCC
 GAM1986 FLJ14251 3' GGCACCTGCCTGTAATCCC 46485 CCT ____
 GGGAT CA CAGGTGCC
 ||||| || |||||
 CCCTA GT GTCCACGG
 AT_ CC
 GAM1986 FLJ20004 3' GGCACCTGTAATCCCA 97008 CCTC
 TGGGAT ACAGGTGCC
 ||||| |||||
 ACCCTA TGTCCACGG
 A____
 GAM1986 FLJ20069 3' GGCACCTGTAATCCCA 34955 CCTC
 TGGGAT ACAGGTGCC
 ||||| |||||
 ACCCTA TGTCCACGG
 A____
 GAM1986 FLJ20700 3' GGCACCTGTAGTCCCA 36012 CCTC
 TGGGAT ACAGGTGCC
 ||||| |||||
 ACCCTG TGTCCACGG
 A____
 GAM1986 FLJ21596 3' GGCACCTTCAAGGAACCCA 46118 A CAC
 TGGG TCCT AGGTGCC
 ||||| |||||
 ACCC AGGA TCCACGG
 A ACT
 GAM1986 FLJ22419 5' CACCGCGGTGGGATTCCA 45530 T A____
 TGGGATCC CAC GGTG
 ||||| ||| |||
 ACCTTAGG GTG CCAC
 _ GCG
 GAM1986 FLJ22477 3' CACCTGCGTGTGGGGACCCA 45668 A ____
 TGGG TCCTCACA GGTG
 ||| ||||| |||
 ACCC AGGGGTGT CCAC
 C GCGT
 GAM1986 FLJ22814 3' GGCACCTGTAATCCCA 46727 CCTC
 TGGGAT ACAGGTGCC
 ||||| |||||
 ACCCTA TGTCCACGG
 A____
 GAM1986 FLJ23022 3' GGCACCTGTAATCCCA 47498 CCTC
 TGGGAT ACAGGTGCC
 ||||| |||||

			ACCCTA TGTCCACGG		
			A___		
GAM1986	FLJ23120	3'	GGCACCTGTAATCCCA 86328	CCTC	
			TGGGAT ACAGGTGCC		
			ACCCTA TGTCCACGG		
			A___		
GAM1986	FLJ23360	3'	GGCACCTGTAGTCCCA 43834	CCTC	
			TGGGAT ACAGGTGCC		
			ACCCTG TGTCCACGG		
			A___		
GAM1986	FLJ23584	3'	GGCACCTGGGAACCCA 45039	A TCA	
			TGGG TCC CAGGTGCC		
			ACCC AGG GTCCACGG		
			A ___		
GAM1986	FLJ30567	3'	GCATTTGAGGATCTCA 59476	CA	
			TGGGATCCTCA GGTGC		
			ACTCTAGGAGT TTACG		
			—		
GAM1986	HT002	3'	GCACTGTGAGGCCCCA 26791	AT G	
			TGGG CCTCACAG TGC		
			ACCC GGAGTGTC ACG		
			C_ _		
GAM1986	IL23A	3'	GGCACCTGTGAGCCA 33891	GATC	
			TGG CTCACAGGTGCC		
			ACC GAGTGTCCACGG		
			—		
GAM1986	KIAA0057	3'	GGCACCTGTAATCCCA 25419	CCTC	
			TGGGAT ACAGGTGCC		
			ACCCTA TGTCCACGG		
			A___		
GAM1986	KIAA0215	3'	GGCATTTGTGAAGGATTCCA 29085	—	
			TGGGATCCT CACAGGTGCC		
			ACCTTAGGA GTGTTTACGG		
			A		
GAM1986	KIAA0266	3'	GGCACCTGTAATCCCA 41639	CCTC	
			TGGGAT ACAGGTGCC		
			ACCCTA TGTCCACGG		
			A___		
GAM1986	KIAA0316	3'	GCACCTGTGAGTCTCA 70245	TC	
			TGGGA CTCACAGGTGC		

ACTCT GAGTGTCCACG

GAM1986 KIAA0574 3' GGCACCTGCTGTGACACCA 69818 GA CT _
TGG TC CA CAGGTGCC
||| || |||||
ACC AG GT GTCCACGG
AC T_ C

GAM1986 KIAA0628 3' GGCGCCTGTAGAATCCCA 29533 C C
TGGGAT CT ACAGGTGCC
||||| || |||||
ACCCTA GA TGTCCGCGG
A _

GAM1986 KIAA0635 3' GGCACCTGTAATCCCA 28417 CCTC
TGGGAT ACAGGTGCC
||||| |||||
ACCCTA TGTCCACGG
A _

GAM1986 KIAA0930 3' GGCACCTGTAATCCCA 71072 CCTC
TGGGAT ACAGGTGCC
||||| |||||
ACCCTA TGTCCACGG
A _

GAM1986 KIAA1164 3' GGCACCTGTCATCCCA 70048 CCTC
TGGGAT ACAGGTGCC
||||| |||||
ACCCTA TGTCCACGG
C _

GAM1986 KIAA1257 3' GGCACCTGTAGTCCCA 63405 CCTC
TGGGAT ACAGGTGCC
||||| |||||
ACCCTG TGTCCACGG
A _

GAM1986 KIAA1396 3' GGCACCTGGAATGCCA 63673 G CC A
TGG AT TC CAGGTGCC
||| || |||||
ACC TA AG GTCCACGG
G _ _

GAM1986 KIAA1862 3' GGCACCAGACGGGATCCCA 69512 CACA
TGGGATCCT GGTGCC
||||| |||||
ACCCTAGGG CCACGG
CAGA

GAM1986 KIAA1977 3' GGCACCTGGAAAATGCCA 74767 G CC A
TGG AT TC CAGGTGCC
||| || |||||
ACC TA AG GTCCACGG
G AA _

GAM1986 LRG 3' GGCACCTGTAGTCCCA 54824 CCTC
TGGGAT ACAGGTGCC
||||| |||||

		ACCCTG TGTCCACGG	
		A__	
GAM1986	MGC15397	3' GGCACCTGTAATCCCA 55554	CCTC
		TGGGAT ACAGGTGCC	
		ACCCTA TGTCCACGG	
		A__	
GAM1986	MGC2663	3' GGCACCTGTAATCCCA 44335	CCTC
		TGGGAT ACAGGTGCC	
		ACCCTA TGTCCACGG	
		A__	
GAM1986	MGC29891	3' GGCACCTGCCTGTAATCCC 58865	CCT _
		GGGAT CA CAGGTGCC	
		CCCTA GT GTCCACGG	
		AT_ CC	
GAM1986	MGC3040	3' GCACCTGGGGATCCCA 67384	T A
		TGGGATCC C CAGGTGC	
		ACCCTAGG G GTCCACG	
		--	
GAM1986	MGC3222	3' GGCACCTGGGCTTCCTA 44546	TC T A
		TGGGA C C CAGGTGCC	
		ATCCT G G GTCCACGG	
		TC _ _	
GAM1986	MGC4248	3' GGCACCTGTAGTCCCA 51314	CCTC
		TGGGAT ACAGGTGCC	
		ACCCTG TGTCCACGG	
		A__	
GAM1986	MGC4504	3' CACCTGCCAAGGATCCCA 44355	CA_
		TGGGATCCT CAGGTG	
		ACCCTAGGA GTCCAC	
		ACC	
GAM1986	MGC4663	3' GGCACCTGTAGTCCCA 44789	CCTC
		TGGGAT ACAGGTGCC	
		ACCCTG TGTCCACGG	
		A__	
GAM1986	MRPL48	5' GGCACCTGTAATCCCA 32661	CCTC
		TGGGAT ACAGGTGCC	
		ACCCTA TGTCCACGG	
		A__	
GAM1986	PRO2015	3' GGCACCTGTAGTTCCA 38164	CCTC
		TGGGAT ACAGGTGCC	

			ACCTTG TGTCCACGG		
			A__		
GAM1986	PRO2859	3'	GGCACTTGTAGTCCCA 38211	CCTC	
			TGGGAT ACAGGTGCC		
			ACCCTG TGTTCACGG		
			A__		
GAM1986	PRO2964	3'	GGCACCTGTAGTCCCA 38261	CCTC	
			TGGGAT ACAGGTGCC		
			ACCCTG TGTCCACGG		
			A__		
GAM1986	PRTD-NY3	3'	GCACTTCAGGGTCCCA 48883	CAC	
			TGGGATCCT AGGTGC		
			ACCCTGGGA TTCACG		
			C__		
GAM1986	PV1	3'	GGTACCCACAGGATCCCA 49377	CACA	
			TGGGATCCT GGTGCC		
			ACCCTAGGA CCATGG		
			CAC_		
GAM1986	SARM	3'	CACCCAGAGGGTAAGGATTCCA 31278	C A_____	
			TGGGATCCT AC GGTG		
			ACCTTAGGA TG CCAC		
			A GGAGAC		
GAM1986	SYAP1	3'	GGCACCTGTAATCCCA 52473	CCTC	
			TGGGAT ACAGGTGCC		
			ACCCTA TGTCCACGG		
			A__		
GAM1986	TACTILE	3'	GGCACCTGTAGTCCCA 20589	CCTC	
			TGGGAT ACAGGTGCC		
			ACCCTG TGTCCACGG		
			A__		
GAM1986	WBSCR23	3'	CACCTGTGAAGGGTCCCA 47417	_	
			TGGGATCCT CACAGGTG		
			ACCCTGGGA GTGTCCAC		
			A		
GAM1986	ZIM3	3'	GGCACCTGTAATCCCA 54639	CCTC	
			TGGGAT ACAGGTGCC		
			ACCCTA TGTCCACGG		
			A__		
GAM1986	LOC126133	5'	GCCTTGCCAGGATCCCA 74910	CA T	
			TGGGATCCT CAGG GC		

	ACCCTAGGA GTTC CG	
	CC _	
GAM1986 LOC126208 3'	GGCCCTTTAGAGGATCCCA 74930	AC_ T
	TGGGATCCTC AGG GCC	
	ACCCTAGGAG TCC CGG	
	ATT _	
GAM1986 LOC126669 3'	GGCACCTGTAGTTCCA 75940	CCTC
	TGGGAT ACAGGTGCC	
	ACCTTG TGTCCACGG	
	A__	
GAM1986 LOC132241 3'	GGCACCGTGCCTGTCCCA 75563	CCT A
	TGGGAT CAC GGTGCC	
	ACCCTG GTG CCACGG	
	TCC _	
GAM1986 LOC143286 5'	GGCTGTGAGAGGATTCCA 83846	A GGT
	TGGGATCCTC CA GCC	
	ACCTTAGGAG GT CGG	
	A GT_	
GAM1986 LOC143631 3'	GCACCTGTGGTTCCCA 77098	TCC
	TGGGA TCACAGGTGC	
	ACCCT GGTGTCCACG	
	T__	
GAM1986 LOC144563 3'	GGCACCTGTAATCCCA 77400	CCTC
	TGGGAT ACAGGTGCC	
	ACCCTA TGTCCACGG	
	A__	
GAM1986 LOC145216 3'	GGCACCTGTAATCCCA 84226	CCTC
	TGGGAT ACAGGTGCC	
	ACCCTA TGTCCACGG	
	A__	
GAM1986 LOC145761 5'	GGCAGAGGTAAGGATTCCA 84482	C AGG
	TGGGATCCT AC TGCC	
	ACCTTAGGA TG ACGG	
	A GAG	
GAM1986 LOC146515 5'	GGTCTCTGAGGATCCC 78519	C GT
	GGGATCCTCA AG GCC	
	CCCTAGGAGT TC TGG	
	C _	
GAM1986 LOC146714 5'	GGTATCTGAGGGACCCCA 84751	A CA
	TGGG TCCT CAGGTGCC	

	ACCC AGGG GTCTATGG	
	C A_	
GAM1986 LOC146923 3'	GGCACCTGTAGTCCCA 78802	CCTC
	TGGGAT ACAGGTGCC	
	ACCCTG TGTCCACGG	
	A_	
GAM1986 LOC147660 3'	GGCACCTGTAGTCTCA 79029	CCTC
	TGGGAT ACAGGTGCC	
	ACTCTG TGTCCACGG	
	A_	
GAM1986 LOC148809 5'	GGCACCTGTAATCCCA 79756	CCTC
	TGGGAT ACAGGTGCC	
	ACCCTA TGTCCACGG	
	A_	
GAM1986 LOC149194 5'	GGCACCTGTAATCCCA 79986	CCTC
	TGGGAT ACAGGTGCC	
	ACCCTA TGTCCACGG	
	A_	
GAM1986 LOC149460 3'	GGCACCTGTAATCCCA 85611	CCTC
	TGGGAT ACAGGTGCC	
	ACCCTA TGTCCACGG	
	A_	
GAM1986 LOC150299 3'	GGCACCTGTAGTCCCA 86169	CCTC
	TGGGAT ACAGGTGCC	
	ACCCTG TGTCCACGG	
	A_	
GAM1986 LOC150358 3'	GGCACCTGTAGTCCCA 86098	CCTC
	TGGGAT ACAGGTGCC	
	ACCCTG TGTCCACGG	
	A_	
GAM1986 LOC151632 3'	GGCACCTGTAATCCCA 86647	CCTC
	TGGGAT ACAGGTGCC	
	ACCCTA TGTCCACGG	
	A_	
GAM1986 LOC152271 3'	GGCACCTGTAATCCCA 81361	CCTC
	TGGGAT ACAGGTGCC	
	ACCCTA TGTCCACGG	
	A_	
GAM1986 LOC152804 3'	GGCACCTGTAATCCCA 87083	CCTC
	TGGGAT ACAGGTGCC	

	ACCCTA	TGTCCACGG		
	A			
GAM1986	LOC155376	3' GGCACCTGTAATCCCA	82247	CCTC
		TGGGAT ACAGGTGCC		
		ACCCTA TGTCCACGG		
		A		
GAM1986	LOC158088	3' GGCACCTGTAGTCCCA	87974	CCTC
		TGGGAT ACAGGTGCC		
		ACCCTG TGTCCACGG		
		A		
GAM1986	LOC158677	5' GGCACCTGTAATCCCA	88250	CCTC
		TGGGAT ACAGGTGCC		
		ACCCTA TGTCCACGG		
		A		
GAM1986	LOC199953	3' GCACCTGTGGTCTGTCCC	89884	CC_
		GGGAT TCACAGGTGC		
		CCCTG GGTGTCCACG		
		TCT		
GAM1986	LOC200251	5' GGCACCTGTAATCCCA	90064	CCTC
		TGGGAT ACAGGTGCC		
		ACCCTA TGTCCACGG		
		A		
GAM1986	LOC200728	3' GGCACCTGTAGTCCCA	91685	CCTC
		TGGGAT ACAGGTGCC		
		ACCCTG TGTCCACGG		
		A		
GAM1986	LOC200904	3' GGCACCTGTAATCCCA	91782	CCTC
		TGGGAT ACAGGTGCC		
		ACCCTA TGTCCACGG		
		A		
GAM1986	LOC200939	3' GCACTTGTGGTCCCA	91799	CCT
		TGGGAT CACAGGTGC		
		ACCCTG GTGTTACG		
GAM1986	LOC200942	3' GGCTGTTGTGAGGACCCA	90378	A GT
		TGGG TCCTCACAG GCC		
		ACCC AGGAGTGTT CGG		
		GT		
GAM1986	LOC201931	3' GGCACCTGTAGTCCCA	90566	CCTC
		TGGGAT ACAGGTGCC		

	ACCCTG TGTCCACGG	
	A__	
GAM1986 LOC202025 5'	ACACTGTTTCAGGATTCCA 91881	C_ _
	TGGGATCCT ACAG GT	
	ACCTTAGGA TGTC CA	
	CT A	
GAM1986 LOC202915 3'	GGCACCTGTGAGGCTGGCC 92020	AT__
	GG CCTCACAGGTGCC	
	CC GGAGTGTCCACGG	
	GGTC	
GAM1986 LOC203083 3'	GGCACCTGTAATCCCA 92092	CCTC
	TGGGAT ACAGGTGCC	
	ACCCTA TGTCCACGG	
	A__	
GAM1986 LOC203276 3'	GGCACCTGTAATCCCA 92125	CCTC
	TGGGAT ACAGGTGCC	
	ACCCTA TGTCCACGG	
	A__	
GAM1986 LOC203305 3'	GGCACCTGTAATCCCA 92178	CCTC
	TGGGAT ACAGGTGCC	
	ACCCTA TGTCCACGG	
	A__	
GAM1986 LOC219347 3'	GGCACCTGTAGTCTCA 94579	CCTC
	TGGGAT ACAGGTGCC	
	ACTCTG TGTCCACGG	
	A__	
GAM1986 LOC219672 5'	GGCACCTGTAATCCCA 92969	CCTC
	TGGGAT ACAGGTGCC	
	ACCCTA TGTCCACGG	
	A__	
GAM1986 LOC219855 3'	GCATGGAGGGTCCCA 93142	A GG
	TGGGATCCTC CA TGC	
	ACCCTGGGAG GT ACG	
	- -	
GAM1986 LOC219919 3'	GGCACCTGTAATCCCA 94928	CCTC
	TGGGAT ACAGGTGCC	
	ACCCTA TGTCCACGG	
	A__	
GAM1986 LOC221271 3'	GGCACCTGTAGTCCCA 93522	CCTC
	TGGGAT ACAGGTGCC	

	ACCCTG TGTCCACGG	
	A__	
GAM1986 LOC221641 5'	GGCACCTGTAATCTCA 95346	CCTC
	TGGGAT ACAGGTGCC	
	ACTCTA TGTCCACGG	
	A__	
GAM1986 LOC221795 3'	GGCACCTGTAATCCCA 94076	CCTC
	TGGGAT ACAGGTGCC	
	ACCCTA TGTCCACGG	
	A__	
GAM1986 LOC253532 3'	GGCACCTGTAATCCCA 97736	CCTC
	TGGGAT ACAGGTGCC	
	ACCCTA TGTCCACGG	
	A__	
GAM1986 LOC254176 3'	GGCACCTGTAATCCCA 99173	CCTC
	TGGGAT ACAGGTGCC	
	ACCCTA TGTCCACGG	
	A__	
GAM1986 LOC254243 3'	GGCACCTGTAATCCCA 99264	CCTC
	TGGGAT ACAGGTGCC	
	ACCCTA TGTCCACGG	
	A__	
GAM1986 LOC254875 3'	GGCACCTGTAATCCCA 97781	CCTC
	TGGGAT ACAGGTGCC	
	ACCCTA TGTCCACGG	
	A__	
GAM1986 LOC255328 3'	GGCACCTGTAATCCCA 98343	CCTC
	TGGGAT ACAGGTGCC	
	ACCCTA TGTCCACGG	
	A__	
GAM1986 LOC256158 5'	GGCACCTGTGGTCCT 99504	CCT
	GGGAT CACAGGTGCC	
	TCCTG GTGTCCACGG	
	—	
GAM1986 LOC256515 3'	GGCACCTGTAATCCCA 98214	CCTC
	TGGGAT ACAGGTGCC	
	ACCCTA TGTCCACGG	
	A__	
GAM1986 LOC256594 3'	GGCACCTGTAATCCCA 98863	CCTC
	TGGGAT ACAGGTGCC	

		ACCCTA TGTCCACGG		
		A____		
GAM1986	LOC57107	3' GGCACCAGGCAGGATCCTA	40191	CACA
		TGGGATCCT GGTGCC		
		ATCCTAGGA CCACGG		
		CGGA		
GAM1986	LOC90038	3' GGCACCTGTAATCCCA	61808	CCTC
		TGGGAT ACAGGTGCC		
		ACCCTA TGTCCACGG		
		A____		
GAM1986	LOC90393	5' GGCACCTGTAGTCCCA	63308	CCTC
		TGGGAT ACAGGTGCC		
		ACCCTG TGTCCACGG		
		A____		
GAM1986	LOC91380	3' GGCACCTGTAATCCCA	66450	CCTC
		TGGGAT ACAGGTGCC		
		ACCCTA TGTCCACGG		
		A____		
GAM1986	LOC92421	3' GGCACCTGTAATCCCA	69727	CCTC
		TGGGAT ACAGGTGCC		
		ACCCTA TGTCCACGG		
		A____		
GAM1986	LOC96597	5' GGCACCTGTAATCCCA	67463	CCTC
		TGGGAT ACAGGTGCC		
		ACCCTA TGTCCACGG		
		A____		
GAM1986	LOC96597	5' GGTCCTAGAAGGATCCCA	67464	CAC T
		TGGGATCCT AGG GCC		
		ACCCTAGGA TCC TGG		
		AGA _		
GAM1987	ABCA1	3' TGTCTGTGTTTTCTTCTTGTGG	19736	TG TCCT_
	TT	GGC CGGGAG CATAGATG		
		TTG GTTCTT GTGTCTGT		
		GT CTTTT		
GAM1987	ABCC3	3' ATCTCCACTCTTGTGGTCA	39609	TG CCTCAT
		TGGC CGGGAGT AGAT		
		ACTG GTTCTCA TCTA		
		GT CC____		
GAM1987	ACAA1	5' TGTCTGTTAACTCCGCGGTCA	9637	G CCTC
		TGGCTGCGG AGT ATAGATG		

			ACTGGCGCC TCA	TGTCTGT		
			— AT—			
GAM1987	ADAMTS4	3'	TATTTATGTGATCCTTTTGGAG	18774	G	— CT
			TCA	TGGCT CGGGAG TC	CATAGATG	
			ACTGA GTTTTC AG	GTATTTAT		
			G	CT T—		
GAM1987	ADORA2B	3'	TATTTATGATCTATTCAGCT	7281	CG—	GTCC
			GGCTG GGA	TCATAGATG		
			TCGAC TCT	AGTATTTAT		
			TTA	—		
GAM1987	AKAP2	3'	GAGCTGGGGGTTCTTGGGCCA	24227	G	GT TAGATG
			TGGCT CGGGA	CCTCA		
			ACCGG GTTCT	GGGGT		
			— TG	CGAGA		
GAM1987	ALDH1A3	3'	GTCTGTGAAATCGCAGTC	7336	GAGTCC	
			GGCTGCGG	TCATAGAT		
			CTGACGCT	AGTGTCTG		
			AA—			
GAM1987	ALPP	3'	ATCTATGCGCCTGTAGTC	69406	AGTCCT	
			GGCTGCGGG	CATAGAT		
			CTGATGTCC	GTATCTA		
			GC—			
GAM1987	ANK1	3'	TGAATGAGGGCTTTTTGTGGCT	40413	TG	— AGATG
			GGC CGGGA	GTCCTCAT		
			TCG GTTTT	CGGGAGTA		
			GT T	AGT		
GAM1987	ANK1	3'	TGAATGAGGGCTTTTTGTGGCT	40414	TG	— AGATG
			GGC CGGGA	GTCCTCAT		
			TCG GTTTT	CGGGAGTA		
			GT T	AGT		
GAM1987	ANK1	3'	TGAATGAGGGCTTTTTGTGGCT	40415	TG	— AGATG
			GGC CGGGA	GTCCTCAT		
			TCG GTTTT	CGGGAGTA		
			GT T	AGT		
GAM1987	ANK1	3'	TGAATGAGGGCTTTTTGTGGCT	40416	TG	— AGATG
			GGC CGGGA	GTCCTCAT		
			TCG GTTTT	CGGGAGTA		
			GT T	AGT		
GAM1987	ARF3	3'	ATCTGCCCTTCCGTGTT	9768	T	TCCTCA
			GGC GCGGGAG	TAGAT		

			TTG TGCCTTC	GTCTA		
			— CCC—			
GAM1987	ARF5	3'	TATGGAAGGGGCTTCCTGGCCA	9785	C	—
			TGGCTG GGGAGTCCT	CATA		
			ACCGGT CCTTCGGGG	GTAT		
			— AAG			
GAM1987	ARG2	3'	TATTTGGTTTTTGCAGTT	8608	T TC	
			GGCTGCGGGAG CC	ATA		
			TTGACGTTTTT GG	TAT		
			T TT			
GAM1987	ARHGEF6	3'	CATCTGCCCCATTCTGTGGTTA	68753	TG	GTCCTCA
			TGGC CGGGA	TAGATG		
			ATTG GTCTT	GTCTAC		
			GT ACCC—			
GAM1987	ASL	3'	CGTTGCTGGGCTTTCGGGGCT	72395	G GG	TCATA
			GGCT CG AGTCC	GATG		
			TCGG GC TCGGG	TTGC		
			G TT TCG—			
GAM1987	ATF2	3'	CATTTATGCGAAATCTGTGGTT	10298	TG	AG CT
			GGC CGGG TC	CATAGATG		
			TTG GTCT AG	GTATTTAC		
			GT AA C—			
GAM1987	ATP7A	3'	CATTTATCACTCTTCTGTATTC	5317	GC	TCCTC
	A		TG TCGGGGAG	ATAGATG		
			AC ATGTCTTC	TATTTAC		
			TT TCAC—			
GAM1987	ATRN	3'	CATCTGTGTGTCCTGCAGCC	24856		GTCCT
			GGCTGCGGGA	CATAGATG		
			CCGACGTCCT	GTGTCTAC		
			GT—			
GAM1987	BACH2	3'	CATTCCTCAGGTTTCTGTGGT	41779	TG	T CAT—
	T		GGC CGGGAG CCT	AGATG		
			TTG GTCTTT GGA	TTTAC		
			GT — CTCC			
GAM1987	BCL11A	3'	TGTCTGTGTTTTTTTGGCAGTT	43470	G	TCCT
			GGCTGC GGAG	CATAGATG		
			TTGACG TTTT	GTGTCTGT		
			G TTT—			
GAM1987	BCL2	3'	CATTCGGTGACTTCCGCATCA	7233	C	— CAT
			TGG TCGGGGAGTC CT	AGATG		

ACT ACGCCTTCAG GG TTTAC
 _ T C_
 GAM1987 BCL2 3' TATCTAATTATTTTGCAGTT 7241 GTCCTCA
 GGCTGCGGGA TAGATG
 ||||| ||||
 TTGACGTTTT ATCTAT
 ATTA_
 GAM1987 BCL2L2 3' CATTTATGATTTATTTGAAGCC 15755 G AGTCC
 A TGGCT CGGG TCATAGATG
 |||| ||| |||||
 ACCGA GTTT AGTATTTAC
 A ATTT_
 GAM1987 BHLHB3 3' GTCTGTGAGAAACCAGCT 48489 GC GAG C
 GGCT GG TC TCATAGAT
 ||| || || |||||
 TCGA CC AG AGTGTCTG
 _ AA _
 GAM1987 C18orf1 3' CATCTGTGACCGTCTGTGTCCA 60862 C AGTCC
 TGG TCGGG TCATAGATG
 || ||||| |||||
 ACC GTGTCT AGTGTCTAC
 T GCC_
 GAM1987 C1QBP 5' CATCTGCACGTGTTGCGAGTC 60856 AGTCCTCA
 GGCTGCGGG TAGATG
 ||||| ||||
 CTGACGCTT GTCTAC
 GTGCAC_
 GAM1987 C20orf1 3' TGTCTCGATTAGACTCCATGTA 25055 _ CTCAT_
 GTTA TGGCTGCG GGAGTC AGATG
 ||||| ||||| ||||
 ATTGATGT CCTCAG TCTGT
 A ATTAGC
 GAM1987 C4orf1 3' TGTCTGTGAGTTTCTTCAGTTA 60227 C TC
 TGGCTG GGGAG CTCATAGATG
 |||| |||| |||||
 ATTGAC TCTTT GAGTGTCTGT
 T _
 GAM1987 CANX 3' ATCTGTTGTTCTGTGGTCA 88865 TG GTCCTC
 TGGC CGGGA ATAGAT
 ||| |||| ||||
 ACTG GTCTT TGTCTA
 GT GT_
 GAM1987 CANX 3' TATCTGATTTTTTTTGTAGCT 88868 TCCTCA
 GGCTGCGGGAG TAGATG
 ||||| ||||
 TCGATGTTTTT GTCTAT
 TTTA_
 GAM1987 CARKL 3' CATCTGTGGTTCCACCTGTAGAC 26101 G AGTCC
 A TG CTGCGGG TCATAGATG
 || ||||| |||||

AC GATGTCC GGTGTCTAC
 A ACTT_
 GAM1987 CCNT2 3' TATTTATGATTTGAATACTGTA 55248 GAG C__
 GCTA TGGCTGCGG TC TCATAGATG
 ||||| || |||||
 ATCGATGTC AG AGTATTTAT
 ATA TTT
 GAM1987 CD164 3' CATCTGATTTGTTCTTGCAG 21195 TCCTCA
 CTGCGGGAG TAGATG
 ||||| |||||
 GACGTTCTT GTCTAC
 GTTTA_
 GAM1987 CD79A 3' TGGGGGCTTCCTTAGTCA 10122 C
 TGGCTG GGGAGTCCTCA
 ||||| |||||
 ACTGAT CCTTCGGGGGT
 T
 GAM1987 CDC25A 5' TGTTTGTGTTTGACCCGCGGGC 10132 G AGTCCT
 G TG CTGCGGG CATAGATG
 || ||||| |||||
 GC GCGCCC GTGTTTGT
 G AGTTT_
 GAM1987 CDC5L 3' ATCTGTGGTTTTTCAGTT 8811 CG GTCC
 GGCTG GGA TCATAGAT
 |||| || |||||
 TTGAC TTT GGTGTCTA
 TT ____
 GAM1987 CGTHBA 3' CATTGTGAAGTGCCCTGTGGC 24888 TG A TC _
 C GGC CGGG G CT CATAGATG
 || |||| | || |||||
 CCG GTCC C GA GTGTTTAC
 GT _GT A
 GAM1987 CHST1 3' TGTCTGTCTGAGTCTCGTGGCC 14704 TG G CTC
 GGC CGGGA TC ATAGATG
 || |||| || |||||
 CCG GCTCT AG TGTCTGT
 GT G TC_
 GAM1987 CLASP1 5' TTA CTGGGGTTCCACAGTCA 65898 C T TAGATG
 TGGCTG GGGAG CCTCA
 ||||| ||||| |||||
 ACTGAC CCTTT GGGGT
 A _ CATTG
 GAM1987 CPSF4 3' CCTGTGGGTCCCTGCAGTC 22927 AGT T ATG
 GGCTGCGGG CC CATAG
 ||||| || |||||
 CTGACGTCC GG GTGTC
 CT_ _ CT
 GAM1987 D12S2489E 5' TATGTGTGGGGACTTCCCAGTT 24763 C G
 GGCTG GGGAGTCCTCATA ATG
 ||||| ||||| ||||| |||||

			TTGAC CCTTCAGGGGTGT TAT		
			— G		
GAM1987 DBY	3'	TATTTATAGTCTCTTGCTA 17407	T TC C		
		TGGC GCGGGAG CT ATAGATG			
		ATCG TGTTCTC GA TATTTAT			
		— T_—			
GAM1987 DCN	5'	TCAGCTTTGAGGGCTCCTGTGG 56870	TG T ATG		
C		GC CGGGAGTCCTCA AG			
		CG GTCCTCGGGAGT TC			
		GT T GACTC			
GAM1987 DFFB	3'	GTCTGTGAGTACCTGGTCA 88781	TG AGTC		
		TGGC CGGG CTCATAGAT			
		ACTG GTCC GAGTGTCTG			
		— AT—			
GAM1987 DGKG	3'	CATTCTTGGGTTTCTGCGCC 9041	T T T TA		
		GGC GCGGGAG CC CA GATG			
		CCG CGTCTTT GG GT TTAC			
		— — — TC			
GAM1987 DHFR	3'	CATTGTAAGACTTTTGGAGCCA 7645	G CTCATA		
		TGGCT CGGGAGTC GATG			
		ACCGA GTTTTCAG TTAC			
		G AATG—			
GAM1987 DIAPH2	3'	TGTCTTCCAGTTTCTTGTGGCT 24598	TG TC CAT		
		GGC CGGGAG CT AGATG			
		TCG GTTCTT GA TCTGT			
		GT T_ CCT			
GAM1987 DRPLA	3'	TGCAGGGCCTCCGCAGCT 10427	GA —		
		GGCTGCGG GTCCT CA			
		TCGACGCC CGGGA GT			
		TC C			
GAM1987 DSCR4	3'	CATCTGTCTGATTCTTGTGTC 20790	T CTC		
		GGC GCGGGAGTC ATAGATG			
		CTG TGTTCTTAG TGTCTAC			
		— TC—			
GAM1987 DTR	3'	CATTCTGCAGATCTTCCGTGG 10455	TG TC _ T		
TCA		TGGC CGGGAG CT CA AGATG			
		ACTG GCCTTC GA GT TTTAC			
		GT TA C C			
GAM1987 E2F3	3'	CATTTAAGCATTCTGTGGC 10465	TG C CA		
		GC CGGGAGT CT TAGATG			

		CG GTCCTTA GA ATTTAC	
		GT C _	
GAM1987 E2F3	3'	GTTTGTGAGTTTCCAGTT 10471	C GG GTC
		GGCTG G A CTCATAGAT	
		TTGAC C T GAGTGTTTG	
		_ TT _	
GAM1987 EIF1A	3'	ATCTGTGGAATCATGGCTA 90004	GCGG G TC
		TGGCT GA TCC ATAGAT	
		ATCGG CT AGG TGTCTA	
		TA_ A _	
GAM1987 EPB42	5'	TGAGAGAGGCGCTTCTGCGGCC 5504	_ ATAGATG
A		TGGCTGCGGGAGT CCTC	
		ACCGGCGTCTTCG GGAG	
		C AGAGT	
GAM1987 ESR1	3'	AGCGTGAGGATTCCCGTAGCT 5509	AGATG
		GGCTGCGGGAGTCCTCAT	
		TCGATGCCCTTAGGAGTG	
		CGAA	
GAM1987 ESR1	3'	TGTGCAGGATTGTTGTGGCTA 5520	TG G _
		TGGC CGG AGTCCT CATA	
		ATCG GTT TTAGGA GTGT	
		GT G C	
GAM1987 ETF1	3'	TATGATGGGGCTTCTGTGCTA 17592	T _
		TGGC GCGGGAGTCC TCATA	
		ATCG TGTCTTCGGG AGTAT	
		_ GT	
GAM1987 EXTL3	3'	TGTCTGTGGGCCGCCCCTGGCC 9340	C AGTC
A		TGGCTG GGG CTCATAGATG	
		ACCGGT CCC GGGTGTCTGT	
		C GCC_	
GAM1987 EYA2	3'	TGTGGCTGGGTTTCTTAGTC 19128	C GT _
		GGCTG GGGA CC TCATA	
		CTGAT TCTT GG GGTGT	
		_ TG TC	
GAM1987 FGF7	3'	CATTTAATTTTCTGTGGTT 10629	TG TCCTCA
		GGC CGGGAG TAGATG	
		TTG GTCCTT ATTTAC	
		GT TTA_	
GAM1987 FLT1	3'	TGTCTGCACCTTCTGCAGCCA 10667	TCCTCA
		TGGCTGCGGGAG TAGATG	

		ACCGACGTCTTC	GTCTGT		
		CAC__			
GAM1987	FSTL1	3' TGTCTTTTCGACTTCTGTGATTA	24007	CT	CTCAT
		TGG GCGGGAGTC	AGATG		
		ATT TGTCTTCAG	TCTGT		
		AG	CTT__		
GAM1987	FZD3	3' TGAAAATTGTTGTAGCTA	34259	G	CC
		TGGCTGCGG	AGT TCA		
		ATCGATGTT	TTA AGT		
		G	AA		
GAM1987	G22P1	5' CATTTGTGTTGTTTCGCCAGCTA	9406	_	AGTCCT
		TGGCTG CGGG	CATAGATG		
		ATCGAC	GCTT GTGTTTAC		
		C	GTT__		
GAM1987	GAN	3' TGTCTGCACATTTTCGTAGT	42124	GG	CCTCA
		GCTGCG	AGT TAGATG		
		TGATGC	TTA GTCTGT		
		TT	CAC__		
GAM1987	GCLC	3' TATCTATGATGTTTCTTTTGCA	9474	TCC__	
		TGCGGGAG	TCATAGATG		
		ACGTTTTC	AGTATCTAT		
		TTTGT			
GAM1987	GEMIN5	3' CATCTTTCACCTCTGCAGTTA	90641	GA	CCTCAT
		TGGCTGCGG	GT AGATG		
		ATTGACGTC	CA TCTAC		
		TC	CTT__		
GAM1987	GFAP	3' CATCCCTGATTCTGTGTTGTTA	10776	T	CTCATA
		TGGC GCGGGAGTC	GATG		
		ATTG	TGTCCTTAG CTAC		
		T	TCC__		
GAM1987	GFAP	3' CATCTGTGGGCACGCTGTGGGC	10777	G TG	GA C
	A	TG C CGG	GT CTCATAGATG		
		AC G GTC	CA GGGTGTCTAC		
		G GT	G_ C		
GAM1987	GFI1	3' TATTTTAAAGATTTCTGAGCTA	19154	G	CTCAT
		TGGCT CGGGAGTC	AGATG		
		ATCGA	GTCTTTAG TTTAT		
		_	AAAT_		
GAM1987	GHRHR	3' TGTCTACCTCTGACTTCTGTGG	7706	TG	CTCA_
	TC	GGC CGGGAGTC	TAGATG		

			CTG GTCTTCAG ATCTGT		
			GT TCTCC		
GAM1987	GLO1	5'	CGTCTGTGATACTGCAGTT 22961	GAGTCC	
			GGCTGCGG TCATAGATG		
			TTGACGTC AGTGTCTGC		
			AT____		
GAM1987	GPC6	3'	TATCTGTGGGGACCTTGT 20333	A	
			GCGGG GTCCTCATAGATG		
			TGTTC CAGGGGTGTCTAT		
			—		
GAM1987	GPR86	3'	TATTGATGAGACTTCCGTAG 43904	C A	
			CTGCGGGAGTC TCAT GATG		
			GATGCCTTCAG AGTA TTAT		
			— G T		
GAM1987	GPX3	3'	CATCTGTGTGCCTGCAGCT 10867	AGTCCT	
			GGCTGCGGG CATAGATG		
			TCGACGTCC GTGTCTAC		
			GT____		
GAM1987	GRIA3	5'	TATTTTGACGACTCCTGAGTT 7716	G C T	
			GGCT CGGGAGTC TCA AGATG		
			TTGA GTCCTCAG AGT TTTAT		
			— C —		
GAM1987	GRN	3'	CGTTTCAGTGGACCCTGTGGCC 10874	TG A TCAT	
	A		TGGC CGGG GTCC AGATG		
			ACCG GTCC CAGG TTTGC		
			GT — TGAC		
GAM1987	HDAC4	3'	GCTCTGGTGGATTTTTGTGGCT 21246	TG TCA TG	
			GGC CGGGAGTCC TAGA		
			TCG GTTTT TAGG GTCT		
			GT TG_ CGT		
GAM1987	HKE4	3'	GTCTGTGTTGCCCGAGCT 23712	G AGTCCT	
			GGCT CGGG CATAGAT		
			TCGA GCCC GTGTCTG		
			— GTT____		
GAM1987	HLA-DRA	3'	TGTCTATTGCCTTTTCCTGTAT 39413	C TCCTC_	
	CTA		TGG TGCGGGAG ATAGATG		
			ATC ATGTCCTT TATCTGT		
			T TTCCGT		
GAM1987	HLA-DRA	3'	TGTCTATTGCCTTTTCCTGTAT 39414	C TCCTC_	
	CTA		TGG TGCGGGAG ATAGATG		

		ATC ATGTCCTT TATCTGT		
		T TTCCGT		
GAM1987 HRH1	3'	TATCTGTGAGTTCTGTTGTGTT 7827	T G TC	
		GGC GCGG AG CTCATAGATG		
		TTG TGTT TC GAGTGTCTAT		
		_ G TT		
GAM1987 HTR2C	3'	CATTTGTTAATGATTCTTGTGT 7868	T CTC_	
CA		TGGC GCGGGAGTC ATAGATG		
		ACTG TGTTCTTAG TGTTTAC		
		_ TAAT		
GAM1987 IGF1	3'	ATCTGTGGCATTGTACCA 7060	C A CCT	
		TGG TGCGGG GT CATAGAT		
		ACC ATGTTT CG GTGTCTA		
		_ A _		
GAM1987 IL1R1	3'	TGTTTATATAATTTTGCAGC 7929	GTCCTC	
		GCTGCGGGA ATAGATG		
		CGACGTTTT TATTTGT		
		AATA_		
GAM1987 IL24	3'	TATTTGTGAGACTGTAAGTTA 23394	GCGGG C	
		TGGCT AGTC TCATAGATG		
		ATTGA TCAG AGTGTTTAT		
		ATG_ _		
GAM1987 ILF1	3'	CATCTGCACATTTCCGTGTTA 16918	T CCTCA	
		TGGC GCGGGAGT TAGATG		
		ATTG TGCCTTTA GTCTAC		
		_ CAC_		
GAM1987 ITGB3BP	3'	TGTCTAGATAAAATTTCTTGCA 27386	TCCTCA_	
GCTA		TGGCTGCGGGAG TAGATG		
		ATCGACGTTCTT ATCTGT		
		TAAAATAG		
GAM1987 IVD	3'	ATCATGGGCCTCGCAGCC 11090	A TCATA	
		GGCTGCGGG GTCC GAT		
		CCGACGCTC CGGG CTA		
		_ TA_		
GAM1987 JAG1	3'	TATTTATTGACTCTTGAGTT 5815	G CTC	
		GGCT CGGGAGTC ATAGATG		
		TTGA GTTCTCAG TATTTAT		
		_ T_		
GAM1987 JAK3	3'	CATTTGGGGGGGCTCCCGTGGC 5828	TG A	
C		GGC CGGGAGTCCTC TAGATG		

		CCG GCCCTCGGGG GTTTAC		
		GT G		
GAM1987	KCNK4	5' TGTCTGTGGACAGTGCAGCT 33991	GGA TC	
		GGCTGCG GTCC ATAGATG		
		TCGACGT CAGG TGTCTGT		
		GA_ _		
GAM1987	KIAA0857	3' GTTTGTGGGGCGAGTGCCA 67256	T GGA T	
		TGGC GC GTCC CATAGAT		
		ACCG TG CGGG GTGTTTG		
		_ AG_ _		
GAM1987	KLK5	5' TGTCTGTGCGTCCTGCACCCA 25787	C GTCCT	
		TGG TGCGGGA CATAGATG		
		ACC ACGTCCT GTGTCTGT		
		C GC_		
GAM1987	KRT16	5' ATGAAGGGCTCCTGCAGT 96887	_	
		GCTGCGGGAGTCCT CAT		
		TGACGTCCTCGGGA GTA		
		A		
GAM1987	LDLR	3' CATTTGTGTTATTATTTTGCAC 6730	C GTCCT_	
	T	GG TGCGGGA CATAGATG		
		TC ACGTTT GTGTTTAC		
		_ ATTATT		
GAM1987	LGMN	3' ATGGGGGCTTCTGTAGCC 20031		
		GGCTGCGGGAGTCCTCAT		
		CCGATGTCTTCGGGGGTA		
GAM1987	LHX1	5' TATTTATTTCCGTTCCCGCCGC 19918	T TCCTC	
	C	GGC GCGGGAG ATAGATG		
		CCG CGCCCTT TATTTAT		
		C GCCTT		
GAM1987	LIPA	3' TATTTGTCTGCTTTTCTTGACAG 5881	TCCTC_	
	C	GCTGCGGGAG ATAGATG		
		CGACGTTCTT TGTTTAT		
		TTCGTC		
GAM1987	LRP8	3' TATTTGTGGGGGAAATGGC 34458	GCGGGAG	
		GCT TCCTCATAGATG		
		CGG GGGGGTGTTTAT		
		TAAAG_		
GAM1987	MEF2C	3' CATTTGTGGCTTTTGTAGTT 11531	TCC	
		GGCTGCGGGAG TCATAGATG		

TTGATGTTTTT GGTGTTTAC
 C__
 GAM1987 MEN1 3' TATCTGTTTTTACTTTTGTGGT 56359 TG CCTC
 C GGC CGGGAGT ATAGATG
 ||| ||||| |||||
 CTG GTTTTCA TGTCTAT
 GT TTTT
 GAM1987 MME 3' CATTTATCATTCTTGTGCCA 8029 T CCTC
 TGGC GCGGGAGT ATAGATG
 ||| ||||| |||||
 ACCG TGTTCTTA TATTTAC
 T C__
 GAM1987 MMP14 3' ATGGGGCCTTTCACAGTTA 18426 C GG T
 TGGCTG G AGTCC CAT
 ||||| | ||||| |||
 ATTGAC C TCGGG GTA
 A TT _
 GAM1987 MMP20 3' TATTTACAAGCAATGGCTTTTG 17675 TG ____ CA
 TGGCCA TGGC CGGGAGTC CT TAGATG
 ||| ||||| || |||||
 ACCG GTTTTCGG GA ATTTAT
 GT TAAC AC
 GAM1987 MPDZ 3' ATCTAATGTTTTGTAGTCA 15147 GTCCT _
 TGGCTGCGGGA CAT AGAT
 ||||| ||| |||||
 ACTGATGTTTT GTA TCTA
 ____ A
 GAM1987 MYCN 3' GAGGTGGCTTTTGCGGCCA 19385 _
 TGGCTGCGGGAGT CCTC
 ||||| ||||| |||||
 ACCGGCGTTTTTCG GGAG
 GT
 GAM1987 MYD88 3' TGTCAGGATGCCTGTGGTCA 11733 TG A C
 TGGC CGGG GTCCT ATA
 ||| ||| ||||| |||
 ACTG GTCC TAGGA TGT
 GT G C
 GAM1987 MYLK2 3' ATGTAGGGCTTCTGTGGTT 53579 TG _
 GGC CGGGAGTCCT CAT
 ||| ||||| ||||| |||
 TTG GTCTTCGGGA GTA
 GT T
 GAM1987 MYO1C 3' CATCTGCATCTTTTGCAGCC 61858 TCCTCA
 GGCTGCGGGAG TAGATG
 ||||| ||||| |||||
 CCGACGTTTTTC GTCTAC
 TAC__
 GAM1987 NCOA3 3' CATCCCTTGACTTTTGTGGCC 22562 TG CTCATA
 GGC CGGGAGTC GATG
 ||| ||||| ||||| |||

CCG GTTTTCAG CTAC
 GT TTCC__
 GAM1987 NFATC1 3' TGTCTGTGTCAGCTGTCTTTGT 21600 ____ G CCT
 AGTTA TGGCTGC GG AGT CATAGATG
 ||||| || ||| |||||
 ATTGATG CT TCG GTGTCTGT
 TTT G ACT
 GAM1987 NFATC3 3' ATTTGTGGGGAAAGTAGC 17048 GGGAG
 GCTGC TCCTCATAGAT
 |||| | |||||
 CGATG AGGGGTGTTTA
 AA__
 GAM1987 NFKBIL2 5' CATCTATGACCACTGCCAGTC 26446 GC G CC
 GGCT GG AGT TCATAGATG
 ||| || ||| |||||
 CTGA CC TCA AGTATCTAC
 __ G CC
 GAM1987 NOC4 3' TGTCCCTGTGGACTCTCTCAGT 21377 C T TA
 T GGCTG GGGAGTCC CA GATG
 |||| ||||| || |||
 TTGAC CTCTCAGG GT CTGT
 T T CC
 GAM1987 NOC4 3' TGTGGGTGTTTCTGTGGTCA 21378 TG TC
 TGGC CGGGAG CTCATA
 ||| |||| | ||||
 ACTG GTCTTT GGGTGT
 GT GT
 GAM1987 NOS1 5' TATTTATGCCGCGTTTCCAGCC 7099 C GG _ CCT
 GGCTG G A GT CATAGATG
 |||| | || |||||
 CCGAC C T CG GTATTTAT
 TT G CC
 GAM1987 NUP62 3' CGTTTGTGCCTCGTCTCGCTGT 25649 T GTCCT
 TA TGGC GCGGGA CATAGATG
 ||| |||| | |||||
 ATTG CGCTCT GTGTTTGC
 T GCTCC
 GAM1987 OVOL1 5' TGTCTGTTCTCTCCCCAGTCA 17074 C TCCTC
 TGGCTG GGGAG ATAGATG
 |||| |||| | |||||
 ACTGAC CCCTC TGTCTGT
 _ TCT_
 GAM1987 OXCT 3' TATGTGATTTTGTGGTTA 6489 TG CT
 TGGC CGGGAGTC CATA
 ||| ||||| |||
 ATTG GTTTT TAG GTAT
 GT T_
 GAM1987 PCDH11X 3' TGTTTGTGTCTCTCTGCTGTCA 28018 T _ TCCT
 TGGC GCGG GAG CATAGATG
 ||| |||| || | |||||

		ACTG CGTC CTC GTGTTTGT	
		T T T__	
GAM1987	PCDH11Y	3' TGTTTGTGTCTCTCTGCTGTCA 53170	T _ TCCT
		TGGC GCGG GAG CATAGATG	
		ACTG CGTC CTC GTGTTTGT	
		T T T__	
GAM1987	PCDHB7	3' TGTAGATTTTCTGCAGTCA 38944	_ CT
		TGGCTGCGGGAG TC CA	
		ACTGACGTCTTT AG GT	
		T AT	
GAM1987	PDCL	3' TGTCTTCTGGCTTTTCAGCT 19403	C T TCAT
		GGCTG GGGAG CC AGATG	
		TCGAC TTTTC GG TCTGT	
		_ _ TCT_	
GAM1987	PFKFB3	3' GTCTGTGTCCCCTCGGCC 83753	C AGTCCT
		GGCTG GGG CATAGAT	
		CCGGC CCC GTGTCTG	
		T CT__	
GAM1987	PFN2	3' CATTTAGTCTTCCTTTTGTAGC 54883	TCCTCA
		GCTGCGGGAG TAGATG	
		CGATGTTTTC ATTTAC	
		CTTCTG	
GAM1987	PFN2	3' CATTTAGTCTTCCTTTTGTAGC 54884	TCCTCA
		GCTGCGGGAG TAGATG	
		CGATGTTTTC ATTTAC	
		CTTCTG	
GAM1987	PIK3CG	3' TATTTTGTAATTACCTGTAGCT 12124	_ CCT T
	A	TGGCTGCGGG AGT CA AGATG	
		ATCGATGTCC TTA GT TTTAT	
		A AT_ _	
GAM1987	PKD2	3' TGTCTGTGGGACTAACTGTATC 33618	C G_ T
	A	TGG TGCGG AGTCC CATAGATG	
		ACT ATGTC TCAGG GTGTCTGT	
		_ AA _	
GAM1987	PKHD1	3' TGTCTCATACATATTTTGCAGC 57719	GTCCTCAT
	TA	TGGCTGCGGGA AGATG	
		ATCGACGTTTT TCTGT	
		ATACATAC	
GAM1987	PLAU	3' CATTTGTGAGGCCCATGGTT 69541	GC AGT
		GGCT GGG CCTCATAGATG	

TTGG CCC GGAGTGTTTAC
 TA ____
 GAM1987 PLGL 3' GTCTGTGAGGGATTGGTTC 12171 T G AG
 C GC GG TCCTCATAGAT
 |||||
 C TG TT GGGAGTGTCTG
 T G A_
 GAM1987 PPARGC1 3' CATTTTGAAGTTTCTGTAGTT 26076 TCC T
 GGCTGCGGGAG TCA AGATG
 ||||| |||||
 TTGATGTCTTT AGT TTTAC
 GA_ _
 GAM1987 PPP2R5E 5' CGTCGCCCCAGGCTCCCCGCAG 21805 _ T CATA_
 CT GGCTGCGGG AG CCT GATG
 ||||| |||||
 TCGACGCCC TC GGA CTGC
 C _ CCCC
 GAM1987 PPP3CC 3' CATTTGTGAAGTCTTGTGCTA 20027 T GTCC
 TGGC GCGGGA TCATAGATG
 ||||| |||||
 ATCG TGTTCT AGTGTTTAC
 _ GA_
 GAM1987 PRELP 3' ATCTATTCTTCTGCAGCC 12255 TCCTC
 GGCTGCGGGAG ATAGAT
 ||||| |||||
 CCGACGTCTTC TATCTA
 T____
 GAM1987 PRG2 5' TGTCTGTGATACAGTTGTGGC 12263 TG GA CC
 GC CGG GT TCATAGATG
 || |||||
 CG GTT CA AGTGTCTGT
 GT GA T_
 GAM1987 PRKY 3' CATCTGTCTCCTTCTGCACCCA 12367 C TCCTC
 TGG TCGGGGAG ATAGATG
 ||||| |||||
 ACC ACGTCTTC TGTCTAC
 C CTC_
 GAM1987 PTGFRN 3' CATCCCAGGCTTCTGCTGCT 67764 T T CATA
 GGC GCGGGAG CCT GATG
 ||||| |||||
 TCG CGTCTTC GGA CTAC
 T _ CC_
 GAM1987 PTP4A2 3' ATCAGGGGCTCTTGCACTA 14438 C CATA
 TGG TCGGGGAGTCCT GAT
 ||||| |||||
 ATC ACGTTCTCGGGG CTA
 _ A_
 GAM1987 PTPN2 3' TATCTATTTAATCTTTGTAGT 12582 TCCTC
 TA TGGCTGCGGGAG ATAGATG
 ||||| |||||

			ATTGATGTTTTC	TATCTAT		
			TAATT			
GAM1987	RAB11A	3'	TGTTTGGATTCTCAGTTA	17416	C	TC
			TGGCTG GGGAGTCC	ATA		
			ATTGAC TCCTTAGG	TGT		
			—	TT		
GAM1987	RAB1A	5'	TGTCTGTCCTCAGCTCGCGTAG	70782	G	CCTC_
	CC		GGCTGCG GAGT	ATAGATG		
			CCGATGC CTCG	TGTCTGT		
			G	ACTCC		
GAM1987	RAB5A	3'	ATTTATGATGCTTAGCCA	16041	GCGG	CC
			TGGCT	GAGT TCATAGAT		
			ACCGA	TTCG AGTATTTA		
			—	T_		
GAM1987	RAD51C	3'	TATTTATTATTTTCGCTGTC	12751	T GG	CCTC
			GGC GCG AGT	ATAGATG		
			CTG CGC TTA	TATTTAT		
			T	TT T_		
GAM1987	RAP1B	3'	CATTTTCAGGCTTCTGCAGCT	32233	T	CAT
			GGCTGCGGGAG CCT	AGATG		
			TCGACGTCTTC GGA	TTTAC		
			—	CT_		
GAM1987	RBM3	3'	TATTTATAAAGGTTTTTGGAGC	71012	G	T C_
	T		GGCT CGGGAG CCT	ATAGATG		
			TCGA GTTTTT GGA	TATTTAT		
			G	— AA		
GAM1987	REGL	3'	TATTTTTGCTGAGTCCTGCAGC	22503	G	CT T
	CA		TGGCTGCGGGA TC	CA AGATG		
			ACCGACGTCCT AG	GT TTTAT		
			G	TC T		
GAM1987	RGL	3'	TATTTATTGAGTTCCTGTGGT	31430	TG	TC _
			GC CGGGAG CTCA	TAGATG		
			TG GTCCTT GAGT	ATTTAT		
			GT	— T		
GAM1987	RGS16	3'	TGTCTGTCCAGCCTTGCAGTCA	12873	A	CCTC
			TGGCTGCGGG GT	ATAGATG		
			ACTGACGTTT CG	TGTCTGT		
			—	ACC_		
GAM1987	RPGR	3'	ATTTATGTTTTACAGTCA	6166	C GG	TCCT
			TGGCTG G AG	CATAGAT		

			ACTGAC C TT GTATTTA		
			A TT ____		
GAM1987	RPN2	5'	TGTGGCGGGCTCTTGGAGCCA 12909	G	_
			TGGCT CGGGAGTCC TCATA		
			ACCGA GTTCTCGGG GGTGT		
			G C		
GAM1987	RPS6KA2	3'	ATCTCGATTCTCGTACCCA 41220	C	CTCAT
			TGG TGCGGGAGTC AGAT		
			ACC ATGCTCTTAG TCTA		
			C C ____		
GAM1987	RPS6KA2	5'	CGTCCCCCGGCCCTGCGGCT 41221	A	CTCATA
			GGCTGCGGG GTC GATG		
			TCGGCGTCC CGG CTGC		
			_ CCCC_		
GAM1987	RPS6KA2	3'	CGTCTGTCCCCAGCTCCCGTGG 41222	TG	CCTC_
			CCA TGGC CGGGAGT ATAGATG		
			ACCG GCCCTCG TGTCTGC		
			GT ACCCC		
GAM1987	RPS6KA2	5'	GTGCCGGGCTCCCTGGCCA 41226	C	T_
			TGGCTG GGGAGTCC CAT		
			ACCGGT CCCTCGGG GTG		
			_ CC		
GAM1987	RRP22	5'	TGTCTGTCTGCCCTCCCGCCGC 22394	T	TCCTC
			CA TGGC GCGGGAG ATAGATG		
			ACCG CGCCCTC TGTCTGT		
			C CCGTC		
GAM1987	RTDR1	5'	CATTTGAAAGGCCTCTGTAGT 27804	GA T	CA_
			T GGCTGCGG G CCT TAGATG		
			TTGATGTC C GGA GTTTAC		
			TC_ AAG		
GAM1987	SERPINB6	3'	CATTTGTGGGATGCCGCA 17091	GA T	
			TGCGG GTCC CATAGATG		
			ACGCC TAGG GTGTTTAC		
			G_ _		
GAM1987	SFRP1	3'	TATTTGTTTCATTTCTGCAG 13027	CCTC	
			CTGCGGGAGT ATAGATG		
			GACGTCTTTA TGTTTAT		
			CTT_		
GAM1987	SFRS7	3'	TATTTAGCAACACTCCATGTAG 60149	_	CCTCA
			CTA TGGCTGCG GGAGT TAGATG		

		ATCGATGT CCTCA	ATTTAT	
		A	CAACG	
GAM1987	SGCG	5'	TGTCTGTGGTAGAGCTCGGGCC 5875	G AGTCC
	A		TGGCT CGGG TCATAGATG	
			ACCGG GCTC GGTGTCTGT	
			_ GAGAT	
GAM1987	SGT	3'	CGTCTGTGAGGTAGGCGCAGT 13039	GGAGT
			GCTGCG CCTCATAGATG	
			TGACGC GGAGTGTCTGC	
			GGAT_	
GAM1987	SH3BP2	3'	CATCTGTGAGGTGCCGAGCT 13053	G GAGT
			GGCT CGG CCTCATAGATG	
			TCGA GCC GGAGTGTCTAC	
			_ GT_	
GAM1987	SHANK2	3'	ATCCATGGCTCTTTGGCCA 25522	C CCT A
			TGGCTG GGGAGT CAT GAT	
			ACCGGT TTCTCG GTA CTA	
			_ _ C	
GAM1987	SLC25A17	5'	CATCTGTGGGAAAAGTGTGGCT 22059	TG GGAG T
			GGC CG TCC CATAGATG	
			TCG GT AGG GTGTCTAC	
			GT GAAA _	
GAM1987	SLC29A1	3'	GTCTGTGTGTCTGCGTCC 18262	C AGTCCT
			GG TGC GGG CATAGAT	
			CC GCGTCT GTGTCTG	
			T GT_	
GAM1987	SLC4A7	3'	TATTTGTGTTTCATTTCTGTAG 14619	CCT_
			CTGCGGGAGT CATAGATG	
			GATGTCTTTA GTGTTTAT	
			CTTT	
GAM1987	SLC7A4	3'	TGTTTATGATCAGCTCCAGCTA 65821	GCG CC_
			TGGCT GGAGT TCATAGATG	
			ATCGA CCTCG AGTATTTGT	
			_ ACT	
GAM1987	SLC7A6	5'	CATTTATGAGGAGGTGGCT 15639	TG GGGAG
			GGC C TCCTCATAGATG	
			TCG G AGGAGTATTAC	
			GT G_	
GAM1987	SLC9A6	3'	ATTTGTTAGTCTGTAGTTA 22061	AGTC C
			TGGCTGCGGG CT ATAGAT	

			ATTGATGTCT	GA TGTTTA		
			_____ T			
GAM1987	SNAI1	3'	TGTCTGCGTGGGTTTTTGTATC	21127	C	GT TCA
	CA		TGG TGCGGGA CC TAGATG			
			ACC ATGTTTT GG GTCTGT			
			T TG TGC			
GAM1987	SNAP23	3'	CATTTATTCACTTCCGTAGCT	15137		CCTC
			GGCTGCGGGAGT ATAGATG			
			TCGATGCCTTCA TATTTAC			
			CT__			
GAM1987	SNAP23	3'	TGTTTATTTTTGCTTTTGTGGT	15144	TG	CCTC
	T		GGC CGGGAGT ATAGATG			
			TTG GTTTTCG TATTTGT			
			GT TTTT			
GAM1987	SNRP70	5'	GTTGCTGAGGGGCTGCCGCAGC	79254	G _	TAGATG
	C		GGCTGCGG AGTCC TCA			
			CCGACGCC TCGGG AGT			
			G G CGTTGT			
GAM1987	SPAP1	3'	CATCTGGTCTAGGGCTTTTGTG	57834	T	CA__
	TT		GGC GCGGGAGTCCT TAGATG			
			TTG TGTTTTCGGGA GTCTAC			
			_ TCTG			
GAM1987	SRGAP1	5'	CATTACACATATTTTTGCATG	72714	_	CCTCA
	CCA		TGGC TGCGGGAGT TAGATG			
			ACCG ACGTTTTTA ATTTAC			
			T TACAC			
GAM1987	SYN3	3'	GTTAGGGCTCCTGTACCCA	14483	C	C
			TGG TGCGGGAGTCCT AT			
			ACC ATGTCCTCGGGA TG			
			C T			
GAM1987	SYN3	3'	GTTAGGGCTCCTGTACCCA	14484	C	C
			TGG TGCGGGAGTCCT AT			
			ACC ATGTCCTCGGGA TG			
			C T			
GAM1987	SYN3	3'	GTTAGGGCTCCTGTACCCA	14485	C	C
			TGG TGCGGGAGTCCT AT			
			ACC ATGTCCTCGGGA TG			
			C T			
GAM1987	SYT4	3'	GTCTGTTCTTTTGTGCCA	63111	T	TCCTC
			TGGC GCGGGAG ATAGAT			

		ACCG TGTTTTC TGTCTG		
		— T —		
GAM1987	TCEB1L	3' TGTCTTCCAGCCTCCTGCAGTC 13608	TC	CAT
	A	TGGCTGCGGGAG CT AGATG		
		ACTGACGTCCTC GA TCTGT		
		C_ CCT		
GAM1987	TCF2	3' GTGACAGGGCTCCCGAGTCA 6618	G	—
		TGGCT CGGGAGTCC TCAT		
		ACTGA GCCCTCGGG AGTG		
		— AC		
GAM1987	TCF7	3' ATCTATGGCAGTCCAGCCA 13614	C	GA CCT
		TGGCTG GG GT CATAGAT		
		ACCGAC CT CG GTATCTA		
		— GA —		
GAM1987	TCP11	3' ATCCCAGGCCCTGCAGCCA 38561	A	T CATA
		TGGCTGCGGG G CCT GAT		
		ACCGACGTCC C GGA CTA		
		— CC —		
GAM1987	TEM6	3' TATCTGACACATCTCTGTAGCC 43041	GA	CCTCA
	A	TGGCTGCGG GT TAGATG		
		ACCGATGTC TA GTCTAT		
		TC CACA_		
GAM1987	TEX15	3' GTTTATGCTTATGCAGTTA 49224	G	TCCT
		TGGCTGCG GAG CATAGAT		
		ATTGACGT TTC GTATTTG		
		A —		
GAM1987	TGFBR3	3' CATGACCCTGGGCTTCTGTACC 13739	C	— AGATG
	A	TGG TGCGGGAGTCC TCAT		
		ACC ATGTCTTCGGG AGTA		
		— TCCC C G		
GAM1987	THOP1	3' CATCTGGAGGGCTTTCGTGGCT 73767	TG	GG A
		GGC CG AGTCCTC TAGATG		
		TCG GC TCGGGAG GTCTAC		
		GT TT —		
GAM1987	TIRAP	3' TGTTTGTGTATCCCTGTGCT 54665	T	— GTCCT
		GGC GC GGGA CATAGATG		
		TCG TG CCCT GTGTTTGT		
		— T AT —		
GAM1987	TLX1	5' TATCTCTGGCTCCTGCATCT 19826	C	T TCAT
		GG TGCGGGAG CC AGATG		

TC ACGTCCTC GG TCTAT
 T _ TC__
 GAM1987 TOP1 3' TGTTTGATTCTCTTAGCTA 13827 C TC
 TGGCTG GGGAGTCC ATA
 ||||| ||||| ||
 ATCGAT CTCTTAGG TGT
 T TT
 GAM1987 TPI1 3' CATCTGCTCCTTCCTGTGGCC 6295 TG TCCTCA
 GGC CGGGAG TAGATG
 || ||||| |||||
 CCG GTCCTT GTCTAC
 GT CCTC__
 GAM1987 TR2 3' TGTCTGTGGGCTGCTGTGGGCT 72780 _TG G T T
 GG C CGG AG CC CATAGATG
 || | || || || |||||
 TC G GTC TC GG GTGTCTGT
 G GT G _ _
 GAM1987 TRHDE 3' TGAAGGGCTTTTATAGTT 26317 CG _
 GGCTG GGAGTCCT CA
 ||||| ||||| ||
 TTGAT TTTCGGGA GT
 AT A
 GAM1987 TRPM6 5' TGTCTGTGATGACAGTGGCCA 35039 TG GGGA C
 TGGC C GTC TCATAGATG
 |||| | || |||||
 ACCG G CAG AGTGTCTGT
 GT A__ T
 GAM1987 TSSC3 3' TATTTATTTTCGCTGGTTCTTTG 13872 _ T TC____
 TAGTCA TGGCTGCGG GAG CC ATAGATG
 ||||| || || |||||
 ACTGATGTT CTT GG TATTTAT
 T _ TCGCTT
 GAM1987 UGT1A1 3' TATCTTTTGGCTTCTGCAG 6630 T TCAT
 CTGCGGGAG CC AGATG
 ||||| || |||||
 GACGTCTTC GG TCTAT
 _ TTT_
 GAM1987 UGT1A4 3' TATCTTTTGGCTTCTGCAG 24057 T TCAT
 CTGCGGGAG CC AGATG
 ||||| || |||||
 GACGTCTTC GG TCTAT
 _ TTT_
 GAM1987 UGT1A9 3' TATCTTTTGGCTTCTGCAG 41053 T TCAT
 CTGCGGGAG CC AGATG
 ||||| || |||||
 GACGTCTTC GG TCTAT
 _ TTT_
 GAM1987 VCL 3' ATCCTGGTTTTTGTAGCC 26582 T TCATA
 GGCTGCGGGAG CC GAT
 ||||| || ||

CCGATGTTTTT GG CTA
 _ TC_
 GAM1987 VEGF 3' TATTTCTGGGATTCCTGTAGAC 14043 G T T
 A TG CTGCGGGAGTCC CA AGATG
 || ||||| || |||||
 AC GATGTCCTTAGG GT TTTAT
 A _ C
 GAM1987 VLGR1 3' TATTTGTATCAGCTTTTGTGCT 50412 T CCTC
 A TGGC GCGGGAGT ATAGATG
 ||| ||||| |||||
 ATCG TGTTTTCG TGTTTAT
 _ ACTA
 GAM1987 WBSCR5 3' TATCTGTGTTCTTTTGTGCTA 42114 T TCCT
 TGGC GCGGGAG CATAGATG
 ||| ||||| |||||
 ATCG TGTTTTC GTGTCTAT
 _ TT_
 GAM1987 WNT2 3' CATCTCCTGGTGTCTGCAGTC 14113 GT TCAT
 A TGGCTGCGGGA CC AGATG
 ||||| || |||||
 ACTGACGTCTT GG TCTAC
 GT TCC_
 GAM1987 WNT8B 3' GTCTGAATCCTCGCAGCCA 60336 _ G CTCAT
 TGGCTGCG GGA TC AGAT
 ||||| || |||||
 ACCGACGC CCT AG TCTG
 T A _
 GAM1987 ZFP37 3' TGTCTGTGTTGGCTTCTGCATC 14161 C CT
 A TGG TGCGGGAGTC CATAGATG
 ||| ||||| |||||
 ACT ACGTCTTCGG GTGTCTGT
 _ TT
 GAM1987 ZNF155 3' TATTTATGGGGTACAACGTGCT 14317 T GGA _
 A TGGC GCG GT CCTCATAGATG
 ||| || |||||
 ATCG TGC CA GGGGTATTTAT
 _ AA_ T
 GAM1987 ZNF198 3' CATTTGTGGCTTTCTGCATCA 14361 C TCC
 TGG TGCGGGAG TCATAGATG
 ||| ||||| |||||
 ACT ACGTCTTT GGTGTTTAC
 _ C_
 GAM1987 ZNF217 3' ATCTGTGAATTGCAGGTA 22541 G GAGTCC
 TG CTGCGG TCATAGAT
 || ||||| |||||
 AT GACGTT AGTGTCTA
 G A_
 GAM1987 ZNF26 3' CGTTTATTATATTTTGCAGTT 73338 GTCCTC
 GGCTGCGGGA ATAGATG
 ||||| |||||

TTGACGTTTT TATTTGC
 ATAT__
 GAM1987 ZNF278 3' TGTTTGGGTTCTGTAGCT 50278 G TC
 GGCTGCGGGA TCC ATA
 ||||| ||| |||
 TCGATGTCTT GGG TGT
 _ TT
 GAM1987 ZNF278 3' TGTTTGGGTTCTGTAGCT 50279 G TC
 GGCTGCGGGA TCC ATA
 ||||| ||| |||
 TCGATGTCTT GGG TGT
 _ TT
 GAM1987 7h3 3' TGTCTGTGAGGACTGGTGTGC 53437 T GG
 GC GCG AGTCCTCATAGATG
 || ||| |||||
 CG TGT TCAGGAGTGTCTGT
 _ GG
 GAM1987 AASDHPPT 3' TGTTTGTGATCTTCCGTATTCA 31856 GC TCC
 TG TGCGGGAG TCATAGATG
 || ||||| |||||
 AC ATGCCTTC AGTGTTTGT
 TT T__
 GAM1987 AF9Q34 3' CATTTGTGTGTTGGCTTTGCAG 51712 G CT__
 CT GGCTGCGG AGTC CATAGATG
 ||||| ||| |||||
 TCGACGTT TCGG GTGTTTAC
 _ TTGT
 GAM1987 AF9Q34 3' TCTAAGACTCTGTGTGGCT 51722 TG _ CTCA TG
 GGC CG GGAGTC TAGA
 ||| ||||| |||||
 TCG GT TCTCAG ATCT
 GT G A__ T
 GAM1987 ALOXE3 3' ATGGAGACTTTTGCAGCCA 41557 CT
 TGGCTGCGGGAGTC CAT
 ||||| ||| |||
 ACCGACGTTTTCAG GTA
 AG
 GAM1987 ARL3 3' CATCTGTGTACACTCCAGCT 16301 GCG CCT
 GGCT GGAGT CATAGATG
 ||| |||| |||||
 TCGA CCTCA GTGTCTAC
 __ CAT
 GAM1987 ATE1 3' TATCTGTGAGAATCTCATAGTT 73019 C GTC
 A TGGCTG GGGA CTCATAGATG
 ||||| ||| |||||
 ATTGAT CTCT GAGTGTCTAT
 A AA_
 GAM1987 AXOT 3' TTATGATTACTGTAGTCA 43383 GAGTCC
 TGGCTGCGG TCATAG
 ||||| |||||

ACTGATGTC AGTATT
 ATT___
 GAM1987 BCMP1 3' CATTTCATGATTTTGTAGTT 49535 CTCAT
 GGCTGCGGGAGTC AGATG
 ||||| ||||
 TTGATGTTTTTAG TTTAC
 TAC___
 GAM1987 BDG-29 3' CGTCTGAAGAGCGTTTTGCGGT 72803 _TC CA
 CA TGGCTGCGGGA G CT TAGATG
 ||||| | || |||||
 ACTGGCGTTTT C GA GTCTGC
 G GA A_
 GAM1987 BTBD1 3' TATCTATGGGATGTGTGGTT 48226 TG GGGA T
 GGC C GTCC CATAGATG
 || | ||| |||||
 TTG G TAGG GTATCTAT
 GT TG__ _
 GAM1987 C1orf16 3' TGTCTGTGCAAGACCTGCAGCT 29917 AGTCCT
 GGCTGCGGG CATAGATG
 ||||| |||||
 TCGACGTCC GTGTCTGT
 AGAAC_
 GAM1987 C20orf103 3' TGTTTGGACTTCTTCCTGTGCC 25328 T ____ TC GATG
 A TGGC GCGGGA GTCC ATA
 ||| |||| | ||| |||
 ACCG TGTCT CAGG TGT
 _ TCTT TT G
 GAM1987 C20orf59 5' TGTCTGTGGGGTTTGAGGCCA 42237 G AGT
 TGGCT CGGG CCTCATAGATG
 |||| ||| |||||
 ACCGG GTTT GGGGTGTCTGT
 A ____
 GAM1987 C21orf108 3' TATCTTTGGGGATTCTTTGGT 90120 C T
 TA TGGCTG GGGAGTCCTCA AGATG
 |||| ||||| |||||
 ATTGGT TCCTTAGGGGT TCTAT
 T T
 GAM1987 C5orf3 5' TTTGTGTGAGGAATTCTTGTCG 38595 T _ GATG
 TT GGC GCGGGAGT CCTCATA
 || ||||| |||||
 TTG TGTTCTTA GGAGTGT
 C A GTTTG
 GAM1987 CAMP-GEFII 3' TGTTTATGGGATGAGATGTGCT 23812 T GGA_ T
 A TGGC GCG GTCC CATAGATG
 ||| || | ||| |||||
 ATCG TGT TAGG GTATTTGT
 _ AGAG _
 GAM1987 CEZANNE 3' GTTTGTGGGAGCCTGGCT 39897 TG AG T
 GGC CGGG TCC CATAGAT
 || ||| || |||||

TCG GTCC AGG GTGTTTG
 _ G _
 GAM1987 CG012 5' ATCTGTGGACATTGTATCA 84143 C GA TC
 TGG TCGGG GTCC ATAGAT
 ||| |||| ||| |||||
 ACT ATGTT CAGG TGTCTA
 _ A _
 GAM1987 CHERP 3' TCTAGATTTCTGTAGCT 22134 TCC A
 GGCTGCGGGAG TC TAGA
 ||||| || |||
 TCGATGTCCTT AG ATCT
 T _ _
 GAM1987 CLIC2 5' CATCTAGAATTTTCTGCGTCA 8915 T TCC A
 TGGC GCGGGAG TC TAGATG
 ||| ||||| || |||||
 ACTG CGTCTTT AG ATCTAC
 _ TA _
 GAM1987 CLSTN3 3' TGCAGGGCTCCCTCAGCT 28882 C _
 GGCTG GGGAGTCCT CA
 |||| ||||| ||
 TCGAC CCCTCGGGA GT
 T C
 GAM1987 CNNM3 3' CGTTTTAGATGGCCCTTGTAGT 34806 A C AT
 T GGCTGCGGG GTC TC AGATG
 ||||| || || |||||
 TTGATGTTT CGG AG TTTGC
 C T AT
 GAM1987 CNOT7 5' TGTCTATGGGGCACCCGCTGCC 26257 T A T
 GGC GCGGG GTCC CATAGATG
 || |||| ||| |||||
 CCG CGCCC CGGG GTATCTGT
 T A _
 GAM1987 CNOT7 5' TGTCTATGGGGCACCCGCTGCC 55061 T A T
 GGC GCGGG GTCC CATAGATG
 || |||| ||| |||||
 CCG CGCCC CGGG GTATCTGT
 T A _
 GAM1987 COLEC10 3' TATTTGCTATTTTCCTGTGACC 22239 CT TCCTCA
 GG GCGGGAG TAGATG
 || ||||| |||||
 CC TGTCTT GTTTAT
 AG TTATC_
 GAM1987 CYP2S1 3' ATTTACACGCTGCAGTT 48368 A CCTCA
 GGCTGCGGG GT TAGAT
 ||||| || |||
 TTGACGTCC CA ATTTA
 G C _
 GAM1987 DC-TM4F2 3' CATCTGTGGGTGGGCCGTGGGT 48896 G TG GAG _
 A TG C CGG TC CTCATAGATG
 || | || || |||||

AT G GCC GG GGGTGTCTAC
 G GT G__ T
 GAM1987 DDX18 3' TTTGTGAGGATTTTGTGGC 23201 TG TG
 GC CGGGAGTCCTCATAGA
 || |||||
 CG GTTTTATAGGAGTGTT
 GT T
 GAM1987 DDX34 5' CATCTGTGGTGGTCCTGTGCC 28664 T GT _
 GGC GCGGA CC TCATAGATG
 ||| ||||| || |||||
 CCG TGTCTT GG GGTGTCTAC
 _ _ T
 GAM1987 DEPP 3' CATTTATGAGCACTGTAGACA 23805 G GAGTC
 TG CTGCGG CTCATAGATG
 || ||||| |||||
 AC GATGTC GAGTATTTAC
 A AC__
 GAM1987 DJ37E16.5 3' CTCTGGGGCTTCTGTGGCCA 40095 TG T T
 TGGC CGGGAGTCC CA AG
 |||| ||||| ||||
 ACCG GTCTTCGGG GT TC
 GT _ C
 GAM1987 DKFZP434B205 3' CGTCAGCAGGGACTTCGTGGCC 75844 TG G CATA
 A TGGC CGG AGTCCT GATG
 |||| ||||| ||||
 ACCG GCT TCAGGG CTGC
 GT _ ACGA
 GAM1987 DKFZP434C1715 3' ATCTATGTATTCTGGCCA 87350 GCG CCT
 TGGCT GGAGT CATAGAT
 |||| ||||| |||||
 ACCGG TCTTA GTATCTA
 _ T__
 GAM1987 DKFZP434E2318 5' GCAGTGGGGGCTTCCGCGGCT 50455 AGATG
 GGCTGCGGGAGTCCTCAT
 |||||
 TCGGCGCCTTCGGGGGTG
 ACGG
 GAM1987 DKFZP434P1750 3' TGTCTCCCCCACTTCCTGGCCA 32029 C CCTCAT
 TGGCTG GGGAGT AGATG
 ||||| ||||| |||||
 ACCGGT CCTTCA TCTGT
 _ CCCCC_
 GAM1987 DLL1 3' TATTTATGGAATATTGTGCCA 20051 T GAG TC
 TGGC GCGG TCC ATAGATG
 |||| ||||| |||||
 ACCG TGTT AGG TATTTAT
 _ ATA _
 GAM1987 DNAJB6 3' TATTTGTCATAGACTTTTGTGAGT 19718 G CTC_
 T GGCT CGGGAGTC ATAGATG
 |||| ||||| |||||

TTGA GTTTTCAG TGTTTAT
 _ ATAC
 GAM1987 EMR2 3' TGAAGTGGCTCTTGCAGCTA 26501 _ _
 TGGCTGCGGGAGTC CT CA
 ||||| ||
 ATCGACGTTCTCGG GA GT
 T A
 GAM1987 ENAH 3' TATTTAAAGTTGATTTCTGCAC 37158 C CTCA_
 TA TGG TGC GGGAGTC TAGATG
 || ||||| ||||
 ATC ACGTCTTTAG ATTTAT
 _ TTGAA
 GAM1987 EZFIT 3' TTTTATAGTGATTTTTGCAGCT 41382 _ C TG
 A TGGCTGCGGGAGTC CT ATAGA
 ||||| || ||||
 ATCGACGTTTTTAG GA TATTT
 T _ TT
 GAM1987 FLJ10233 5' TGTTTGGGCTGTCCCTGTGGCT 36390 TG _ TC GATG
 GGC CGGG AGTCC ATA
 || ||| |||| ||
 TCG GTCC TCGGG TGT
 GT CTG TT
 GAM1987 FLJ10468 3' GTCTACCCTCTCGCACTCA 36634 GC TCCTCA
 TG TGC GGGAG TAGAT
 || ||||| ||||
 AC ACGCTCTC ATCTG
 TC CC____
 GAM1987 FLJ10546 5' GTTTGTGACACAGTAGCCA 60183 GGGAGTCC
 TGGCTGC TCATAGAT
 ||||| |||||
 ACCGATG AGTGTTTG
 ACAC____
 GAM1987 FLJ10713 3' TGTTTATGGGCCATGCAGACT 37013 _ _ AGTC
 GG CTGCG GG CTCATAGATG
 || |||| || |||||
 TC GACGT CC GGGTATTTGT
 A A ____
 GAM1987 FLJ10774 3' TGTCTGTGAGCTCAACCTGGCT 45420 C _ TC
 A TGGCTG GG GAG CTCATAGATG
 |||| || || |||||
 ATCGGT CC CTC GAGTGTCTGT
 _ AA _
 GAM1987 FLJ10813 3' ATTTAATGTCTGCAGCCA 37228 GA CCTCA
 TGGCTGCGG GT TAGAT
 ||||| || ||||
 ACCGACGTC TA ATTTA
 TG ____
 GAM1987 FLJ10900 3' CATCTTCTTTCACTCCTGTGGC 66203 TG CCTCAT
 C GGC CGGGAGT AGATG
 || ||||| ||||

CCG GTCCTCA TCTAC
 GT CTTTCT
 GAM1987 FLJ10900 3' CATCTTCTTTGACTCCTGTGGC 66204 TG CTCAT
 C GGC CGGGAGTC AGATG
 ||| ||||| ||||
 CCG GTCCTCAG TCTAC
 GT TTTCT
 GAM1987 FLJ11164 3' CGTCTCTGCTCCTTGTGGTTA 37699 TG _ CCTCAT
 TGGC CG GGAGT AGATG
 |||| || |||| ||||
 ATTG GT CCTCG TCTGC
 GT T TC____
 GAM1987 FLJ11210 3' ATTTAGTATCTTGCAGCTA 60317 GTCCTCA
 TGGCTGCGGGA TAGAT
 ||||| ||||
 ATCGACGTTCT ATTTA
 ATG____
 GAM1987 FLJ12428 5' GTCTGTGAGGGCAGACTG 43267 GA_
 CGG GTCCTCATAGAT
 ||| |||||
 GTC CGGGAGTGTCTG
 AGA
 GAM1987 FLJ12610 5' GAGAGTGGGCGCTCTCGCGGCC 45858 C AGATG
 GGCTGCGGGAGT CTCAT
 ||||| ||||
 CCGGCGCTCTCG GGGTG
 C AGAGA
 GAM1987 FLJ13052 3' GGAGATGAGGGTTTCCGGGGCT 43755 G GT AGATG
 A TGGCT CGGGA CCTCAT
 |||| |||| ||||
 ATCGG GCCTT GGAGTA
 G TG GAGGG
 GAM1987 FLJ13063 5' GTGGTCGGACTTCTGGGCT 72301 G _
 GGCT CGGGAGTCC TCAT
 ||| ||||| ||||
 TCGG GTCTTCAGG GGTG
 _ CT
 GAM1987 FLJ13166 3' TATCTATGGCTGGTTTTGCACT 47190 C GT _
 A TGG TGCGGGA CC TCATAGATG
 ||| ||||| || |||||
 ATC ACGTTTT GG GGTATCTAT
 _ _ TC
 GAM1987 FLJ13197 3' TGTTTGAAGTGCTCCTGCAGCT 45190 TC _ TAGATG
 A TGGCTGCGGGAG CT CA
 ||||| || ||
 ATCGACGTCCTC GA GT
 GT A TTGT
 GAM1987 FLJ13322 3' TGTCAGTGGAGGGTCTCTGCA 45634 _ G _ A
 GCCA TGGCTGCGG GA TCCTC AT GATG
 ||||| || |||| || ||||

ACCGACGTC CT GGGAG TG CTGT
 T G G A
 GAM1987 FLJ13390 5' TGTTTAAAAGTGCCTTGTGGC 42842 TG A TC CA
 T GGC CGGG G CT TAGATG
 ||| |||| | || |||||
 TCG GTTC C GA ATTTGT
 GT G GT AA
 GAM1987 FLJ13441 3' TGTTTATGTGGCTTGTGTGCT 43923 T G T T
 GGC GCG GAG CC CATAGATG
 ||| ||| ||| || |||||
 TCG TGT TTC GG GTATTTGT
 _ G _ T
 GAM1987 FLJ13441 3' TGTTTATGTGGCTTGTGTGCT 43924 T G T T
 GGC GCG GAG CC CATAGATG
 ||| ||| ||| || |||||
 TCG TGT TTC GG GTATTTGT
 _ G _ T
 GAM1987 FLJ13479 5' TGTCAGGCTCCGCGGCCA 45557 G T C
 TGGCTGCGG AG CCT ATA
 ||||| || ||| |||
 ACCGGCGCC TC GGA TGT
 _ _ C
 GAM1987 FLJ13910 3' TGT TTGTGAGGAGAAAGAGTAC 43253 C GGGAG_
 T GG TGC TCCTCATAGATG
 || ||| |||||
 TC ATG AGGAGTGT TTGT
 _ AGAAAG
 GAM1987 FLJ14075 3' TGTCTGTGTATTGCCTGTGTT 46584 T AGTCCT
 GGC GCGGG CATAGATG
 ||| |||| |||||
 TTG TGTCC GTGTCTGT
 _ GTTAT_
 GAM1987 FLJ14249 3' TGTCTGTGGGGACATCGGTGT 42648 T G GA
 GC GC G GTCCTCATAGATG
 || ||| |||||
 TG TG C CAGGGGTGTCTGT
 _ G TA
 GAM1987 FLJ14251 5' TGTGCGCTGGGCTCCCGCCGCT 46494 T T___ GATG
 GGC GCGGGAGTCC CATA
 ||| ||||| |||
 TCG CGCCCTCGGG GTGT
 C TCGC
 GAM1987 FLJ14326 3' CATCTGTGTCCCCGCATGTTA 50762 _ AGTCCT
 TGGC TGCGGG CATAGATG
 ||| |||| |||||
 ATTG ACGCCC GTGTCTAC
 T CT___
 GAM1987 FLJ14596 5' CGTCTATGATCCAGGCCCTGGC 52516 C AGTCC_
 CA TGGCTG GGG TCATAGATG
 ||||| ||| |||||

ACCGGT CCC AGTATCTGC
 _ GGACCT
 GAM1987 FLJ14621 5' GTCTCTGGCCCTGCGGTCA 52539 A T TCAT
 TGGCTGCGGG G CC AGAT
 ||||| || ||||
 ACTGGCGTCC C GG TCTG
 _ _ TC_
 GAM1987 FLJ14668 3' CATTTTGCCTGGGGCTTGTGC 52587 G _ T
 AGCT GGCTGCG GAGTCCT CA AGATG
 ||||| ||||| || ||||
 TCGACGT TTCGGGG GT TTTAC
 G TCC T
 GAM1987 FLJ14751 3' TGTCTGTTTCCTAATATCTTGT 52672 TG GTCCTC_
 GGCT GGC CGGGA ATAGATG
 || |||| |||||
 TCG GTTCT TGTCTGT
 GT ATAATCCTT
 GAM1987 FLJ14803 3' CATCTACCTGATTCTTGTACCA 52692 C CTCA
 TGG TGCGGGAGTC TAGATG
 || ||||| |||||
 ACC ATGTTCTTAG ATCTAC
 _ TCC_
 GAM1987 FLJ14816 3' TGTCTGGGAGTCAGGACTCCTG 52711 T CA_
 TGTT GGC GCGGGAGTCCT TAGATG
 || ||||| |||||
 TTG TGTCTCAGGA GTCTGT
 _ CTGAGG
 GAM1987 FLJ20086 3' TATTTGTGAGGATGATGCTGGT 35015 _ GGA
 GCT GCG GTCCTCATAGATG
 || || |||||
 TGG CGT TAGGAGTGTAT
 T AG_
 GAM1987 FLJ20132 5' CATCTACAACTCCTGTGGC 35086 TG CCTCA
 GC CGGGAGT TAGATG
 || ||||| |||||
 CG GTCCTCA ATCTAC
 GT AAC_
 GAM1987 FLJ20273 3' CATTTGTATAGAGGTTTTTGT 39245 T T _
 GTT GGC GCGGGAG CCTC ATAGATG
 || ||||| |||||
 TTG TGTTTTT GGAG TGTTTAC
 T _ ATA
 GAM1987 FLJ20330 5' TGTCTGTGCGATTGCGCGGCT 39147 TG _ CT
 GGC CGG GAGTC CATAGATG
 || || ||||| |||||
 TCG GCC CTTAG GTGTCTGT
 _ G C_
 GAM1987 FLJ20401 5' TGTCTGTGGAGCTGCGGCCA 35583 GAG TC
 TGGCTGCGG TCC ATAGATG
 ||||| || |||||

ACCGGCGTC AGG TGTCTGT
 G__ __
 GAM1987 FLJ20701 3' ATCTGTGTGTCCGTATCT 36022 C AGTCCT
 GG TCGGG CATAGAT
 || ||||| |||||
 TC ATGCCT GTGTCTA
 T GT____
 GAM1987 FLJ20772 3' TGAGGAGGCTTCTGTGGTT 36089 TG ____
 GGC CGGGAGT CCTCA
 ||| ||||| |||||
 TTG GTCTTCG GGAGT
 GT GA
 GAM1987 FLJ20847 5' CATTTATGAGCATCTACTTGCG 96485 _ TC_
 GCT GGCTGCGGG AG CTCATAGATG
 ||||| || |||||
 TCGGCGTTC TC GAGTATTTAC
 A TAC
 GAM1987 FLJ20972 3' CATTTACCCTCTTCCTGTGGTT 47383 TG TCCTCA
 GGC CGGGAG TAGATG
 ||| ||||| |||||
 TTG GTCCTT ATTTAC
 GT CTCCC_
 GAM1987 FLJ21404 3' TATTTAGTTATTGTTTTGTAGC 50802 GTCCTCA
 T GGCTGCGGGA TAGATG
 ||||| |||||
 TCGATGTTTT ATTTAT
 GTTATTG
 GAM1987 FLJ21551 3' TATTTATGATATTTCTGCAGAC 46041 _ CC
 T GG CTGCGGGAGT TCATAGATG
 || ||||| |||||
 TC GACGTCTTTA AGTATTTAT
 A T_
 GAM1987 FLJ22353 3' TGTCTGTGGGAGCCTTGCAGTC 45035 A TC
 A TGGCTGCGGG G CTCATAGATG
 ||||| | |||||
 ACTGACG TTC C GGGTGTCTGT
 _ GA
 GAM1987 FLJ22389 5' CATCTTGACATTTCCGTGGC 46791 TG CC T
 GC CGGGAGT TCA AGATG
 || ||||| ||| |||||
 CG GCCTTTA AGT TCTAC
 GT C_ _
 GAM1987 FLJ22405 5' ATGGGGATATCTGTGGCCA 42814 TG A
 TGGC CGGG GTCCTCAT
 ||| ||| |||||
 ACCG GTCT TAGGGGTA
 GT A
 GAM1987 FLJ23047 3' TATCTATTATTCTGTTGTAGTC 44934 G TCCTC
 A TGGCTGCGG AG ATAGATG
 ||||| || |||||

		ACTGATGTT TC TATCTAT	
		G TTAT_	
GAM1987	FLJ23091 3'	GAGGAAGATTTCCTGCAGCCA 46664	_____
		TGGCTGCGGGAG TCCTC	
		ACCGACGTCCTT AGGAG	
		AGA	
GAM1987	FLJ23306 3'	CATCTCAAGTGGTATTTGTAGC 44846	AG _ CAT
	CA	TGGCTGCGGG TC CT AGATG	
		ACCGATGTTT GG GA TCTAC	
		AT T AC_	
GAM1987	FLJ23519 3'	TGTCTGGTGGTTTCTTGTGGTT 50966	TG T TCA
		GGC CGGGAG CC TAGATG	
		TTG GTTCTT GG GTCTGT	
		GT T TG_	
GAM1987	FLJ25473 3'	TATCTGTGTTTCCTTTTTAGTT 59138	C_ TCCT
		GGCTG GGGAG CATAGATG	
		TTGAT TCCTT GTGTCTAT	
		TTT T_	
GAM1987	FLJ31978 3'	TGCAGGGCTTTGCAGCCA 59010	G _
		TGGCTGCGG AGTCCT CA	
		ACCGACGTT TCGGGA GT	
		_ C	
GAM1987	FLJ32926 3'	TCTCTGGGCTTCCTGGTCA 58637	C TCAT
		TGGCTG GGGAGTCC AGA	
		ACTGGT CCTTCGGG TCT	
		_ TC_	
GAM1987	FPGT 3'	TATCTGTGGGGGAAGTGGTAGT 15182	GGGAG
		GCTGC TCCTCATAGATG	
		TGATG GGGGGTGTCTAT	
		GTGAA	
GAM1987	GBTS1 5'	GTCTGGGGTTCTTGCAGCT 59726	GT CAT
		GGCTGCGGGA CCT AGAT	
		TCGACGTTCT GGG TCTG	
		TG _	
GAM1987	GMEB2 3'	TGTCTGGAAGGGCTGTCTGTGG 25670	TG _ CA
	CT	GGC CGGG AGTCCT TAGATG	
		TCG GTCT TCGGGA GTCTGT	
		GT G AG	
GAM1987	GMNN 3'	TGTGAATAGGATTTTCTCAGTT 32472	C GG _ GATG
		GGCTG G AGTCC TCATA	

			TTGAC C TTAGG AGTGT		
			T TT ATA		
GAM1987	GP5	3'	CATTTGTTTCTGGGTTCTGCAG 16866	G TC__	
	TT		GGCTGCGGGA TCC ATAGATG		
			TTGACGTCTT GGG TGTTTAC		
			_ TCTT		
GAM1987	GRID1	3'	TATTTATGAGGGTGATAACTAG 69026	CGGGA_	
	CC		GGCTG GTCCTCATAGATG		
			CCGAT TGGGAGTATTTAT		
			CAATAG		
GAM1987	GTPBP5	3'	TGTCTGTGGTTTAAAGTCTTTGC 65983	_ GTCC__	
	AGTCA		TGGCTGCGG GA TCATAGATG		
			ACTGACGTT CT GGTGTCTGT		
			T GAATTT		
GAM1987	HEF1	3'	CATTTGTGAGTGTTTCAGTCA 22156	GCGG GT_	
			TGGCT GA C CTCATAGATG		
			ACTGA CT G GAGTGTTTAC		
			___ TG T		
GAM1987	HNK-1ST	5'	CGTCTTCCTTACTTCCGCTGCC 17948	T CCTCAT	
			GGC GCGGGAGT AGATG		
			CCG CGCCTTCA TCTGC		
			T TTCCT_		
GAM1987	HSMPP8	3'	TGTCTGTAAACCTCTTGCA GTT 95144	TCCTC	
	A		TGGCTGCGGGAG ATAGATG		
			ATTGACGTTCTC TGTCTGT		
			CAAA_		
GAM1987	HSPC002	3'	ATCTGGGTTCTCCAGTCA 31719	C GT TCAT	
			TGGCTG GGGA CC AGAT		
			ACTGAC CTCT GG TCTA		
			_ TG _		
GAM1987	HSPC065	3'	GTCATGGGGGCTCCCTGGCCA 27159	C A G	
			TGGCTG GGGAGTCCTCAT GAT		
			ACCGGT CCCTCGGGGGTA CTG		
			_ _		
GAM1987	HSPC189	3'	CATCTTCCTGGGGCTTCTGCGC 96987	T CAT_	
	T		GGC GCGGGAGTCCT AGATG		
			TCG CGTCTTCGGGG TCTAC		
			_ TCCT		
GAM1987	HSPC228	3'	CATTTATGTTTTGTCTGTGGTT 33647	TG AGTCCT	
			GGC CGGG CATAGATG		

TTG GTCT GTATTTAC
 GT GTTTT_
 GAM1987 HSXIAPAF1 3' CATCTATGACAAAACCACAGCC 34459 C GAGTCC
 A TGGCTG GG TCATAGATG
 ||||| || |||||
 ACCGAC CC AGTATCTAC
 A AAAAC_
 GAM1987 humNRDR 3' CGTCTTACTCGGGATTCTGCT 41011 T CAT_
 GTT GGC GCGGGAGTCCT AGATG
 || ||||| |||||
 TTG CGTCCTTAGGG TCTGC
 T CTCAT
 GAM1987 IL-17RC 3' CATCCCCCGGGGACTCCCGCGC 52177 T ATA_
 C GGC GCGGGAGTCCTC GATG
 || ||||| |||||
 CCG CGCCCTCAGGGG CTAC
 _ CCCC
 GAM1987 IMAP1 5' CAGGTTGGGGCTTCTTGTGGCC 56235 TG T TAGATG
 A TGGC CGGGAG CCTCA
 |||| ||||| |||||
 ACCG GTTCTT GGGGT
 GT C TGGAC
 GAM1987 JM11 3' TGTCTGTGATTTTCGGAGCT 54375 G GG TCC
 GGCT CG AG TCATAGATG
 |||| || || |||||
 TCGA GC TT AGTGTCTGT
 G TT _
 GAM1987 KIAA0010 3' TATTTGTGGTTTTTTTCTCAGC 28592 C GG TCC
 TA TGGCTG G AG TCATAGATG
 ||||| | || |||||
 ATCGAC C TT GGTGTTTAT
 T TT TTT
 GAM1987 KIAA0077 3' CATTTTGGTGGTTTCTGTGTTA 67578 T GT C T
 TGGC GCGGGA C TCA AGATG
 |||| ||||| | || |||||
 ATTG TGTCTT G GGT TTTAC
 _ TG T _
 GAM1987 KIAA0089 3' CATAGGAGGGCTTCCTGCAGCT 70504 _ ATAG
 GGCTGCGGGA GTCCTC ATG
 ||||| ||||| |||||
 TCGACGTCCT CGGGAG TAC
 T GA_
 GAM1987 KIAA0211 3' TATTTGTA CTGCTCTCGTGCCA 28287 T CCTC
 TGGC GCGGGAGT ATAGATG
 |||| ||||| |||||
 ACCG TGCTCTCG TGTTTAT
 _ TCA_
 GAM1987 KIAA0212 3' TATCCTGCAGGGCTTTTGCAGT 28629 _ TA
 T GGCTGCGGGAGTCCT CA GATG
 ||||| ||||| |||||

TTTGACGTTTTTCGGGA GT CTAT
 C C_
 GAM1987 KIAA0284 3' TTCTCAGGATTCTTTTCAGCT 63807 CG CAT TG
 GGCTG GGAGTCCT AGA
 |||| ||||| ||
 TCGAC TCTTAGGA TCT
 TT C_ TT
 GAM1987 KIAA0286 3' CATTTAATTTTTCTCTGGCAGT 68857 G TCCTCA
 TA TGGCTGC GGAG TAGATG
 ||||| ||| |||||
 ATTGACG TCTC ATTTAC
 G TTTTAA
 GAM1987 KIAA0295 3' AGCTGGTGGACTCCTGTGGCTA 68659 TG TCA ATG
 TGGC CGGGAGTCC TAG
 ||| ||||| ||
 ATCG GTCCTCAGG GTC
 GT TG_ GAC
 GAM1987 KIAA0295 3' TATCTGTGGCACTGGCCTGCAG 68673 _ C T
 C GCTGCGGG AGT C CATAGATG
 ||||| ||| |||||
 CGACGTCC TCA G GTGTCTAT
 GG C_
 GAM1987 KIAA0298 3' AGAATGAGGACTTCTGTGCT 77074 T AGATG
 GGC GCGGGAGTCCTCAT
 ||| |||||
 TCG TGTCTTCAGGAGTA
 _ AGAG
 GAM1987 KIAA0298 3' TGTTTGTGAGGATACTGGAGGT 77082 G_ GA
 CA TGGCT CGG GTCCTCATAGATG
 |||| ||| |||||
 ACTGG GTC TAGGAGTGTGTTGT
 AG A_
 GAM1987 KIAA0356 5' TGAGGGGCTGCCGCGGCC 66780 G _
 GGCTGCGG AGTCC TCA
 ||||| ||||| ||
 CCGGCGCC TCGGG AGT
 G G
 GAM1987 KIAA0391 3' ATCAGAGGCTCTTGAGCT 28599 G T ATA
 GGCT CGGGAG CCTC GAT
 ||| ||||| ||| ||
 TCGA GTTCTC GGAG CTA
 _ _ A_
 GAM1987 KIAA0416 3' CGTTTATATTCATTTCTGTAGC 32090 CCTC
 GCTGCGGGAGT ATAGATG
 ||||| |||||
 CGATGTCTTTA TATTTGC
 CTTA
 GAM1987 KIAA0450 5' TGTCTCTTTGGTCTTGCAAGTC 28377 GT TCAT
 GGCTGCGGGA CC AGATG
 ||||| || |||||

CTGACGTTCT GG TCTGT
 _ TTTC
 GAM1987 KIAA0461 3' TGT TTGTTTATTGTGTGGCCA 71396 TG G GTCCTC
 TGGC CG GA ATAGATG
 ||| ||| |||||
 ACCG GT TT TGT TTGT
 GT G ATTT_
 GAM1987 KIAA0471 5' TATCTGAACTCTCCTGCATCA 30045 C TCCTCA
 TGG TGC GGGAG TAGATG
 || ||||| |||||
 ACT ACGTCCTC GTCTAT
 _ TCAA_
 GAM1987 KIAA0472 3' TGTCTGGTTCCTGCTGTCTGCA 72374 _ CCTCA_
 GCCA TGGCTGCGGG AGT TAGATG
 ||||| ||| |||||
 ACCGACGTCT TCG GTCTGT
 G TCCTTG
 GAM1987 KIAA0493 3' TTTATATGTGGACTTCTGTTGT 64941 T T GATG
 CA TGGC GCGGGAGTCC CATA
 ||| ||||| |||
 ACTG TGTCTTCAGG GTAT
 T T ATTTA
 GAM1987 KIAA0523 5' TGCAGGACCCTGTGGCCA 68357 TG A _
 TGGC CGGG GTCCT CA
 ||| ||| ||||| ||
 ACCG GTCC CAGGA GT
 GT _ C
 GAM1987 KIAA0544 3' TGTCTCAGGCTTCTGTGGC 71478 TG T CAT
 GC CGGGAG CCT AGATG
 || ||||| ||| |||||
 CG GTCTTC GGA TCTGT
 GT _ C_
 GAM1987 KIAA0553 3' TATTGGGATTTTGTAGCTA 70452 G C
 TGGCT CGGGAGTCCT ATA
 ||||| ||||| |||
 ATCGA GTTTT TAGGG TAT
 _ T
 GAM1987 KIAA0599 3' TTGTGCTGACCCTGTGGTT 77706 TG A CT
 GGC CGGG GTC CATAG
 ||| ||| ||| |||||
 TTG GTCC CAG GTGTT
 GT _ TC
 GAM1987 KIAA0637 3' CATTT CAGGTTTCTGCATTCA 29922 GC T CAT
 TG TGC GGGAG CCT AGATG
 || ||||| ||| |||||
 AC ACGTCTTT GGA TTTAC
 TT _ C_
 GAM1987 KIAA0652 3' CATCTGTGAAGAGTCTCAGCCA 29120 CG G C
 TGGCTG GGA TC TCATAGATG
 ||||| ||| || ||||| |||

			ACCGAC TCT AG AGTGTCTAC		
			___ G A		
GAM1987	KIAA0700	3'	ATCAAGATTCTGTACCA 72514 C	CTCATA	
			TGG TCGGGGAGTC GAT		
			ACC ATGTCCTTAG CTA		
			___ AA___		
GAM1987	KIAA0705	3'	TCCCTTGTTGGGGGCTTTGGCAG 25484	G	ATG
			CTA TGGCTGC GGAGTCCTCATAG		
			ATCGACG TTTCGGGGGTGTT		
			G CCCTT		
GAM1987	KIAA0716	3'	TATCTTGCAAGTTTTGCAGTCA 28837	GTCCT T	
			TGGCTGCGGGA CA AGATG		
			ACTGACGTTTT GT TCTAT		
			GAAC_ _		
GAM1987	KIAA0748	5'	TATCTACAATGGCTTCTGCAGC 29618	CTCA	
			CA TGGCTGCGGGAGTC TAGATG		
			ACCGACGTCTTCGG ATCTAT		
			TAAC		
GAM1987	KIAA0863	3'	CATCTATTGTTTCTGCAGTT 96950	TCCTC	
			GGCTGCGGGAG ATAGATG		
			TTGACGTCCTT TATCTAC		
			TGT_		
GAM1987	KIAA0863	3'	CATCTATTGTTTCTGCAGTT 96951	TCCTC	
			GGCTGCGGGAG ATAGATG		
			TTGACGTCCTT TATCTAC		
			TGT_		
GAM1987	KIAA0914	3'	TTCTTCAGGACTTCCTCAGCT 30297	C	CAT TG
			GGCTG GGGAGTCCT AGA		
			TCGAC CCTTCAGGA TCT		
			T CT_ TT		
GAM1987	KIAA0937	3'	TATCTGTGAGGGATTTGGGTTA 93226	G	AG
			TGGCT CGGG TCCTCATAGATG		
			ATTGG GTTT GGGAGTGTCTAT		
			_ A_		
GAM1987	KIAA1023	3'	CGTTTGCTCTCCCGTGGCT 34679	TG	TCCTCA
			GGC CGGGAG TAGATG		
			TCG GCCCTC GTTTGC		
			GT TC_		
GAM1987	KIAA1036	3'	ATCTCATTCCTGTTGTCA 30485	T	CCTCAT
			TGGC GCGGGAGT AGAT		

		ACTG TGTCTTA	TCTA	
		T C		
GAM1987 KIAA1069	3'	CATTTGGCTCCCGATCCTGTAG	68528	GTCCTCA
		TTA	TGGCTGCGGA	TAGATG
		ATTGATGTCCT	GTTTAC	
		AGCCCTCG		
GAM1987 KIAA1094	5'	GTCTAGGGCGTCCGTAGTC	30480	GA CAT G
		GGCTGCGG	GTCCT AGAT	
		CTGATGCC	CGGGA TCTG	
		TG		
GAM1987 KIAA1136	3'	CATTTATGCAATCTGCAGCTA	92958	AGTCCT
		TGGCTGCGGG	CATAGATG	
		ATCGACGTCT	GTATTTAC	
		AAC		
GAM1987 KIAA1209	3'	CATTTTAGGGTTTTTGCTA	61401	T GT CAT
		TGGC GCGGGA	CCT AGATG	
		ATCG TGT	TTTAC	
		TG		
GAM1987 KIAA1240	3'	TATCTTCATTCATTGTAGCC	67292	CCTCAT
		GGCTGCGG	GAGT AGATG	
		CCGATGTT	CTTA TCTAT	
		A CT		
GAM1987 KIAA1254	3'	TGTTTGTGTTAAATTTGCAGC	70570	AGTCCT
		GCTGCGGG	CATAGATG	
		CGACGTTT	GTGTTTGT	
		AAATT		
GAM1987 KIAA1255	3'	TGTCTGTGGAGTCCTCAGTCA	67748	C G TC
		TGGCTG GGA	TCC ATAGATG	
		ACTGAC TCCT	AGG TGTCTGT	
		G		
GAM1987 KIAA1266	3'	TGTTTGTGGGTATGAGTCTGTG	66702	TG G
		TGGCCA	TGGC CG GGA TC CTCATAGATG	
		ACCG GT TCT	AG GGGTGT	
		GT G G	TAT	
GAM1987 KIAA1271	3'	CATCTGTTCCGTTCCCTGCAGT	70130	TCCTC
		GCTGCGGGAG	ATAGATG	
		TGACGTCCTT	TGTCTAC	
		GCCT		
GAM1987 KIAA1383	3'	TATGAAAGGTTTCTGTGGCTA	70342	TG T
		TGGC CGGGAG	CC TCATA	

ATCG GTCTTT GG AGTAT
 GT _ AA
 GAM1987 KIAA1437 3' ATTTGTGTTTTCTGCGTC 61212 T TCCT
 GGC GCGGGAG CATAGAT
 ||| ||||| |||||
 CTG CGTCTTT GTGTTTA
 _ T____
 GAM1987 KIAA1535 3' TATCTTCCTGTTCTGTAGC 80216 TCCTCAT
 GCTGCGGGAG AGATG
 ||||| |||||
 CGATGTCCTT TCTAT
 GTCCT____
 GAM1987 KIAA1554 3' TATCTAGTCCTTTCTGTGGTT 96861 TG TCCTCA
 GGC CGGGAG TAGATG
 ||| ||||| |||||
 TTG GTCTTT ATCTAT
 GT CCTG____
 GAM1987 KIAA1673 3' TGTAGATTCTTGTGTCA 71331 T CT
 TGGC GCGGGAGTC CA
 ||| ||||| ||
 ACTG TGTTCTTAG GT
 _ AT
 GAM1987 KIAA1681 3' TATCTATAAGGCTTTTGTGTT 61715 T T C
 GGC GCGGGAG CCT ATAGATG
 ||| ||||| ||| |||||
 TTG TGTTTTTC GGA TATCTAT
 _ _ A
 GAM1987 KIAA1727 3' CGTTTGTGGGAATCCACGTGG 64756 TG _ G
 TT GGC CG GGA TCCTCATAGATG
 ||| || ||| |||||
 TTG GC CCT AGGGGTGTTTGC
 GT A A
 GAM1987 KIAA1729 5' CATTTGTTCTCACTGCAGCTA 90588 _ TCCTC
 TGGCTGCGG GAG ATAGATG
 ||||| ||| |||||
 ATCGACGTC CTC TGTTTAC
 A T____
 GAM1987 KIAA1786 3' TATCTGTGGTTTCACTTTCCGT 66634 TG _ CC____
 GGTT GGC CGGGA GT TCATAGATG
 ||| ||||| || |||||
 TTG GCCTT CA GGTGTCTAT
 GT T CTTT
 GAM1987 KIAA1814 5' CGTCCACTGGACTCCTGCGCCA 70876 T TCATA
 TGGC GCGGGAGTCC GATG
 ||| ||||| |||
 ACCG CGTCCTCAGG CTGC
 _ TCAC____
 GAM1987 KIAA1887 5' AGAGCTGGGGGCCCTGTGGCCA 77275 TG A TAGATG
 TGGC CGGG GTCCTCA
 ||| ||| |||||

ACCG GTCC CGGGGGT
 GT _ CGAGAC
 GAM1987 KIAA1906 3' TATTTATACAAGTGCTTTGTGG 73575 TG G TC C__
 CCA TGGC CGG AG CT ATAGATG
 |||| ||| || || |||||
 ACCG GTT TC GA TATTTAT
 GT _ GT ACA
 GAM1987 KIAA1912 3' CATTTAAAATAAGCTTTTGTGC 73756 T CCTCA_
 C GGC GCGGGAGT TAGATG
 ||| ||||| |||||
 CCG TGTTTTCG ATTTAC
 _ AATAAA
 GAM1987 KIAA1937 3' TATCTGCTGTCCACTCTCGCTG 74073 T CCT _
 TC GGC GCGGGAGT CA TAGATG
 ||| ||||| || |||||
 CTG CGCTCTCA GT GTCTAT
 T CCT C
 GAM1987 KIAA1944 3' AGACTGAGGTTTCTGCAGCCA 76076 T TAGATG
 TGGCTGCGGGAG CCTCA
 ||||| |||||
 ACCGACGTCTTT GGAGT
 _ CAGAG
 GAM1987 LACE1 3' TATTTGGCCTTATTTCTGCACC 93479 C CCTCA
 A TGG TGC GGGAGT TAGATG
 ||| ||||| |||||
 ACC ACGTCTTTA GTTTAT
 _ TTCCG
 GAM1987 LENE 3' ATCAAGACTCCTGAAGCCA 38475 G CTCATA
 TGGCT CGGGAGTC GAT
 ||||| ||||| |||
 ACCGA GTCCTCAG CTA
 A AA__
 GAM1987 LENG5 3' GCTGTGTTTTTGTAGTTA 44191 TCCT ATG
 TGGCTGCGGGAG CATAG
 ||||| |||||
 ATTGATGTTTTT GTGTC
 _ GG
 GAM1987 LIPG 3' ATGAAGACTTTTGCAGCCA 21230 C
 TGGCTGCGGGAGTC TCAT
 ||||| ||||| |||||
 ACCGACGTTTTTCAG AGTA
 A
 GAM1987 LNX 3' TGTTTGTGTCTCCTGTGACTA 51914 CT TCCT
 TGG GCGGGAG CATAGATG
 ||| ||||| |||||
 ATC TGTCTC GTGTTTGT
 AG T__
 GAM1987 LYPLA3 3' TGTGCCACAGGACTCCTGTGGC 25565 TG _ GATG
 T GGC CCGGAGTCCT CATA
 ||| ||||| ||||| |||||

			TCG GTCCTCAGGA GTGT			
			GT CACC			
GAM1987	MACF1	5'	GGTTTGGGGATTCTCAGCAGTT 53432	_		TAGATG
			GGCTGC GGGAGTCCTCA			
			TTGACG CTCTTAGGGGT			
			A TTGGC			
GAM1987	MAD4	3'	GTTAGGGCTCCTGGAGCCA 22279	G		C
			TGGCT CGGGAGTCCT AT			
			ACCGA GTCCTCGGGA TG			
			G T			
GAM1987	MAT2B	3'	TATTTTCAGGATTTTTGAAGCT 26128	G		CAT
			GGCT CGGGAGTCCT AGATG			
			TCGA GTTTTTAGGA TTTAT			
			A CT_			
GAM1987	MEP50	3'	TGTCTATGAGGAATTGGCC 44319	GCGGGAG		
			GGCT TCCTCATAGATG			
			CCGG AGGAGTATCTGT			
			TTA__			
GAM1987	MGC15854	5'	CGTTGCGCCCGACTCTCCGCGG 59500	_		CTCATA
			TTA TGGCTGCGG GAGTC GATG			
			ATTGGCGCC CTCAG TTGC			
			T CCCGCG			
GAM1987	MGC16075	5'	CATTTATGTCCTCTGTAGC 52252	G		TCCT
			GCTGCGG AG CATAGATG			
			CGATGTC TC GTATTAC			
			_ CT_			
GAM1987	MGC18079	5'	CATCTCCGAGGGGTCTGTGGC 59032	TG	G	AT
			T GGC CGGGA TCCTC AGATG			
			TCG GTCCT GGGAG TCTAC			
			GT G CC			
GAM1987	MGC2477	5'	TGTGGTTTCCTGCAGTCA 44315	T	T	
			TGGCTGCGGGAG CC CA			
			ACTGACGTCCTT GG GT			
			T T			
GAM1987	MGC26651	3'	CATTTGCATTCTTCTGCAGTC 58950			TCCTCA
			GGCTGCGGGAG TAGATG			
			CTGACGTCTTC GTTTAC			
			TTAC__			
GAM1987	MRPS7	5'	TGTGGGGTCTCGTGGCCA 32557	TG		AGT
			TGGC CGGG CCTCATA			

ACCG GCTC GGGGTGT
 GT CT_
 GAM1987 MYT1 3' CGTTTGC GTGTCGGCTCTTGCG 16978 CT ____
 GT GCTGCGGGAGTC CAT AGATG
 ||||| ||| |||||
 TGGCGTTCTCGG GTG TTTGC
 CT CG
 GAM1987 MYT1L 5' GTCTGTGTATTTTGAGCCA 67366 G GTCCT
 TGGCT CGGGA CATAGAT
 ||||| |||||
 ACCGA GTTTT GTGTCTG
 _ AT____
 GAM1987 NEUROD6 3' TGTTTACTAGTTTCTGCAGT 42995 TC CA
 GCTGCGGGAG CT TAGATG
 ||||| || |||||
 TGACGTCTTT GA ATTTGT
 _ TC
 GAM1987 NPD009 5' CATTTTGCATTCTGCAGTCA 40721 CCT T
 TGGCTGCGGGAGT CA AGATG
 ||||| || |||||
 ACTGACGTCCTTA GT TTTAC
 C__ _
 GAM1987 NXPH3 3' TGTTTATGGGGACGGAGGCAGC 66350 GGGA
 T GGCTGC GTCCTCATAGATG
 ||||| |||||
 TCGACG CAGGGGTATTTGT
 GAGG
 GAM1987 OCIA 5' TGTCTGGATGACTTCTTGCGGC 35656 _ C A
 T GGCTGCGGGA GTC TC TAGATG
 ||||| ||| || |||||
 TCGGCGTTCT CAG AG GTCTGT
 T T _
 GAM1987 OSBPL6 3' TATCGCAGGACTCCTGGGCCA 51687 G CATA
 TGGCT CGGGAGTCCT GATG
 ||||| ||||| |||||
 ACCGG GTCCTCAGGA CTAT
 _ CG__
 GAM1987 p25 3' TGTCTGTGGGGGTTTCTCTGCC 23840 TGC GT
 A TGGC GGGA CCTCATAGATG
 ||||| ||||| |||||
 ACCG TCTT GGGGTGTCTGT
 TC_ TG
 GAM1987 PADI1 3' GTCCGTGGTTCCTGGGCT 62705 G TCC TA
 GGCT CGGGAG TCA GAT
 ||||| ||||| ||| |||
 TCGG GTCCTT GGT CTG
 _ _ GC
 GAM1987 PGRMC2 3' CATCAAGGGACTCCTGTGTCA 21977 T CATA
 TGGC GCGGGAGTCCT GATG
 ||||| ||||| ||||| |||||

ACTG TGTCTCAGGG CTAC
 _ AA_
 GAM1987 PIK3C3 5' CATTATGTTGTTTTCCTGTA 60553 C TCCT_
 CC GG TCGGGAG CATAGATG
 || ||||| |||||
 CC ATGTCCTT GTATTAC
 _ TTTGTT
 GAM1987 POLR2J2 3' CGTCTGCCCCATGGGACTTCTG 60006 T ____
 TAGT GCTGCGGGAGTCC CAT AGATG
 ||||| || |||||
 TGATGTCTTCAGG GTA TCTGC
 _ CCCC
 GAM1987 PRC1 3' CATCTCCCCATTCTGTGCC 15626 T CCTCAT
 GGC GCGGGAGT AGATG
 || ||||| |||||
 CCG TGTCTTA TCTAC
 _ CCCCC_
 GAM1987 PRO0461 3' TATTAGAGCTGCTGTAGCT 49210 G TC A
 GGCTGCGG AG CTC TAGATG
 ||||| || |||||
 TCGATGTC TC GAG ATTTAT
 G _ _
 GAM1987 PRO1596 3' TATTGTTTCCATTTTGTGCC 49222 T CCTC
 A TGGC GCGGGAGT ATAGATG
 |||| ||||| |||||
 ACCG TGTTTTTA TGTTTAT
 _ CCTT
 GAM1987 PRO1855 3' TGTCTATGACAGCTCTAGTT 38146 GCG CC
 GGCT GGAGT TCATAGATG
 |||| |||| |||||
 TTGA TCTCG AGTATCTGT
 _ AC
 GAM1987 PSR 3' CATTTTGCTGTATTCTTGCAGC 65780 CCTCAT
 T GGCTGCGGGAGT AGATG
 ||||| |||||
 TCGACGTTCTTA TTTAC
 TGTCGT
 GAM1987 PTK6 3' TGTCTGTGGGGTGGTTCCGGGC 21083 G GT_
 T GGCT CGGGA CCTCATAGATG
 |||| |||| |||||
 TCGG GCCTT GGGGTGTCTGT
 _ GGT
 GAM1987 RAB14 3' ATTTATGATTCAGTGGCT 33332 TG GG TCC
 GGC C GAG TCATAGAT
 || | || |||||
 TCG G CTT AGTATTTA
 GT A_ _
 GAM1987 RAB14 3' CATTATCTTCTCTCTCGTGCT 33333 T TCCTC
 GGC GCGGGAG ATAGATG
 || ||||| |||||

			TCG TGCTCTC	TATTTAC		
			—	TCTTC		
GAM1987	RGS17	3'	ATGGGGATTCTCTGGTT	25771	C	
			GGCTG GGGAGTCCTCAT			
			TTGGT TCCTTAGGGGTA			
			C			
GAM1987	RNF38	3'	TGTCTGCCTCTTCCTGCAGTT	43263		TCCTCA
			GGCTGCGGGAG	TAGATG		
			TTGACGTCCTT	GTCTGT		
			CTCC—			
GAM1987	SCYA22	3'	ATCTATGCCTTTCTGGCT	92579	C GG	TCCT
			GGCTG G AG	CATAGAT		
			TCGGT C TC	GTATCTA		
			— TT C—			
GAM1987	SDS3	3'	GATGGATTTCTGTAGCCA	69748		—
			TGGCTGCGGGAGTCC	TC		
			ACCGATGTCTTTAGG	AG		
			T			
GAM1987	SEEK1	5'	CGTCTCAAATAGACTCTGCAGC	26808	G	CTCAT—
	CA		TGGCTGCGG	AGTC	AGATG	
			ACCGACGTC	TCAG	TCTGC	
			—	ATAAAC		
GAM1987	SEF	3'	ATCAAGTTTCTTGCAGCT	69994		TC CATA
			GGCTGCGGGAG	CT	GAT	
			TCGACGTTCTT	GA	CTA	
			T_ A—			
GAM1987	SGK2	5'	CATCTTGGACTTCTGGAGCTA	33250	G	TCAT
			TGGCT CGGGAGTCC	AGATG		
			ATCGA GTCTTCAGG	TCTAC		
			G	T—		
GAM1987	SH120	3'	GTCTATGGTAGCTGAGCCA	33392	G	GAGTCC
			TGGCT CGG	TCATAGAT		
			ACCGA GTC	GGTATCTG		
			—	GAT—		
GAM1987	SIRPB1	3'	ATCTGAAGTTCCTGCATCA	21356	C	TC CA
			TGG TGCGGGAG	CT	TAGAT	
			ACT ACGTCCTT	GA	GTCTA	
			—	— A—		
GAM1987	SLC19A3	3'	CATCTATGGGCCAGGTGCAGT	48240		GGAGTC
			GCTGCG	CTCATAGATG		

TGACGT GGGTATCTAC
 GGACC_
 GAM1987 SLC38A1 5' CATTTTCCCGGCCTCCGCAGCC 48421 GA CTCAT
 A TGGCTGCGG GTC AGATG
 ||||| ||| ||||
 ACCGACGCC CGG TTTAC
 TC CCCT_
 GAM1987 SLC39A3 5' CGTCTGTGGGGTCGAGACTGCG 58601 GG ____
 CGGCC GGCTGCG AGT CCTCATAGATG
 ||||| ||| |||||
 CCGGCGC TCA GGGGTGTCTGC
 G_ GAGCT
 GAM1987 SLC5A6 3' CATCTATCTACCTGACTCCTGA 41177 G CTC____
 GCCA TGGCT CGGGAGTC ATAGATG
 |||| ||||| |||||
 ACCGA GTCCTCAG TATCTAC
 _ TCCATC
 GAM1987 SLK 3' TGTCTGTAGCACTTTCTTGCAG 28892 _ C C
 TTA TGGCTGCGGGA GT CT ATAGATG
 ||||| || || |||||
 ATTGACGTTCT CA GA TGTCTGT
 TT C _
 GAM1987 SPRY1 3' TATTTGTGAAGGACTCAGCCA 65635 GCGG _
 TGGCT GAGTCCT CATAGATG
 |||| ||||| |||||
 ACCGA CTCAGGA GTGTTTAT
 _ A
 GAM1987 SQRDL 3' CATCTTGATGGCTTCTGGGCC 41348 G C AT
 A TGGCT CGGGAGTC TC AGATG
 |||| ||||| || |||||
 ACCGG GTCTTCGG AG TCTAC
 _ T GT
 GAM1987 SSR3 3' TGTCTATGGGTGGCCTGTGGT 24041 TG AGT T
 GC CGGG CC CATAGATG
 || |||| || |||||
 TG GTCC GG GTATCTGT
 GT GGT _
 GAM1987 STARD7 3' ATTTGTGGGAGTGTTGTCA 39736 T GGAG T
 TGGC GCG TCC CATAGAT
 |||| ||| ||| |||||
 ACTG TGT AGG GTGTTTA
 T G_____
 GAM1987 STIP-1 3' ATTTGTGTGCCTCTGGTCA 70237 C AGTCCT
 TGGCTG GGG CATAGAT
 ||||| ||| |||||
 ACTGGT TCC GTGTTTA
 C GT_____
 GAM1987 TCBAP0758 3' AGAATGAGGGTTCCCCAGCC 49096 C GT AGATG
 GGCTG GGGG CCTCAT
 |||| |||| |||||

CCGAC CCCT GGAGTA
 C TG AGAA
 GAM1987 TRIM4 5' CGTCTGGCCTCCCCGCGGCC 53406 _ T TCAT
 GGCTGCGGG AG CC AGATG
 ||||| || || ||||
 CCGGCGCCC TC GG TCTGC
 C C ____
 GAM1987 VMP 3' ATTTATGCCCGTGGTTA 55759 TG AGTCCT G
 TGGC CGGG CATAGAT
 ||| ||| |||||
 ATTG GCCC GTATTTA
 GT _____ G
 GAM1987 VMP 3' TGTTTGTGATGTTTTGTGGCT 55766 TG TCC
 GGC CGGGAG TCATAGATG
 || ||||| |||||
 TCG GTTTTT AGTGTGTGT
 GT GT_
 GAM1987 XT2 3' TGTCTGTGGGAGCAGTGGCT 42477 TG GGGAG
 GGC C TCCTCATAGATG
 || | |||||
 TCG G AGGGGTGTCTGT
 GT ACG_
 GAM1987 YAP1 3' CATTTGTGTTATTTTCAGTCA 21458 CG CCT
 TGGCTG GGAGT CATAGATG
 |||| ||| |||||
 ACTGAC TTTTA GTGTTTAC
 _ TT_
 GAM1987 ZNF213 3' CATCTGTGGCCACCTCCCGGGC 65697 G TCC_
 T GGCT CGGGAG TCATAGATG
 ||| ||||| |||||
 TCGG GCCCTC GGTGTCTAC
 _ CACC
 GAM1987 ZNF304 3' CATCTGTATCTCCTGTGGCCA 40680 TG TCCTC
 TGGC CGGGAG ATAGATG
 ||| ||||| |||||
 ACCG GTCCTC TGTCTAC
 GT TA_
 GAM1987 LOC113386 3' TGTCTGTCTCATTTCTGCATTC 57870 GC CCTC
 G TGCGGGAGT ATAGATG
 | ||||| |||||
 C ACGTCTTTA TGTCTGT
 TT CTC_
 GAM1987 LOC115219 3' CATTTATGGGGACTGGGAAGTC 73692 _ GCGGG
 CA TGG CT AGTCCTCATAGATG
 ||| || |||||
 ACC GA TCAGGGGTATTTAC
 T AGGG_
 GAM1987 LOC116068 3' TATTTGAAAGCACTTTTGTAGT 74108 C CA
 T GGCTGCGGGAGT CT TAGATG
 ||||| || |||||

		TTGATGTTTTCA GA GTTTAT		
		C AA		
GAM1987	LOC116113 3'	CGTTTGCTGGGGGCTCCTCCAG 93835	C	_
	CC	GGCTG GGGAGTCCTCA TAGATG		
		CCGAC TCCTCGGGGGT GTTTGC		
		C C		
GAM1987	LOC119188 5'	GTCTATGAGTGTGCAGACA 74403	G	GGAGTC
		TG CTGCG CTCATAGAT		
		AC GACGT GAGTATCTG		
		A GT____		
GAM1987	LOC122786 3'	TGTCTGTGCTGTCCCTCCTGTG 74624	T	TCCT__
	CT	GGC GCGGGAG CATAGATG		
		TCG TGTCTC GTGTCTGT		
		_ CCTGTC		
GAM1987	LOC126364 3'	TGTTTGTGGGCCAGCCAGCAGC 76203	G	AGTC
	C	GGCTGC GG CTCATAGATG		
		CCGACG CC GGGTGTGTTGT		
		A GACC		
GAM1987	LOC127262 3'	TATCTCGAGTGCCTGCAGTT 76604	AGTC	AT
		GGCTGCGGG CTC AGATG		
		TTGACGTCC GAG TCTAT		
		GT__ C_		
GAM1987	LOC127702 3'	CATCTGTGGGGGCTTCCTCTCC 75984	CTGC	
		GG GGGAGTCCTCATAGATG		
		CC CCTTCGGGGGTGTCTAC		
		TCT_		
GAM1987	LOC128844 5'	ATCTGTGTCCCCGCTGTT 76294	T	AGTCCT
		GGC GCGGG CATAGAT		
		TTG CGCCC GTGTCTA		
		T CT____		
GAM1987	LOC130612 3'	TGTCTATGGGGCAAAGTGTAGC 75475	GAGT	
		GCTGCGG CCTCATAGATG		
		CGATGTC GGGGTATCTGT		
		AAAC		
GAM1987	LOC130612 3'	TGTCTGTCTAGACTCTGCAGTC 75476	G	CTC
	A	TGGCTGCGG AGTC ATAGATG		
		ACTGACGTC TCAG TGTCTGT		
		_ ATC		
GAM1987	LOC132112 3'	ATTTAAGATTTTGTACCA 75531	C	CTCA
		TGG TGCGGGAGTC TAGAT		

	ACC ATGTTTTTAG	ATTTA		
	— A —			
GAM1987	LOC132617 3'	TATGATGGATTCCTGAGCTA	76420	G —
		TGGCT CGGGAGTCC TCATA		
		ATCGA GTCCTTAGG AGTAT		
		— T		
GAM1987	LOC136288 5'	CATCTGTCTTTTCCCGCAGC	75767	TCCTC
		GCTGCGGGAG ATAGATG		
		CGACGCCCTT TGTCTAC		
		TTC —		
GAM1987	LOC142893 5'	CATTTGTGGAAATCTGCAGT	83758	AG TC
		GCTGCGGG TCC ATAGATG		
		TGACGTCT AGG TGTTTAC		
		AA —		
GAM1987	LOC142955 5'	GTTTGTGGGCTACAGCCA	76964	CG GAGTC
		TGGCTG G CTCATAGAT		
		ACCGAC C GGGTGTTTG		
		AT —		
GAM1987	LOC142955 3'	TATCCCTTGAGGACTTCTGTGC	76965	T TA_
	T	GGC GCGGGAGTCCTCA GATG		
		TCG TGTCTTCAGGAGT CTAT		
		— TCC		
GAM1987	LOC143497 5'	CATCTGTGATCCACTGCACTA	77085	C GAGTCC
		TGG TGCGG TCATAGATG		
		ATC ACGTC AGTGTCTAC		
		— ACCT —		
GAM1987	LOC143828 3'	TATTTGTCATAGACTTTTGAGT	73186	G CTC_
	T	GGCT CGGGAGTC ATAGATG		
		TTGA GTTTTCAG TGTTTAT		
		— ATAC		
GAM1987	LOC145225 3'	CATTTATGAAGCCCTGGGCT	84264	G A CC
		GGCT CGGG GT TCATAGATG		
		TCGG GTCC CG AGTATTTAC		
		— _ A_		
GAM1987	LOC145501 3'	CATTTGGGCAGCTTCTGTGGT	77764	TG CC A
		GC CGGGAGT TC TAGATG		
		TG GTCTTCG GG GTTTAC		
		GT AC —		
GAM1987	LOC145508 3'	ATTTGTCTTTTGTGGCCA	77775	TG TCCTC
		TGGC CGGGAG ATAGAT		

	ACCG GTTTTT TGTTTA	
	GT C____	
GAM1987 LOC145601 3'	TATCTGTGGCTGGTTTTAGCCA 84355	CGG T ____
	TGGCTG GAG CC TCATAGATG	
	ACCGAT TTT GG GGTGTCTAT	
	____ _ TC	
GAM1987 LOC145624 5'	CATCTGTTTCTCTCATTGTAGT 84401	_ TCCTC
TA	TGGCTGCGG GAG ATAGATG	
	ATTGATGTT CTC TGTCTAC	
	A TCTT_	
GAM1987 LOC145815 3'	TGGGGTTTTTGCCTA 84525 T T	
	TGGC GCGGGAG CCTCA	
	ATCG CGTTTTT GGGGT	
	____ _	
GAM1987 LOC145826 5'	AGCCTGGGGTTTTTATGGTCA 84526	CG T TAGATG
	TGGCTG GGAG CCTCA	
	ACTGGT TTTT GGGGT	
	AT _ CCGAG	
GAM1987 LOC145845 3'	CATTTAACATAATCCTTGCAGC 84545	_ GTCCTCA
TA	TGGCTGCG GGA TAGATG	
	ATCGACGT CCT ATTTAC	
	T AATACA_	
GAM1987 LOC146083 5'	TGTCTGTGTCAGATTTGTAGCT 84585	GG CT_
	GGCTGC GAGTC CATAGATG	
	TCGATG TTTAG GTGTCTGT	
	____ ACT	
GAM1987 LOC146108 5'	CGTCTCACGGTCCCGCGGCCA 78149	GT TCAT
	TGGCTGCGGGA CC AGATG	
	ACCGGCGCCCT GG TCTGC	
	____ CAC_	
GAM1987 LOC146226 5'	TGTTTGGACCAGTTCTTGCC 84599	T ____ TC GATG
A	TGGC GCGGGA GTCC ATA	
	ACCG TGTCT CAGG TGT	
	_ TGAC TT G	
GAM1987 LOC146272 3'	TATCCATGGCTCCTGCAGCC 78331	CCT A
	GGCTGCGGGAGT CAT GATG	
	CCGACGTCCTCG GTA CTAT	
	____ C	
GAM1987 LOC146517 3'	ATCTGGGTCTTTGCAGCT 78504	G T CAT
	GGCTGCGG AG CCT AGAT	

		TCGACGTT TC GGG TCTA		
		_ T _		
GAM1987	LOC146669 3'	CATCTCGCTCACCCCTGTAGCC 78659	A	CCTCAT
	A	TGGCTGCGGG GT AGATG		
		ACCGATGTCC CA TCTAC		
		C CTCGC_		
GAM1987	LOC146856 5'	CATTTAAGCATTCCTGTGGC 83699	TG	C CA
		GC CGGGAGT CT TAGATG		
		CG GTCCTTA GA ATTTAC		
		GT C _		
GAM1987	LOC147080 3'	TGTTTGTGCACAACTTCAGCCA 85054	C	GA CCT
		TGGCTG GG GT CATAGATG		
		ACCGAC TC CA GTGTTTGT		
		T AA C_		
GAM1987	LOC147343 5'	CGTCTGGCCCTCACTGTGGCTA 85126	TG	_ TC CAT
		TGGC CGG GAG CT AGATG		
		ATCG GTC CTC GG TCTGC		
		GT A CC _		
GAM1987	LOC147463 3'	CATCTATGCATGTTTTTGAGTT 79003	G	TCCT
		GGCT CGGGAG CATAGATG		
		TTGA GTTTTT GTATCTAC		
		_ GTAC		
GAM1987	LOC147837 5'	GTCTGTGTAGCCTCAGTC 79207	C	AGTCCT
		GGCTG GGG CATAGAT		
		CTGAC TCC GTGTCTG		
		_ GAT_		
GAM1987	LOC148398 3'	TGTGGGGCTTCAGCAGCCA 79575	G	T
		TGGCTGC GGAGTCC CATA		
		ACCGACG CTTCTGGG GTGT		
		A _		
GAM1987	LOC148764 5'	CGTCCCTGGTTCCTGCAGCT 79736	T	TCATA
		GGCTGCGGGAG CC GATG		
		TCGACGTCCTT GG CTGC		
		_ TCC_		
GAM1987	LOC148809 3'	CATCTCAAGACTTTTGTACC 79749	C	CTCAT
		GG TGCGGGAGTC AGATG		
		CC ATGTTTTCAG TCTAC		
		_ AAC_		
GAM1987	LOC149401 5'	CATCTTGACAGAGGAGCTTCTG 80111	_	AT_
	CAGTT	GGCTGCGGGAG TCCTC AGATG		

	TTGACGTCTTC AGGAG TCTAC	
	G ACAGT	
GAM1987 LOC149414 5'	CGTCTGGGGCCCCCGCGGCT 85571	A CAT
	GGCTGCGGG GTCCT AGATG	
	TCGGCGCCC CGGGG TCTGC	
	C ____	
GAM1987 LOC149420 3'	ATCTATGTGCTTGGAGCCA 80153	G AGTCCT
	TGGCT CGGG CATAGAT	
	ACCGA GTTC GTATCTA	
	G GT____	
GAM1987 LOC149670 3'	GTGAGGGTCCTGCAGTCA 80308	G
	TGGCTGCGGGA TCCTCAT	
	ACTGACGTCCT GGGAGTG	
	—	
GAM1987 LOC149684 5'	CTCTGCCTGGACTCCTGCGG 85763	TCA TG
	CTGCGGGAGTCC TAGA	
	GGCGTCCTCAGG GTCT	
	TCC CT	
GAM1987 LOC149705 3'	TGTGGATTCTTGTAGCTA 85790	T
	TGGCTGCGGGAGTCC CA	
	ATCGATGTTCTTAGG GT	
	T	
GAM1987 LOC149837 5'	TGTGCTGCGGGCATCCTGTGGT 85911	TG _ T TAGATG
CA	TGGC CGGGA GTCC CA	
	ACTG GTCCT CGGG GT	
	GT A C CGTGT	
GAM1987 LOC149935 3'	TGTCTGTGAGCCAGTTCAGCT 60938	C AGTC
	GGCTG GGG CTCATAGATG	
	TCGAC CTT GAGTGTCTGT	
	_ GACC	
GAM1987 LOC150211 5'	CATCTGTGACTGAGTCACAGTC 80628	CGG G C_
A	TGGCTG GA TC TCATAGATG	
	ACTGAC CT AG AGTGTCTAC	
	A_ G TC	
GAM1987 LOC150481 3'	CTTCCTGGGGGCCTCCTGTGGT 80700	TG _ TAGATG
T	GGC CGGGAG TCCTCA	
	TTG GTCCTC GGGGGT	
	GT C CCTTCA	
GAM1987 LOC151171 5'	CATCAGGCAGGGCTCCTGAGCC 80945	G CATA
A	TGGCT CGGGAGTCCT GATG	

ACCGA GTCCTCGGGA CTAC
 _ CGGA
 GAM1987 LOC151473 3' CATCTCTAGACTCTCGTGTT 81050 T CTCAT
 GGC GCGGGAGTC AGATG
 ||| ||||| ||||
 TTG TGCTCTCAG TCTAC
 _ ATC_
 GAM1987 LOC151473 3' TTTTATGAGGGAATTCTGCAG 81053 G_ TG
 CTA TGGCTGCGGGA TCCTCATAGA
 ||||| |||||
 ATCGACGTCTT GGGAGTATTT
 AA TTA
 GAM1987 LOC151568 5' CATCTGTGAGGTGGAGGGCT 57492 GCGGGA T
 GGCT G CCTCATAGATG
 ||| | |||||
 TCGG T GGAGTGTCTAC
 GAGG_
 GAM1987 LOC152343 5' TATCTAAATGTATTCTTGTAAC 81435 C CCTCA
 CA TGG TGCGGGAGT TAGATG
 ||| ||||| ||||
 ACC ATGTTCTTA ATCTAT
 A TGTA
 GAM1987 LOC152453 5' CGTTTGTGAGGGCCAGGCT 81471 GCGGGA
 GGCT GTCCTCATAGATG
 ||| |||||
 TCGG CGGGAGTGTTTGC
 AC_
 GAM1987 LOC152667 3' CATCTGTGGCCTGAATCGTGT 81522 G G C_
 GCG GA TC TCATAGATG
 ||| || |||||
 TGT CT AG GGTGTCTAC
 G A TCC
 GAM1987 LOC152926 5' CATCTGTGACTGGCTGCGATC 81630 GC GAGT _
 G TGCGG CC TCATAGATG
 | |||| || |||||
 C GCGTC GG AGTGTCTAC
 TA _ TC
 GAM1987 LOC153020 5' CATTTGTGGGCGCGCGGC 81646 GGA T T
 GCTGCG G CC CATAGATG
 |||| | || |||||
 CGGCGC C GG GTGTTTAC
 G_ _
 GAM1987 LOC153416 3' CATTTTCAGGCTTCTGCAGCT 61157 T CAT
 GGCTGCGGGAG CCT AGATG
 ||||| || |||||
 TCGACGTCTTC GGA TTTAC
 _ CT_
 GAM1987 LOC153688 5' CATCTTTCAGTCCTGCAGCT 87301 GTC CAT
 GGCTGCGGGA CT AGATG
 ||||| || |||||

TCGACGTCCT GA TCTAC
 ____ CTT

GAM1987 LOC154141 5' TGTCTATGAGTGCTTTTGCACT 87387 C TC
 A TGG TGC GGGAG CTCATAGATG
 ||| ||||| |||||
 ATC ACGTTTTC GAGTATCTGT
 _ GT

GAM1987 LOC154739 5' CATCTAACTGTATTTTTGTGCC 87433 T CCTCA
 GGC GCGGGAGT TAGATG
 ||| ||||| |||||
 CCG TGTTTTTA ATCTAC
 _ TGTC A

GAM1987 LOC155004 5' CGTTTGAAAGGATTTCTCAGCC 82156 C CA
 GGCTG GGGAGTCCT TAGATG
 |||| ||||| |||||
 CCGAC TCTTTAGGA GTTTGC
 _ AA

GAM1987 LOC155179 3' CGTTTGCTCTCCCGTGGCT 82228 TG TCCTCA
 GGC CGGGAG TAGATG
 ||| ||||| |||||
 TCG GCCCTC GTTTGC
 GT TC____

GAM1987 LOC155434 3' CATTTGTGTGATTTTCGTACCA 87688 C G CT
 TGG TGCGG AGTC CATAGATG
 ||| ||||| ||||| |||||
 ACC ATGCT TTAG GTGTTTAC
 _ _ T_

GAM1987 LOC157653 5' CATTTAAAGATTTCTGAGCTA 82442 G CTCA
 TGGCT CGGGAGTC TAGATG
 |||| ||||| |||||
 ATCGA GTCTTTAG ATTTAC
 _ AA__

GAM1987 LOC157918 3' TGTCTGTGGACGTGCGTGGCT 87934 TG GGA TC
 GGC CG GTCC ATAGATG
 ||| || ||||| |||||
 TCG GC CAGG TGTCTGT
 GT GTG _

GAM1987 LOC158116 3' CATTTAATTTTCTGTGGTT 60949 TG TCCTCA
 GGC CGGGAG TAGATG
 ||| ||||| |||||
 TTG GTCCTT ATTTAC
 GT TTA____

GAM1987 LOC158191 3' CTTCTGGGGGCTCCTGTGGT 82673 TG _ TAGATG
 T GGC CGGGAG TCCTCA
 ||| ||||| |||||
 TTG GTCCTC GGGGGT
 GT C CCTTCA

GAM1987 LOC158377 5' ATGGGACCCCGTGGTCA 88130 TG A T
 TGGC CGGG GTCC CAT
 |||| ||||| ||||| |||||

	ACTG GCCC CAGG GTA		
	GT _ _		
GAM1987 LOC158431 3'	ATGAAGGGTTTTCCGTGGCTA 88165	TG	_ GT _
	TGGC CGGG A CCT CAT		
	ATCG GCCT T GGA GTA		
	GT TTG A		
GAM1987 LOC159110 3'	TGTGGGGTTATTCGTAGCTA 82997	AGT	
	TGGCTGCGGG CCTCATA		
	ATCGATGCTT GGGGTGT		
	ATT		
GAM1987 LOC159116 3'	TGTGGGGTTATTCGTAGCTA 82980	AGT	
	TGGCTGCGGG CCTCATA		
	ATCGATGCTT GGGGTGT		
	ATT		
GAM1987 LOC166765 3'	TATTTATGTAGCAACTTTTGTG 83548	T	C_ _
CCA	TGGC GCGGGAGT CT CATAGATG		
	ACCG TGTTTTCA GA GTATTTAT		
	_ AC T		
GAM1987 LOC168448 3'	TATTTATGGCCAGTTTTGGGGC 83583	G	GTCC
CA	TGGCT CGGGA TCATAGATG		
	ACCGG GTTTT GGTATTTAT		
	G GACC		
GAM1987 LOC170082 3'	TATTTATATTGTGCCTTGTGGC 83450	TG	A CCTC_
CA	TGGC CGGG GT ATAGATG		
	ACCG GTTC CG TATTTAT		
	GT _ TGTTA		
GAM1987 LOC170132 5'	TGTCTGCCTCTGGTTCCTGCAT 83464	C	T TCA__
CA	TGG TGCGGGAG CC TAGATG		
	ACT ACGTCCTT GG GTCTGT		
	_ _ TCTCC		
GAM1987 LOC196047 5'	CATCTTGGGCTTTGGTGGCT 91147	TG G	TCAT
	GGC C GGAGTCC AGATG		
	TCG G TTTCGGG TCTAC		
	GT G T__		
GAM1987 LOC196337 5'	CATCCTGGGGGAGTTTCGCAGC 89021	GG G	ATA
TA	TGGCTGCG A TCCTC GATG		
	ATCGACGC T AGGGG CTAC		
	TT G GTC		
GAM1987 LOC196411 3'	GTCTGTGTGCCTGTATCA 89050	C	AGTCCT
	TGG TGCGGG CATAGAT		

	ACT ATGTCC	GTGTCTG		
	— GT —			
GAM1987	LOC196477 3'	CATTTGCAGGCTCTTGTGTCA	89063	T T CA
		TGGC GCGGGAG CCT TAGATG		
		ACTG TGTTCTC GGA GTTTAC		
		— — C —		
GAM1987	LOC199676 3'	GTGAGGGTTCCTGTGAGCC	91361	— GT
		GGCT GCGGGA CCTCAT		
		CCGA TGTCCT GGAGTG		
		G TG		
GAM1987	LOC199718 5'	CATCTACAGAAGGCCCTGCAGC	89704	A C A —
	TA	TGGCTGCGGG GTC TC TAGATG		
		ATCGACGTCC CGG AG ATCTAC		
		— A AC		
GAM1987	LOC199729 3'	TATCTACCTGTACTTTTGCATC	73396	C CCTCA
	CA	TGG TGCGGGAGT TAGATG		
		ACC ACGTTTTCA ATCTAT		
		T TGTCC		
GAM1987	LOC199848 5'	CATCTGGCAGCTCTCGCACTCA	91453	GC CCTCA
		TG TGCGGGAGT TAGATG		
		AC ACGCTCTCG GTCTAC		
		TC ACG —		
GAM1987	LOC199858 3'	GTCTGTGAGGGTGTTGCCA	89800	T GGAG
		TGGC GCG TCCTCATAGAT		
		ACCG TGT GGGAGTGTCTG		
		T —		
GAM1987	LOC200169 3'	CGTTTGTGAACATTCTTGGAGC	91554	G CC
	T	GGCT CGGGAGT TCATAGATG		
		TCGA GTTCTTA AGTGTTTGC		
		G CA		
GAM1987	LOC200325 5'	GTCTCGGTTTCCTGCGGCC	91579	T TCAT
		GGCTGCGGGAG CC AGAT		
		CCGGCGTCCTT GG TCTG		
		— C —		
GAM1987	LOC200609 5'	TCTAAGATTTTTGTAGTT	91669	CTCA
		GGCTGCGGGAGTC TAGA		
		TTGATGTTTTTAG ATCT		
		A —		
GAM1987	LOC200779 5'	TGTGGGCTTTCTGCGGCC	90291	— T
		GGCTGCGGGA GTCC CA		

		CCGGCGTCTT CGGG GT		
		T T		
GAM1987	LOC200940 5'	CATCTGTGCTCTGGCCCCTGGC 90389	C A	CT__
	CA	TGGCTG GGG GTC CATAGATG		
		ACCGGT CCC CGG GTGTCTAC		
		_ _ TCTC		
GAM1987	LOC201283 3'	CATTTGTGAATACTCTGCACTA 61049	C G	CC
		TGG TGCGG AGT TCATAGATG		
		ATC ACGTC TCA AGTGTTTAC		
		_ _ TA		
GAM1987	LOC202025 5'	TATCTGTGCACAATTTTGTGCC 91891	T	GTCCT
	A	TGGC GCGGGA CATAGATG		
		ACCG TGTTTT GTGTCTAT		
		_ AACAC		
GAM1987	LOC202134 5'	CATTTGCCACCTTTTGCAGTT 91918		TCCTCA
		GGCTGCGGGAG TAGATG		
		TTGACGTTTTC GTTTAC		
		CACC__		
GAM1987	LOC202181 5'	CGTCTGTGAAAACCCACAGCT 90636	C A	CC
	A	TGGCTG GGG GT TCATAGATG		
		ATCGAC CCC CA AGTGTCTGC		
		A _ AA		
GAM1987	LOC202934 3'	TATCTGTGTTCTCTTGTATCT 92053	C	TCCT
		GG TGCGGGAG CATAGATG		
		TC ATGTTCTC GTGTCTAT		
		T TT__		
GAM1987	LOC203276 3'	CATCTAACTGTATTTTTGTGTC 92114	C	CCTCA
	CA	TGG TGCGGGAGT TAGATG		
		ACC GTGTTTTTA ATCTAC		
		T TGTCA		
GAM1987	LOC203305 3'	CATCTAACTGTATTTTTGTGTC 92167	C	CCTCA
	CA	TGG TGCGGGAGT TAGATG		
		ACC GTGTTTTTA ATCTAC		
		T TGTCA		
GAM1987	LOC203378 5'	CATCTATGAAGTCCCACAGCT 92284	C	GTCC
		GGCTG GGGA TCATAGATG		
		TCGAC CCCT AGTATCTAC		
		A GA__		
GAM1987	LOC203378 5'	TATTTATGGAACACTTCCTGTG 92301	T	_ CC_
	CCA	TGGC GCGGGA GT TCATAGATG		

	ACCG TGCCT CA GGTATTTAT		
	— T CAA		
GAM1987 LOC203523 3'	TGTCTATGGGGTTCTCTGCAG 90941	—	GT
	CTGCGG GA CCTCATAGATG		
	GACGTC CT GGGGTATCTGT		
	T TG		
GAM1987 LOC219401 5'	GTTTTATCCTGGGGCACTTGTA 94387	A C—	TG
	GTCA TGGCTGCGGG GTCCT ATAGA		
	ACTGATGTTT CCGGG TATTT		
	A TCC TGT		
GAM1987 LOC219404 3'	TATTTATGAAAAGCTGTAGCC 95149		GAGTCC
	GGCTGCGG TCATAGATG		
	CCGATGTC AGTATTTAT		
	GAAA—		
GAM1987 LOC219594 3'	TGTCTTCCAGCCTCCTGCAGTC 92460		TC CAT
	A TGGCTGCGGGAG CT AGATG		
	ACTGACGTCCTC GA TCTGT		
	C_ CCT		
GAM1987 LOC219627 3'	TATCTGGTGGCTTTTGTATC 93811	C	T TCA
	GG TGCGGGAG CC TAGATG		
	CT ATGTTTTT C GG GTCTAT		
	— — TG—		
GAM1987 LOC220110 5'	TATTTAAAAGACTTCTGCATC 95116	C	CTCA
	GG TGCGGGAGTC TAGATG		
	CT ACGTCTTCAG ATTTAT		
	— AAA—		
GAM1987 LOC220370 3'	CATAGGAGGATTTTCCAGCCA 94396	C GG	ATAG
	TGGCTG G AGTCCTC ATG		
	ACCGAC C TTAGGAG TAC		
	— TT GA—		
GAM1987 LOC220477 5'	CATTATAATGGGCTTTTGCATC 76503	C	TCATA
	GG TGCGGGAGTCC GATG		
	TC ACGTTTTTCGGG TTAC		
	— TAATA		
GAM1987 LOC221543 5'	AACCTGGGGTTTCTGGGCTA 95352	G T	TAGATG
	TGGCT CGGGAG CCTCA		
	ATCGG GTCTTT GGGGT		
	— — CCAAG		
GAM1987 LOC221663 3'	CATTTGTGACATTTGTAGT 95457	A	CTC
	GCTGCGGG GTC ATAGATG		

	TGATGTTT CAG TGTTTAC		
	A ____		
GAM1987 LOC221692 3'	TGTCTGTCTCTCAGGATTCCCA 93862	C	C ____
	CAGCT GGCTG GGGAGTCCT ATAGATG		
	TCGAC CCCTTAGGA TGTCTGT		
	A CTCTC		
GAM1987 LOC221814 5'	TATTTGTGAGTGTGTAGTCA 95561	GGAGTC	
	TGGCTGCG CTCATAGATG		
	ACTGATGT GAGTGTTTAT		
	GT ____		
GAM1987 LOC221927 5'	TGTTTGTGGCCTCGGCGGCCA 94223	G GA CCT	
	TGGCTGC G GT CATAGATG		
	ACCGGCG C CG GTGTTTGT		
	G TC ____		
GAM1987 LOC222234 3'	TATCTGACTTCTTCTGCAGCCA 95902	TCCTCA	
	TGGCTGCGGGAG TAGATG		
	ACCGACGTCTTC GTCTAT		
	TTCA ____		
GAM1987 LOC253287 5'	CATCCAGTGGGTTTCTGCAGCT 99351	GT TCATA	
	GGCTGCGGGA CC GATG		
	TCGACGTCTT GG CTAC		
	TG TGAC ____		
GAM1987 LOC253613 3'	TGTGGAATTTCTGCGGTTA 97920	_ T	
	TGGCTGCGGGAGT CC CA		
	ATTGGCGTCTTTA GG GT		
	A T		
GAM1987 LOC253983 3'	CGTTTGTGGGGACCTCCTGGTC 98428	C GA	
A	TGGCTG GG GTCCTCATAGATG		
	ACTGGT CC CAGGGGTGTTTGC		
	_ TC		
GAM1987 LOC254115 5'	TATCTGCTCACTCCTGTGGCC 96372	TG CCTCA	
	GGC CGGGAGT TAGATG		
	CCG GTCCTCA GTCTAT		
	GT CTC ____		
GAM1987 LOC254170 3'	TGTAGAATTCCTGTGGTTA 96599	TG C _	
	TGGC CGGGAGT CT CA		
	ATTG GTCCTTA GA GT		
	GT A T		
GAM1987 LOC254243 3'	CATCTAACTGTATTTTGTGTC 99253	C CCTCA	
CA	TGG TGCGGGAGT TAGATG		

ACC GTGTTTTTA ATCTAC
 T TGTCA
 GAM1987 LOC254423 3' AGACTGGGTGCTCTTGCAGCCA 99299 TC TAGATG
 TGGCTGCGGGAG CTCA
 ||||| ||||
 ACCGACGTTCTC GGGT
 GT CAGAA
 GAM1987 LOC254746 5' TTGTGGTGTTCCTGTGGCT 96850 TG TC T
 GGC CGGGAG C CATAG
 || ||||| | ||||
 TCG GTCCTT G GTGTT
 GT GT_
 GAM1987 LOC255654 5' TATCTGTGAGCAGTTCTGTGTT 98672 CT GTC
 CA TGG GCGGGA CTCATAGATG
 || ||||| |||||
 ACT TGTCTT GAGTGTCTAT
 TG GAC
 GAM1987 LOC256130 5' CATTTGTGGAATATTGTGTGCC 97756 T G GTCC
 A TGGC GCG GA TCATAGATG
 |||| || || |||||
 ACCG TGT TT GGTGTTTAC
 _ G ATAA
 GAM1987 LOC256401 3' TGTTTATGGCCAGTTTGGGGC 97721 G GTCC
 CA TGGCT CGGGA TCATAGATG
 |||| |||| |||||
 ACCGG GTTTT GGTATTTGT
 G GACC
 GAM1987 LOC256436 3' CATCTGCTCCTTCCTGTGGCC 96248 TG TCCTCA
 GGC CGGGAG TAGATG
 || ||||| |||||
 CCG GTCCTT GTCTAC
 GT CCTC_
 GAM1987 LOC256536 3' TCTCCAGGATTCCCGCAGT 96363 CAT TG
 GCTGCGGGAGTCCT AGA
 ||||| |||||
 TGACGCCCTTAGGA TCT
 CC_ T
 GAM1987 LOC256714 3' GTTTATGAGCTTCAGCTA 98045 C GAGTC
 TGGCTG GG CTCATAGAT
 |||| || |||||
 ATCGAC TC GAGTATTTG
 T _____
 GAM1987 LOC257054 3' GTGGGGCCTCTGCAGCCA 97376 GA T
 TGGCTGCGG GTCC CAT
 ||||| |||||
 ACCGACGTC CGGG GTG
 TC _
 GAM1987 LOC257426 3' CGTCTGTGCTTGTGGCTA 67217 TG AGTCCT
 TGGC CGGG CATAGATG
 |||| || |||||

	ATCG GTTC GTGTCTGC		
	GT _____ C		
GAM1987 LOC257596 5'	AACCTGGGGTTTCTGGGCTA 99754	G	T TAGATG
	TGGCT CGGGAG CCTCA		
	ATCGG GTCTTT GGGGT		
	_____ CCAAG		
GAM1987 LOC51075 3'	TATTTATGTTTTCCCTTTGGCT 32554	GC_	TCCT
	GGCT GGGAG CATAGATG		
	TCGG CCCTT GTATTTAT		
	TTT TT__		
GAM1987 LOC54516 3'	TATTTATAGACTTTCGTAGCT 39285	GG	CTC
	GGCTGCG AGTC ATAGATG		
	TCGATGC TCAG TATTTAT		
	TT A__		
GAM1987 LOC57109 3'	CATCAGGGGTTTCCTGTGGCC 40203	TG	T ATA
	GGC CGGGAG CCTC GATG		
	CCG GTCCTT GGGG CTAC		
	GT T A__		
GAM1987 LOC90038 3'	CATCTAACTGTATTTTGTGTC 61796	C	CCTCA
CA	TGG TGCGGGAGT TAGATG		
	ACC GTGTTTTTA ATCTAC		
	T TGTCA		
GAM1987 LOC90230 3'	CATTTGTGTCATCTTGTTGCCA 62525	T	GTCCT
	TGGC GCGGGA CATAGATG		
	ACCG TGTTCT GTGTTTAC		
	T ACT__		
GAM1987 LOC90322 3'	TATTTATGATACTGCATGCT 62945	_	GAGTCC
	GGC TGCGG TCATAGATG		
	TCG ACGTC AGTATTTAT		
	T AT__		
GAM1987 LOC90918 5'	CATTTATGAAAAGCCTATAGTT 64997	CG	AGTCC
A	TGGCTG GG TCATAGATG		
	ATTGAT CC AGTATTTAC		
	AT GAAA_		
GAM1987 LOC91531 5'	ATCTGTCCCTTCCGTGTT 66940	T	TCCTC
	GGC GCGGGAG ATAGAT		
	TTG TGCCTTC TGTCTA		
	_ CC__		
GAM1987 LOC91947 3'	TGTTTATTGACTTCTGAGTTA 68225	G	CTC
	TGGCT CGGGAGTC ATAGATG		

ATTGA GTCTTCAG TATTTGT
 _ T_
 GAM1987 LOC92223 5' CATCCAGGGTTCCTGTGTTCA 69047 CT GT CATA
 TGG GCGGGA CCT GATG
 ||| ||||| ||| ||||
 ACT TGTTCT GGA CTAC
 TG TG C_
 GAM1987 LOC92231 3' GTTTGTGGCGCTGTTGCCA 69093 T GA CCT
 TGGC GCGG GT CATAGAT
 |||| |||| || |||||
 ACCG TGTC CG GTGTTTG
 T G_ _
 GAM1987 LOC92293 3' TGTTTGGAGGGTTTTTGAGTT 69323 G GT A
 GGCT CGGGA CCTC TAGATG
 |||| |||| ||| |||||
 TTGA GTTTT GGAG GTTTGT
 _ TG _
 GAM1987 LOC92370 3' TGTTTATGATGATTGTGGT 69667 TG GGA C
 GC CG GTC TCATAGATG
 || || ||| |||||
 TG GT TAG AGTATTTGT
 GT _ T
 GAM1987 LOC92840 3' CGTCCTCGGGGCCCTGCAGCC 57245 A CATA
 A TGGCTGCGGG GTCCT GATG
 ||||| |||| |||
 ACCGACGTCC CGGGG CTGC
 C CTC_
 GAM1987 LOC93408 3' TGTGACAGGGAGCTCTTGCAGC 57292 _ _ GATG
 CA TGGCTGCGGGAG TCC TCATA
 ||||| ||| ||||
 ACCGACGTTCTC AGG AGTGT
 G GAC
 GAM1987 LOC93496 3' CATCTAACTTCCACTTTCGTGT 72862 T GG CCTCA_
 CA TGGC GCG AGT TAGATG
 |||| ||| ||| |||||
 ACTG TGC TCA ATCTAC
 _ TT CCTTCA
 GAM1988 ALG6 5' TTCAAGAAGTGATAACAT 26235 CAC
 ATGT CACTTCTTGAA
 |||| |||||
 TACA GTGAAGAACTT
 ATA
 GAM1988 COL19A1 3' TTAGTTCCTGGTAACAT 10266 C CTTCTT
 ATGT ACCA GAACTAA
 |||| ||| |||||
 TACA TGGT CTTGATT
 A C_
 GAM1988 GCA 3' TAGTTCAATCTGTAGTGAAATA 25179 G C TTC
 TAT TCAC AC TTGAACTA
 ||| |||| || |||||

ATA AGTG TG AACTTGAT
 A A TCT
 GAM1988 PLA2G2D 3' TCATGTGAAGTGGTGTGCATA 25722 T T__
 TATG CACCACTTC TGA
 |||| ||||| ||
 ATAC GTGGTGAAG ACT
 T TGT
 GAM1988 DKFZp727G131 3' CTTAGCCAGGCGTGGTGGCA 59695 TT AA
 TGTCAACCAC CTTG CTAAG
 ||||| ||| ||||
 ACGGTGGTG GGAC GATTC
 C_ C_
 GAM1988 PRO2032 5' TCAAGAAGTGAAACATA 38392 CAC
 TATGT CACTTCTTGA
 |||| |||||
 ATACA GTGAAGAACT
 AA_
 GAM1989 DLEC1 3' CATCTGGCCCTCCCTTG 96278 A A C
 CAAGG AGGGC GG GTG
 |||| |||| ||
 GTTCC TCCCG TC TAC
 C G _
 GAM1989 DLEC1 3' CATCTGGCCCTCCCTTG 96279 A A C
 CAAGG AGGGC GG GTG
 |||| |||| ||
 GTTCC TCCCG TC TAC
 C G _
 GAM1989 PIP5K1A 3' TATCCCACCCTGCCTTGATA 14520 A CA C
 TATCAAGG AGGG GG GTG
 ||||| ||| ||
 ATAGTTCC TCCC CC TAT
 G A_ C
 GAM1989 SOX11 3' ACCCACCCCCCTTGGA 13308 AA CA C
 TATCAAGG GGG GG GT
 ||||| ||| ||
 ATGGTTCC CCC CC CA
 CC A_ _
 GAM1989 CHL1 3' TGTTACCTTTCCTCAATA 22768 CA CA
 TAT AGGAAGGG GGCG
 || ||||| ||
 ATA TCCTTCC TTGT
 AC A_
 GAM1989 EPB41L1 3' CATTCTGCCCTTCCCTGA 71104 A C
 TCA GGAAGGGCAGG GTG
 || ||||| ||
 AGT CCTTCCCGTCT TAC
 C _
 GAM1989 FLJ00060 3' CATACCCCCTGCCCTCCTCTGA 61741 _ A CGTG
 TCA AGGA GGGCAGG ATG
 || ||| ||||| ||

AGT TCCT CCCGTCC TAC
 C _ CCCA
 GAM1989 FLJ10898 5' CACCACAGCCCTTTCTCAATA 60126 CA AGGC
 TAT AGGAAGGGC GTG
 ||| ||||| |||
 ATA TCTTTCCCG CAC
 AC ACAC
 GAM1989 FLJ22557 3' ATCATCCCATCCTTAATA 45581 C A CAGGC
 TAT AAGGA GGG GTGAT
 ||| |||| ||| |||||
 ATA TTCCT CCC TACTA
 A A _____
 GAM1989 KIAA0574 3' CATCCCCTGCCCTCCCCTGA 69808 A A CGT
 TCA GG AGGGCAGG GATG
 ||| || ||||| |||||
 AGT CC TCCCGTCC CTAC
 C C C____
 GAM1989 KIAA0632 3' CACCTCAGAAACCCTTCCTTGA 32071 CA____ C
 TCAAGGAAGGG GG GTG
 ||||| || |||
 AGTTCCTTCCC CT CAC
 AAAGA C
 GAM1989 KIAA1045 3' CATCACATGTCCTTCC 71599 GGC
 GGAAGGGCA GTGATG
 ||||| |||||
 CCTTCCTGT CACTAC
 A____
 GAM1989 KIAA1354 5' CAGTGACTGCCTTCCCTTGATA 61572 A G _
 TATCAAGG AGGGCAG CG TG
 ||||| ||||| || |||
 ATAGTTCC TTCCGTC GT AC
 C A G
 GAM1989 MGC20460 5' CACCGCCTCCTACCTTCTT 54901 C____ _
 AGGAAGGG AGGCG TG
 ||||| ||||| |||
 TTCTTCCC TCCGC AC
 ATCC C
 GAM1989 LOC158476 3' CACGCCCCGCCCCCCCCATTGA 88186 _ AA_ A
 TCAA GG GGGC GGC GTG
 ||| || ||| |||||
 AGTT CC CCG CCGCAC
 A CCC C
 GAM1989 LOC90459 3' CACACCCGCCTAATTTTGT 63550 A_ A C
 CAAGGA GGGC GG GTG
 ||||| ||| || |||
 GTTTTT TCCG CC CAC
 AA C A
 GAM1990 DLEC1 3' CATCTGGCCCTCCCTTG 96278 A A C
 CAAGG AGGGC GG GTG
 ||||| ||||| || |||

			GTTCC TCCCG TC TAC			
			C G _			
GAM1990	DLEC1	3'	CATCTGGCCCTCCCTTG	96279	A A C	
			CAAGG AGGGC GG GTG			
			GTTCC TCCCG TC TAC			
			C G _			
GAM1990	PIP5K1A	3'	TATCCCACCCTGCCTTGATA	14520	A CA C	
			TATCAAGG AGGG GG GTG			
			ATAGTTCC TCCC CC TAT			
			G A_ C			
GAM1990	SOX11	3'	ACCCACCCCCCCTTGGA	13308	AA CA C	
			TATCAAGG GGG GG GT			
			ATGGTTCC CCC CC CA			
			CC A_ _			
GAM1990	CHL1	3'	TGTTACCTTTCCTCAATA	22768	CA CA	
			TAT AGGAAGGG GGCG			
			ATA TCCTTTCC TTGT			
			AC A_			
GAM1990	EPB41L1	3'	CATTCTGCCCTTCCCTGA	71104	A C	
			TCA GGAAGGGCAGG GTG			
			AGT CCTTCCCGTCT TAC			
			C _			
GAM1990	FLJ00060	3'	CATACCCCCTGCCCTCCTCTGA	61741	_ A CGTG	
			TCA AGGA GGGCAGG ATG			
			AGT TCCT CCCGTCC TAC			
			C _ CCCA			
GAM1990	FLJ10898	5'	CACCACAGCCCTTTCTCAATA	60126	CA AGGC	
			TAT AGGAAGGGC GTG			
			ATA TCTTTCCCG CAC			
			AC ACAC			
GAM1990	FLJ22557	3'	ATCATCCCATCCTTAATA	45581	C A CAGGC	
			TAT AAGGA GGG GTGAT			
			ATA TTCCT CCC TACTA			
			A A _ _ _			
GAM1990	KIAA0574	3'	CATCCCCTGCCCTCCCCTGA	69808	A A CGT	
			TCA GG AGGGCAGG GATG			
			AGT CC TCCCGTCC CTAC			
			C C C_			
GAM1990	KIAA0632	3'	CACCTCAGAAACCCTTCCTTGA	32071	CA_ C	
			TCAAGGAAGGG GG GTG			

AGTTCCTTCCC CT CAC
 AAAGA C
 GAM1990 KIAA1045 3' CATCACATGTCCTTCC 71599 GGC
 GGAAGGGCA GTGATG
 ||||| ||||
 CCTTCCTGT CACTAC
 A__
 GAM1990 KIAA1354 5' CAGTGACTGCCTTCCCTTGATA 61572 A G _
 TATCAAGG AGGGCAG CG TG
 ||||| ||||| || ||
 ATAGTTCC TTCCGTC GT AC
 C A G
 GAM1990 MGC20460 5' CACCGCCTCCTACCCTTCTT 54901 C__ _
 AGGAAGGG AGGCG TG
 ||||| |||| ||
 TTCTTCCC TCCGC AC
 ATCC C
 GAM1990 LOC158476 3' CACGCCCGCCCCCCCCATTGA 88186 _ AA_ A
 TCAA GG GGGC GGC GTG
 ||| || ||| |||||
 AGTT CC CCG CCGCAC
 A CCC C
 GAM1990 LOC90459 3' CACACCCGCCTAATTTTGT 63550 A_ A C
 CAAGGA GGGC GG GTG
 ||||| ||| || |||
 GTTTTT TCCG CC CAC
 AA C A
 GAM1991 SCAMP1 3' GCTAAATAAATATTCTCC 18013 T C
 GGA AATATT ATTTAGC
 || ||||| |||||
 CCT TTATAA TAAATCG
 C A
 GAM1991 SCAMP1 3' GCTAAATAAATATTCTCC 54501 T C
 GGA AATATT ATTTAGC
 || ||||| |||||
 CCT TTATAA TAAATCG
 C A
 GAM1991 NX-17 3' TGAATATCAGCCCCTAATA 40706 ATA_
 TATTAGGG ATATTCA
 ||||| |||||
 ATAATCCC TATAAGT
 CGAC
 GAM1991 LOC161589 3' GCTAAATGAATATTATCCCTAA 83159
 TA TATTAGGGATAATATTCATTTAGC
 |||||
 ATAATCCCTATTATAAGTAAATCG
 GAM1992 BPAG1 3' CTGAGAAGCTGAATGATA 32075 G TAGAT
 TATTATTCAG T TCTCAG
 ||||| |||||

ATAGTAAGTC A AGAGTC
 G____
 GAM1992 PRKG2 3' CTGCTTTTAACTGAAAATA 21824 A TTCT
 TATT TTCAGGTTAGA CAG
 |||| ||||| ||
 ATAA AAGTCCAATTT GTC
 _ TC_
 GAM1992 APOL2 3' TCTGAGAACCAACCAATGAA 48794 _ AGA
 TTCA GGTT TTCTCAGA
 |||| ||| |||||
 AAGT CCAA AAGAGTCT
 AA CC_
 GAM1992 CYYR1 3' CTGAGAATGCTGAATA 54760 GTTAG
 TATTCAG ATTCTCAG
 ||||| |||||
 ATAAGTC TAAGAGTC
 G____
 GAM1992 FLJ12661 3' CTGAGAACTGCAATGAACAAT 47854 A GGT A
 ATT TTCA TAG TTCTCAG
 ||| ||| ||| |||||
 TAA AAGT GTC AAGAGTC
 C AAC _
 GAM1992 KIAA1045 3' TCTGAGAACACTTGAG 71612 TAGA
 TTCAGGT TTCTCAGA
 ||||| |||||
 GAGTTCA AAGAGTCT
 C____
 GAM1992 LOC152756 3' TGAAAACCTGAAAATA 87056 A AGATTC
 TATT TTCAGGTT TCA
 |||| ||||| ||
 ATAA AAGTCCAA AGT
 _ A____
 GAM1993 CDH12 3' CTTATCATTTAAAGTGGTGTA 15777 CCCAA GA
 TACACCACT GAA ATAAG
 ||||| ||| ||||
 ATGTGGTGA TTT TATTC
 AA__ AC
 GAM1993 GOCAP1 3' ATTGTTCTTGGGAGCAGTGTA 43007 CA G
 TACAC CTCCCAAGAA AAT
 |||| ||||| |||
 ATGTG GAGGGTTCTT TTA
 AC G
 GAM1993 DKFZp434N2435 5' CTTATTACTGTGGGGTGGT 98090 T AGAAG
 ACCAC CCCA AATAAG
 |||| ||| |||||
 TGGTG GGGT TTATTC
 _ GTCA_
 GAM1993 DKFZP564I122 3' CTTATTCTTCTCCCTCATGTGT 63877 CACTCCCA
 A TACAC AGAAGAATAAG
 |||| |||||

		ATGTG TCTTCTTATTC	
		TACTCCC_	
GAM1993	FLJ21791	3' CTTATTTGCAGAAAGTGGTGTA 62126	CCCAAGAA
		TACACCACT GAATAAG	
		ATGTGGTGA TTTATTC	
		AGACG__	
GAM1993	HMP19	3' CTTATTCTTTGTTAGGAAAATG 88860	CCAC CAA_
	TA	TACA TCC GAAGAATAAG	
		ATGT AGG TTTCTTATTC	
		AAA_ ATTG	
GAM1993	KIAA1579	3' TACTCTTAGTGGTGTA 37154	CCCAAG A
		TACACCACT AAGA TA	
		ATGTGGTGA TTCT AT	
		_____ C	
GAM1993	KIAA1719	3' TCTGTCTTGGGAGTGGTGTA 68742	_
		TACACCACTCCCAAGA AGA	
		ATGTGGTGAGGGTTCT TCT	
		G	
GAM1993	KIAA1853	3' TTTTCTTGAAGCAGTG 69929	CA C
		CAC CT CCAAGAAGAA	
		GTG GA GGTTCTTTTT	
		AC A	
GAM1993	KIAA1877	3' CTTATTCTTCTGCCATGAGT 66748	CCA_
		ACTC AGAAGAATAAG	
		TGAG TCTTCTTATTC	
		TACCG	
GAM1993	KIAA1906	3' CTTATTCTTCTTGACTTTTGG 73571	CTCC_
		CCA CAAGAAGAATAAG	
		GGT GTTCTTCTTATTC	
		TTTCA	
GAM1993	OSBPL11	3' CTTAATTTCCCAAGAGTGGTG 43206	CCAA AA
		CACCACTC GAAG TAAG	
		GTGGTGAG CTTT ATTC	
		AACC A_	
GAM1993	YME1L1	3' TCATTCTTGATGTGGTGTA 58438	TCC _
		TACACCAC CAAGAA GA	
		ATGTGGTG GTTCTT CT	
		TA_ A	
GAM1993	YME1L1	3' TCATTCTTGATGTGGTGTA 27323	TCC _
		TACACCAC CAAGAA GA	

			ATGTGGTG GTTCTT CT		
			TA_ A		
GAM1993	ZNF262	3'	CTTATTTTGTGGGAGT 18723	A	
			ACTCCCAAG AGAATAAG		
			TGAGGGTTT TTTTATTC		
			G		
GAM1993	LOC91960	3'	TGTGGCTTGGAACGTGGTGTA 68294	TC_ AAGA	
			TACACCAC CCAAG ATA		
			ATGTGGTG GGTTT TGT		
			CAA GG_		
GAM1994	AQP6	3'	GGCCCCAGGCCCCAGC 55008	A CTC	
			GCTG GGCCTGGG GCC		
			CGAC CCGGACCC CGG		
			C _		
GAM1994	GCK	5'	CCCAAGCGCCCAGCAATG 5682	A _ _	
			CATTGCTG GGC CT GGG		
			GTAACGAC CCG GA CCC		
			_ C A		
GAM1994	GGT1	5'	TGTCCCCAGGCCTCAGCAA 26439	CT	
			TTGCTGAGGCCTGGG CG		
			AACGACTCCGGACCC GT		
			CT		
GAM1994	GNAT1	3'	GACGCACAGACTCAGCAAT 5721	GC G _	
			ATTGCTGAG CTG GC TC		
			TAACGACTC GAC CG AG		
			A_ A C		
GAM1994	HAS3	3'	AGGCAAGCGTGTTCAGCA 19231	CCT G C	
			TGCTGAGG G GCT GCCT		
			ACGACTCT T CGA CGGA		
			TG_ G A		
GAM1994	P23	3'	AGGCGAGCCCTCCCCAGCA 22751	A CCT	
			TGCTG GG GGGCTCGCCT		
			ACGAC CC CCCGAGCGGA		
			_ CT_		
GAM1994	SF1	3'	AGGCAGACAGCCTCAGCAA 17339	C GG C	
			TTGCTGAGGC TG CT GCCT		
			AACGACTCCG AC GA CGGA		
			_ A_ _		
GAM1994	SYN3	3'	GTCGCCTAGTCAGACCTCAGCA 14482	C _ _ _ _ CTGG	
AT			ATTGCTGAGG CTG GG C		

			TAACGACTCC GAC	CC	G	
			A TGA__T GCTC			
GAM1994	SYN3	3'	GTCGCCTAGTCAGACCTCAGCA	56904	C	_____ CTCG
	AT		ATTGCTGAGG CTG	GG	C	
			TAACGACTCC GAC	CC	G	
			A TGA__T GCTC			
GAM1994	SYN3	3'	GTCGCCTAGTCAGACCTCAGCA	56906	C	_____ CTCG
	AT		ATTGCTGAGG CTG	GG	C	
			TAACGACTCC GAC	CC	G	
			A TGA__T GCTC			
GAM1994	WNT5A	3'	CTCAGAAGCATCAGCAATG	14120	G	__
			CATTGCTGA GC	CTGGG		
			GTAACGACT CG	GA CTC		
			A AA			
GAM1994	ARGBP2	5'	AGGCAAGCTTTCCTGCAAT	14589	TG	CCT C
			ATTGC AGG	GGGCT GCCT		
			TAACG TCC	TTCGA CGGA		
			__ CT_	A		
GAM1994	ATP9B	3'	AGGCAAGCCCAGGGCACAG	78971	AG	_ C
			CTG GCC	TGGGCT GCCT		
			GAC CGG	ACCCGA CGGA		
			A_ G	A		
GAM1994	ATP9B	3'	AGGCAAGCCCAGGGCACAG	78972	AG	_ C
			CTG GCC	TGGGCT GCCT		
			GAC CGG	ACCCGA CGGA		
			A_ G	A		
GAM1994	ATP9B	3'	AGGCAAGCCCAGGGCACAG	78973	AG	_ C
			CTG GCC	TGGGCT GCCT		
			GAC CGG	ACCCGA CGGA		
			A_ G	A		
GAM1994	ATP9B	3'	AGGCGAGCCCAGGGCACAG	78974	AG	_
			CTG GCC	TGGGCTCGCCT		
			GAC CGG	ACCCGAGCGGA		
			A_ G			
GAM1994	CALN1	3'	AGGCAAACCCAGTGGTTTCAGA	49659	G	__ CTC
	AATG		CATT CTGAGGCC	TGGG GCCT		
			GTAA GACTTTGG	ACCC CGGA		
			A	TG AAA		
GAM1994	CNR2	3'	GCGAGCCTCCAGGCCAGCAAT	10234	A	__
	G		CATTGCTG	GGCCTGG GCTCGC		

		GTAACGAC CCGGACC CGAGCG		
		— TC		
GAM1994	DKFZp434A171 3'	GGCTCGCCTAAACATAACCTCA 71342	CCT_____	CTCG
		GCAAT ATTGCTGAGG GGG CC		
		TAACGACTCC TCC GG		
		AATACAAA__ GCTC		
GAM1994	DKFZp762L0311 3'	GTCGCCTAGACGGGCTTCAACA 38672	C _____	CTCG
		ATG CATTG TGAGGCCTG GG C		
		GTAAC ACTTCGGGC CC G		
		A AGA__T GCTC		
GAM1994	FLJ12076 3'	AGCACCTGTGCCCTCAGCAATG 48020	_CT_ _	
		CATTGCTGAGG C GG GCT		
		GTAACGACTCC G CC CGA		
		C TGT A		
GAM1994	FLJ20297 3'	AGGCAGGTGGGCCCCAGCAA 35369	A GG TC	
		TTGCTG GGCCT GC GCCT		
		AACGAC CCGGG TG CGGA		
		C __ GA		
GAM1994	FLJ20297 3'	AGGCAGGTGGGCCCCAGCAA 36076	A GG TC	
		TTGCTG GGCCT GC GCCT		
		AACGAC CCGGG TG CGGA		
		C __ GA		
GAM1994	KIAA1069 3'	AGTTCCAAACCCAGCAATG 68525	A CC _	
		CATTGCTG GG TGGG CT		
		GTAACGAC CC ACCT GA		
		C AA T		
GAM1994	KIAA1272 3'	AGGCCTCACACAGGCCTCAGAA 70731	G GGCTC_	
		ATG CATT CTGAGGCCTG GCCT		
		GTAA GACTCCGGAC CGGA		
		A AACTC		
GAM1994	MGC:5244 3'	GGCCGGACCTCAGCAAT 49151	_ TG	
		ATTGCTGAGG CC GGCT		
		TAACGACTCC GG CCGG		
		A _		
GAM1994	LOC149194 3'	GCAAGCCCAGGTTGCCAGT 79984	A_ C	
		GCTG GGCCTGGGCT GC		
		TGAC TTGGACCCGA CG		
		CG A		
GAM1994	LOC150207 3'	GGCCGGACCTCAGCAAT 80596	_ TG	
		ATTGCTGAGG CC GGCT		

		TAACGACTCC GG CCGG		
		A _		
GAM1994	LOC158281 3'	AGGCGAGCCCTCCCCAGCA 82734	A	CCT
		TGCTG GG GGGCTCGCCT		
		ACGAC CC CCCGAGCGGA		
		_ CT_		
GAM1994	LOC163479 5'	AGGCATATTCAAACCTCAGCAA 83021	GCC	CTC
		TTGCTGAG TGGG GCCT		
		AACGACTC ACTT CGGA		
		AAA ATA		
GAM1994	LOC220020 5'	GATCCAGACCTCACCAATG 95045	C	C C
		CATTG TGAGG CTGGG TC		
		GTAAC ACTCC GACCT AG		
		C A _		
GAM1994	LOC256286 3'	GGCCGGACCTCAGCAAT 96895	_	TG
		ATTGCTGAGG CC GGCT		
		TAACGACTCC GG CCGG		
		A _		
GAM1994	LOC91632 3'	AGCCGGACCTCAGCAAT 67314	_	TG
		ATTGCTGAGG CC GGCT		
		TAACGACTCC GG CCGA		
		A _		
GAM1994	LOC93538 5'	AGACGAGAACCTGCCTCAGCAA 72952	CT G_	C
		TTGCTGAGGC GG CTCG CT		
		AACGACTCCG CC GAGC GA		
		T_ AA A		
GAM1995	DPP6 3'	TCCCACTCAGCTATGCTA 56325	C	A
		TAGCAT GCTGAGTG GGA		
		ATCGTA CGACTCAC CCT		
		T _		
GAM1995	FBXL7 3'	TTCTGTTCACCTCAACAATGC 25501	CGC	GG
		GCAT TGAGTGA ACGGAA		
		CGTA ACTCACT TGTCTT		
		ACA _		
GAM1995	HSA243396 3'	TCCCATGTTTCAGCAATGT 37846	C _	A
		GCAT GCTGA GTG GGA		
		TGTA CGACT TAC CCT		
		A TG _		
GAM1995	OSBP2 5'	CCGCCCCCACTGGCCGCT 48480	ATC	G A A
		AGC GCT AGTG GG CGG		

		TCG CGG TCAC CC GCC		
		C__ _ C C		
GAM1995 TANK	5'	TCCATCCTTTATAGTGATGCTA 56825	AGT	C
		TAGCATCGCTG GAGGA GGA		
		ATCGTAGTGAT TTCCT CCT		
		AT_ A		
GAM1995 TANK	5'	TCCATCCTTTATAGTGATGCTA 16077	AGT	C
		TAGCATCGCTG GAGGA GGA		
		ATCGTAGTGAT TTCCT CCT		
		AT_ A		
GAM1995 LOC126823	5'	TCCACACTCAGCGACGCTA 75081	A	A
		TAGC TCGCTGAGTG GGA		
		ATCG AGCGACTCAC CCT		
		C A		
GAM1995 LOC149420	3'	TCCACCCTCACTTTGCCTGC 80158	TC T	AC
		GCA GC GAGTGAGG GGA		
		CGT CG TTCACTCC CCT		
		C_ T CA		
GAM1995 LOC158969	3'	CCATCCCCACCGCCACTGCT 82933	TC_ T A	A C
		AGCA GC G GTG GGA GG		
		TCGT CG C CAC CCT CC		
		CAC __ C A		
GAM1996 HCS	3'	GGCGTGAGCCACCAGGCC 38986	GGGA	
		GGGCCTGGTGGTT GTC		
		CCCGGACCACCGA CGG		
		GTG_		
GAM1996 IFI16	5'	GTGACTCAACCAAGGCC 71748	GG	GG
		GGCCT TGGTT GAGTCAC		
		CCGGA ACCAA CTCAGTG		
		— —		
GAM1996 MHC2TA	3'	GGTGTGAACCACACACCC 5991	CC	GGGAGT
		GGG TGGTGGTT CACC		
		CCC ACCACCAA GTGG		
		AC GT_____		
GAM1996 NEU3	5'	GGCATAAGCCACCAGGCC 22830	GGGA	
		GGGCCTGGTGGTT GTC		
		CCCGGACCACCGA CGG		
		ATA_		
GAM1996 PER2	3'	GGCGACTGCCACCACACCC 43355	CC	TGGG A
		GGG TGGTGGT AGTC CC		

CCC ACCACCG TCAG GG
 AC ____ C
 GAM1996 ZNF135 3' TGACCATGGGACCAAGCTC 14305 C GGGA_
 GGGC TGGTGGTT GTCA
 ||| ||||| |||
 CTCG ACCACCAG CAGT
 A GGTAC
 GAM1996 C11orf9 3' ACTCCCAACCACCAAGACC 26113 GCC
 GG TGGTGGTTGGGAGT
 || |||||
 CC ACCACCAACCCTCA
 AGA
 GAM1996 DKFZp434K1210 3' GACAACCCCCAGCTTCAGGTCC 34690 T A_
 GGGCCTGG GGTTGGG GTC
 ||||| ||||| |||
 CCTGGACT TCGACCC CAG
 _ CCAA
 GAM1996 DKFZp547H025 3' GGTGTGAGCCACCAGGCC 39777 GGGAGT
 GGGCCTGGTGGTT CACC
 ||||| ||||| |||
 CCCGGACCACCGA GTGG
 GT____
 GAM1996 GLE1L 3' GTAACATCATAACCAGGCCT 9476 GGTTGG C
 GGGCCTGGT GAGT AC
 ||||| ||| ||
 TCCGGACCA CTCA TG
 ATA____ A
 GAM1996 IRF7 3' GACCCCCAGCCCCGGGCC 15736 T A
 GGGCCTGG GGTTGGG GTC
 ||||| ||||| |||
 CCCGGGCC CCGACCC CAG
 _ C
 GAM1996 KIAA0469 3' GGCGTGAACCACACGCCC 29986 C GGGA
 GGGC TGGTGGTT GTC
 ||| ||||| |||
 CCCG ACCACCAA CGG
 C GTG_
 GAM1996 KIAA1922 3' GTGAGAACCACCAAATC 74002 CC GGGAG
 GGG TGGTGGTT TCAC
 ||| ||||| |||
 CTC ACCACCAA AGTG
 AA G____
 GAM1996 LY75 3' GGCAACTGCCACCATGCCC 11395 C T GA
 GGGC TGGTGGT GG GTC
 ||| ||||| || |||
 CCCG ACCACCG TC CGG
 T _ AA
 GAM1996 SQV7L 5' GGTGTGAACCACCATGCCC 71099 C GGGAGT
 GGGC TGGTGGTT CACC
 ||| ||||| |||

CCGG ACCACCAA GTGG
 T GT____
 GAM1996 LOC123876 5' GACTCCCAAGCCCAGCCC 74717 CT GG
 GGGC GGT TTGGGAGTC
 |||| ||| |||||
 CCGG CCG AACCCCTCAG
 AC ____
 GAM1996 LOC146894 3' AGGTGACTCCGAGTCCAGCCC 59853 C TGG G
 GGGC TGG TT GGAGTCACCT
 |||| ||| || |||||
 CCGG ACC GA CCTCAGTGGA
 _ T__ G
 GAM1996 LOC147136 3' GTGACTCCAGCCCAAGCCC 78865 C TG
 GGGC TGG GTTGGGAGTCAC
 |||| ||| |||||
 CCGG ACC CGACCCTCAGTG
 A ____
 GAM1996 LOC158954 3' TGACCATGGGACCACCAAGCTC 61064 C GGGA_
 GGGC TGGTGGTT GTCA
 |||| ||||| |||
 CTCG ACCACCAG CAGT
 A GGTAC
 GAM1996 LOC200301 5' ACCCCGACCACGCCC 90129 CTG A
 GGGC GTGGTTGGG GT
 |||| ||||| ||
 CCGG CACCAGCCC CA
 ____ _
 GAM1996 LOC253367 3' CTCCCGACCACCAGACCC 99436 C
 GGG CTGGTGGTTGGGAG
 ||| |||||
 CCC GACCACCAGCCCTC
 A
 GAM1996 LOC90170 5' GACATAAAAACCGCCAGACCC 62377 C GGGA_
 GGG CTGGTGGTT GTC
 ||| ||||| |||
 CCC GACCGCCAA CAG
 A AAATA
 GAM1996 LOC90591 3' GGTGACCGCCACCACGCCC 64180 C TGGGA
 GGGC TGGTGGT GTCACC
 |||| ||||| |||||
 CCGG ACCACCG CAGTGG
 C C____
 GAM1996 LOC92267 3' GGCATGAGCCACCAAGCCC 69173 C GGGA
 GGGC TGGTGGTT GTC
 |||| ||||| |||
 CCGG ACCACCGA CGG
 A GTA_
 GAM1997 HNRPH3 3' CCCTTCAGCACTTGACCGAA 25208 G G CT
 TTCGGTCA AGTG TG GGG
 ||||| |||| || |||

			AAGCCAGT TCAC AC CCC		
			— G TT		
GAM1997	PLOD3	3'	CTCAACCACTCTGCC 8431 T	GC	
			GG CAGAGTGGT TGGG		
			CC GTCTCACCA ACTC		
			— —		
GAM1997	PTHLH	3'	TCCTTTACCACTCTACC 12546 C	CT	
			GGT AGAGTGGTG GGGA		
			CCA TCTCACCAT TCCT		
			— T—		
GAM1997	CECR7	3'	TTCCCAGTGCCTGGCCGAA 80451	GAGT TG	
			TTCGGTCA GG CTGGGAA		
			AAGCCGGT CC GACCCTT		
			— GT		
GAM1997	CHST3	3'	CCCAGCCAGCGCTCCAGCC 16232	CA G —	
			GGT GAGTG TG CTGGG		
			CCG CTCGC AC GACCC		
			AC G C		
GAM1997	FLJ00026	3'	TTCCCAAATGGACTCTGACC 65624	GGTGC	
			GGTCAGAGT TGGGAA		
			CCAGTCTCA ACCCTT		
			GGTAA		
GAM1997	KIAA1884	3'	TCCCAGCAGCCGCTGACC 73731	GA —	
			GGTCA GTGG TGCTGGGA		
			CCAGT CGCC ACGACCCT		
			— G		
GAM1997	SSB-4	3'	GTTCCAGGAGGCCCAACCG 55964	CAGAGT G—	
			CGGT GGT CTGGGAAC		
			GCCA CCG GACCCTTG		
			AC— GAG		
GAM1997	LOC90381	3'	GTTCAGAGCACCTAACC 63215	CAG T GG	
			GGT AG GGTGCT GAAC		
			CCA TC CCACGA CTTG		
			A— — GA		
GAM1998	KIAA1069	3'	TGACCTACATTCAACTGCAA 68535	— C—	
			TTGCAGTTGAA GT GTCG		
			AACGTCAACTT CA CAGT		
			A TC		
GAM1998	NICN1	3'	TGGCGACTTCATCTGCAA 51261	T	
			TTGCAG TGAAGTCGTCG		

		AACGTC ACTTCAGCGGT	
		T	
GAM1998	TEX27	3' GCTGAACACCTGCAACTGCAA 41952	A TC CG
		TTGCAGTTG AG GT TAGC	
		AACGTCAAC TC CA GTCG	
		G CA A_	
GAM1998	LOC142948	3' TGGCCACCGGCCCAACTGCAG 83782	AA TC A
		TTGCAGTTG GTCG GT GCCA	
		GACGTCAAC CGGC CA CGGT	
		C_ _ C	
GAM1998	LOC146488	5' GCTACAACCGCTTCAACAACAA 71359	CA C C
		TTG GTTGAAGT GT GTAGC	
		AAC CAACTTCG CA CATCG	
		AA C A	
GAM1998	LOC147080	3' TGCACAACCTTCAGCCACAA 85053	CA C C
		TTG GTTGAAGT GT GTA	
		AAC CGACTTCA CA CGT	
		AC A _	
GAM1998	LOC152845	5' GCGGTGACCTCAGCTGCAA 60958	A GT
		TTGCAGTTGA GTC CGT	
		AACGTCGACT CAG GCG	
		C TG	
GAM1998	LOC203052	3' ACCACCATTTCAACTGCA 92073	C C
		TGCAGTTGAAGT GT GT	
		ACGTCAACTTTA CA CA	
		C C	
GAM1998	LOC204084	5' GGCCAGACCTCCAAGTGCAG 91000	A TC GTA
		TTGCAGTTG AG GTC GCC	
		GACGTCAAC TC CAG CGG	
		C _ AC_	
GAM1999	ALDH3A2	5' CAGCCCGCTGCCAGAGCCGGGG 69796	ATG_ A
	A	TCCCTGGCTT AGC GGCTG	
		AGGGGCCGAG TCG CCGAC	
		ACCG C	
GAM1999	CAPNS1	3' CAGCCTGCCAGGCCAGG 10013	TA A
		CCTGGCT TG GCAGGCTG	
		GGACCGG AC CGTCCGAC	
		_ _	
GAM1999	CASP10	3' CAGCCTGCTTTCACACTAAGGA 53218	C CTTAT
		TCC TGG GAGCAGGCTG	

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AGG ATC TTCGTCCGAC
A ACACT
GAM1999 DLEC1 3' TGGCCCCACAAGCCAGG 24723 A AGCA
CCTGGCTT TG GGCTG
||||| || |||
GGACCGAA AC CCGGT
C C__
GAM1999 DLEC1 3' TGGCCCCACAAGCCAGG 24733 A AGCA
CCTGGCTT TG GGCTG
||||| || |||
GGACCGAA AC CCGGT
C C__
GAM1999 DYT1 3' CAGCCCACTCATCGCAGGG 5477 G TT CA
CCCTG C ATGAG GGCTG
|||| | ||| |||
GGGAC G TACTC CCGAC
_ C_ AC
GAM1999 LPIN1 5' CAGCCTGCTGAGAACTAG 67985 C ATG
CTGG TT AGCAGGCTG
||| || |||||
GATC AA TCGTCCGAC
_ GAG
GAM1999 RCV1 5' CAGCCTGCGGCCAGGGG 12801 TATGA
TCCCTGGCT GCAGGCTG
||||| |||||
GGGGACCGG CGTCCGAC

GAM1999 TNXB 5' CTCAGCCTTGGGCCAAGCCTGG 51634 CT TA A __
A TCC GGCT TG GC AGGCTGAG
||| ||| || || |||||
AGG CCGA AC CG TCCGACTC
T_ _ _ GGT
GAM1999 C20orf150 3' CAGCCTGCCCTCAAGCCAAGGA 66009 C ATGA
TCC TGGCTT GCAGGCTG
||| ||||| |||||
AGG ACCGAA CGTCCGAC
A CTCC
GAM1999 C20orf39 5' CAGCCTGCCGGCCAGGCGA 46571 _ TAT A
TC CCTGGCT G GCAGGCTG
|| ||||| | |||||
AG GGACCGG C CGTCCGAC
C _ _ _
GAM1999 CBX6 3' CAGCCTGCCTGAAGCAAAGGA 27407 CTG ATGA
TCC GCTT GCAGGCTG
||| ||| |||||
AGG CGAA CGTCCGAC
AAA GTC_
GAM1999 CD84 3' CTCAGCCTGTAAGCAAAGCAGG 81570 G A A__
CCTG CTT TG GCAGGCTGAG
|||| ||| |||||

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GGAC GAA AC TGTCCGACTC
— — GAA
GAM1999 CYP2D6 3' CAGCCTGCTCCTAGCCCAGAGG 5451 — C T
CC CTGG TTA GAGCAGGCTG
|| ||| ||| |||||
GG GACC GAT CTCGTCCGAC
A C C
GAM1999 DKFZP586J0619 3' CTCAGCCTGCCCAGCAGGGA 82317 G TAT A
TCCCTG CT G GCAGGCTGAG
||||| || | |||||
AGGGAC GA C CGTCCGACTC
— — — C
GAM1999 FKHL18 3' CAGCCCTGGTGAGCCAAGGA 80370 C G CA
TCC TGGCTTAT AG GGCTG
||| ||||| || |||||
AGG ACCGAGTG TC CCGAC
A G —
GAM1999 FLJ14800 3' CAACCTGCTCAGGCACCACAGA 52684 CC CTTA C
TC TGG TGAGCAGG TG
|| ||| ||||| ||
AG ACC ACTCGTCC AC
AC ACGG A
GAM1999 FLJ14957 3' CTCAGCCCACTCATACCTAGAG 52816 C CT CA
A TC CTGG TATGAG GGCTGAG
|| ||| ||||| |||||
AG GATC ATACTC CCGACTC
A C_ AC
GAM1999 HIC2 3' CAGCCTGGAGCCAGG 65861 ATGAG
CCTGGCTT CAGGCTG
||||| |||||
GGACCGAG GTCCGAC
— — —
GAM1999 KIAA1023 3' CAGGCTCAGAAGCCAGGGA 34677 A AGG
TCCCTGGCTT TGAGC CTG
||||||| ||||| |||
AGGGACCGAA ACTCG GAC
G —
GAM1999 KIAA1655 5' CTCAGCCCACTCCCAAACCAG 67183 C AT CA
CTGG TT GAG GGCTGAG
|||| || ||| |||||
GACC AA CTC CCGACTC
A CC AC
GAM1999 MGC35521 3' CTCAGGTGTCAGTAAGCCAG 59666 GA GG
CTGGCTTAT GCA CTGAG
||||||| ||| |||||
GACCGAATG TGT GACTC
AC G_
GAM1999 MGC5508 3' CAGCCTGCCTCACCAGGGA 44264 CTTA —
TCCCTGG TGAG CAGGCTG
||||| ||| |||||

AGGGACC ACTC GTCCGAC
 _____ C
 GAM1999 PADI1 3' CAGCCTGCACTGAGTCA 62700 TGA
 TGGCTTA GCAGGCTG
 ||||| |||||
 ACTGAGT CGTCCGAC
 CA_
 GAM1999 RIN3 5' CTCAGCCTGCCTCCCCAAGGGA 46162 _ CTTAT _
 TCCCT GG GAG CAGGCTGAG
 ||||| || ||| |||||
 AGGGA CC CTC GTCCGACTC
 A C_____ C
 GAM1999 SOX17 3' CAGCCTGCAGGCCAG 42630 ATGA
 CTGGCTT GCAGGCTG
 ||||| |||||
 GACCGGA CGTCCGAC

 GAM1999 SP140 3' AGTATCTCATCAGCCAGGGA 24326 T CAG
 TCCCTGGCT ATGAG GCT
 ||||| ||||| |||
 AGGGACCGA TACTC TGA
 C TA_
 GAM1999 VI 3' CAGCCGCTAGGCCAGGGA 26486 ATG A
 TCCCTGGCTT AGC GGCTG
 ||||| ||| |||||
 AGGGACCGGA TCG CCGAC
 _____ _
 GAM1999 LOC112817 5' CAGTGGCCACAAGTCAGGGA 57319 A A AG
 TCCCTGGCTT TG GC GCTG
 ||||| || || |||||
 AGGGA CTGAA AC CG TGAC
 C _ G_
 GAM1999 LOC129676 5' CTCAGCCTGCAGACACAGGGA 76232 GCTTATGA
 TCCCTG GCAGGCTGAG
 ||||| |||||
 AGGGAC CGTCCGACTC
 ACAGA_____
 GAM1999 LOC134266 3' CTCAGCCTACCAAGTAGCCAGG 75644 TATGAGC
 CCTGGCT AGGCTGAG
 ||||| |||||
 GGACCGA TCCGACTC
 TGAACCA
 GAM1999 LOC150248 3' CCACCTCATCAGCCAGGGA 86126 T CA
 TCCCTGGCT ATGAG GG
 ||||| ||||| ||
 AGGGACCGA TACTC CC
 C CA
 GAM1999 LOC155179 3' CAGGCTCAGAAGCCAGGGA 82225 A AGG
 TCCCTGGCTT TGAGC CTG
 ||||| ||||| |||

AGGGACCGAA ACTCG GAC
 G ____
 GAM1999 LOC158056 5' CTCAGCCCAGGAGAGCCAGGGG 82589 ATGAGCA
 TCCCTGGCTT GGCTGAG
 ||||| |||||
 GGGGACCGAG CCGACTC
 AGGAC__
 GAM1999 LOC219405 3' CAGCCTGCTCTACCCAGAGA 92450 C CTTAT
 TC CTGG GAGCAGGCTG
 || ||| |||||
 AG GACC CTCGTCCGAC
 A CAT__
 GAM1999 LOC221496 3' TCAGCCTGCTCCCTGGGA 93643 T CTTAT
 TCCC GG GAGCAGGCTGA
 ||| || |||||
 AGGG CC CTCGTCCGACT
 T ____
 GAM1999 LOC222031 3' CAGCCTGTCTAACCCAAAGA 95672 CC C T G
 TC TGG TTA GA CAGGCTG
 || ||| ||| |||||
 AG ACC AAT CT GTCCGAC
 AA C _ _
 GAM1999 LOC51320 3' CTGCAACTAATAAGCCAAGGA 34028 C GA__
 TCC TGGCTTAT GCAG
 ||| ||||| |||
 AGG ACCGAATA CGTC
 A ATCAA
 GAM2000 PVR 3' ATAAATCACATCATTAGCATG 22488 GTATT
 CA ATGATGTGATTTAT
 || |||||
 GT TACTACACTAAATA
 ACGAT
 GAM2000 FLJ20033 3' TATATCATAATCTGGCA 34823 T
 TGCCAG ATTATGATGTG
 ||||| |||||
 ACGGTC TAATACTATAT
 -
 GAM2000 FLJ21313 3' TACATCATATACTGACA 43933 C T
 TG CAGTAT ATGATGTG
 || ||||| |||||
 AC GTCATA TACTACAT
 A _
 GAM2000 LOC219333 3' ATAATGTTTCATCATAACCCTAG 95183 C TA TGAT
 CA TGC AG TTATGATG TTAT
 ||| || ||||| |||
 ACG TC AATACTAC AATA
 A CC TTGT
 GAM2001 DMD 5' ACCTGAGAAACAAGGAGA 15699 _ A
 TCTCCTTG TC CAGGT
 ||||| || |||

			AGAGGAAC AG GTCCA		
			AA A		
GAM2001	DMD	5'	ACCTGAGAAACAAGGAGA 15713	___	A
			TCTCCTTG TC CAGGT		
			AGAGGAAC AG GTCCA		
			AA A		
GAM2001	DMD	5'	ACCTGAGAAACAAGGAGA 15718	___	A
			TCTCCTTG TC CAGGT		
			AGAGGAAC AG GTCCA		
			AA A		
GAM2001	KCNS2	3'	AGTTTTAGTACCAAAACAAAGA 68843	C	CACA _
	GA		TCTC TTGT GGT TTAAAACT		
			AGAG AACA CCA GATTTTGA		
			A AAA_ T		
GAM2001	KCNS3	3'	TTTAAATTACTGACAAGTAGA 11197	C	CA
			TCT CTTGTCA GGTTTAAA		
			AGA GAACAGT TTAAATTT		
			T CA		
GAM2001	NTRK2	3'	AGCCTGTGTATAAAAAAGA 21633	CC_	_
			TCT TTGT CACAGGTT		
			AGA AATA GTGTCCGA		
			AAA T		
GAM2001	PPP1R12B	3'	AGTTTTCTTGACACAAG 50378		TTT
			CTTGTCACAGG AAAACT		
			GAACAGTGTTT TTTTGA		
			C_		
GAM2001	PYCR1	5'	AGTTGACACCCCAACAAGGA 70638		CACA_ TTAA
	GA		TCTCCTTGTT GGT AACT		
			AGAGGAACA CCA TTGA		
			ACACC CAG_		
GAM2001	SPTBN2	5'	AGCCTCTGGCCACAAGGAGA 23691	___	C
			TCTCCTTGTT CA AGGTT		
			AGAGGAACA GT TCCGA		
			CCG C		
GAM2001	STK4	3'	AGTTTTAAACCCAGGAACAGA 21863		CTTG ACA_
	GA		TCTC TC GGTTTAAACT		
			AGAG AG CCAAATTTTGA		
			ACA_ GACC		
GAM2001	TEX15	3'	TAAATGTGACAAGAGA 49225	C	GG
			TCTC TTGTCACA TTTA		

AGAG AACAGTGT AAAT
 _ A_
 GAM2001 TGM2 5' AGTTCTAAACTTGAACAA 17241 CA A
 TTGT CAGGTTTA AACT
 |||| ||||| ||||
 AACA GTTCAAAT TTGA
 AA C
 GAM2001 CTCFL 3' AGTTTTAAACCTTGAATGAGA 83390 CTTG C
 TCTC TCA AGGTTTAAACT
 |||| || ||||| ||||
 AGAG AGT TCCAAATTTTGA
 TA__ _
 GAM2001 FLJ21657 3' AGCCTGTGTGACAAAGGGA 42795 C _
 TCTC TTGTCACA GGTT
 |||| ||||| ||||
 AGGG AACAGTGT CCGA
 A GT
 GAM2001 FLJ21816 3' GTTTTAAATATAAAGGAGA 45475 GTCACAG
 TCTCCTT GTTTAAAC
 ||||| |||||
 AGAGGAA TAAATTTTG
 ATA____
 GAM2001 H11 5' TATTCCTGTGACAGGAGA 27639 T TT
 TCTCCT GTCACAGG TA
 ||||| ||||| ||
 AGAGGA CAGTGTCC AT
 _ TT
 GAM2001 HSA275986 3' TTGAGCCTATGAGAAAGAGA 37860 C G C
 TCTC TT TCA AGGTTTAA
 |||| || || |||||
 AGAG AA AGT TCCGAGTT
 A G A
 GAM2001 KIAA1423 3' TTTAAGCCCAAAAGGAGA 62399 GTCACA
 TCTCCTT GGTTTAA
 ||||| |||||
 AGAGGAA CCGAATT
 AAC____
 GAM2001 OS4 3' AGTCTCAAACCTGTGGGGAAGG 20382 _G AAA
 AG CTCCT T TCACAGGTTT ACT
 ||||| ||||| ||||| ||||
 GAGGA G GGTGTCCAAA TGA
 A G CTC
 GAM2001 PB1 3' TTTTAAACCTGTTACATTGA 36884 CT C
 TC TGT ACAGGTTTAAAA
 || ||||| |||||
 AG ACA TGTCCAAATTTT
 TT T
 GAM2001 PRO1866 5' TTTTAGAGACAAGGA 38151 ACAGG
 TCCTTGTC TTAAAA
 ||||| |||||

AGGAACAG AGATTTT

GAM2001 LOC151778 5' CTTGTATGAAGACAAGGAGA 71948

TCTCCTTGTC ACAGG

||||||| ||||

AGAGGAACAG TGTTT

AAGTA

GAM2001 LOC152179 5' AGTTTAAAAAGAAGAAAGGAG 86741

G ACAGG

A

TCTCCTT TC TTAAAACT

||||| || |||||

AGAGGAA AG AAATTTTGA

_ AAGAA

GAM2001 LOC220965 3' AGTTTAATTATATACAAGGAGA 93088

CACA TA

TCTCCTTGT GGTT AAAC

||||||| ||| ||||

AGAGGAACA TTAA TTTGA

TATA _

GAM2001 LOC256307 3' AGTCTTGGAGTCAGACAAGGA 98839

ACA _ A

TCCTTGTC GG TTAA ACT

||||||| || ||||| |||

AGGAACAG CT AGGTT TGA

A_ G C

GAM2001 LOC256598 5' CTTGTAAGAAGACAAGGAGA 98105

TCTCCTTGTC ACAGG

||||||| ||||

AGAGGAACAG TGTTT

AAGAA

GAM2002 ATP2B2 5' CAGCCATCACCCGGCAGC 9846 A

GCT CTGGGTGA GCTG

||| ||||| ||||

CGA GGCCCACT CGAC

C AC

GAM2002 BSCL2 5' GGA CTACCGGCTTTACCTCCC 51994

T_ T_ ACTA

AGTAGCT

AGCTACTGGG GAGC GG CC

||||||| |||| || ||

TCGATGACCC TTCG CC GG

TCCCAT G_ ATCA

GAM2002 IMPA2 5' AGTGTGTGCTCACCCACAGC 96944

AC _ G

GCT TGGGTGAGC TG ACT

||| ||||| || ||||

CGA ACCCACTCG GT TGA

C_ T G

GAM2002 KCNE1L 3' AGTCCAGCTTCCAGTTGC 25388 T GT

GC ACTGG GAGCTGACT

|| ||||| |||||

CG TGACC TTCGACCTGA

T _

GAM2002 KRTHA1 3' GGCAGCCAAGAACTCACCCAA 11237 AC

C_ A A

AGC

GCT TGGGTGAG TGG CT CC

||| ||||| ||| || ||

CGA ACCCACTC ACC GA GG
 A_ AAAGA _ C
 GAM2002 MADH7 3' AGTATTGCTCACCCAGTGC 20922 T TGG
 GC ACTGGGTGAGC ACT
 || ||||| ||
 CG TGACCCACTCG TGA
 _ TTA
 GAM2002 RXRA 3' GTTGTTCACCCAGAGC 12922 A TG
 GCT CTGGGTGAGC GAC
 || ||||| ||
 CGA GACCCACTTG TTG
 _ _
 GAM2002 SQSTM1 3' GTACCAGCAGCCCAGCACATAG 15329 ____ GA T__ ACTA
 CT AGCTA CTGGGT GC GG C
 |||| |||| || || |
 TCGAT GACCCG CG CC G
 ACAC A_ A__ ATC
 GAM2002 TPI1 3' AGCCCAGAAGCCAGTAACT 6294 C GAG A
 AG TACTGGGT CTGG CT
 || ||||| |||| ||
 TC ATGACCCG GACC GA
 A AA_ C
 GAM2002 TRHDE 3' GGTATTCTACCCAGTAG 26316 CTGG
 CTACTGGGTGAG ACT
 ||||| ||
 GATGACCCACTC TGG
 TTA_
 GAM2002 C11orf21 3' AGTCCAGCCCATGGAGC 27100 A GG A
 GCT CT GTG GCTGGACT
 ||| || |||||
 CGA GG TAC CGACCTGA
 _ _ C
 GAM2002 CAPN6 3' CAGCATTTTCACCCAGCAGC 27398 A ____
 GCT CTGGGTGA GCTG
 || ||||| ||
 CGA GACCCACT CGAC
 C TTA
 GAM2002 DT1P1A10 3' AGTTTCTGGGCCACCTAGCA 62246 A _ A ____
 GC GCT CT GGGTG GCT GGACT
 ||| || |||| ||||
 CGA GA CCCAC CGG TTTGA
 C T C GTC
 GAM2002 FLJ12700 3' GGCAGTCCACAGGCCTACAGCT 46657 AC GAGC A
 AGCT TGGGT TGGACT CC
 |||| |||| |||| ||
 TCGA ATCCG ACCTGA GG
 C_ GAC_ C
 GAM2002 FLJ32780 3' AGTCCTCTGGTCCCACAGCT 59297 AC _G CT
 AGCT TGGG T AG GGACT
 |||| |||| | || ||||

TCGA ACCC G TC CCTGA
C_ T G T_
GAM2002 HRD1 3' CCTGTCTCACCCAGCAGC 70148 A _T
GCT CTGGGTGAG C GG
||| ||||| | ||
CGA GACCCACTC G CC
C T T
GAM2002 KIAA0356 3' GGTCTATGGGCCCACCCAGTGC 66779 T A ____
GC ACTGGGTG GCT GGACT
|| ||||| ||| |||||
CG TGACCCAC CGG TCTGG
_ C GTA
GAM2002 KIAA0984 3' AGCTCACTCACCCACCAGCT 66137 AC C GA
AGCT TGGGTGAG TG CT
||| ||||| || ||
TCGA ACCCACTC AC GA
CC _ TC
GAM2002 KIAA1598 5' GTAGTCCAAGTGGGATATTAGC 37639 ____ G GAGC
GCTA CT GGT TGGACTAC
||| || ||| |||||
CGAT GG TCA ACCTGATG
TATA G ____
GAM2002 KIAA1681 3' AGTCCAAGTCCAGTAACT 61714 C GTGA _
AG TACTGG GCT GGACT
|| ||||| ||| |||||
TC ATGACC TGA CCTGA
A ____ A
GAM2002 MGC17303 3' GGCAGTCAGATCCACCCAGTGC 58233 T AG_ G A
T AGC ACTGGGTG CTG ACT CC
||| ||||| ||| ||| ||
TCG TGACCCAC GAC TGA GG
_ CTA _ C
GAM2002 PDE4DIP 5' CCAGTGGTCACCCAGTAGC 97175 _ T____
GCTACTGGGTGA GC GG
||||||| || ||
CGATGACCCACT TG CC
GG A____
GAM2002 SLC26A10 5' CCGGTAACCCAACAGTGGCT 56842 ____ GA T____
AGCTACT GGGT GC GG
||||| ||| || ||
TCGGTGA CCCA TG CC
CAA A_ G____
GAM2002 USP2 5' AGCCGGGACTCACCCGCAGCT 16108 AC _ A
AGCT TGGGTGAG CTGG CT
||| ||||| ||| ||
TCGA GCCCACTC GGCC GA
C_ AG _
GAM2002 LOC143425 3' CTACTIONCAGTAGCT 89013 C
AGCTACTGGGTGAG TGG
||||||| ||| |||

TCGATGACTCACTC ATC

GAM2002 LOC145828 5' AGTCCCTCCCAGTGGCT 84537 TGAGCT
AGCTACTGGG GGACT
||||||| ||||
TCGGTGACCC CCTGA
TC____

GAM2002 LOC151174 5' GGCCCGGCTCACCCACAGCT 86438 ACT A
AGCT GGGTGAGCTGG CT
||| ||||||||| ||
TCGA CCCACTCGGCC GG
CAC C

GAM2002 LOC158055 3' AGGCCTCCACCCAGTGCT 82576 T AGCT A
AGC ACTGGGTG GG CT
||| ||||||| |||
TCG TGACCCAC CC GA
CT__ G

GAM2002 LOC158696 3' GTAGATCCACCAATAGCT 82861 C GTGAGC _
AGCTA TGG TGG A CTAC
||||| ||| ||| |||
TCGAT ACC ACCT GATG
A _____ A

GAM2002 LOC196027 3' GGTTTTCACCCAGTAGTT 88940 CTG
AGCTACTGGGTGAG GACT
||||||||| |||
TTGATGACCCACTT TTGG

GAM2002 LOC200812 5' CAGCCCATCCAGTATGCT 90301 _ A
AGC TACTGGGTG GCTG
||| ||||||| |||
TCG ATGACCTAC CGAC
T C

GAM2002 LOC253836 5' CAGCGCTTCACCCAGTGC 99465 T ____
GC ACTGGGTGA GCTG
|| ||||||| |||
CG TGACCCACT CGAC
TCG

GAM2002 LOC256436 3' AGCCCAGAAGCCCAGTAACT 96247 C GAG A
AG TACTGGGT CTGG CT
|| ||||||| ||| ||
TC ATGACCCG GACC GA
A AA_ C

GAM2002 LOC256492 5' TCCAGCTCAGTACAGCAGC 99434 A GG_
GCT CTG TGAGCTGGA
||| ||| |||||||
CGA GAC ACTCGACCT
C ATG

GAM2002 LOC56181 3' GTCACCTCACTCAGCAGCT 97284 A CTG
AGCT CTGGGTGAG GAC
||||| ||| |||

			TCGA GACTCACTC CTG		
			C A__		
GAM2002	LOC92148	5'	TCTACACACCCAGTACT 68888	C	AGC
			AG TACTGGGTG TGGA		
			TC ATGACCCAC ATCT		
			_ AC_		
GAM2003	BACH2	3'	CTGTCAAGCAATGGATAAACAG 41782	C	GGGA__
			CTCT AGAGTTGTT ATCCA GACAG		
			TCTCGACAA TAGGT CTGTC		
			A AACGAA		
GAM2003	CHRNA1	3'	CTGTCTCCCTGAAGAGTGAAC 5375	C__	
			GTTTCAT CAGGGAGACAG		
			CAAGTG GTCCCTCTGTC		
			AGAA		
GAM2003	FZD8	3'	CCATGGATAACAACCTCT 49873	C	G
			AGAGTTGTT ATCCA GG		
			TCTCAACAA TAGGT CC		
			_ A		
GAM2003	HHIP	5'	CTGTCCCACCTAAACAACCTC 42753		CATCCAG A
			GAGTTGTT GG GACAG		
			CTCAACAA CC CTGTC		
			ATCCA__ _		
GAM2003	MME	3'	TCCCTATGGAGGAACAACCTCT 8034	A	_
			AGAGTTGTTC TCCA GGGA		
			TCTCAACAAG AGGT CCCT		
			G AT		
GAM2003	MME	3'	TCCCTATGGAGGAACAACCTCT 24437	A	_
			AGAGTTGTTC TCCA GGGA		
			TCTCAACAAG AGGT CCCT		
			G AT		
GAM2003	MME	3'	TCCCTATGGAGGAACAACCTCT 24439	A	_
			AGAGTTGTTC TCCA GGGA		
			TCTCAACAAG AGGT CCCT		
			G AT		
GAM2003	MME	3'	TCCCTATGGAGGAACAACCTCT 24441	A	_
			AGAGTTGTTC TCCA GGGA		
			TCTCAACAAG AGGT CCCT		
			G AT		
GAM2003	MTCP1	5'	CTACATGGATAACAACCTCT 27242	C	GGG
			AGAGTTGTT ATCCA AG		

TCTCAACAA TAGGT TC
 _ ACA
 GAM2003 NR1D1 3' TGTCTCCCCACAACCCT 41672 A TCATCCA
 AG GTTGT GGGAGACA
 || |||| |||||
 TC CAACA CCCTCTGT
 C CC____
 GAM2003 NR1I2 3' TGTCTCCCTAGGGAATTC 42088 GTTCA _
 GAGTT TCC AGGGAGACA
 |||| ||| |||||
 CTTAA GGG TCCCTCTGT
 _____ A
 GAM2003 NR1I2 3' TGTCTCCCTAGGGAATTC 15304 GTTCA _
 GAGTT TCC AGGGAGACA
 |||| ||| |||||
 CTTAA GGG TCCCTCTGT
 _____ A
 GAM2003 PCOLN3 3' CTGCCCTGTTGCCAAACAACCTC 12411 ____ TC _
 GAGTTGTT CA CAGGG AG
 ||||| || |||||
 CTCAACAA GT GTCCC TC
 ACC T_ G
 GAM2003 PFN2 3' TGTCTTCATCAACAACCCT 12063 A CATCCAG
 AG GTTGT GGAGACA
 || |||| |||||
 TC CAACAA CTTCTGT
 C CTA____
 GAM2003 PFN2 3' TGTCTTCATCAACAACCCT 54890 A CATCCAG
 AG GTTGT GGAGACA
 || |||| |||||
 TC CAACAA CTTCTGT
 C CTA____
 GAM2003 TNS 3' CTGTCTCCCTAACTCAACTGCT 42950 _ TTCATCC
 AG AGTTG AGGGAGACAG
 || |||| |||||
 TC TCAAC TCCCTCTGTC
 G TCAA____
 GAM2003 FLJ10511 3' CCCTAGAAAAACAACCTCT 36686 CA C
 AGAGTTGTT TC AGGG
 ||||| || ||||
 TCTCAACAA AG TCCC
 AA A
 GAM2003 FLJ20195 3' CCCGATGAACACCTCT 35216 T CA
 AGAG TGTTCATC GGG
 ||| ||||| ||
 TCTC ACAAGTAG CCC
 C _
 GAM2003 HAAO 3' TCCCTGCCAAACAACCTCT 60173 CATC
 AGAGTTGTT CAGGGA
 ||||| |||||

		TCTCAACAA GTCCCT		
		ACC_		
GAM2003 KIAA0843	3'	CTGAACAACCAGACAGACAACT 30801		CA CA GAGA_
	CT	AGAGTTGTT TC GG CAG		
		TCTCAACAG AG CC GTC		
		AC A_ AACAA		
GAM2003 KIAA1497	5'	CTGTCCTTGTATGAGCAAC 68121	C	GA
		GTTGTTTCAT CAGGGA CAG		
		CAACGAGTA GTTCCT GTC		
		T _		
GAM2003 KIAA1710	3'	TCTCCATACATGAACAATCT 63181	G	CCAG
		AGA TTGTTTCAT GGAGA		
		TCT AACAAGTA CCTCT		
		_ CATA		
GAM2003 PDE7B	3'	CTGCCGAAATGAGCAACTC 38949		CCA G
		GAGTTGTTTCAT GG AG		
		CTCAACGAGTA CC TC		
		AAG G		
GAM2003 SEC24B	3'	CTGCATTGTTGGATGACAACTC 21984	T	G GA
	T	AGAGTTGT CATCCAG GA CAG		
		TCTCAACA GTAGGTT TT GTC		
		_ G AC		
GAM2003 LOC124753	5'	CTGCCTCCCTGGCTTCCATCTC 74803	T	TTCAT A
		GAG TG CCAGGGAG CAG		
		CTC AC GGTCCCTC GTC		
		T CTTC_ C		
GAM2003 LOC142948	3'	CTACCGGGAGGAATGAATAACT 83777		___ A G
	C	GAGTTGTTCA TCC GG AG		
		CTCAATAAGT AGG CC TC		
		AAGG G A		
GAM2003 LOC153914	5'	CCACTAAAGTGAACAACTC 81898		CC_ _
		GAGTTGTTTCAT AG GG		
		CTCAACAAGTG TC CC		
		AAA A		
GAM2003 LOC219445	5'	CTCCCTGGTTCAAACAATTC 93202		CAT_
		GAGTTGTT CCAGGGAG		
		CTTAACAA GGTCCCTC		
		ACTT		
GAM2003 LOC219914	5'	CCACTGGGAGGAACGAACAACT 94967		A_____ _
	C	GAGTTGTTCC TCCAG GG		

CTCAACAAG GGGTC CC
 CAAGGA A
 GAM2004 CD1D 5' CCCAAGAATGCTACTTCAG 80268 A G A
 CT AAGTAGCGT CT GGG
 || ||||| || |||
 GA TTCATCGTA GA CCC
 C A A
 GAM2004 GGA1 3' CCCCCAGCTATTTGCACTCTGG 26277 A A T__ A
 CTA AGT GCG GCT GGGG
 ||| ||| ||| |||
 GGT TCA CGT CGA CCCC
 C _ TTAT C
 GAM2004 KCND3 3' CCCCTAGCACTGAGACTT 18352 AG_
 AAGT C GTGCTAGGGG
 |||| | |||||
 TTCA G CACGATCCCC
 GA T
 GAM2004 LETM1 3' GCCCCTGGGCTCCTTCAG 25555 A T GTG
 CT AAG AGC CTAGGGGC
 || ||| ||| |||||
 GA TTC TCG GGTCCCCG
 C C _
 GAM2004 PDE4A 3' GCCCCCGCCCCACTTCTAG 21685 _ AGC CTA
 CTA AAGT GTG GGGGC
 ||| ||| ||| |||||
 GAT TTCA CGC CCCCG
 C CCC C_
 GAM2004 RAD51L3 5' CCCCCAGCCCTACCCTTGG 56884 A_ CGT A
 CTAA GTAG GCT GGGG
 |||| ||| ||| |||
 GGTT CATC CGA CCCC
 CC C_ C
 GAM2004 SFTPA2 3' CCCCAGGCAGCCACTCCTAG 23627 A_ A G A
 CTA AGT GC TGCT GGGG
 ||| ||| ||| ||| |||
 GAT TCA CG ACGG CCCC
 CC C _ A
 GAM2004 TNFAIP6 5' GCCCCTAACAGGCTGTACTT 60166 T ____
 AAGTAGCG GCT AGGGGC
 ||||| ||| |||||
 TTCATTGT CGG TCCCCG
 _ ACAA
 GAM2004 CGI-01 3' GCCCCTAGCACACACTGC 32505 C_
 GTAG GTGCTAGGGGC
 |||| ||||| |||||
 CGTC CACGATCCCCG
 ACA
 GAM2004 DKFZP566M114 5' CCCCAGGTCTTTACTTTA 50448 CGT A
 TAAAGTAG GCT GGGG
 ||||| ||| |||

ATTCATT TGG CCCC
 TC_ A
 GAM2004 FLJ10357 3' GCCCTGCCACCACTATCTCTAG 36552 A _ C_ CTA
 CTA AG TAG GTG GGGGC
 ||| ||| ||| ||||
 GAT TC ATC CAC TCCCG
 C T AC CG_
 GAM2004 FLJ10687 3' CCCCTCCAGACTACTTTA 36945 CG CT
 TAAAGTAG TG AGGGG
 ||||| || ||||
 ATTCATC AC TCCCC
 AG C_
 GAM2004 FLJ11722 3' GCCCCAGGGTTTATTTTAG 47003 GCG G A
 CTAAAGTA T CT GGGGC
 ||||| | || ||||
 GATTTTAT G GA CCCCG
 TT_ G C
 GAM2004 FLJ12587 3' GCCCCTGGGGGCCTCTTCAG 42780 A TA GTG
 CT AAG GC CTAGGGGC
 || ||| || |||||
 GA TTC CG GGTCCCCG
 C TC GG_
 GAM2004 KIAA0356 3' GCCCCTAGCTCTTCTCTAG 66774 A T CGT
 CTA AG AG GCTAGGGGC
 ||| || |||||
 GAT TC TC CGATCCCCG
 C T T__
 GAM2004 KIAA0399 3' GCCCTGTGCACACTCCTTTAG 31363 T C TA
 CTAAAG AG GTGC GGGGC
 ||||| || ||| ||||
 GATTTC TC CACG TCCCG
 C A TG
 GAM2004 KIAA1634 3' CCCCAAACATCACTACTTTA 64123 C_ CTA
 TAAAGTAG GTG GGGG
 ||||| ||| |||
 ATTCATC TAC CCCC
 AC AAA
 GAM2004 KIAA1718 3' GCCCAGGGCATGCTACTTTA 64977 AG
 TAAAGTAGCGTGCT GGGC
 ||||| ||||| |||
 ATTCATCGTACGG CCG
 GA
 GAM2004 RAB3D 3' CCCCTAGCACTCCGGCTCT 16258 T ____
 AG AGC GTGCTAGGGG
 || ||| |||||
 TC TCG CACGATCCCC
 _ GCCT
 GAM2004 LOC123036 3' GCCCCATTCTTACTTTG 74647 C_ CTA
 TAAAGTAG GTG GGGGC
 ||||| ||| ||||

GTTTCATT TAC CCCCG
 CT ____
 GAM2004 LOC146174 3' GCCATTTTACAGCACTTTAG 78200 A _ CTAGG
 CTAAAGT GC GTG GGC
 ||||| || ||| |||
 GATTTC A CG CAT CCG
 _ A TTTA_
 GAM2004 LOC151451 3' CCCCTCACCAACTACTTTA 81048 C__ CT
 TAAAGTAG GTG AGGGG
 ||||| || |||||
 ATTTTCATC CAC TCCCC
 AAC ____
 GAM2004 LOC201158 3' GCCCCCAGCAGCGCTGCTTTG 61087 _ A
 TAAAGTAG CGTGCT GGGGC
 ||||| ||||| |||||
 GTTTCGTC GCACGA CCCCG
 C C
 GAM2004 LOC219842 5' GCCCCTCTGCCTCCTCTAG 94891 A T C GCT
 CTA AG AG GT AGGGGC
 ||| ||| ||| |||||
 GAT TC TC CG TCCCCG
 C C _ TC_
 GAM2005 LARGE 3' AATAATTATGCTTCCCATC 56925 CCTT
 GATGGGAAGT ATTATT
 ||||| |||||
 CTACCCTTCG TAATAA
 TAT_
 GAM2006 NEURL 3' CCACTATGGGTCTCCACTACCC 16127 T CC C
 A
 TGGGT AGTGG GCTCA AGTGG
 |||| |||| |||| |||||
 ACCCA TCACC TGGGT TCACC
 _ TC A
 GAM2006 FLJ12154 3' CACTGTGAACAGTAAGCCA 41955 G G GCCGC
 TGG TTA TG TCACAGTG
 ||| ||| || |||||
 ACC AAT AC AGTGTCAC
 G G A____
 GAM2006 FLJ14082 3' CCACTGTGAGCACTCCACCCA 47318 TAGT CC_
 TGGGT GG GCTCACAGTGG
 |||| || ||||| |||||
 ACCCA CC CGAGTGTCACC
 ____ TCA
 GAM2006 LOC197408 5' CCACTCTGCTGCGGCCACATAA 91316 _ T_ C
 CCCA
 TGGGTTA GTGGCCGC CA AGTGG
 ||||| ||||| || |||||
 ACCCAAT CACCGGCG GT TCACC
 A TC C
 GAM2007 AMPH 3' CGACTACACTGAGGCA 9686 CCAC _
 TGTCTCAGTGT AG CG
 ||||| || |||

ACGGAGTCACA TC GC
 _____ A
 GAM2007 B3GAT1 3' TGCTGGGACACTGAGCA 38456 T A
 TG CTCAGTGTCC CAGCG
 || ||||| ||||
 AC GAGTCACAGG GTCGT

— —
 GAM2007 B3GAT1 3' TGCTGGGACACTGAGCA 55059 T A
 TG CTCAGTGTCC CAGCG
 || ||||| ||||
 AC GAGTCACAGG GTCGT

— —
 GAM2007 BF 5' GCTTGGACACTGAGCCA 9922 T C
 TG CTCAGTGTCCA AGC
 || ||||| ||||
 AC GAGTCACAGGT TCG
 C —

GAM2007 D10S170 3' TGCAGTGGAACTGAGTCA 19550 T _ A
 TG CTCAGTGT CCAC GCG
 || ||||| ||||
 AC GAGTCACA GGTG CGT
 T A A

GAM2007 DTNB 3' CTGACGACGACTGAGACA 53679 _ CA
 TGTCTCAGT GTC CAG
 ||||| ||||
 ACAGAGTCA CAG GTC
 G CA

GAM2007 EZH1 3' ATGCACTGTGTCTCCCACTG 10547 C_____ C ____
 AGA TCTCAGTGT CACAG GCA T
 ||||| ||||| |
 AGAGTCACA GTGTC CGT A
 CCCTCT A ____

GAM2007 GNAS 3' TGCGCTGTGGACACTGAGA 33918
 TCTCAGTGTCCACAGCGCA
 ||||| ||||| |||||
 AGAGTCACAGGTGTCGCGT

GAM2007 IAPP 5' TGCTGACATTGAAACA 6444 C CAC
 TGT TCAGTGTC AGCG
 || ||||| ||||
 ACA AGTTACAG TCGT
 A ____

GAM2007 KPNA3 3' TGCGCTGTGGATCAAGACA 11224 CAGT
 TGTCT GTCCACAGCGCA
 |||| ||||| |||||
 ACAGA TAGGTGTCGCGT
 AC__

GAM2007 PABPN1 5' GCGCCGTGGACATAGGC 17357 CA A
 GTCT GTGTCCAC GCGC
 |||| ||||| ||||

CGGA TACAGGTG CGCG
 — C
 GAM2007 SPTBN4 3' GCACTGTGGGCACAAAGACA 48157 CA C
 TGTCT GTGTCCACAG GC
 |||| ||||| ||
 ACAGA CACGGGTGTC CG
 AA A
 GAM2007 VENTX2 3' TGCATGAAACCTGAGACA 27869 T CCA GC
 TGTCTCAG GT CA GCA
 ||||| || || ||
 ACAGAGTC CA GT CGT
 — AA_ A_
 GAM2007 CDIPT 5' GCGCTGCGGGGCTGGGACA 21976 G A
 TGTCTCAGT TCC CAGCGC
 ||||| || |||||
 ACAGGGTCG GGG GTCGCG
 — C
 GAM2007 DKFZP434I216 5' CGCGGTTCACTGAGAC 78232 CC A
 GTCTCAGTGT AC GCG
 ||||| || ||
 CAGAGTCACA TG CGC
 CT G
 GAM2007 DKFZP434K046 3' TGCAATGAACCTGAGACA 93410 T C CA
 TGTCTCAG GT CA GCG
 ||||| || || ||
 ACAGAGTC CA GT CGT
 — A AA
 GAM2007 DKFZP547L112 5' CGCACTGGACTGAGGCA 67129 GT CA
 TGTCTCA GTCCA GCG
 ||||| |||| ||
 ACGGAGT CAGGT CGC
 — CA
 GAM2007 DKFZP667O116 3' TGCACTGTGGAACAGAGCTGAG 95942 — — C
 AC GTCTCAGT GT CCACAG GCA
 ||||| || ||||| ||
 CAGAGTCG CA GGTGTC CGT
 AGA A A
 GAM2007 DREV1 3' TGCAGTGAACACTGAGTCA 32620 T C A
 TG CTCAGTGT CAC GCG
 || ||||| || ||
 AC GAGTCACA GTG CGT
 T A A
 GAM2007 FAM3A 3' GCGCTGCCGGGCGGACA 41732 CAGT A_
 TGTCT GTCC CAGCGC
 |||| || |||||
 ACAGG CGGG GTCGCG
 — CC
 GAM2007 FLJ14100 3' CGCTGGCGCTGAGACA 47333 CCA
 TGTCTCAGTGT CAGCG
 ||||| ||||

ACAGAGTCGCG GTCGC

GAM2007 FLJ20288 5' GCACTGTGGATCCAGAGACA 45445 AGT C
TGTCTC GTCCACAG GC
||||| ||||| ||
ACAGAG TAGGTGTC CG
ACC A

GAM2007 FLJ21945 3' TGCTTGACACTGGACA 48096 T CAC
TGTC CAGTGTC AGCG
||| ||||| |||
ACAG GTCACAG TCGT

— T—
GAM2007 FLJ23790 5' TGCGCTGTTGATAAGAT 59275 CAG C
GTCT TGTC ACAGCGCA
||| ||| |||||
TAGA ATAG TGTCGCGT
— T

GAM2007 HUMGT198A 3' TGCAGGCAACACTGAGACA 33792 — ACA
TGTCTCAGTGT CC GCG
||||||| || |||
ACAGAGTCACA GG CGT
AC A—

GAM2007 HUMGT198A 3' TGCAGGCAACACTGAGACA 26140 — ACA
TGTCTCAGTGT CC GCG
||||||| || |||
ACAGAGTCACA GG CGT
AC A—

GAM2007 KIAA0258 3' GCGAAACGGACACTGAACA 29471 C ACAG
TGT TCAGTGTCC CGC
||| ||||| |||
ACA AGTCACAGG GCG
— CAAA

GAM2007 KIAA0775 5' CGCGGGCACCCTGAGACA 28953 — ACA
TGTCTCA GTGTCC GCG
||||| ||||| |||
ACAGAGT CACGGG CGC
CC —

GAM2007 KIAA0795 5' TGCGCCAGTTTGCTGAGACA 47233 TCCACA
TGTCTCAGTG GCGCA
||||||| |||||
ACAGAGTCGT CGCGT
TTGAC—

GAM2007 KIAA1091 3' TGCGCTGTGATGACGAGA 70265 AGT —
TCTC GTC CACAGCGCA
||| ||| |||||
AGAG CAG GTGTCGCGT
— TA

GAM2007 KIAA1679 3' TGCGCTGTGGAGGAGG 70718 AGTG
TCTC TCCACAGCGCA
||| |||||

			GGAG AGGTGTCGCGT		
			G___		
GAM2007	MGC10067	3'	TGCTGGACACTGAAGCA	59592	TC CA
			TG TCAGTGTCCA GCG		
			AC AGTCACAGGT CGT		
			GA ___		
GAM2007	MGC15875	5'	CGCTGGCCCTGAGGCA	53014	T CCA
			TGTCTCAG GT CAGCG		
			ACGGAGTC CG GTCGC		
			C ___		
GAM2007	STI2	3'	TGCACTGTGGACACAGTGAG	90408	___ C
			CTCA GTGTCCACAG GCA		
			GAGT CACAGGTGTC CGT		
			GA A		
GAM2007	TMSB10	3'	TGCACTGTGAACCTGGGCA	41192	T T C C
			TGTC CAG GT CACAG GCA		
			ACGG GTC CA GTGTC CGT		
			_ _ A A		
GAM2007	TREX1	5'	TGCGCTGTCTGCGGGACA	54384	AGT CC
			TGTCTC GT ACAGCGCA		
			ACAGGG CG TGTCGCGT		
			___ TC		
GAM2007	TREX1	5'	TGCGCTGTCTGCGGGACA	54390	AGT CC
			TGTCTC GT ACAGCGCA		
			ACAGGG CG TGTCGCGT		
			___ TC		
GAM2007	ZNF185	3'	CGTGGTGGACACTAACACA	24094	CTC A
			TGT AGTGTCCAC GCG		
			ACA TCACAGGTG TGC		
			CAA G		
GAM2007	LOC146337	3'	CGCTGTGGACTGAGCTGCA	84639	___ GT
			TGT CTCA GTCCACAGCG		
			ACG GAGT CAGGTGTCCG		
			TC ___		
GAM2007	LOC150094	3'	TGCCGACGCTGAGACA	86007	CACA
			TGTCTCAGTGTC GCG		
			ACAGAGTCGCAG CGT		
			C___		
GAM2007	LOC155006	3'	CTTTGAGAGACTGAGACA	82170	G _ C
			TGTCTCAGT TC CA AG		

		ACAGAGTCA AG GT TC	
		G A T	
GAM2007	LOC197342 3'	CGCCATGTGGGTGTTAGACA 89361	C TG _
		TGTCT AG TCCACA GCG	
		ACAGA TT GGGTGT CGC	
		_ GT AC	
GAM2007	LOC220739 3'	TGCTGAGACTGAGACA 94531	G CAC
		TGTCTCAGT TC AGCG	
		ACAGAGTCA AG TCGT	
		G _	
GAM2007	LOC257109 5'	GCGCGATCTACACTGAGACA 97307	CCACA
		TGTCTCAGTGT GCGC	
		ACAGAGTCACA CGCG	
		TCTAG	
GAM2007	LOC83985 5'	GCGCTGTGTGTCTACTGAGAC 50175	TC_
		GTCTCAGTG CACAGCGC	
		CAGAGTCAT GTGTCGCG	
		CTGT	
GAM2007	LOC91363 3'	TGCGCCATGTGTTGCTCAGACA 66353	C TC _
		TGTCT AGTG CACA GCGCA	
		ACAGA TCGT GTGT CGCGT	
		C T_ AC	
GAM2008	ALDH3B2 5'	CAGGACCTGCATAAGCCAGCT 7340	A_ AA TTA
		GGC GC ATG CAGGTCCTG	
		TCG CG TAC GTCCAGGAC	
		AC AA _	
GAM2008	BAP1 3'	CAGGACCTGGCCCTTCTGCCT 17396	C AT TA
		AGGCAG AA GT CAGGTCCTG	
		TCCGTC TT CG GTCCAGGAC	
		_ CC _	
GAM2008	CSF1R 3'	CAGGACCTCTTAGTCTCTGCC 19053	CAAA TTAC
		GGCAG TG AGGTCCTG	
		CCGTC AT TCCAGGAC	
		TCTG TC_	
GAM2008	DLG5 5'	CAGGACCTGCAGCGACTACTCC 83812	C CAAA A
		GG AG TGTT CAGGTCCTG	
		CC TC GCGA GTCCAGGAC	
		_ ATCA C	
GAM2008	EFNA3 3'	CAGGACCTTGCCCTGCTCACC 18250	C_ AAT TAC
		GG AGCA GT AGGTCCTG	

			CC TCGT CG TCCAGGAC		
			AC CC_ T__		
GAM2008	GARP	3'	GACCTTGTTTTGCTGTCT 19781	TGTT _	
			AGGCAGCAAA ACA GGTC		
			TCTGTCGTTT TGT CCAG		
			____ T		
GAM2008	GNAS	3'	CAGGACCTGCTTCGCTGCC 33915	AAATGTTA	
			GGCAGC CAGGTCCTG		
			CCGTCG GTCCAGGAC		
			CTTC____		
GAM2008	NLGN2	5'	CAGAACCTGCACGGGGCGCTGC 89530	AAA_ TA C	
	C		GGCAGC TGT CAGGT CTG		
			CCGTCG GCA GTCCA GAC		
			CGGG C_ A		
GAM2008	PRDM4	3'	CAGGACCTGCCTTAAGTCTCC 25741	C AAT ____	
	T		AGG AGCA GTTA CAGGTCCTG		
			TCC TCGT CAAT GTCCAGGAC		
			_ ____ TCC		
GAM2008	TRPS1	3'	ACCCATAAATTGTTGCCT 26922	ATG CA	
			AGGCAGCAA TTA GGT		
			TCCGTTGTT AAT CCA		
			A__ AC		
GAM2008	ABCC13	3'	GATGTTTAACATTTCTGCC 57811	C CAG	
			GGCAG AAATGTTA GTC		
			CCGTC TTTACAAT TAG		
			_ TTG		
GAM2008	ARHGDIG	3'	CAGGACTTGAGAACACCTGTGC 8618	G AA A_	
	CT		AGGCA CA TGTT CAGGTCCTG		
			TCCGT GT ACAA GTTCAGGAC		
			_ CC GA		
GAM2008	DKFZP434J046	5'	AGGACCTGGATTGCTACTT 71533	C ATGTTA	
			AGG AGCAA CAGGTCCT		
			TTC TCGTT GTCCAGGA		
			A AG____		
GAM2008	FLJ13215	3'	CAGGACCAGGATTTTCTACC 47194	C C G ACA	
			GG AG AAAT TT GGTCCTG		
			CC TC TTTA GA CCAGGAC		
			A T G ____		
GAM2008	FLJ13215	3'	CAGGACCAGGATTTTCTACC 47195	C C G ACA	
			GG AG AAAT TT GGTCCTG		

CC TC TTTA GA CCAGGAC
 A T G ____
 GAM2008 FLJ22169 5' ATCTATAACATTTGCTGCT 44228 C
 GGCAGCAAATGTTA AGGT
 |||||
 TCGTCGTTTACAAT TCTA
 A
 GAM2008 HRH3 3' CAGGACACTGCCTTTGCTGCCT 24315 T TTA _
 AGGCAGCAAA G CAG GTCCTG
 ||||| | |||||
 TCCGTCGTTT C GTC CAGGAC
 C ____ A
 GAM2008 HSPC128 3' CAGGTTAAAATATCTGCTGCCT 27179 A ACAGGT
 AGGCAGCA ATGTT CCTG
 ||||| ||||| |||||
 TCCGTCGT TATAA GGAC
 C AATT__
 GAM2008 KIAA0977 3' GATATGACATTTGCTGCCT 30435 CAG
 AGGCAGCAAATGTTA GTC
 ||||| ||||| |||||
 TCCGTCGTTTACAGT TAG
 A__
 GAM2008 KIAA1233 3' CTGTACACCTGCTGCCT 63756 AA T
 AGGCAGCA TGT ACAG
 ||||| |||||
 TCCGTCGT ACA TGTC
 CC _
 GAM2008 LYPLA2 3' CAGGACCTCACTCACTAGCC 24386 _ CAAA TTAC
 GGC AG TG AGGTCCTG
 ||| || |||||
 CCG TC AC TCCAGGAC
 A ____ TCAC
 GAM2008 SSI-1 3' AGGACCTGAACTCGCACCT 14982 CA AAAT A
 AGG GC GTT CAGGTCCT
 ||| || |||||
 TCC CG CAA GTCCAGGA
 A_ CT__ _
 GAM2008 LOC145098 5' CTGTGTTAACATTTGCCAACC 77535 CA_ ____
 GG GCAAATGT TACAG
 || ||||| |||||
 CC CGTTTACA GTGTC
 AAC ATT
 GAM2008 LOC149668 5' CAGGACCTCCCAGCCACTGCCT 85695 CAAA TTAC
 AGGCAG TG AGGTCCTG
 ||||| || |||||
 TCCGTC AC TCCAGGAC
 ACCG CC__
 GAM2008 LOC150368 3' CAGGACCTCTCCTTGCTACT 80513 C ATGTTAC
 GG AGCAA AGGTCCTG
 || ||||| |||||

		TC TCGTT TCCAGGAC		
		A CCTC__		
GAM2008	LOC201917 5'	CAGGCTTCCAACCTTTGCTGCC 91872	T	AC T
	T	AGGCAGCAAA GTT AGG CCTG		
		TCCGTCGTTT CAA TTC GGAC		
		T CC _		
GAM2008	LOC202134 5'	CAGTGGCTAGCATTTGCCACCT 91917	CA	ACA _
		AGG GCAAATGTT GGTC CTG		
		TCC CGTTTACGA TCGG GAC		
		AC _ T		
GAM2008	LOC221143 3'	AGGACCTTGGCCTCTGCCT 95212	CAAAT	C
		AGGCAG GTTA AGGTCCT		
		TCCGTC CGGT TCCAGGA		
		TC__ _		
GAM2008	LOC221336 3'	ACTTATGTAACATTTGCTACCT 93888	C	_
		AGG AGCAAATGTTACA GGT		
		TCC TCGTTTACAATGT TCA		
		A AT		
GAM2008	LOC222066 5'	AGGAGAGACATTTGCCACT 94310	CA	ACAGG
		GG GCAAATGTT TCCT		
		TC CGTTTACAG AGGA		
		AC AG__		
GAM2008	LOC255397 5'	AGGACCTGCCCCACTGCC 99366	CAAA	TTA
		GGCAG TG CAGGTCCT		
		CCGTC AC GTCCAGGA		
		__ CC_		
GAM2009	CML66 3'	GGCTAGAATCTCATGTTTTAT 68784	A	_
		ATAGAACAT AGATTT CC		
		TATTTTGTA TCTAAG GG		
		C ATC		
GAM2009	NDST4 5'	AATACTGGATATCTCATGTTCT 42918	A	T A
	A	TAGAACAT AGAT TCCA TATT		
		ATCTTGTA TCTA AGGT ATAA		
		C T C		
GAM2009	LOC151361 5'	AATATTGGAAAGACTTGTTCTT 86499	T	TAAGA
	C	A AGAACA TTTCCAATATT		
		C TCTTGT AAAGGTTATAA		
		T TCAG_		
GAM2009	LOC253150 3'	AATATTGGAAATTTTATTTT 97255	C	
		GAA ATAAGATTTCCAATATT		

CTT TATTTTAAAGGTTATAA

GAM2010 EDNRA 3' CCAAGAAGAAATGCTTTC 64799 T GATT C
GAGA CATT TCTTC TGG
||||| |||||
CTTT GTAA AGAAG ACC
C ____ A

GAM2010 PRPH 3' CCCGATAAGAAGCCAATGATC 21831 AT CC
GATCATTG TTCTT TGGG
||||||| |||||
CTAGTAAC AAGAA GCCC
CG TA

GAM2010 TMEM2 3' CCCAGAAAGCTTAATGAT 26336 TTT C
ATCATTGA CTT CTGGG
||||||| |||
TAGTAATT GAA GACCC
C__ A

GAM2010 TNFSF4 3' CCTTATGAAAAATAATGATCTC 13912 A_ TTCCT
T AGAGATCATTG TTTC GG
||||||| ||| ||
TCTCTAGTAAT AAAG CC
AA TATT_

GAM2010 DCLRE1A 3' CCCAGGAAAAATATAAACTCT 69683 ATCATTG C
AGAG ATTT TTCCTGGG
||| ||| |||||
TCTC TAAA AAGGACCC
AAAATA_ _

GAM2010 DKFZp434F2322 3' CCCATCTGAATCAGTAATCCCT 70300 A C CTTCC
AG GAT ATTGATTT TGGG
|| ||| ||||| |||
TC CTA TGA CTAAG ACCC
C A TCT_

GAM2010 DKFZP566G1424 5' CCTGGAAGAAACCCATAATCCC 85941 A CAT A_ T
T AG GAT TG TTTCTTCC GG
|| ||| ||| ||||| ||
TC CTA AC AAAGAAGG CC
C AT_ CC T

GAM2010 FLJ14326 3' CCATGAGTCAATGACCTC 50764 A TTCT C
GAG TCATTGAT TC TGG
||| ||||| |||
CTC AGTAACTG AG ACC
C ____ T

GAM2010 FLJ20170 5' CCAGGAAACCAGATCTC 35164 AT ATTTC
GAGATC TG TTCCTGG
||||| || |||||
CTCTAG AC AAGGACC
__ CA__

GAM2010 FLJ20249 3' CCCAGAAAGGAAACTGATCTCT 80220 TTGA C
AGAGATCA TTTCTT CTGGG
||||||| ||||| |||||

TCTCTAGT AAGGAA GACCC
 CA__ A
 GAM2010 KIAA0295 3' CCCAGGAAGCTTTCCAGTGATC 68661 ATTT_
 TC GAGATCATTG CTCCTGCG
 ||||| |||||
 CTCTAGTGAC GAAGGACCC
 CTTTC
 GAM2010 KIAA0825 3' CCCAGGAAGACACTGACCTGCT 61683 _ A T ATT
 AG AG TCA TG TCTTCCTGGG
 || || || || |||||
 TC TC AGT AC AGAAGGACCC
 G C C ____
 GAM2010 KIAA1190 3' CCCAAAAAAGTTGATCTCT 71644 TTG C CC
 AGAGATCA ATTT TT TGGG
 ||||| ||| || |||
 TCTCTAGT TGAA AA ACCC
 ____ A A_
 GAM2010 MGC4638 3' CCAGAAAGCATGATTTC 49733 T ATTT C
 GAGATCAT G CTT CTGG
 ||||| | ||| |||
 CTTTAGTA C GAA GACC
 ____ A
 GAM2010 PLPL 3' CCAGGAAAAAGAGTCTC 39820 CATTGA C
 GAGAT TTT TTCCTGG
 |||| ||| |||||
 CTCTG AAA AAGGACC
 AG_____
 GAM2010 RIN3 5' CCCAGGAAAAAACGGATCTCT 46161 ATTGA C
 AGAGATC TTT TTCCTGGG
 ||||| ||| |||||
 TCTCTAG AAA AAGGACCC
 GC__ A
 GAM2010 SLC26A1 3' CCCAAACACTCAGAAATCAAGA 42126 ATCA TCC____
 ACCTCT AGAG TTGATTCT TGGG
 ||| ||||| |||
 TCTC AACTAAAGA ACCC
 CAAG CTCACAA
 GAM2010 LOC121838 5' CCAGGAAGGACAATCTCTC 76512 TC AT
 GAGA ATTG TTCTTCCTGG
 ||| ||| |||||
 CTCT TAAC AGGAAGGACC
 C_ _
 GAM2010 LOC200138 5' CCCAGGAAAAAATCAATGATCT 91540 C
 C GAGATCATTGATTT TTCCTGGG
 ||||| |||||
 CTCTAGTAACTAAA AAGGACCC
 A
 GAM2010 LOC220000 3' CCAGGAAGATCTGGCCTCT 93231 AT TT TT
 AGAG CA GA TCTTCCTGG
 ||| || ||| |||||

		TCTC GT CT AGAAGGACC		
		CG _ _		
GAM2010	LOC221550 5'	CCCAGGAAAAAGAATAGATC 93745	_ GA C	
		GATC ATT TTT TTCCTGGG		
		CTAG TAA AAA AAGGACCC		
		A G_ _		
GAM2010	LOC255721 3'	CCAGGAAGATCTGGCCTCT 96487	AT TT TT	
		AGAG CA GA TCTTCCTGG		
		TCTC GT CT AGAAGGACC		
		CG _ _		
GAM2010	LOC257495 5'	CCCAGGAAAAAGAATAGATC 99572	_ GA C	
		GATC ATT TTT TTCCTGGG		
		CTAG TAA AAA AAGGACCC		
		A G_ _		
GAM2010	LOC257576 5'	CCCAGGAAAAAGAATAGATC 99709	_ GA C	
		GATC ATT TTT TTCCTGGG		
		CTAG TAA AAA AAGGACCC		
		A G_ _		
GAM2011	ALDH1A1 3'	GTGACTCTTGAAGTACTTA 7306	C GA G	
		TAAGTGCT CAAG GGT GC		
		ATTCATGA GTTC TCA TG		
		A _ G		
GAM2011	ARHGAP6 3'	TGGCCACTGGCACACTTA 26433	CT AGGAG	
		TAAGTG CCA GTGGCCA		
		ATTCAC GGT CACCGGT		
		AC _ _ _		
GAM2011	ARHGAP6 3'	TGGCCACTGGCACACTTA 26434	CT AGGAG	
		TAAGTG CCA GTGGCCA		
		ATTCAC GGT CACCGGT		
		AC _ _ _		
GAM2011	ASH1 5'	GGCCACCCCTCTTCCCCACTT 38089	CTCCA_ A	
		AAGTG AGG GGTGGCC		
		TTCAC TCC CCACCGG		
		CCCTTC C		
GAM2011	ENG 3'	GCCACTGGCTTGGAACAC 5498	C GA	
		GTG TCCAAG GGTGGC		
		CAC AGGTTC TCACCG		
		A GG		
GAM2011	GALNT3 3'	CACTCCACTTGAAGCACTTA 16825	C GA_	
		TAAGTGCT CAAG G GTG		

		ATTCACGA GTTC C CAC	
		A AC T	
GAM2011 HDAC4	3'	GTGGGGCTCTCTTGAGCAC 21249	GA GG
		GTGCTCCAAG GGT CCAC	
		CACGAGGTTC TCG GGTG	
		TC G_	
GAM2011 ROCK2	3'	GTGGCCTCAAAGGCACTTA 66623	CCAAG G
		TAAGTGCT GAGGT GC	
		ATTCACGG CTCCG TG	
		AAA__ G	
GAM2011 SNCAIP	3'	GCCACCTATAAGCTTGGGGCAC 97609	G_____
		GTGCTCCAAG AGGTGGC	
		CACGGGGTTC TCCACCG	
		GAATA	
GAM2011 CLIPR-59	3'	TGGTCACCCTGAAGCCCTTA 32022	T CCAA A
		TAAG GCT GG GGTGGCCA	
		ATTC CGA TC CCACTGGT	
		C AG__ _	
GAM2011 FLJ10620	3'	GTGGCCCGTGCCAAAGCACTTA 36865	CCAA AGGT
		TAAGTGCT GG GGCCAC	
		ATTCACGA CC CCGGTG	
		AA__ GTGC	
GAM2011 FLJ14681	3'	GTGGCTCCCCAGAGCACTT 52597	CAA A TG
		AAGTGCTC GG GG GCCAC	
		TTCACGAG CC CC CGGTG	
		A__ _ CT	
GAM2011 FLJ23360	3'	GCCACCTCCTGCTGGGCAC 43831	CA_
		GTGCTC AGGAGGTGGC	
		CACGGG TCCTCCACCG	
		TCG	
GAM2011 FLJ23375	5'	GTGGCCATGCTCTTGAGCACT 46953	AG
		AGTGCTCCAAGG GTGGCCAC	
		TCACGAGTTCT TACCGGTG	
		CG	
GAM2011 KIAA0232	3'	GTAGCATGCCTGGAGCATCA 73123	A A AG_ G
		A GTGCTCCA GG GT GC	
		A TACGAGGT CC CG TG	
		C _ GTA A	
GAM2011 KLHL8	3'	GTTAACCCTGTAGCACTTA 63517	CCA AGG
		TAAGTGCT AGG TGGC	

ATTCACGA TCC ATTG
 TG_ CA_
 GAM2011 KLHL8 3' TGCCACCTTTCAACACTT 63521 CTCCAA C
 AAGTG GGAGGTGG CA
 |||| ||||| ||
 TTCAC TTTCCACC GT
 AAC__ A
 GAM2011 MGC13090 3' GTGGCCACTTGGCCAAAGCGC 52122 CCAA _
 GTGCT GG AGGTGGCCAC
 |||| || |||||
 CGCGA CC TTCACCGGTG
 AA__ GG
 GAM2011 MGC33177 3' ATTTACCTTAGAGCATTTA 58626 C _
 TAAGTGCTC AAGG AGGT
 ||||| ||| |||
 ATTTACGAG TTCC TTTA
 A A
 GAM2011 PPP1R13B 3' CCATCACCTTGGAGCACT 31656 A
 AGTGCTCCAAGG GGTGG
 ||||| |||
 TCACGAGGTTCC CTACC
 A
 GAM2011 SHANK3 3' GTGACCACCTCCTTCGCAGC 66110 CC_ C
 GCT AAGGAGGTGG CAC
 || ||||| |||
 CGA TTCCTCCACC GTG
 CGC A
 GAM2011 SIAT8C 5' GCCACCTCCTCGCCGGCAC 32447 CCA_
 GTGCT AGGAGGTGGC
 |||| |||||
 CACGG TCCTCCACCG
 CCGC
 GAM2011 WAC 5' GCAGCCTTACCAGGCACTTA 34034 CCAAG G
 TAAGTGCT GAGGT GC
 ||||| ||| ||
 ATTCACGG TTCCG CG
 ACCA_ A
 GAM2011 YAP 5' GGCCACCCCCTCTTCCTCACTT 58202 CTCCA_ A
 AAGTG AGG GGTGGCC
 |||| || |||||
 TTCAC TCC CCACCGG
 TCCTTC C
 GAM2011 LOC140275 3' ATCTCCCTTAAAGTACTTA 75295 CC _
 TAAGTGCT AAGG AGGT
 ||||| ||| |||
 ATTCATGA TTCC TCTA
 AA C
 GAM2011 LOC146488 5' GTGGCCACACCTGGAACACT 71361 C A AG
 AGTG TCCA GG GTGGCCAC
 ||| ||| || |||||

	TCAC AGGT CC CACCGGTG		
	A _ A_		
GAM2011 LOC146713 3'	GGTCACCTCGGAGCCACT 84738	_	AAG
	AGTG CTCC GAGGTGGCC		
	TCAC GAGG CTCCACTGG		
	C _		
GAM2011 LOC148137 3'	CCTCCCTCCTTGAAGCACTT 59094	C	T_
	AAGTGCT CAAGGAGG GG		
	TTCACGA GTTCCTCC CC		
	A CT		
GAM2011 LOC150203 3'	GTGACCATTGTTGGAGCAC 61136	G _	G
	GTGCTCCAA GA GGT GC		
	CACGAGGTT TT CCA TG		
	G A G		
GAM2011 LOC151521 3'	GTGGCCACACTTGAAACAC 86624	CTC	GAG
	GTG CAAG GTGGCCAC		
	CAC GTTC CACCGGTG		
	AAA A_		
GAM2011 LOC151996 5'	GTAGCCATGACATTGGAGCAC 86722	GGAG	C
	GTGCTCCAA GTGGC AC		
	CACGAGGTT TACCG TG		
	ACAG A		
GAM2011 LOC152790 5'	GCACGCTTCTTAAAGCACT 87060	CCA	_
	AGTGCT AGGAGGTG GC		
	TCACGA TTCTTCGC CG		
	AA_ A		
GAM2011 LOC153688 3'	GTGGCCACTTGATTAGAGACCT 87330	TG C	GG
	AG CTC AA AGGTGGCCAC		
	TC GAG TT TTCACCGGTG		
	CA A AG		
GAM2011 LOC154860 3'	GCGGCCTCTGGAGCCTTA 87505	T	AG G
	TAAG GCTCCA GAGGT GC		
	ATTC CGAGGT CTCCG CG		
	_ _ G		
GAM2011 LOC164714 5'	GGCTGGCGTCCTTGGAGC 88587	G	_
	GCTCCAAGGA GT GGCC		
	CGAGGTTTCCT CG TCGG		
	G G		
GAM2011 LOC196374 3'	GCCACCTCCTTCCTGAACAC 89029	C C_	
	GTG TC AAGGAGGTGGC		

CAC AG TTCCTCCACCG
A TCC
GAM2011 LOC196955 3' GCAGGCCTTGGAGCCTTA 77868 T AGGTG
TAAG GCTCCAAGG GC
||||| ||
ATTC CGAGGTTCC CG
_ GGA_
GAM2011 LOC199720 3' TGGCCAAGCTGGAGCACT 89706 AG AGG
AGTGCTCCA G TGGCCA
||||| | |||||
TCACGAGGT C ACCGGT
_ GA_
GAM2011 LOC200138 5' GTGGCCACCTCCTTGGAGCACT 91543
TA TAAGTGCTCCAAGGAGGTGGCCAC
|||||
ATTCACGAGGTTCTCCACCGGTG

GAM2011 LOC203378 5' TGGTCAACCTTGGAACATT 92309 C AGG
AGTG TCCAAGG TGGCCA
||||| |||||
TTAC AGGTTCC ACTGGT
A A_
GAM2011 LOC205258 5' CACTGCTCCTCAGAGCACTTG 92361 CA _
TAAGTGCTC AGGAG GTG
||||| |||||
GTTACAGAG TCCTC CAC
AC GT
GAM2011 LOC222160 3' TGGCTCTCACTTTGGAGCACTT 95795 A GT
A TAAGTGCTCCAAGG G GGCCA
||||| | |||||
ATTCACGAGGTTTC C TCGGT
A TC
GAM2012 C7orf2 3' AGCGACCTGCAGACGGCGTCTT 42635 C A T_____ CGAC
CTGCCA TG CAGAAGAC C CAG CT
|| ||||| | ||| ||
AC GTCTTCTG G GTC GA
C C GCAGAC_ CAGC
GAM2012 DIAPH2 3' CAGGGCTGAACGTCTTCTGG 24588 AC GA
CCAGAAGAC TCAGC CTG
||||| |||||
GGTCTTCTG AGTCG GGAC
CA _
GAM2012 EPO 5' CAGGTCGCTGAGGGACCCCGGC 7683 AGAAGACA
GCC CTCAGCGACCTG
||| |||||
CGG GAGTCGCTGGAC
CCCCAGG_
GAM2012 NID 3' CAGATTGAAAAGTGTCTCTGG 11805 A CAG C
C GCCAGA GACACT CGA CTG
||||| ||||| ||| |||

	CGGTCT CTGTGA GTT GAC		
	C AAA A		
GAM2012 FLJ11106	3' AGCCAGTAAAGAATACTTCTGG 37616	ACA_ CA GAC	
CA	TGCCAGAAG CT GC CT		
	ACGGTCTTC GA TG GA		
	ATAA AA ACC		
GAM2012 FLJ20300	3' TTTCTGGAATGTCTTCTGGCA 35381	C_ C	
	TGCCAGAAGACA TCAG GA		
	ACGGTCTTCTGT GGTC TT		
	AA T		
GAM2012 FLJ23360	5' CAGGTCGCTGGCCGGCTCTGCA 43825	C A ACAC	
	TGC AGA G TCAGCGACCTG		
	ACG TCT C GGTCTGCTGGAC		
	_ _ GGCC		
GAM2012 KIAA1061	3' CAGGGAGGTAAATGCCTTTTGG 71718	A CTCAGCGA	
CA	TGCCAGAAG CA CCTG		
	ACGGTTTTC GT GGAC		
	C AAATGGAG		
GAM2012 MGC14386	3' AGGTCATCGTCTTCTGTCA 54325	C ACTCAGC	
	TG CAGAAGAC GACCT		
	AC GTCTTCTG CTGGA		
	T CTA_____		
GAM2012 TRIM11	3' CAGGCCACTGAGTGTTTTGGC 73189	AG CGA	
	GCCAGA AACTCAG CCTG		
	CGGTTT TGTGAGTC GGAC		
	_ ACC		
GAM2012 LOC120856	3' GCTGAATGTTTTCTGACA 74472	C C	
	TG CAGAAGACA TCAGC		
	AC GTCTTTTGT AGTCG		
	A A		
GAM2012 LOC144564	3' TGCTGAGTGTCTGAGCA 77407	_ AA	
	TGC CAG GAACTCAGCG		
	ACG GTC CTGTGAGTCGT		
	AC _		
GAM2012 LOC145748	3' GCAGTGTCTTCTTGCA 84472	C CA	
	TGC AGAAGAACT GC		
	ACG TCTTCTGTGA CG		
	T _		
GAM2012 LOC148887	5' CAGATCTTAGCACCTTCTGGCA 85393	ACA C C C	
	TGCCAGAAG CT AG GA CTG		

		ACGGTCTTC GA TT CT GAC		
		CAC _ _ A		
GAM2012	LOC150606 3'	GACCTGCAAGTCTGTTTCTGGC 86269	AC_ T_____	CGAC
	A	TGCCAGAAG AC CAG C		
		ACGGTCTTT TG GTC G		
		GTC AAC___ CAG		
GAM2012	LOC152078 3'	TGCAAGTGTCTTCGAGCA 81291	CA	CA
		TGC GAAGACACT GCG		
		ACG CTTCTGTGA CGT		
		AG A_		
GAM2012	LOC152282 5'	GCTGAGTGCCTCCTAGCA 81405	C A A	
		TGC AG AG CACTCAGC		
		ACG TC TC GTGAGTCG		
		A C C		
GAM2012	LOC220072 3'	TGCTGAGTGTCTGCAGCA 95083	___ AA	
		TGC CAG GACACTCAGCG		
		ACG GTC CTGTGAGTCGT		
		AC _		
GAM2012	LOC254173 5'	CAGGTCGTGCGTCCTTTGACA 98642	C A	ACTCA
		TG CAGA GAC GCGACCTG		
		AC GTTT CTG TGCTGGAC		
		A C CG___		
GAM2012	LOC255506 5'	CAGGTGAAAAGTGTCTTCCTGC 98824	CA	CAG G
	A	TGC GAAGACACT C ACCTG		
		ACG CTTCTGTGA G TGGAC		
		TC AAA_		
GAM2013	BCR 3'	ACCCGAGGGCGCCCCAAGCCA 41480	ACAA	GG A
		TGGCTTGGG GCT TC GGT		
		ACCGAACCC CGG AG CCA		
		CG_ G_ C		
GAM2013	BCR 3'	ACCCGAGGGCGCCCCAAGCCA 41481	ACAA	GG A
		TGGCTTGGG GCT TC GGT		
		ACCGAACCC CGG AG CCA		
		CG_ G_ C		
GAM2013	CARD10 3'	ACCTGCACCTTCTCCCCAAGCC 28034	ACA CT _	
	A	TGGCTTGGG AG GGT CAGGT		
		ACCGAACCC TC CCA GTCCA		
		C_ TT C		
GAM2013	DYRK3 3'	ACCTAACCAGCTTGTATTGGCC 14555	TGGG	C
	A	TGGCT ACAAGCTGGT AGGT		

			ACCGG TGTTCGACCA TCCA		
			TTA_ A		
GAM2013	GGA3	3'	GCCAGCTTGTCCCAGCCA 26587	T	
			TGGCT GGGACAAGCTGGT		
			ACCGA CCCTGTTTCGACCG		
			-		
GAM2013	KLK13	3'	CCTGAATGTCCCAACCCA 32145	C	AGCTGG
			TGG TTGGGACA TCAGG		
			ACC AACCTGT AGTCC		
			C A_____		
GAM2013	PIK3R2	3'	ACCGAGGACCCGCCCAAGC 18507		ACAA T A__
			GCTTGGG GC GGTC GGT		
			CGAACCC CG CCAG CCA		
			_____ C GAG		
GAM2013	TLR5	3'	CCAACCTATCTCAAGCCA 13781		C C
			TGGCTTGGGA AAG TGG		
			ACCGAACTCT TTC ACC		
			A A		
GAM2013	C20orf150	3'	CAGCCTGCCCTCAAGCCA 66008		_ A A
			TGGCTTG GG CA GCTG		
			ACCGAAC CC GT CGAC		
			T C C		
GAM2013	C20orf51	3'	CCAGGCCACCCCAAGTCA 42287		ACAAGC A_
			TGGCTTGGG TGGTC GG		
			ACTGAACCC ACCGG CC		
			C_____ AC		
GAM2013	CES2	5'	CCTTTCCCGGCCCAAGCCA 15262		GACAA TC_
			TGGCTTGG GCTGG AGG		
			ACCGAACC CGGCC TCC		
			_____ CTT		
GAM2013	DKFZP761F241	3'	ACCTGACCTCACTCCCAGCCA 49579		T CAAGCT
			TGGCT GGGA GGTCAGGT		
			ACCGA CCCT CCAGTCCA		
			_ CACT__		
GAM2013	FLJ10898	5'	CCAGACCACCCCAAGCCA 60128		ACAAGC A_
			TGGCTTGGG TGGTC GG		
			ACCGAACCC ACCAG CC		
			C_____ AA		
GAM2013	FLJ25193	3'	CCTGACTTGCCCCAACCCA 59357		C ACAA T
			TGG TTGGG GC GGTCAGG		

		ACC AACCC CG TCAGTCC		
		C ____ T		
GAM2013	PRO1866	5' TCAGTCCATCCCAAGCCA 38149	CAA	
		TGGCTTGGGA GCTGG		
		ACCGAACCT TGACT		
		ACC		
GAM2013	RABL4	5' CCTTCCCGTCCCAGGCCA 23410	AAGCT TC	
		TGGCTTGGGAC GG AGG		
		ACCGGACCCTG CC TCC		
		____ CT		
GAM2013	SIRPB1	3' CCCTCCCTGTCCCAGGCCA 21362	T AGCT TCA	
		TGGCT GGGACA GG GG		
		ACCGA CCCTGT CC CC		
		_ C__ TCC		
GAM2013	TBL1Y	3' ACCAACTTGTCCCAGGCCA 53857	C	
		TGGCTTGGGACAAG TGGT		
		ACCGGACCCTGTTC ACCA		
		A		
GAM2013	USP19	3' CCTGCCTGCCCCAGGCCA 90401	ACAA T T	
		TGGCTTGGG GC GG CAGG		
		ACCGGACCC CG CC GTCC		
		____ T _		
GAM2013	LOC149153	5' CTCTTCAGTCATCCCAAGCCA 85528	CAA TC	
		TGGCTTGGGA GCTGG AG		
		ACCGAACCT TGACT TC		
		AC_ TC		
GAM2013	LOC196759	3' ACCTAGGAGCTCCCCAAGCCA 88907	ACA GG _	
		TGGCTTGGG AGCT TC AGGT		
		ACCGAACCC TCGA GG TCCA		
		C_ _ A		
GAM2013	LOC199864	3' ACCTAGGAGCTCCCCAAGCCA 91456	ACA GG _	
		TGGCTTGGG AGCT TC AGGT		
		ACCGAACCC TCGA GG TCCA		
		C_ _ A		
GAM2013	LOC220045	3' ACCTAGGGGCTCCCCAAGCCA 95033	ACA GG _	
		TGGCTTGGG AGCT TC AGGT		
		ACCGAACCC TCGG GG TCCA		
		C_ _ A		
GAM2014	CDH12	3' CTTATCATTTAAAGTGGTGTA 15777	CCCAA GA	
		TACACCACT GAA ATAAG		

ATGTGGTGA TTT TATTC
 AA___ AC
 GAM2014 GOCAP1 3' ATTGTTCTTGGGAGCAGTGTA 43007 CA G
 TACAC CTCCCAAGAA AAT
 |||| ||||| ||
 ATGTG GAGGGTTCTT TTA
 AC G
 GAM2014 DKFZp434N2435 5' CTTATTACTGTGGGGTGGT 98090 T AGAAG
 ACCAC CCCA AATAAG
 |||| || ||||
 TGGTG GGGT TTATTC
 _ GTCA_
 GAM2014 DKFZP564I122 3' CTTATTCTTCTCCCTCATGTGT 63877 CACTCCCA
 A TACAC AGAAGAATAAG
 |||| |||||
 ATGTG TCTTCTTATTC
 TACTCCC_
 GAM2014 FLJ21791 3' CTTATTTGCAGAAGTGGTGTA 62126 CCCAAGAA
 TACACCACT GAATAAG
 ||||| ||||
 ATGTGGTGA TTTATTC
 AGACG_
 GAM2014 HMP19 3' CTTATTCTTTGTTAGGAAAATG 88860 CCAC CAA_
 TA TACA TCC GAAGAATAAG
 ||| || |||||
 ATGT AGG TTTCTTATTC
 AAA_ ATTG
 GAM2014 KIAA1719 3' TCTGTCTTGGGAGTGGTGTA 68742 _
 TACACCACTCCCAAGA AGA
 ||||| |||||
 ATGTGGTGAGGGTTCT TCT
 G
 GAM2014 KIAA1853 3' TTTTCTTGGAAGCAGTG 69929 CA C
 CAC CT CCAAGAAGAA
 || |||||
 GTG GA GGTTCTTTT
 AC A
 GAM2014 KIAA1877 3' CTTATTCTTCTGCCATGAGT 66748 CCA_
 ACTC AGAAGAATAAG
 ||| |||||
 TGAG TCTTCTTATTC
 TACCG
 GAM2014 KIAA1906 3' CTTATTCTTCTTGACTTTTGG 73571 CTCC_
 CCA CAAGAAGAATAAG
 || |||||
 GGT GTTCTTCTTATTC
 TTTCA
 GAM2014 OSBPL11 3' CTTAATTTCCCAAGAGTGGTG 43206 CCAA AA
 CACCACTC GAAG TAAG
 ||||| ||| |||

			GTGGTGAG CTTT ATTC		
			AACC A_		
GAM2014 YME1L1	3'	TCATTCTTGATGTGGTGTA	58438	TCC	_
		TACACCAC CAAGAA GA			
		ATGTGGTG GTTCTT CT			
		TA_ A			
GAM2014 ZNF262	3'	CTTATTTTGTGGGAGT	18723	A	
		ACTCCCAAG AGAATAAG			
		TGAGGGTTT TTTTATTC			
		G			
GAM2014 LOC91960	3'	TGTGGCTTGGAACGTGGTGTA	68294	TC_	AAGA
		TACACCAC CCAAG ATA			
		ATGTGGTG GGTTT TGT			
		CAA GG_			
GAM2015 DPH2L1	3'	CTGACAAAGTCATCCCCTCTCA	9112	C	_ CTCA
GG		CCT GAGAGGGGGG GAT TCAG			
		GGA CTCTCCCCT CTG AGTC			
		_ A AAAC			
GAM2015 MEF2D	3'	ATGGCCCTCCCCCTCCCCAGG	20979	CGA	ATC
		CCT GAGGGGGG TCAT			
		GGA CTCCCCCT GGTA			
		CCC CCC			
GAM2015 SORCS2	3'	ATGAGGGTCCCTCTCAGAG	40797	GA	AT
		CTC GAGGGGGG CTCAT			
		GAG CTCTCCCT GAGTA			
		A_ GG			
GAM2015 CACNG4	3'	CTGACTTTGTCCCCTCCCCGA	27708	AGA	CTCA
		TCG GGGGGGAT TCAG			
		AGC CTCCCCTG AGTC			
		CC_ TTTC			
GAM2015 CYP2A7	5'	TGGAGTCCCCCCTCCTGAG	48356	A	CT
		CTCG GAGGGGGGAT CA			
		GAGT CTCCCCCCTG GT			
		C AG			
GAM2015 FLJ20457	3'	GATGGCCTTCCCCTCTGA	35671	G	ATC
		TC AGAGGGGGG TCATC			
		AG TCTCCCCTT GGTA			
		_ CC_			
GAM2015 HABP2	5'	CTGACATTTTCCCCCCTAAAG	15951	CGAG	TCTCA_
G		CCT AGGGGGGA TCAG			

GGA TCCCCCT AGTC
 AA__ TTTTAC
 GAM2015 KLF12 3' ATGAGATTCTCTCAGAGG 33276 GAGA
 CCTC GGGGGGATCTCAT
 ||| |||||
 GGAG CTCTCTTAGAGTA
 A__
 GAM2015 SDCCAG3 3' TGACGGCCCCCTCAGAGG 22806 GA A _
 CCTC GAGGGGGG TC TCA
 ||| ||||| ||
 GGAG CTCCCCC GG AGT
 A_ _ C
 GAM2015 XPO5 3' CTGACAAGAGGGTTTCCCCGAG 92874 AGA GG AT A__
 CTCG GGG G CTC TCAG
 ||| || | || |||
 GAGC CCC T GAG AGTC
 _ TT GG AAC
 GAM2015 LOC147599 3' AGGCTCCCCTCTCTCAAGG 85159 C _
 CCT GAGAGGGGGGA TCT
 || ||||| ||
 GGA CTCTCTCCCCT GGA
 A C
 GAM2015 LOC200314 3' TGTGACCCCCCTCAAGG 91608 C A A T
 CCT GAG GGGGGG TC CA
 || || ||||| ||
 GGA CTC CCCCCC AG GT
 A _ C T
 GAM2015 LOC222414 3' TGTAATCCCCCCTCAAGG 95975 C A CT
 CCT GAG GGGGGGAT CA
 || || ||||| ||
 GGA CTC CCCCCTA GT
 A C AT
 GAM2016 PCDH1 3' GCGCCGGCCAGCTCCCAA 51577 AA G
 TTG GGCTGGCCGG CGT
 || ||||| ||
 AAC TCGACCGGCC GCG
 CC _
 GAM2016 BMF 3' GGTGCCAGCCAGCCT 54287 C GT
 AGGCTGGC GGGC ACC
 ||||| ||| ||
 TCCGACCG CCG TGG
 A _
 GAM2016 C20orf43 3' GTCCTGGCCAGCCTTCAA 60614 _
 TTGAAGGCTGGCCGGG C
 ||||| ||||| |
 AACTCCGACCGGTCC G
 T
 GAM2016 CECR2 3' GTGGCCAGCCAGCCTTCAG 49437 CG G
 TTGAAGGCTGGC GGC TAC
 ||||| ||| ||

		GA	CTTCCG	ACCG	CCG	GTG	
			A				
GAM2016	D21S2056E 3'	GTGGCAGGCGCCAGCCTCCGA	14870	A	CGG	GTA	
		TTG AGGCTGGC	GC CCAC				
		AGC TCCGACCG	CG GGTG				
		C					
GAM2016	FLJ13154 3'	GGAGGCCCCAGCCATGCCTTCA	45110		C	C A	
	A	TTGAAGGC TGGC	GGG GT CC				
		AACTTCCG ACCG	CCC CG GG				
		T	A				
GAM2016	KIAA0157 3'	GTTTAGCAGCAGCCTTCAA	50751			CG	
		TTGAAGGCTG	GC GGC				
		AACTTCCGAC	CG TTG				
		GA	AT				
GAM2016	ZDHC8 3'	CGCCAGGCCAGCCCCAA	64620	AA	G		
		TTG GGCTGGCC	GGCG				
		AAC CCGACCGG	CCGC				
		CC	A				
GAM2016	ZNF259 3'	GTGGCTCAAGGGCCAGCCTCCA	73022	A		G	
	G	TTG AGGCTGGCC	GGGC TAC				
		GAC TCCGACCGG	CTCG GTG				
		C	GAA				
GAM2016	LOC124222 3'	GCACTTGGACAGCCTTCAA	74750		G	C	
		TTGAAGGCTG	CCGGG GT				
		AACTTCCGAC	GGTTC CG				
		A	A				
GAM2016	LOC136345 3'	GCCCCAGCCAGCTCTTCAA	76714		C	C	
		TTGAAG GCTGGC	GGG GT				
		AACTTC CGACCG	CCC CG				
		T	A				
GAM2016	LOC144848 3'	GCACCAAGGCCAGCCTCCAG	73959	A	G	C	
		TTG AGGCTGGCC	GG GT				
		GAC TCCGACCGG	CC CG				
		C	AA A				
GAM2016	LOC145748 3'	GGA	CTCAACCAGCTTTCAA	84475	CCG	C A	
		TTGAAGGCTGG	GG GT CC				
		AACTTTCGACC	CT CA GG				
		AA					
GAM2016	LOC149837 3'	GTGGAGTACAAACAGCCTTCAA	85905		GCCGG	GTA	
		TTGAAGGCTG	GC CCAC				

AACTTCCGAC TG GGTG
 AAACA A__
 GAM2016 LOC155032 5' GCCCCAGCCAGCTCTTCAA 87595 _ C C
 TTGAAG GCTGGC GGG GT
 ||||| ||||| || ||
 AACTTC CGACCG CCC CG
 T A _
 GAM2016 LOC204804 3' GTGATCCTCCCAGCTCAGCCTT 91051 _ C CGTAC
 CAA TTGAAGGCTG GC GGG CAC
 ||||| || || ||
 AACTTCCGAC CG CCC GTG
 T A TCCTA
 GAM2016 LOC256471 3' GCGGTGAGCCAGTCTCCAA 97544 A _ G_
 TTG AGGCTGGC CG GC
 || ||||| || ||
 AAC TCTGACCG GT CG
 C A GG
 GAM2017 AQP6 5' TTGGAAGTGTCTACAACACGAG 55023 A A CGC
 CTC TG TGTA GCAGTCCAA
 || || || || |||||
 GAG AC ACAT TGTCAGGTT
 C A C__
 GAM2017 PAX2 3' TGGACTGCGCGGCGCCGTGAG 15664 A A
 CTCATG TGT CGCGCAGTCCA
 ||||| || |||||
 GAGTGC GCG GCGCGTCAGGT
 C _
 GAM2017 PAX2 3' TGGACTGCGCGGCGCCGTGAG 15669 A A
 CTCATG TGT CGCGCAGTCCA
 ||||| || |||||
 GAGTGC GCG GCGCGTCAGGT
 C _
 GAM2017 CLIC5 3' TTGGAAGTGGTGGCATCATG 34186 A G
 CATGATGT CGC CAGTCCAA
 ||||| || |||||
 GTACTACG GTG GTCAGGTT
 _ _
 GAM2017 DKFZP547L112 3' TGGACTATGGCACCAGAG 67134 A A ACG C
 CTC TG TGT CG AGTCCA
 || || || || |||||
 GAG AC ACG GT TCAGGT
 _ C _ A
 GAM2017 DKFZP547L112 3' TGGACTGCGGCACCTGAG 67135 TGA ACG
 CTCA TGT CGCAGTCCA
 || || || |||||
 GAGT ACG GCGTCAGGT
 CC_ _
 GAM2017 FLJ10377 3' TGGACTGTGTACATCTGA 36565 T GC
 TCA GATGTAC GCAGTCCA
 || ||||| |||||

AGT CTACATG TGTCAGGT

GAM2017 FLJ12057 3' TGA[—]ACTGCGTCATGGG 45797 ATGTAC C
CTCATG GCGCAGT CA
||||| ||||| ||
GGGTAC TCGTCA GT

_____ A
GAM2017 LGALS12 3' TGGACTGCACTCACAGAG 53548 A A TACGC
CTC TG TG GCAGTCCA
||| ||| |||||
GAG AC AC CGTCAGGT

— — TCA—
GAM2017 MISS 3' TTGGATGCGTAGTACATCAT 58642 — G
ATGATGTAC GCGCA TCCAA
||||||| ||||| |||||
TACTACATG TCGGT AGGTT

A —
GAM2017 SMARCE1 3' TTTGGACCATTTAGCATCATGA 13266 ACGCGCA
G CTCATGATGT GTCCAAA
||||||| |||||
GAGTACTACG CAGGTTT

ATTTAC—
GAM2017 LOC118738 3' CTGGCACACATCATGGG 76003 AC G
CTCATGATGT GC CAG
||||||| |||||
GGGTACTACA CG GTC

CA —
GAM2017 LOC153894 3' TTGGATGTGTAGTACATCAT 81880 — G
ATGATGTAC GCGCA TCCAA
||||||| ||||| |||||
TACTACATG TGTGT AGGTT

A —
GAM2018 IL13RA1 3' ACATTGGTAGCCAGCCAG 9564 AG G
CTGGCTGGCT GC GGTGT
||||||| |||||
GACCGACCGA TG TTACA

— G
GAM2018 SLC25A13 5' CGCCAGCCAGCCAGTCA 27288 T A
TGA CTGGCTGGCT GGCG
||| ||||| |||||
ACT GACCGACCGA CCGC

— —
GAM2018 SLC7A8 3' ACACCCGCACACAGCCAGC 25298 AG—
GCTGGCT GCGGGTGT
||||| |||||
CGACCGA CGCCCACA
CACA

GAM2018 KIAA0337 3' ACACCCACTGGCCAGCCAGGCC 29474 AT GC
A TG CTGGCTGGCTAG GGGTGT
|| ||||| |||||

AC GACCGACCGGTC CCCACA
 CG A_
 GAM2018 MGC16186 5' ACAGCTAGCCAGCCAGCCAG 51408 A _ G
 CTGGCTGGCT GGC GG TGT
 ||||| ||| ||
 GACCGACCGA CCG TC ACA
 _ A G
 GAM2018 LOC158226 3' ACACCCGCGCACCAGCCAGG 82695 CTAG
 TCTGGCTGG GCGGGTGT
 ||||| |||||
 GGACCGACC CGCCCACA
 ACG_
 GAM2018 LOC256537 5' CACCCGCTGCCAAACCA 96935 C_ TA
 TGG TGGC GGCGGGTG
 ||| ||| |||||
 ACC ACCG TCGCCAC
 AA _
 GAM2019 AGRN 3' CCAGGCAGCCGTGCTGCA 79584 CA _
 TGCAGCAC GCTGC TGG
 ||||| |||||
 ACGTCGTG CGACG ACC
 C_ G
 GAM2019 ALEX1 5' CTGCCTCAGAGCCGGCCCGCA 33974 AGCA A G GA
 TGC CC GCT CTG GCAG
 ||| ||| ||| |||
 ACG GG CGA GAC CGTC
 CCC_ C _ TC
 GAM2019 AP1B1 3' CCACCGACTGGCAGCTGCA 8516 A_ C C
 TGCAGC CCAG TG TGG
 ||||| ||||| |||
 ACGTCG GGTC GC ACC
 AC A C
 GAM2019 ATM 3' CTGCCGGGTAGCTGGGGCTACA 57144 C A GGA
 TG AGC CCAGCTGCT GCAG
 || ||| ||||| |||
 AC TCG GGTCGATGG CGTC
 A G GC_
 GAM2019 BDP1 3' CTGCCGGGTAGCTGGGACTACA 37966 C CA GGA
 TG AG CCAGCTGCT GCAG
 || ||| ||||| |||
 AC TC GGTCGATGG CGTC
 A AG GC_
 GAM2019 CAPON 5' CTGCTCTGGGGCCGGCGCCGC 64659 A A A G TG
 GC GC CC GCT C GAGCAG
 || ||| ||| |||||
 CG CG GG CGG G CTCGTC
 C C C _GT
 GAM2019 CTF1 3' CCAGCAGCTGGGACTACA 9009 C CA
 TG AG CCAGCTGCTGG
 || ||| |||||

AC TC GGTGACGACC
 A AG
 GAM2019 DDB2 3' CTGCTCCAGAGTTGGTGACACA 5456 CAG G
 TG CACCAGCT CTGGAGCAG
 || ||||| |||||
 AC GTGGTTGA GACCTCGTC
 ACA _
 GAM2019 ENDOGL1 3' CTGCCCCCTGAGCAGCTGGGAC 18823 C CA _ A
 TACA TG AG CCAGCTGCT GG GCAG
 || || ||||| || ||||
 AC TC GGTGACGA CC CGTC
 A AG GTC C
 GAM2019 FCRH1 3' CTGCTGAGTAGCTGGGACTACA 54726 C CA GG
 TG AG CCAGCTGCT AGCAG
 || || ||||| ||||
 AC TC GGTGATGA TCGTC
 A AG G_
 GAM2019 FTH1 5' GCTCCAGCGCCGCGCA 68713 A ACCA T
 TGC GC GC GCTGGAGC
 ||| || || |||||
 ACG CG CG CGACCTCG
 _ C _ _
 GAM2019 GAB2 3' CCACAGCTGGTGCTCA 55404 C C
 TG AGCACCAGCTG TGG
 || ||||| ||||
 AC TCGTGGTCGAC ACC
 _ _
 GAM2019 GAB2 3' CCACAGCTGGTGCTCA 25457 C C
 TG AGCACCAGCTG TGG
 || ||||| ||||
 AC TCGTGGTCGAC ACC
 _ _
 GAM2019 HTR4 3' GCCCTGGCTGTGCTGCA 7885 C GCT A
 TGCAGCAC AGCT GG GC
 ||||| |||| || ||
 ACGTCGTG TCGG CC CG
 _ T _ _
 GAM2019 KLHL3 3' TTCCAAGCAGGTGCTGCA 88855 A GC
 TGCAGCAC GCT TGGAG
 ||||| |||| ||||
 ACGTCGTGG CGA ACCTT
 A _
 GAM2019 LPIN1 3' CTGCTCCAGCAAGTAGCT 67987 ACCA _
 AGC GCT GCTGGAGCAG
 ||| || |||||
 TCG TGA CGACCTCGTC
 A _ A
 GAM2019 MAD2L2 3' GCCTAGGGCAGTGCTGCA 22018 CA G A
 TGCAGCAC GCT CTGG GC
 ||||| |||| ||||

ACGTCGTG CGG GATC CG

A _ _ _

GAM2019 MPST 3' TGCCCACCTGGTGCTG 41210 CTGC A

CAGCACCAG TGG GCA

||||||| ||| |||

GTCGTGGTC ACC CGT

C _ _ _

GAM2019 MSF 3' GCCCCCACTGGGCTGCA 89466 A C CT A

TGCAGC CCAG TG GG GC

||||| |||| || || ||

ACGTCG GGTC AC CC CG

_ _ C _ _

GAM2019 OLFM1 3' GTATTTGCAGCTGGAAGCTGCA 27345 CA TG A

TGCAG CCAGCTGC G GC

|||| | ||||| | ||

ACGTC GGTCGACG T TG

AA TT A

GAM2019 PTPN18 3' CTGCCGAGTAGCTGGGACTACA 27650 C CA GGA

TG AG CCAGCTGCT GCAG

|| || ||||| |||

AC TC GGTCGATGA CGTC

A AG GC _

GAM2019 RPS18 5' CCGCCGCTTGTGCTGCA 42880 C T T

TGCAGCAC AGC GC GG

|||||| | || ||

ACGTCGTG TCG CG CC

T C _

GAM2019 SBF1 3' CTGGTCCAGCCAGCGGCTGCA 66069 ACCA _ G

TGCAGC GCTG CTGGA CAG

|||| | ||| |||| |||

ACGTCG CGAC GACCT GTC

G _ C G

GAM2019 SCGB1A1 3' CTGCTCCAGCCTCTGCCGCT 13983 AC CT

AGC CAG GCTGGAGCAG

|| | ||| |||||

TCG GTC CGACCTCGTC

CC TC

GAM2019 SLC8A2 5' CTGCTCCAGGCTGTAGCCGCA 66934 A AC TG

TGC GC CAGC CTGGAGCAG

|| | ||| |||||

ACG CG GTCG GACCTCGTC

C AT _

GAM2019 STARD5 3' GCTCCCTCAGTCCTGTGCTGCA 48318 CA_ CT

TGCAGCAC GCTG GGAGC

|||||| | || ||||

ACGTCGTG TGAC CCTCG

TCC TC

GAM2019 TARBP2 3' CTGCAGGAGCTGGTGGTGCA 57004 G G G

TGCA CACCAGCT CTG AG

|||| | |||| | || ||

ACGT GTGGTCGA GAC TC
 G G G
 GAM2019 ARHGAP8 3' CTGCCCCAGCCCTCTGGTGT 35201 CT_ A
 GCACCAG GCTGG GCAG
 ||||| |||| ||||
 TGTGGTC CGACC CGTC
 TCC C
 GAM2019 BCKDK 3' CTGCTCCACACACTGCTGCA 60494 CCAGC C
 TGCAGCA TG TGGAGCAG
 ||||| || |||||
 ACGTCGT AC ACCTCGTC
 CAC__ _
 GAM2019 C11orf21 3' CTGAGATGGCAACTGGCACCGG 27103 AGCA_ C GAG
 CA TGC CCAG TGCTG CAG
 || |||| |||| ||
 ACG GGTC ACGGT GTC
 GCCAC A AGA
 GAM2019 C14orf3 5' CTGCCGGGCGGCTGGCACT 25049 CA GGA
 AG CCAGCTGCT GCAG
 || ||||| ||||
 TC GGTGGGCGG CGTC
 AC GC_
 GAM2019 CDCA4 3' CTGCTCTGTTAGACTGGTGCTG 36086 _ CT
 CAGCACCAG CTG GGAGCAG
 ||||| || |||||
 GTCGTGGTC GAT TCTCGTC
 A TG
 GAM2019 CITED2 5' CTGCCCCAGCGGCCGCTGCG 21401 ACCA A
 TGCAGC GCTGCTGG GCAG
 |||| | ||||| ||||
 GCGTCG CGGCGACC CGTC
 C__ C
 GAM2019 COPS7B 3' CTGGGGCAGCTGGCACTCA 42999 C CA GG
 TG AG CCAGCTGCT AG
 || || ||||| ||
 AC TC GGTGACGG TC
 _ AC GG
 GAM2019 CXYorf1 3' CCATCGTACAGTGGTGCTGCA 82908 G C____
 TGCAGCACCA CTG TGG
 ||||| || ||
 ACGTCGTGGT GAC ACC
 _ ATGCT
 GAM2019 CXYorf1 5' TGCTCCAGAGCGCCTGCA 82922 CACCA G
 TGCAG GCT CTGGAGCA
 |||| || |||||
 ACGTC CGA GACCTCGT
 CG__ _
 GAM2019 D2S448 3' CTGCTCCAACAGCCAAATGC 73890 GCACCA C
 GCA GCTG TGGAGCAG
 || |||| |||||

CGT CGAC ACCTCGTC
 AAAC__ A
 GAM2019 FER1L4 3' CTGCTCTGTGCAGCTGGCCCGC 48119 AGCA _
 A TGC CCAGCTGC TGGAGCAG
 ||| ||||| |||||
 ACG GGTGACG GTCTCGTC
 CCC_ T
 GAM2019 FLJ10604 3' CTCCAGCTTTCTGGTGTGACA 36858 CA CT_
 TG GCACCAG GCTGGAG
 || ||||| |||||
 AC TGTGGTC CGACCTC
 AC TTT
 GAM2019 FLJ10640 5' CCGAGTAGCTGGGACTACA 39232 C CA _
 TG AG CCAGCTGCT GG
 || || ||||| ||
 AC TC GGTGATGA CC
 A AG G
 GAM2019 FLJ11125 5' CCACGTAGCTGGGGCTACA 60322 C A _
 TG AGC CCAGCTGC TGG
 || || ||||| ||
 AC TCG GGTGATG ACC
 A G C
 GAM2019 FLJ11280 5' CTGGAAGGCAGCTGGCACTGGC 37786 _ CA GGAG
 A TGC AG CCAGCTGCT CAG
 ||| || ||||| ||
 ACG TC GGTGACGG GTC
 G AC AAG_
 GAM2019 FLJ12581 3' CCGAGCAGCTGGGACTACA 46334 C CA _
 TG AG CCAGCTGCT GG
 || || ||||| ||
 AC TC GGTGACGA CC
 A AG G
 GAM2019 FLJ12697 3' GCCCCAGCAGCCCCCGCGCA 94158 A ACCA A
 TGC GC GCTGCTGG GC
 ||| || ||||| ||
 ACG CG CGACGACC CG
 _ CCCC C
 GAM2019 FLJ13710 3' CTGCCCCATCCCTGGTGCT 46098 CTGC A
 AGCACCAG TGG GCAG
 ||||| || ||||
 TCGTGGTC ACC CGTC
 CCT_ C
 GAM2019 FLJ14681 5' CTGCCTGGGGCGGTGCTGCA 52595 A G TG A
 TGCAGCACC GCT C G GCAG
 ||||| || | ||||
 ACGTCGTGG CGG G C CGTC
 _ _GT_
 GAM2019 FLJ14871 3' TCAGCAATGGTGCTGCA 52731 GC
 TGCAGCACCA TGCTGG
 ||||| |||||

ACGTCGTGGT ACGACT
 A_
 GAM2019 FLJ20150 3' CTGCTCCAGCTGTTACATGCA 35140 GCACC T
 TGCA AGC GCTGGAGCAG
 ||| ||| |||||
 ACGT TTG CGACCTCGTC
 ACAC_ T
 GAM2019 FLJ30678 5' CTGCCCCAGCAGCGGCCTG 58981 CA A A
 CAG CC GCTGCTGG GCAG
 ||| || ||||| |||
 GTC GG CGACGACC CGTC
 C_ _ C
 GAM2019 HCA112 3' CTGCTCCAGCAGCACTTGC 38082 CCA
 GCA GCTGCTGGAGCAG
 ||| |||||
 CGT CGACGACCTCGTC
 TCA
 GAM2019 HEMK 3' CTGTCGGGGCAGCTGGGGCCAC 32956 CA A GGA
 A TG GC CCAGCTGCT GCAG
 || || ||||| |||
 AC CG GGTCGACGG TGTC
 AC G GGC
 GAM2019 ITGB8 5' CTGCTCCGCAGACGGGGCTGCA 11055 A AG_ T
 TGCAGC CC CTGC GGAGCAG
 ||||| || ||| |||||
 ACGTCG GG GACG CCTCGTC
 _ GCA _
 GAM2019 KIAA0084 5' GCTCCAGCGGCTGCTGT 68709 CCA
 GCAGCA GCTGCTGGAGC
 ||||| |||||
 TGTCGT CGGCGACCTCG
 _
 GAM2019 KIAA0290 3' CTGCCCCAGCTCTACACTGC 66716 CACC CT A
 GCAG AG GCTGG GCAG
 ||| || ||||| |||
 CGTC TC CGACC CGTC
 ACA_ T_ C
 GAM2019 KIAA0415 3' GCCCAGGCCAGCTGGTGCT 94163 _ A
 AGCACCAGCTG CTGG GC
 ||||| ||| |||
 TCGTGGTCGAC GACC CG
 CG _
 GAM2019 KIAA0453 3' CTGCCCTGTGGGCTGGTGCTTC 69605 C _TG T A
 A TG AGCACCAG C C GG GCAG
 || ||||| | || |||
 AC TCGTGGTC G G CC CGTC
 T G GT T _
 GAM2019 KIAA0532 3' CCAAGCAGCTGGGACTACA 71319 C CA _
 TG AG CCAGCTGCT GG
 || || ||||| ||

		AC TC GGTCGACGA CC		
		A AG A		
GAM2019 KIAA0720	3'	CTCTAGTAGCTGGA	62981	CA
		TGCAG CCAGCTGCTGGAG		
		ACGTC GGTCGATGATCTC		
		AA		
GAM2019 KIAA0934	3'	CTGCCCCAGTGTGACCCTGCA	64883	CACCA T A
		TGCAG GC GCTGG GCAG		
		ACGTC TG TGACC CGTC		
		CCAG_ _ C		
GAM2019 KIAA1160	3'	CTGCAGACACAGGCTGGTGCTG	40756	GC GA_
	CA	TGCAGCACCAGCT TG GCAG		
		ACGTCGTGGTCGG AC CGTC		
		AC AGA		
GAM2019 KIAA1169	5'	CCAAGCAGCTGGA	35878	C CA _
		TG AG CCAGCTGCT GG		
		AC TC GGTCGACGA CC		
		A AA A		
GAM2019 KIAA1464	3'	CTCGGGACAGCTGTGTGCTGCA	68818	_ _ G
		TGCAGCAC CAGCTG CT GAG		
		ACGTCGTG GTCGAC GG CTC		
		T A G		
GAM2019 KIAA1465	3'	CTGCCTAGTAGCTGGG	61494	C CA A
		TG AG CCAGCTGCTGG GCAG		
		AC TC GGTCGATGATC CGTC		
		A AG _		
GAM2019 KIAA1671	3'	CTGCTCCAACCTGGTGCTG	66281	CTGC
		CAGCACCAG TGGAGCAG		
		GTCGTGGTC ACCTCGTC		
		CA_		
GAM2019 KIAA1821	3'	CTGCCTGAGTAGCTGGG	72264	C CA _ A
	A	TG AG CCAGCTGCT GG GCAG		
		AC TC GGTCGATGA TC CGTC		
		A AG G _		
GAM2019 MGC1842	5'	CTGCTCCAGGATGGTGCTGCA	66254	GCTG
		TGCAGCACCA CTGGAGCAG		
		ACGTCGTGGT GACCTCGTC		
		AG_		
GAM2019 MGC3178	3'	CTGCTCTGGCCCTGGTGCTGCA	48718	G CT TG
		TGCA CACCAG GC GAGCAG		

ACGT GTGGTC CG CTCGTC
 _ C_ GT
 GAM2019 MGC34923 5' CCAGCAGCTGGTGCTCA 59195 C
 TG AGCACCAGCTGCTGG
 || |||||
 AC TCGTGGTCGACGACC
 _
 GAM2019 moblak 3' CCAGCAGCTGGGACTACA 56389 C CA
 TG AG CCAGCTGCTGG
 || || |||||
 AC TC GGTCGACGACC
 A AG
 GAM2019 NDRG4 3' CTGGGCCAGCTGGTGCTGTA 40381 CT AG
 TGCAGCACCAGCTG GG CAG
 ||||| || |||
 ATGTCGTGGTCGAC CC GTC
 _ GG
 GAM2019 NDRG4 3' CTGGGCCAGCTGGTGCTGTA 43578 CT AG
 TGCAGCACCAGCTG GG CAG
 ||||| || |||
 ATGTCGTGGTCGAC CC GTC
 _ GG
 GAM2019 NR4A3 5' CCGGTGCAGCGCGGCCGCA 23718 A A A_ _
 TGC GC CC GCTGC TGG
 ||| || |||| |||
 ACG CG GG CGACG GCC
 C C CG TG
 GAM2019 NSAP1 5' CTGCCTCAGCCAGTAGCGCA 22086 A ACCA _ GA
 TGC GC GCTG CTG GCAG
 ||| || |||| ||||
 ACG CG TGAC GAC CGTC
 _ A_ C TC
 GAM2019 PDCD5 5' CTGCTCCAGCGCTGACGC 17483 AC T
 GC CAGC GCTGGAGCAG
 || |||||
 CG GTCG CGACCTCGTC
 CA _
 GAM2019 PDZD2 5' CTCCTCTACCA GTGGCTGCA 81720 ACCA C C
 TGCAGC GCTG TGGAG AG
 |||| ||||| ||
 ACGTCG TGAC ATCTC TC
 G_ C C
 GAM2019 PPP1R16B 3' TTCAAAGCAGGTGCTGCA 62042 A GC
 TGCAGCACC GCT TGGAG
 ||||| || ||||
 ACGTCGTGG CGA ACCTT
 A A_
 GAM2019 PSIP2 5' CTGCGGCAGCTGGTGGCGCA 53781 AG G
 TGC CACCAGCTGCTG AG
 || ||||| ||

ACG GTGGTCGACGGC TC
 CG G
 GAM2019 RAB40C 3' CTGCCCACAGCACTGGTGCTCA 41279 C C GA_
 TG AGCACCAG TGCTG GCAG
 || ||||| |||| ||||
 AC TCGTGGTC ACGAC CGTC
 _ _ ACC
 GAM2019 RAB40C 3' CTGCCCCAGCAGCCCCTCTGCA 41280 CACCA A
 TGCAG GCTGCTGG GCAG
 |||| ||||| ||||
 ACGTC CGACGACC CGTC
 TCCC_ C
 GAM2019 SFXN5 3' CTGCCAGCCGCTGGTGC 58652 T GA
 GCACCAGC GCTG GCAG
 ||||| |||| ||||
 CGTGGTCG CGAC CGTC
 C _
 GAM2019 SIMRP7 3' CTGCTCCAGCAGACCATCTGCA 93972 CACCAG
 TGCAG CTGCTGGAGCAG
 |||| |||||
 ACGTC GACGACCTCGTC
 TACCA_
 GAM2019 ZNF297B 5' CTGTTGCGGCAGCTGAGGCTAC 82704 C AC G
 A TG AGC CAGCTGCTG AGCAG
 || ||||| ||||
 AC TCG GTCGACGGC TTGTC
 A GA G
 GAM2019 LOC123242 5' CTGAGGCCAGCTGGTGCTG 76114 CT AG_
 CAGCACCAGCTG GG CAG
 ||||| || ||||
 GTCGTGGTCGAC CC GTC
 _ GGA
 GAM2019 LOC126603 5' TGCTTCGCTGATCCTGCA 75914 CAC TGCT
 TGCAG CAGC GGAGCA
 |||| |||| ||||
 ACGTC GTCG CTTCGT
 CTA _
 GAM2019 LOC127841 5' CTGCTCCCCAGCAGCTGGTGC 75186 _
 GCACCAGCTGCT GGAGCAG
 ||||| |||||
 CGTGGTCGACGA CCTCGTC
 CC
 GAM2019 LOC130074 3' CCACAGCTGGTGCTGCA 76624 C
 TGCAGCACCAGCTG TGG
 ||||| ||||
 ACGTCGTGGTCGAC ACC
 _
 GAM2019 LOC132166 3' CCAGCCGCTGGTGTGCA 75535 G T
 TGCA CACCAGC GCTGG
 |||| ||||| ||||

ACGT GTGGTCG CGACC
 _ C
 GAM2019 LOC132332 5' CTGCCCTTGACTGGTGCTCA 76666 C CTGCT A
 TG AGCACCAG GG GCAG
 || ||||| || ||||
 AC TCGTGGTC CC CGTC
 _ AGTT_ _
 GAM2019 LOC142820 3' GCTCCAGCTGCACTGCA 76916 CACCA T
 TGCAG GC GCTGGAGC
 |||| || |||||
 ACGTC CG CGACCTCG
 A_ T
 GAM2019 LOC143785 5' CCAGACGCTGGTGTGCA 77102 G TG
 TGCA CACCAGC CTGG
 ||| ||||| |||
 ACGT GTGGTCG GACC
 _ CA
 GAM2019 LOC146229 3' CCAAGTAGCTGGGACTACA 78267 C CA _
 TG AG CCAGCTGCT GG
 || || ||||| ||
 AC TC GGTCGATGA CC
 A AG A
 GAM2019 LOC146268 3' CTCTGGCTGGTGTGCTGC 78338 GCT
 GCAGCACCAGCT GGAG
 ||||| |||
 CGTCGTGGTCGG TCTC
 _
 GAM2019 LOC147080 5' CCGAGCAGCTGGGACTACA 85031 C CA _
 TG AG CCAGCTGCT GG
 || || ||||| ||
 AC TC GGTCGACGA CC
 A AG G
 GAM2019 LOC147160 5' CTGCTCCAGCACGTGTGC 85075 CA _
 GCAC GC TGCTGGAGCAG
 |||| || |||||
 CGTG TG ACGACCTCGTC
 _ C
 GAM2019 LOC148089 3' CCGGCAGCTAGTGGCA 79329 AG C
 TGC CAC AGCTGCTGG
 ||| || |||||
 ACG GTG TCGACGGCC
 _ A
 GAM2019 LOC150166 5' CTGCTCCAGCAGCCGGGCCTGC 86037 CA A
 A TGCAG CC GCTGCTGGAGCAG
 |||| || |||||
 ACGTC GG CGACGACCTCGTC
 CG C
 GAM2019 LOC151178 5' CTTGCAGCTGAAGCTGCA 80959 AC T
 TGCAGC CAGCTGC GG
 |||| ||||| ||

	ACGTCG GTCGACG TC	
	AA T	
GAM2019 LOC151568 5'	CTGCTCCGGCATCCAGCGCTGC 57495	ACCAGC
	GCAGC TGCTGGAGCAG	
	CGTCG ACGGCCTCGTC	
	CGACCT	
GAM2019 LOC153205 5'	CTGCTCCTGACACGTGCTGCA 87157	CAGCTGCT
	TGCAGCAC GGAGCAG	
	ACGTCGTG CCTCGTC	
	CACAGT__	
GAM2019 LOC154084 3'	CTGCCCCAGTAGCATCTGCA 87377	CACCA A
	TGCAG GCTGCTGG GCAG	
	ACGTC CGATGACC CGTC	
	TA__ C	
GAM2019 LOC154813 5'	CCACCAATGGTGCTGCA 82057	GC C
	TGCAGCACCA TG TGG	
	ACGTCGTGGT AC ACC	
	A_ C	
GAM2019 LOC155006 3'	CTGCTCTGCCCTGATGTGCA 82168	G C CT T
	TGCA CA CAG GC GGAGCAG	
	ACGT GT GTC CG TCTCGTC	
	_ A C_ _	
GAM2019 LOC166129 5'	CTGCTCCAAGCAGCAGCGGCTG 88609	ACCA _
CA	TGCAGC GCTGCT GGAGCAG	
	ACGTCG CGACGA CCTCGTC	
	GCGA A	
GAM2019 LOC196500 5'	GCTCCAGCGCCCTGCCGC 89084	A CCA T
	GC GCA GC GCTGGAGC	
	CG CGT CG CGACCTCG	
	C CC_ _	
GAM2019 LOC200093 3'	CCATTGTACAGTGGTGCTGCA 63765	G C_____
	TGCAGCACCA CTG TGG	
	ACGTCGTGGT GAC ACC	
	_ ATGTT	
GAM2019 LOC200093 5'	TGCTCCAGGGCGCCTGCA 63778	CACCA G
	TGCAG GCT CTGGAGCA	
	ACGTC CGG GACCTCGT	
	CG__ _	
GAM2019 LOC253001 5'	CTGAGGCCAGCTGGTGCTG 97993	CT AG_
	CAGCACCAGCTG GG CAG	

GTCGTGGTCGAC CC GTC
 _ GGA
 GAM2019 LOC254266 5' CCACCGTGCTGGTGCTCA 99196 C _ C
 TG AGCACCAGC TG TGG
 || ||||| || |||
 AC TCGTGGTCG GC ACC
 _ T C
 GAM2019 LOC255189 5' GCTCCCCATTGTGCTGCA 98376 C C CT
 TGCAGCAC AG TG GGAGC
 ||||| || || |||||
 ACGTCGTG TT AC CCTCG
 _ _ CC
 GAM2019 LOC255738 5' CTGCCACGTGGCTGGCATTGC 98629 CA TG _ A
 A TGCAG CCAGC C TGG GCAG
 |||| |||| | || ||||
 ACGTT GGTCTG G ACC CGTC
 AC GT C _
 GAM2019 LOC91040 3' CCATCGTACAGTGGTGCTGCA 65339 G C____
 TGCAGCACCA CTG TGG
 ||||| || || |||
 ACGTCGTGGT GAC ACC
 _ ATGCT
 GAM2019 LOC91040 5' TGCTCCAGAGCGCCTGCA 65353 CACCA G
 TGCAG GCT CTGGAGCA
 |||| || |||||
 ACGTC CGA GACCTCGT
 CG____ _
 GAM2020 DPH2L1 3' CTGACAAAGTCATCCCCTCTCA 9112 C _ CTCA
 GG CCT GAGAGGGGG GAT TCAG
 || ||||| || |||
 GGA CTCTCCCCT CTG AGTC
 _ A AAAC
 GAM2020 MEF2D 3' ATGGCCCTCCCCCTCCCCAGG 20979 CGA ATC
 CCT GAGGGGGG TCAT
 || ||||| |||
 GGA CTCCCCCT GGTA
 CCC CCC
 GAM2020 SORCS2 3' ATGAGGGTCCCTCTCAGAG 40797 GA AT
 CTC GAGGGGGG CTCAT
 || ||||| |||||
 GAG CTCTCCCT GAGTA
 A_ GG
 GAM2020 CACNG4 3' CTGACTTTGTCCCCTCCCCGA 27708 AGA CTCA
 TCG GGGGGGAT TCAG
 || ||||| |||
 AGC CTCCCCTG AGTC
 CC_ TTTC
 GAM2020 CYP2A7 5' TGGAGTCCCCCTCCTGAG 7544 A CT
 CTCG GAGGGGGGAT CA
 |||| ||||| ||

GAGT CTCCCCCCTG GT
 C AG
 GAM2020 FLJ20457 3' GATGGCCTTCCCCTCTGA 35671 G ATC
 TC AGAGGGGGG TCATC
 || ||||| ||||
 AG TCTCCCCTT GGTAG
 _ CC_
 GAM2020 HABP2 5' CTGACATTTTCCCCCCTAAAG 15951 CGAG TCTCA_
 G CCT AGGGGGGA TCAG
 || ||||| ||||
 GGA TCCCCCCT AGTC
 AA_ TTTTAC
 GAM2020 KLF12 3' ATGAGATTCTCTCAGAGG 33276 GAGA
 CCTC GGGGGGATCTCAT
 ||| |||||
 GGAG CTCTCTTAGAGTA
 A_
 GAM2020 SDCCAG3 3' TGACGGCCCCCCTCAGAGG 22806 GA A _
 CCTC GAGGGGGG TC TCA
 ||| ||||| || |||
 GGAG CTCCCCC GG AGT
 A_ _ C
 GAM2020 XPO5 3' CTGACAAGAGGGTTTCCCCGAG 92874 AGA GG AT A_
 CTCG GGG G CTC TCAG
 ||| || | || ||||
 GAGC CCC T GAG AGTC
 _ TT GG AAC
 GAM2020 LOC147599 3' AGGCTCCCCTCTCTCAAGG 85159 C _
 CCT GAGAGGGGGGA TCT
 ||| ||||| |||
 GGA CTCTCTCCCCT GGA
 A C
 GAM2020 LOC200314 3' TGTGACCCCCCCTCAAGG 91608 C A A T
 CCT GAG GGGGGG TC CA
 ||| || ||||| || ||
 GGA CTC CCCCCC AG GT
 A _ C T
 GAM2020 LOC222414 3' TGTAATCCCCCCTCAAGG 95975 C A CT
 CCT GAG GGGGGGAT CA
 ||| || ||||| ||
 GGA CTC CCCCCCTA GT
 A C AT
 GAM2021 A1BG 3' GACAGGGTCTCACTGTGTT 56291 A CA
 AACACGGTGA ACCC TC
 ||||| ||| ||
 TTGTGTCACT TGGG AG
 C AC
 GAM2021 A1BG 3' GAGATGGGGTTTACCTTGTT 56292 C
 AACA GGTGAAACCCCATCTC
 ||| |||||

			TTGT CCACTTTGGGGTAGAG		
			T		
GAM2021	ADAMTS4	3'	GAGACAGGGTTTCACCATGTT 18762	C	CA
			AACA GGTGAAACCC TCTC		
			TTGT CCACTTTGGG AGAG		
			A AC		
GAM2021	ADAMTS4	3'	GAGACGGGGTTTCACCATGTT 18763	C	A
			AACA GGTGAAACCC TCTC		
			TTGT CCACTTTGGGG AGAG		
			A C		
GAM2021	APAF1	3'	GAGACGGGGTTTCACCATGTT 8587	C	A
			AACA GGTGAAACCC TCTC		
			TTGT CCACTTTGGGG AGAG		
			A C		
GAM2021	APAF1	3'	GAGACGGGGTTTCACCATGTT 25973	C	A
			AACA GGTGAAACCC TCTC		
			TTGT CCACTTTGGGG AGAG		
			A C		
GAM2021	APM1	3'	ATGGGGTTTCGTCATGTT 17759	C GT	
			AACA G GAAACCCCAT		
			TTGT C CTTTGGGGTA		
			A TG		
GAM2021	APOL1	3'	GAGATGGGGTTTCACCATGTT 14740	C	
			AACA GGTGAAACCCCATCTC		
			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2021	APPL	3'	GAGACGGGGTTTCACCGTGTT 24948		A
			AACACGGTGAAACCC TCTC		
			TTGTGCCACTTTGGGG AGAG		
			C		
GAM2021	ARCN1	3'	GAGACGGGGTTTCACCGTGTT 9754		A
			AACACGGTGAAACCC TCTC		
			TTGTGCCACTTTGGGG AGAG		
			C		
GAM2021	ATP1B2	3'	GAGATGGAGTTTCGCTCTTGT 9835	C _	C
			ACA G GTGAAAC CCATCTC		
			TGT C CGCTTTG GGTAGAG		
			T T A		
GAM2021	ATP7A	3'	GAGACGGGGTTTCGCCATGTT 5322	C	A
			AACA GGTGAAACCC TCTC		

			TTGT CCGCTTTGGGG AGAG		
			A C		
GAM2021	AXL	3'	GAGACAGGGTTTCACCATGTT 9905	C	CA
			AACA GGTGAAACCC TCTC		
			TTGT CCACTTTGGG AGAG		
			A AC		
GAM2021	AXL	3'	GAGACAGGGTTTCACCATGTT 41886	C	CA
			AACA GGTGAAACCC TCTC		
			TTGT CCACTTTGGG AGAG		
			A AC		
GAM2021	BRIP1	3'	GAGATGGGGTTTCACCATGTT 50209	C	
			AACA GGTGAAACCCCATCTC		
			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2021	C14orf1	3'	GAGACGGGGTTTCACTCTGT 24169	C	A
			ACA GGTGAAACCC TCTC		
			TGT TCACTTTGGGG AGAG		
			C C		
GAM2021	C14orf1	3'	GAGATGGGGTCTTACTATGTT 24170	CG	A
			AACA GTGA ACCCATCTC		
			TTGT CATT TGGGGTAGAG		
			AT C		
GAM2021	C7	3'	GAGATGGGTTTCACCATGTT 6986	C	C
			AACA GGTGAAACCC ATCTC		
			TTGT CCACTTTGGG TAGAG		
			A _		
GAM2021	CA14	3'	ATGAGGAAATCGCTGTGTT 25057	AAC	_
			AACACGGTGA CC CAT		
			TTGTGTCGCT GG GTA		
			AAA A		
GAM2021	CASP10	3'	GAGATGGGGTTTCACTATGTT 53222	CG	
			AACA GTGAAACCCCATCTC		
			TTGT CACTTTGGGGTAGAG		
			AT		
GAM2021	CASP10	3'	GAGATGGGGTTTCACTATGTT 53258	CG	
			AACA GTGAAACCCCATCTC		
			TTGT CACTTTGGGGTAGAG		
			AT		
GAM2021	CASP2	3'	GAGACAGGGTTTCACCATGTT 53288	C	CA
			AACA GGTGAAACCC TCTC		

			TTGT CCACTTTGGG AGAG		
			A AC		
GAM2021	CASP2	3'	GAGACAGGGTTTCACCATGTT 53304	C	CA
			AACA GGTGAAACCC TCTC		
			TTGT CCACTTTGGG AGAG		
			A AC		
GAM2021	CASP2	3'	GAGACAGGGTTTCACCATGTT 53333	C	CA
			AACA GGTGAAACCC TCTC		
			TTGT CCACTTTGGG AGAG		
			A AC		
GAM2021	CASP2	3'	GAGACAGGGTTTCACCATGTT 8709	C	CA
			AACA GGTGAAACCC TCTC		
			TTGT CCACTTTGGG AGAG		
			A AC		
GAM2021	CASP8	3'	GAGACAGGGTTTCACTGTGTT 8753		CA
			AACACGGTGAAACCC TCTC		
			TTGTGTCACTTTGGG AGAG		
			AC		
GAM2021	CASP8	3'	GAGACAGGGTTTCACTGTGTT 54076		CA
			AACACGGTGAAACCC TCTC		
			TTGTGTCACTTTGGG AGAG		
			AC		
GAM2021	CASP8	3'	GAGACAGGGTTTCACTGTGTT 54099		CA
			AACACGGTGAAACCC TCTC		
			TTGTGTCACTTTGGG AGAG		
			AC		
GAM2021	CASP8	3'	GAGACAGGGTTTCACTGTGTT 54115		CA
			AACACGGTGAAACCC TCTC		
			TTGTGTCACTTTGGG AGAG		
			AC		
GAM2021	CBFA2T2	3'	GAGACGGGGTTTCTCCTTGTT 18711	C T	A
			AACA GG GAAACCCC TCTC		
			TTGT CC CTTTGGGG AGAG		
			T T C		
GAM2021	CDC6	3'	GAGACAGGGTTTTACCATGTT 8821	C	CA
			AACA GGTGAAACCC TCTC		
			TTGT CCATTTTGGG AGAG		
			A AC		
GAM2021	CIAS1	5'	GAGATGGAGTCTTGCTGTGT 18097	TG A C	
			ACACGG A AC CCATCTC		

			TGTGTC T TG GGTAGAG		
			GT C A		
GAM2021	CLECSF11	5'	GAGATGGGGTTTCACTATGTT 56149	CG	
			AACA GTGAAACCCCATCTC		
			TTGT CACTTTGGGGTAGAG		
			AT		
GAM2021	CLNS1A	3'	GAGAGCTCCTTTCGCCATGTT 8921	C	CCCCA
			AACA GGTGAAA TCTC		
			TTGT CCGCTTT AGAG		
			A CCTCG		
GAM2021	CNGA1	5'	GAGATGGGATTTCACCATGTT 60240	C	C
			AACA GGTGAAA CCCATCTC		
			TTGT CCACTTT GGGTAGAG		
			A A		
GAM2021	CNN2	3'	GAGATGGGGTTTCCCCATGTT 16461	C T	
			AACA GG GAAACCCCATCTC		
			TTGT CC CTTTGGGGTAGAG		
			A C		
GAM2021	CR1	3'	GAGACGGGGTTTCACTATGTT 6944	C	A
			AACA GGTGAAACCCC TCTC		
			TTGT CCACTTTGGGG AGAG		
			A C		
GAM2021	CRTAP	3'	GAGACGGGGTTTTGCCATGTT 22080	C TG	A
			AACA GG AAACCCC TCTC		
			TTGT CC TTTGGGG AGAG		
			A GT C		
GAM2021	CTF1	3'	GAGACGAGGTTTTCGCCATGTT 9016	C	CCA
			AACA GGTGAAACC TCTC		
			TTGT CCGCTTTGG AGAG		
			A AGC		
GAM2021	CXCL16	3'	GAGACGGGGTTTCACTATGTT 42169	C	A
			AACA GGTGAAACCCC TCTC		
			TTGT CCACTTTGGGG AGAG		
			A C		
GAM2021	CYP1A2	3'	GAGACGAGGTTTCACTGTGTT 7515		CCA
			AACACGGTGAAACC TCTC		
			TTGTGTCACTTTGG AGAG		
			AGC		
GAM2021	CYP1A2	3'	GAGACGGGGTTTCACTATGTT 7516	C	CA
			AACA GGTGAAACCCC TCTC		

			TTGT CCACTTTGGG AGAG		
			A C_		
GAM2021	CYP1A2	3'	GAGATGGGGTTTCACCATGTT 7517	C	
			AACA GGTGAAACCCCATCTC		
			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2021	CYP1B1	3'	GAGATGAGGTCAGTTGTGTT 5446	GG GAA C	
			AACAC T ACC CATCTC		
			TTGTG G TGG GTAGAG		
			TT AC_ A		
GAM2021	CYP2B6	3'	GAGATGGGGTTTCACTGTGT 7562		
			ACACGGTGAACCCCATCTC		
			TGTGTCACCTTTGGGGTAGAG		
GAM2021	CYP4F3	3'	GAGGCGGGGTTTCGCCATGTT 8008	C	AT
			AACA GGTGAAACCCC CTC		
			TTGT CCGCTTTGGGG GAG		
			A CG		
GAM2021	CYP51	3'	GAGACGGGGGTTTCACTATGTT 7616	CG	A_
			AACA GTGAAACCCC TCTC		
			TTGT CACTTTGGGG AGAG		
			AT GC		
GAM2021	DFFB	3'	GAGACGGGGTTCACCATGTT 88771	C	A
			AACA GGTGAAACCCC TCTC		
			TTGT CCACTTTGGGG AGAG		
			A C		
GAM2021	DHFR	3'	GAGATGGGGTTCACCATGTT 7648	C	
			AACA GGTGAAACCCCATCTC		
			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2021	DSC3	3'	GAGACGGGGTTCCTGTGTT 44623		A
			AACACGGTGAACCCC TCTC		
			TTGTGTCACCTTTGGGG AGAG		
			C		
GAM2021	DSC3	3'	GAGACGGGGTTCCTGTGTT 10440		A
			AACACGGTGAACCCC TCTC		
			TTGTGTCACCTTTGGGG AGAG		
			C		
GAM2021	EHD2	3'	GAGACGGGGTTCACCATGTT 28222	C	A
			AACA GGTGAAACCCC TCTC		

			TTGT CCACTTTGGGG AGAG		
			A C		
GAM2021	EIF2S3	3'	GAGACGGGGTTTCAGCATGTT 9208	CGG	A
			AACA TGAAACCCC TCTC		
			TTGT ACTTTGGGG AGAG		
			ACG C		
GAM2021	ENDOGL1	3'	GAGATGTGGTCTCGCCGTGT 18824	A	C
			ACACGGTGA ACC CATCTC		
			TGTGCCGCT TGG GTAGAG		
			C T		
GAM2021	EPB72	3'	GAGACGGGGTTTCACCATGTT 15876	C	A
			AACA GGTGAAACCCC TCTC		
			TTGT CCACTTTGGGG AGAG		
			A C		
GAM2021	EPB72	3'	GAGATGGAGTTTCACTCTTGT 15877	C_	C
			ACA G GTGAAAC CCATCTC		
			TGT C CACTTTG GG TAGAG		
			T T A		
GAM2021	F2RL2	3'	GAGACGGGGTTTCACCATGTT 15897	C	A
			AACA GGTGAAACCCC TCTC		
			TTGT CCACTTTGGGG AGAG		
			A C		
GAM2021	F2RL3	3'	AGACGGAGTTTCACCATGTT 15487	C	C A
			AACA GGTGAAAC CC TCT		
			TTGT CCACTTTG GG AGA		
			A A C		
GAM2021	FANCF	3'	GAGACGGGGTTTCACCATG 42980	C	A
			CA GGTGAAACCCC TCTC		
			GT CCACTTTGGGG AGAG		
			A C		
GAM2021	FCAR	3'	GAGATGGGGTTTCACTGTGTT 56574		
			AACACGGTGAAACCCCATCTC		
			TTGTGTCACTTTGGGGTAGAG		
GAM2021	FCAR	3'	GAGATGGGGTTTCACTGTGTT 56593		
			AACACGGTGAAACCCCATCTC		
			TTGTGTCACTTTGGGGTAGAG		
GAM2021	FCAR	3'	GAGATGGGGTTTCACTGTGTT 56605		
			AACACGGTGAAACCCCATCTC		

TTGTGTCACTTTGGGGTAGAG

GAM2021 FCAR 3' GAGATGGGGTTTCACTGTGTT 56617
AACACGGTGAAACCCCATCTC
|||||
TTGTGTCACTTTGGGGTAGAG

GAM2021 FCAR 3' GACAGGGTTTCACCATGTT 56635 C CA
AACAGGTGAAACCC TC
||| ||||| ||
TTGT CCACTTTGGG AG
A AC

GAM2021 FCAR 3' GAGATGGGGTTTCACTGTGTT 10589
AACACGGTGAAACCCCATCTC
|||||
TTGTGTCACTTTGGGGTAGAG

GAM2021 FCGR2A 3' GAGACAGGGTTTCGCAATGTT 80029 CG CA
AACAGTGAAACCC TCTC
||| ||||| |||
TTGT CGCTTTGGG AGAG
AA AC

GAM2021 FEZ1 3' GAGATGGGAGTTTCACCATGTT 42870 C _
AACAGGTGAAAC CCCATCTC
||| ||||| |||||
TTGT CCACTTTG GGGTAGAG
A A

GAM2021 FGF5 3' GAGACGGGGTTTCACCATGTT 16760 C A
AACAGGTGAAACCCC TCTC
||| ||||| |||
TTGT CCACTTTGGGG AGAG
A C

GAM2021 FGF5 3' GAGACGGGGTTTCACCATGTT 53660 C A
AACAGGTGAAACCCC TCTC
||| ||||| |||
TTGT CCACTTTGGGG AGAG
A C

GAM2021 FSHPRH1 5' GAGACATTGGTCTCACTGTGTT 23067 A CCA_
AACACGGTGA ACC TCTC
||||| ||| |||
TTGTGTCACT TGG AGAG
C TTAC

GAM2021 FUT1 3' GAGACAGGGTTTCACCATGTT 5592 C CA
AACAGGTGAAACCC TCTC
||| ||||| |||
TTGT CCACTTTGGG AGAG
A AC

GAM2021 FUT1 3' GAGACGGGGTTTCATCGTGTT 5594 A
AACACGGTGAAACCCC TCTC
||||| |||

			TTGTGCTACTTTGGGG AGAG		
			C		
GAM2021	G6PC	3'	GAGATGGGATTTTCATCATGTT 5661	C	C
			AACA GGTGAAA CCCATCTC		
			TTGT CTACTTT GGGTAGAG		
			A A		
GAM2021	GHR	3'	GAGACGGGGTTTCACCATGTT 5700	C	A
			AACA GGTGAAACCCC TCTC		
			TTGT CCACTTTGGGG AGAG		
			A C		
GAM2021	GM2A	3'	GAGATGGGGTTTCACCATGTT 68382	C	
			AACA GGTGAAACCCCATCTC		
			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2021	GNE	3'	GACAGGGTTTCACCATGTT 19670	C	CA
			AACA GGTGAAACCC TC		
			TTGT CCACTTTGGG AG		
			A AC		
GAM2021	GPR4	3'	GAGACAGGGTCTCACTGTGTT 60578		A CA
			AACACGGTGA ACCC TCTC		
			TTGTGTCACT TGGG AGAG		
			C AC		
GAM2021	GPR81	3'	GAGACAGGGTTTTGCCATGTT 51750	C TG	CA
			AACA GG AAACCC TCTC		
			TTGT CC TTTGGG AGAG		
			A GT AC		
GAM2021	GRAF	3'	GAGATGGGGTTTTGCCATGTT 31237	C TG	
			AACA GG AAACCCCATCTC		
			TTGT CC TTTGGGGTAGAG		
			A GT		
GAM2021	GRINL1A	3'	GAGATGGGGTCTTGCTCTGT 70062	C TG A	
			ACA GG A ACCCCATCTC		
			TGT TC T TGGGGTAGAG		
			C GT C		
GAM2021	GRM7	5'	GAGATTGGGTTTCACCATGTT 7787	C	C
			AACA GGTGAAACCC ATCTC		
			TTGT CCACTTTGGG TAGAG		
			A T		
GAM2021	HCS	3'	GAGATGGAGTTTTGCCATGT 38980	C TG	C
			ACA GG AAAC CCATCTC		

			TGT CC TTTG GGTAGAG		
			A GT A		
GAM2021	HCS	3'	GAGATGGTGTTCACCATGTT 38981	C	C
			AACA GGTGAAAC CCATCTC		
			TTGT CCACTTTG GGTAGAG		
			A T		
GAM2021	HTR1D	3'	AGACGGGGTTTCATCATGTT 7834	C	A
			AACA GGTGAAACCCC TCT		
			TTGT CTACTTTGGGG AGA		
			A C		
GAM2021	HUNK	3'	ATGGGGTTTCGCCATGTT 28176	C	
			AACA GGTGAAACCCCAT		
			TTGT CCGCTTTGGGGTA		
			A		
GAM2021	HUS1	3'	GAGACAGGGTCTCACTGTGTT 92739		A CA
			AACACGGTGA ACCC TCTC		
			TTGTGTCACT TGGG AGAG		
			C AC		
GAM2021	HYAL4	5'	GAGATGGGGTTTCACCGTGTT 25369		
			AACACGGTGAAACCCCATCTC		
			TTGTGCCACTTTGGGGTAGAG		
GAM2021	IGF1	3'	GAGACGGGGTTTACCATGTT 7074	C	A
			AACA GGTGAAACCCC TCTC		
			TTGT CCATTTTGGGG AGAG		
			A C		
GAM2021	IGF1	3'	GAGATGGGGTCTCGCACTGT 7075	AA__	
			ACGGTG ACCCCATCTC		
			TGTCAC TGGGGTAGAG		
			GCTC		
GAM2021	IL11	3'	GAGACAGGGTTTCACCATGTT 7185	C	CA
			AACA GGTGAAACCC TCTC		
			TTGT CCACTTTGGG AGAG		
			A AC		
GAM2021	IMPA2	5'	GAGATGGGGCTTCGCCATG 96947	C	A
			CA GGTGAA CCCCATCTC		
			GT CCGCTT GGGGTAGAG		
			A C		
GAM2021	INMT	3'	GAGACGGAGTTTCGCTCTGT 23216	C	C A
			ACA GGTGAAAC CC TCTC		

			TGT TCGCTTTG GG AGAG		
			C A C		
GAM2021	INMT	3'	GATATGGGGTTTCACCGTGTT 23217	C	
			AACACGGTGAAACCCCAT TC		
			TTGTGCCACTTTGGGGTA AG		
			T		
GAM2021	JAK3	3'	GAGATGAGGTTTCACCATG 5831	C	C
			CA GGTGAAACC CATCTC		
			GT CCACTTTGG GTAGAG		
			A A		
GAM2021	JRK	3'	GAGACAGGGTCTCACTGTGTT 87827	A	CA
			AACACGGTGA ACCC TCTC		
			TTGTGTCACT TGGG AGAG		
			C AC		
GAM2021	LLGL1	3'	GAGATGGGGTTTCACCATGTT 67419	C	
			AACA GGTGAAACCCCATCTC		
			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2021	LNK	3'	GAGACAGGGTTTCACCATGTT 19645	C	CA
			AACA GGTGAAACCC TCTC		
			TTGT CCACTTTGGG AGAG		
			A AC		
GAM2021	LTB4R	5'	GAGACGGGGTTTCACCATGTT 7464	C	A
			AACA GGTGAAACCC TCTC		
			TTGT CCACTTTGGGG AGAG		
			A C		
GAM2021	LYZ	3'	GAGACAGGGTTTCACCGTGTT 5895		CA
			AACACGGTGAAACCC TCTC		
			TTGTGCCACTTTGGG AGAG		
			AC		
GAM2021	MAGEA10	3'	AGATTCTTCACTGTGTT 41084		ACCCC
			AACACGGTGAA ATCT		
			TTGTGTCACTT TAGA		
			CT__		
GAM2021	MAK	3'	GAGACAGGGTTTCACCATGTT 20947	C	CA
			AACA GGTGAAACCC TCTC		
			TTGT CCACTTTGGG AGAG		
			A AC		
GAM2021	MDM2	3'	GAGACAGGGTTTCACCGTGTT 23458		CA
			AACACGGTGAAACCC TCTC		

			TTGTGCCACTTTGGG AGAG		
			AC		
GAM2021	MDM2	3'	GAGACAGGGTTTCACCGTGTT 23471		CA
			AACACGGTGAAACCC TCTC		
			TTGTGCCACTTTGGG AGAG		
			AC		
GAM2021	MDM2	3'	GAGACAGGGTTTCACCGTGTT 23484		CA
			AACACGGTGAAACCC TCTC		
			TTGTGCCACTTTGGG AGAG		
			AC		
GAM2021	MDM2	3'	GAGACAGGGTTTCACCGTGTT 23497		CA
			AACACGGTGAAACCC TCTC		
			TTGTGCCACTTTGGG AGAG		
			AC		
GAM2021	MDM2	3'	GAGACAGGGTTTCACCGTGTT 11493		CA
			AACACGGTGAAACCC TCTC		
			TTGTGCCACTTTGGG AGAG		
			AC		
GAM2021	MEF2A	5'	GAGATGGAGTTTCACCATGTT 20000	C	C
			AACA GGTGAAAC CCATCTC		
			TTGT CCACTTTG GG TAGAG		
			A A		
GAM2021	MEFV	3'	GAGACGGGGTTTCACCATGTT 5938	C	A_
			AACA GGTGAAACCCC TCTC		
			TTGT CCACTTTGGGG AGAG		
			A GC		
GAM2021	MHC2TA	3'	GAGACAGGGTTTTGCCGTGTT 5985	TG	CA
			AACACGG AAACCC TCTC		
			TTGTGCC TTTGGG AGAG		
			GT AC		
GAM2021	MLANA	3'	GAGACGGGGTTTCTCCATGTT 19763	C T	A
			AACA GG GAAACCCC TCTC		
			TTGT CC CTTTGGGG AGAG		
			A T C		
GAM2021	MLANA	3'	GAGATGGAGTTTCGCTTTTGTT 19764	C_	C
			AACA GGTGAAAC CCATCTC		
			TTGT TCGCTTTG GG TAGAG		
			TT A		
GAM2021	MPL	3'	GAGACAGGGTTTTGCCATGTT 19355	C TG	CA
			AACA GG AAACCC TCTC		

			TTGT CC TTTGGG AGAG		
			A GT AC		
GAM2021	MRPL49	3'	GAGATGGGGTTTCACCATGTT 70169	C	
			AACA GGTGAAACCCCATCTC		
			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2021	MTR	3'	GAGACAGGATTTCACTGTGTT 6018	C	CA
			AACACGGTGAAA CC TCTC		
			TTGTGTCACTTT GG AGAG		
			A AC		
GAM2021	NCOA6	5'	GAGGCGGGGTTTCGCCATGTT 26836	C	AT
			AACA GGTGAAACCCC CTC		
			TTGT CCGCTTTGGGG GAG		
			A CG		
GAM2021	NCOA6	5'	GATGGGGTTTCATCATGTT 26837	C	
			AACA GGTGAAACCCCATC		
			TTGT CTACTTTGGGGTAG		
			A		
GAM2021	NDRG3	3'	GAGATGGAGTTTCACCATGTT 50122	C	C
			AACA GGTGAAAC CCATCTC		
			TTGT CCACTTTG GG TAGAG		
			A A		
GAM2021	NQO1	3'	GAGACGGCGTTTCACCATGTT 8049	C	C A
			AACA GGTGAAAC CC TCTC		
			TTGT CCACTTTG GG AGAG		
			A C C		
GAM2021	PCDHA9	3'	GAGATGGGGTTTCACCGTGTT 26620		
			AACACGGTGAAACCCCATCTC		
			TTGTGCCACTTTGGGGTAGAG		
GAM2021	PCDHA9	3'	GAGATGGGGTTTCATCATGTT 26621	C	
			AACA GGTGAAACCCCATCTC		
			TTGT CTACTTTGGGGTAGAG		
			A		
GAM2021	PDGFB	3'	GAGATGGAGTTTGCTGTTG 12025	C	G C
			A ACGGT AAAC CCATCTC		
			G TGTCG TTTG GG TAGAG		
			T _ A		
GAM2021	PER2	3'	GAGACAGGGTTTCACCATGTT 43352	C	CA
			AACA GGTGAAACCC TCTC		

			TTGT CCACTTTGGG AGAG		
			A AC		
GAM2021	PEX14	3'	GAGATGGGGGCTCACTCC 64402 C AA		
			A GGTGA CCCCATCTC		
			C TCACT GGGGTAGAG		
			C CG		
GAM2021	PIGR	3'	GAGACAAAGTCTCACTGTGT 72998 A CCCA		
			ACACGGTGA AC TCTC		
			TGTGTCACT TG AGAG		
			C AAAC		
GAM2021	PIGR	3'	GAGACAGGGTTTCACCGTGTT 72999 CA		
			AACACGGTGAAACCC TCTC		
			TTGTGCCACTTTGGG AGAG		
			AC		
GAM2021	PIGR	3'	GAGACAGGGTTTCGCCATGTT 73000 C CA		
			AACA GGTGAAACCC TCTC		
			TTGT CCGCTTTGGG AGAG		
			A AC		
GAM2021	PIK3C2B	3'	GAGACGGGGTTTCACCATGTT 12101 C A		
			AACA GGTGAAACCCC TCTC		
			TTGT CCACTTTGGGG AGAG		
			A C		
GAM2021	PIK3CD	3'	GAGACGGGGTTTCACCATGTT 18492 C A_		
			AACA GGTGAAACCCC TCTC		
			TTGT CCACTTTGGGG AGAG		
			A GC		
GAM2021	PIK3CD	3'	GAGATGGGGTCTTCCTCTGTT 18494 C T _		
			AACA GG GAA ACCCCATCTC		
			TTGT TC CTT TGGGGTAGAG		
			C _ C		
GAM2021	POU2AF1	3'	GAGACGGGGTTTCACCATGTT 21743 C A		
			AACA GGTGAAACCCC TCTC		
			TTGT CCACTTTGGGG AGAG		
			A C		
GAM2021	PPP1R12B	3'	GAGATGGGGTTTTGCCATGTT 50388 C TG		
			AACA GG AAACCCCATCTC		
			TTGT CC TTTGGGGTAGAG		
			A GT		
GAM2021	PRKR	3'	AGACAGGGTTTCACCATGTT 12339 C CA		
			AACA GGTGAAACCC TCT		

			TTGT CCACTTTGGG AGA		
			A AC		
GAM2021	PRKWNK3	3'	GATGGGGTTTCACTATGTT 62233	CG	
			AACA GTGAAACCCCATC		
			TTGT CACTTTGGGGTAG		
			AT		
GAM2021	PTGIS	3'	GAGACGGGGTTTCCCATGTT 8209	C T	A
			AACA GG GAAACCCC TCTC		
			TTGT CC CTTTGGGG AGAG		
			A C C		
GAM2021	PTGIS	3'	GAGATGGGATTTCACCGT 8210	C	
			ACGGTGAAA CCCATCTC		
			TGCCACTTT GGGTAGAG		
			A		
GAM2021	RAB36	3'	GAGAGAGGTTTCACCATGTT 18169	C	CCA
			AACA GGTGAAACC TCTC		
			TTGT CCACTTTGG AGAG		
			A AG_		
GAM2021	RAB36	3'	GAGATGGAGTTTCACCCTTGT 18170	C_	C
			ACA GGTGAAAC CCATCTC		
			TGT CCACTTTG GGTAGAG		
			TC A		
GAM2021	RAB36	3'	GAGATGGGGTTTCTCCATGTT 18171	C T	
			AACA GG GAAACCCCATCTC		
			TTGT CC CTTTGGGGTAGAG		
			A T		
GAM2021	RABL2A	3'	GAGACGGGGTTTCACCATGTT 26407	C	A
			AACA GGTGAAACCCC TCTC		
			TTGT CCACTTTGGGG AGAG		
			A C		
GAM2021	RABL2B	3'	GAGACGGGGTTTCACCATGTT 23978	C	A
			AACA GGTGAAACCCC TCTC		
			TTGT CCACTTTGGGG AGAG		
			A C		
GAM2021	RAD52	3'	GAGACGGGGTCTGGCTGTGTT 57034	GAA	A
			AACACGGT ACCCC TCTC		
			TTGTGTCG TGGGG AGAG		
			GTC C		
GAM2021	RAD52	3'	GAGACGGGGTCTGGCTGTGTT 57045	GAA	A
			AACACGGT ACCCC TCTC		

			TTGTGTCG TGGGG AGAG		
			GTC C		
GAM2021	RAD52	3'	GAGACGGGGTCTGGCTGTGTT 57051	GAA	A
			AACACGGT ACCCC TCTC		
			TTGTGTCG TGGGG AGAG		
			GTC C		
GAM2021	RAD52	3'	GAGACGGGGTCTGGCTGTGTT 12758	GAA	A
			AACACGGT ACCCC TCTC		
			TTGTGTCG TGGGG AGAG		
			GTC C		
GAM2021	RBBP9	3'	GAGACAGGGTTTCACCATGTT 70691	C	CA
			AACA GGTGAAACCC TCTC		
			TTGT CCACTTTGGG AGAG		
			A AC		
GAM2021	RBM8A	3'	GAGATAGAGTCTTGCTGTGTT 18806	TG A	CCC
			AACACGG A AC ATCTC		
			TTGTGTC T TG TAGAG		
			GT C AGA		
GAM2021	RBM8A	3'	GAGATGGGGTCTTGCTGTGTT 18807	TG A	
			AACACGG A ACCCATCTC		
			TTGTGTC T TGGGGTAGAG		
			GT C		
GAM2021	RGR	3'	GAGATAAGGTCTCATTGTG 12860	A	CC
			CACGGTGA ACC ATCTC		
			GTGTTACT TGG TAGAG		
			C AA		
GAM2021	RGS9	5'	AGACGGGGTTTTGTCATGTT 15169	C TG	A
			AACA GG AAACCCC TCT		
			TTGT CT TTTGGGG AGA		
			A GT C		
GAM2021	RGS9	3'	AGATGGGGTAGATTGTG 15172	GAA	
			CACGGT ACCCATCT		
			GTGTTA TGGGGTAGA		
			GA_		
GAM2021	RHD	3'	AGATGGGGTTTCACCATGTT 32807	C	
			AACA GGTGAAACCCCATCT		
			TTGT CCACTTTGGGGTAGA		
			A		
GAM2021	RHD	3'	GACAGGGTTTCACCATGTT 32828	C	CA
			AACA GGTGAAACCC TC		

			TTGT CCACTTTGGG AG		
			A AC		
GAM2021	RHD	3'	AGATGGGGTTTCACCATGTT 33132	C	
			AACA GGTGAAACCCCATCT		
			TTGT CCACTTTGGGGTAGA		
			A		
GAM2021	RHD	3'	GACAGGGTTTCACCATGTT 33143	C	CA
			AACA GGTGAAACCC TC		
			TTGT CCACTTTGGG AG		
			A AC		
GAM2021	RPH3AL	3'	GAGATGGGGTTTCTCCATGTT 23734	C T	
			AACA GG GAAACCCCATCTC		
			TTGT CC CTTTGGGGTAGAG		
			A T		
GAM2021	RPP30	3'	GAGACGGGGTTTCACCGTGTT 22199		A
			AACACGGTGAAACCCC TCTC		
			TTGTGCCACTTTGGGG AGAG		
			C		
GAM2021	SAS	3'	GAGACAGGGTTTCACCATGTT 21101	C	CA
			AACA GGTGAAACCC TCTC		
			TTGT CCACTTTGGG AGAG		
			A AC		
GAM2021	SCML2	3'	GAGATGGAGTTTCACTCTTGT 21425	C _	C
			ACA G GTGAAAC CCATCTC		
			TGT C CACTTTG GG TAGAG		
			T T A		
GAM2021	SCML2	3'	GAGATGGGGTTTCTCCATGTT 21426	C T	
			AACA GG GAAACCCCATCTC		
			TTGT CC CTTTGGGGTAGAG		
			A T		
GAM2021	SEDL	3'	GAGATGGAGTTTCGCTCTGTT 28099	C	C
			AACA GGTGAAAC CCATCTC		
			TTGT TCGCTTTG GG TAGAG		
			C A		
GAM2021	SERPINB9	3'	GAGACGGGGTTTCACCGTGTT 16021		A
			AACACGGTGAAACCCC TCTC		
			TTGTGCCACTTTGGGG AGAG		
			C		
GAM2021	SH3GL3	5'	GAGATGGGGTTTCACCATGTT 13108	C	C
			AACA GGTGAAACCC ATCTC		

			TTGT CCACTTTGGG TAGAG		
			A _		
GAM2021	SHOX	3'	GAGACGGCGTTTCACCGTGTT 6575	C	A
			AACACGGTGAAAC CC TCTC		
			TTGTGCCACTTTG GG AGAG		
			C C		
GAM2021	SHOX	3'	GAGATGGGGTTTGACCATGTT 23520	C	G
			AACA GGT AAACCCCATCTC		
			TTGT CCA TTTGGGGTAGAG		
			A G		
GAM2021	SIGLEC11	3'	GAGACAGGGTTTTGCCATGTT 54654	C	TG CA
			AACA GG AAACCC TCTC		
			TTGT CC TTTGGG AGAG		
			A GT AC		
GAM2021	SIL	5'	GAGACGGGGTTTCACCATGTT 13155	C	A
			AACA GGTGAAACCCC TCTC		
			TTGT CCACTTTGGGG AGAG		
			A C		
GAM2021	SLC15A1	3'	GAGATGGGGTTTCACCATGTT 18642	C	
			AACA GGTGAAACCCCATCTC		
			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2021	SLC17A5	3'	GAGATGGGGTCTCGTTTTGT 25833	CG	A
			ACA GTGA ACCCCATCTC		
			TGT TGCT TGGGGTAGAG		
			TT C		
GAM2021	SLC3A2	5'	GAGACGGGGTCTGACTGTGTT 11522	GAA	A
			AACACGGT ACCCC TCTC		
			TTGTGTCA TGGGG AGAG		
			GTC C		
GAM2021	SLC3A2	5'	GAGTTGGGGTCTCACTGTGTT 11523	A	T
			AACACGGTGA ACCCCA CTC		
			TTGTGTCACT TGGGGT GAG		
			C T		
GAM2021	SMAC	5'	GAGATGGGGTTTCACCATGTT 58022	C	
			AACA GGTGAAACCCCATCTC		
			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2021	SNAP23	3'	GAGACAGGGTTTCACCATGT 56336	C	CA
			ACA GGTGAAACCC TCTC		

			TGT CCACTTTGGG AGAG		
			A AC		
GAM2021	SNAP23	3'	GAGACAGGGTTTCACCATGT 15139	C	CA
			ACA GGTGAAACCC TCTC		
			TGT CCACTTTGGG AGAG		
			A AC		
GAM2021	SPN	3'	GAGACAGAGTTTCGCTTTGT 13375	C	CCCA
			ACA GGTGAAAC TCTC		
			TGT TCGCTTTG AGAG		
			T AGAC		
GAM2021	SPN	3'	GAGATGGGGTTTCACCATGTT 13376	C	
			AACA GGTGAAACCCCATCTC		
			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2021	TAF11	3'	GAGATGGGGTCTTGCTTTGTT 20121	C	TG A
			AACA GG A ACCCCATCTC		
			TTGT TC T TGGGGTAGAG		
			T GT C		
GAM2021	TAPBP	3'	GAGACGGGGTTTCACCATGTT 13562	C	A
			AACA GGTGAAACCCC TCTC		
			TTGT CCACTTTGGGG AGAG		
			A C		
GAM2021	TAPBP	3'	GAGACGGGGTTTCACCGTGTT 13563		A
			AACACGGTGAAACCCC TCTC		
			TTGTGCCACTTTGGGG AGAG		
			C		
GAM2021	TAPBP	3'	GAGACGGGGTTTCACCGTGTT 13564		A
			AACACGGTGAAACCCC TCTC		
			TTGTGCCACTTTGGGG AGAG		
			C		
GAM2021	TAT	3'	GAGACAGGGTTTCACCATGTT 6255	C	CA
			AACA GGTGAAACCC TCTC		
			TTGT CCACTTTGGG AGAG		
			A AC		
GAM2021	TBXA2R	3'	GAGACGGGGTTTCACCGTGTT 8358		A
			AACACGGTGAAACCCC TCTC		
			TTGTGCCACTTTGGGG AGAG		
			C		
GAM2021	TEM7	3'	GAGACAGGGTCTCACTGTGT 40261	A	CA
			ACACGGTGA ACCC TCTC		

			TGTGTC	ACT	TGGG	AGAG		
			C	AC				
GAM2021	TERF1	3'	GAGGCGGGGTTTCACCATG	34394	C	AT		
			CA GGTGAAACCCC	CTC				
			GT CCACTTTGGGG	GAG				
			A	CG				
GAM2021	TERF2	3'	GAGACGGGGTTTCACCGTGTT	20152		A		
			AACACGGTGAAACCCC	TCTC				
			TTGTGCCACTTTGGGG	AGAG				
			C					
GAM2021	TIM3	3'	GAGACAGGGTTTCACCATGTT	52356	C	CA		
			AACA GGTGAAACCC	TCTC				
			TTGT CCACTTTGGG	AGAG				
			A	AC				
GAM2021	TMPRSS3	3'	GAGACAGGGTTTCACCATGTT	51516	C	CA		
			AACA GGTGAAACCC	TCTC				
			TTGT CCACTTTGGG	AGAG				
			A	AC				
GAM2021	TMPRSS3	3'	GAGACAGGGTTTCACCATGTT	51543	C	CA		
			AACA GGTGAAACCC	TCTC				
			TTGT CCACTTTGGG	AGAG				
			A	AC				
GAM2021	TMPRSS3	3'	GAGACAGGGTTTCACCATGTT	44025	C	CA		
			AACA GGTGAAACCC	TCTC				
			TTGT CCACTTTGGG	AGAG				
			A	AC				
GAM2021	TNFAIP2	3'	GAGACAGGGTCTTGCTGTGTT	21921		TG A	CA	
			AACACGG A ACCC	TCTC				
			TTGTGTC T TGGG	AGAG				
			GT C	AC				
GAM2021	TNFRSF10B	3'	GAGACGGGGTTTCACCATGTT	15227	C	A		
			AACA GGTGAAACCCC	TCTC				
			TTGT CCACTTTGGGG	AGAG				
			A	C				
GAM2021	TP53	3'	GAGATGGGGTCTCACAGTGTT	6801	G	A		
			AACAC GTGA ACCCATCTC					
			TTGTG CACT TGGGGTAGAG					
			A	C				
GAM2021	TP53BP2	5'	GAGATAGAGTTTCATCATGTT	19461	C	CCC		
			AACA GGTGAAAC	ATCTC				

			TTGT CTA CTTTG TAGAG		
			A AGA		
GAM2021	TPMT	3'	GAGACGGGGTTTCACCATGTT 6310	C	A
			AACA GGTGAAACCCC TCTC		
			TTGT CCACTTTGGGG AGAG		
			A C		
GAM2021	TRAF5	3'	GAGACGGAGTTTTGCCATGTT 17275	C TG	C A
			AACA GG AAAC CC TCTC		
			TTGT CC TTTG GG AGAG		
			A GT A C		
GAM2021	TRIM9	5'	GAGACGGAGTTTCGCTCTTGT 31453	C _	C A
			ACA G GTGAAAC CC TCTC		
			TGT C CGCTTTG GG AGAG		
			T T A C		
GAM2021	TRPM6	3'	GAGATGGGGTTTCACCATGTT 35033	C	
			AACA GGTGAAACCCCATCTC		
			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2021	TRPV1	3'	GAGACGGGGTTTCACCATGTT 38697	C	A
			AACA GGTGAAACCCC TCTC		
			TTGT CCACTTTGGGG AGAG		
			A C		
GAM2021	TRPV1	3'	GATATGGGGTTTCGCCATGTT 38698	C	C
			AACA GGTGAAACCCCAT TC		
			TTGT CCGCTTTGGGGTA AG		
			A T		
GAM2021	TRPV1	3'	GAGACGGGGTTTCACCATGTT 55676	C	A
			AACA GGTGAAACCCC TCTC		
			TTGT CCACTTTGGGG AGAG		
			A C		
GAM2021	TRPV1	3'	GATATGGGGTTTCGCCATGTT 55677	C	C
			AACA GGTGAAACCCCAT TC		
			TTGT CCGCTTTGGGGTA AG		
			A T		
GAM2021	TRPV1	3'	GAGACGGGGTTTCACCATGTT 55713	C	A
			AACA GGTGAAACCCC TCTC		
			TTGT CCACTTTGGGG AGAG		
			A C		
GAM2021	TRPV1	3'	GATATGGGGTTTCGCCATGTT 55714	C	C
			AACA GGTGAAACCCCAT TC		

			TTGT CCGCTTTGGGGTA AG		
			A T		
GAM2021	TRPV1	3'	GAGACGGGGTTTCACCATGTT 55744	C	A
			AACA GGTGAAACCCC TCTC		
			TTGT CCACTTTGGGG AGAG		
			A C		
GAM2021	TRPV1	3'	GATATGGGGTTTCGCCATGTT 55745	C	C
			AACA GGTGAAACCCCAT TC		
			TTGT CCGCTTTGGGGTA AG		
			A T		
GAM2021	UGDH	3'	GAGACAGGGTTTCACCATGT 13997	C	CA
			ACA GGTGAAACCC TCTC		
			TGT CCACTTTGGG AGAG		
			A AC		
GAM2021	VENTX2	3'	ATGGGGTTTCACCATGTT 27853	C	
			AACA GGTGAAACCCCAT		
			TTGT CCACTTTGGGGTA		
			A		
GAM2021	VHL	3'	GAGACAGTGTTTCGCCATGTT 6857	C	CCCA
			AACA GGTGAAAC TCTC		
			TTGT CCGCTTTG AGAG		
			A TGAC		
GAM2021	VHL	3'	GAGACGGGGTTTCACCATGTT 6858	C	A
			AACA GGTGAAACCCC TCTC		
			TTGT CCACTTTGGGG AGAG		
			A C		
GAM2021	VIPR2	3'	GAGACAGGGTTTCACCATGTT 14063	C	CA
			AACA GGTGAAACCC TCTC		
			TTGT CCACTTTGGG AGAG		
			A AC		
GAM2021	WBSCR5	5'	GAGATGGAATTTACCGTGTT 51629		CC
			AACACGGTGAAA CCATCTC		
			TTGTGCCACTTT GGTAAGAG		
			AA		
GAM2021	WBSCR5	5'	GAGATGGAATTTACCGTGTT 42111		CC
			AACACGGTGAAA CCATCTC		
			TTGTGCCACTTT GGTAAGAG		
			AA		
GAM2021	XRCC2	3'	GAGACGGGGTTTCACCATGTT 19501	C	A
			AACA GGTGAAACCCC TCTC		

			TTGT CCACTTTGGGG AGAG		
			A C		
GAM2021	YES1	3'	GAGACGCAGTTTTCACCGTGTT 19536		CCCA
			AACACGGTGAAAC TCTC		
			TTGTGCCACTTTG AGAG		
			ACGC		
GAM2021	ZNF157	3'	AGACGGGTTTTCACCATGTT 14323	C	CA
			AACA GGTGAAACCC TCT		
			TTGT CCACTTTGGG AGA		
			A C_		
GAM2021	ZNF253	3'	GAGATGGAGTTTCACTCTTGT 41079	C_	C
			ACA G GTGAAAC CCATCTC		
			TGT C CACTTTG GG TAGAG		
			T T A		
GAM2021	ZNF264	3'	GAGACGGGGTTTTCACCATGTT 14215	C	A
			AACA GGTGAAACCCC TCTC		
			TTGT CCACTTTGGGG AGAG		
			A C		
GAM2021	ZNF74	5'	GAGACGGGGTTTTGCCATGTT 14261	C TG	A
			AACA GG AAACCCC TCTC		
			TTGT CC TTTGGGG AGAG		
			A GT C		
GAM2021	AAK1	3'	GAGATGGGGTTTCTCCATGTT 30524	C T	
			AACA GG GAAACCCCATCTC		
			TTGT CC CTTTGGGGTAGAG		
			A T		
GAM2021	ANAPC11	5'	GAGACGGAGTTTCGTCATGTT 33633	C GT	C A
			AACA G GAAAC CC TCTC		
			TTGT C CTTTG GG AGAG		
			A TG A C		
GAM2021	ANKT	3'	GAGACAGGGTCTCACTGTGTT 33457	A	CA
			AACACGGTGA ACCC TCTC		
			TTGTGTCACT TGGG AGAG		
			C AC		
GAM2021	AP3S2	3'	GAGACAGGGTTTTCACCATGTT 20652	C	CA
			AACA GGTGAAACCC TCTC		
			TTGT CCACTTTGGG AGAG		
			A AC		
GAM2021	APOL2	3'	GAGACGGGGTTTCACTGTGTT 48789		A
			AACACGGTGAAACCCC TCTC		

			TTGTGTCACTTTGGGG AGAG		
			C		
GAM2021	ARHF	3'	GAGACAGGGTTTCACCATGTT 39269	C	CA
			AACA GGTGAAACCC TCTC		
			TTGT CCACTTTGGG AGAG		
			A AC		
GAM2021	ARHGAP11A	3'	GAGACGGTTTCACCGTGTT 29448		CCA
			AACACGGTGAAACC TCTC		
			TTGTGCCACTTTGG AGAG		
			C_		
GAM2021	ARHGAP5	5'	GAGATGGGGTTTCTCCATGTT 77602	C T	
			AACA GG GAAACCCCATCTC		
			TTGT CC CTTTGGGGTAGAG		
			A T		
GAM2021	ATP1B4	3'	GAGACAGGGTTTCACCATGTT 24844	C	CA
			AACA GGTGAAACCC TCTC		
			TTGT CCACTTTGGG AGAG		
			A AC		
GAM2021	ATP1B4	3'	GAGATGGAGTTTCGCTGTTGT 24845	_	C
			ACA CGGTGAAAC CCATCTC		
			TGT GTCGCTTTG GG TAGAG		
			T A		
GAM2021	BA108L7.2	3'	GAGATGGGGTTTCACCATGTT 49075	C	_
			AACA GGTGAAACCCC ATCTC		
			TTGT CCACTTTGGGG TAGAG		
			A G		
GAM2021	BAGE	3'	GAGATGGAGTTTCACTGTGT 8639	C	
			ACACGGTGAAAC CCATCTC		
			TGTGTCACTTTG GG TAGAG		
			A		
GAM2021	BNIP-S	3'	GAGACGGGGTTTCACCATGTT 57089	C	A
			AACA GGTGAAACCCC TCTC		
			TTGT CCACTTTGGGG AGAG		
			A C		
GAM2021	BRAG	3'	GAGATGGGGTCTCGCCGTGTT 30101		A
			AACACGGTGA ACCCATCTC		
			TTGTGCCGCT TGGGGTAGAG		
			C		
GAM2021	C13orf1	3'	GAGATGGGGTTTCACCATGTT 40362	C	
			AACA GGTGAAACCCCATCTC		

			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2021	C1orf24	3'	GAGATGGGTTTTACCATGTT 54790	C	C
			AACA GGTGAAA CCCATCTC		
			TTGT CCACTTT GGGTAGAG		
			A T		
GAM2021	C1QR1	3'	GAGATGATGCACTGTGTT 24870	AAACCC	
			AACACGGTG CATCTC		
			TTGTGTCAC GTAGAG		
			GTA__		
GAM2021	C20orf142	3'	GAGATGGGTTTCTCCATGTT 75283	C T	
			AACA GG GAAACCCCATCTC		
			TTGT CC CTTTGGGGTAGAG		
			A T		
GAM2021	C21orf25	3'	GAGATGGAGTTTCACTCTGTT 64295	C	C
			AACA GGTGAAAC CCATCTC		
			TTGT TCACTTTG GGTAGAG		
			C A		
GAM2021	C6orf5	3'	GAGACAGGGTTTCATATTG 31991	CG	CA
			CA GTGAAACCC TCTC		
			GT TACTTTGGG AGAG		
			TA AC		
GAM2021	C6orf5	3'	GAGACAGGGTTTTGCCATGTT 31992	C TG	CA
			AACA GG AAACCC TCTC		
			TTGT CC TTTGGG AGAG		
			A GT AC		
GAM2021	C9orf9	3'	GAGACAGCGTTTCACCATGTT 39020	C	CCCA
			AACA GGTGAAAC TCTC		
			TTGT CCACTTTG AGAG		
			A CGAC		
GAM2021	C9orf9	3'	GAGATGGAGTTTCACTCTGT 39022	C	C
			ACA GGTGAAAC CCATCTC		
			TGT TCACTTTG GGTAGAG		
			C A		
GAM2021	CCRN4L	3'	GAGACGGGGTTTCACCGTGTT 25068		A
			AACACGGTGAAACCC TCTC		
			TTGTGCCACTTTGGGG AGAG		
			C		
GAM2021	CDC14B	3'	GAGACAGGGTTTCACCATGTT 54005	C	CA
			AACA GGTGAAACCC TCTC		

			TTGT CCACTTTGGG AGAG		
			A AC		
GAM2021	CEACAM8	3'	GAGACGGGGTTTCACTGTG 10181		A
			CACGGTGAAACCCC TCTC		
			GTGTCACTTTGGGG AGAG		
			C		
GAM2021	CENPH	3'	GAGACGGGGTTTCACCGTGTT 43566		A
			AACACGGTGAAACCCC TCTC		
			TTGTGCCACTTTGGGG AGAG		
			C		
GAM2021	CGI-96	3'	GGGTGGATTTCATCGTGT 32295		CC
			ACACGGTGAAA CCATCT		
			TGTGCTACTTT GGTGGG		
			A_		
GAM2021	CHSY1	3'	GAGACGGGGTTTCACCATG 30569	C	A
			CA GGTGAAACCCC TCTC		
			GT CCACTTTGGGG AGAG		
			A C		
GAM2021	CIP29	3'	GAGACGGGGTTTCACCATGTT 51377	C	A
			AACA GGTGAAACCCC TCTC		
			TTGT CCACTTTGGGG AGAG		
			A C		
GAM2021	COLEC12	3'	GAGAGGGGTTTCACAGTGTT 48612	G	A
			AACAC GTGAAACCCC TCTC		
			TTGTG CACTTTGGGG AGAG		
			A _		
GAM2021	CPSF2	3'	GAGACAGGGTTTCACCATGTT 62270	C	CA
			AACA GGTGAAACCC TCTC		
			TTGT CCACTTTGGG AGAG		
			A AC		
GAM2021	CPSF2	3'	GAGACGGGGTTTCTCCATGTT 62271	C T	A
			AACA GG GAAACCCC TCTC		
			TTGT CC CTTTGGGG AGAG		
			A T C		
GAM2021	DBR1	3'	GACAGGGTTTCACCGTGTT 33065		CA
			AACACGGTGAAACCC TC		
			TTGTGCCACTTTGGG AG		
			AC		
GAM2021	DBR1	3'	GAGATGGAGTTTCACTCTTGT 33066	C _	C
			ACA G GTGAAAC CCATCTC		

			TGT C CACTTTG GGTAGAG		
			TT A		
GAM2021	DCOHM	3'	GAGATGGAGTTTCGCTCTTGT 50523	C _	C
			ACA G GTGAAAC CCATCTC		
			TGT C CGCTTTG GGTAGAG		
			TT A		
GAM2021	DCOHM	3'	GAGATGGGGTCTCGTTCTGT 50525	_	A
			ACGG TGA ACCCCATCTC		
			TGTC GCT TGGGGTAGAG		
			TT C		
GAM2021	DCOHM	3'	GAGATGGGGTTTCGCCATGTT 50526	C	
			AACA GGTGAAACCCCATCTC		
			TTGT CCGCTTTGGGGTAGAG		
			A		
GAM2021	DKFZp434A2417	3'	GAGACGGGGTTTCTCCATGTT 66679	C T	A
			AACA GG GAAACCCC TCTC		
			TTGT CC CTTTGGGG AGAG		
			A T C		
GAM2021	DKFZP434B044	3'	GAGATGGGGTTTCATTATGTT 49718	CG	
			AACA GTGAAACCCCATCTC		
			TTGT TACTTTGGGGTAGAG		
			AT		
GAM2021	DKFZP434D146	3'	GAGACAGGGTTTCATCATGTT 32135	C	CA
			AACA GGTGAAACCC TCTC		
			TTGT CTACTTTGGG AGAG		
			A AC		
GAM2021	DKFZP434F0318	3'	GAGACAGGGTTTCGCCATGTT 48758	C	CA
			AACA GGTGAAACCC TCTC		
			TTGT CCGCTTTGGG AGAG		
			A AC		
GAM2021	DKFZp434F1719	3'	GAGATGGGATTTCGCCATGTT 51015	C	C
			AACA GGTGAAA CCCATCTC		
			TTGT CCGCTTT GGGTAGAG		
			A A		
GAM2021	DKFZp547G183	3'	GAGATGGGGCAACTGAGT 38643	A	GAAA
			AC CGGT CCCCATCTC		
			TG GTCA GGGGTAGAG		
			A AC_		
GAM2021	DKFZp547H025	3'	GAGATGAGGTTTCACCATGTT 39773	C	C
			AACA GGTGAAACC CATCTC		

		TTGT CCACTTTGG GTAGAG		
		A A		
GAM2021	DKFZP564G092 5'	GAGACGGAGTTTCGCTCTTGT	32160	C _ C A
		ACA G GTGAAAC CC TCTC		
		TGT C CGCTTTG GG AGAG		
		T T A C		
GAM2021	DKFZP564O0423 3'	GAGATGGGGTCTCACTATGTT	93350	CG A
		AACA GTGA ACCCCATCTC		
		TTGT CACT TGGGGTAGAG		
		AT C		
GAM2021	DKFZP586A0522 3'	GAGACAGGGTCTCACTGTGTT	26727	A CA
		AACACGGTGA ACCC TCTC		
		TTGTGTCACT TGGG AGAG		
		C AC		
GAM2021	DKFZp761J139 5'	GAGATGGGGTTTGACCATGTT	51106	C G
		AACA GGT AAACCCCATCTC		
		TTGT CCA TTTGGGGTAGAG		
		A G		
GAM2021	DKFZp761N1114 3'	GAGACGGGATTTACCGTGTT	79786	C A
		AACACGGTGAAA CCC TCTC		
		TTGTGCCACTTT GGG AGAG		
		A C		
GAM2021	DKFZp761O0113 5'	GAGACGGGGTTTCTCCATGTT	37893	C T A
		AACA GG GAAACCCC TCTC		
		TTGT CC CTTTGGGG AGAG		
		A T C		
GAM2021	DKFZp761O0113 5'	GAGATGGAGTTTCGCTCTTGT	37894	C _ C
		ACA G GTGAAAC CCATCTC		
		TGT C CGCTTTG GG TAGAG		
		T T A		
GAM2021	DKFZp762P2111 3'	AGATGGAGTTTCACTCTTGT	87623	C _ C
		ACA G GTGAAAC CCATCT		
		TGT C CACTTTG GG TAGA		
		T T A		
GAM2021	DKFZp762P2111 3'	GAGACAGGGTTTCATCATGTT	87635	C CA
		AACA GGTGAAACCC TCTC		
		TTGT CTACTTTGGG AGAG		
		A AC		
GAM2021	DSCR6 3'	GAGACTCGGTTTCACCATGTT	39068	C CCA
		AACA GGTGAAACC TCTC		

		TTGT CCACTTTGG AGAG		
		A CTC		
GAM2021	EREG	3' GAGGCGGGGTTTCACCATGTT 9307	C	AT
		AACA GGTGAAACCCC CTC		
		TTGT CCACTTTGGGG GAG		
		A CG		
GAM2021	ERO1L	3' GAGACAAGGTTTTGCTGTGTT 28159	TG	CCA
		AACACGG AAACC TCTC		
		TTGTGTC TTTGG AGAG		
		GT AAC		
GAM2021	EVI5	3' GAGACAGGTGTCTCACTGTGTT 20209	A _	CA
		AACACGGTGA AC CC TCTC		
		TTGTGTCACT TG GG AGAG		
		C T AC		
GAM2021	EVI5	3' GAGATGGGGTTTCACCATGTT 20211	C	
		AACA GGTGAAACCCCATCTC		
		TTGT CCACTTTGGGGTAGAG		
		A		
GAM2021	EVI5	3' GAGATGGGGTTTCGCTATGTT 20212	CG	
		AACA GTGAAACCCCATCTC		
		TTGT CGCTTTGGGGTAGAG		
		AT		
GAM2021	FBP17	3' GAGACAGGGTTTCACCGTGTT 73150		CA
		AACACGGTGAAACCC TCTC		
		TTGTGCCACTTTGGG AGAG		
		AC		
GAM2021	FER1L4	3' GAGACAGGGTTTCACCATGTT 48122	C	CA
		AACA GGTGAAACCC TCTC		
		TTGT CCACTTTGGG AGAG		
		A AC		
GAM2021	FKBP9	3' GAGACGGGGTTTCACCGTGTT 95716		A
		AACACGGTGAAACCCC TCTC		
		TTGTGCCACTTTGGGG AGAG		
		C		
GAM2021	FLJ10101	3' GAGATAAGGCTTGCTGTGT 45600	TG A	CC
		ACACGG A ACC ATCTC		
		TGTGTC T TGG TAGAG		
		GT C AA		
GAM2021	FLJ10232	5' GAGATGGGGTTTGCTATGTT 36380	CG TG	
		AACA G AAACCCCATCTC		

			TTGT C TTTGGGGTAGAG		
			AT GT		
GAM2021	FLJ10298	3'	GAGACGGGGTTTCACCATGTT 36458	C	A
			AACA GGTGAAACCCC TCTC		
			TTGT CCACTTTGGGG AGAG		
			A C		
GAM2021	FLJ10346	5'	GAGGCAGGGTTTCACCATGTT 36524	C	CA
			AACA GGTGAAACCCC TCTC		
			TTGT CCACTTTGGG GGAG		
			A AC		
GAM2021	FLJ10535	3'	GAGACGGGGTTTCATTATGTT 36747	CG	A
			AACA GTGAAACCCC TCTC		
			TTGT TACTTTGGGG AGAG		
			AT C		
GAM2021	FLJ10535	3'	GAGATGGGGTTTCACCATGTT 36748	C	
			AACA GGTGAAACCCCATCTC		
			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2021	FLJ10560	3'	GAGACGGGGTTTCACCGTGTT 36795		A
			AACACGGTGAAACCCC TCTC		
			TTGTGCCACTTTGGGG AGAG		
			C		
GAM2021	FLJ10713	3'	GAGATGGGGTTTCACCATGTT 37003	C	
			AACA GGTGAAACCCCATCTC		
			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2021	FLJ10901	3'	GAGATGGGGTTTCATCATGTT 37363	C	
			AACA GGTGAAACCCCATCTC		
			TTGT CTACTTTGGGGTAGAG		
			A		
GAM2021	FLJ10956	3'	GAGACGGGGTTTCACCATGTT 37467	C	A
			AACA GGTGAAACCCC TCTC		
			TTGT CCACTTTGGGG AGAG		
			A C		
GAM2021	FLJ11186	3'	GAGATGGGGTTTCGTCATGTT 37726	C GT	
			AACA G GAAACCCCATCTC		
			TTGT C CTTTGGGGTAGAG		
			A TG		
GAM2021	FLJ11193	3'	GAGATGGGGTCTCACCATGTT 37750	C A	
			AACA GGTGA ACCCCATCTC		

		TTGT CCACT TGGGGTAGAG		
		A C		
GAM2021	FLJ12363	3' GATGGGGTTTCACCATGTT 50636	C	
		AACA GGTGAAACCCCATC		
		TTGT CCACTTTGGGGTAG		
		A		
GAM2021	FLJ12581	3' GAGACAGGGTTTCACTGTGTT 46335		CA
		AACACGGTGAAACCC TCTC		
		TTGTGTCACTTTGGG AGAG		
		AC		
GAM2021	FLJ12649	3' GAGATAGGGTTTTACCATGTT 45091	C	C
		AACA GGTGAAACCC ATCTC		
		TTGT CCATTTTGGG TAGAG		
		A A		
GAM2021	FLJ12668	3' GAGATGAGGTTTTCACCTTGTT 47159	C	C
		AACA GGTGAAACC CATCTC		
		TTGT CCACTTTGG GTAGAG		
		T A		
GAM2021	FLJ12687	3' GAGACAGGGTTTTCACCATGTT 46751	C	CA
		AACA GGTGAAACCC TCTC		
		TTGT CCACTTTGGG AGAG		
		A AC		
GAM2021	FLJ12876	3' GAGACGGGGTTTCACTGTG 43092		A
		CACGGTGAAACCCC TCTC		
		GTGTCACCTTTGGGG AGAG		
		C		
GAM2021	FLJ12891	3' GAGACGGGGTCTTGTTGTGT 46924	TG A	A
		ACACGG A ACCCC TCTC		
		TGTGTT T TGGGG AGAG		
		GT C C		
GAM2021	FLJ12903	3' GAGACGGAGTTTCGCTGTTGT 43071	—	C A
		ACA CGGTGAAAC CC TCTC		
		TGT GTCGCTTTG GG AGAG		
		T A C		
GAM2021	FLJ12960	3' GAGATGGGGTTTCACCGT 45298		
		ACGGTGAAACCCCATCTC		
		TGCCACTTTGGGGTAGAG		
GAM2021	FLJ12973	3' GAGATGGGGTTTCATCATGTT 46642	C	
		AACA GGTGAAACCCCATCTC		

			TTGT CTACTTTGGGGTAGAG		
			A		
GAM2021	FLJ12975	3'	AGACGGGGTTTCGCCTTGTT 70180	C	A
			AACA GGTGAAACCCC TCT		
			TTGT CCGCTTTGGGG AGA		
			T C		
GAM2021	FLJ13072	5'	GAGACAGGGTTTCACCATGTT 91391	C	CA
			AACA GGTGAAACCC TCTC		
			TTGT CCACTTTGGG AGAG		
			A AC		
GAM2021	FLJ13114	3'	GAGATGGAGTTTCACCATGTT 44903	C	C
			AACA GGTGAAAC CCATCTC		
			TTGT CCACTTTG GGTAGAG		
			A A		
GAM2021	FLJ13188	3'	GAGACAGAGTTTTGCTGTGTT 42190	TG	CCCA
			AACACGG AAAC TCTC		
			TTGTGTC TTTG AGAG		
			GT AGAC		
GAM2021	FLJ13197	3'	GAGACAAGAGTTTCACCATGTT 45180	C	CCCA_
			AACA GGTGAAAC TCTC		
			TTGT CCACTTTG AGAG		
			A AGAAC		
GAM2021	FLJ13305	5'	GAGATGGGGTTTCACCATGTT 91711	C	
			AACA GGTGAAACCCCATCTC		
			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2021	FLJ13456	3'	GAGACAGAGTTTCACTCTGT 66547	C	CCCA
			ACA GGTGAAAC TCTC		
			TGT TCACTTTG AGAG		
			C AGAC		
GAM2021	FLJ13769	5'	GAGATGGGGTTTCACTATGTT 47250	CG	
			AACA GTGAAACCCCATCTC		
			TTGT CACTTTGGGGTAGAG		
			AT		
GAM2021	FLJ14442	3'	GAGATGGGGTTTTACCATGTT 52384	C	
			AACA GGTGAAACCCCATCTC		
			TTGT CCATTTTGGGGTAGAG		
			A		
GAM2021	FLJ14950	3'	GAGACAGGGTTTCACCATGTT 52789	C	CA
			AACA GGTGAAACCC TCTC		

		TTGT CCACTTTGGG AGAG		
		A AC		
GAM2021	FLJ14957	3' GAGACGGGGTTTCACCATGTT 52820	C	A
		AACA GGTGAAACCCC TCTC		
		TTGT CCACTTTGGGG AGAG		
		A C		
GAM2021	FLJ14957	3' GAGATGGAGTTTCATTCTTGT 52821	C_	C
		ACA GGTGAAAC CCATCTC		
		TGT TTACTTTG GG TAGAG		
		TC A		
GAM2021	FLJ20033	3' GAGATGGGATTCCTTTCTTGT 34819	T	C_____
		ACGG GAAA CCCATCTC		
		TGTT CTTT GGGTAGAG		
		_ CCTTA		
GAM2021	FLJ20034	3' GAGATGGGGTCTCTCCATGTT 34847	C T A	
		AACA GG GA ACCCATCTC		
		TTGT CC CT TGGGGTAGAG		
		A T C		
GAM2021	FLJ20136	3' GAGATGAGTTTCACCATGTT 35098	C	CC
		AACA GGTGAAAC CATCTC		
		TTGT CCACTTTG GTAGAG		
		A A_		
GAM2021	FLJ20147	3' GAGATAGGGTCTTGCTGTGTT 35134	TG A	C
		AACACGG A ACCC ATCTC		
		TTGTGTC T TGGG TAGAG		
		GT C A		
GAM2021	FLJ20344	3' GAGACAGGGTTTCACCATGTT 35482	C	CA
		AACA GGTGAAACCC TCTC		
		TTGT CCACTTTGGG AGAG		
		A AC		
GAM2021	FLJ20507	3' GAGACAGGGTTTCACCATGTT 35740	C	CA
		AACA GGTGAAACCC TCTC		
		TTGT CCACTTTGGG AGAG		
		A AC		
GAM2021	FLJ20507	3' GAGACAGGGTTTCACCATGTT 60845	C	CA
		AACA GGTGAAACCC TCTC		
		TTGT CCACTTTGGG AGAG		
		A AC		
GAM2021	FLJ20511	3' GAGGCGCAGTTTCACCGTGTT 35774		CCCA
		AACACGGTGAAAC TCTC		

		TTGTGCCACTTTG GGAG		
		ACGC		
GAM2021	FLJ20729	3' GAGATGGGGTCTTGGAGTG 36083	GG	A
		CAC TGA ACCCCATCTC		
		GTG GTT TGGGGTAGAG		
		AG C		
GAM2021	FLJ20813	3' GAGATGGGCTTTCACTACGTT 36132	AC	C
		AAC GGTGAAA CCCATCTC		
		TTG TCACTTT GGGTAGAG		
		CA C		
GAM2021	FLJ20897	5' GAGACGGGGTTTCAACGTGTT 51475	G	A
		AACACG TGAAACCCC TCTC		
		TTGTGC ACTTTGGGG AGAG		
		A C		
GAM2021	FLJ20958	3' GAGATGGGATCACTATGTT 42309	CG	AAC
		AACA GTGA CCCATCTC		
		TTGT CACT GGGTAGAG		
		AT A__		
GAM2021	FLJ21302	3' GAGACAGGGTTTCACCATGTT 43509	C	CA
		AACA GGTGAAACCC TCTC		
		TTGT CCACTTTGGG AGAG		
		A AC		
GAM2021	FLJ21324	5' GAGATGGGGTTTCACCATGTT 92855	C	
		AACA GGTGAAACCCCATCTC		
		TTGT CCACTTTGGGGTAGAG		
		A		
GAM2021	FLJ21603	3' GAGATGGGGTTTCACCCTGTT 45772	C	
		AACA GGTGAAACCCCATCTC		
		TTGT CCACTTTGGGGTAGAG		
		C		
GAM2021	FLJ22002	3' GAGATGAGGTTTCGCCATGTT 46198	C	C
		AACA GGTGAAACC CATCTC		
		TTGT CCGCTTTGG GTAGAG		
		A A		
GAM2021	FLJ22167	5' GAGATGGGGTCTCACTGTGTT 44872	A	
		AACACGGTGA ACCCCATCTC		
		TTGTGTCACT TGGGGTAGAG		
		C		
GAM2021	FLJ22329	3' GAGACGGGGTTTCACCATGTT 45401	C	A
		AACA GGTGAAACCCC TCTC		

			TTGT CCACTTTGGGG AGAG		
			A C		
GAM2021	FLJ22529	3'	GAGACAGGGTTTCATCATGTT 45944	C	CA
			AACA GGTGAAACCC TCTC		
			TTGT CTACTTTGGG AGAG		
			A AC		
GAM2021	FLJ22684	3'	GAGACAGGGTTTCACCATGTT 47469	C	CA
			AACA GGTGAAACCC TCTC		
			TTGT CCACTTTGGG AGAG		
			A AC		
GAM2021	FLJ22794	3'	GAGACAGGGTTTCACCATGTT 93247	C	CA
			AACA GGTGAAACCC TCTC		
			TTGT CCACTTTGGG AGAG		
			A AC		
GAM2021	FLJ22969	3'	GAGACAGGGTTTCACCATGTT 69205	C	CA
			AACA GGTGAAACCC TCTC		
			TTGT CCACTTTGGG AGAG		
			A AC		
GAM2021	FLJ23024	3'	GAGACGGGGTTTCACCATGTT 46842	C	A
			AACA GGTGAAACCCC TCTC		
			TTGT CCACTTTGGGG AGAG		
			A C		
GAM2021	FLJ23392	3'	GAGACAGGGTTTCACCATGTT 45892	C	CA
			AACA GGTGAAACCC TCTC		
			TTGT CCACTTTGGG AGAG		
			A AC		
GAM2021	FLJ23392	3'	GAGACAGGGTTTCACCGTGTT 45893		CA
			AACACGGTGAAACCC TCTC		
			TTGTGCCACTTTGGG AGAG		
			AC		
GAM2021	FLJ23392	3'	GAGACGGGGTTTCACCGTGTT 45894		A
			AACACGGTGAAACCCC TCTC		
			TTGTGCCACTTTGGGG AGAG		
			C		
GAM2021	FLJ23519	3'	GAGATGGGGTTTCACCGTGTT 50951		
			AACACGGTGAAACCCCATCTC		
			TTGTGCCACTTTGGGGTAGAG		
GAM2021	FLJ23556	3'	GAGACGGGGTTTCACCGTGTT 46442		A
			AACACGGTGAAACCCC TCTC		

			TTGTGCCACTTTGGGG AGAG		
			C		
GAM2021	FLJ23556	3'	GAGATGGAGTTTTGCTCTGT 46443	C TG	C
			ACA GG AAAC CCATCTC		
			TGT TC TTTG GGTAGAG		
			C GT A		
GAM2021	FLJ25416	5'	GAGATGGGGTTTCACCATGTT 59455	C	
			AACA GGTGAAACCCCATCTC		
			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2021	FLJ30532	3'	GAGATGGAGTTTCGCTCTTGT 59220	C _	C
			ACA G GTGAAAC CCATCTC		
			TGT C CGCTTTG GGTAGAG		
			T T A		
GAM2021	FLJ31153	3'	GAGATGGGGTTTCACCATG 58748	C	
			CA GGTGAAACCCCATCTC		
			GT CCACTTTGGGGTAGAG		
			A		
GAM2021	FLJ32865	3'	GAGACGGGGTTTCTCCGTGTT 58812	T	A
			AACACGG GAAACCCC TCTC		
			TTGTGCC CTTTGGGG AGAG		
			T C		
GAM2021	FLJ32894	3'	GAGATGGGATTTCACTGTGTT 58998	C	
			AACACGGTGAAA CCCATCTC		
			TTGTGTCACTTT GGGTAGAG		
			A		
GAM2021	GMFB	3'	GAGGTTTTGTTTACCTGTT 15940	C	CCC
			AACA GGTGAAAC ATCTC		
			TTGT CCACTTTG TGGAG		
			_ TTT		
GAM2021	GMPPB	5'	GAGACAGGGTTTCACCAGGTT 97447	AC	CA
			AAC GGTGAAACCC TCTC		
			TTG CCACTTTGGG AGAG		
			GA AC		
GAM2021	GNG4	3'	AGACGGGGTTTCACCATGTT 16837	C	A
			AACA GGTGAAACCCC TCT		
			TTGT CCACTTTGGGG AGA		
			A C		
GAM2021	GOLGA3	3'	ATGGGGTTTCACCATGTT 20880	C	
			AACA GGTGAAACCCCAT		

			TTGT CCACTTTGGGGTA		
			A		
GAM2021	GREB1	3'	GAGACGGGGTTTCACCATGTT 28568	C	A
			AACA GGTGAAACCCC TCTC		
			TTGT CCACTTTGGGG AGAG		
			A C		
GAM2021	GREB1	3'	GAGATGGGGTTTCGCCAGGTT 28569	AC	
			AAC GGTGAAACCCCATCTC		
			TTG CCGCTTTGGGGTAGAG		
			GA		
GAM2021	GRWD	3'	GAGACGGGGTTTCACCATGTT 49783	C	A
			AACA GGTGAAACCCC TCTC		
			TTGT CCACTTTGGGG AGAG		
			A C		
GAM2021	GT650	3'	GAGATGGGATCCTATGTGTT 54552	GT_ AAC	
			AACACG GA CCCATCTC		
			TTGTGT CT GGGTAGAG		
			ATC A__		
GAM2021	GTF2E1	3'	GAGGCAGGGTTTCACCATGTT 19799	C	CA
			AACA GGTGAAACCC TCTC		
			TTGT CCACTTTGGG GGAG		
			A AC		
GAM2021	GTPBG3	3'	GAGACAAGGTTTCACCATGTT 51897	C	CCA
			AACA GGTGAAACC TCTC		
			TTGT CCACTTTGG AGAG		
			A AAC		
GAM2021	H-plk	5'	GAGATGGAGTCTTGCTGTGT 32383	TG A C	
			ACACGG A AC CCATCTC		
			TGTGTC T TG GGTAGAG		
			GT C A		
GAM2021	H2AV	3'	GACGTGGGGTTTCACCATGTT 57630	C	C
			AACA GGTGAAACCCCAT TC		
			TTGT CCACTTTGGGGTG AG		
			A C		
GAM2021	HARS2	3'	GAGACGGGGTTTACCATGTT 55865	C	A
			AACA GGTGAAACCCC TCTC		
			TTGT CCATTTTGGGG AGAG		
			A C		
GAM2021	HCA4	3'	GAGACGGGGTTTGGCCATGTT 78041	C TG	A
			AACA GG AAACCCC TCTC		

		TTGT CC TTTGGGG AGAG	
		A GT C	
GAM2021 HCGIV.9	3'	GAGACAGGGTTTTTTGTTGTT 39131	_ T CA
		AACA CGG GAAACCC TCTC	
		TTGT GTT TTTTGGG AGAG	
		T _ AC	
GAM2021 HPIP	3'	GAGATGGGAGAGGAGCCTGTT 40424	C GAAAC_
		AACA GGT CCCATCTC	
		TTGT CCG GGGTAGAG	
		_ AGGAGA	
GAM2021 HRH4	3'	AGACAGGGTATTGCCGTGTT 41522	TG A CA
		AACACGG A ACCC TCT	
		TTGTGCC T TGGG AGA	
		GT A AC	
GAM2021 HRH4	3'	GAGATGAAGTCTCACTGTGTT 41540	A CC
		AACACGGTGA AC CATCTC	
		TTGTGTCACT TG GTAGAG	
		C AA	
GAM2021 HSA277841	3'	GAGATGGGGTCTCCTGTTGTT 38268	_ T AA
		AACA CGG GA CCCCATCTC	
		TTGT GTC CT GGGGTAGAG	
		T _ _	
GAM2021 HSMPP8	3'	GAGACGGAGTTTCGCTCTTGT 95134	C _ C A
		ACA G GTGAAAC CC TCTC	
		TGT C CGCTTTG GG AGAG	
		T T A C	
GAM2021 HSMPP8	3'	GAGATGGGGTTTATCCATGTT 95135	C TG
		AACA GG AAACCCCATCTC	
		TTGT CC TTTGGGGTAGAG	
		A TA	
GAM2021 HSNV1	3'	GACATGGGGTTTCACCATGTT 34435	C C
		AACA GGTGAAACCCCAT TC	
		TTGT CCACTTTGGGGTA AG	
		A C	
GAM2021 HSNV1	3'	GAGATGGGGTTTCGCCATGTT 34436	C
		AACA GGTGAAACCCCATCTC	
		TTGT CCGCTTTGGGGTAGAG	
		A	
GAM2021 HSPC065	3'	GAGATGGGGTTTCACCATGTT 27152	C
		AACA GGTGAAACCCCATCTC	

			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2021	HSPC065	3'	GAGATGGGGTTTCACGATGTT 27153	CG	
			AACA GTGAAACCCCATCTC		
			TTGT CACTTTGGGGTAGAG		
			AG		
GAM2021	HSPC232	3'	GAGATGGGGTTCACCATGTT 33657	C	A
			AACA GGTGAA CCCCATCTC		
			TTGT CCACTT GGGGTAGAG		
			A _		
GAM2021	ICK	3'	GAGACGGGGTTTCACTGTGTT 30596		A
			AACACGGTGAAACCCC TCTC		
			TTGTGTCACTTTGGGG AGAG		
			C		
GAM2021	JAM1	3'	GAGACAGGGTTTCACCATGTT 34228	C	CA
			AACA GGTGAAACCC TCTC		
			TTGT CCACTTTGGG AGAG		
			A AC		
GAM2021	JAM1	3'	GAGACAGGGTTTCACCATGTT 58515	C	CA
			AACA GGTGAAACCC TCTC		
			TTGT CCACTTTGGG AGAG		
			A AC		
GAM2021	JAM1	3'	GAGACAGGGTTTCACCATGTT 58543	C	CA
			AACA GGTGAAACCC TCTC		
			TTGT CCACTTTGGG AGAG		
			A AC		
GAM2021	JAM1	3'	GAGACAGGGTTTCACCATGTT 58572	C	CA
			AACA GGTGAAACCC TCTC		
			TTGT CCACTTTGGG AGAG		
			A AC		
GAM2021	KIAA0063	3'	GAGATGGGGTTTCTCCATGTT 30258	C T	
			AACA GG GAAACCCCATCTC		
			TTGT CC CTTTGGGGTAGAG		
			A T		
GAM2021	KIAA0082	3'	GAGATGGGGCCACCTG 93782	C	AAA
			CA GGTG CCCCATCTC		
			GT CCAC GGGGTAGAG		
			_ C _		
GAM2021	KIAA0161	3'	GAGACGGAGTTTCGCTTTTGT 29201	C_	C A
			ACA GGTGAAAC CC TCTC		

			TGT TCGCTTTG GG AGAG		
			TT A C		
GAM2021	KIAA0161	3'	GAGACGGGGTTTCACCATGTT 29202	C	A
			AACA GGTGAAACCCC TCTC		
			TTGT CCACTTTGGGG AGAG		
			A C		
GAM2021	KIAA0186	3'	CGAGATGGGGTTTCACCATGTT 41106	C	—
			AACA GGTGAAACCCCATCTC	G	
			TTGT CCACTTTGGGGTAGAG	C	
			A		
GAM2021	KIAA0186	3'	GAGACAGAGTTTTACCATGTT 41108	C	CCCA
			AACA GGTGAAAC TCTC		
			TTGT CCATTTTG AGAG		
			A AGAC		
GAM2021	KIAA0205	3'	GAGATGGGGTTTCACCATGTT 30214	C	
			AACA GGTGAAACCCCATCTC		
			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2021	KIAA0210	5'	GGAGGAGTTTCACCATGTT 29164	C	C A
			AACA GGTGAAAC CC TCT		
			TTGT CCACTTTG GG AGG		
			A A _		
GAM2021	KIAA0426	3'	GAGACGGGGTTTCACCATGTT 28927	C	A
			AACA GGTGAAACCCC TCTC		
			TTGT CCACTTTGGGG AGAG		
			A C		
GAM2021	KIAA0459	3'	GAGACGGGGTTTCACCATGTT 61653	C	A
			AACA GGTGAAACCCC TCTC		
			TTGT CCACTTTGGGG AGAG		
			A C		
GAM2021	KIAA0469	3'	GAGACAGGGTCTTGCTGTGTT 29981		TG A CA
			AACACGG A ACCC TCTC		
			TTGTGTC T TGGG AGAG		
			GT C AC		
GAM2021	KIAA0469	3'	GAGACGGGATTTCACTGTGTT 29982		C A
			AACACGGTGAAA CCC TCTC		
			TTGTGTCACTTT GGG AGAG		
			A C		
GAM2021	KIAA0495	3'	GAGATGGGATTTACCATGTT 63268	C	C
			AACA GGTGAAA CCCATCTC		

			TTGT CCACTTT GGGTAGAG		
			A A		
GAM2021	KIAA0513	5'	GAGACAGGGTTTCGCCATGTT 29031	C	CA
			AACA GGTGAAACCC TCTC		
			TTGT CCGCTTTGGG AGAG		
			A AC		
GAM2021	KIAA0513	3'	GAGATGGGGTTTCACCATG 29032	C	
			CA GGTGAAACCCCATCTC		
			GT CCACTTTGGGGTAGAG		
			A		
GAM2021	KIAA0527	3'	GAGATGGAGTTTCACCATGTT 97498	C	C
			AACA GGTGAAAC CCATCTC		
			TTGT CCACTTTG GGTAGAG		
			A A		
GAM2021	KIAA0555	3'	GAGACAGGGTTTCACTATG 29550	CG	CA
			CA GTGAAACCC TCTC		
			GT CACTTTGGG AGAG		
			AT AC		
GAM2021	KIAA0557	3'	GAGACGGGGCCTTGCTGTGT 78563	TG AA	A
			ACACGG A CCCC TCTC		
			TGTGTC T GGGG AGAG		
			GT CC C		
GAM2021	KIAA0557	3'	GAGATGGGGTTTCTCCATGTT 78564	C T	
			AACA GG GAAACCCCATCTC		
			TTGT CC CTTTGGGGTAGAG		
			A T		
GAM2021	KIAA0561	3'	GACGGGGTTTCACCATGTT 66478	C	A
			AACA GGTGAAACCCC TC		
			TTGT CCACTTTGGGG AG		
			A C		
GAM2021	KIAA0563	5'	GAGGCGGAGTTTCGCCATGTT 29884	C	C AT
			AACA GGTGAAAC CC CTC		
			TTGT CCGCTTTG GG GAG		
			A A CG		
GAM2021	KIAA0599	3'	GAGACGGGGTTTCGCCGTGTT 77693		A
			AACACGGTGAAACCCC TCTC		
			TTGTGCCGCTTTGGGG AGAG		
			C		
GAM2021	KIAA0682	3'	GACGGGGTTTCACCATGT 30023	C	A
			ACA GGTGAAACCCC TC		

			TGT CCACTTTGGGG AG		
			A C		
GAM2021	KIAA0682	3'	GAGACTGGGTTTCACCATGT 30024	C	CA
			ACA GGTGAAACCC TCTC		
			TGT CCACTTTGGG AGAG		
			A TC		
GAM2021	KIAA0737	3'	GAGACAGGGTTTCACCATGTT 29809	C	CA
			AACA GGTGAAACCC TCTC		
			TTGT CCACTTTGGG AGAG		
			A AC		
GAM2021	KIAA0737	3'	GAGATGGGGTCTCACTATGTT 29810	CG	A
			AACA GTGA ACCCATCTC		
			TTGT CACT TGGGGTAGAG		
			AT C		
GAM2021	KIAA0759	3'	ATGGGGTTTTAAATTGTT 67882	CGG	
			AACA TGAAACCCCAT		
			TTGT ATTTTGGGGTA		
			TAA		
GAM2021	KIAA0798	3'	GAGACGGGGTTTCACTGTGTT 28447		A
			AACACGGTGAAACCCC TCTC		
			TTGTGTCACTTTGGGG AGAG		
			C		
GAM2021	KIAA0828	3'	GAGACAGGGTTTCACTATGTT 82115	CG	CA
			AACA GTGAAACCC TCTC		
			TTGT CACTTTGGG AGAG		
			AT AC		
GAM2021	KIAA0831	3'	GAGACGGGGGTTTTACCATGT 30637	C	_ A_
			ACA GGTGAAA CCCC TCTC		
			TGT CCACTTT GGGG AGAG		
			A T GC		
GAM2021	KIAA0841	3'	GACGGGGTTTCATCATGTT 71896	C	A
			AACA GGTGAAACCCC TC		
			TTGT CTACTTTGGGG AG		
			A C		
GAM2021	KIAA0861	3'	GAGACGGGGTTTCCCCGTGTT 90349	T	A
			AACACGG GAAACCCC TCTC		
			TTGTGCC CTTTGGGG AGAG		
			C C		
GAM2021	KIAA0884	3'	GAGGTGAGGTTTCACCATGTT 70753	C	C
			AACA GGTGAAACC CATCTC		

			TTGT CCACTTTGG GTGGAG		
			A A		
GAM2021	KIAA0889	3'	GAGACGGGGTTTCACCGTGTT 31777		A
			AACACGGTGAAACCCC TCTC		
			TTGTGCCACTTTGGGG AGAG		
			C		
GAM2021	KIAA0918	3'	AGATGGGGCTACTGTTGTT 73518	_	AAA
			AACA CGGTG CCCCATCT		
			TTGT GTCAT GGGGTAGA		
			T C_		
GAM2021	KIAA0931	3'	GAGACGGGGTTTCACCATGTT 68012	C	A
			AACA GGTGAAACCCC TCTC		
			TTGT CCACTTTGGGG AGAG		
			A C		
GAM2021	KIAA0961	3'	GAGATGGGGTTTCACCATGTT 30400	C	
			AACA GGTGAAACCCCATCTC		
			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2021	KIAA1010	3'	GAGATGGGGTCTTGCTATGTT 72542	CG TG A	
			AACA G A ACCCATCTC		
			TTGT C T TGGGGTAGAG		
			AT GT C		
GAM2021	KIAA1041	3'	GAGATGGGGTTTCACCATGTT 30823	C	
			AACA GGTGAAACCCCATCTC		
			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2021	KIAA1054	3'	GAGGTGGGGTTTCACCGTGTT 68965		
			AACACGGTGAAACCCCATCTC		
			TTGTGCCACTTTGGGGTGGAG		
GAM2021	KIAA1115	5'	GAGACAGGGTTTCGCCATGTT 30691	C	CA
			AACA GGTGAAACCC TCTC		
			TTGT CCGCTTTGGG AGAG		
			A AC		
GAM2021	KIAA1143	3'	GAGACGGGGTTTCACTTTGTT 69242	C	A
			AACA GGTGAAACCCC TCTC		
			TTGT TCACTTTGGGG AGAG		
			T C		
GAM2021	KIAA1161	5'	GAGATGGGGTTTACCATGTT 82646	C	A
			AACA GGTGAA CCCCATCTC		

			TTGT CCATTT GGGGTAGAG		
			A _		
GAM2021	KIAA1198	3'	GAGACAGTGTTCACCATGTT 64036	C	CCCA
			AACA GGTGAAAC TCTC		
			TTGT CCACTTTG AGAG		
			A TGAC		
GAM2021	KIAA1198	3'	GAGACGGGGTTTCACCATGTT 64037	C	A
			AACA GGTGAAACCCC TCTC		
			TTGT CCACTTTGGGG AGAG		
			A C		
GAM2021	KIAA1198	3'	GAGACGGGGTTTCACCATGTT 64038	C	A
			AACA GGTGAAACCCC TCTC		
			TTGT CCACTTTGGGG AGAG		
			A C		
GAM2021	KIAA1198	3'	GAGACGGGGTTTCACCGTGTT 64039		A
			AACACGGTGAAACCCC TCTC		
			TTGTGCCACTTTGGGG AGAG		
			C		
GAM2021	KIAA1198	3'	GAGATGGGGTTTCACCATGTT 64040	C	
			AACA GGTGAAACCCCATCTC		
			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2021	KIAA1198	3'	GAGATGGGGTTTCTCCATGTT 64041	C T	
			AACA GG GAAACCCCATCTC		
			TTGT CC CTTTGGGGTAGAG		
			A T		
GAM2021	KIAA1200	3'	GAGACGGGGTTTCACCATGTT 63038	C	A
			AACA GGTGAAACCCC TCTC		
			TTGT CCACTTTGGGG AGAG		
			A C		
GAM2021	KIAA1210	3'	GAGACGGGGTTTCACCATGTT 98070	C	A
			AACA GGTGAAACCCC TCTC		
			TTGT CCACTTTGGGG AGAG		
			A C		
GAM2021	KIAA1254	3'	GAGATGGGGTTTCACCATGTT 70561	C	
			AACA GGTGAAACCCCATCTC		
			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2021	KIAA1373	3'	GAGATGGGGTTTTACCCTGTT 71506	C	
			AACA GGTGAAACCCCATCTC		

			TTGT CCATTTTGGGGTAGAG		
			C		
GAM2021	KIAA1443	3'	GAGACGGGTTTCATCATGTT 64571	C	CA
			AACA GGTGAAACCC TCTC		
			TTGT CTACTTTGGG AGAG		
			A C_		
GAM2021	KIAA1456	3'	GAGACGGGGTTTCACCGTGTT 67555		A
			AACACGGTGAAACCCC TCTC		
			TTGTGCCACTTTGGGG AGAG		
			C		
GAM2021	KIAA1465	3'	GAGACGGGGTTTCACCATGTT 61496	C	A
			AACA GGTGAAACCCC TCTC		
			TTGT CCACTTTGGGG AGAG		
			A C		
GAM2021	KIAA1467	3'	GAGACGGGGTTTCACCATGTT 72068	C	A
			AACA GGTGAAACCCC TCTC		
			TTGT CCACTTTGGGG AGAG		
			A C		
GAM2021	KIAA1493	3'	GAGATGGGGTTTCACCTTGTT 64841	C	
			AACA GGTGAAACCCCATCTC		
			TTGT CCACTTTGGGGTAGAG		
			T		
GAM2021	KIAA1497	5'	GAGACAGGGTTTCACCATGTT 68123	C	CA
			AACA GGTGAAACCC TCTC		
			TTGT CCACTTTGGG AGAG		
			A AC		
GAM2021	KIAA1530	3'	GAGACGGGATTTCACTGTGTT 68561	C	A
			AACACGGTGAAA CCC TCTC		
			TTGTGTCACTTT GGG AGAG		
			A C		
GAM2021	KIAA1530	3'	GAGATGAGGTCTCACTGTGTT 68562	A	C
			AACACGGTGA ACC CATCTC		
			TTGTGTCACT TGG GTAGAG		
			C A		
GAM2021	KIAA1617	3'	GAGACAGGGTTTCACCATGTT 93078	C	CA
			AACA GGTGAAACCC TCTC		
			TTGT CCACTTTGGG AGAG		
			A AC		
GAM2021	KIAA1649	5'	AGAGTCTCACTGTGTT 51214	A	CCCA
			AACACGGTGA AC TCT		

		TTGTGTCACT TG AGA		
		C _		
GAM2021	KIAA1649	3' GAGATGAGGTTTCACCGTGTT 51238	C	
		AACACGGTGAAACC CATCTC		
		TTGTGCCACTTTGG GTAGAG		
		A		
GAM2021	KIAA1655	3' GAGACAGGTTTCACCATGTT 67187	C	CCA
		AACA GGTGAAACC TCTC		
		TTGT CCACTTTGG AGAG		
		A AC_		
GAM2021	KIAA1668	3' GAGACGGGGTTTCACCGTGTT 67069		A
		AACACGGTGAAACCCC TCTC		
		TTGTGCCACTTTGGGG AGAG		
		C		
GAM2021	KIAA1712	3' GAGACAGGGTTTCACCATGTT 68158	C	CA
		AACA GGTGAAACCC TCTC		
		TTGT CCACTTTGGG AGAG		
		A AC		
GAM2021	KIAA1727	3' GAGATGGGATCTCACTATGTT 64761	CG	AAC
		AACA GTGA CCCATCTC		
		TTGT CACT GGGTAGAG		
		AT CTA		
GAM2021	KIAA1737	3' ATGGGGTTTACCGTGTT 67931		
		AACACGGTGAAACCCCAT		
		TTGTGCCATTTTGGGGTA		
GAM2021	KIAA1737	3' GAGATGGAGTTTCGCTCTTGT 67942	C_	C
		ACA G GTGAAAC CCATCTC		
		TGT C CGCTTTG GGTAGAG		
		T T A		
GAM2021	KIAA1821	3' GAGACAGGGTCTCACTGTGTT 72265	A	CA
		AACACGGTGA ACCC TCTC		
		TTGTGTCACT TGGG AGAG		
		C AC		
GAM2021	KIAA1877	3' GAGACAGGGTTTCACCGTGTT 66749		CA
		AACACGGTGAAACCC TCTC		
		TTGTGCCACTTTGGG AGAG		
		AC		
GAM2021	KIAA1971	3' GAGACAAGGTTTCGCTATGTT 74680	CG	CCA
		AACA GTGAAACC TCTC		

		TTGT CGCTTTGG AGAG		
		AT AAC		
GAM2021 KIAA1971	3'	GAGACGAGGTTTCACCGTGTT 74681		CCA
		AACACGGTGAAACC TCTC		
		TTGTGCCACTTTGG AGAG		
		AGC		
GAM2021 KIAA1975	5'	GAGATGGGGTTTCACCATGTT 74422	C	
		AACA GGTGAAACCCCATCTC		
		TTGT CCACTTTGGGGTAGAG		
		A		
GAM2021 KLK7	3'	GAGACAGGGTTTCACCATGTT 58390	C	CA
		AACA GGTGAAACCC TCTC		
		TTGT CCACTTTGGG AGAG		
		A AC		
GAM2021 KLK7	3'	GAGACAGGGTTTCACCATGTT 18544	C	CA
		AACA GGTGAAACCC TCTC		
		TTGT CCACTTTGGG AGAG		
		A AC		
GAM2021 LAMP3	3'	GACGGGGTTTCACCATGTT 60204	C	A
		AACA GGTGAAACCCC TC		
		TTGT CCACTTTGGGG AG		
		A C		
GAM2021 LAMP3	3'	GAGACGGAGTTTCACTCTTGT 60205	C _	C A
		ACA G GTGAAAC CC TCTC		
		TGT C CACTTTG GG AGAG		
		T T A C		
GAM2021 LHFPL2	3'	GAGATGGAATGGGACAACCGCA 70499	A_	GAAA ____
GTT		AAC CGGT CC CCATCTC		
		TTG GCCA GG GGTAGAG		
		AC ACAG TAA		
GAM2021 LIECG3	3'	GAGGGGGGTCTCACTGTGTT 88799	A	A
		AACACGGTGA ACCCC TCTC		
		TTGTGTCACT TGGGG GGAG		
		C _		
GAM2021 LY75	3'	GAGATGGGGTTTCACCATGTT 11394	C	
		AACA GGTGAAACCCCATCTC		
		TTGT CCACTTTGGGGTAGAG		
		A		
GAM2021 MAP-1	3'	GAGACGGGGTTTCACCATGTT 42441	C	A
		AACA GGTGAAACCCC TCTC		

			TTGT CCACTTTGGGG AGAG		
			A C		
GAM2021	MCLC	3'	GAGATGGGGTTTCACCATGTT 31382	C	
			AACA GGTGAAACCCCATCTC		
			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2021	MCM10	3'	GAGATGGGGTTTTGCCATGTT 38177	C TG	
			AACA GG AAACCCCATCTC		
			TTGT CC TTTGGGGTAGAG		
			A GT		
GAM2021	MEF-2	3'	GAGACTGGGTTTCACCATGTT 65022	C CA	
			AACA GGTGAAACCC TCTC		
			TTGT CCACTTTGGG AGAG		
			A TC		
GAM2021	MGC10200	3'	GAGATGGGGTTTCACCATGTT 59644	C	
			AACA GGTGAAACCCCATCTC		
			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2021	MGC11386	3'	GAGATGGGGATCTCACTGTGTT 53065	AA_	
			AACACGGTGA CCCCATCTC		
			TTGTGTCACT GGGGTAGAG		
			CTA		
GAM2021	MGC12466	3'	GAGATGGGATCTCGCTGT 79797	AAC	
			ACGGTGA CCCATCTC		
			TGTCGCT GGGTAGAG		
			CTA		
GAM2021	MGC12518	3'	GAGTGAGGGTTTCACCATGTT 64777	C _ T	
			AACA GGTGAAACCC CA CTC		
			TTGT CCACTTTGGG GT GAG		
			A A _		
GAM2021	MGC13007	5'	GAATTGGTTCACCTGTGTT 51279	A CCA	
			AACACGGTG AACC TC		
			TTGTGTCACT TTGG AG		
			C TTA		
GAM2021	MGC13061	3'	GAGATGGGATCTCACTAGGTT 51289	AC AAC	
			AAC GGTGA CCCATCTC		
			TTG TCACT GGGTAGAG		
			GA CTA		
GAM2021	MGC15563	3'	GAGATGGGATCTCACCATGTT 52861	C AAC	
			AACA GGTGA CCCATCTC		

			TTGT CCACT GGGTAGAG		
			A CTA		
GAM2021	MGC21675	3'	GAGATGGGGTTTCACCATGTT 54593	C	
			AACA GGTGAAACCCCATCTC		
			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2021	MGC2474	3'	GAGATGGGGTTCCCACTATGT 43958	CG	A_
			ACA GTG AACCCCATCTC		
			TGT CAC TTGGGGTAGAG		
			AT CC		
GAM2021	MGC2474	3'	GAGATGGGGTTTCACCATGTT 43959	C	
			AACA GGTGAAACCCCATCTC		
			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2021	MGC29898	3'	GAGATGGGATCTCACTCTGTT 59586	C	AAC
			AACA GGTGA CCCATCTC		
			TTGT TCACT GGGTAGAG		
			C CTA		
GAM2021	MGC4766	5'	GAGACGGGGTTTCACCGTGTT 49558		A
			AACACGGTGAAACCCC TCTC		
			TTGTGCCACTTTGGGG AGAG		
			C		
GAM2021	moblak	3'	GAGACAGGGTTTCACCGTGTT 56400		CA
			AACACGGTGAAACCCC TCTC		
			TTGTGCCACTTTGGGG AGAG		
			AC		
GAM2021	MOCS3	3'	GAGGGGGTTTCACCATGTT 27932	C	A
			AACA GGTGAAACCCC TC		
			TTGT CCACTTTGGGG AG		
			A G		
GAM2021	MRPS27	3'	GAGATGGGGTTTCACCATGTT 31330	C	
			AACA GGTGAAACCCCATCTC		
			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2021	MSP	3'	GAGATGAGGATTCATCTGT 50243	A	C
			ACGGTGAA CC CATCTC		
			TGTCATT GG GTAGAG		
			A A		
GAM2021	MtFMT	3'	GAGATGGGGTTTCACCATGTT 58336	C	
			AACA GGTGAAACCCCATCTC		

			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2021	MYO5C	3'	GAGACAGGTTTCACCATGTT 38719	C	CCA
			AACA GGTGAAACC TCTC		
			TTGT CCACTTTGG AGAG		
			A AC_		
GAM2021	NDP52	3'	GAGACAGGGTTTCACTATGTT 20671	CG	CA
			AACA GTGAAACCC TCTC		
			TTGT CACTTTGGG AGAG		
			AT AC		
GAM2021	NDUFC2	3'	GAGACGGGGTTTCACCATGTT 17031	C	A
			AACA GGTGAAACCCC TCTC		
			TTGT CCACTTTGGGG AGAG		
			A C		
GAM2021	NFAT5	3'	GAGATGGGGTTTTGCCATGTT 57790	C TG	
			AACA GG AAACCCCATCTC		
			TTGT CC TTTGGGGTAGAG		
			A GT		
GAM2021	NINJ2	3'	GAGACGGGGTTTCTCCATGTT 33725	C T	A
			AACA GG GAAACCCC TCTC		
			TTGT CC CTTTGGGG AGAG		
			A T C		
GAM2021	Nup43 TT	3'	GAGACGACAGGGTTTCACCATG 45347	C	CA__
			AACA GGTGAAACCC TCTC		
			TTGT CCACTTTGGG AGAG		
			A ACAGC		
GAM2021	Nup43	3'	GAGATGGGGTTTCACTGTGTT 45348		
			AACACGGTGAAACCCCATCTC		
			TTGTGTCACTTTGGGGTAGAG		
GAM2021	NXN	3'	GAGATGGGGTTTCACCATGTT 42675	C	
			AACA GGTGAAACCCCATCTC		
			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2021	OCT11	3'	GAGATGGGGTTTCACCATGTT 27590	C	
			AACA GGTGAAACCCCATCTC		
			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2021	OR51E2	3'	GAGACAGAGTTTCACCATGTT 48509	C	CCCA
			AACA GGTGAAAC TCTC		

			TTGT CCACTTTG AGAG		
			A AGAC		
GAM2021	OR51E2	3'	GAGATGGGGTCTCGCTCTGT 48510	C	A
			ACA GGTGA ACCCCATCTC		
			TGT TCGCT TGGGGTAGAG		
			C C		
GAM2021	OSBPL2	3'	GAGACGGAGTTTCACTCTTGT 29900	C _	C A
			ACA G GTGAAAC CC TCTC		
			TGT C CACTTTG GG AGAG		
			T T A C		
GAM2021	OSBPL2	3'	GAGACGGAGTTTCACTCTTGT 58486	C _	C A
			ACA G GTGAAAC CC TCTC		
			TGT C CACTTTG GG AGAG		
			T T A C		
GAM2021	PASK	5'	GAGACGGGGTTTCTCCATGTT 31412	C T	A
			AACA GG GAAACCCC TCTC		
			TTGT CC CTTTGGGG AGAG		
			A T C		
GAM2021	PELI1	5'	GAGACGGGGTTTCACCATGTT 40641	C	A
			AACA GGTGAAACCCC TCTC		
			TTGT CCACTTTGGGG AGAG		
			A C		
GAM2021	PELI1	5'	GAGATGGGGTTTCACCATGTT 40642	C	
			AACA GGTGAAACCCCATCTC		
			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2021	PIG7	3'	GAGATGGGGTCTTACTATGTT 17970	CG	A
			AACA GTGA ACCCCATCTC		
			TTGT CATT TGGGGTAGAG		
			AT C		
GAM2021	PIP5K1C	3'	GAGACGAGGGTGCTGTGT 71301	GAA	CA_
			ACACGGT ACCC TCTC		
			TGTGTCG TGGG AGAG		
			_ AGC		
GAM2021	PRO0365	5'	GAGACGGGGTTTCACTATGTT 26982	CG	A
			AACA GTGAAACCCC TCTC		
			TTGT CACTTTGGGG AGAG		
			AT C		
GAM2021	PRO1992	3'	GAGATGGGGTTTACCATGT 26906	C	
			ACA GGTGAAACCCCATCTC		

			TGT CCATTTTGGGGTAGAG		
			A		
GAM2021	PRO2955	3'	GAGACAGGGTTTTACCATGTT 38239	C	CA
			AACA GGTGAAACCC TCTC		
			TTGT CCATTTTGGG AGAG		
			A AC		
GAM2021	PSPH	3'	GAGACGGGGTTTGACCGTGTT 17134	G	A
			AACACGGT AAACCCC TCTC		
			TTGTGCCA TTTGGGG AGAG		
			G C		
GAM2021	PSTPIP2	3'	GAGACAGGGTTTTACCATGTT 44655	C	CA
			AACA GGTGAAACCC TCTC		
			TTGT CCATTTTGGG AGAG		
			A AC		
GAM2021	PTPN3	3'	GAGATGGGACAGTGTCTC 12586	A	___
			GGTGA AC CCCATCTC		
			CTACT TG GGGTAGAG		
			G ACA		
GAM2021	PTPRT	3'	GAGATGGGGCACCAGTG 56494	_	AAA
			CAC GGTG CCCCATCTC		
			GTG CCAC GGGGTAGAG		
			A ___		
GAM2021	RAB21	3'	GAGACGGGGTTTCACCAGGTT 31089	AC	A
			AAC GGTGAAACCCC TCTC		
			TTG CCACTTTGGGG AGAG		
			GA C		
GAM2021	RAB33B	3'	GATGGGGTTTCACCATGTT 49328	C	
			AACA GGTGAAACCCCATC		
			TTGT CCACTTTGGGGTAG		
			A		
GAM2021	RAP140	3'	GAGACAGGGTTTCACTGTGTT 31515		CA
			AACACGGTGAAACCC TCTC		
			TTGTGTCACTTTGGG AGAG		
			AC		
GAM2021	RES4-25	3'	GAGACGGGGTTTCTCCATGTT 65267	C T	A
			AACA GG GAAACCCC TCTC		
			TTGT CC CTTTGGGG AGAG		
			A T C		
GAM2021	RNF8	3'	GAGACAGGGTTTCACCATGTT 15568	C	CA
			AACA GGTGAAACCC TCTC		

			TTGT CCACTTTGGG AGAG		
			A AC		
GAM2021	RNO2	5'	GAGATGGGGTGTCAACCATGTT 53937	C	A
			AACA GGTGA ACCCCATCTC		
			TTGT CCACT TGGGGTAGAG		
			A G		
GAM2021	SAMHD1	3'	GAGACAAGGTTTTGCTCTGTT 61985	C TG	CCA
			AACA GG AAACC TCTC		
			TTGT TC TTTGG AGAG		
			C GT AAC		
GAM2021	SC4MOL	3'	GAGATGGGGTTTCTCGATGTT 23105	_	T
			AACA CGG GAAACCCCATCTC		
			TTGT GCT CTTTGGGGTAGAG		
			A _		
GAM2021	SCAMP-4	3'	GAGACAGAGTTTCACTCTGT 55348	C	CCCA
			ACA GGTGAAAC TCTC		
			TGT TCACTTTG AGAG		
			C AGAC		
GAM2021	SCAMP-4	3'	GATGGGGTTTCAACCATGTT 55350	C	
			AACA GGTGAAACCCCATC		
			TTGT CCACTTTGGGGTAG		
			A		
GAM2021	SCYA22	3'	GAGACGGGGTTTTGCCATGTT 92595	C TG	A
			AACA GG AAACCCC TCTC		
			TTGT CC TTTGGGG AGAG		
			A GT C		
GAM2021	SCYA22	3'	GAGATGGAGTTTCGCTCTTGT 92596	C _	C
			ACA G GTGAAAC CCATCTC		
			TGT C CGCTTTG GGTAGAG		
			T T A		
GAM2021	SCYA28	3'	GACGGGGTTTCACCGTGTT 39543		A
			AACACGGTGAAACCCC TC		
			TTGTGCCACTTTGGGG AG		
			C		
GAM2021	SERF1B	3'	GAGATGGGGTTTCAACCATGTT 43697	C	
			AACA GGTGAAACCCCATCTC		
			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2021	SFXN2	3'	GAGACGGGGTTTCAACCATG 74376	C	A
			CA GGTGAAACCCC TCTC		

			GT CCACTTTGGGG AGAG		
			A C		
GAM2021	SIRPB1	3'	GAGATGGGGTTTCTCCATGTT 21367	C T	
			AACA GG GAAACCCCATCTC		
			TTGT CC CTTTGGGGTAGAG		
			A T		
GAM2021	SLC12A8	3'	GAGACAGGGTTTCACCATGTT 45237	C	CA
			AACA GGTGAAACCC TCTC		
			TTGT CCACTTTGGG AGAG		
			A AC		
GAM2021	SLC16A4	3'	GAGGCGGGGTTTCACCATGTT 17451	C	AT
			AACA GGTGAAACCC CTC		
			TTGT CCACTTTGGGG GAG		
			A CG		
GAM2021	SLC19A3	3'	GAGATGGGGTTTCACAATGTT 48243	CG	
			AACA GTGAAACCCCATCTC		
			TTGT CACTTTGGGGTAGAG		
			AA		
GAM2021	SLC2A10	3'	GAGATGGGGTTTCACTGTGTT 48552		
			AACACGGTGAAACCCCATCTC		
			TTGTGTCACTTTGGGGTAGAG		
GAM2021	SREC	3'	GAGACAGGGTTTCACCATGTT 14903	C	CA
			AACA GGTGAAACCC TCTC		
			TTGT CCACTTTGGG AGAG		
			A AC		
GAM2021	SS-56	3'	GAGACGGAGTTTCACCATGTT 60351	C	C A
			AACA GGTGAAAC CC TCTC		
			TTGT CCACTTTG GG AGAG		
			A A C		
GAM2021	STAF65(gamma)	3'	GAGATGAGGTTTCACCGTGTT 30069		C
			AACACGGTGAAACC CATCTC		
			TTGTGCCACTTTGG GTAGAG		
			A		
GAM2021	STARD7	3'	GAGATGGAGTTTCACTCTGTT 58370	C	C
			AACA GGTGAAAC CCATCTC		
			TTGT TCACTTTG GG TAGAG		
			C A		
GAM2021	STARD7	3'	GAGATGGAGTTTCACTCTGTT 39741	C	C
			AACA GGTGAAAC CCATCTC		

			TTGT TCACTTTG GGTAGAG		
			C A		
GAM2021	STRBP	5'	GAGACGGGGTTTTGCCATGTT 37819	C TG	A
			AACA GG AAACCCC TCTC		
			TTGT CC TTTGGGG AGAG		
			A GT C		
GAM2021	SULT1C2	3'	GAGACGAGGTTTCACCGTGTT 22713		CCA
			AACACGGTGAAACC TCTC		
			TTGTGCCACTTTGG AGAG		
			AGC		
GAM2021	SUN1	3'	GAGACAGGGTTTCACTGTGTT 47914		CA
			AACACGGTGAAACCC TCTC		
			TTGTGTCACTTTGGG AGAG		
			AC		
GAM2021	SYT13	3'	GAGATGGGGTTTCACCATGTT 95101	C	
			AACA GGTGAAACCCCATCTC		
			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2021	TADA3L	3'	GAGACGGGGTTTCACCGTGTT 56807		A
			AACACGGTGAAACCCC TCTC		
			TTGTGCCACTTTGGGG AGAG		
			C		
GAM2021	TBCC	3'	GAGACGGGGTTTCGCCATGTT 13604	C	A
			AACA GGTGAAACCCC TCTC		
			TTGT CCGCTTTGGGG AGAG		
			A C		
GAM2021	TCL6	5'	GAGACGAGGTTTCACCATGTT 40478	C	CCA
			AACA GGTGAAACC TCTC		
			TTGT CCACTTTGG AGAG		
			A AGC		
GAM2021	TCL6	5'	GAGACGAGGTTTCACCATGTT 40510	C	CCA
			AACA GGTGAAACC TCTC		
			TTGT CCACTTTGG AGAG		
			A AGC		
GAM2021	TCL6	3'	GAGACAGGGTTTCACCGTGTT 27759		CA
			AACACGGTGAAACCC TCTC		
			TTGTGCCACTTTGGG AGAG		
			AC		
GAM2021	TCL6	5'	GAGACGAGGTTTCACCATGTT 27760	C	CCA
			AACA GGTGAAACC TCTC		

			TTGT CCACTTTGG AGAG		
			A AGC		
GAM2021	TCL6	3'	GAGACAGGGTTTCACCGTGTT 25907		CA
			AACACGGTGAAACCC TCTC		
			TTGTGCCACTTTGGG AGAG		
			AC		
GAM2021	TCL6	5'	GAGACGAGGTTTCACCATGTT 25908	C	CCA
			AACA GGTGAAACC TCTC		
			TTGT CCACTTTGG AGAG		
			A AGC		
GAM2021	THEA	3'	GAGACACTTTTCACTGTGTT 66889		CCCCA
			AACACGGTGAAA TCTC		
			TTGTGTCACTTT AGAG		
			CAC__		
GAM2021	THEA	3'	GAGATGGGGTTTCACTGTGTT 66890		
			AACACGGTGAAACCCCATCTC		
			TTGTGTCACTTTGGGGTAGAG		
GAM2021	TRIM16	3'	GAGATGGGGTTTCAACCATGTT 22372	C	
			AACA GGTGAAACCCCATCTC		
			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2021	TRIM5	3'	GAGACGGGGTTTCCCCATGTT 53471	C T	A
			AACA GG GAAACCCC TCTC		
			TTGT CC CTTTGGGG AGAG		
			A C C		
GAM2021	TRIM5	3'	GAGACGGGGTTTCCCCATGTT 53540	C T	A
			AACA GG GAAACCCC TCTC		
			TTGT CC CTTTGGGG AGAG		
			A C C		
GAM2021	TRIM6	3'	GAGATAGGGTTTCAACCGTGTT 55181		C
			AACACGGTGAAACCC ATCTC		
			TTGTGCCACTTTGGG TAGAG		
			A		
GAM2021	TU12B1-TY	3'	GAGACGGGGTTTCAACCATGTT 33849	C	A
			AACA GGTGAAACCCC TCTC		
			TTGT CCACTTTGGGG AGAG		
			A C		
GAM2021	TU12B1-TY	3'	GAGATGGGGTTTCAACCATGTT 33850	C	
			AACA GGTGAAACCCCATCTC		

			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2021	TU12B1-TY 3'	GAGATGGGGTTTCTCCATG	33851	C T	
		CA GG GAAACCCCATCTC			
		GT CC CTTTGGGGTAGAG			
		A T			
GAM2021	TUSP 3'	GAGATGGGGTTTTGCCATGTT	40028	C TG	
		AACA GG AAACCCCATCTC			
		TTGT CC TTTGGGGTAGAG			
		A GT			
GAM2021	UBF-fl 3'	GATGGGGTTTTACCATGTT	52625	C	
		AACA GGTGAAACCCCATC			
		TTGT CCATTTTGGGGTAG			
		A			
GAM2021	VDU1 3'	GAGATGGGGTTTCACCATGTT	31125	C	
		AACA GGTGAAACCCCATCTC			
		TTGT CCACTTTGGGGTAGAG			
		A			
GAM2021	WBSCR23 3'	GAGACGGGGTTTCACCATGTT	47435	C	A
		AACA GGTGAAACCCC TCTC			
		TTGT CCACTTTGGGG AGAG			
		A C			
GAM2021	LOC112687 3'	GAGATGGGGTTTGCCATGT	73235	C G	
		ACA GGT AAACCCCATCTC			
		TGT CCG TTTGGGGTAGAG			
		A _			
GAM2021	LOC112817 3'	GAGACAGAGTTTCACTCTGT	57326	C	CCCA
		ACA GGTGAAAC TCTC			
		TGT TCACTTTG AGAG			
		C AGAC			
GAM2021	LOC112817 3'	GAGATGGGGTTTCACCGTGTT	57327		
		AACACGGTGAAACCCCATCTC			
		TTGTGCCACTTTGGGGTAGAG			
GAM2021	LOC113523 5'	GAGACAGGGTTTCACCATGTT	73423	C	CA
		AACA GGTGAAACCC TCTC			
		TTGT CCACTTTGGG AGAG			
		A AC			
GAM2021	LOC115219 5'	GAGACGGGGTTTCATCATGTT	73695	C	A
		AACA GGTGAAACCCC TCTC			

		TTGT CTA	TTTTGGGG	AGAG		
		A	C			
GAM2021	LOC115648 3'	GAGACGGGGTTTCACCATGTT	60022	C	A	
		AACA GGTGAAACCCC	TCTC			
		TTGT CCA	TTTGGGG	AGAG		
		A	C			
GAM2021	LOC116411 5'	GAGACGGGGTTTCGCTGTGTT	74300		A	
		AACACGGTGAAACCCC	TCTC			
		TTGTGTCGCTTTGGGG	AGAG			
		C				
GAM2021	LOC120114 3'	GAGATGGGGTTTCACCATGTT	76045	C		
		AACA GGTGAAACCCC	ATCTC			
		TTGT CCA	TTTGGGGTAGAG			
		A				
GAM2021	LOC120224 5'	GAGACAGGGTTTCACCATGTT	57888	C	CA	
		AACA GGTGAAACCC	TCTC			
		TTGT CCA	TTTGGG	AGAG		
		A	AC			
GAM2021	LOC120224 5'	GAGATGGAGTTTTGCTTTTGT	57889	C_ TG	C	
		ACA GG AAAC	CCATCTC			
		TGT TC	TTTG GGTAGAG			
		TT GT	A			
GAM2021	LOC120939 3'	GAGAGGGGGTTTCACCATGTT	76762	C	A	
		AACA GGTGAAACCCC	TCTC			
		TTGT CCA	TTTGGGG	AGAG		
		A	G			
GAM2021	LOC126364 3'	GAGATGGGGTTTCGCCATGTT	76192	C		
		AACA GGTGAAACCCC	ATCTC			
		TTGT CCGCTTTGGGG	TAGAG			
		A				
GAM2021	LOC126661 3'	GAGATGGGGTTTCACCATGTT	75057	C		
		AACA GGTGAAACCCC	ATCTC			
		TTGT CCA	TTTGGGGTAGAG			
		A				
GAM2021	LOC126669 3'	GAGACGAAGTCTCGCTGTGTT	75935	A	CCCA	
		AACACGGTGA AC	TCTC			
		TTGTGTCGCT TG	AGAG			
		C	AAGC			
GAM2021	LOC126669 3'	GAGATGGGGTTTCGCCGT	75936			
		ACGGTGAAACCCC	ATCTC			

TGCCGCTTTGGGGTAGAG

GAM2021	LOC128077	3'	GAGACAGGGTTTCACCATGTT	75215	C	CA
			AACA GGTGAAACCC TCTC			
			TTGT CCACTTTGGG AGAG			
			A AC			
GAM2021	LOC128077	3'	GAGACGGGGTTTCACCATGTT	75217	C	A
			AACA GGTGAAACCC TCTC			
			TTGT CCACTTTGGG AGAG			
			A C			
GAM2021	LOC128989	3'	GAGACGGGGTTTCACCATGTT	75317	C	A
			AACA GGTGAAACCC TCTC			
			TTGT CCACTTTGGG AGAG			
			A C			
GAM2021	LOC129880	3'	GAGACGGGGTTTCGCTGTGTT	75406		A
			AACACGGTGAAACCC TCTC			
			TTGTGTCGCTTTGGG AGAG			
			C			
GAM2021	LOC130813	3'	GAGATGGGGTTTCTCCATGTT	76275	C T	
			AACA GG GAAACCCCATCTC			
			TTGT CC CTTTGGGGTAGAG			
			A T			
GAM2021	LOC132241	5'	GAGAGTGGGTTTCACTATGTT	75562	CG	CA
			AACA GTGAAACCC TCTC			
			TTGT CACTTTGGG AGAG			
			AT TG			
GAM2021	LOC132625	3'	GAGATGGGGTTTCACCATGTT	76440	C	
			AACA GGTGAAACCCCATCTC			
			TTGT CCACTTTGGGGTAGAG			
			A			
GAM2021	LOC135154	3'	AGACAAGGTTTCACCATGTT	75718	C	CCA
			AACA GGTGAAACC TCT			
			TTGT CCACTTTGG AGA			
			A AAC			
GAM2021	LOC142820	5'	GAGACGGAGTTTGGCCATGTT	76913	C TG	C A
			AACA GG AAAC CC TCTC			
			TTGT CC TTTG GG AGAG			
			A GT A C			
GAM2021	LOC143187	3'	GAGATGGAGTTTTCACCATGTT	59758	C	C
			AACA GGTGAAAC CCATCTC			

		TTGT CCACTTTG GGTAGAG			
		A A			
GAM2021	LOC143916 3'	GAGATGGGGTTTCACCTTGTT 77141	C		
		AACA GGTGAAACCCCATCTC			
		TTGT CCACTTTGGGGTAGAG			
		T			
GAM2021	LOC144317 5'	GAGACTGGGGTTTCTCCATGTT 77295	C T	—	
		AACA GG GAAACCCCA TCTC			
		TTGT CC CTTTGGGGT AGAG			
		A T C			
GAM2021	LOC144519 5'	GAGACGGGGTTTTGCCATGTT 77374	C TG	A	
		AACA GG AAACCCC TCTC			
		TTGT CC TTTGGGG AGAG			
		A GT C			
GAM2021	LOC144667 3'	GAGATGGGGTCTCCCTATGTT 84087	CG T	A	
		AACA G GA ACCCATCTC			
		TTGT C CT TGGGGTAGAG			
		AT C C			
GAM2021	LOC144871 3'	ATGGGGTTTCACTGTGTT 84118			
		AACACGGTGAAACCCCAT			
		TTGTGTCACTTTGGGGTA			
GAM2021	LOC145082 5'	GAGACGAGGTTTTGCCATGTT 84189	C TG	CCA	
		AACA GG AAACC TCTC			
		TTGT CC TTTGG AGAG			
		A GT AGC			
GAM2021	LOC145268 5'	GAGACAGAGTTTCACCATGTT 77579	C	CCCA	
		AACA GGTGAAAC TCTC			
		TTGT CCACTTTG AGAG			
		A AGAC			
GAM2021	LOC145453 5'	GAGACAGGGTCTCACTGTGT 77663	A	CA	
		ACACGGTGA ACCC TCTC			
		TGTGTCACT TGGG AGAG			
		C AC			
GAM2021	LOC145453 5'	GAGATGGGGTTTTGTCATGTT 77664	C TG		
		AACA GG AAACCCCATCTC			
		TTGT CT TTTGGGGTAGAG			
		A GT			
GAM2021	LOC146050 3'	GAGATGGGGTTTCACCATGTT 78117	C		
		AACA GGTGAAACCCCATCTC			

		TTGT CCACTTTGGGGTAGAG		
		A		
GAM2021	LOC146050 3'	GAGATGGGGTTTCTCCATGTT 78118	C	T
		AACA GG GAAACCCCATCTC		
		TTGT CC CTTTGGGGTAGAG		
		A T		
GAM2021	LOC146229 3'	GACGGGGTTTCACCATGTT 78279	C	A
		AACA GGTGAAACCCC TC		
		TTGT CCACTTTGGGG AG		
		A C		
GAM2021	LOC146229 3'	GAGACGGGGTTTCACCATGTT 78282	C	A
		AACA GGTGAAACCCC TCTC		
		TTGT CCACTTTGGGG AGAG		
		A C		
GAM2021	LOC146229 3'	GAGACGGGGTTTTACCGTGTT 78283		A
		AACACGGTGAAACCCC TCTC		
		TTGTGCCATTTTGGGG AGAG		
		C		
GAM2021	LOC146229 3'	GAGATGGAGTTTCATTCTTGT 78284	C_	C
		ACA GGTGAAAC CCATCTC		
		TGT TTACTTTG GG TAGAG		
		TC A		
GAM2021	LOC146346 5'	GAGACGGGGTTTCACCGTGTT 78397		A
		AACACGGTGAAACCCC TCTC		
		TTGTGCCACTTTGGGG AGAG		
		C		
GAM2021	LOC146429 5'	AGACAGGGTTTCACCATG 84658	C	CA
		CA GGTGAAACCC TCT		
		GT CCACTTTGGG AGA		
		A AC		
GAM2021	LOC146603 5'	GAGACGGGGTTTCACCGTGTT 78595		A
		AACACGGTGAAACCCC TCTC		
		TTGTGCCACTTTGGGG AGAG		
		C		
GAM2021	LOC146784 5'	GAGATGGAGTTTCACTCTTGT 78712	C_	C
		ACA G GTGAAAC CCATCTC		
		TGT C CACTTTG GG TAGAG		
		T T A		
GAM2021	LOC146784 5'	GAGATGGGGTTTTCACCATGTT 78713	C	
		AACA GGTGAAACCCCATCTC		

		TTGT CCACTTTGGGGTAGAG		
		A		
GAM2021	LOC146839 3'	GAGACGGGGTTTCACCGTGTT 84842		A
		AACACGGTGAAACCCC TCTC		
		TTGTGCCACTTTGGGG AGAG		
		C		
GAM2021	LOC146894 3'	GAGATGGGGTTTCACCATGTT 59862	C	
		AACA GGTGAAACCCCATCTC		
		TTGT CCACTTTGGGGTAGAG		
		A		
GAM2021	LOC146901 3'	GAGACGGGGTTTCACCATGTT 84901	C	A
		AACA GGTGAAACCCC TCTC		
		TTGT CCACTTTGGGG AGAG		
		A C		
GAM2021	LOC146909 3'	GAGATGGGGTTTCACCGTGTT 78772		
		AACACGGTGAAACCCCATCTC		
		TTGTGCCACTTTGGGGTAGAG		
GAM2021	LOC147054 3'	GATGGGGTTTCTCCATGTT 85007	C T	
		AACA GG GAAACCCCATC		
		TTGT CC CTTTGGGGTAG		
		A T		
GAM2021	LOC147071 5'	GAGACGGAGTTTCACCATGTT 73365	C	C A
		AACA GGTGAAAC CC TCTC		
		TTGT CCACTTTG GG AGAG		
		A A C		
GAM2021	LOC147080 5'	GAGACAAGGTTTCACCATGTT 85037	C	CCA
		AACA GGTGAAACC TCTC		
		TTGT CCACTTTGG AGAG		
		A AAC		
GAM2021	LOC147166 3'	GAGATGGGGTTTCACCATGTT 78889	C	
		AACA GGTGAAACCCCATCTC		
		TTGT CCACTTTGGGGTAGAG		
		A		
GAM2021	LOC147276 3'	GAGATGGAGTTTCACTCTTGT 78963	C _	C
		ACA G GTGAAAC CCATCTC		
		TGT C CACTTTG GGTAGAG		
		T T A		
GAM2021	LOC147429 3'	GAGATGGGGTTTCACCATGTT 78996	C	
		AACA GGTGAAACCCCATCTC		

		TTGT CCACTTTGGGGTAGAG		
		A		
GAM2021	LOC147694 3'	GAGACGGGGTTTCACCGTGTT 79097		A
		AACACGGTGAAACCCC TCTC		
		TTGTGCCACTTTGGGG AGAG		
		C		
GAM2021	LOC147841 3'	GAGATGGAGTTTCACCATG 79229	C	C
		CA GGTGAAAC CCATCTC		
		GT CCACTTTG GGTAGAG		
		A A		
GAM2021	LOC148137 3'	GAGACGGTGTTTCACTGTGTT 59099		C A
		AACACGGTGAAAC CC TCTC		
		TTGTGTCACTTTG GG AGAG		
		T C		
GAM2021	LOC148137 3'	GAGATGGAGTTTCACCCTTGT 59100	C_	C
		ACA GGTGAAAC CCATCTC		
		TGT CCACTTTG GGTAGAG		
		TC A		
GAM2021	LOC148147 3'	GAGATGAGGTTTCACCTTGTT 79399	C	C
		AACA GGTGAAACC CATCTC		
		TTGT CCACTTTGG GTAGAG		
		T A		
GAM2021	LOC148189 5'	GAGACGGGGTTTCACCATGTT 79448	C	A
		AACA GGTGAAACCCC TCTC		
		TTGT CCACTTTGGGG AGAG		
		A C		
GAM2021	LOC148887 5'	GAGACAGGGTTTCACCATGTT 85401	C	CA
		AACA GGTGAAACCC TCTC		
		TTGT CCACTTTGGG AGAG		
		A AC		
GAM2021	LOC149171 5'	GAGATGGGGTTTCTCCATGTT 79968	C	T
		AACA GG GAAACCCCATCTC		
		TTGT CC CTTTGGGGTAGAG		
		A T		
GAM2021	LOC149478 3'	GAGACGGGGTTTCACCATGTT 80170	C	A_
		AACA GGTGAAACCCC TCTC		
		TTGT CCACTTTGGGG AGAG		
		A GC		
GAM2021	LOC149577 3'	GAGATGGGGTTTGGCCATGTT 85677	C	TG
		AACA GG AAACCCCATCTC		

		TTGT CC TTTGGGGTAGAG		
		A GT		
GAM2021	LOC149684 5'	GAGATGGGGGCTCCCTATGTT 85764	CG T	AA
		AACA G GA CCCCATCTC		
		TTGT C CT GGGGTAGAG		
		AT C CG		
GAM2021	LOC149692 3'	GAGACAGGGTTTCACCATGTT 85735	C	CA
		AACA GGTGAAACCC TCTC		
		TTGT CCACTTTGGG AGAG		
		A AC		
GAM2021	LOC149703 5'	GAGACGGGGTTTTGCCATGTT 85820	C TG	A
		AACA GG AAACCCC TCTC		
		TTGT CC TTTGGGG AGAG		
		A GT C		
GAM2021	LOC149711 3'	GAGATGGGGTTTTACCATGTT 85852	C	
		AACA GGTGAAACCCCATCTC		
		TTGT CCATTTTGGGGTAGAG		
		A		
GAM2021	LOC149821 5'	GACGGAGTTTCACCGTGTT 85932	C A	
		AACACGGTGAAAC CC TC		
		TTGTGCCACTTTG GG AG		
		A C		
GAM2021	LOC150054 5'	GATGGGGTTTCCCATGTT 85974	C T	
		AACA GG GAAACCCCATC		
		TTGT CC CTTTGGGGTAG		
		A _		
GAM2021	LOC150166 5'	ATGGGGTTTCACCATGTT 86032	C	
		AACA GGTGAAACCCCAT		
		TTGT CCACTTTGGGGTA		
		A		
GAM2021	LOC150225 3'	GAGACGGTTTCACCATGT 86193	C	CCA
		ACA GGTGAAACC TCTC		
		TGT CCACTTTGG AGAG		
		A C__		
GAM2021	LOC150282 5'	GAGATGGCGTTTCACCATGTT 80544	C	C
		AACA GGTGAAAC CCATCTC		
		TTGT CCACTTTG GG TAGAG		
		A C		
GAM2021	LOC150397 3'	GAGACGCAGTTTCACCGTGTT 80663		CCCA
		AACACGGTGAAAC TCTC		

		TTGTGCCACTTTG AGAG		
		ACGC		
GAM2021	LOC150630 5'	GAGAGGGGGTTTCACCGTG 86301	A	
		CACGGTGAAACCCC TCTC		
		GTGCCACTTTGGGG AGAG		
		G		
GAM2021	LOC150696 3'	GAGACGGGGTTTTGCCATGTT 59159	C TG	A
		AACA GG AAACCCC TCTC		
		TTGT CC TTTGGGG AGAG		
		A GT C		
GAM2021	LOC150960 3'	GAGATGGGGTCTCACCCCTGTT 80875	C	A
		AACA GGTGA ACCCCATCTC		
		TTGT CCACT TGGGGTAGAG		
		C C		
GAM2021	LOC151050 5'	GAGACAGAGTTTCACCATGTT 80917	C	CCCA
		AACA GGTGAAAC TCTC		
		TTGT CCACTTTG AGAG		
		A AGAC		
GAM2021	LOC151057 3'	GAGACGGGGTTTCACCATGTT 86388	C	A
		AACA GGTGAAACCCC TCTC		
		TTGT CCACTTTGGGG AGAG		
		A C		
GAM2021	LOC151178 5'	AGATGGGGTCAGCGCCTG 80949	C	AA_
		CA GGTG ACCCCATCT		
		GT CCGC TGGGGTAGA		
		_ GAC		
GAM2021	LOC151201 3'	GAGACGGGGTTTCACCATGTT 86477	C	A
		AACA GGTGAAACCCC TCTC		
		TTGT CCACTTTGGGG AGAG		
		A C		
GAM2021	LOC151475 5'	GAGACGAGGTTTCACCATGTT 86593	C	CCA
		AACA GGTGAAACC TCTC		
		TTGT CCACTTTGG AGAG		
		A AGC		
GAM2021	LOC151701 3'	GAGACGGGGTTTCACCATGTT 86672	C	A
		AACA GGTGAAACCCC TCTC		
		TTGT CCACTTTGGGG AGAG		
		A C		
GAM2021	LOC151826 3'	GAGACAGGGTTTCACCGTGTT 81182		CA
		AACACGGTGAAACCC TCTC		

		TTGTGCCACTTTGGG AGAG		
		AC		
GAM2021	LOC151877 3'	GAGATGGGGTCTTGCTGTGTT 86698	TG A	
		AACACGG A ACCCATCTC		
		TTGTGTC T TGGGGTAGAG		
		GT C		
GAM2021	LOC151979 5'	GAGACGGGGTTTCACCATGTT 81249	C	A
		AACA GGTGAAACCCC TCTC		
		TTGT CCACTTTGGGG AGAG		
		A C		
GAM2021	LOC152137 3'	AGAGCGGGTTTCACCATGTT 81305	C	CA
		AACA GGTGAAACCCC TCT		
		TTGT CCACTTTGGG AGA		
		A CG		
GAM2021	LOC152343 3'	GACTGGGTTTCACCATGTT 81427	C	CA
		AACA GGTGAAACCCC TC		
		TTGT CCACTTTGGG AG		
		A TC		
GAM2021	LOC152343 3'	GAGATGGAGTCTTGCTGTGT 81428	TG A C	
		ACACGG A AC CCATCTC		
		TGTGTC T TG GGTAGAG		
		GT C A		
GAM2021	LOC152445 3'	GAGACAGGGTTTCACCATGTT 86948	C	CA
		AACA GGTGAAACCCC TCTC		
		TTGT CCACTTTGGG AGAG		
		A AC		
GAM2021	LOC152719 5'	GAGACGGGGTTTCACCATGTT 87029	C	A
		AACA GGTGAAACCCC TCTC		
		TTGT CCACTTTGGGG AGAG		
		A C		
GAM2021	LOC152794 5'	GAGATGGGGTTTCATCATGTT 81559	C	
		AACA GGTGAAACCCCATCTC		
		TTGT CTACTTTGGGGTAGAG		
		A		
GAM2021	LOC153077 3'	GAGATGGGGCTTCACCATGTT 87126	C	A
		AACA GGTGAA CCCCATCTC		
		TTGT CCACTT GGGGTAGAG		
		A C		
GAM2021	LOC153606 5'	GAGATAGGGTTTCACCATGTT 87257	C	C
		AACA GGTGAAACCCC ATCTC		

		TTGT CCACTTTGGG TAGAG		
		A A		
GAM2021	LOC153688 3'	GAGACAGGATTTTCATCGTGTT 87315	C	CA
		AACACGGTGAAA CC TCTC		
		TTGTGCTACTTT GG AGAG		
		A AC		
GAM2021	LOC153688 3'	GAGACAGGGTTTCACCATGTT 87316	C	CA
		AACA GGTGAAACCC TCTC		
		TTGT CCACTTTGGG AGAG		
		A AC		
GAM2021	LOC153769 3'	GAGATGGGGTCCAAGCCTG 81806	C	GAA_
		CA GGT ACCCCATCTC		
		GT CCG TGGGGTAGAG		
		_ AACC		
GAM2021	LOC153883 5'	ATGGGGTTTTACCATGTT 81887	C	
		AACA GGTGAAACCCCAT		
		TTGT CCATTTTGGGGTA		
		A		
GAM2021	LOC153910 5'	GAGACAGGGTTTTGCCATGTT 81907	C	TG CA
		AACA GG AAACCC TCTC		
		TTGT CC TTTGGG AGAG		
		A GT AC		
GAM2021	LOC154282 5'	GAGATGGTGTTCACCATGTT 87404	C	C
		AACA GGTGAAAC CCATCTC		
		TTGT CCACTTTG GGTAGAG		
		A T		
GAM2021	LOC154877 5'	GAGACAGGGTTTCACCCTGTT 87550	C	CA
		AACA GGTGAAACCC TCTC		
		TTGT CCACTTTGGG AGAG		
		C AC		
GAM2021	LOC154877 3'	GAGATGGGGTCTTGCTATGT 87551	CG	TG A
		ACA G A ACCCCATCTC		
		TGT C T TGGGGTAGAG		
		AT GT C		
GAM2021	LOC154877 5'	GAGATGGGGTTTTGCCATGTT 87552	C	TG
		AACA GG AAACCCCATCTC		
		TTGT CC TTTGGGGTAGAG		
		A GT		
GAM2021	LOC154877 3'	GAGTCGGGGTTTCACCATGTT 87553	C	AT
		AACA GGTGAAACCC CTC		

		TTGT CCACTTTGGGG GAG		
		A CT		
GAM2021	LOC154930 3'	GAGACAGGATTTTACTGTGTT 82092	C	CA
		AACACGGTGAAA CC TCTC		
		TTGTGTCATTTT GG AGAG		
		A AC		
GAM2021	LOC157247 5'	GAGACGGGGTTTCACCAAGTGT 82298	_	A
		ACAC GGTGAAACCCC TCTC		
		TGTG CCACTTTGGGG AGAG		
		A C		
GAM2021	LOC157506 3'	GAGACGGGGTTTCACCATGTT 82367	C	A
		AACA GGTGAAACCCC TCTC		
		TTGT CCACTTTGGGG AGAG		
		A C		
GAM2021	LOC157798 5'	GAGACGGAGTCTTGCTGTGT 87858	TG A	C A
		ACACGG A AC CC TCTC		
		TGTGTC T TG GG AGAG		
		GT C A C		
GAM2021	LOC157798 5'	GAGACGGGGTTTCACCTTGTT 87859	C	A
		AACA GGTGAAACCCC TCTC		
		TTGT CCACTTTGGGG AGAG		
		T C		
GAM2021	LOC157858 5'	GAGACAGGGTTTCACTATGT 87888	CG	CA
		ACA GTGAAACCC TCTC		
		TGT CACTTTGGG AGAG		
		AT AC		
GAM2021	LOC158014 5'	GAGACGGAGTTTACCATGTT 82559	C	C A
		AACA GGTGAAAC CC TCTC		
		TTGT CCACTTTG GG AGAG		
		A A C		
GAM2021	LOC158014 5'	GAGATAGAGTTTCACTCTTGT 82560	C_	CCC
		ACA G GTGAAAC ATCTC		
		TGT C CACTTTG TAGAG		
		T T AGA		
GAM2021	LOC158014 5'	GAGATGGGGTCTCGCTATGTT 82561	CG	A
		AACA GTGA ACCCATCTC		
		TTGT CGCT TGGGGTAGAG		
		AT C		
GAM2021	LOC158310 5'	GAGACAGGGTTTCAACAATGTT 88082	CG	CA
		AACA GTGAAACCC TCTC		

		TTGT CACTTTGGG AGAG		
		AA AC		
GAM2021	LOC158402 5'	GAGGGGGGTTTCACCGTGTT 88148	A	
		AACACGGTGAAACCCC TCTC		
		TTGTGCCACTTTGGGG GGAG		
GAM2021	LOC158476 3'	GAGACAGGGTTTCACCATGTT 88194	C	CA
		AACA GGTGAAACCC TCTC		
		TTGT CCACTTTGGG AGAG		
		A AC		
GAM2021	LOC158549 5'	GAGATAGGGGTTTCACCGTGTT 88224		—
		AACACGGTGAAACCCC ATCTC		
		TTGTGCCACTTTGGGG TAGAG		
		A		
GAM2021	LOC158668 3'	GAGGTGGGGTTTCACCATG 69901	C	
		CA GGTGAAACCCCATCTC		
		GT CCACTTTGGGGTGGAG		
		A		
GAM2021	LOC158865 5'	GAGATGGGGACTTCACCGTGTT 88309	A_	
		AACACGGTGAA CCCCATCTC		
		TTGTGCCACTT GGGGTAGAG		
		CA		
GAM2021	LOC160646 3'	GAGATGGGGCTTCACCATGTT 83113	C	A
		AACA GGTGAA CCCCATCTC		
		TTGT CCACTT GGGGTAGAG		
		A C		
GAM2021	LOC161829 3'	GAGATGGGGTTTCACCATGTT 83190	C	
		AACA GGTGAAACCCCATCTC		
		TTGT CCACTTTGGGGTAGAG		
		A		
GAM2021	LOC162427 3'	ATGGGGTTTCACCATGTT 83220	C	
		AACA GGTGAAACCCCAT		
		TTGT CCACTTTGGGGTA		
		A		
GAM2021	LOC169611 3'	GAGACAGAGTTTCGCTTTTGTT 83649	C_	CCCA
		AACA GGTGAAAC TCTC		
		TTGT TCGCTTTG AGAG		
		TT AGAC		
GAM2021	LOC170082 5'	GAGATGGGGTTTCACCATGTT 83443	C	
		AACA GGTGAAACCCCATCTC		

			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2021	LOC196047	5'	GAGCCAGGGTTTCACCATGT	91154	C CAT
			ACA GGTGAAACCC CTC		
			TGT CCACTTTGGG GAG		
			A ACC		
GAM2021	LOC196205	3'	AGATGGGGCATCATGT	88973	C AAA
			ACA GGTG CCCCATCT		
			TGT CTAC GGGGTAGA		
			A _		
GAM2021	LOC196411	3'	GAGATGGGGTTTCACTATGTT	89047	CG
			AACA GTGAAACCCCATCTC		
			TTGT CACTTTGGGGTAGAG		
			AT		
GAM2021	LOC196529	3'	GAGACAGGGTCTCACTGTGTT	89133	A CA
			AACACGGTGA ACCC TCTC		
			TTGTGTCACT TGGG AGAG		
			C AC		
GAM2021	LOC196529	3'	GAGACAGGGTTTCACTACGTT	89134	AC CA
			AAC GGTGAAACCC TCTC		
			TTG TCACTTTGGG AGAG		
			CA AC		
GAM2021	LOC197358	3'	GAGACGGGGTTTCATCATGTT	89432	C A
			AACA GGTGAAACCC TCTC		
			TTGT CTACTTTGGGG AGAG		
			A C		
GAM2021	LOC197358	3'	GAGATGGGGTTTCACCATGTT	89433	C
			AACA GGTGAAACCCCATCTC		
			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2021	LOC199699	3'	AGACAGGGTTTCACCGTGTT	89664	CA
			AACACGGTGAAACCC TCT		
			TTGTGCCACTTTGGG AGA		
			AC		
GAM2021	LOC199786	3'	GAGACGGTGGGTTTCACCATGTT	89753	C _ A
			AACA GGTGAAACC CC TCTC		
			TTGT CCACTTTGG GG AGAG		
			A T C		
GAM2021	LOC199786	3'	GAGATGGGGTTTCACCATGTT	89754	C
			AACA GGTGAAACCCCATCTC		

		TTGT CCACTTTGGGGTAGAG		
		A		
GAM2021	LOC199906 3'	AGACAGGGTTTCATCATGTT 89842	C	CA
		AACA GGTGAAACCC TCT		
		TTGT CTACTTTGGG AGA		
		A AC		
GAM2021	LOC200014 3'	GAGACGGTGTTTCACCATGTT 89935	C	C A
		AACA GGTGAAAC CC TCTC		
		TTGT CCACTTTG GG AGAG		
		A T C		
GAM2021	LOC200107 5'	GATCCGGTTTCATCGTGTT 89987		CC
		AACACGGTGAAACC ATC		
		TTGTGCTACTTTGG TAG		
		CC		
GAM2021	LOC200169 5'	GAGACGGAGTTTCACCATGTT 91556	C	C A
		AACA GGTGAAAC CC TCTC		
		TTGT CCACTTTG GG AGAG		
		A A C		
GAM2021	LOC200268 3'	GAGATGGGATTTTGCCATGTT 90086	C TG	C
		AACA GG AAA CCCATCTC		
		TTGT CC TTT GGGTAGAG		
		A GT A		
GAM2021	LOC200301 5'	GAGACGGGGTTTCACCGTGTT 90140		A
		AACACGGTGAAACCCC TCTC		
		TTGTGCCACTTTGGGG AGAG		
		C		
GAM2021	LOC200310 3'	GAGACGGGGTTTCACCATGTT 66327	C	A
		AACA GGTGAAACCCC TCTC		
		TTGT CCACTTTGGGG AGAG		
		A C		
GAM2021	LOC200316 3'	GACTGGGTTTCACCATGTT 90181	C	CA
		AACA GGTGAAACCC TC		
		TTGT CCACTTTGGG AG		
		A TC		
GAM2021	LOC200316 3'	GAGACGGAGTTTCACTCTGT 90182	C	C A
		ACA GGTGAAAC CC TCTC		
		TGT TCACTTTG GG AGAG		
		C A C		
GAM2021	LOC200316 5'	GAGACGGGGTTTCTCCATGTT 90183	C T	A
		AACA GG GAAACCCC TCTC		

		TTGT CC CTTTGGGG AGAG		
		A T C		
GAM2021	LOC200339 3'	GAGATGGGATTTTCCCTTGTT 91616	C TG C	
		AACA GG AAA CCCATCTC		
		TTGT CC TTT GGGTAGAG		
		T CT A		
GAM2021	LOC200407 3'	GAGACAGGGTTTTGCCATGTT 91627	C TG CA	
		AACA GG AAACCC TCTC		
		TTGT CC TTTGGG AGAG		
		A GT AC		
GAM2021	LOC200845 5'	GAGATGGGGTTTCACTATGTT 90317	CG	
		AACA GTGAAACCCCATCTC		
		TTGT CACTTTGGGGTAGAG		
		AT		
GAM2021	LOC200860 3'	GAGACGGGGTTTCGCTCTTGT 91748	C _ A	
		ACA G GTGAAACCC TCTC		
		TGT C CGCTTTGGGG AGAG		
		T T C		
GAM2021	LOC200860 3'	GAGACGGGGTTTCTCCATGTT 91749	C T A	
		AACA GG GAAACCC TCTC		
		TTGT CC CTTTGGGG AGAG		
		A T C		
GAM2021	LOC201164 3'	GAGACAGGGTTTCACCATGTT 89494	C CA	
		AACA GGTGAAACCC TCTC		
		TTGT CCACTTTGGG AGAG		
		A AC		
GAM2021	LOC201173 5'	GAGACGGAGTTTCACCATGTT 88685	C C A	
		AACA GGTGAAAC CC TCTC		
		TTGT CCACTTTG GG AGAG		
		A A C		
GAM2021	LOC201220 5'	GAGATGGAGTTTCACCATGTT 88720	C C	
		AACA GGTGAAAC CCATCTC		
		TTGT CCACTTTG GGTAGAG		
		A A		
GAM2021	LOC201294 3'	GAGACGGGGTTTCACCATGTT 89584	C A	
		AACA GGTGAAACCC TCTC		
		TTGT CCACTTTGGGG AGAG		
		A C		
GAM2021	LOC201411 3'	GAGACAGGGTTTCACCATGTT 63642	C CA	
		AACA GGTGAAACCC TCTC		

	TTGT CCACTTTGGG AGAG		
	A AC		
GAM2021 LOC201411 3'	GAGATGGAGTTTCGTTCTCGT 63643	___	C
	ACGG TGAAAC CCATCTC		
	TGCT GCTTTG GGTAGAG		
	CTT A		
GAM2021 LOC201626 3'	GAGATGGAGTTTCACTCTTGT 90433	C _	C
	ACA G GTGAAAC CCATCTC		
	TGT C CACTTTG GGTAGAG		
	T T A		
GAM2021 LOC201627 3'	GAGATGGGGTTTCTCCATGTT 90455	C T	
	AACA GG GAAACCCCATCTC		
	TTGT CC CTTTGGGGTAGAG		
	A T		
GAM2021 LOC201696 3'	GAGATGGAGTTTCACTCTTGT 63820	C _	C
	ACA G GTGAAAC CCATCTC		
	TGT C CACTTTG GGTAGAG		
	T T A		
GAM2021 LOC202347 3'	GAGATGACTTAAATCACTGTGT 91945		AACCC_
T	AACACGGTGA CATCTC		
	TTGTGTCACT GTAGAG		
	AAATTCA		
GAM2021 LOC202460 5'	GAGATGGGGTTTCACCATGT 90671	C	
	ACA GGTGAAACCCCATCTC		
	TGT CCACTTTGGGGTAGAG		
	A		
GAM2021 LOC202908 5'	GAGATGAGGTTTCACTCTGTT 90724	C	C
	AACA GGTGAAACC CATCTC		
	TTGT TCACTTTGG GTAGAG		
	C A		
GAM2021 LOC202908 5'	GAGATGGGGTCTCACCCCTGT 90725	C	A
	ACA GGTGA ACCCCATCTC		
	TGT CCACT TGGGGTAGAG		
	C C		
GAM2021 LOC203197 3'	GAGATGGGGTTTCGCCATGTT 90812	C	
	AACA GGTGAAACCCCATCTC		
	TTGT CCGCTTTGGGGTAGAG		
	A		
GAM2021 LOC203339 3'	GAGATGGGGTTTCACCATGTT 92211	C	
	AACA GGTGAAACCCCATCTC		

	TTGT CCACTTTGGGGTAGAG		
	A		
GAM2021 LOC203350 3'	GAGACGGGGTTTCACCGTGTT 92240	A	
	AACACGGTGAAACCCC TCTC		
	TTGTGCCACTTTGGGG AGAG		
	C		
GAM2021 LOC203369 3'	GATGGGGTTTCACTGTGTT 90889		
	AACACGGTGAAACCCCATC		
	TTGTGTCACTTTGGGGTAG		
GAM2021 LOC204804 3'	GAGACAGGGTCTCACTGTGT 91043	A	CA
	ACACGGTGA ACCC TCTC		
	TGTGTCACT TGGG AGAG		
	C AC		
GAM2021 LOC204804 3'	GAGATGAGGTTTACCTTGTT 91044	C	C
	AACA GGTGAAACC CATCTC		
	TTGT CCACTTTGG GTAGAG		
	T A		
GAM2021 LOC205251 5'	GACAGGGTTTCACCATGTT 92357	C	CA
	AACA GGTGAAACCC TC		
	TTGT CCACTTTGGG AG		
	A AC		
GAM2021 LOC219445 5'	GACGGGGTTTCACCGTGTT 93204		A
	AACACGGTGAAACCCC TC		
	TTGTGCCACTTTGGGG AG		
	C		
GAM2021 LOC219735 3'	GAGACGGGGTTTCACCGTGTT 94728		A
	AACACGGTGAAACCCC TCTC		
	TTGTGCCACTTTGGGG AGAG		
	C		
GAM2021 LOC219736 3'	GAGATGGGGTTTTGCCATGTT 94741	C	TG
	AACA GG AAACCCCATCTC		
	TTGT CC TTTGGGGTAGAG		
	A GT		
GAM2021 LOC219894 3'	GAGATGGGGTTTTCACCGTGTT 94905		
	AACACGGTGAAACCCCATCTC		
	TTGTGCCACTTTGGGGTAGAG		
GAM2021 LOC220064 3'	GAGATGGGGTTTTGCCTTGTT 95066	C	TG
	AACA GG AAACCCCATCTC		

		TTGT CC TTTGGGGTAGAG		
		T GT		
GAM2021	LOC220074 3'	GAGACAAGGTTTCGCCATGTT 59978	C	CCA
		AACA GGTGAAACC TCTC		
		TTGT CCGCTTTGG AGAG		
		A AAC		
GAM2021	LOC220074 3'	GAGACGGGGTTTCACCATGTT 59981	C	A
		AACA GGTGAAACCCC TCTC		
		TTGT CCACTTTGGGG AGAG		
		A C		
GAM2021	LOC220074 3'	GAGATGGGGTTTCGCCATGTT 59982	C	
		AACA GGTGAAACCCCATCTC		
		TTGT CCGCTTTGGGGTAGAG		
		A		
GAM2021	LOC221042 3'	GAGACGGGGTTTGCTGTGTT 94802	G	A
		AACACGGT AAACCCC TCTC		
		TTGTGTCG TTTGGGG AGAG		
		- C		
GAM2021	LOC221060 3'	GACGGTGTTCACCATGTT 94832	C	C A
		AACA GGTGAAAC CC TC		
		TTGT CCACTTTG GG AG		
		A T C		
GAM2021	LOC221271 3'	GAGGGGGTTTCATCATGTT 93518	C	A
		AACA GGTGAAACCCC TC		
		TTGT CTACTTTGGGG AG		
		A G		
GAM2021	LOC221296 3'	GAGACGGGGTTTCACCATG 93609	C	A
		CA GGTGAAACCCC TCTC		
		GT CCACTTTGGGG AGAG		
		A C		
GAM2021	LOC221663 5'	GAGACAAGGTTTCACTATGTT 95461	CG	CCA
		AACA GTGAAACC TCTC		
		TTGT CACTTTGG AGAG		
		AT AAC		
GAM2021	LOC221814 3'	GAGATGAAGGGGTTTCCAGGTT 95556	ACGGT	___
		AAC GAAACCCC ATCTC		
		TTG CTTTGGGG TAGAG		
		GAC__ AAG		
GAM2021	LOC221964 3'	GAGACAGGGTTTTGCCGTGTT 95606	TG	CA
		AACACGG AAACCC TCTC		

		TTGTGCC TTTGGG AGAG		
		GT AC		
GAM2021	LOC222068 3'	GAGATGGGGTTTTACCATGTT 94276	C	
		AACA GGTGAAACCCCATCTC		
		TTGT CCATTTTGGGGTAGAG		
		A		
GAM2021	LOC222070 5'	GAGACGGTGTTCACCATGTT 95816	C	C A
		AACA GGTGAAAC CC TCTC		
		TTGT CCACTTTG GG AGAG		
		A T C		
GAM2021	LOC222224 5'	GAGACAGGGTTTCACCATGTT 95872	C	CA
		AACA GGTGAAACCC TCTC		
		TTGT CCACTTTGGG AGAG		
		A AC		
GAM2021	LOC245771 5'	GAGATGGGGTTTCATCATGTT 94477	C	
		AACA GGTGAAACCCCATCTC		
		TTGT CTACTTTGGGGTAGAG		
		A		
GAM2021	LOC253664 3'	GAGATGGGGTTTCCCATGTT 96466	C T	
		AACA GG GAAACCCCATCTC		
		TTGT CC CTTTGGGGTAGAG		
		A C		
GAM2021	LOC253666 3'	GAGACGGGGTTTCACCATGTT 96761	C	A
		AACA GGTGAAACCC TCTC		
		TTGT CCACTTTGGGG AGAG		
		A C		
GAM2021	LOC253805 3'	GAGATAGGGTTTCACAATGTT 98176	CG	C
		AACA GTGAAACCC ATCTC		
		TTGT CACTTTGGG TAGAG		
		AA A		
GAM2021	LOC254018 5'	GAGATGGGGTTTCGCCATGTT 98740	C	
		AACA GGTGAAACCCCATCTC		
		TTGT CCGCTTTGGGGTAGAG		
		A		
GAM2021	LOC254100 3'	GAGATGGGGTTTCGTCATGTT 98155	C GT	
		AACA G GAAACCCCATCTC		
		TTGT C CTTTGGGGTAGAG		
		A TG		
GAM2021	LOC254268 3'	GAGATGGGGTTTCACCATGTT 97143	C	
		AACA GGTGAAACCCCATCTC		

		TTGT CCACTTTGGGGTAGAG		
		A		
GAM2021	LOC254295 5'	GAGACGGGGTTTCACCGTGTT 97891		A
		AACACGGTGAAACCCC TCTC		
		TTGTGCCACTTTGGGG AGAG		
		C		
GAM2021	LOC254351 5'	GACGGGGTTTCTCCGTGTT 96688	T	A
		AACACGG GAAACCCC TC		
		TTGTGCC CTTTGGGG AG		
		T C		
GAM2021	LOC254351 3'	GAGACGGAGTTTTCACCCTTGT 96689	C_	C A
		ACA GGTGAAAC CC TCTC		
		TGT CCACTTTG GG AGAG		
		TC A C		
GAM2021	LOC254413 5'	GAGACAGGGAGAGCTGTGTT 98913	GAAA	CA
		AACACGGT CCC TCTC		
		TTGTGTCTG GGG AGAG		
		AGA_ AC		
GAM2021	LOC254655 3'	GAGACGGGGTTTCACCATGTT 97220	C	A
		AACA GGTGAAACCCC TCTC		
		TTGT CCACTTTGGGG AGAG		
		A C		
GAM2021	LOC254778 3'	AGACAGGATTTTGCTGTGTT 97826	TG	C CA
		AACACGG AAA CC TCT		
		TTGTGTC TTT GG AGA		
		GT A AC		
GAM2021	LOC255037 3'	GAGACGAAGTCTCGCTGTGT 98439	A	CCCA
		ACACGGTGA AC TCTC		
		TGTGTCGCT TG AGAG		
		C AAGC		
GAM2021	LOC255308 3'	GAGACGGGGTTTCGGCATGTT 96176	CGG	A
		AACA TGAAACCCC TCTC		
		TTGT GCTTTGGGG AGAG		
		ACG C		
GAM2021	LOC255338 5'	GAGACAGGGGCATCACTGTGTT 97632	AA	CA
		AACACGGTGA CCC TCTC		
		TTGTGTCACT GGG AGAG		
		AC AC		
GAM2021	LOC255465 3'	GAGACGGGGTTTCACCATGTT 99114	C	CA
		AACA GGTGAAACCCC TCTC		

		TTGT CCACTTTGGG AGAG		
		A C_		
GAM2021	LOC255497 3'	GAGACGGGGTTTCACCATGTT 98985	C	A
		AACA GGTGAAACCCC TCTC		
		TTGT CCACTTTGGGG AGAG		
		A C		
GAM2021	LOC256221 3'	GAGACGGGGTTTCACCGTGTT 96910		A
		AACACGGTGAAACCCC TCTC		
		TTGTGCCACTTTGGGG AGAG		
		C		
GAM2021	LOC256306 3'	GAGACGGGGTTTCACCATGTT 98515	C	A
		AACA GGTGAAACCCC TCTC		
		TTGT CCACTTTGGGG AGAG		
		A C		
GAM2021	LOC256965 5'	GAGATAGGTTCACTGTG 99418	A CC	
		CACGGTGAA CC ATCTC		
		GTGTCACTT GG TAGAG		
		_ A_		
GAM2021	LOC257465 3'	GAGATGGTGTTTCACCATGTT 82496	C	C
		AACA GGTGAAAC CCATCTC		
		TTGT CCACTTTG GG TAGAG		
		A T		
GAM2021	LOC257486 3'	GAGACGGGGTTTCACCATGTT 69771	C	A
		AACA GGTGAAACCCC TCTC		
		TTGT CCACTTTGGGG AGAG		
		A C		
GAM2021	LOC51008 5'	GAGATGGGGTTTCTCCATGTT 32533	C T	
		AACA GG GAAACCCCATCTC		
		TTGT CC CTTTGGGGTAGAG		
		A T		
GAM2021	LOC51193 5'	GAGACGGGGTTTCCCATGTT 33367	C T	A
		AACA GG GAAACCCC TCTC		
		TTGT CC CTTTGGGG AGAG		
		A C C		
GAM2021	LOC51219 5'	GAGACGGGGTTTCTCCATGT 33545	C T	A
		ACA GG GAAACCCC TCTC		
		TGT CC CTTTGGGG AGAG		
		A T C		
GAM2021	LOC51696 3'	GAGACAGCGTTTCACCATGTT 33083	C	CCCA
		AACA GGTGAAAC TCTC		

		TTGT CCACTTTG AGAG		
		A CGAC		
GAM2021	LOC56181	5' GAGACAGGGCTTCACTGTGTT 97273	A	CA
		AACACGGTGAA CCC TCTC		
		TTGTGTCACTT GGG AGAG		
		C AC		
GAM2021	LOC57107	3' GAGATGGGGTTTCACTATGTT 40188	CG	
		AACA GTGAAACCCCATCTC		
		TTGT CACTTTGGGGTAGAG		
		AT		
GAM2021	LOC57146	3' GATGGGGTTTCACCATGTT 40296	C	
		AACA GGTGAAACCCCATC		
		TTGT CCACTTTGGGGTAG		
		A		
GAM2021	LOC81034	3' ATGGGGTTTCACCATGTT 48581	C	
		AACA GGTGAAACCCCAT		
		TTGT CCACTTTGGGGTA		
		A		
GAM2021	LOC89231	3' GAGATGGGGTCTCACTATGTT 94299	CG	A
		AACA GTGA ACCCCATCTC		
		TTGT CACT TGGGGTAGAG		
		AT C		
GAM2021	LOC89919	3' GAGACGGGGTTTCACCATGTT 61374	C	A
		AACA GGTGAAACCCC TCTC		
		TTGT CCACTTTGGGG AGAG		
		A C		
GAM2021	LOC89932	3' GAGACGGGGTTTCTCCATGTT 61462	C T	A
		AACA GG GAAACCCC TCTC		
		TTGT CC CTTTGGGG AGAG		
		A T C		
GAM2021	LOC89932	3' GAGATGGGGTTTCACCATGTT 61463	C	
		AACA GGTGAAACCCCATCTC		
		TTGT CCACTTTGGGGTAGAG		
		A		
GAM2021	LOC90288	3' GAGACGGGGTTTCACAGTGTT 62789	G	A
		AACAC GTGAAACCCC TCTC		
		TTGTG CACTTTGGGG AGAG		
		A C		
GAM2021	LOC90288	3' GAGAGGGAGTCTCACCGTGT 62790	A _	A
		ACACGGTGAC AC CCC TCTC		

			TGTGCCACT TG GGG AGAG		
			C A _		
GAM2021	LOC90333	3'	GAGACTGGGTTTCACCGTGTT 62959		CA
			AACACGGTGAAACCC TCTC		
			TTGTGCCACTTTGGG AGAG		
			TC		
GAM2021	LOC90459	3'	GAGGCGGGGTTTCACCATGTT 63556	C	AT
			AACA GGTGAAACCCC CTC		
			TTGT CCACTTTGGGG GAG		
			A CG		
GAM2021	LOC90485	3'	GAGGCAGGGTTTCACCATGTT 63700	C	CA
			AACA GGTGAAACCC TCTC		
			TTGT CCACTTTGGG GGAG		
			A AC		
GAM2021	LOC90485	3'	GAGGCGGGGTTTCACCATGTT 63701	C	AT
			AACA GGTGAAACCCC CTC		
			TTGT CCACTTTGGGG GAG		
			A CG		
GAM2021	LOC90591	3'	GAGACGGAGTTTCATCGTGTT 64170		C A
			AACACGGTGAAAC CC TCTC		
			TTGTGCTACTTTG GG AGAG		
			A C		
GAM2021	LOC91012	5'	GAGACAAGGTTTTGCCATGTT 65245	C TG	CCA
			AACA GG AAACC TCTC		
			TTGT CC TTTGG AGAG		
			A GT AAC		
GAM2021	LOC91115	3'	GAGATGGAGTTTCACTCTTGT 65565	C _	C
			ACA G GTGAAAC CCATCTC		
			TGT C CACTTTG GG TAGAG		
			T T A		
GAM2021	LOC91115	3'	GAGATGGGGTTTCACTGTGTT 65566		
			AACACGGTGAAACCCCATCTC		
			TTGTGTCACTTTGGGGTAGAG		
GAM2021	LOC91115	3'	GAGATGGGGTTTCATCATGTT 65567	C	
			AACA GGTGAAACCCCATCTC		
			TTGT CTACTTTGGGGTAGAG		
			A		
GAM2021	LOC91250	5'	GAGATGGGGTTTCATCATGTT 65916	C	
			AACA GGTGAAACCCCATCTC		

			TTGT CTA	TTTGGGG	TAGAG		
			A				
GAM2021	LOC91291	5'	GAGACAAGG	TTTCACCCTGTT	66089	C	CCA
			AACA	GGTGAAACC	TCTC		
			TTGT	CCACTTTGG	AGAG		
			C	AAC			
GAM2021	LOC91373	3'	GAGATGGGG	TTTGACCGTGTT	66414	G	
			AACACGGT	AAACCCCATCTC			
			TTGTGCCA	TTTGGGGTAGAG			
			G				
GAM2021	LOC91561	5'	GACGGGG	TTTCTCCATGTT	67044	C T	A
			AACA	GGGAAACCCC	TC		
			TTGT	CCCTTTGGGG	AG		
			A	T	C		
GAM2021	LOC91893	3'	GAGACGAGG	TTTCACCGTGTT	68072		CCA
			AACACGGT	GAAACC	TCTC		
			TTGTGCCA	CTTTGG	AGAG		
			AGC				
GAM2021	LOC92148	5'	GAGACGGGG	TTTCACCGTGTT	68879		A
			AACACGGT	GAAACCCC	TCTC		
			TTGTGCCA	CTTTGGGG	AGAG		
			C				
GAM2021	LOC92303	3'	GAGATGGGG	TTTCACCATGTT	69392	C	C
			AACA	GGTGAAACCC	ATCTC		
			TTGT	CCACTTTGGG	TAGAG		
			A				
GAM2021	LOC92482	3'	GAGATGAGG	TCTTGCTTTGTT	70021	C TG A	C
			AACA	GG AACC	CATCTC		
			TTGT	TC T TGG	G TAGAG		
			T	GT C	A		
GAM2021	LOC92661	5'	GAGGCGGGG	TTTCACTGTGTT	70630		AT
			AACACGGT	GAAACCCC	CTC		
			TTGTGTCA	CTTTGGGG	GAG		
			CG				
GAM2021	LOC92689	3'	GAGACAGGG	TTTCACCATGTT	70775	C	CA
			AACA	GGTGAAACCC	TCTC		
			TTGT	CCACTTTGGG	AGAG		
			A	AC			
GAM2021	LOC92697	5'	GAGACGGGG	TTTCGCTGTGTT	70811		A
			AACACGGT	GAAACCCC	TCTC		

			TTGTGTCGCTTTGGGG AGAG		
			C		
GAM2021	LOC92841	3'	GAGACAGGGTTTCACCATGTT 71253	C	CA
			AACA GGTGAAACCC TCTC		
			TTGT CCACTTTGGG AGAG		
			A AC		
GAM2021	LOC92841	3'	GAGACGGGGTTTCACCATGTT 71254	C	A
			AACA GGTGAAACCC TCTC		
			TTGT CCACTTTGGGG AGAG		
			A C		
GAM2021	LOC93129	3'	GAGACGGGGTTTCGCTGT 71957		A
			ACGGTGAAACCC TCTC		
			TGTCGCTTTGGGG AGAG		
			C		
GAM2021	LOC93349	3'	GAGACGGGGTTTCACTATGTT 57268	CG	A
			AACA GTGAAACCC TCTC		
			TTGT CACTTTGGGG AGAG		
			AT C		
GAM2022	GPD1	3'	TCATGCCACCACATTTG 60398	C	C
			TAAATG GGTGGCAT GA		
			GTTTAC CCACCGTA CT		
			A _		
GAM2022	IL5RA	5'	TCGCATGGCCACCGCATTT 6906		AT__
			AAATGCGGTGGC CGA		
			TTTACGCCACCG GCT		
			GTAC		
GAM2022	MYO1C	3'	TGCCGATGCCAAATATTTG 61873	CGG	A
			TAAATG TGGCATCG CA		
			GTTTAT ACCGTAGC GT		
			AA_ C		
GAM2022	C6orf37	3'	TGTCACACTGCATTTA 68097		GCATC
			TAAATGCGGTG GACA		
			ATTTACGTCAC CTGT		
			A__		
GAM2022	DNAJC6	3'	TTGCAGAACCACCGCATT 29498		CA GA
			AATGCGGTGG TC CAA		
			TTACGCCACC AG GTT		
			A_ AC		
GAM2022	FLJ11210	3'	GTCGATGTGCATGCTTTTA 60319	T	GTG
			TAAA GCG GCATCGAC		

	ATTT CGT TGTAGCTG	
	T ACG	
GAM2022 FLJ12476 3'	TCGATCTTCTGCATTTA 43270	T C
	TAAATGCGG GG ATCGA	
	ATTTACGTC TC TAGCT	
	T _	
GAM2022 KIAA1034 3'	TCGATGGCATCCGCATTTG 63134	_ G
	TAAATGCGG TG CATCGA	
	GTTTACGCC AC GTAGCT	
	T G	
GAM2022 KIAA1987 3'	TCATGTAAGTGCATTTA 89391	G C
	TAAATGCGGT GCAT GA	
	ATTTACGTCA TGTA CT	
	A _	
GAM2022 MGC16063 3'	TGTCCTGGCCACTGCATT 54929	ATC
	AATGCGGTGGC GACA	
	TTACGTCACCG CTGT	
	GTC	
GAM2022 LOC147949 3'	TGTCAGATGTCCACATTGCA 79279	_ _ _
	TGCG GTGG CATC GACA	
	ACGT CACC GTAG CTGT	
	TA T A	
GAM2022 LOC150577 3'	GTCCTCACCGCATTTG 86258	CATC
	TAAATGCGGTGG GAC	
	GTTTACGCCACT CTG	
	C _	
GAM2022 LOC158219 3'	TGTGTGTCACCACATTT 82694	C CG
	AAATG GGTGGCAT ACA	
	TTTAC CCACTGTG TGT	
	A _	
GAM2022 LOC202020 3'	TGTCTCACACATTTA 90605	C CATC
	TAAATG GGTGG GACA	
	ATTTAC CCACT CTGT	
	A _	
GAM2022 LOC90826 5'	TGTCGATGCAGGTTTATTTG 64788	CGGTG
	TAAATG GCATCGACA	
	GTTTAT CGTAGCTGT	
	TTGGA	
GAM2022 LOC93587 3'	TTGTCTTTACCTGCATTTA 73042	_ CATC
	TAAATGC GGTGG GACAA	

ATTTACG CCATT CTGTT
 T T___
 GAM2023 ATOX1 5' ACGGTGACCCGCGTGTGCG 15748 G _ AA
 CG ATG GC GTCACCGT
 || ||| || |||||
 GC TGT CG CAGTGGCA
 G G CC
 GAM2023 ATP8B2 5' ACGGTGAAGTGATCTGTGAA 65828 G AAG
 TTCACGGAT GC TCACCGT
 ||||| || |||||
 AAGTGTCTA TG AGTGGCA
 G A___
 GAM2023 MUCDHL 3' ACGGTGACCTCTGGCACCG 88633 A G A___
 CGG TG CA GTCACCGT
 ||| || |||||
 GCC AC GT CAGTGGCA
 _ G CTC
 GAM2023 CGRP-RCP 3' ACGGTGACTCATGCTTGT 27882 GAT _
 ACG GGCA AGTCACCGT
 || ||| |||||
 TGT TCGT TCAGTGGCA
 _ AC
 GAM2023 FLJ10898 3' ACAGTGAATGTAGTCCGTGAA 60121 G AG C
 TTCACGGAT GCA TCAC GT
 ||||| || ||| ||
 AAGTGCCTG TGT AGTG CA
 A A_ A
 GAM2023 FLJ10932 3' ACAGTGCCTTTCCATCCGTGAA 37421 C T C
 TTCACGGATGG AAG CAC GT
 ||||| ||| ||| ||
 AAGTGCCTACC TTC GTG CA
 T C A
 GAM2023 FLJ22477 3' ACGGTGACTGTGGCCTTGAA 45664 C ATG A
 TTCA GG GCA GTCACCGT
 ||| || ||| |||||
 AAGT CC TGT CAGTGGCA
 T GG_ _
 GAM2023 MGC3020 3' ACGGTGACTAAAAGCCCCTGAA 44121 C AT A___
 TTCA GG GGC AGTCACCGT
 ||| || ||| |||||
 AAGT CC CCG TCAGTGGCA
 _ _ AAAA
 GAM2023 LOC168283 5' ACGGTGGTGCACCATCCTGAA 83575 C CAA
 TTCA GGATGG GTCACCGT
 ||| ||||| |||||
 AAGT CCTACC TGGTGGCA
 _ ACG
 GAM2023 LOC200125 5' GGTTCCTCTGCCATCCTGAA 91537 C _ TC
 TTCA GGATGGCA AG ACC
 ||| ||||| || |||

		AAGT CCTACCGT TC TGG		
		— C CT		
GAM2023	LOC202134 5'	GGATGCCTGCCATTCATGAA 91924	C	A CA
		TTCA GGATGGCA GT CC		
		AAGT CTTACCGT CG GG		
		A C TA		
GAM2024	CENPF 3'	ACACATTTTATTCTTCTAAT 33415		CTAAC
		ATTAGAAGAATGAA GTGT		
		TAATCTTCTTATTT CACA		
		TA__		
GAM2025	CDH12 3'	CTTATCATTTAAAGTGGTGTA 15777		CCCAA GA
		TACACCACT GAA ATAAG		
		ATGTGGTGA TTT TATTC		
		AA__ AC		
GAM2025	GOCAP1 3'	ATTGTTCTTGGGAGCAGTGTA 43007	CA	G
		TACAC CTCCCAAGAA AAT		
		ATGTG GAGGGTTCTT TTA		
		AC G		
GAM2025	DKFZp434N2435 5'	CTTATTACTGTGGGGTGGT 98090	T	AGAAG
		ACCAC CCCA AATAAG		
		TGGTG GGGT TTATTC		
		— GTCA_		
GAM2025	DKFZP564I122 3'	CTTATTCTTCTCCCTCATGTGT 63877		CACTCCCA
	A	TACAC AGAAGAATAAG		
		ATGTG TCTTCTTATTC		
		TACTCCC_		
GAM2025	FLJ21791 3'	CTTATTTGCAGAAAGTGGTGTA 62126		CCCAAGAA
		TACACCACT GAATAAG		
		ATGTGGTGA TTTATTC		
		AGACG__		
GAM2025	HMP19 3'	CTTATTCTTTGTTAGGAAAATG 88860	CCAC	CAA_
	TA	TACA TCC GAAGAATAAG		
		ATGT AGG TTTCTTATTC		
		AAA_ ATTG		
GAM2025	KIAA1719 3'	TCTGTCTTGGGAGTGGTGTA 68742		—
		TACACCACTCCCAAGA AGA		
		ATGTGGTGAGGGTTCT TCT		
		G		
GAM2025	KIAA1853 3'	TTTTTCTTGGAAGCAGTG 69929	CA	C
		CAC CT CCAAGAAGAA		

		GTG GA GGTTCCTTTT		
		AC A		
GAM2025 KIAA1877	3'	CTTATTCTTCTGCCATGAGT 66748	CCA__	
		ACTC AGAAGAATAAG		
		TGAG TCTTCTTATTC		
		TACCG		
GAM2025 KIAA1906	3'	CTTATTCTTCTTGACTTTTGG 73571	CTCC_	
		CCA CAAGAAGAATAAG		
		GGT GTTCTTCTTATTC		
		TTTCA		
GAM2025 OSBPL11	3'	CTTAATTTCCCAAGAGTGGTG 43206	CCAA AA	
		CACCACTC GAAG TAAG		
		GTGGTGAG CTTT ATTC		
		AACC A_		
GAM2025 YME1L1	3'	TCATTCTTGATGTGGTGTA 58438	TCC _	
		TACACCAC CAAGAA GA		
		ATGTGGTG GTTCTT CT		
		TA_ A		
GAM2025 ZNF262	3'	CTTATTTTGTGTTGGGAGT 18723	A	
		ACTCCCAAG AGAATAAG		
		TGAGGGTTT TTTTATTC		
		G		
GAM2025 LOC91960	3'	TGTGGCTTGGAACGTGGTGTA 68294	TC_ AAGA	
		TACACCAC CCAAG ATA		
		ATGTGGTG GGTC TGT		
		CAA GG_		
GAM2026 FLJ20559	3'	GAACCTTCACCAAGATACAA 35833	CCG CGT	
		TTGTA TGGTGA GGTC		
		AACAT ACCACT CCAAG		
		AGA T_		
GAM2026 HT002	3'	GGTCCCCACCGACACAA 26799	AC ACGT TT	
		TTGT CGTGGTG GG CC		
		AACA GCACCAC CC GG		
		CA _ CT		
GAM2026 INA	3'	GGATATTTGTGTCACCAGAACAC 52175	ACCG TG _	
AA		TTGT TGGTGACG GT TCC		
		AACA ACCACTGT TA AGG		
		CAAG TT T		
GAM2026 KIAA1553	3'	GGAACCACATCAGCAGCAA 93567	ACCG G C	
		TTGT TG TGA GTGGTTCC		

			AACG AC ACT CACCAAGG		
			_____ G A		
GAM2026	LOC222224	3'	GAAGTGAGTCACCACAGCACGA 95871	ACC	GT G
			TTGT GTGGTGAC G TTC		
			AGCA CACCACTG T AAG		
			CGA AG G		
GAM2027	AQP6	3'	GGCCCCAGGCCCCAGC 55008	A	CTC
			GCTG GGCCTGGG GCC		
			CGAC CCGGACCC CGG		
			C _____		
GAM2027	GCK	5'	CCCAAGCGCCCAGCAATG 5682	A	_ _
			CATTGCTG GGC CT GGG		
			GTAACGAC CCG GA CCC		
			_ C A		
GAM2027	GGT1	5'	TGTCCCCAGGCCTCAGCAA 26439		CT
			TTGCTGAGGCCTGGG CG		
			AACGACTCCGGACCC GT		
			CT		
GAM2027	GNAT1	3'	GACGCACAGACTCAGCAAT 5721	GC	G _
			ATTGCTGAG CTG GC TC		
			TAACGACTC GAC CG AG		
			A_ A C		
GAM2027	HAS3	3'	AGGCAAGCGTGTTCAGCA 19231	CCT	G C
			TGCTGAGG G GCT GCCT		
			ACGACTCT T CGA CGGA		
			TG_ G A		
GAM2027	P23	3'	AGGCGAGCCCTCCCCAGCA 22751	A	CCT
			TGCTG GG GGGCTCGCCT		
			ACGAC CC CCCGAGCGGA		
			_ CT_		
GAM2027	SF1	3'	AGGCAGACAGCCTCAGCAA 17339	C	GG C
			TTGCTGAGGC TG CT GCCT		
			AACGACTCCG AC GA CGGA		
			_ A_ _		
GAM2027	SYN3	3'	GTCGCCTAGTCAGACCTCAGCA 14482	C	_____ CTCG
	AT		ATTGCTGAGG CTG GG C		
			TAACGACTCC GAC CC G		
			A TGA__T GCTC		
GAM2027	SYN3	3'	GTCGCCTAGTCAGACCTCAGCA 56904	C	_____ CTCG
	AT		ATTGCTGAGG CTG GG C		

			TAACGACTCC GAC	CC	G	
			A TGA__T GCTC			
GAM2027	SYN3	3'	GTCGCCTAGTCAGACCTCAGCA	56906	C _____	CTCG
	AT		ATTGCTGAGG CTG	GG	C	
			TAACGACTCC GAC	CC	G	
			A TGA__T GCTC			
GAM2027	WNT5A	3'	CTCAGAAGCATCAGCAATG	14120	G _	
			CATTGCTGA GC CTGGG			
			GTAACGACT CG GACTC			
			A AA			
GAM2027	ARGBP2	5'	AGGCAAGCTTTCCCTGCAAT	14589	TG CCT	C
			ATTGC AGG GGGCT GCCT			
			TAACG TCC TTCGA CGGA			
			_ CT_ A			
GAM2027	ATP9B	3'	AGGCAAGCCCAGGGCACAG	78971	AG _	C
			CTG GCC TGGGCT GCCT			
			GAC CGG ACCCGA CGGA			
			A_ G A			
GAM2027	ATP9B	3'	AGGCAAGCCCAGGGCACAG	78972	AG _	C
			CTG GCC TGGGCT GCCT			
			GAC CGG ACCCGA CGGA			
			A_ G A			
GAM2027	ATP9B	3'	AGGCAAGCCCAGGGCACAG	78973	AG _	C
			CTG GCC TGGGCT GCCT			
			GAC CGG ACCCGA CGGA			
			A_ G A			
GAM2027	ATP9B	3'	AGGCGAGCCCAGGGCACAG	78974	AG _	
			CTG GCC TGGGCTCGCCT			
			GAC CGG ACCCGAGCGGA			
			A_ G			
GAM2027	CALN1	3'	AGGCAAACCCAGTGGTTTCAGA	49659	G _	CTC
	AATG		CATT CTGAGGCC TGGG GCCT			
			GTAA GACTTTGG ACCC CGGA			
			A TG AAA			
GAM2027	CNR2	3'	GCGAGCCTCCAGGCCAGCAAT	10234	A _	
	G		CATTGCTG GGCCTGG GCTCGC			
			GTAACGAC CCGGACC CGAGCG			
			_ TC			
GAM2027	DKFZp434A171	3'	GGCTCGCCTAAACATAACCTCA	71342	CCT_____	CTCG
	GCAAT		ATTGCTGAGG GGG CC			

		TAACGACTCC	TCC	GG		
		AATACAAA__	GCTC			
GAM2027	DKFZp762L0311	3'	GTCGCCTAGACGGGCTTCAACA	38672	C	_____CTCG
		ATG	CATTG TGAGGCCTG	GG	C	
			GTAAC ACTTCGGGC	CC	G	
			A	AGA__T	GCTC	
GAM2027	FLJ12076	3'	AGCACCTGTGCCCTCAGCAATG	48020		_CT_ _
			CATTGCTGAGG	C	GG	GCT
			GTAACGACTCC	G	CC	CGA
			C	TGT	A	
GAM2027	FLJ20297	3'	AGGCAGGTGGGCCCCAGCAA	35369	A	GG TC
			TTGCTG GGCCT	GC	GCCT	
			AACGAC CCGGG	TG	CGGA	
			C	_	GA	
GAM2027	FLJ20297	3'	AGGCAGGTGGGCCCCAGCAA	36076	A	GG TC
			TTGCTG GGCCT	GC	GCCT	
			AACGAC CCGGG	TG	CGGA	
			C	_	GA	
GAM2027	KIAA1069	3'	AGTTCCAAACCCCAGCAATG	68525	A	CC _
			CATTGCTG	GG	TGGG	CT
			GTAACGAC	CC	ACCT	GA
			C	AA	T	
GAM2027	KIAA1272	3'	AGGCCTCACACAGGCCTCAGAA	70731	G	GGCTC_
		ATG	CATT	CTGAGGCCTG	GCCT	
			GTAA GACTCCGGAC	CGGA		
			A	ACACTC		
GAM2027	MGC:5244	3'	GGCCGGACCTCAGCAAT	49151		_ TG
			ATTGCTGAGG	CC	GGCT	
			TAACGACTCC	GG	CCGG	
			A	_		
GAM2027	LOC149194	3'	GCAAGCCCAGGTTGCCAGT	79984	A_	C
			GCTG	GGCCTGGGCT	GC	
			TGAC	TTGGACCCGA	CG	
			CG	A		
GAM2027	LOC150207	3'	GGCCGGACCTCAGCAAT	80596		_ TG
			ATTGCTGAGG	CC	GGCT	
			TAACGACTCC	GG	CCGG	
			A	_		
GAM2027	LOC158281	3'	AGGCGAGCCCTCCCCAGCA	82734	A	CCT
			TGCTG	GG	GGGCTCGCCT	

ACGAC CC CCCGAGCGGA
 _ CT_
 GAM2027 LOC163479 5' AGGCATATTCAAACCTCAGCAA 83021 GCC CTC
 TTGCTGAG TGGG GCCT
 ||||| ||| |||
 AACGACTC ACTT CGGA
 AAA ATA
 GAM2027 LOC220020 5' GATCCAGACCTCACCAATG 95045 C C C
 CATTG TGAGG CTGGG TC
 |||| |||| |||| ||
 GTAAC ACTCC GACCT AG
 C A _
 GAM2027 LOC256286 3' GGCCGGACCTCAGCAAT 96895 _ TG
 ATTGCTGAGG CC GGCT
 ||||| || |||
 TAACGACTCC GG CCGG
 A _
 GAM2027 LOC91632 3' AGCCGGACCTCAGCAAT 67314 _ TG
 ATTGCTGAGG CC GGCT
 ||||| || |||
 TAACGACTCC GG CCGA
 A _
 GAM2027 LOC93538 5' AGACGAGAACCTGCCTCAGCAA 72952 CT G_ C
 TTGCTGAGGC GG CTCG CT
 ||||| || ||| ||
 AACGACTCCG CC GAGC GA
 T_ AA A
 GAM2028 HSPE1 3' GCTGCCCATTCCTGAAGTT 10972 C_ CTC A
 AACTTCAG GA GG CAGC
 ||||| || || |||
 TTGAAGTC CT CC GTCG
 AC TAC _
 GAM2028 IFNW1 5' CTGGAGTTTAGCTGAAGTCTA 10982 A _ GGA
 TA ACTTCAGC GACTC CAG
 || ||||| |||| |||
 AT TGAAGTCG TTGAG GTC
 C AT _
 GAM2028 LPIN2 3' GCTGTCTGTGTGCTGAAG 28433 G T
 CTTTCAGC AC CGGACAGC
 ||||| || |||||
 GAAGTCG TG GTCTGTCTG
 _ T
 GAM2028 DKFZP434C131 3' GCTGCTTCACACTGAGGTTTCAG 69640 A CGACTC A
 CT AACTTCAG GG CAGC
 || ||||| || |||
 GA TTGGAGTC TC GTCG
 C AACT_ _
 GAM2028 HSD17B12 3' CTATCCGAGGTAATTTTGAAGT 32861 CGA_ C
 TTA TAACTTCAG CTCGGA AG
 ||||| |||| ||

		ATTGAAGTT	GAGCCT TC		
		TTAATG	A		
GAM2028	KIAA0097	3'	CTGTCCGTGGATGAGTTTAG	96500	T GCGACT
			CTAAACT CA	CGGACAG	
			GATTTGA GT	GCCTGTC	
			_ AGGT_		
GAM2028	KIAA0125	3'	GCTGTCCGGATGAAGT	29569	GCGAC
			ACTTCA	TCGGACAGC	
			TGAAGT	GGCCTGTCG	
			A_		
GAM2028	KIAA1371	3'	TTGGCCACTGAAGTTTAG	90480	CGACTC A
			CTAAACTTCAG	GG CAG	
			GATTTGAAGTC	CC GTT	
			A_ G		
GAM2028	PEAS	3'	CTGTACTCTGAAGTTCAG	55139	A CGACTC _
			CT AACTTCAG	GG ACAG	
			GA TTGAAGTC	TC TGTC	
			C _ A		
GAM2028	LOC128843	5'	CTGGAGGTTCTGAAGTTCAG	76292	A C CGGA
			CT AACTTCAG GACT	CAG	
			GA TTGAAGTC TTGG	GTC	
			C C AG_		
GAM2028	LOC145622	5'	GCCATCGGTGCGCTGAAG	77817	_ T ACA
			CTTCAGCG AC CGG	GC	
			GAAGTCGC TG GCT	CG	
			G _ AC_		
GAM2028	LOC202459	3'	TCCTGTCAATGAAGTTTA	59933	GC TC
			TAAACTTCA GAC	GGA	
			ATTTGAAGT CTG	CCT	
			AA T_		
GAM2028	LOC257445	5'	GCTGCTTCACACTGAGGTTTCAG	98383	A CGACTC A
			CT AACTTCAG	GG CAGC	
			GA TTGGAGTC	TC GTCG	
			C ACACT_ _		
GAM2029	ADAM17	3'	CACTACACTCCAGCCTGGGTGA	41842	C
			TCGCCCAGGCTGGAGTG	AGTG	
			AGTGGGTCCGACCTCAC	TCAC	
			A		
GAM2029	ADAM17	3'	CACTACACTCCAGCCTGGGTGA	41843	C
			TCGCCCAGGCTGGAGTG	AGTG	

			AGTGGGTCCGACCTCAC TCAC		
			A		
GAM2029	ADAT1	3'	GCACTCCAGCCTGGGTGA 24917		
			TCGCCCAGGCTGGAGTGC		
			AGTGGGTCCGACCTCACG		
GAM2029	ADCY2	3'	CACTGCACTCCAGCCTGGGTGA 65645		
			TCGCCCAGGCTGGAGTGCAGTG		
			AGTGGGTCCGACCTCACGTCAC		
GAM2029	AICDA	3'	GCACTCCAGCCTGGGCGA 40694		
			TCGCCCAGGCTGGAGTGC		
			AGCGGGTCCGACCTCACG		
GAM2029	AK1	3'	CACTGCACTCCAGCCTGGGTGA 6633		
			TCGCCCAGGCTGGAGTGCAGTG		
			AGTGGGTCCGACCTCACGTCAC		
GAM2029	ALPP	3'	CACTGCACTGCAGCCTGGGCGA 69409		G
			TCGCCCAGGCTG AGTGCAGTG		
			AGCGGGTCCGAC TCACGTCAC		
			G		
GAM2029	ANKH	3'	GCACTCCAGCCTGGGTGA 55069		
			TCGCCCAGGCTGGAGTGC		
			AGTGGGTCCGACCTCACG		
GAM2029	APOL1	3'	CACTGCACTCCAGCCTGGGTGA 14731		
			TCGCCCAGGCTGGAGTGCAGTG		
			AGTGGGTCCGACCTCACGTCAC		
GAM2029	ARHGEF6	3'	CACTGCACTCCAACCTAGGT 68752	C	C
			GCC AGG TGGAGTGCAGTG		
			TGG TCC ACCTCACGTCAC		
			A A		
GAM2029	ATM	3'	CACTACACTCCAGCCTGGGAGA 5290	G	C
			TC CCCAGGCTGGAGTG AGTG		
			AG GGGTCCGACCTCAC TCAC		
			A A		
GAM2029	ATM	3'	GCACTCCAGCCTGGGTGA 5295		
			TCGCCCAGGCTGGAGTGC		

AGTGGGTCCGACCTCACG

GAM2029	BCAS1	3'	GCACTCCACCCTGGGCGA	14712	C
			TCGCCCAGG TGGAGTGC		
			AGCGGGTCC ACCTCACG		
			C		
GAM2029	BPHL	3'	CACTGCACTCCAACCTGGGC	16334	C
			GCCCAGG TGGAGTGCAGTG		
			CGGGTCC ACCTCACGTCAC		
			A		
GAM2029	BRCA1	5'	GCACTCCAGCCTGGGCGA	24561	
			TCGCCCAGGCTGGAGTGC		
			AGCGGGTCCGACCTCACG		
GAM2029	BRCA1	3'	GCACTCCAGCCTGGGTGA	24562	
			TCGCCCAGGCTGGAGTGC		
			AGTGGGTCCGACCTCACG		
GAM2029	BRCA1	3'	GCACTCCAGCCTGGGTGA	24563	
			TCGCCCAGGCTGGAGTGC		
			AGTGGGTCCGACCTCACG		
GAM2029	BRCA1	3'	GCACTCCAGCCTGGGTGA	24564	
			TCGCCCAGGCTGGAGTGC		
			AGTGGGTCCGACCTCACG		
GAM2029	BRCA1	3'	GCACTCCAGCCTGGGTGA	24565	
			TCGCCCAGGCTGGAGTGC		
			AGTGGGTCCGACCTCACG		
GAM2029	C1orf1	3'	GCATTCCAGCCTAGGCGA	8678	C
			TCGCC AGGCTGGAGTGC		
			AGCGG TCCGACCTTACG		
			A		
GAM2029	CARKL	3'	GCACTCCAGCCTGGGTGA	26103	
			TCGCCCAGGCTGGAGTGC		
			AGTGGGTCCGACCTCACG		
GAM2029	CASP10	3'	ACTGCACTCCAGCTTGGGC	53196	
			GCCCAGGCTGGAGTGCAGT		

CGGGTTCGACCTCACGTCA

GAM2029 CASP10 3' ACTGCACTCCAGCTTGGGC 53238
GCCCAGGCTGGAGTGCAGT
|||||
CGGGTTCGACCTCACGTCA

GAM2029 CD28 3' GCTCTCCAGCCTGGGCGA 21553 T
TCGCCCAGGCTGGAG GC
|||||
AGCGGGTCCGACCTC CG

T
GAM2029 CD68 3' CACTGCACTCCAGCCTGGGCGA 60503
TCGCCCAGGCTGGAGTGCAGTG
|||||
AGCGGGTCCGACCTCACGTCAC

GAM2029 CDC25C 3' GACACTGCAGAAACCCTGAGC 10133 C CTGGAG
GC CAGG TGCAGTGTG
|| |||
CG GTCC ACGTCACAG
A CAAAG_

GAM2029 CPT2 3' CACTGCACTCCGGCCTGGGCGA 5421
TCGCCCAGGCTGGAGTGCAGTG
|||||
AGCGGGTCCGGCCTCACGTCAC

GAM2029 CRACC 3' CACTGCACTCCGGCCTAGGC 41308 C
GCC AGGCTGGAGTGCAGTG
||| |||
CGG TCCGGCCTCACGTCAC
A

GAM2029 CUBN 3' CACTACACTCCAGCCTGGGCGA 8417 C
TCGCCCAGGCTGGAGTG AGTG
|||||
AGCGGGTCCGACCTCAC TCAC
A

GAM2029 CYP4F3 3' CACTGCACTCCAGCCTGGGTGA 7996
TCGCCCAGGCTGGAGTGCAGTG
|||||
AGTGGGTCCGACCTCACGTCAC

GAM2029 DBT 3' GCACTCCAGCCTGGGCGA 10374
TCGCCCAGGCTGGAGTGC
|||||
AGCGGGTCCGACCTCACG

GAM2029 DFFA 3' CACTGCACTCCAGCCTGGGC 16589
GCCCAGGCTGGAGTGCAGTG
|||||

CGGGTCCGACCTCACGTCAC

GAM2029	DGKI	5'	CACTGCAATCCAGCCTGGGCGA 17524	G
			TCGCCCAGGCTGGA TGCAGTG	
			AGCGGGTCCGACCT ACGTCAC	
			A	
GAM2029	DLX4	3'	GACACCTTCACTCCAGCTGG 57111	G CA_
			CCAG CTGGAGTG GTGTC	
			GGTC GACCTCAC CACAG	
			TTC	
GAM2029	DMC1	3'	CACTGCACTCCAGCCTAGGTGA 23940	C
			TCGCC AGGCTGGAGTGCAGTG	
			AGTGG TCCGACCTCACGTCAC	
			A	
GAM2029	DSC1	3'	CACTGCACTCCAGCCTGGGC 44600	
			GCCCAGGCTGGAGTGCAGTG	
			CGGGTCCGACCTCACGTCAC	
GAM2029	DSC1	3'	CACTGCACTCCAGCCTGGGC 44601	
			GCCCAGGCTGGAGTGCAGTG	
			CGGGTCCGACCTCACGTCAC	
GAM2029	DVL3	3'	GCACTCCAGCCTGGGTGA 16646	
			TCGCCCAGGCTGGAGTGC	
			AGTGGGTCCGACCTCACG	
GAM2029	EGFL4	3'	CACTGCACTCCAACCTGGGTGA 62454	C
			TCGCCCAGG TGGAGTGCAGTG	
			AGTGGGTCC ACCTCACGTCAC	
			A	
GAM2029	EGFL5	3'	ATTTCACTCCAGCCTGGGCGA 87906	C
			TCGCCCAGGCTGGAGTG AGT	
			AGCGGGTCCGACCTCAC TTA	
			T	
GAM2029	F2RL3	3'	CACTGCACTCCAGCCTGGGC 15499	
			GCCCAGGCTGGAGTGCAGTG	
			CGGGTCCGACCTCACGTCAC	
GAM2029	F2RL3	3'	CACTGCACTCCAGCCTGGGCGA 15500	
			TCGCCCAGGCTGGAGTGCAGTG	

AGCGGGTCCGACCTCACGTCAC

GAM2029 FANCC 3' GACTGCACTCCAGCCTGGGC 71041
GCCCAGGCTGGAGTGCAGTGTG
|||||||
CGGGTCCGACCTCACGTCACAG

GAM2029 FCAR 3' GCACTCCAGCCTGGGTGA 56576
TCGCCCAGGCTGGAGTGC
|||||||
AGTGGGTCCGACCTCACG

GAM2029 FCAR 3' GCACTCCAGCCTGGGTGA 56577
TCGCCCAGGCTGGAGTGC
|||||||
AGTGGGTCCGACCTCACG

GAM2029 FCMD 3' GCACTTCAGCCTGGGCGA 23038
TCGCCCAGGCTGGAGTGC
|||||||
AGCGGGTCCGACTTCACG

GAM2029 FGF2 3' CACTGCAGTCCAGCCTAGGC 10613 C G
GCC AGGCTGGA TGCAGTG
||| ||||| |||||
CGG TCCGACCT ACGTCAC
A G

GAM2029 FGFR1 3' CACTGCACTCCAGCCTGGGTGA 7015
TCGCCCAGGCTGGAGTGCAGTG
|||||||
AGTGGGTCCGACCTCACGTCAC

GAM2029 FUT6 3' GCACTCCAACCTGGACGA 5639 C C
TCG CCAGG TGGAGTGC
||| ||||| |||||
AGC GGTCC ACCTCACG
A A

GAM2029 GALNT7 3' GCACTCCAACCTGGGTGA 34280 C
TCGCCCAGG TGGAGTGC
||||||| |||||
AGTGGGTCC ACCTCACG
A

GAM2029 GRAF 3' GCACTCCAGCCTGGGTGA 31239
TCGCCCAGGCTGGAGTGC
|||||||
AGTGGGTCCGACCTCACG

GAM2029 GTF2F1 3' CACTGCACTCCAGCCTGGGTGA 10889
TCGCCCAGGCTGGAGTGCAGTG
|||||||

AGTGGGTCCGACCTCACGTCAC

GAM2029 HIP1 3' CACTGCACTCCAGCCTGAGTGA 19249 C
TCGC CAGGCTGGAGTGCAGTG
|||||
AGTG GTCCGACCTCACGTCAC
A

GAM2029 HLA-E 3' ACTGCACTCCAGCCTGGGTGA 92668
TCGCCCAGGCTGGAGTGCAGT
|||||
AGTGGGTCCGACCTCACGTCA

GAM2029 HRH1 3' CACTGCACTCCAGCCTGGGC 7816
GCCCAGGCTGGAGTGCAGTG
|||||
CGGGTCCGACCTCACGTCAC

GAM2029 IL2RA 3' CACTGCACTCCAGCCTGGGC 6448
GCCCAGGCTGGAGTGCAGTG
|||||
CGGGTCCGACCTCACGTCAC

GAM2029 IRAK1 3' ACTGCACTCCAGCCTGGGTGA 9606
TCGCCCAGGCTGGAGTGCAGT
|||||
AGTGGGTCCGACCTCACGTCA

GAM2029 IRAK4 3' CACTGCACTCCAGCCTGGGTGA 61841
TCGCCCAGGCTGGAGTGCAGTG
|||||
AGTGGGTCCGACCTCACGTCAC

GAM2029 KAI1 3' TACTGCACTCCAGCCTGGGGGA 11128 G
TC CCCAGGCTGGAGTGCAGTG
|| |||||
AG GGGTCCGACCTCACGTCAT
G

GAM2029 KCNA7 3' CACTGCACTCCAGCCTGGGC 49891
GCCCAGGCTGGAGTGCAGTG
|||||
CGGGTCCGACCTCACGTCAC

GAM2029 KCNA7 3' CACTGCACTCCAGCCTGGGC 49892
GCCCAGGCTGGAGTGCAGTG
|||||
CGGGTCCGACCTCACGTCAC

GAM2029 KCNJ5 3' CACTGCACTCCAGCCTGGGCGA 7968
TCGCCCAGGCTGGAGTGCAGTG
|||||

AGCGGGTCCGACCTCACGTCAC

GAM2029 KIF1B 3' GCACTCCAGCCTGGGTGA 31267
TCGCCCAGGCTGGAGTGC
|||||||
AGTGGGTCCGACCTCACG

GAM2029 KIF3B 3' TACTGCATTCCAGCCTGGGTGA 17809
TCGCCCAGGCTGGAGTGCAGTG
|||||||
AGTGGGTCCGACCTTACGTCAT

GAM2029 KNSL1 3' CACTACACTCCAGCCTGGGC 16939 C
GCCCAGGCTGGAGTG AGTG
|||||||
CGGGTCCGACCTCAC TCAC
A

GAM2029 LAMP2 3' GCACTCCAGCCTTGGGCGA 26573 _
TCGCCCCA GGCTGGAGTGC
|||||
AGCGGGT CCGACCTCACG
T

GAM2029 LDLR 3' CACTGCACTCCAGCCTGGGC 6726
GCCCAGGCTGGAGTGCAGTG
|||||||
CGGGTCCGACCTCACGTCAC

GAM2029 LPIN1 3' TACTGCACTCCAGCCTGGGTGA 67991
TCGCCCAGGCTGGAGTGCAGTG
|||||||
AGTGGGTCCGACCTCACGTCAT

GAM2029 LRRC2 3' ACTGCACTCCAGCCTGGGTGA 44732
TCGCCCAGGCTGGAGTGCAGT
|||||||
AGTGGGTCCGACCTCACGTCA

GAM2029 LRRC2 3' GCACTGCCCTCCAGCCTGGGT 44745 T
GA TCGCCCAGGCTGGAG GCAGTGTC
|||||||
AGTGGGTCCGACCTC CGTCACAG
C

GAM2029 MAFF 3' CACTGCACTCCAGCCTGGGC 25575
GCCCAGGCTGGAGTGCAGTG
|||||||
CGGGTCCGACCTCACGTCAC

GAM2029 MDM4 3' CACTGCACTCCAGCCTGGGTGA 11506
TCGCCCAGGCTGGAGTGCAGTG
|||||||

AGTGGGTCCGACCTCACGTCAC

GAM2029 MEN1 5' CACTGCATTCCAGCCTGGGCGA 56342
TCGCCCAGGCTGGAGTGCAGTG
|||||||
AGCGGGTCCGACCTTACGTCAC

GAM2029 MTMR8 3' CACTGCACTCCAGCCTGGGCGA 31906
TCGCCCAGGCTGGAGTGCAGTG
|||||||
AGCGGGTCCGACCTCACGTCAC

GAM2029 MYO1B 3' CACTGCACTCCAGCCCGGGTGA 25242 A
TCGCCC GGCTGGAGTGCAGTG
||||| |||||
AGTGGG CCGACCTCACGTCAC
C

GAM2029 MYO1C 3' CACTGCACTCCAGCCTGGGC 61855
GCCCAGGCTGGAGTGCAGTG
|||||||
CGGGTCCGACCTCACGTCAC

GAM2029 NFKBIL2 3' CACTGCACTCCAGCCTGGGCGA 26444
TCGCCCAGGCTGGAGTGCAGTG
|||||||
AGCGGGTCCGACCTCACGTCAC

GAM2029 NKX3A 3' CACTGCAATCCAGCCTGGGC 21611 G
GCCCAGGCTGGA TGCAGTG
||||||| |||||
CGGGTCCGACCT ACGTCAC
A

GAM2029 NPHS1 3' CACTGCACTCCAGCCTGGGCGA 17367
TCGCCCAGGCTGGAGTGCAGTG
|||||||
AGCGGGTCCGACCTCACGTCAC

GAM2029 NUP62 3' CACTGCACTCCAGCCTAGGC 25643 C
GCC AGGCTGGAGTGCAGTG
||| |||||
CGG TCCGACCTCACGTCAC
A

GAM2029 OPTN 3' CACTGCACTCCAGCCTGGGTGA 42050
TCGCCCAGGCTGGAGTGCAGTG
|||||||
AGTGGGTCCGACCTCACGTCAC

GAM2029 P53AIP1 3' CACTGCACTCCAGCCTGGGCGA 42334
TCGCCCAGGCTGGAGTGCAGTG
|||||||

AGCGGGTCCGACCTCACGTCAC

GAM2029 PA2G4 3' CACTGCACTCCAGCCTGGGTGA 71825
TCGCCCAGGCTGGAGTGCAGTG
|||||||
AGTGGGTCCGACCTCACGTCAC

GAM2029 PAICS 3' CACTGCACTCCAACCTGGGC 22256 C
GCCCAGG TGGAGTGCAGTG
||||| |||||
CGGGTCC ACCTCACGTCAC
A

GAM2029 PCDH11X 3' CACTGCACTCCAGCCTGGGTGA 28007
TCGCCCAGGCTGGAGTGCAGTG
|||||||
AGTGGGTCCGACCTCACGTCAC

GAM2029 PCDH11Y 3' CACTGCACTCCAGCCTGGGTGA 53156
TCGCCCAGGCTGGAGTGCAGTG
|||||||
AGTGGGTCCGACCTCACGTCAC

GAM2029 PDCL 3' ATTGCACTCCAACCTGGGCGA 19393 C
TCGCCCAGG TGGAGTGCAGT
||||| |||||
AGCGGGTCC ACCTCACGTTA
A

GAM2029 PDE4C 3' CACTGCACTCCAGCCTGGGC 8099
GCCCAGGCTGGAGTGCAGTG
|||||||
CGGGTCCGACCTCACGTCAC

GAM2029 PIK3CG 3' ACACTCTTATCAGCCTGGGC 12115 AGTGC
GCCCAGGCTGG AGTGT
||||| |||
CGGGTCCGACT TCACA
ATTC_

GAM2029 PLA2G2D 3' GCACTGCACTCCAGCCTGGGC 25715
GCCCAGGCTGGAGTGCAGTGTC
|||||||
CGGGTCCGACCTCACGTCACAG

GAM2029 POLH 3' CACCGCACTCCAGCCTGGGC 22473 A
GCCCAGGCTGGAGTGC GTG
||||||| |||
CGGGTCCGACCTCACG CAC
C

GAM2029 PPP1R12B 3' CACTGCACTCCAGCCTGGGTGA 50344
TCGCCCAGGCTGGAGTGCAGTG
|||||||

AGTGGGTCCGACCTCACGTCAC

GAM2029 PRKY 3' GCACTCCAGGCTGGACGA 12376 C G
TCG CCAG CTGGAGTGC
||| ||| |||||
AGC GGTC GACCTCACG
A G

GAM2029 PRKY 3' CACTGCACTCCAGCCAGGGCGA 12363 A
TCGCCC GGCTGGAGTGCAGTG
||||| |||||
AGCGGG CCGACCTCACGTCAC
A

GAM2029 PSMB9 3' CACTACACTCCAGCCTGGG 12492 C
CCCAGGCTGGAGTG AGTG
||||| |||
GGGTCCGACCTCAC TCAC
A

GAM2029 PSMB9 3' CACTGCACTCCAGTCTGGACGA 12495 C
TCG CCAGGCTGGAGTGCAGTG
||| |||||
AGC GGTCTGACCTCACGTCAC
A

GAM2029 PSMB9 3' GCACTCCAGCCTGGGCGA 12505
TCGCCCAGGCTGGAGTGC
|||||
AGCGGGTCCGACCTCACG

GAM2029 PTGIS 3' GCACTCCAGCCTGGGCGA 8213
TCGCCCAGGCTGGAGTGC
|||||
AGCGGGTCCGACCTCACG

GAM2029 PTGS1 3' ACACTGCAGTTTCCTGG 55469 CT G
CCAGG GGA TGCAGTGT
||||| ||| |||||
GGTCC TTT ACGTCACA
— G

GAM2029 RBL1 3' CACTGCACTCCAGCCTGGGC 12785
GCCCAGGCTGGAGTGCAGTG
|||||
CGGGTCCGACCTCACGTCAC

GAM2029 RBM3 3' CACTGTACTCCAGCCTGGGC 71005
GCCCAGGCTGGAGTGCAGTG
|||||
CGGGTCCGACCTCATGTCAC

GAM2029 RFC2 3' GCACTCCAGCCTGGGCGA 12841
TCGCCCAGGCTGGAGTGC
|||||

AGCGGGTCCGACCTCACG

GAM2029 ROCK2 3' CACTGCACTCCAGCCTGGGC 66614
GCCCAGGCTGGAGTGCAGTG
|||||||
CGGGTCCGACCTCACGTCAC

GAM2029 SCAP2 3' CACTGCACTCCAGCCTGGGCGA 15424
TCGCCCAGGCTGGAGTGCAGTG
|||||||
AGCGGGTCCGACCTCACGTCAC

GAM2029 SFRS2IP 5' GCACTCCAGCCTGGGTGA 17542
TCGCCCAGGCTGGAGTGC
|||||||
AGTGGGTCCGACCTCACG

GAM2029 SIGLEC11 3' CACTGCACTCCAGCCTGGGC 54650
GCCCAGGCTGGAGTGCAGTG
|||||||
CGGGTCCGACCTCACGTCAC

GAM2029 SIM2 3' CACTGCACTCCAGCCTGGGT 18622
GCCCAGGCTGGAGTGCAGTG
|||||||
TGGGTCCGACCTCACGTCAC

GAM2029 SLC14A1 3' CACTGCACTCCAACCTGGGTGA 32410 C
TCGCCCAGG TGGAGTGCAGTG
|||||||
AGTGGGTCC ACCTCACGTCAC
A

GAM2029 SLC14A2 3' CACTGCACTCCAGCCTGGGC 24112
GCCCAGGCTGGAGTGCAGTG
|||||||
CGGGTCCGACCTCACGTCAC

GAM2029 SLC17A5 3' CACTGCACTCCAGCCTGGGCGA 25829
TCGCCCAGGCTGGAGTGCAGTG
|||||||
AGCGGGTCCGACCTCACGTCAC

GAM2029 SLC26A4 3' CACTGCACTCCAGCCTGGGCGA 6522
TCGCCCAGGCTGGAGTGCAGTG
|||||||
AGCGGGTCCGACCTCACGTCAC

GAM2029 SLC31A1 3' GCACTCCAGCCTGGGTGA 10278
TCGCCCAGGCTGGAGTGC
|||||||

AGTGGGTCCGACCTCACG

GAM2029 SLC7A5 3' GCCCCTCCAGCCTGGGGA 14466 G CA
TC CCCAGGCTGGAGTG GT
|| ||||| ||
AG GGTCCGACCTCAC CG

— CC
GAM2029 SMARCC2 3' ACCCTCCCCAGCCTGGAGA 13256 GC AGTGC T
TC CCAGGCTGG AG GT
|| ||||| || ||
AG GGTCCGACC TC CA
A_ CC_ C

GAM2029 SMG1 3' CACTGCACTCCAGCCTGGGC 31343
GCCCAGGCTGGAGTGCAGTG
|||||
CGGGTCCGACCTCACGTCAC

GAM2029 SRGAP1 5' CACTGCACTCCAGCCTGGGC 72712
GCCCAGGCTGGAGTGCAGTG
|||||
CGGGTCCGACCTCACGTCAC

GAM2029 STAT3 3' GCACTCCATCCTGGGCGA 13437 C
TCGCCCAGG TGGAGTGC
||||| |||||
AGCGGGTCC ACCTCACG
T

GAM2029 SULT2A1 3' CACTGCACTCCAGCCTGGGTGA 72224
TCGCCCAGGCTGGAGTGCAGTG
|||||
AGTGGGTCCGACCTCACGTCAC

GAM2029 TBX1 3' CACTGCACTCCAGCCTGGGTGA 55538
TCGCCCAGGCTGGAGTGCAGTG
|||||
AGTGGGTCCGACCTCACGTCAC

GAM2029 TEM7 3' CACTGCACTCCAGCCTGGGTGA 40248
TCGCCCAGGCTGGAGTGCAGTG
|||||
AGTGGGTCCGACCTCACGTCAC

GAM2029 TNFRSF1B 3' CACTACACTCCAGCCTGAGC 8384 C C
GC CAGGCTGGAGTG AGTG
|| ||||| ||||
CG GTCCGACCTCAC TCAC
A A

GAM2029 TNFRSF1B 3' CACTGCACTCCAGCCTGGGCGA 8387
TCGCCCAGGCTGGAGTGCAGTG
|||||

AGCGGGTCCGACCTCACGTCAC

GAM2029 TNFSF14 3' CACTGCACTCCAACCTGGG 15078 C
CCCAGG TGGAGTGCAGTG
||||| |||||||||
GGGTCC ACCTCACGTCAC

A

GAM2029 TRIM14 3' CACTGCACTCCAGCCTGGGC 29505
GCCCAGGCTGGAGTGCAGTG
|||||||||||||||
CGGGTCCGACCTCACGTCAC

GAM2029 TRIM14 3' CACTGCACTCCAGCCTGGGGA 29506 G
TC CCCAGGCTGGAGTGCAGTG
|| |||||||||||||
AG GGGTCCGACCTCACGTCAC

—

GAM2029 TSNAX 3' CACTGCACTCCAGCCTGGGT 21154
GCCCAGGCTGGAGTGCAGTG
|||||||||||||||
TGGGTCCGACCTCACGTCAC

GAM2029 UBE2B 3' GCACTCCAGCCTGGGTGA 13937
TCGCCCAGGCTGGAGTGC
|||||||||||
AGTGGGTCCGACCTCACG

GAM2029 UBE2G2 3' CACTGCACTCCAGCCTGGGC 65480
GCCCAGGCTGGAGTGCAGTG
|||||||||||||||
CGGGTCCGACCTCACGTCAC

GAM2029 UBE2G2 3' CACTGCACTCCAGCCTGGGC 65481
GCCCAGGCTGGAGTGCAGTG
|||||||||||||||
CGGGTCCGACCTCACGTCAC

GAM2029 USP14 3' CACTGCACTCCAGCCTGGGTGA 18931
TCGCCCAGGCTGGAGTGCAGTG
|||||||||||||||
AGTGGGTCCGACCTCACGTCAC

GAM2029 VHL 3' GCACTCCAGCCTGGGGGA 6860 G
TC CCCAGGCTGGAGTGC
|| |||||||||||||
AG GGGTCCGACCTCACG

G

GAM2029 VHL 3' GCACTCTAACCTGGGCGA 6861 C
TCGCCCAGG TGGAGTGC
||||||| |||||

AGCGGGTCC ATCTCACG

A

GAM2029 WIG1 3' CACTGCACTCCAGCCTGGGTGA 96096
TCGCCCAGGCTGGAGTGCAGTG
|||||
AGTGGGTCCGACCTCACGTCAC

GAM2029 XRCC2 3' GCACTCCCGCCTGGGCGA 19503 T
TCGCCCAGGC GGAGTGC
|||||
AGCGGGTCCG CCTCACG

C

GAM2029 XT3 3' ACTCCACTCCAGTCTGGGCGA 39900 C
TCGCCCAGGCTGGAGTGC AGT
|||||
AGCGGGTCTGACCTCAC TCA

C

GAM2029 ZNF264 3' CACTGCACTCCAGCCTGGGC 14202
GCCCAGGCTGGAGTGCAGTG
|||||
CGGGTCCGACCTCACGTCAC

GAM2029 ZNF264 3' CACTGCACTCCAGCCTGGGC 14203
GCCCAGGCTGGAGTGCAGTG
|||||
CGGGTCCGACCTCACGTCAC

GAM2029 ZNF36 3' ACACTGCACTCCAGCCTGGGTG 95572
A TCGCCCAGGCTGGAGTGCAGTGT
|||||
AGTGGGTCCGACCTCACGTCACA

GAM2029 ZNF91 3' GCACTCAAGCCTGGGCGA 14282 G
TCGCCCAGGCT GAGTGC
|||||
AGCGGGTCCGA CTCACG

A

GAM2029 AF020591 3' CACTGCACTCCAGCCTGGGC 27906
GCCCAGGCTGGAGTGCAGTG
|||||
CGGGTCCGACCTCACGTCAC

GAM2029 ALTE 3' GCACTCCAGCCTGGGCGA 61003
TCGCCCAGGCTGGAGTGC
|||||
AGCGGGTCCGACCTCACG

GAM2029 APXL2 3' CACTGCACTCCAGCCTGGGCGA 75672
TCGCCCAGGCTGGAGTGCAGTG
|||||

AGCGGGTCCGACCTCACGTCAC

GAM2029 ARNTL2 3' CACTGCACCCCAGCCTGGGCGA 39840 A
TCGCCCAGGCTGG GTGCAGTG
|||||||
AGCGGGTCCGACC CACGTCAC
C

GAM2029 ARNTL2 3' CACTGCACTCCAGTCTGGGC 39841
GCCCAGGCTGGAGTGCAGTG
|||||||
CGGGTCTGACCTCACGTCAC

GAM2029 BIRC1 3' CACTGCATTCCAGCCTGGGC 16987
GCCCAGGCTGGAGTGCAGTG
|||||||
CGGGTCCGACCTTACGTCAC

GAM2029 BIVM 3' CACTGCACTCCAGCCTGGGC 35154
GCCCAGGCTGGAGTGCAGTG
|||||||
CGGGTCCGACCTCACGTCAC

GAM2029 BLOV1 3' CACTGCACTCCAGCCTGGGCGA 76791
TCGCCCAGGCTGGAGTGCAGTG
|||||||
AGCGGGTCCGACCTCACGTCAC

GAM2029 BTN3A2 3' CACTGCACTCCAGCCTGGGAGA 23872 G
TC CCCAGGCTGGAGTGCAGTG
|| |||||
AG GGGTCCGACCTCACGTCAC
A

GAM2029 C12orf2 3' TACTGCACTCCAGCCTGGGT 83685
GCCCAGGCTGGAGTGCAGTG
|||||||
TGGGTCCGACCTCACGTCAT

GAM2029 C13orf1 3' CACTGCACTCCAGCCTAGGC 40357 C
GCC AGGCTGGAGTGCAGTG
|| |||||
CGG TCCGACCTCACGTCAC
A

GAM2029 C1orf24 3' GCACTCCAGCTTGGGCGA 54792
TCGCCCAGGCTGGAGTGC
|||||||
AGCGGGTTCGACCTCACG

GAM2029 C1QTNF2 3' CACTGCACTCCAGCCTGGGC 49970
GCCCAGGCTGGAGTGCAGTG
|||||||

CGGGTCCGACCTCACGTCAC

GAM2029	C20orf106	3'	CACTGCACTCCAGCCCAGGTGA	55898	CA
			TCGCC	GGCTGGAGTGCAGTG	
			AGTGG	CCGACCTCACGTCAC	
			AC		
GAM2029	C20orf108	3'	CACTGCACTCCAGCCTGGGCGA	55876	
			TCGCCCAGGCTGGAGTGCAGTG		
			AGCGGGTCCGACCTCACGTCAC		
GAM2029	C20orf142	3'	CACTGCACTCCAGCCTGAGCGA	75274	C
			TCGC	CAGGCTGGAGTGCAGTG	
			AGCG	GTCCGACCTCACGTCAC	
			A		
GAM2029	C20orf172	3'	CACTGCACTCCAGCCTGAGCGA	46764	C
			TCGC	CAGGCTGGAGTGCAGTG	
			AGCG	GTCCGACCTCACGTCAC	
			A		
GAM2029	C20orf183	3'	CACTGCACTCCAGGCTGGGCGA	48528	G
			TCGCCCAG	CTGGAGTGCAGTG	
			AGCGGGTC	GACCTCACGTCAC	
			G		
GAM2029	C20orf29	3'	ACTTCACTCCAGCCTGGGC	37705	C
			GCCCAGGCTGGAGTG	AGT	
			CGGGTCCGACCTCAC	TCA	
			T		
GAM2029	C22orf20	3'	ATTTCATTCCAGCCTGGGC	48192	C
			GCCCAGGCTGGAGTG	AGT	
			CGGGTCCGACCTTAC	TTA	
			T		
GAM2029	C6orf29	3'	CACTGCACTCCAACCTGGGTGA	48264	C
			TCGCCCAGG	TGGAGTGCAGTG	
			AGTGGGTCC	ACCTCACGTCAC	
			A		
GAM2029	C6orf5	3'	CACTGCACTCCAGCCTGGGC	31976	
			GCCCAGGCTGGAGTGCAGTG		
			CGGGTCCGACCTCACGTCAC		
GAM2029	C9orf5	3'	CACTGCACTCCAGCCTGGGTGA	50103	
			TCGCCCAGGCTGGAGTGCAGTG		

AGTGGGTCCGACCTCACGTCAC

GAM2029 CAMKK2 5' GCACTCCAGCGTGGGCGA 22623 G
TCGCCCCA GCTGGAGTGC
||||| |||||||
AGCGGGT CGACCTCACG
G

GAM2029 CAMKK2 5' TACTGCACTCCAGCCTGGGC 22629
GCCCAGGCTGGAGTGCAGTG
|||||||
CGGGTCCGACCTCACGTCAT

GAM2029 CBCIP2 3' CACTGCACTCCAGCCTGGGCGA 52654
TCGCCCAGGCTGGAGTGCAGTG
|||||||
AGCGGGTCCGACCTCACGTCAC

GAM2029 CCR6 3' GCACTCCAGCCTGGGTGA 49403
TCGCCCAGGCTGGAGTGC
|||||||
AGTGGGTCCGACCTCACG

GAM2029 CDT1 3' GCACTCCAGCCTGGGTGA 78162
TCGCCCAGGCTGGAGTGC
|||||||
AGTGGGTCCGACCTCACG

GAM2029 cerk 3' CACTGCACTCCAGCCTGGGC 43160
GCCCAGGCTGGAGTGCAGTG
|||||||
CGGGTCCGACCTCACGTCAC

GAM2029 CG012 5' CACTGCACTCCAGCCCAGGTGA 84147 CA
TCGCC GGCTGGAGTGCAGTG
|||| |||||||
AGTGG CCGACCTCACGTCAC
AC

GAM2029 CG012 5' CACTGCACTCCAGCCTGGGC 84148
GCCCAGGCTGGAGTGCAGTG
|||||||
CGGGTCCGACCTCACGTCAC

GAM2029 COE2 3' CACTGCACTCCAGCCTGGGTGA 64906
TCGCCCAGGCTGGAGTGCAGTG
|||||||
AGTGGGTCCGACCTCACGTCAC

GAM2029 CPR2 3' CACTGCACTCCAGCCTGGGT 48827
GCCCAGGCTGGAGTGCAGTG
|||||||

TGGGTCCGACCTCACGTCAC

GAM2029 CPR2 3' CACTGCAGTCCAGCCTGGGCGA 48828 G
TCGCCCAGGCTGGA TGCAGTG
||||||| |||||
AGCGGGTCCGACCT ACGTCAC
G

GAM2029 DCOHM 3' CACTGCACTCCAGCCTGGGTGA 50512
TCGCCCAGGCTGGAGTGCAGTG
|||||||
AGTGGGTCCGACCTCACGTCAC

GAM2029 DIS3 3' CACTGCACTCCAGCCTGGGTGA 30912
TCGCCCAGGCTGGAGTGCAGTG
|||||||
AGTGGGTCCGACCTCACGTCAC

GAM2029 dJ383J4.3 3' CACTGCACTCCAGCCTGGGC 67490
GCCCAGGCTGGAGTGCAGTG
|||||||
CGGGTCCGACCTCACGTCAC

GAM2029 DKFZP434B168 3' ACTGTGCTCCAGCCTGGGCGA 31862 TG
TCGCCCAGGCTGGAG CAGT
||||||| |||
AGCGGGTCCGACCTC GTCA
GT

GAM2029 DKFZP434C171 3' CACTGCACTCCAGCCCGGGTGA 32185 A
TCGCCC GGCTGGAGTGCAGTG
||||| |||||
AGTGGG CCGACCTCACGTCAC
C

GAM2029 DKFZp434E169 3' GCACGCCAGCCTGGGCGA 51078 A
TCGCCCAGGCTGG GTGC
||||||| |||
AGCGGGTCCGACC CACG
G

GAM2029 DKFZp434E2220 5' GCACTCCAGCCTGGGCGA 34713
TCGCCCAGGCTGGAGTGC
|||||||
AGCGGGTCCGACCTCACG

GAM2029 DKFZP434F091 3' GCACTCCAGCCTGTGCGA 31896 C
TCGC CAGGCTGGAGTGC
||| |||||
AGCG GTCCGACCTCACG
T

GAM2029 DKFZp434G171 3' CACTGCACTCCAGCCTGGGAGA 80236 G
TC CCCAGGCTGGAGTGCAGTG
|| |||||

	AG GGGTCCGACCTCACGTCAC	
	A	
GAM2029 DKFZP434I1735 3'	CACTGCACTCCAGCCTGGGCGA 89166	
	TCGCCCAGGCTGGAGTGCAGTG	
	AGCGGGTCCGACCTCACGTCAC	
GAM2029 DKFZP434K1421 3'	CACTGCACTCCAACCTGGGC 50465	C
	GCCCAGG TGGAGTGCAGTG	
	CGGGTCC ACCTCACGTCAC	
	A	
GAM2029 DKFZP434N1511 3'	CACTGCACTCCAGCCTGGGC 93052	
	GCCCAGGCTGGAGTGCAGTG	
	CGGGTCCGACCTCACGTCAC	
GAM2029 DKFZp547I094 3'	GACACCTAGTGACCAGCCTGGG 50558	AG A__
	CCCAGGCTGG TGC GTGTC	
	GGGTCCGACC GTG CACAG	
	A_ ATC	
GAM2029 DKFZp547I094 3'	GCACTCCAGCCTGGGCGG 50559	
	TCGCCCAGGCTGGAGTGC	
	GGCGGGTCCGACCTCACG	
GAM2029 DKFZP564A022 3'	CACTGCACTCCAGCCTGGGC 48971	
	GCCCAGGCTGGAGTGCAGTG	
	CGGGTCCGACCTCACGTCAC	
GAM2029 DKFZP564B1023 3'	CACTGCACTCCAGCCTGGGC 49362	
	GCCCAGGCTGGAGTGCAGTG	
	CGGGTCCGACCTCACGTCAC	
GAM2029 DKFZP564B1023 3'	GCACTGCCCTCCAGCCTGG 49365	T
	CCAGGCTGGAG GCAGTGTG	
	GGTCCGACCTC CGTCACAG	
	C	
GAM2029 DKFZP564I0422 3'	ACTGCACTCCAGCCTGGGC 49508	
	GCCCAGGCTGGAGTGCAGT	
	CGGGTCCGACCTCACGTCA	
GAM2029 DKFZP564I052 3'	CACTGCACTCCAGGCTGGGC 67280	G
	GCCCAG CTGGAGTGCAGTG	

CGGGTC GACCTCACGTCAC
G
GAM2029 DKFZP564M182 3' CACTGCACTCCAGCCTGGGCGG 78620
TCGCCCAGGCTGGAGTGCAGTG
|||||
GGCGGGTCCGACCTCACGTCAC

GAM2029 DKFZP564M182 3' GATCCTGCACTCCAGCCTGGGC 78631 TG
GCCCAGGCTGGAGTGCAG TC
||||| ||
CGGGTCCGACCTCACGTC AG
CT

GAM2029 DKFZp566H0824 3' CACTGCACTCCAGCCTGGGC 34478
GCCCAGGCTGGAGTGCAGTG
|||||
CGGGTCCGACCTCACGTCAC

GAM2029 DKFZp566H0824 5' GCAGTCCAGCCTGGGCGA 34486 G
TCGCCCAGGCTGGA TGC
||||| |||
AGCGGGTCCGACCT ACG
G

GAM2029 DKFZp727G131 3' CACTGCATTCCAGCCTGGGC 59692
GCCCAGGCTGGAGTGCAGTG
|||||
CGGGTCCGACCTTACGTCAC

GAM2029 DPCR1 3' ACACTGCACTGAGTCCTAAAGG 55995 C__ _ GG
CC AGG CT AGTGCAGTGT
|| ||| || |||||
GG TCC GA TCACGTCACA
AAA T G_

GAM2029 DRF1 3' CACTGCACTCCAGCCTGGGCGA 47740
TCGCCCAGGCTGGAGTGCAGTG
|||||
AGCGGGTCCGACCTCACGTCAC

GAM2029 DRF1 3' TACTGCACTCCAGCCTGGGTGA 47756
TCGCCCAGGCTGGAGTGCAGTG
|||||
AGTGGGTCCGACCTCACGTCAT

GAM2029 DTX2 3' ACTTCCCCAGCCTGGACGG 72418 C ____
TCG CCAGGCTGG AGT
||| ||||| |||
GGC GGTCCGACC TCA
A CCT

GAM2029 ET 3' CACTGCACTCCAGGCTGGGC 44466 G
GCCCAG CTGGAGTGCAGTG
||||| |||||

			CGGGTC GACCTCACGTCAC			
			G			
GAM2029	ET	3'	GCACTCCAGCCTGGATGA 44471	C		
			TCG CCAGGCTGGAGTGC			
			AGT GGTCCGACCTCACG			
			A			
GAM2029	EVI5	3'	CACTGCACTCCAACCTGGGC 20201	C		
			GCCCAGG TGGAGTGCAGTG			
			CGGGTCC ACCTCACGTCAC			
			A			
GAM2029	FBXO27	3'	CACTGCACTCCAGCCTGGGC 75006			
			GCCCAGGCTGGAGTGCAGTG			
			CGGGTCCGACCTCACGTCAC			
GAM2029	FBXO27	3'	CACTGCACTCCAGCCTGGGTGA 75007			
			TCGCCCAGGCTGGAGTGCAGTG			
			AGTGGGTCCGACCTCACGTCAC			
GAM2029	FBXO3	3'	ACACTGCAGATAAGCCAGGC 25153	CA	GGAG	
			GCC GGCT TGCAGTGT			
			CGG CCGA ACGTCACA			
			A_ ATAG			
GAM2029	FBXO6	3'	CACTGCACTCCAGCCTGGGTGA 37989			
			TCGCCCAGGCTGGAGTGCAGTG			
			AGTGGGTCCGACCTCACGTCAC			
GAM2029	FBXO9	3'	ATTCCACTCCAGCCTGAGC 54240	C	C	
			GC CAGGCTGGAGTG AGT			
			CG GTCCGACCTCAC TTA			
			A C			
GAM2029	FKBP14	3'	CACTGCACTCCAGCCTGGGTGA 36064			
			TCGCCCAGGCTGGAGTGCAGTG			
			AGTGGGTCCGACCTCACGTCAC			
GAM2029	FKSG17	3'	GCACTCCAGCCTGGGTGA 50155			
			TCGCCCAGGCTGGAGTGC			
			AGTGGGTCCGACCTCACG			
GAM2029	FKSG43	5'	CACTGCACTCCAGCCTGGGTGA 50162			
			TCGCCCAGGCTGGAGTGCAGTG			

AGTGGGTCCGACCTCACGTCAC

GAM2029 FKSG44 5' CACTGCACTCCAGCCTGGGCGA 49962
TCGCCCAGGCTGGAGTGCAGTG
|||||||
AGCGGGTCCGACCTCACGTCAC

GAM2029 FLJ00060 3' CACTGCACTCCAGCCTGGGCGA 61739
TCGCCCAGGCTGGAGTGCAGTG
|||||||
AGCGGGTCCGACCTCACGTCAC

GAM2029 FLJ10008 3' CACTGCACTCCAGCCTGGGCGA 36181
TCGCCCAGGCTGGAGTGCAGTG
|||||||
AGCGGGTCCGACCTCACGTCAC

GAM2029 FLJ10043 3' CACTGCACTCCAGCCTGGGTGA 36229
TCGCCCAGGCTGGAGTGCAGTG
|||||||
AGTGGGTCCGACCTCACGTCAC

GAM2029 FLJ10058 3' CACTGCACTCCAGCCTGGGC 36260
GCCCAGGCTGGAGTGCAGTG
|||||||
CGGGTCCGACCTCACGTCAC

GAM2029 FLJ10460 3' GCACTCCAACCTGGGTGA 36618 C
TCGCCCAGG TGGAGTGC
|||||||
AGTGGGTCC ACCTCACG

A
GAM2029 FLJ10466 5' ACACTGCTTGTGCGCCTGGGC 36628 T AGT
GCCCAGGC GG GCAGTGT
||||||| || |||||
CGGGTCCG CT CGTCACA
_ GTT

GAM2029 FLJ10650 3' CACTGCACTCCAGCCTGGGCGA 36900
TCGCCCAGGCTGGAGTGCAGTG
|||||||
AGCGGGTCCGACCTCACGTCAC

GAM2029 FLJ10704 3' CACTGCACTCCAGCCTGGACGA 36976 C
TCG CCAGGCTGGAGTGCAGTG
||| |||||
AGC GGTCCGACCTCACGTCAC

A
GAM2029 FLJ10803 3' CACTGCACTCCAGCCTGGGC 37199
GCCCAGGCTGGAGTGCAGTG
|||||||

CGGGTCCGACCTCACGTCAC

GAM2029 FLJ10826 3' CACTGCACTCCAGCCTGGGC 37244
GCCCAGGCTGGAGTGCAGTG
|||||||
CGGGTCCGACCTCACGTCAC

GAM2029 FLJ10830 3' CACTGCACTCCAGCCTGGGCGA 37263
TCGCCCAGGCTGGAGTGCAGTG
|||||||
AGCGGGTCCGACCTCACGTCAC

GAM2029 FLJ10936 3' CACTGTACTCCAGCCTGGGC 37438
GCCCAGGCTGGAGTGCAGTG
|||||||
CGGGTCCGACCTCATGTCAC

GAM2029 FLJ10989 3' GCACTGCACTCCAGCCTGGGTG 37503
A TCGCCCAGGCTGGAGTGCAGTGT
|||||||
AGTGGGTCCGACCTCACGTCACG

GAM2029 FLJ10998 3' GCACTCCAGCCTGGGTGA 37520
TCGCCCAGGCTGGAGTGC
|||||||
AGTGGGTCCGACCTCACG

GAM2029 FLJ11017 3' ACATTGTACCCAACCTGG 37543 C A
CCAGG TGG GTGCAGTGT
||||| ||| |||||
GGTCC ACC CATGTTACA
A _

GAM2029 FLJ11036 3' CACTGCACTCCAGCCTGGGCGA 37552
TCGCCCAGGCTGGAGTGCAGTG
|||||||
AGCGGGTCCGACCTCACGTCAC

GAM2029 FLJ11106 3' CACTGCACTCCAGCCTGGGTGA 37619
TCGCCCAGGCTGGAGTGCAGTG
|||||||
AGTGGGTCCGACCTCACGTCAC

GAM2029 FLJ11126 3' CACTGCACTCCAGCCTGGGT 37648
GCCCAGGCTGGAGTGCAGTG
|||||||
TGGGTCCGACCTCACGTCAC

GAM2029 FLJ11151 3' CACTGCACTCCAGCCTGGGC 68471
GCCCAGGCTGGAGTGCAGTG
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CGGGTCCGACCTCACGTCAC

GAM2029 FLJ11301 3' GCACTCCAGCCTGGGCGA 37806
TCGCCCAGGCTGGAGTGC
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AGCGGGTCCGACCTCACG

GAM2029 FLJ11700 3' TACTGCACTCCAGCCTGGGC 46566
GCCCAGGCTGGAGTGCAGTG
|||||||
CGGGTCCGACCTCACGTCAT

GAM2029 FLJ11710 5' CACTGTACTCCAGCCTGGGC 46242
GCCCAGGCTGGAGTGCAGTG
|||||||
CGGGTCCGACCTCATGTCAC

GAM2029 FLJ11715 3' GACACTGCACTCCAGCCTGGGT 44979
GA TCGCCCAGGCTGGAGTGCAGTGTG
|||||||
AGTGGGTCCGACCTCACGTCACAG

GAM2029 FLJ11726 3' GCACTCCAGCCTGGGCGA 47023
TCGCCCAGGCTGGAGTGC
|||||||
AGCGGGTCCGACCTCACG

GAM2029 FLJ11800 3' CACTGCATTCCAGCCTGGGC 47036
GCCCAGGCTGGAGTGCAGTG
|||||||
CGGGTCCGACCTTACGTCAC

GAM2029 FLJ11827 3' CACTGCACTTCAGCCTGGGC 47678
GCCCAGGCTGGAGTGCAGTG
|||||||
CGGGTCCGACTTCACGTCAC

GAM2029 FLJ11996 3' ACTGCACTCCAACCTGGGC 47049 C
GCCCAGG TGGAGTGCAGT
||||| |||||
CGGGTCC ACCTCACGTCA
A

GAM2029 FLJ12190 3' TACTGCACTCCAGCCTGGGC 47571
GCCCAGGCTGGAGTGCAGTG
|||||||
CGGGTCCGACCTCACGTCAT

GAM2029 FLJ12294 3' CACTGCACTCCAGCCTGGGTGA 47710
TCGCCCAGGCTGGAGTGCAGTG
|||||||

AGTGGGTCCGACCTCACGTCAC

GAM2029 FLJ12298 3' CACTGCACTCCAGCCTGGGC 50596
GCCCAGGCTGGAGTGCAGTG
|||||||
CGGGTCCGACCTCACGTCAC

GAM2029 FLJ12586 3' CACTGCACTCCAGCCTGGGTGA 45206
TCGCCCAGGCTGGAGTGCAGTG
|||||||
AGTGGGTCCGACCTCACGTCAC

GAM2029 FLJ12592 3' GACATGGCCTCCAGCCTGGGTG 50651
A TCGCCCAGGCTGGAG GC GTGTC
||||||| || |||||
AGTGGGTCCGACCTC CG TACAG
— G

GAM2029 FLJ12618 3' CACTGCACTCCAGCCTGGGTGA 46504
TCGCCCAGGCTGGAGTGCAGTG
|||||||
AGTGGGTCCGACCTCACGTCAC

GAM2029 FLJ12666 3' CACTGCACTCCAGCCTGGGC 45065
GCCCAGGCTGGAGTGCAGTG
|||||||
CGGGTCCGACCTCACGTCAC

GAM2029 FLJ12671 3' CACTGCACTCCAGCCTGGGTGA 49104
TCGCCCAGGCTGGAGTGCAGTG
|||||||
AGTGGGTCCGACCTCACGTCAC

GAM2029 FLJ12687 3' CACTGCACTCCAGCCTGGGTGA 46748
TCGCCCAGGCTGGAGTGCAGTG
|||||||
AGTGGGTCCGACCTCACGTCAC

GAM2029 FLJ12800 3' CACTGCACTCCAGGCTGGGCGA 43526
TCGCCCAG CTGGAGTGCAGTG
||||| |||||
AGCGGGTC GACCTCACGTCAC
G

GAM2029 FLJ12921 3' CACTGCACTCCAGCCTGGGCGA 46394
TCGCCCAGGCTGGAGTGCAGTG
|||||||
AGCGGGTCCGACCTCACGTCAC

GAM2029 FLJ12949 3' CACTGCACTCCAGCCTGGGC 43724
GCCCAGGCTGGAGTGCAGTG
|||||||

CGGGTCCGACCTCACGTCAC

GAM2029 FLJ13117 3' CACTGCACTCCAGCCTGGGAGA 43804 G
TC CCCAGGCTGGAGTGCAGTG
|| |||||
AG GGGTCCGACCTCACGTCAC
A

GAM2029 FLJ13162 3' ATTGCACTCCGGCCTGGGC 47181
GCCCAGGCTGGAGTGCAGT
|||||
CGGGTCCGGCCTCACGTTA

GAM2029 FLJ13456 3' CACTGCACTCCAGCCTGG 66532
CCAGGCTGGAGTGCAGTG
|||||
GGTCCGACCTCACGTCAC

GAM2029 FLJ13456 3' CACTGCACTCCAGCCTGGGTGA 66533
TCGCCCAGGCTGGAGTGCAGTG
|||||
AGTGGGTCCGACCTCACGTCAC

GAM2029 FLJ13611 3' GCACTCTAGCCTGAGCGA 46866 C
TCGC CAGGCTGGAGTGC
||| |||||
AGCG GTCCGATCTCACG
A

GAM2029 FLJ13621 3' CACTGCACTCCAGCCTGGGCGA 47218
TCGCCCAGGCTGGAGTGCAGTG
|||||
AGCGGGTCCGACCTCACGTCAC

GAM2029 FLJ13769 3' GCACTCCAGCCTGGGTGA 47252
TCGCCCAGGCTGGAGTGC
|||||
AGTGGGTCCGACCTCACG

GAM2029 FLJ13848 3' GCACTCCAGCCTAGGCGA 45822 C
TCGCC AGGCTGGAGTGC
||| |||||
AGCGG TCCGACCTCACG
A

GAM2029 FLJ13952 3' CACTGCACTCCAGCCTGGGC 46007
GCCCAGGCTGGAGTGCAGTG
|||||
CGGGTCCGACCTCACGTCAC

GAM2029 FLJ14011 3' CACTGCACTCCAGTCTGGGC 42313
GCCCAGGCTGGAGTGCAGTG
|||||

CGGGTCTGACCTCACGTCAC

GAM2029 FLJ14100 3' TACTGCACTCCAGCCTGGGCGA 47339
TCGCCCAGGCTGGAGTGCAGTG
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AGCGGGTCCGACCTCACGTCAT

GAM2029 FLJ14117 3' CACTATACTCCAGCCTGGGC 43218 C
GCCCAGGCTGGAGTGCAGTG
|||||||
CGGGTCCGACCTCAT TCAC

A

GAM2029 FLJ14327 3' CACTGCACTCCAGCCTGG 46675
CCAGGCTGGAGTGCAGTG
|||||||
GGTCCGACCTCACGTCAC

GAM2029 FLJ14346 3' ACTGGACTCCAGCCTGGGC 47352 G
GCCCAGGCTGGAGT CAGT
|||||||
CGGGTCCGACCTCA GTCA

G

GAM2029 FLJ14346 3' CACTGCACTCCAGCCTGGGGGA 47358 G
TC CCCAGGCTGGAGTGCAGTG
|| |||||
AG GGGTCCGACCTCACGTCAC

G

GAM2029 FLJ14397 3' GCACTCCAGCCTGGGTGA 52327
TCGCCCAGGCTGGAGTGC
|||||||
AGTGGGTCCGACCTCACG

GAM2029 FLJ14399 3' TACTGCACTCCAGCCTGGGC 52342
GCCCAGGCTGGAGTGCAGTG
|||||||
CGGGTCCGACCTCACGTCAT

GAM2029 FLJ14457 3' CACTGCACTCCAGCCTGGGAGA 52402 G
TC CCCAGGCTGGAGTGCAGTG
|| |||||
AG GGGTCCGACCTCACGTCAC

A

GAM2029 FLJ14466 3' CACTGCACTCCAACCTGGGC 52422 C
GCCCAGG TGGAGTGCAGTG
||||| |||||
CGGGTCC ACCTCACGTCAC

A

GAM2029 FLJ14490 3' CACTGCACTCCAGCCTGGGC 52438
GCCCAGGCTGGAGTGCAGTG
|||||||

CGGGTCCGACCTCACGTCAC

GAM2029 FLJ14621 3' CACTGCACTCCAGCCTGGGC 52534
GCCCAGGCTGGAGTGCAGTG
|||||||
CGGGTCCGACCTCACGTCAC

GAM2029 FLJ20004 3' CACTGCACTCCAGCCTGGGC 34749
GCCCAGGCTGGAGTGCAGTG
|||||||
CGGGTCCGACCTCACGTCAC

GAM2029 FLJ20004 3' CACTGCACTCCAGCCTGGGTGA 34750
TCGCCCAGGCTGGAGTGCAGTG
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AGTGGGTCCGACCTCACGTCAC

GAM2029 FLJ20006 3' CACTGCAATCCAGCCTGGGCGA 34779 G
TCGCCCAGGCTGGA TGCAGTG
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AGCGGGTCCGACCT ACGTCAC
A

GAM2029 FLJ20019 3' CACTGCACTCCAGCCTAGGTGA 34814 C
TCGCC AGGCTGGAGTGCAGTG
|||||
AGTGG TCCGACCTCACGTCAC
A

GAM2029 FLJ20045 3' GCACTCCAGCCTGGGTGA 34886
TCGCCCAGGCTGGAGTGC
|||||||
AGTGGGTCCGACCTCACG

GAM2029 FLJ20069 3' GCACTCCAGCCTGGGGGA 34953 G
TC CCCAGGCTGGAGTGC
||
AG GGTCCGACCTCACG
G

GAM2029 FLJ20084 3' CACTGCACTCCAGCCTGGGC 34995
GCCCAGGCTGGAGTGCAGTG
|||||||
CGGGTCCGACCTCACGTCAC

GAM2029 FLJ20211 3' AACTGCACTCCAGCCTGGGCG 35248
A TCGCCCAGGCTGGAGTGCAGTGT
|||||||
AGCGGGTCCGACCTCACGTCACA

GAM2029 FLJ20211 3' CACTGCACTCCAGCCTGGGC 35257
GCCCAGGCTGGAGTGCAGTG
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CGGGTCCGACCTCACGTCAC

GAM2029 FLJ20241 3' CACTGCACTCCAGCCTGG 35289
CCAGGCTGGAGTGCAGTG
|||||
GGTCCGACCTCACGTCAC

GAM2029 FLJ20627 3' CACTGCACTCCAGCCAGGGC 35907 A
GCCC GGCTGGAGTGCAGTG
||| |||||
CGGG CCGACCTCACGTCAC
A

GAM2029 FLJ20700 3' CACTGCACTCCAGCCTGGGCGA 35999
TCGCCCAGGCTGGAGTGCAGTG
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AGCGGGTCCGACCTCACGTCAC

GAM2029 FLJ20802 3' CACTGCACTCCAGCCTGGGCGA 36107
TCGCCCAGGCTGGAGTGCAGTG
|||||
AGCGGGTCCGACCTCACGTCAC

GAM2029 FLJ20825 3' CACTGCAGTCCAGCCTGGGC 36142 G
GCCCAGGCTGGA TGCAGTG
||||| |||||
CGGGTCCGACCT ACGTCAC
G

GAM2029 FLJ21144 3' CACTGCACTCCAGCCTGGGC 43190
GCCCAGGCTGGAGTGCAGTG
|||||
CGGGTCCGACCTCACGTCAC

GAM2029 FLJ21162 3' CACTGCACTCCAGCCTGGG 46368
CCCAGGCTGGAGTGCAGTG
|||||
GGGTCCGACCTCACGTCAC

GAM2029 FLJ21415 3' ACTTGCTCCAGCCTGGGTGA 45683 C
TCGCCCAGGCTGGAGTG AGT
||||| |||
AGTGGGTCCGACCTCGT TCA

GAM2029 FLJ21687 3' CACTGCACTCCAGCCTGGGTGA 46292
TCGCCCAGGCTGGAGTGCAGTG
|||||
AGTGGGTCCGACCTCACGTCAC

GAM2029 FLJ21870 3' GACACTGCACTCCAGCCTGGGC 43745
GCCCAGGCTGGAGTGCAGTGC
|||||

CGGGTCCGACCTCACGTCACAG

GAM2029 FLJ22054 3' CACTGCACTCCAGCCTGGGC 96046
GCCCAGGCTGGAGTGCAGTG
|||||||
CGGGTCCGACCTCACGTCAC

GAM2029 FLJ22313 3' GCACTCCACCCTGGGCGA 42579 C
TCGCCCAGG TGGAGTGC
||||| |||||
AGCGGGTCC ACCTCACG
C

GAM2029 FLJ22316 3' CACTGCACTCCAGCCTGGGC 47612
GCCCAGGCTGGAGTGCAGTG
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CGGGTCCGACCTCACGTCAC

GAM2029 FLJ22415 3' GCACTCCAGCCTGGGTGA 93120
TCGCCCAGGCTGGAGTGC
|||||||
AGTGGGTCCGACCTCACG

GAM2029 FLJ22474 3' CACTGCACTCCAGCCTGGGC 45611
GCCCAGGCTGGAGTGCAGTG
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CGGGTCCGACCTCACGTCAC

GAM2029 FLJ22814 3' CACTGCACTCCAACCTGGGTGA 46718 C
TCGCCCAGG TGGAGTGCAGTG
||||| |||||
AGTGGGTCC ACCTCACGTCAC
A

GAM2029 FLJ22814 3' CACTGCACTCCAGCCTGGGTGA 46719
TCGCCCAGGCTGGAGTGCAGTG
|||||||
AGTGGGTCCGACCTCACGTCAC

GAM2029 FLJ22965 3' GCACTCTAGCCTGGGCGA 42298
TCGCCCAGGCTGGAGTGC
|||||||
AGCGGGTCCGATCTCACG

GAM2029 FLJ23022 5' GACACCGCCTTCTAGCCCAGGC 47496 CA T A
GCC GGCTGGAG GC GTGTC
|| ||||| || |||||
CGG CCGATCTT CG CACAG
AC C C

GAM2029 FLJ23022 3' GCACTCCAGCCTGGGCGA 47497
TCGCCCAGGCTGGAGTGC
|||||||

AGCGGGTCCGACCTCACG

GAM2029 FLJ23040 3' CACTGCACTCCAGCCTGGGC 47982
GCCCAGGCTGGAGTGCAGTG
|||||||
CGGGTCCGACCTCACGTCAC

GAM2029 FLJ23185 3' GACACTGCACTCCAGCCTTGGC 47513 C
GCC AGGCTGGAGTGCAGTGTC
||| |||||
CGG TCCGACCTCACGTCACAG
T

GAM2029 FLJ23185 3' GACACTGCACTCCAGCCTTGGC 47514 C
GCC AGGCTGGAGTGCAGTGTC
||| |||||
CGG TCCGACCTCACGTCACAG
T

GAM2029 FLJ23229 3' CACTGGACTCCAGCCTGG 47529 G
CCAGGCTGGAGT CAGTG
||||||| |||||
GGTCCGACCTCA GTCAC
G

GAM2029 FLJ23499 3' GCTCTCCAGCCTGGGCGA 43138 T
TCGCCCAGGCTGGAG GC
||||||| ||
AGCGGGTCCGACCTC CG
T

GAM2029 FLJ23556 3' CACTGCACTCCAGCCTGGGCGA 46432
TCGCCCAGGCTGGAGTGCAGTG
|||||||
AGCGGGTCCGACCTCACGTCAC

GAM2029 FLJ30681 3' TACTGCACTCCAGCCTAGGC 93439 C
GCC AGGCTGGAGTGCAGTG
||| |||||
CGG TCCGACCTCACGTCAT
A

GAM2029 FLJ31168 3' CACTGCACTCCAGCCTGGGCGA 59177
TCGCCCAGGCTGGAGTGCAGTG
|||||||
AGCGGGTCCGACCTCACGTCAC

GAM2029 FLJ31455 3' GCACTCCAGCCTGGGTGA 59286
TCGCCCAGGCTGGAGTGC
|||||||
AGTGGGTCCGACCTCACG

GAM2029 FLJ31952 3' CACTGTACTCCAGCCTGGGC 59042
GCCCAGGCTGGAGTGCAGTG
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CGGGTCCGACCTCATGTCAC

GAM2029 FLJ32915 5' CACTGCACTCCAGCCTGGGCGA 59428
TCGCCCAGGCTGGAGTGCAGTG
|||||
AGCGGGTCCGACCTCACGTCAC

GAM2029 FUSIP1 3' CACTGCACTCCAGCCTGGGC 55035
GCCCAGGCTGGAGTGCAGTG
|||||
CGGGTCCGACCTCACGTCAC

GAM2029 GALNT6 3' CACTGCACTCCAGCCTGGGC 24242
GCCCAGGCTGGAGTGCAGTG
|||||
CGGGTCCGACCTCACGTCAC

GAM2029 GNB4 3' CACTGCACTCCAGCCTAGGCGA 41565 C
TCGCC AGGCTGGAGTGCAGTG
|||||
AGCGG TCCGACCTCACGTCAC
A

GAM2029 GP5 3' GCACTCTAGCCTGGGCGA 16876
TCGCCCAGGCTGGAGTGC
|||||
AGCGGGTCCGATCTCACG

GAM2029 GTF3C4 3' ACTTCCTCCAGCCTGAAGA 25206 GCC TGC
TC CAGGCTGGAG AGT
|| ||||| ||
AG GTCCGACCTC TCA
AA_ CT_

GAM2029 GTPBP5 3' CACTGCACTCCAGCCTGAGCGA 65969 C
TCGC CAGGCTGGAGTGCAGTG
|||||
AGCG GTCCGACCTCACGTCAC
A

GAM2029 GTPBP5 3' CACTGCACTCCAGCCTGAGTGA 65970 C
TCGC CAGGCTGGAGTGCAGTG
|||||
AGTG GTCCGACCTCACGTCAC
A

GAM2029 GTSE1 3' CACTGCACTCCAGCCTGGGC 33562
GCCCAGGCTGGAGTGCAGTG
|||||
CGGGTCCGACCTCACGTCAC

GAM2029 HCGIX 3' CACTACACTCCAGCCTGGGTGA 20712 C
TCGCCCAGGCTGGAGTGCAGTG
|||||

AGTGGGTCCGACCTCAC TCAC

A

GAM2029 HEI10 3' CACTGCACTCCAGCCTGGGC 41294
GCCCAGGCTGGAGTGCAGTG
|||||||
CGGGTCCGACCTCACGTCAC

GAM2029 HES2 3' CACTGCACTCCAGGCTGGGCGA 39370 G
TCGCCCAG CTGGAGTGCAGTG
||||| |||||
AGCGGGTC GACCTCACGTCAC

G

GAM2029 HIC 3' ACCTGCACTCCAGCCTGGGC 68040 T
GCCCAGGCTGGAGTGCAG GT
||||||| ||
CGGGTCCGACCTCACGTC CA

GAM2029 HSD17B7 3' CACTGCACTCCAGCCTGGGTGA 33481
TCGCCCAGGCTGGAGTGCAGTG
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AGTGGGTCCGACCTCACGTCAC

GAM2029 HSMPP8 3' CACTGCACTCCAGCCTGAGTGA 95128 C
TCGC CAGGCTGGAGTGCAGTG
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AGTG GTCCGACCTCACGTCAC

A

GAM2029 HSPC043 3' CACTGCACTCCAGCCTGGGTGA 68349
TCGCCCAGGCTGGAGTGCAGTG
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AGTGGGTCCGACCTCACGTCAC

GAM2029 ICAM4 3' CACTGCACTCCAGCCTGGGGGA 9534 G
TC CCCAGGCTGGAGTGCAGTG
|| |||||
AG GGGTCCGACCTCACGTCAC

G

GAM2029 ICAM4 3' CACTGCACTCCAGCCTGGGGGA 9535 G
TC CCCAGGCTGGAGTGCAGTG
|| |||||
AG GGGTCCGACCTCACGTCAC

G

GAM2029 IL-23R 3' CACTGCACTCCAGCCTGGGC 59129
GCCCAGGCTGGAGTGCAGTG
|||||||
CGGGTCCGACCTCACGTCAC

GAM2029 IL10RB 3' GCACTGCACTCCAGCCTGGGTG 7128
A TCGCCCAGGCTGGAGTGCAGTGT
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AGTGGGTCCGACCTCACGTCACG

GAM2029 IMAGE:4907098 3' CACTGCACTCCAGCCTGGGCGA 57752
TCGCCCAGGCTGGAGTGCAGTG
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AGCGGGTCCGACCTCACGTCAC

GAM2029 JDD1 3' GCACTCCAGCCTGGGTGA 63915
TCGCCCAGGCTGGAGTGC
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AGTGGGTCCGACCTCACG

GAM2029 KCNH6 3' CACTGCACTCCAGCCTGGGTGA 48569
TCGCCCAGGCTGGAGTGCAGTG
|||||||
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GAM2029 KIAA0184 3' TACTGCACTCCAGCCTGGGTGA 65814
TCGCCCAGGCTGGAGTGCAGTG
|||||||
AGTGGGTCCGACCTCACGTCAT

GAM2029 KIAA0189 3' GACACTGCCCAGGCCAAGC 28942 CCA _ AGT
GC GGC TGG GCAGTGTC
|| ||| |||
CG CCG ACC CGTCACAG
AA_ G _

GAM2029 KIAA0226 3' CACCGCACTCCAGCCTGGGTGA 64253 A
TCGCCCAGGCTGGAGTGC GTG
||||||| |||
AGTGGGTCCGACCTCACG CAC
C

GAM2029 KIAA0355 3' CACTGCACTCCAGCCTGGGTGA 28700
TCGCCCAGGCTGGAGTGCAGTG
|||||||
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GAM2029 KIAA0391 3' TACTGCACTCCAGCCTAGGTGA 28617 C
TCGCC AGGCTGGAGTGCAGTG
|||| |||||
AGTGG TCCGACCTCACGTCAT
A

GAM2029 KIAA0408 3' CACTGCACTCCAGCCTGGGTGA 28795
TCGCCCAGGCTGGAGTGCAGTG
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GAM2029 KIAA0446 5' CACTGCACTCCAGCCTGGGCGA 69443
TCGCCCAGGCTGGAGTGCAGTG
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AGCGGGTCCGACCTCACGTCAC

GAM2029 KIAA0451 5' CACTACACTTCAGCCTGGGC 29763 C
GCCCAGGCTGGAGTG AGTG
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CGGGTCCGACTTCAC TCAC

A

GAM2029 KIAA0472 3' CACTGCACTCCAGCCTGGGC 72340
GCCCAGGCTGGAGTGCAGTG
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CGGGTCCGACCTCACGTCAC

GAM2029 KIAA0472 3' CACTGCACTCCAGCCTGGGC 72341
GCCCAGGCTGGAGTGCAGTG
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GAM2029 KIAA0472 3' GCACTCCAGCCTGGGCGA 72355
TCGCCCAGGCTGGAGTGC
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AGCGGGTCCGACCTCACG

GAM2029 KIAA0475 3' GCACTCCAGCCTGGGAGA 30119 G
TC CCCAGGCTGGAGTGC
|| |||||
AG GGGTCCGACCTCACG
A

GAM2029 KIAA0563 3' CACTGCACTCCAGCCTGGGCGA 29871
TCGCCCAGGCTGGAGTGCAGTG
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GAM2029 KIAA0565 3' GCACTCCAACCTGGGCGA 67439 C
TCGCCCAGG TGGAGTGC
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AGCGGGTCC ACCTCACG
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GAM2029 KIAA0596 3' GCACTCCAACCTAGGTGA 63493 C C
TCGCC AGG TGGAGTGC
|||| ||| |||||
AGTGG TCC ACCTCACG
A A

GAM2029 KIAA0635 3' GCACTCCAGCCTGGGTGA 28416
TCGCCCAGGCTGGAGTGC
|||||||
AGTGGGTCCGACCTCACG

GAM2029 KIAA0643 3' CACTGCACTCCAGCCTGGGTGA 45972
TCGCCCAGGCTGGAGTGCAGTG
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AGTGGGTCCGACCTCACGTCAC

GAM2029 KIAA0694 3' CACTGCACTCCAGCCTGGGC 72965
GCCCAGGCTGGAGTGCAGTG
|||||||
CGGGTCCGACCTCACGTCAC

GAM2029 KIAA0738 3' CACTGCACTCCAGCCTGGGGGA 28884 G
TC CCCAGGCTGGAGTGCAGTG
|| |||||
AG GGGTCCGACCTCACGTCAC
G

GAM2029 KIAA0872 3' CACTGCACTCCAGCCTGGGTGA 30743
TCGCCCAGGCTGGAGTGCAGTG
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GAM2029 KIAA0876 3' CACTGCACTCCAGCCTGGGC 65315
GCCCAGGCTGGAGTGCAGTG
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GAM2029 KIAA0889 3' CACTGCACTCCAGCCTGGGTGA 31761
TCGCCCAGGCTGGAGTGCAGTG
|||||||
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GAM2029 KIAA0889 3' GCACTCCAGCCTGGGTGA 31778
TCGCCCAGGCTGGAGTGC
|||||||
AGTGGGTCCGACCTCACG

GAM2029 KIAA0892 3' GACACTGCACTCCAGCCTGGGT 71570
GA TCGCCCAGGCTGGAGTGCAGTGTC
|||||||
AGTGGGTCCGACCTCACGTCACAG

GAM2029 KIAA0894 3' GCACTCCAGCCTGGGTGA 30334
TCGCCCAGGCTGGAGTGC
|||||||
AGTGGGTCCGACCTCACG

GAM2029 KIAA1001 3' CACTGCACTCCAGCCTGGGTGA 31002
TCGCCCAGGCTGGAGTGCAGTG
|||||||
AGTGGGTCCGACCTCACGTCAC

GAM2029 KIAA1030 3' ACTTCACTCCAGCCTGGGTGA 94970 C
TCGCCCAGGCTGGAGTGC AGT
|||||||

AGTGGGTCCGACCTCAC TCA

T

GAM2029 KIAA1032 3' ACTGCACTCCAGCCTGGGC 66719
GCCCAGGCTGGAGTGCAGT
|||||||
CGGGTCCGACCTCACGTCA

GAM2029 KIAA1143 3' CACTGCACTCCAGCCTGGGC 69231
GCCCAGGCTGGAGTGCAGTG
|||||||
CGGGTCCGACCTCACGTAC

GAM2029 KIAA1143 3' CTGAGCCCAGCCTGGGCGA 69238 A G
TCGCCCAGGCTGG GT CAG
||||||| || |||
AGCGGGTCCGACC CG GTC

— A

GAM2029 KIAA1164 3' GCACTCCAGCCTGGGTGA 70045
TCGCCCAGGCTGGAGTGC
|||||||
AGTGGGTCCGACCTCACG

GAM2029 KIAA1228 3' CACTGCACTCCAGCCTGGGC 65669
GCCCAGGCTGGAGTGCAGTG
|||||||
CGGGTCCGACCTCACGTAC

GAM2029 KIAA1271 3' CACTGCACTCCAACCTGGGTGA 70129 C
TCGCCCAGG TGGAGTGCAGTG
||||||| |||||
AGTGGGTCC ACCTCACGTAC

A

GAM2029 KIAA1271 3' GCGCTCCAGCCTGGGCGA 70142
TCGCCCAGGCTGGAGTGC
|||||||
AGCGGGTCCGACCTCGCG

GAM2029 KIAA1277 3' CACTGCACTCCAGCCTGG 65072
CCAGGCTGGAGTGCAGTG
|||||||
GGTCCGACCTCACGTAC

GAM2029 KIAA1328 3' GCACTCCAGCCTGGGTGA 62324
TCGCCCAGGCTGGAGTGC
|||||||
AGTGGGTCCGACCTCACG

GAM2029 KIAA1340 3' GCACTCCAGCCTGGGCGA 69697
TCGCCCAGGCTGGAGTGC
|||||||

AGCGGGTCCGACCTCACG

GAM2029 KIAA1404 3' GCACTCCAGTCTGGGCGA 62690
TCGCCCAGGCTGGAGTGC
|||||||
AGCGGGTCTGACCTCACG

GAM2029 KIAA1456 5' CACTGCACTCCAGCCTGGGTGA 67535
TCGCCCAGGCTGGAGTGCAGTG
|||||||
AGTGGGTCCGACCTCACGTCAC

GAM2029 KIAA1456 3' CACTGCACTGCAGCCTGGGC 67536 G
GCCCAGGCTG AGTGCAGTG
|||||||
CGGGTCCGAC TCACGTCAC
G

GAM2029 KIAA1486 3' CACTGCACTCCAGCCTGGGTGA 67970
TCGCCCAGGCTGGAGTGCAGTG
|||||||
AGTGGGTCCGACCTCACGTCAC

GAM2029 KIAA1497 5' CACTGCACTCCAGCCTGGGCGA 68116
TCGCCCAGGCTGGAGTGCAGTG
|||||||
AGCGGGTCCGACCTCACGTCAC

GAM2029 KIAA1503 3' CACTACACTCCAGCCTGGGCGA 68896 C
TCGCCCAGGCTGGAGTG AGTG
|||||||
AGCGGGTCCGACCTCAC TCAC
A

GAM2029 KIAA1508 3' CACTGCACTCCAGCCTGGGTGA 62544
TCGCCCAGGCTGGAGTGCAGTG
|||||||
AGTGGGTCCGACCTCACGTCAC

GAM2029 KIAA1554 3' CACTGCACTCCAACCTGGGTGA 96854 C
TCGCCCAGG TGGAGTGCAGTG
|||||||
AGTGGGTCC ACCTCACGTCAC
A

GAM2029 KIAA1559 3' CACTGCACTCCAGCCTGGGT 73448
GCCCAGGCTGGAGTGCAGTG
|||||||
TGGGTCCGACCTCACGTCAC

GAM2029 KIAA1559 3' CACTGCACTCCAGCCTGGGTGA 73449
TCGCCCAGGCTGGAGTGCAGTG
|||||||

AGTGGGTCCGACCTCACGTCAC

GAM2029 KIAA1641 3' CACTGCACTCCAGCCTGAGC 81017 C
GC CAGGCTGGAGTGCAGTG
|| |||||
CG GTCCGACCTCACGTCAC
A

GAM2029 KIAA1649 3' CACTGCACTCCAGCCTGTGC 51219 C
GC CAGGCTGGAGTGCAGTG
|| |||||
CG GTCCGACCTCACGTCAC
T

GAM2029 KIAA1674 3' CACTGCACTCCAGCCTGGGCGA 69331
TCGCCCAGGCTGGAGTGCAGTG
|||||
AGCGGGTCCGACCTCACGTCAC

GAM2029 KIAA1727 3' CACTGCACTCCAGCCTGGATGA 64751 C
TCG CCAGGCTGGAGTGCAGTG
||| |||||
AGT GGTCCGACCTCACGTCAC
A

GAM2029 KIAA1786 3' CACTGCACCCAGCCCGGGTGA 66629 A A
TCGCCC GGCTGG GTGCAGTG
||||| |||||
AGTGGG CCGACC CACGTCAC
C C

GAM2029 KIAA1871 3' CACTGCACTCCAGCCTGGGC 61896
GCCCAGGCTGGAGTGCAGTG
|||||
CGGGTCCGACCTCACGTCAC

GAM2029 KIAA1872 3' CACTGCACTCCAGCCTGGGAGA 63598 G
TC CCCAGGCTGGAGTGCAGTG
|| |||||
AG GGGTCCGACCTCACGTCAC
A

GAM2029 KIAA1872 3' CACTGCACTCCAGCCTGGGC 63599
GCCCAGGCTGGAGTGCAGTG
|||||
CGGGTCCGACCTCACGTCAC

GAM2029 KIAA1872 3' CACTGCATTCCAGCCTGGGCGA 63600
TCGCCCAGGCTGGAGTGCAGTG
|||||
AGCGGGTCCGACCTTACGTCAC

GAM2029 KIAA1879 3' CACTGCACTCCAGCCTGGGAGA 73931 G
TC CCCAGGCTGGAGTGCAGTG
|| |||||

		AG GGGTCCGACCTCACGTCAC		
		A		
GAM2029	KIAA1941	3'	CACTGCACTCCAGCCCGGGCGA 75335	A
			TCGCCC GGCTGGAGTGCAGTG	
			AGCGGG CCGACCTCACGTCAC	
			C	
GAM2029	KIAA1948	5'	CACTGCACTCCAGCCTGGGTGA 83295	
			TCGCCCAGGCTGGAGTGCAGTG	
			AGTGGGTCCGACCTCACGTCAC	
GAM2029	KIAA1948	3'	CACTGCACTCCAGCCTGGGTGA 83296	
			TCGCCCAGGCTGGAGTGCAGTG	
			AGTGGGTCCGACCTCACGTCAC	
GAM2029	KIAA1951	3'	CACTGCACTCCAGCCTGGGCGA 74147	
			TCGCCCAGGCTGGAGTGCAGTG	
			AGCGGGTCCGACCTCACGTCAC	
GAM2029	KIAA1951	3'	CACTGCACTCCAGTCTGGGC 74148	
			GCCCAGGCTGGAGTGCAGTG	
			CGGGTCTGACCTCACGTCAC	
GAM2029	KIAA1954	3'	TACTGCATTCCAGCCTGAGC 78229	C
			GC CAGGCTGGAGTGCAGTG	
			CG GTCCGACCTTACGTCAT	
			A	
GAM2029	KIAA1958	3'	CACTGCACTCCAGCCTGGGC 82777	
			GCCCAGGCTGGAGTGCAGTG	
			CGGGTCCGACCTCACGTCAC	
GAM2029	KIAA1979	3'	ACATTAACTCTAGCCTGAGC 89643	C
			GC CAGGCTGGAGTG AGTGT	C
			CG GTCCGATCTCAC TTACA	
			A A	
GAM2029	KR18	3'	CACTGCACTCCAGCCTGGGC 53883	
			GCCCAGGCTGGAGTGCAGTG	
			CGGGTCCGACCTCACGTCAC	
GAM2029	KREMEN	3'	CACCACACTCCAGCCTGAGC 50226	C
			GC CAGGCTGGAGTG GTG	CA

			CG GTCCGACCTCAC CAC	
			A AC	
GAM2029	LANO	3'	CACTGCACTCCAGCCCGGGTGA 47970	A
			TCGCCC GGCTGGAGTGCAGTG	
			AGTGGG CCGACCTCACGTCAC	
			C	
GAM2029	LIM	3'	CACTGCACTCCAGCCTGGGTGA 22319	
			TCGCCCAGGCTGGAGTGCAGTG	
			AGTGGGTCCGACCTCACGTCAC	
GAM2029	LRG	3'	GCACTCTAGCCTGGGCGA 54821	
			TCGCCCAGGCTGGAGTGC	
			AGCGGGTCCGATCTCACG	
GAM2029	LSR68	3'	CACTGCACTCCAGCCTGGGCGA 38551	
			TCGCCCAGGCTGGAGTGCAGTG	
			AGCGGGTCCGACCTCACGTCAC	
GAM2029	MAWBP	3'	CACTGCACTCCAGCCTGGGC 42378	
			GCCCAGGCTGGAGTGCAGTG	
			CGGGTCCGACCTCACGTCAC	
GAM2029	MCAM	3'	CACTGCACTCCAGCCTGGGC 22456	
			GCCCAGGCTGGAGTGCAGTG	
			CGGGTCCGACCTCACGTCAC	
GAM2029	MESDC2	3'	CACTGCACTCCAGCCTGGATGA 72909	C
			TCG CCAGGCTGGAGTGCAGTG	
			AGT GGTCCGACCTCACGTCAC	
			A	
GAM2029	MGC10200	3'	CACTGCACTCCAGTCTGGGC 59636	
			GCCCAGGCTGGAGTGCAGTG	
			CGGGTCTGACCTCACGTCAC	
GAM2029	MGC10765	3'	CACTGCACTCCAGCCTAGGCGA 44556	C
			TCGCC AGGCTGGAGTGCAGTG	
			AGCGG TCCGACCTCACGTCAC	
			A	
GAM2029	MGC11386	3'	CACTGCACTCCAGCCTGGGC 53058	
			GCCCAGGCTGGAGTGCAGTG	

CGGGTCCGACCTCACGTCAC

GAM2029 MGC13008 3' CTCACTCCAGCCTGGGC 52057 C
GCCCAGGCTGGAGTG AG
||||||| ||
CGGGTCCGACCTCAC TC

—
GAM2029 MGC13053 3' CACTGCACTCCAGCCTGGGCGA 52098
TCGCCCAGGCTGGAGTGCAGTG
|||||||
AGCGGGTCCGACCTCACGTCAC

GAM2029 MGC13053 3' CACTGCACTCCAGCCTGGGCGA 52099
TCGCCCAGGCTGGAGTGCAGTG
|||||||
AGCGGGTCCGACCTCACGTCAC

GAM2029 MGC14407 3' CACTGCACTCCAGCCTGGGTGA 52970
TCGCCCAGGCTGGAGTGCAGTG
|||||||
AGTGGGTCCGACCTCACGTCAC

GAM2029 MGC14436 3' CACTGCACTCCAGCCTGGGTGA 52922
TCGCCCAGGCTGGAGTGCAGTG
|||||||
AGTGGGTCCGACCTCACGTCAC

GAM2029 MGC14799 3' GCACTCCAGCCTGGGTGA 51330
TCGCCCAGGCTGGAGTGC
|||||||
AGTGGGTCCGACCTCACG

GAM2029 MGC15397 3' CACTGCACTCCAGCCTGGGTGA 55551
TCGCCCAGGCTGGAGTGCAGTG
|||||||
AGTGGGTCCGACCTCACGTCAC

GAM2029 MGC16037 3' CACTGCACTCCAGCCTGG 52890
CCAGGCTGGAGTGCAGTG
|||||||
GGTCCGACCTCACGTCAC

GAM2029 MGC16142 3' CACTGCACTCCAGTCTGGGC 52261
GCCCAGGCTGGAGTGCAGTG
|||||||
CGGGTCTGACCTCACGTCAC

GAM2029 MGC16175 3' CACTGCACTCCAGCCTGGGC 52274
GCCCAGGCTGGAGTGCAGTG
|||||||

CGGGTCCGACCTCACGTCAC

GAM2029 MGC16384 5' ACACTGCATTTCCTCAAGG 54932 CA CT
CC GG GGAGTGCAGTGT
|| || |||||
GG CC CTTTACGTCACA
AA C_

GAM2029 MGC16703 3' CACTGCACTCCAGCCTGGGC 73488
GCCCAGGCTGGAGTGCAGTG
|||||
CGGGTCCGACCTCACGTCAC

GAM2029 MGC20235 3' ACTGCACTCCAGCCTGGGC 59546
GCCCAGGCTGGAGTGCAGT
|||||
CGGGTCCGACCTCACGTCA

GAM2029 MGC23244 3' CACTGCACTCCAGCCTGGGCGA 58828
TCGCCCAGGCTGGAGTGCAGTG
|||||
AGCGGGTCCGACCTCACGTCAC

GAM2029 MGC2562 3' CACTGCACTCCAGCCTGGAAGA 51429 GC
TC CCAGGCTGGAGTGCAGTG
|| |||||
AG GGTCCGACCTCACGTCAC
AA

GAM2029 MGC2562 3' CACTGCACTCCAGCCTGGGCGA 51430
TCGCCCAGGCTGGAGTGCAGTG
|||||
AGCGGGTCCGACCTCACGTCAC

GAM2029 MGC2663 3' CACTGCACTCCAGCCTGGGCGA 44332
TCGCCCAGGCTGGAGTGCAGTG
|||||
AGCGGGTCCGACCTCACGTCAC

GAM2029 MGC3101 5' CACTGCACTCCAGCCTGGGTGA 44101
TCGCCCAGGCTGGAGTGCAGTG
|||||
AGTGGGTCCGACCTCACGTCAC

GAM2029 MGC3207 3' CACTGCACTCCAGCCTGGGC 63233
GCCCAGGCTGGAGTGCAGTG
|||||
CGGGTCCGACCTCACGTCAC

GAM2029 MGC3329 3' CACTGCACTACAGCCTGGGCGA 44240 G
TCGCCCAGGCTG AGTGCAGTG
|||||

AGCGGGTCCGAC TCACGTCAC

A

GAM2029 MGC4562 3' CACTGCATTCCAGCCTGGGC 56734
GCCCAGGCTGGAGTGCAGTG
|||||
CGGGTCCGACCTTACGTCAC

GAM2029 MGC4663 3' CACTGCACTCCAGCCTGGGC 44783
GCCCAGGCTGGAGTGCAGTG
|||||
CGGGTCCGACCTCACGTCAC

GAM2029 MGC5457 3' GCACTCCAGCCTGGGTGA 51939
TCGCCCAGGCTGGAGTGC
|||||
AGTGGGTCCGACCTCACG

GAM2029 MOST2 5' CACTGCACTCCAGCCTGGGC 40055
GCCCAGGCTGGAGTGCAGTG
|||||
CGGGTCCGACCTCACGTCAC

GAM2029 MRP63 3' GCACTCCAGCCTGGGAGA 44047 G
TC CCCAGGCTGGAGTGC
|| |||||
AG GGGTCCGACCTCACG
A

GAM2029 MRPL48 5' CACTACACTCCAGCCTGCGC 32655 C C
GC CAGGCTGGAGTG AGTG
|| ||||| ||||
CG GTCCGACCTCAC TCAC
C A

GAM2029 MRPS18B 3' GCACTCCAGCCTGGGTGA 26751
TCGCCCAGGCTGGAGTGC
|||||
AGTGGGTCCGACCTCACG

GAM2029 My015 3' CACTGCACTCCAGCCTGGGAGA 67228 G
TC CCCAGGCTGGAGTGCAGTG
|| |||||
AG GGGTCCGACCTCACGTCAC
A

GAM2029 NMNAT 3' CACTGCACTCCAGCCTGGGC 43280
GCCCAGGCTGGAGTGCAGTG
|||||
CGGGTCCGACCTCACGTCAC

GAM2029 NMNAT 3' GCACTCCAGCCTGGGTGA 43288
TCGCCCAGGCTGGAGTGC
|||||

AGTGGGTCCGACCTCACG

GAM2029	NMT2	3'	CACTGCACTCCAGCCTGGGTGA 17854	
			TCGCCCAGGCTGGAGTGCAGTG	
			AGTGGGTCCGACCTCACGTCAC	
GAM2029	Nup43	3'	ACTTCACTCCAGCCTGGGC 45340	C
			GCCCAGGCTGGAGTG AGT	
			CGGGTCCGACCTCAC TCA	
			T	
GAM2029	NY-BR-1	3'	GCACTCCAGCCTAGGTGA 54852	C
			TCGCC AGGCTGGAGTGC	
			AGTGG TCCGACCTCACG	
			A	
GAM2029	OR51E2	3'	CACTACACTCCAGCCTGGGC 48505	C
			GCCCAGGCTGGAGTG AGTG	
			CGGGTCCGACCTCAC TCAC	
			A	
GAM2029	ORC6L	3'	CACCGCACTCCAGCCTGGGTGA 27488	A
			TCGCCCAGGCTGGAGTGC GTG	
			AGTGGGTCCGACCTCACG CAC	
			C	
GAM2029	PAFAH2	3'	CACTGCACTCCAGCCTGGGTGA 6497	
			TCGCCCAGGCTGGAGTGCAGTG	
			AGTGGGTCCGACCTCACGTCAC	
GAM2029	PB1	3'	ACTCTACTCCAGCCTGGGC 36869	C
			GCCCAGGCTGGAGTG AGT	
			CGGGTCCGACCTCAT TCA	
			C	
GAM2029	PDCD7	3'	GCACTCCAGCCTGGGAGA 72606	G
			TC CCCAGGCTGGAGTGC	
			AG GGGTCCGACCTCACG	
			A	
GAM2029	phorbolin-1	3'	TACTGCACTCCAGCCTGGGCGA 90212	
			TCGCCCAGGCTGGAGTGCAGTG	
			AGCGGGTCCGACCTCACGTCAT	
GAM2029	POFUT1	3'	CACTGCATTCCAGCCTGGGC 70972	
			GCCCAGGCTGGAGTGCAGTG	

CGGGTCCGACCTTACGTCAC

GAM2029 POLYDOM 3' CACTGCACTCCAGCCTGGGC 44685
GCCCAGGCTGGAGTGCAGTG
|||||||
CGGGTCCGACCTCACGTCAC

GAM2029 PRIC285 3' CACTGCACTCCAGCCTGGGTGA 62110
TCGCCCAGGCTGGAGTGCAGTG
|||||||
AGTGGGTCCGACCTCACGTCAC

GAM2029 PRO0038 3' CACTGCACTCCAGCCTGGGTGA 26929
TCGCCCAGGCTGGAGTGCAGTG
|||||||
AGTGGGTCCGACCTCACGTCAC

GAM2029 PRO0478 5' CACTGCACTCCAGCCTGG 27023
CCAGGCTGGAGTGCAGTG
|||||||
GGTCCGACCTCACGTCAC

GAM2029 PRO0478 3' CACTGCACTCCAGCCTGGGGGA 27024 G
TC CCCAGGCTGGAGTGCAGTG
|| |||||
AG GGGTCCGACCTCACGTCAC
G

GAM2029 PRO1386 3' CACTGTACTCCAGCCTGGGC 49213
GCCCAGGCTGGAGTGCAGTG
|||||||
CGGGTCCGACCTCATGTCAC

GAM2029 PRO1942 5' CACTACACTCCAGCCTGG 38382 C
CCAGGCTGGAGTG AGTG
||||||| |||
GGTCCGACCTCAC TCAC
A

GAM2029 PRO2133 3' CACTGCACTCCAGTCTGGGC 38399
GCCCAGGCTGGAGTGCAGTG
|||||||
CGGGTCTGACCTCACGTCAC

GAM2029 PROL2 3' CACTGCACTCCAGCCTGGGT 23321
GCCCAGGCTGGAGTGCAGTG
|||||||
TGGGTCCGACCTCACGTCAC

GAM2029 PSR 3' GCCACTCCAGCCTGGGTGA 65788 —
TCGCCCAGGCTGGAGTG C
||||||| |

AGTGGGTCCGACCTCAC G

C

GAM2029 PTK6 3' CACTGCACTCCAGCCTGGGCGA 21069
TCGCCCAGGCTGGAGTGCAGTG
|||||
AGCGGGTCCGACCTCACGTCAC

GAM2029 PTRF 3' GACACTGCACTCCAGCCTGGGT 64238
GA TCGCCCAGGCTGGAGTGCAGTGTC
|||||
AGTGGGTCCGACCTCACGTCACAG

GAM2029 PTRF 5' GACACTGCGGCGCGTGGACGA 64239 C G TGGAG
TCG CCA GC TGCAGTGTC
||| ||| || |||||
AGC GGT CG GCGTCACAG
A G CG__

GAM2029 Rabip4R 3' CACTGCACTCCAACCTGGGTGA 36274 C
TCGCCCAGG TGGAGTGCAGTG
||||| |||||
AGTGGGTCC ACCTCACGTCAC
A

GAM2029 RHOBTB3 3' CACTGCACTCCAGCCTGGGTGA 30422
TCGCCCAGGCTGGAGTGCAGTG
|||||
AGTGGGTCCGACCTCACGTCAC

GAM2029 Rpo1-2 3' CACCACACTCCAGCCTGGGCGA 39211 CA
TCGCCCAGGCTGGAGTG GTG
||||| |||
AGCGGGTCCGACCTCAC CAC
AC

GAM2029 Rpo1-2 3' CACTGCACTCCAGCCTGGGTGA 39214
TCGCCCAGGCTGGAGTGCAGTG
|||||
AGTGGGTCCGACCTCACGTCAC

GAM2029 RRP4 3' ACCACACTCCAGCCTGGGTGA 27350 CA
TCGCCCAGGCTGGAGTG GT
||||| ||
AGTGGGTCCGACCTCAC CA
AC

GAM2029 SAMHD1 3' GCACTCCAGCCTGGGTGA 61988
TCGCCCAGGCTGGAGTGC
|||||
AGTGGGTCCGACCTCACG

GAM2029 SC65 3' CACCGCACTCCAGCCTGGGCGA 22286 A
TCGCCCAGGCTGGAGTGC GTG
||||| |||

		AGCGGGTCCGACCTCACG CAC	
		C	
GAM2029	SC65	3' CACTGCACTCCAGCCTGGGCGA 22289	
		TCGCCCAGGCTGGAGTGCAGTG	
		AGCGGGTCCGACCTCACGTCAC	
GAM2029	SCAND2	3' CACTGCACTCCAGCCTGGGCGA 54415	
		TCGCCCAGGCTGGAGTGCAGTG	
		AGCGGGTCCGACCTCACGTCAC	
GAM2029	SCAND2	3' CACTGCATTCCAGCCTGGGCGA 54416	
		TCGCCCAGGCTGGAGTGCAGTG	
		AGCGGGTCCGACCTTACGTCAC	
GAM2029	SCIN	3' CACCACACTCCAGCCTGGGC 53598	CA
		GCCCAGGCTGGAGTG GTG	
		CGGGTCCGACCTCAC CAC	
		AC	
GAM2029	SCYA5	3' ACTTCACTCCAGCCTGGGTGA 12954	C
		TCGCCCAGGCTGGAGTG AGT	
		AGTGGGTCCGACCTCAC TCA	
		T	
GAM2029	SCYA5	3' CACTGCACTCCAGCCTGGGCGA 12961	
		TCGCCCAGGCTGGAGTGCAGTG	
		AGCGGGTCCGACCTCACGTCAC	
GAM2029	SIAT4A	3' CACTGCACTCCAGCCTGGG 13135	
		CCCAGGCTGGAGTGCAGTG	
		GGGTCCGACCTCACGTCAC	
GAM2029	SMA3	3' CACTGCACTCCAGCCTGGGTGA 23257	
		TCGCCCAGGCTGGAGTGCAGTG	
		AGTGGGTCCGACCTCACGTCAC	
GAM2029	SNAPC1	3' CACTGCACTCCAGCCTGGGC 13274	
		GCCCAGGCTGGAGTGCAGTG	
		CGGGTCCGACCTCACGTCAC	
GAM2029	SPRY4	3' CACTACACTCCAGCCTGGGTGA 48997	C
		TCGCCCAGGCTGGAGTG AGTG	

AGTGGGTCCGACCTCAC TCAC

A

GAM2029 SPRY4 3' GCACTCCAGCCTGGGTGA 49016
TCGCCCAGGCTGGAGTGC
|||||
AGTGGGTCCGACCTCACG

GAM2029 SPRY4 3' GCACTCCAGCCTTGGCGA 49017 C
TCGCC AGGCTGGAGTGC
|||||
AGCGG TCCGACCTCACG

T

GAM2029 SPTLC2 3' GCACTCCAGCCTGGGTGA 17994
TCGCCCAGGCTGGAGTGC
|||||
AGTGGGTCCGACCTCACG

GAM2029 SPTLC2 3' GCACTCCAGCCTTGGCGA 17995 C
TCGCC AGGCTGGAGTGC
|||||
AGCGG TCCGACCTCACG

T

GAM2029 SYAP1 3' CACTGCACTCCAGCCTGGGTGA 52469
TCGCCCAGGCTGGAGTGCAGTG
|||||
AGTGGGTCCGACCTCACGTCAC

GAM2029 THEA 3' CACTGCACTCCAGCCCAGGC 66877 CA
GCC GGCTGGAGTGCAGTG
|||
CGG CCGACCTCACGTCAC

AC

GAM2029 THEA 3' CACTGCACTCCAGCCTGGGTGA 66878
TCGCCCAGGCTGGAGTGCAGTG
|||||
AGTGGGTCCGACCTCACGTCAC

GAM2029 TIP47 3' GCACTCCAGCCTGGGGGA 20604 G
TC CCCAGGCTGGAGTGC
||
AG GGGTCCGACCTCACG

G

GAM2029 TMG4 3' CACTGCATTCCAGCCTGGGCGA 44211
TCGCCCAGGCTGGAGTGCAGTG
|||||
AGCGGGTCCGACCTTACGTCAC

GAM2029 TOMM70A 3' CACTGCACTCCAGCCTGGGC 29737
GCCCAGGCTGGAGTGCAGTG
|||||

CGGGTCCGACCTCACGTCAC

GAM2029 TOR1B 3' GACATGGGCCAGACTG 27974 G A G G
CAG CTGG GT CA TGTC
||| ||| || |||
GTC GACC CG GT ACAG
A _ G _

GAM2029 TRIAD3 3' CACTGCACTCCAGCCTGAGC 96131 C
GC CAGGCTGGAGTGCAGTG
|| |||||
CG GTCCGACCTCACGTCAC
A

GAM2029 UBCE7IP5 3' CACTGTACTCCAGCCTGGGCGA 30842
TCGCCCAGGCTGGAGTGCAGTG
|||||||
AGCGGGTCCGACCTCATGTCAC

GAM2029 UST 3' CACTGCACTCCAGCCTGGGTGA 20350
TCGCCCAGGCTGGAGTGCAGTG
|||||||
AGTGGGTCCGACCTCACGTCAC

GAM2029 VPS4B 3' GCACTCCAGCCTGGGCGA 18023
TCGCCCAGGCTGGAGTGC
|||||||
AGCGGGTCCGACCTCACG

GAM2029 WBSCR21 3' CACTACACTCCAGCCTAGGC 49296 C C
GCC AGGCTGGAGTG AGTG
||| |||||
CGG TCCGACCTCAC TCAC
A A

GAM2029 WBSCR23 5' CACTGCACTCCAGCCTGGGCGA 47422
TCGCCCAGGCTGGAGTGCAGTG
|||||||
AGCGGGTCCGACCTCACGTCAC

GAM2029 WBSCR23 3' CACTGCACTCCAGCCTGGGCGA 47423
TCGCCCAGGCTGGAGTGCAGTG
|||||||
AGCGGGTCCGACCTCACGTCAC

GAM2029 WBSCR23 3' CACTGCACTCCAGCCTGGGCGA 47424
TCGCCCAGGCTGGAGTGCAGTG
|||||||
AGCGGGTCCGACCTCACGTCAC

GAM2029 WBSCR23 3' CACTGCACTCCAGCCTGGGTGA 47425
TCGCCCAGGCTGGAGTGCAGTG
|||||||

AGTGGGTCCGACCTCACGTCAC

GAM2029 WIRE 3' CACTGCACTCCAGCCTGGGCGA 78904
TCGCCCAGGCTGGAGTGCAGTG
|||||
AGCGGGTCCGACCTCACGTCAC

GAM2029 WSB1 3' CACTGCACTCCAACCTGG 56965 C
CCAGG TGGAGTGCAGTG
|||||
GGTCC ACCTCACGTCAC
A

GAM2029 WSB1 3' CACTGCACTCCAACCTGG 56966 C
CCAGG TGGAGTGCAGTG
|||||
GGTCC ACCTCACGTCAC
A

GAM2029 YME1L1 3' CACTGCACTCCAGCCTGGGC 58426
GCCCAGGCTGGAGTGCAGTG
|||||
CGGGTCCGACCTCACGTCAC

GAM2029 YME1L1 3' CACTGCACTCCAGCCTGGGTGA 58427
TCGCCCAGGCTGGAGTGCAGTG
|||||
AGTGGGTCCGACCTCACGTCAC

GAM2029 ZAK 3' CACTACACTCCAGCCTGGATGA 34098 C C
TCG CCAGGCTGGAGTG AGTG
||| |||||
AGT GGTCCGACCTCAC TCAC
A A

GAM2029 ZFD25 3' CACTACACTCCAGCCAAAGC 33107 CCA C
GC GGCTGGAGTG AGTG
|| |||||
CG CCGACCTCAC TCAC
AAA A

GAM2029 ZFP106 3' TACTGCACTCCAGCCTGGGCGA 42739
TCGCCCAGGCTGGAGTGCAGTG
|||||
AGCGGGTCCGACCTCACGTCAT

GAM2029 ZNF271 3' CACTGCATTCCAGCCTGGGC 96958
GCCCAGGCTGGAGTGCAGTG
|||||
CGGGTCCGACCTTACGTCAC

GAM2029 ZNF297B 3' CACCACACTCCAGCCTGCGCGA 26643 C CA
TCGC CAGGCTGGAGTG GTG
||| ||||| |||

		AGCG GTCCGACCTCAC CAC	
		C AC	
GAM2029	ZNF297B	5' CACTACACTCCAGCCTGGGT 26644	C
		GCCCAGGCTGGAGTG AGTG	
		TGGGTCCGACCTCAC TCAC	
		A	
GAM2029	ZNF297B	5' CACTGCACTCCAGCCTGGGC 26648	
		GCCCAGGCTGGAGTGCAGTG	
		CGGGTCCGACCTCACGTCAC	
GAM2029	ZNF333	3' CACTGCACTCCAGCCTGGGC 51587	
		GCCCAGGCTGGAGTGCAGTG	
		CGGGTCCGACCTCACGTCAC	
GAM2029	ZNF339	3' GCACTGCACTCCAGCCTGGGC 41393	
		GCCCAGGCTGGAGTGCAGTGTC	
		CGGGTCCGACCTCACGTCACAG	
GAM2029	LOC112687	3' CACTGCACTCCAGCCTGGGC 73223	
		GCCCAGGCTGGAGTGCAGTG	
		CGGGTCCGACCTCACGTCAC	
GAM2029	LOC113523	3' TACTGCACTCCAGCCTGGGCGA 73432	
		TCGCCCAGGCTGGAGTGCAGTG	
		AGCGGGTCCGACCTCACGTCAT	
GAM2029	LOC115129	5' CACTGCACTCCAGCCTGGGC 73606	
		GCCCAGGCTGGAGTGCAGTG	
		CGGGTCCGACCTCACGTCAC	
GAM2029	LOC115129	5' CACTGCACTGCAGCCCGGGCGA 73607	A G
		TCGCCC GGCTG AGTGCAGTG	
		AGCGGG CCGAC TCACGTCAC	
		C G	
GAM2029	LOC115129	3' CACTGCATTCCAGCCTGAGCGA 73608	C
		TCGC CAGGCTGGAGTGCAGTG	
		AGCG GTCCGACCTTACGTCAC	
		A	
GAM2029	LOC115196	3' CACTGCACTCCAGCCTGGGAGA 73651	G
		TC CCCAGGCTGGAGTGCAGTG	

	AG GGGTCCGACCTCACGTCAC	
	A	
GAM2029 LOC115273 3'	CACTGCACTCCAGCCTGGGC 73748	
	GCCCAGGCTGGAGTGCAGTG	
	CGGGTCCGACCTCACGTCAC	
GAM2029 LOC115761 3'	CACTGCACTCCAGTCTGGGC 93395	
	GCCCAGGCTGGAGTGCAGTG	
	CGGGTCTGACCTCACGTCAC	
GAM2029 LOC116143 3'	CACTGCACTCCAGCCTGGGC 74178	
	GCCCAGGCTGGAGTGCAGTG	
	CGGGTCCGACCTCACGTCAC	
GAM2029 LOC116143 3'	GCACTCCAGCCCTGGCGA 74186	CA
	TCGCC GGCTGGAGTGC	
	AGCGG CCGACCTCACG	
	TC	
GAM2029 LOC116236 3'	CACTGCACTCCAGCCTGGGCGA 74239	
	TCGCCCAGGCTGGAGTGCAGTG	
	AGCGGGTCCGACCTCACGTCAC	
GAM2029 LOC116349 3'	CACTGTACTCCAGCCTGGGC 74271	
	GCCCAGGCTGGAGTGCAGTG	
	CGGGTCCGACCTCATGTCAC	
GAM2029 LOC120406 3'	CACCACACTCCAGCCTGGGTGA 76063	CA
	TCGCCCAGGCTGGAGTG GTG	
	AGTGGGTCCGACCTCAC CAC	
	AC	
GAM2029 LOC122704 3'	GCACTCCAACCTGGGCGA 74607	C
	TCGCCCAGG TGGAGTGC	
	AGCGGGTCC ACCTCACG	
	A	
GAM2029 LOC122970 3'	CACTGCACTCCAGCCCAGGT 74640	CA
	GCC GGCTGGAGTGCAGTG	
	TGG CCGACCTCACGTCAC	
	AC	
GAM2029 LOC126282 3'	CACTGCACTCCAGCCTGGGTGA 74945	
	TCGCCCAGGCTGGAGTGCAGTG	

AGTGGGTCCGACCTCACGTCAC

GAM2029 LOC126669 3' GCACTCCAGCCTGAGTGA 75937 C
TCGC CAGGCTGGAGTGC
|||||
AGTG GTCCGACCTCACG
A

GAM2029 LOC127262 3' GCACTCCAGCCCGGGCGA 76599 A
TCGCCC GGCTGGAGTGC
|||||
AGCGGG CCGACCTCACG
C

GAM2029 LOC127294 3' ACACCTTCATCCAGGCTGGGCG 75141 G GTGCA
A TCGCCCAG CTGGA GTGT
||||| |||||
AGCGGGTC GACCT CACA
G ACTTC

GAM2029 LOC127428 3' CACTGCACTCCAGCCTGGGC 75156
GCCCAGGCTGGAGTGCAGTG
|||||
CGGGTCCGACCTCACGTCAC

GAM2029 LOC130026 3' CACTGCACTCCAGCCTAGGC 57433 C
GCC AGGCTGGAGTGCAGTG
|||
CGG TCCGACCTCACGTCAC
A

GAM2029 LOC130535 3' CACTGCACTCCAGCCTGGGTGA 76645
TCGCCCAGGCTGGAGTGCAGTG
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AGTGGGTCCGACCTCACGTCAC

GAM2029 LOC131965 3' GCACTCCAGCCTGGGCGA 75524
TCGCCCAGGCTGGAGTGC
|||||
AGCGGGTCCGACCTCACG

GAM2029 LOC133926 3' TACTGCACTCCAGCCTGGGCGA 75633
TCGCCCAGGCTGGAGTGCAGTG
|||||
AGCGGGTCCGACCTCACGTCAT

GAM2029 LOC134147 3' TACTGCACTCCAGCCTGG 57966
CCAGGCTGGAGTGCAGTG
|||||
GGTCCGACCTCACGTCAT

GAM2029 LOC134265 3' CACTGCACTCCAGCCTAAGC 75655 CC
GC AGGCTGGAGTGCAGTG
|| |||||

CG TCCGACCTCACGTCAC

AA

GAM2029 LOC138389 3' CACTGTACTCCAGCCTGGGC 76726
GCCCAGGCTGGAGTGCAGTG
|||||||
CGGGTCCGACCTCATGTCAC

GAM2029 LOC142948 3' CACTGCACTCCAGCCTGGGTGA 83773
TCGCCCAGGCTGGAGTGCAGTG
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AGTGGGTCCGACCTCACGTCAC

GAM2029 LOC143310 3' CACTGCACCCCAGCCTGGGTGA 77036 A
TCGCCCAGGCTGG GTGCAGTG
||||||| |||||
AGTGGGTCCGACC CACGTCAC
C

GAM2029 LOC143465 3' ACTTCACTCCAGCCTGGGTGA 83865 C
TCGCCCAGGCTGGAGTG AGT
||||||| |||
AGTGGGTCCGACCTCAC TCA
T

GAM2029 LOC143888 3' CACTGCACTCCAGCCTGGGTGA 77167
TCGCCCAGGCTGGAGTGCAGTG
|||||||
AGTGGGTCCGACCTCACGTCAC

GAM2029 LOC143943 3' CACTGCACTCCAGCCTGGGTGA 83915
TCGCCCAGGCTGGAGTGCAGTG
|||||||
AGTGGGTCCGACCTCACGTCAC

GAM2029 LOC144262 5' GACACTGCACCCTATGGGC 77260 GGCT A
GCCCA GG GTGCAGTGTC
|||| || |||||
CGGGT CC CACGTCACAG
AT__ _

GAM2029 LOC144289 3' CACTGCACTCCAGCCTGGGTGA 83952
TCGCCCAGGCTGGAGTGCAGTG
|||||||
AGTGGGTCCGACCTCACGTCAC

GAM2029 LOC144308 5' ACACTGCACTCCAGCCTGGGTG 83976
A TCGCCCAGGCTGGAGTGCAGTGT
|||||||
AGTGGGTCCGACCTCACGTCACA

GAM2029 LOC144519 5' CACTGCACTCCAGCCTGGGCGA 77369
TCGCCCAGGCTGGAGTGCAGTG
|||||||

AGCGGGTCCGACCTCACGTCAC

GAM2029 LOC144583 3' ATTGCACTCCAGCCCGAGTGA 77412 CCA
TCGC GGCTGGAGTGCAGT
|||| |||||||||
AGTG CCGACCTCACGTTA
AGC

GAM2029 LOC144817 3' ATTGCACTCCAGCCCAGGGGA 77506 G A_
TC CCC GGCTGGAGTGCAGT
|| ||| |||||||||
AG GGG CCGACCTCACGTTA
_ AC

GAM2029 LOC144845 3' CACTACACTCCAGCCCGGGCGA 57453 A C
TCGCCC GGCTGGAGTG AGTG
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AGCGGG CCGACCTCAC TCAC
C A

GAM2029 LOC145231 3' TACTGCACTCCAGCCTGGGTGA 84258
TCGCCCAGGCTGGAGTGCAGTG
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GAM2029 LOC145333 3' CACTGCACTCCAGCCTGGGCGA 84291
TCGCCCAGGCTGGAGTGCAGTG
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GAM2029 LOC145387 3' GCACTCCAGCCTGGGCGA 84337
TCGCCCAGGCTGGAGTGC
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AGCGGGTCCGACCTCACG

GAM2029 LOC145438 3' CACTGCACTCCAGCCTGGGCGA 84309
TCGCCCAGGCTGGAGTGCAGTG
|||||||||||||
AGCGGGTCCGACCTCACGTCAC

GAM2029 LOC145453 3' CACTGCACTTCAGCCTGGGC 77654
GCCCAGGCTGGAGTGCAGTG
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GAM2029 LOC145482 3' GCACTCCAGCCTGGGCGA 77745
TCGCCCAGGCTGGAGTGC
|||||||||||||
AGCGGGTCCGACCTCACG

GAM2029 LOC145608 5' CACTGCACTCCAGCCTGGGTGA 84377
TCGCCCAGGCTGGAGTGCAGTG
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AGTGGGTCCGACCTCACGTCAC

GAM2029 LOC145609 3' CACTGCACTCCAGCCTGGGTGA 84362
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GAM2029 LOC145663 3' CACTGCACTCCAGCCTGGGCGA 84416
TCGCCCAGGCTGGAGTGCAGTG
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GAM2029 LOC145820 3' CACTGCACTCCAGCCTGGGCGA 77973
TCGCCCAGGCTGGAGTGCAGTG
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GAM2029 LOC145945 5' GATACTGTACTCCAGCCTGAGC 84566 C
GC CAGGCTGGAGTGCAGTGTC
|| |||||
CG GTCCGACCTCATGTCATAG
A

GAM2029 LOC146229 3' CACTACACTCCAGCCTGGGCGA 78265 C
TCGCCCAGGCTGGAGTGCAGTG
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AGCGGGTCCGACCTCAC TCAC
A

GAM2029 LOC146475 5' GCACTCAAGCCTGGGCGA 84691 G
TCGCCCAGGCT GAGTGC
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AGCGGGTCCGA CTCACG
A

GAM2029 LOC146728 3' CACTGCACTCCAGCCTGGG 84761
CCCAGGCTGGAGTGCAGTG
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GAM2029 LOC146756 3' CACTGCACTCCAGCCTGGGCGA 84795
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GAM2029 LOC146839 5' CACTGCACTCCAGCCTGGGC 84837
GCCCAGGCTGGAGTGCAGTG
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CGGGTCCGACCTCACGTCAC

GAM2029 LOC146895 3' GCACTCCAGCCTGGGTGA 84869
TCGCCCAGGCTGGAGTGC
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AGTGGGTCCGACCTCACG

GAM2029 LOC146923 3' CACTGCACTCCAGCCTGGGCGA 78796
TCGCCCAGGCTGGAGTGCAGTG
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GAM2029 LOC146958 3' CACTGCACTCCAGCCTGGGTGA 84941
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GAM2029 LOC147071 3' CACTGCACTCCAGCCTGGGCGA 73354
TCGCCCAGGCTGGAGTGCAGTG
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GAM2029 LOC147660 3' CACTGCACTCCAGGCTGGGCGA 79025 G
TCGCCCAG CTGGAGTGCAGTG
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AGCGGGTC GACCTCACGTCAC
G

GAM2029 LOC147664 3' ATTCCACTCCAGCCTGGGC 79042 C
GCCCAGGCTGGAGTG AGT
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C

GAM2029 LOC147669 3' GCACTCCAGCCTGGGTGA 85183
TCGCCCAGGCTGGAGTGC
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GAM2029 LOC147727 5' CACTGCACTCCAGTCTGGGCGA 79130
TCGCCCAGGCTGGAGTGCAGTG
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GAM2029 LOC147727 5' GCACTCCAGCCTGGGCGA 79137
TCGCCCAGGCTGGAGTGC
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AGCGGGTCCGACCTCACG

GAM2029 LOC147837 3' CACTGCACTCCAGCCTGGGC 79202
GCCCAGGCTGGAGTGCAGTG
|||||||
CGGGTCCGACCTCACGTCAC

GAM2029 LOC147837 3' GCACTGCACCCCAGCCTGGGCG 79206 A
A TCGCCCAGGCTGG GTGCAGTGT
||||||| |||||

		AGCGGGTCCGACC CACGTCACG		
		C		
GAM2029	LOC147990 3'	CACTGCACTCCAGCCTGGGC 85214		
		GCCCAGGCTGGAGTGCAGTG		
		CGGGTCCGACCTCACGTCAC		
GAM2029	LOC148166 3'	CACTGCACTCCAGCCTAGGCGA 79412	C	
		TCGCC AGGCTGGAGTGCAGTG		
		AGCGG TCCGACCTCACGTCAC		
		A		
GAM2029	LOC148254 3'	CACTGCACTCCAGCCTGGGAGA 79499	G	
		TC CCCAGGCTGGAGTGCAGTG		
		AG GGGTCCGACCTCACGTCAC		
		A		
GAM2029	LOC148343 3'	GCACACCAGCCTGGGCGA 79545	A	
		TCGCCCAGGCTGG GTGC		
		AGCGGGTCCGACC CACG		
		A		
GAM2029	LOC148397 3'	CACTGCACCCCAGCCTGGGC 79561	A	
		GCCCAGGCTGG GTGCAGTG		
		CGGGTCCGACC CACGTCAC		
		C		
GAM2029	LOC148413 3'	GCACTGCACTCATGCAGCGG 79580	CCAG TG	
		TCGC GC GAGTGCAGTGTC		
		GGCG CG CTCACGTCACAG		
		A__ TA		
GAM2029	LOC148479 5'	CACCTCCAGCCCGGGCGA 79608	A	TGCA
		TCGCCC GGCTGGAG GTG		
		AGCGGG CCGACCTC CAC		
		C		
GAM2029	LOC148534 3'	CACTGCACTCCAGCCTGGGCGA 79631		
		TCGCCCAGGCTGGAGTGCAGTG		
		AGCGGGTCCGACCTCACGTCAC		
GAM2029	LOC148809 5'	ATTGCACTCCAGCCTGGGTGA 79746		
		TCGCCCAGGCTGGAGTGCAGT		
		AGTGGGTCCGACCTCACGTTA		
GAM2029	LOC148809 3'	GCACTGTACTCCAGCCTGGGCG 79755		
A		TCGCCCAGGCTGGAGTGCAGTGT		

AGCGGGTCCGACCTCATGTCACG

GAM2029 LOC148936 3' ACACTGCACTCCAGGTTGGGC 85444 G
GCCCAG CTGGAGTGCAGTGT
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CGGGTT GACCTCACGTCACA
G

GAM2029 LOC148938 3' ACACTGCACTCCAGGCTGGGC 85426 G
GCCCAG CTGGAGTGCAGTGT
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CGGGTC GACCTCACGTCACA
G

GAM2029 LOC149073 3' ACTCCACTCCAGCCTGGGC 85478 C
GCCCAGGCTGGAGTG AGT
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CGGGTCCGACCTCAC TCA
C

GAM2029 LOC149175 3' CACTGCACTCCAGCCTGGGCGA 79949
TCGCCCAGGCTGGAGTGCAGTG
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GAM2029 LOC149628 3' CACTGCACTCCAGCCTGGGTGA 80277
TCGCCCAGGCTGGAGTGCAGTG
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GAM2029 LOC149672 5' CACTACACTCCAGCCTGGGC 80336 C
GCCCAGGCTGGAGTG AGTG
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CGGGTCCGACCTCAC TCAC
A

GAM2029 LOC149705 3' GCACTCCAGCCTGGGTGA 85781
TCGCCCAGGCTGGAGTGC
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GAM2029 LOC149711 3' CACTGCACTCCAGCCTGGGTGA 85844
TCGCCCAGGCTGGAGTGCAGTG
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GAM2029 LOC149912 3' GCACTCCAGCCTGGGCGA 85881
TCGCCCAGGCTGGAGTGC
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AGCGGGTCCGACCTCACG

GAM2029 LOC149952 3' ACTTTGCATTCCAGCCTGGGC 80371 T
GCCCAGGCTGGAGTGCAG GT
||||||| ||

CGGGTCCGACCTTACGTT CA

T

GAM2029 LOC150095 3' CACTGCACTCCAGCCTGGGC 85991
GCCCAGGCTGGAGTGCAGTG
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CGGGTCCGACCTCACGTCAC

GAM2029 LOC150185 3' CACTGCACTCCAGCCTGGGTGA 86063
TCGCCCAGGCTGGAGTGCAGTG
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AGTGGGTCCGACCTCACGTCAC

GAM2029 LOC150225 3' CACTGCACTCCAGCCTGGGCG 86183
CGCCCAGGCTGGAGTGCAGTG
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GAM2029 LOC150225 3' CACTGCACTGCAGCCTGGGCGA 86184 G
TCGCCCAGGCTG AGTGCAGTG
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AGCGGGTCCGAC TCACGTCAC
G

GAM2029 LOC150244 3' GCACTCCAGCCTGGGCGA 80550
TCGCCCAGGCTGGAGTGC
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AGCGGGTCCGACCTCACG

GAM2029 LOC150245 3' CACTGCACTCCAGCCTGGGTGA 86110
TCGCCCAGGCTGGAGTGCAGTG
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AGTGGGTCCGACCTCACGTCAC

GAM2029 LOC150358 3' CACTGCATTCCAGCCTGGGCGA 86089
TCGCCCAGGCTGGAGTGCAGTG
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GAM2029 LOC150577 3' CACTGCACTCCAGCCTGGATGA 86251 C
TCG CCAGGCTGGAGTGCAGTG
||| |||||
AGT GGTCCGACCTCACGTCAC
A

GAM2029 LOC150630 5' CACTGCACTCCAGCCTGGGC 86293
GCCCAGGCTGGAGTGCAGTG
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GAM2029 LOC151196 3' CACTGCACTCCAGCCTGGGC 86449
GCCCAGGCTGGAGTGCAGTG
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CGGGTCCGACCTCACGTCAC

GAM2029 LOC151248 5' CACTGCACTCCCGCCTGGGCGA 80987 T
TCGCCCAGGC GGAGTGCAGTG
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C

GAM2029 LOC151429 3' CACTGCACTCCAGCCTGGGCGA 86523
TCGCCCAGGCTGGAGTGCAGTG
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GAM2029 LOC151429 3' CACTGCACTCCAGCCTGGGTGA 86524
TCGCCCAGGCTGGAGTGCAGTG
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GAM2029 LOC151556 3' CACTGCACTCCAGCCTGAGC 81076 C
GC CAGGCTGGAGTGCAGTG
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GAM2029 LOC151632 3' CACTGCACTCCAGCCTGGGC 86639
GCCCAGGCTGGAGTGCAGTG
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GAM2029 LOC151720 3' CACTGCACTCCAGCCTGGGCGA 81147
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GAM2029 LOC151904 3' CACTGCACTCCAGCCTGGGC 81203
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GAM2029 LOC152002 3' CACTGCACTCCAGCCTGGACGA 81264 C
TCG CCAGGCTGGAGTGCAGTG
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GAM2029 LOC152106 3' GCACTCCAGCCTGGTCGA 70595 C
TCG CCAGGCTGGAGTGC
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AGC GGTCCGACCTCACG
T

GAM2029 LOC152313 3' CACTGCACTCCAGCCTGGGTGA 86847
TCGCCCAGGCTGGAGTGCAGTG
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GAM2029 LOC152316 3' CACTGCATTCCAGCCTAGGC 86790 C
GCC AGGCTGGAGTGCAGTG
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CGG TCCGACCTTACGTCAC
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GAM2029 LOC152426 3' TACTGCACTCCAGCCTGGGCGA 86901
TCGCCCAGGCTGGAGTGCAGTG
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GAM2029 LOC152445 3' CACTGCACTCCAGCCTGAGTGA 86937 C
TCGC CAGGCTGGAGTGCAGTG
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A

GAM2029 LOC152804 3' CACTGCACTCCAGCCTGGGC 87071
GCCCAGGCTGGAGTGCAGTG
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GAM2029 LOC153077 3' ACTGCACTCCAGCCTGGGC 87105
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GAM2029 LOC153146 3' CACTGCACTCCAGCCTGGGTGA 87144
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GAM2029 LOC153338 3' CACTGCACTCCAGCCTGGGTGA 87193
TCGCCCAGGCTGGAGTGCAGTG
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GAM2029 LOC153579 3' CACTGCACTCCAGCCTGGGCGA 81765
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GAM2029 LOC153682 3' CACCACACTCCAGCCTGAGCGA 87269 C CA
TCGC CAGGCTGGAGTG GTG
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AGCG GTCCGACCTCAC CAC
A AC

GAM2029 LOC153688 3' CACTGCACTCCAGCCTGGGCGA 87299
TCGCCCAGGCTGGAGTGCAGTG
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GAM2029 LOC154791 3' ACTCACTCCAGCCTGGGC 82045 C
GCCCAGGCTGGAGTG AGT
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GAM2029 LOC154877 3' CACTGCACTCCAGCCTAGGTGA 87532 C
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A

GAM2029 LOC155006 3' CACTGCACTCCAGCCTGGGCGG 82165
TCGCCCAGGCTGGAGTGCAGTG
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GAM2029 LOC155054 3' CACTGCACTCCAGCCTGGGTGA 82200
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GAM2029 LOC155072 3' CACTACACTCCAACCTGGGTGA 87655 C C
TCGCCCAGG TGGAGTG AGTG
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AGTGGGTCC ACCTCAC TCAC
A A

GAM2029 LOC155376 3' CACTACACTCCAGCCTGGGTGA 82241 C
TCGCCCAGGCTGGAGTG AGTG
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AGTGGGTCCGACCTCAC TCAC
A

GAM2029 LOC157562 5' ACCTCACTCCAGCCTGGGC 87770 C T
GCCCAGGCTGGAGTG AG GT
||||||| ||
CGGGTCCGACCTCAC TC CA

GAM2029 LOC157737 3' CACTGCACTCCAGCCTGGGC 87842
GCCCAGGCTGGAGTGCAGTG
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GAM2029 LOC158160 3' CACTGCACTCCAGCCTGGGTGA 73471
TCGCCCAGGCTGGAGTGCAGTG
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GAM2029 LOC158187 3' CACTGCACTCCAGCCTGGGTGA 87988
TCGCCCAGGCTGGAGTGCAGTG
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AGTGGGTCCGACCTCACGTCAC

GAM2029 LOC158235 3' CACTGTACTCCAGCCTGGGC 88000
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CGGGTCCGACCTCATGTCAC

GAM2029 LOC158292 5' CACTGCACTCCAGCCTGGGC 88040
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GAM2029 LOC158292 5' CACTGCACTCCAGCCTGGGCGA 88041
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GAM2029 LOC158677 5' CACTGCACTCCAGCCTGGGTGA 88247
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GAM2029 LOC158819 3' CACTGCACTCCAGCCTGGGTGA 88271
TCGCCCAGGCTGGAGTGCAGTG
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AGTGGGTCCGACCTCACGTCAC

GAM2029 LOC158987 3' CACTGCACTCCAGCCTGGGC 88319
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GAM2029 LOC159036 3' GACACTGCACTCCAGCCTGGGC 88348
GA TCGCCCAGGCTGGAGTGCAGTGTC
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GAM2029 LOC159053 3' CACTGCACTCCAGCCTGGGC 88365
GCCCAGGCTGGAGTGCAGTG
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CGGGTCCGACCTCACGTCAC

GAM2029 LOC159199 5' GACACTTCCTGTCCAGCCTGGG 83060 G GTGC_
GA TC CCCAGGCTGGA AGTGTC
|| ||||| |||||
AG GGGTCCGACCT TCACAG
_ GTCCT

GAM2029 LOC161244 5' GACACCCTCCAACCTGGGCGG 88452 C TGCA
TCGCCCAGG TGGAG GTGTC
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GGCGGGTCC ACCTC CACAG
A C____
GAM2029 LOC162962 3' GCACTCCAGCCTGGGTGA 83258
TCGCCCAGGCTGGAGTGC
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AGTGGGTCCGACCTCACG

GAM2029 LOC163412 5' GACAGTCCCCAGCCTGGC 83013 C AGT AG
GCC AGGCTGG GC TGTC
||| ||||| || ||||
CGG TCCGACC TG ACAG
_ CC_ _
GAM2029 LOC196047 5' GCACTCCAGCCTGGGTGA 91156
TCGCCCAGGCTGGAGTGC
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AGTGGGTCCGACCTCACG

GAM2029 LOC196761 3' ACTGCACTCCAGCCTGGGCGA 91113
TCGCCCAGGCTGGAGTGCAGT
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AGCGGGTCCGACCTCACGTCA

GAM2029 LOC197196 3' CACTGCACTCCAGCCTGGGCGA 91298
TCGCCCAGGCTGGAGTGCAGTG
|||||
AGCGGGTCCGACCTCACGTAC

GAM2029 LOC197201 3' CACTGCACTCCAGCCTGGGC 89267
GCCCAGGCTGGAGTGCAGTG
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CGGGTCCGACCTCACGTAC

GAM2029 LOC199676 3' CACTGCACTCCAGCCTGGGAGA 91358 G
TC CCCAGGCTGGAGTGCAGTG
|| |||||
AG GGGTCCGACCTCACGTAC
A

GAM2029 LOC199729 3' TACTGCACTCCAGCCAGGGC 73395 A
GCCC GGCTGGAGTGCAGTG
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CGGG CCGACCTCACGTCAT
A

GAM2029 LOC199733 3' CACTGCACTCCAACCTGGGC 91435 C
GCCCAGG TGGAGTGCAGTG
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A

GAM2029 LOC199786 3' CACTGCACTCCAGCCTGGGTGA 89743
TCGCCCAGGCTGGAGTGCAGTG
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GAM2029 LOC199858 3' CACTGCACTCCAGCCTGGGCGA 89793
TCGCCCAGGCTGGAGTGCAGTG
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GAM2029 LOC199923 3' CACTGCACTCCAGCCTGGACGA 89864 C
TCG CCAGGCTGGAGTGCAGTG
||| |||||
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A

GAM2029 LOC199923 3' CACTGCACTCCAGCCTGGGC 89865
GCCCAGGCTGGAGTGCAGTG
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GAM2029 LOC200014 3' CACTGCACTCCAGCCTGGGCGA 89922
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AGCGGGTCCGACCTCACGTCAC

GAM2029 LOC200853 3' GCACTCCAGCCTGGGAGA 90330 G
TC CCCAGGCTGGAGTGC
|| |||||
AG GGGTCCGACCTCACG
A

GAM2029 LOC200918 3' GCGCTCCAGCCTGGGCGA 90368
TCGCCCAGGCTGGAGTGC
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AGCGGGTCCGACCTCGCG

GAM2029 LOC200940 3' CACTGCACTCCAGCCTGGGCGA 90387
TCGCCCAGGCTGGAGTGCAGTG
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GAM2029 LOC201109 3' ACACCTGCCAGGCCTGGGC 91325 GGAGT _
GCCCAGGCT GCAG TGT
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AC__ C

GAM2029 LOC201173 3' CACTGCACTCCAGCCTGGGCGA 88673
TCGCCCAGGCTGGAGTGCAGTG
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GAM2029 LOC201220 3' CACTGCACTCCAGCCTGGGTGA 88708
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GAM2029 LOC201689 3' CACTGCACTCCAGCCTGGGTGA 67732
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GAM2029 LOC201705 3' ACACTGCACTCCAGCCTGGGTG 91851
A TCGCCCAGGCTGGAGTGCAGTGT
|||||||
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GAM2029 LOC201895 3' CACTGCATTCCAGCCTAAGC 90541 CC
GC AGGCTGGAGTGCAGTG
|| |||||
CG TCCGACCTTACGTCAC
AA

GAM2029 LOC201911 3' GACACTGCGCTCCAGCCTGGGC 91863
GCCCAGGCTGGAGTGCAGTGTC
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CGGGTCCGACCTCGCGTCACAG

GAM2029 LOC201931 3' CACTGCACTCCAGCCTGGGCGA 90561
TCGCCCAGGCTGGAGTGCAGTG
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GAM2029 LOC202781 3' GCACTCCAGCCTGGGCGA 91972
TCGCCCAGGCTGGAGTGC
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GAM2029 LOC202781 3' TTGAGTCCAGCCTGGACGA 91977 C GTG
TCG CCAGGCTGGA CAG
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AGC GGTCCGACCT GTT
A GA_

GAM2029 LOC202868 3' CACTGCACTCCAACCTGGGTGA 91991 C
TCGCCCAGG TGGAGTGCAGTG
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A

GAM2029 LOC203083 3' CACTGCACTCCAGCCTGGGC 92082
GCCCAGGCTGGAGTGCAGTG
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GAM2029 LOC203246 3' GCACTCCCGCCTGGGCGA 90832 T
TCGCCCAGGC GGAGTGC
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AGCGGGTCCG CCTCAG

C

GAM2029 LOC203350 3' TACTGCACTCCAGCCTGGATGA 92248 C
TCG CCAGGCTGGAGTGCAGTG
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AGT GGTCCGACCTCACGTCAT

A

GAM2029 LOC203378 3' CACTGTACTCCAGCCTGGGCGA 92281
TCGCCCAGGCTGGAGTGCAGTG
|||||||
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GAM2029 LOC205327 3' TACTGCACTCCAACCTGGGC 91071 C
GCCCAGG TGGAGTGCAGTG
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CGGGTCC ACCTCACGTCAT

A

GAM2029 LOC219347 3' CACTGCACTCCAGCCTGGGC 94574
GCCCAGGCTGGAGTGCAGTG
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CGGGTCCGACCTCACGTCAC

GAM2029 LOC219540 3' CACTGCACTCCAGCCTGGGCGA 95240
TCGCCCAGGCTGGAGTGCAGTG
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GAM2029 LOC219649 3' CACTGCACTCCAGCCTGGGCGA 94545
TCGCCCAGGCTGGAGTGCAGTG
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GAM2029 LOC219722 5' CACTGCACTTCAGCCTGG 94674
CCAGGCTGGAGTGCAGTG
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GGTCCGACTTCACGTCAC

GAM2029 LOC219919 3' CACTGCACTCCAGCCTGGGC 94919
GCCCAGGCTGGAGTGCAGTG
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GAM2029 LOC220038 3' GCATTCCAGCCTGGGCGA 93376
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GAM2029 LOC220070 3' CACTGCACTCCAGCCTGG 59940
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GAM2029 LOC220549 3' CACTGCACTCCAGCCTGGGTGA 94505
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GAM2029 LOC220992 3' CACTGCACTCCAGCCTGGGC 93109
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GAM2029 LOC221042 3' CACTGCACTCCAGCCTGGGTGA 94794
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GAM2029 LOC221069 3' CACCGCACTCCAGCCTGGGCGA 94817 A
TCGCCCAGGCTGGAGTGC GTG
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C

GAM2029 LOC221178 3' CACTGCACTCCAGCCTGGGAGA 95167 G
TC CCCAGGCTGGAGTGCAGTG
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A

GAM2029 LOC221271 3' ACACCGTACTCCAGCCTGGGCG 93484 A A
TCGCCCAGGCTGGAGTGC GTGT
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C

GAM2029 LOC221271 3' CACTACACTCCAGCCTGGGC 93497 C
GCCCAGGCTGGAGTG AGTG
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A

GAM2029 LOC221271 3' CACTGCACTCCAGCCTGGGTGA 93500
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GAM2029 LOC221288 3' GCACTCCAGCCTGGGCGA 95260
TCGCCCAGGCTGGAGTGC
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GAM2029 LOC221410 3' CACTGCACTCCAGCCTGGGTGA 93690
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GAM2029 LOC221477 3' ACTTCATTCCAGCCTGGGCGA 93762 C
TCGCCCAGGCTGGAGTG AGT
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T

GAM2029 LOC221490 3' CACTGCACTGCAGCCTAGGCGA 95298 C G
TCGCC AGGCTG AGTGCAGTG
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AGCGG TCCGAC TCACGTCAC
A G

GAM2029 LOC221543 3' CACTGCACTCCAGCCTGGGC 95365
GCCCAGGCTGGAGTGCAGTG
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GAM2029 LOC221543 5' CACTGCACTCCAGCCTGGGCGA 95366
TCGCCCAGGCTGGAGTGCAGTG
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GAM2029 LOC221795 3' CACTGCACTCCAGCCTGGGC 94069
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GAM2029 LOC221943 5' CACTGCACTCCAGCCTGGGCGA 95618
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GAM2029 LOC221954 5' CACTGCACTCCAGCCTGGGC 95640
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GAM2029 LOC221954 5' CACTGCACTCCAGCCTGGGTGA 95641
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GAM2029 LOC222060 5' GCACTCCAGCCTGGGCGA 95755
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GAM2029 LOC222160 3' CACTGCACTCCAGCCTGGGC 95773
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GAM2029 LOC222160 5' CACTGCACTCCAGCCTGGGCGA 95774
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GAM2029 LOC222865 3' CACTGCACTCCAGCCTGAGTGA 94439 C
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GAM2029 LOC253039 3' CACTGCACTCCAGCCTGGGCGA 97864
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GAM2029 LOC253532 3' CACTACACTCCAGCCTGGGTGA 97730 C
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|||||
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GAM2029 LOC253639 3' CACTGCACTCCAGCCTGGGCGA 97511
TCGCCCAGGCTGGAGTGCAGTG
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GAM2029 LOC253778 5' CACTGCATTCCAGCCTGGGCGA 96523
TCGCCCAGGCTGGAGTGCAGTG
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GAM2029 LOC253786 3' CACTGCACTCCAGCCTGGGC 98830
GCCCAGGCTGGAGTGCAGTG
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GAM2029 LOC253832 3' GCACTCCAGCCTGGGCGA 96592
TCGCCCAGGCTGGAGTGC
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GAM2029 LOC254041 5' CACTGCACTACAGCCTGGACGA 96551 C G
TCG CCAGGCTG AGTGCAGTG
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GAM2029 LOC254100 3' CACTGCACTCCAGCCTGGGC 98149
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GAM2029 LOC254176 3' CACTGCACTCCAGCCTGGGC 99163
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GAM2029 LOC254428 3' ACACTGCACCTTATCCCAGG 97192 CA C GA
CC GG TG GTGCAGTGT
|| || || |||||
GG CC AT CACGTCACA
AC T TC

GAM2029 LOC254531 5' CACTGCACTCCAGCCTGGGTGA 96664
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GAM2029 LOC254756 3' CACTGCACTCCAGCCTGGGC 99211
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GAM2029 LOC254808 3' CACTGCACTCCAGCCTGGGC 98802
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GAM2029 LOC254875 3' CACTACACTCCAGCCTGGGTGA 97774 C
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GAM2029 LOC255030 5' CACTGCACTCCAGCCTGGGTGA 99081
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GAM2029 LOC255177 3' CACTGCACTCCAGCCTAGGC 98388 C
GCC AGGCTGGAGTGCAGTG
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A

GAM2029 LOC255196 3' CACTGCACTACAACCTGGGC 98950 C G
GCCCAGG TG AGTGCAGTG
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A A

GAM2029 LOC255231 3' CACTACACTCCAGCCTGGGTGA 97116 C
TCGCCCAGGCTGGAGTG AGTG
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A

GAM2029 LOC255326 3' CACTGCACTCCAGCCTGGGTGA 98116
TCGCCCAGGCTGGAGTGCAGTG
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GAM2029 LOC255328 3' GCACTCCAGCCTGGGTGA 98340
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GAM2029 LOC255374 5' CACTGCACTCCTGCCTGGGC 97788 T
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T

GAM2029 LOC255523 3' CACTGTACTCCAGCCTGGGC 96735
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GAM2029 LOC255671 3' CACTGCACTCCAGCCTGGGT 99067
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GAM2029 LOC255671 5' CACTGCACTCCAGCCTGGGTGA 99068
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GAM2029 LOC255671 5' GCACTCCAGCCTGGGCGA 99072
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GAM2029 LOC256207 3' GCACTCCAACCTGGGCGA 96878 C
TCGCCCAGG TGGAGTGC
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A

GAM2029 LOC256515 3' CACTGCACTCCAGCCTGGGC 98205
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GAM2029 LOC256520 3' GCCCTCCAGCCTGGGCGA 97668 T
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C

GAM2029 LOC256594 3' CACTGCACTCCAGCCTGGGC 98856
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GAM2029 LOC256980 3' GCACTCCAGCCTGGTCGA 96929 C
TCG CCAGGCTGGAGTGC
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T

GAM2029 LOC257539 3' ACTGCACTCCAGCCTGGGTGA 99542
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GAM2029 LOC257578 3' ACTGCACTCCAGCCTGGGTGA 99654
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GAM2029 LOC257596 3' CACTGCACTCCAGCCTGGGC 99768
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GAM2029 LOC257596 5' CACTGCACTCCAGCCTGGGCGA 99769
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AGCGGGTCCGACCTCACGTCAC

GAM2029 LOC51145 3' ACTCCCCTCCAGCCTGGGCGA 32917 TGC
TCGCCCAGGCTGGAG AGT
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CCC

GAM2029 LOC51212 3' CACTGCACTCCAGCCTGGGTGA 33498
TCGCCCAGGCTGGAGTGCAGTG
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GAM2029 LOC51336 3' ACCTCACTCCAGCCTGGGTGA 34064 C T
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GAM2029 LOC57118 3' CACTGCACTCCAGCCTGGGTGA 40216
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GAM2029 LOC63929 3' ACTGCACTCCAGCCTGGGTGA 42275
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GAM2029 LOC85479 5' CACTGCACTCCAGCCTGGGCGA 53561
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GAM2029 LOC89890 3' CACTGCACTCCAGCCTGGATGA 61203 C
TCG CCAGGCTGGAGTGCAGTG
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AGT GGTCCGACCTCACGTCAC
A

GAM2029 LOC90072 3' CACTGCACTCCAGCCTGGGGA 61951 G
TC CCCAGGCTGGAGTGCAGTG
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AG GGGTCCGACCTCACGTCAC

—
GAM2029 LOC90072 5' CACTGCACTCCAGCCTGGGTGA 61952
TCGCCCAGGCTGGAGTGCAGTG
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GAM2029 LOC90141 3' GCACTCCAGCCTGGATGA 62304 C
TCG CCAGGCTGGAGTGC
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GAM2029 LOC90233 3' CACTGCACTCCAGCCCAGGC 57190 CA
GCC GGCTGGAGTGCAGTG
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AC

GAM2029 LOC90321 3' CACTGCACTCCAACCTGGGTGA 62930 C
TCGCCCAGG TGGAGTGCAGTG
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GAM2029 LOC90393 5' CACTGCACTCCAGCCTGGGTGA 63304
TCGCCCAGGCTGGAGTGCAGTG
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GAM2029 LOC90573 5' GCACTGCAGTCCAGCCTGGGCG 63958 G
A TCGCCCAGGCTGGA TGCAGTGT
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AGCGGGTCCGACCT ACGTCACG
 G
 GAM2029 LOC90624 3' CACTGCACTCCAGCCTGGGGGA 64366 G
 TC CCCAGGCTGGAGTGCAGTG
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 GAM2029 LOC90841 5' CACTGCACTCCAGCCTGGGTGA 64864
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 GAM2029 LOC91056 3' CACTGCACTCCAGCCTGGGCGA 96401
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 GAM2029 LOC91064 3' GCACTCCAGCGTGGGCGA 65386 G
 TCGCCCA GCTGGAGTGC
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 G
 GAM2029 LOC91250 5' GCACTCCAGCCTGAGTGA 65917 C
 TCGC CAGGCTGGAGTGC
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 A
 GAM2029 LOC91286 3' CACTGCACTCCAGCCTGG 66057
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 GAM2029 LOC91380 3' CACTGCACTCCAGCCTGGGTGA 66438
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 GAM2029 LOC91442 3' CACTGCACTCCAGCCTGGGC 66641
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 GAM2029 LOC91547 3' CACTGCACTCCAGCCTGGGCGA 66998
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 GAM2029 LOC91750 3' CACTGCACTCCAGCCTGGGC 67649
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GAM2029 LOC91812 3' CACTGCACTCCAGCCTGGGC 67814
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GAM2029 LOC91862 3' CACTGCACTCCAGCCCAGGTGA 54570 CA
TCGCC GGCTGGAGTGCAGTG
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AGTGG CCGACCTCACGTCAC
AC

GAM2029 LOC91963 5' CACTGCACTCCAGCCTGGGC 68314
GCCCAGGCTGGAGTGCAGTG
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GAM2029 LOC92078 3' TACTGCACTCCAGCCTGGGTGA 68610
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AGTGGGTCCGACCTCACGTCAT

GAM2029 LOC92228 3' CACTGCACTCCCAGCCTGGGC 69069 —
GCCCAGGCTGG AGTGCAGTG
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CGGGTCCGACC TCACGTCAC
C

GAM2029 LOC92267 3' GACACCATTGCACTCCAGCCTG 69170 —
GGC GCCCAGGCTGGAGTGCA GTGTC
|||||
CGGGTCCGACCTCACGT CACAG
TAC

GAM2029 LOC92360 3' CACTGCACTCCAGCCTGGGTGA 69623
TCGCCCAGGCTGGAGTGCAGTG
|||||
AGTGGGTCCGACCTCACGTCAC

GAM2029 LOC92421 3' CACTGCACTCCAGACTGGGC 69723 G
GCCCAG CTGGAGTGCAGTG
|||||
CGGGTC GACCTCACGTCAC
A

GAM2029 LOC92465 5' GACACTGCACTCCAGCCTGGGC 69950
GA TCGCCCAGGCTGGAGTGCAGTGTC
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AGCGGGTCCGACCTCACGTCACAG

GAM2029 LOC92482 3' CACTGCACCCCAGCCTGGGC 70017 A
GCCCAGGCTGG GTGCAGTG
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CGGGTCCGACC CACGTCAC
C

GAM2029 LOC92492 3' CACTGCACTCCAGCCTGGATGA 70081 C
TCG CCAGGCTGGAGTGCAGTG
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A

GAM2029 LOC92499 5' CACTGCACTACAGCCTGGACGA 70102 C G
TCG CCAGGCTG AGTGCAGTG
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AGC GGTCCGAC TCACGTCAC
A A

GAM2029 LOC92568 3' CACTGCACTCCAGCCTGGGTGA 70326
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GAM2029 LOC92573 3' GCACTCCAGCCTGGGTGA 70375
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GAM2029 LOC92659 3' CACTGCACTCCAGCCTGGGCGA 70608
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GAM2029 LOC92973 5' CACTGCACTCCAGCCTGGGC 71586
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GAM2029 LOC93070 3' CACTGTACTCCAGCCTGGGC 71802
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GAM2029 LOC93613 5' GACACTGCACCCTGACTGGGGA 73074 G GCT A
TC CCCAG GG GTGCAGTGT
|| ||| || |||||
AG GGGTC CC CACGTCACAG
_ AGT _

GAM2030 ADCY2 3' GGGAGGCCGAGGAGAGAGGATC 65650 ACCTG
A
TGATCC CCTCGGCCTCCC
||||| |||||

			ACTAGG GGAGCCGGAGGG		
			AGAGA		
GAM2030	AICDA	3'	GGGAGGCCGAGCCGGGCGGATC 40697	A	C
	A		TGATCC CCTG CTCGGCCTCCC		
			ACTAGG GGGC GAGCCGGAGGG		
			C C		
GAM2030	AK1	3'	GGGAAGCTGAGGCAGGAGGATC 6640	A	C
	A		TGATCC CCTGCCTCGGC TCCC		
			ACTAGG GGACGGAGTCG AGGG		
			A A		
GAM2030	ALDH3B1	3'	GGGAGGCCGAGGCAGGCGGATC 93159	A	
	A		TGATCC CCTGCCTCGGCCTCCC		
			ACTAGG GGACGGAGCCGGAGGG		
			C		
GAM2030	ALDH8A1	3'	GGGAGGCCAAGGTGGGTGGATC 42915	TG	C
	A		TGATCCACC CCT GGCCTCCC		
			ACTAGGTGG GGA CCGGAGGG		
			GT A		
GAM2030	ALPP	3'	GGGAGGCCGAGGTGGGCGGATC 69419	A	TG
	A		TGATCC CC CCTCGGCCTCCC		
			ACTAGG GG GGAGCCGGAGGG		
			C GT		
GAM2030	ANKH	3'	GGGAGGCCAAGGAGGGTGGATC 55071	G	C
	A		TGATCCACCT CCT GGCCTCCC		
			ACTAGGTGGG GGA CCGGAGGG		
			A A		
GAM2030	APOL1	3'	GGGAGGCCAAGGCGGGCGGATC 14741	A	C
	A		TGATCC CCTGCCT GGCCTCCC		
			ACTAGG GGGCGGA CCGGAGGG		
			C A		
GAM2030	ATF5	3'	GGGAGGCCAAGGCAGGAGGATC 24823	A	C
	GT		ATGATCC CCTGCCT GGCCTCCC		
			TGCTAGG GGACGGA CCGGAGGG		
			A A		
GAM2030	ATM	3'	GGGAGGCCGAGGTGAGCGGATC 5298	AC	_
	A		TGATCC CT GCCTCGGCCTCCC		
			ACTAGG GA TGGAGCCGGAGGG		
			C_ G		
GAM2030	ATM	3'	GGGAGGCCGAGGTGAGCGGATC 57135	AC	_
	A		TGATCC CT GCCTCGGCCTCCC		

		ACTAGG GA TGGAGCCGGAGGG	
		C_ G	
GAM2030	ATP1A2	3' GGGAGGCCGAGGCAGGTGGATC 7366	
	AT	ATGATCCACCTGCCTCGGCCTCCC	
		TACTAGGTGGACGGAGCCGGAGGG	
GAM2030	BCAS1	3' GGGAGGCCGAGGCAGGTGGATC 14714	
	A	TGATCCACCTGCCTCGGCCTCCC	
		ACTAGGTGGACGGAGCCGGAGGG	
GAM2030	BHMT2	3' GGGAGGCCGAGGCGGGCGGATC 34738	A
	A	TGATCC CCTGCCTCGGCCTCCC	
		ACTAGG GGGCGGAGCCGGAGGG	
		C	
GAM2030	BRCA1	3' GGGAGGCCAAGGTGGGCAGATC 24448	CA TG C
	A	TGATC CC CCT GGCCTCCC	
		ACTAG GG GGA CCGGAGGG	
		AC GT A	
GAM2030	BRCA1	3' GGGAGGCCAAGGTGGGCAGATC 24460	CA TG C
	A	TGATC CC CCT GGCCTCCC	
		ACTAG GG GGA CCGGAGGG	
		AC GT A	
GAM2030	BRCA1	3' GGGAGGCCAAGGTGGGCAGATC 24471	CA TG C
	A	TGATC CC CCT GGCCTCCC	
		ACTAG GG GGA CCGGAGGG	
		AC GT A	
GAM2030	BRCA1	3' GGGAGGCCAAGGTGGGCAGATC 24480	CA TG C
	A	TGATC CC CCT GGCCTCCC	
		ACTAG GG GGA CCGGAGGG	
		AC GT A	
GAM2030	BRCA1	3' GGGAGGCCAAGGTGGGCAGATC 24488	CA TG C
	A	TGATC CC CCT GGCCTCCC	
		ACTAG GG GGA CCGGAGGG	
		AC GT A	
GAM2030	BRCA1	3' GGGAGGCCAAGGTGGGCAGATC 24496	CA TG C
	A	TGATC CC CCT GGCCTCCC	
		ACTAG GG GGA CCGGAGGG	
		AC GT A	
GAM2030	BRCA1	3' GGGAGGCCAAGGTGGGCAGATC 24506	CA TG C
	A	TGATC CC CCT GGCCTCCC	

			ACTAG GG GGA CCGGAGGG AC GT A		
GAM2030	BRCA1	3'	GGGAGGCCAAGGTGGGCAGATC 24515	CA TG C	
	A		TGATC CC CCT GGCCTCCC 		
			ACTAG GG GGA CCGGAGGG AC GT A		
GAM2030	BRCA1	3'	GGGAGGCCAAGGTGGGCAGATC 24523	CA TG C	
	A		TGATC CC CCT GGCCTCCC 		
			ACTAG GG GGA CCGGAGGG AC GT A		
GAM2030	BRCA1	3'	GGGAGGCCAAGGTGGGCAGATC 24531	CA TG C	
	A		TGATC CC CCT GGCCTCCC 		
			ACTAG GG GGA CCGGAGGG AC GT A		
GAM2030	BRCA1	3'	GGGAGGCCAAGGTGGGCAGATC 24571	CA TG C	
	A		TGATC CC CCT GGCCTCCC 		
			ACTAG GG GGA CCGGAGGG AC GT A		
GAM2030	C21orf5	3'	GGGAGGCCAAGGCAGGCAGATC 18886	CA C	
	A		TGATC CCTGCCT GGCCTCCC 		
			ACTAG GGACGGA CCGGAGGG AC A		
GAM2030	CARKL	3'	GGAGGCTGAGGCAGGAAAATCA 26105	CCA	
			TGAT CCTGCCTCGGCCTCC 		
			ACTA GGACGGAGTCGGAGG AAA		
GAM2030	CASP6	3'	GGAAGGCTGAGGCAGGAGAATC 8734	CCA	—
	A		TGAT CCTGCCTCGGCCT CC 		
			ACTA GGACGGAGTCGGA GG AGA A		
GAM2030	CASP6	3'	GGAAGGCTGAGGCAGGAGAATC 53365	CCA	—
	A		TGAT CCTGCCTCGGCCT CC 		
			ACTA GGACGGAGTCGGA GG AGA A		
GAM2030	CD28	3'	GGGAGGCCGAGGTGGGCAGATC 21555	CA TG	
	A		TGATC CC CTCGGCCTCCC 		
			ACTAG GG GGAGCCGGAGGG AC GT		
GAM2030	CD68	3'	GGGAGGCTGAGGCAGGTGGATC 60506		
	A		TGATCCACCTGCCTCGGCCTCCC 		

ACTAGGTGGACGGAGTCGGAGGG

GAM2030 CHST5 3' GAGGCTGAGGCGGGTGGATCA 25090
TGATCCACCTGCCTCGGCCTC
|||||
ACTAGGTGGGCGGAGTCGGAG

GAM2030 COG7 3' GGGAGGCCAAGCCAGATGGATC 68257 C C C
AT ATGATCCA CTG CT GGCCTCCC
||||| ||| || |||||
TACTAGGT GAC GA CCGGAGGG
A C A

GAM2030 CORO2A 3' GGGAGGCCGAGGCTGGTGGATC 54497 T
A TGATCCACC GCCTCGGCCTCCC
||||| |||||
ACTAGGTGG CGGAGCCGGAGGG
T

GAM2030 CORO2A 3' GGGAGGCCGAGGCTGGTGGATC 14105 T
A TGATCCACC GCCTCGGCCTCCC
||||| |||||
ACTAGGTGG CGGAGCCGGAGGG
T

GAM2030 CPM 3' GGGAGGCCAAGGTGGGCGGATC 60409 A TG C
A TGATCC CC CCT GGCCTCCC
||||| || ||| |||||
ACTAGG GG GGA CCGGAGGG
C GT A

GAM2030 CPT2 3' GAGGCTGAGGCGGGTGGATCA 5425
TGATCCACCTGCCTCGGCCTC
|||||
ACTAGGTGGGCGGAGTCGGAG

GAM2030 CPT2 3' GGGAGGCCGGGCATGGTGGCTC 5427 T _ T
AT ATGA CCACC TGCC CGGCCTCCC
||| |||| ||| |||||
TACT GGTGG ACGG GCCGGAGGG
C T _

GAM2030 CRACC 3' GGGAGGCCAAGGTGGGTGGGTC 41313 TG C
AT ATGATCCACC CCT GGCCTCCC
||||| ||| |||||
TACTGGGTGG GGA CCGGAGGG
GT A

GAM2030 CTMP 3' GGAGGCCGAGGCAGGCGGATT 54952 A
GATCC CCTGCCTCGGCCTCC
||||| |||||
TTAGG GGACGGAGCCGGAGG
C

GAM2030 CTSS 3' GGGAGGCCAAGGCAGGCATATC 15820 CCA C
A TGAT CCTGCCT GGCCTCCC
||| ||||| |||||

			ACTA GGACGGA CCGGAGGG	
			TAC A	
GAM2030	CUBN	3'	GGGAGGCCGAGGCAGGTTGATC 8422	C
	A		TGATC ACCTGCCTCGGCCTCCC	
			ACTAG TGGACGGAGCCGGAGGG	
			T	
GAM2030	CYP3A4	3'	GGAGGCTGAGGCAGGAGAATCA 34364	CCA
			TGAT CCTGCCTCGGCCTCC	
			ACTA GGACGGAGTCGGAGG	
			AGA	
GAM2030	CYP4F3	3'	GGGAGGTTGATGCAGGAGAATC 8013	CCA C
	A		TGAT CCTGC TCGGCCTCCC	
			ACTA GGACG AGTTGGAGGG	
			AGA T	
GAM2030	DBT	3'	GGGAGGCCGAGGTGGCCAGATC 10376	CAC TG
	A		TGATC C CCTCGGCCTCCC	
			ACTAG G GGAGCCGGAGGG	
			ACC GT	
GAM2030	DBT	3'	GGGAGGCTGAAGCAGGAGGATC 10377	A C
	A		TGATCC CCTGC TCGGCCTCCC	
			ACTAGG GGACG AGTCGGAGGG	
			A A	
GAM2030	DDOST	3'	GGGAGGCCGAGGCAGGCGGCTC 19065	T A
	A		TGA CC CCTGCCTCGGCCTCCC	
			ACT GG GGACGGAGCCGGAGGG	
			C C	
GAM2030	DFFA	3'	GGGAGGCCGAGGGGGCGGATC 16596	A G
	GT		ATGATCC CCT CCTCGGCCTCCC	
			TGCTAGG GGG GGAGCCGGAGGG	
			C G	
GAM2030	DHFR	3'	GGGAGGCTAAGGCAGGCAGATC 7653	CA CG
	A		TGATC CCTGCCT GCCTCCC	
			ACTAG GGACGGA CGGAGGG	
			AC AT	
GAM2030	DMC1	3'	GGGAGGCCGAGGCAGGTGGATC 23946	
	A		TGATCCACCTGCCTCGGCCTCCC	
			ACTAGGTGGACGGAGCCGGAGGG	
GAM2030	DVL3	3'	GGGAGGCTGAGACAGGTGGATC 16649	C
	A		TGATCCACCTG CTCGGCCTCCC	

		ACTAGGTGGAC GAGTCGGAGGG	
		A	
GAM2030	EGFL5	3' GGGAGGCCGAGGCGGGTGGATC 87917	
	A	TGATCCACCTGCCTCGGCCTCCC	
		ACTAGGTGGGCGGAGCCGGAGGG	
GAM2030	EGFL5	3' GGGAGGCTGAGGCAGGAGAATC 87918	CCA
	A	TGAT CCTGCCTCGGCCTCCC	
		ACTA GGACGGAGTCGGAGGG	
		AGA	
GAM2030	EIF2AK3	3' GCCGTAGTAAGAAATGGATCAT 17901	C__ _ CT
		ATGATCCA CT GC CGGC	
		TACTAGGT GA TG GCCG	
		AAA A AT	
GAM2030	F2R	3' GGGAGGCTGAGGCGGGTGGATC 10572	
	A	TGATCCACCTGCCTCGGCCTCCC	
		ACTAGGTGGGCGGAGTCGGAGGG	
GAM2030	F2RL3	3' GGAAGGCCGAGGTGGGCAGATC 15519	CA TG _
	AT	ATGATC CC CCTCGGCCT CC	
		TACTAG GG GGAGCCGGA GG	
		AC GT A	
GAM2030	FANCC	3' GGGAGGCCAAGGCAGGGGGATT 71046	A C
	A	TGATCC CCTGCCT GGCCTCCC	
		ATTAGG GGACGGA CCGGAGGG	
		G A	
GAM2030	FANCD2	3' GGGAGGCCGATGTGGGCAGATC 53531	CA TG C
	A	TGATC CC C TCGGCCTCCC	
		ACTAG GG G AGCCGGAGGG	
		AC GT T	
GAM2030	FCAR	3' GGAGGCTGAGGCAGGAGAATCA 56637	CCA
		TGAT CCTGCCTCGGCCTCC	
		ACTA GGACGGAGTCGGAGG	
		AGA	
GAM2030	FCMD	3' GAGAAGCTAAGGCAGGTGGATC 23037	CG _
	A	TGATCCACCTGCCT GC CTC	
		ACTAGGTGGACGGA CG GAG	
		AT AA	
GAM2030	FCMD	3' GGAGGCTGAGGCAGGAGAATCA 23041	CCA
		TGAT CCTGCCTCGGCCTCC	

			ACTA GGACGGAGTCGGAGG		
			AGA		
GAM2030	FGF2	3'	GGGAGGCCAAAGCAGGAGGATC 10620	A	CTC
	G		TGATCC CCTGC GGCCTCCC		
			GCTAGG GGACG CCGGAGGG		
			A AAA		
GAM2030	FGFR2	3'	GGGAGGCCGAGGCAGGCGGATC 43654	A	
	AT		ATGATCC CCTGCCTCGGCCTCCC		
			TACTAGG GGACGGAGCCGGAGGG		
			C		
GAM2030	FGFR2	3'	GGGAGGCCGAGGCAGGCGGATC 43667	A	
	AT		ATGATCC CCTGCCTCGGCCTCCC		
			TACTAGG GGACGGAGCCGGAGGG		
			C		
GAM2030	FLRT2	5'	GAGACCGAGGCAGAAGAATCAT 25998	CCAC	C
			ATGAT CTGCCTCGG CTC		
			TACTA GACGGAGCC GAG		
			AGAA A		
GAM2030	FLRT2	5'	GGGAGGCTGAAGCAGGAGGACC 26003	A A	C
	A		TG TCC CCTGC TCGGCCTCCC		
			AC AGG GGACG AGTCGGAGGG		
			C A A		
GAM2030	FUT6	3'	GGGAGGCCGAGGCAGGCGGATC 5642	A	
	A		TGATCC CCTGCCTCGGCCTCCC		
			ACTAGG GGACGGAGCCGGAGGG		
			C		
GAM2030	GAS7	3'	GGGAGGCCGAGGTGGGCAGATC 20857	CA	TG
	A		TGATC CC CCTCGGCCTCCC		
			ACTAG GG GGAGCCGGAGGG		
			AC GT		
GAM2030	GNE	3'	GGGAGGCCGAGGCGGGCGGATC 19672	A	
	A		TGATCC CCTGCCTCGGCCTCCC		
			ACTAGG GGGCGGAGCCGGAGGG		
			C		
GAM2030	GP2	3'	GGGAGGCTGAGGCAGGTGGATC 9482		
	A		TGATCCACCTGCCTCGGCCTCCC		
			ACTAGGTGGACGGAGTCGGAGGG		
GAM2030	GP6	3'	GGGAGGCCAAGGCAGGAGGATC 33473	A	C
	G		TGATCC CCTGCCT GGCCTCCC		

			GCTAGG GGACGGA CCGGAGGG		
			A A		
GAM2030	GPR81	3'	GGGAGACTGAGGCGGATCA 51753	ACCT	C
			TGATCC GCCTCGG CTCCC		
			ACTAGG CGGAGTC GAGGG		
			_____ A		
GAM2030	GPRK7	3'	GGGAGGCCAAGGCAGATGGATC 58315	C	C
	AT		ATGATCCA CTGCCT GGCCTCCC		
			TACTAGGT GACGGA CCGGAGGG		
			A A		
GAM2030	GRAF	3'	GGGAGGCCGAGGCGGGCGGATC 31240	A	
	A		TGATCC CCTGCCTCGGCCTCCC		
			ACTAGG GGGCGGAGCCGGAGGG		
			C		
GAM2030	GRM6	3'	GGGAGGCCGAGGCAGGTGGATC 7768		
	A		TGATCCACCTGCCTCGGCCTCCC		
			ACTAGGTGGACGGAGCCGGAGGG		
GAM2030	GRPR	3'	GGGAGGCCCAAATGATGGATCA 19207	CCTGCCTC	
			TGATCCA GGCCTCCC		
			ACTAGGT CCGGAGGG		
			AGTAAAC_		
GAM2030	HCS	3'	GGGAGGCCAAGGCAGGCAGATC 38987	CA	C
	A		TGATC CCTGCCT GGCCTCCC		
			ACTAG GGACGGA CCGGAGGG		
			AC A		
GAM2030	HIP1	3'	GGAGGCTGAGACAGGAGAATCA 19257	CCA	C
			TGAT CCTG CTCGGCCTCC		
			ACTA GGAC GAGTCGGAGG		
			AGA A		
GAM2030	HIP1	3'	GGGAGGCAGGGGCGGGTGGATC 19258		G
	A		TGATCCACCTGCCTC GCCTCCC		
			ACTAGGTGGGCGGGG CGGAGGG		
			A		
GAM2030	HIP1	3'	GGGAGGCCAAGACGGGATG 19259	_ C C	
			CA CCTG CT GGCCTCCC		
			GT GGGC GA CCGGAGGG		
			A A A		
GAM2030	HLA-E	3'	GGGAGGCCGAGGAGGGCAGATC 92676	CA	G
	A		TGATC CCT CCTCGGCCTCCC		

			ACTAG GGG GGAGCCGGAGGG	
			AC A	
GAM2030	HRH1	3'	GGGAGGCCGAGGCACGAGAATC 7823	CCACC
	G		TGAT TGCCTCGGCCTCCC	
			GCTA ACGGAGCCGGAGGG	
			AGAGC	
GAM2030	HSPA5	3'	AGGCTGAGGCAGGAGAATCA 19278	CCA
			TGAT CCTGCCTCGGCCT	
			ACTA GGACGGAGTCGGA	
			AGA	
GAM2030	HSPA5	3'	GGGAGGCCAAGGCGGGTGGATC 19286	C
	A		TGATCCACCTGCCT GGCCTCCC	
			ACTAGGTGGGCGGA CCGGAGGG	
			A	
GAM2030	HUNK	3'	GGGAGGCCGAGGCAGGTGGATC 28187	
	G		TGATCCACCTGCCTCGGCCTCCC	
			GCTAGGTGGACGGAGCCGGAGGG	
GAM2030	IAPP	3'	GGGAGGCCGAGGCAGGCAGATC 6442	CA
	A		TGATC CCTGCCTCGGCCTCCC	
			ACTAG GGACGGAGCCGGAGGG	
			AC	
GAM2030	ICA1	3'	GGAGGCTGAGGCAGGAGGATCA 42518	A
			TGATCC CCTGCCTCGGCCTCC	
			ACTAGG GGACGGAGTCGGAGG	
			A	
GAM2030	IFIT4	3'	GGGAGGCCGAGGTGGGCGGATC 71495	A TG
	A		TGATCC CC CCTCGGCCTCCC	
			ACTAGG GG GGAGCCGGAGGG	
			C GT	
GAM2030	IFNAR1	3'	GGGAGGCTGAGGCAGGCAGATC 7141	CA
	AT		ATGATC CCTGCCTCGGCCTCCC	
			TACTAG GGACGGAGTCGGAGGG	
			AC	
GAM2030	IL10	3'	GGGAGGCTGAGGCGGGTGGATC 6928	
	A		TGATCCACCTGCCTCGGCCTCCC	
			ACTAGGTGGGCGGAGTCGGAGGG	
GAM2030	IL11	3'	GGGAGGACGAAGCGAGTGGATC 7190	C C G
	A		TGATCCAC TGC TCG CCTCCC	

			ACTAGGTG GCG AGC GGAGGG		
			A A A		
GAM2030	IL13RA1	3'	GGGAGTCCGAGGCGGGCGGATC 9574	A	C
	A		TGATCC CCTGCCTCGG CTCCC		
			ACTAGG GGGCGGAGCC GAGGG		
			C T		
GAM2030	IL17R	3'	GGGAGGCCGAGGCAGGTGGATC 27558		
	A		TGATCCACCTGCCTCGGCCTCCC		
			ACTAGGTGGACGGAGCCGGAGGG		
GAM2030	IL18	3'	GAGGCTGAGGCAGGAGAATCA 9593	CCA	
			TGAT CCTGCCTCGGCCTC		
			ACTA GGACGGAGTCGGAG		
			AGA		
GAM2030	IL18	3'	GGGAGGCTGAGGCGGGCAGATC 9595	CA	
	A		TGATC CCTGCCTCGGCCTCCC		
			ACTAG GGGCGGAGTCGGAGGG		
			AC		
GAM2030	IL4R	5'	AGGCTGAGGCGGGCAGATCA 6456	CA	
			TGATC CCTGCCTCGGCCT		
			ACTAG GGGCGGAGTCGGA		
			AC		
GAM2030	IL6R	3'	GGGAGGTCGAGGCAGGAGGATC 6914	A	
	A		TGATCC CCTGCCTCGGCCTCCC		
			ACTAGG GGACGGAGCTGGAGGG		
			A		
GAM2030	IRAK1	3'	GGGAGGCCAAGGCAGGAGGATC 9615	A	C
	G		TGATCC CCTGCCT GGCCTCCC		
			GCTAGG GGACGGA CCGGAGGG		
			A A		
GAM2030	IRAK4	3'	GGGAGGCCGAGGCAGGCAGATC 61846	CA	
	A		TGATC CCTGCCTCGGCCTCCC		
			ACTAG GGACGGAGCCGGAGGG		
			AC		
GAM2030	ITCH	3'	GGGAGGCCGAGGCAGGAGGATC 49756	A	
			GATCC CCTGCCTCGGCCTCCC		
			CTAGG GGACGGAGCCGGAGGG		
			A		
GAM2030	ITGAL	3'	GGGAGGCCAAGGAGGGTGGATC 11048	G	C
	A		TGATCCACCT CCT GGCCTCCC		

			ACTAGGTGGG GGA CCGGAGGG	
			A A	
GAM2030 KAI1	3'		GGGAGGCCGAGGCGGGTGGATC 11127	
A			TGATCCACCTGCCTCGGCCTCCC	
			ACTAGGTGGGCGGAGCCGGAGGG	
GAM2030 KCNA7	3'		AGGCCGGGCGCGGTGGCTCAT 49886	T _ T
			ATGA CCACC TGCC CGGCCT	
			TACT GGTGG GCGG GCCGGA	
			C C _	
GAM2030 KCNA7	3'		GGGAGGCCGAGGTGGGCAAATT 49903	CCA TG
A			TGAT CC CCTCGGCCTCCC	
			ATTA GG GGAGCCGGAGGG	
			AAC GT	
GAM2030 KCNJ5	3'		GGGAGGCCGAGGCGGGTGGATC 7976	
AT			ATGATCCACCTGCCTCGGCCTCCC	
			TACTAGGTGGGCGGAGCCGGAGGG	
GAM2030 KIF1B	3'		GGGAGGCCGAGGCGGGCAGATC 31268	CA
A			TGATC CCTGCCTCGGCCTCCC	
			ACTAG GGGCGGAGCCGGAGGG	
			AC	
GAM2030 KIF3B	3'		GGGAGGCCGAGGTGGGTGGACC 17807	A TG
A			TG TCCACC CCTCGGCCTCCC	
			AC AGGTGG GGAGCCGGAGGG	
			C GT	
GAM2030 KMO	3'		GGGAGGCCAACGCCTAAAGATC 14846	CACCT CTC
AT			ATGATC GC GGCCTCCC	
			TACTAG CG CCGGAGGG	
			AAATC CAA	
GAM2030 LAMC2	3'		GGGAGACTGAAGCGGGTGGATC 38767	C C
A			TGATCCACCTGC TCGG CTCCC	
			ACTAGGTGGGCG AGTC GAGGG	
			A A	
GAM2030 LAMP2	3'		GGGAGGCCGAAGTGGGTGGATC 26574	TG C
A			TGATCCACC C TCGGCCTCCC	
			ACTAGGTGG G AGCCGGAGGG	
			GT A	
GAM2030 LAMP2	3'		GGGAGGCTGAGGCAGGAGAATC 26575	CCA
A			TGAT CCTGCCTCGGCCTCCC	

			ACTA GGACGGAGTCGGAGGG		
			AGA		
GAM2030	LDLR	3'	GGGAGGCCGAGGCGGGTGGATC 6740		
	AT		ATGATCCACCTGCCTCGGCCTCCC		
			TACTAGGTGGGCGGAGCCGGAGGG		
GAM2030	LEP	3'	GGGAGGCCAAGGTGGGGGGATC 5865	A TG C	
	A		TGATCC CC CCT GGCCTCCC		
			ACTAGG GG GGA CCGGAGGG		
			G GT A		
GAM2030	LILRB1	3'	GGGAGGCCGAGGCGGGCAGATC 22875	CA	
	A		TGATC CCTGCCTCGGCCTCCC		
			ACTAG GGGCGGAGCCGGAGGG		
			AC		
GAM2030	LRRC2	3'	GGGAGGCCGAAGTGGGTGGATC 44756	TG C	
	A		TGATCCACC C TCGGCCTCCC		
			ACTAGGTGG G AGCCGGAGGG		
			GT A		
GAM2030	LRRC2	3'	GGGAGGCCGAGATGGGTGAATC 44757	C GC	
	AT		ATGAT CACCT CTCGGCCTCCC		
			TACTA GTGGG GAGCCGGAGGG		
			A TA		
GAM2030	LUZP1	3'	GGAGGCTGAGGCAGGAGAATCA 54402	CCA	
			TGAT CCTGCCTCGGCCTCC		
			ACTA GGACGGAGTCGGAGG		
			AGA		
GAM2030	LUZP1	3'	GGGAGGCCAAGGCAGGCGGATC 54403	A C	
	A		TGATCC CCTGCCT GGCCTCCC		
			ACTAGG GGACGGA CCGGAGGG		
			C A		
GAM2030	MAFF	3'	GGGAGGCTGAGGCAGGAGGATC 25582	A	
	A		TGATCC CCTGCCTCGGCCTCCC		
			ACTAGG GGACGGAGTCGGAGGG		
			A		
GAM2030	MAPRE1	3'	GGAAGTGCAGCAGGCAGGTGAT 25593	C CG_ _ _	
	CAT		ATGATC ACCTGCCT GC CT CC		
			TACTAG TGGACGGA CG GA GG		
			_ CGA T A		
GAM2030	MAPT	3'	GGAGGCCGAGGCAGGGG 20966	A	
			CC CCTGCCTCGGCCTCC		

GG GGACGGAGCCGGAGG

GAM2030 MAPT 3' GGAGGCCGAGGCAGGGG 34178 A
CC CCTGCCTCGGCCTCC
|| |||||
GG GGACGGAGCCGGAGG

GAM2030 MAPT 3' GGAGGCCGAGGCAGGGG 34181 A
CC CCTGCCTCGGCCTCC
|| |||||
GG GGACGGAGCCGGAGG

GAM2030 MAPT 3' GGAGGCCGAGGCAGGGG 34183 A
CC CCTGCCTCGGCCTCC
|| |||||
GG GGACGGAGCCGGAGG

GAM2030 MBD4 3' GGAAGGCTGAGGCAGGAGGATC 15387 A
AT ATGATCC CCTGCCTCGGCCT CC
||||| ||||| ||
TACTAGG GGACGGAGTCGGA GG
A A

GAM2030 MCM4 3' GGGAGGCCAATGTGGGTGGATC 62580 TG CTC
AT ATGATCCACC C GGCCTCCC
||||| | |||||
TACTAGGTGG G CCGGAGGG
GT TAA

GAM2030 MLLT4 3' GGGAGGCCAAGGCGGGCAGATC 72901 CA C
A TGATC CCTGCCT GGCCTCCC
|||| ||||| |||||
ACTAG GGGCGGA CCGGAGGG
AC A

GAM2030 MMP19 3' GGGAGGCTGAAGCAGGAGGATC 11637 A C
A TGATCC CCTGC TCGGCCTCCC
|||| |||| |||||
ACTAGG GGACG AGTCGGAGGG
A A

GAM2030 MMP19 3' GGGAGGCTGAAGCAGGAGGATC 43305 A C
A TGATCC CCTGC TCGGCCTCCC
|||| |||| |||||
ACTAGG GGACG AGTCGGAGGG
A A

GAM2030 MOG 3' GGGAGGCCGAGGCGGGCGAATC 11674 CCA
A TGAT CCTGCCTCGGCCTCCC
||| |||||
ACTA GGGCGGAGCCGGAGGG
AGC

GAM2030 MS4A1 3' GGGAGGCCGAGGTGGGCAGATC 5551 CA TG
A TGATC CC CTCGGCCTCCC
|||| || |||||

			ACTAG GG GGAGCCGGAGGG		
			AC GT		
GAM2030	MSH3	3'	GGGAGGCCAAGGTAGGCAGATC 11692	CA	C
	A		TGATC CCTGCCT GGCCTCCC		
			ACTAG GGATGGA CCGGAGGG		
			AC A		
GAM2030	MSL3L1	3'	GAGACTGGGGCAGGAGGATCA 55320	A	C
			TGATCC CCTGCCTCGG CTC		
			ACTAGG GGACGGGGTC GAG		
			A A		
GAM2030	MTMR8	3'	GGGAGGCCAAGGCGGGCGGATC 31913	A	C
	AT		ATGATCC CCTGCCT GGCCTCCC		
			TACTAGG GGGCGGA CCGGAGGG		
			C A		
GAM2030	MYO1B	3'	GGGAGGCGGAGGCAGGTGGATC 25246		G
	A		TGATCCACCTGCCTC GCCTCCC		
			ACTAGGTGGACGGAG CGGAGGG		
			G		
GAM2030	MYO1C	3'	GGGAGGCTGAGGCAGGAGAATC 61868	CCA	
	A		TGAT CCTGCCTCGGCCTCCC		
			ACTA GGACGGAGTCGGAGGG		
			AGA		
GAM2030	NFKBIL2	3'	GGGAGGCCCAGGCGGGCGGATC 26454	A	C
	A		TGATCC CCTGCCT GGCCTCCC		
			ACTAGG GGGCGGA CCGGAGGG		
			C C		
GAM2030	NPHP1	3'	GGGAGGCCGAGGTGGGTGGATC 63147	TG	
	A		TGATCCACC CCTCGGCCTCCC		
			ACTAGGTGG GGAGCCGGAGGG		
			GT		
GAM2030	NPHS1	3'	GGGAGGCTGAGGCGGGTGGATC 17373		
	A		TGATCCACCTGCCTCGGCCTCCC		
			ACTAGGTGGGCGGAGTCGGAGGG		
GAM2030	NT5C2	3'	GGGAGGCCGAGACAGGCGGATC 25266	A	C
	A		TGATCC CCTG CTCGGCCTCCC		
			ACTAGG GGAC GAGCCGGAGGG		
			C A		
GAM2030	NUP62	3'	GGGAGGCTGAGGCAGGAGAATC 33787	CCA	
	A		TGAT CCTGCCTCGGCCTCCC		

			ACTA GGACGGAGTCGGAGGG	
			AGA	
GAM2030	OPA3	3'	GGGAGGCCGAGGCGGGCGGATC 47847	A
	A		TGATCC CCTGCCTCGGCCTCCC	
			ACTAGG GGGCGGAGCCGGAGGG	
			C	
GAM2030	P2RX7	3'	GGGAGGCCGAGGCAGGCAGATC 11928	CA
	A		TGATC CCTGCCTCGGCCTCCC	
			ACTAG GGACGGAGCCGGAGGG	
			AC	
GAM2030	PA2G4	3'	GGGAGGCTGAGGCGGGTGGATC 71830	
	A		TGATCCACCTGCCTCGGCCTCCC	
			ACTAGGTGGGCGGAGTCGGAGGG	
GAM2030	PAICS	3'	GGGAGGCTGAAGCAAGCAGATC 22265	CACC C
	A		TGATC TGC TCGGCCTCCC	
			ACTAG ACG AGTCGGAGGG	
			ACGA A	
GAM2030	PCDH11X	3'	GGGAGGCCGAGGCGGGTGGATC 53131	
	A		TGATCCACCTGCCTCGGCCTCCC	
			ACTAGGTGGGCGGAGCCGGAGGG	
GAM2030	PCDH11X	3'	GGGAGGCCGAGGTGGGTGGATC 53132	TG
	A		TGATCCACC CCTCGGCCTCCC	
			ACTAGGTGG GGAGCCGGAGGG	
			GT	
GAM2030	PCDH11Y	3'	GGGAGGCCGAGGCGGGTGGATC 53164	
	A		TGATCCACCTGCCTCGGCCTCCC	
			ACTAGGTGGGCGGAGCCGGAGGG	
GAM2030	PCDH11Y	3'	GGGAGGCCGAGGCGGGTGGATC 53165	
	A		TGATCCACCTGCCTCGGCCTCCC	
			ACTAGGTGGGCGGAGCCGGAGGG	
GAM2030	PCDH11Y	3'	GGGAGGCCGAGGCGGGTGGATC 53183	
	A		TGATCCACCTGCCTCGGCCTCCC	
			ACTAGGTGGGCGGAGCCGGAGGG	
GAM2030	PCDH11Y	3'	GGGAGGCCGAGGCGGGTGGATC 53184	
	A		TGATCCACCTGCCTCGGCCTCCC	

ACTAGGTGGGCGGAGCCGGAGGG

GAM2030	PCDHB9	3'	GGGAGGCCAAGGCGGGCAGATC 39448	CA	C
	A		TGATC CCTGCCT GGCCTCCC		
			ACTAG GGGCGGA CCGGAGGG		
			AC A		
GAM2030	PDE4C	3'	GGGAGGCTGAGGCAGGAGAATC 8105	CCA	
	A		TGAT CCTGCCTCGGCCTCCC		
			ACTA GGACGGAGTCGGAGGG		
			AGA		
GAM2030	PDE4C	3'	GGGAGGCTGAGGCAGGTGGATC 8106		
	A		TGATCCACCTGCCTCGGCCTCCC		
			ACTAGGTGGACGGAGTCGGAGGG		
GAM2030	PHKB	3'	GGGAGGCTGAGGCAGGTGGATC 6100		
	A		TGATCCACCTGCCTCGGCCTCCC		
			ACTAGGTGGACGGAGTCGGAGGG		
GAM2030	PIK3R2	3'	GGGAGGCCAAGACGGGCGGATC 18516	A	C C
			GATCC CCTG CT GGCCTCCC		
			CTAGG GGGC GA CCGGAGGG		
			C A A		
GAM2030	PKD2	3'	GGGAGGCCGAAACAGGCGAATC 60719	CCA	CC
	A		TGAT CCTG TCGGCCTCCC		
			ACTA GGAC AGCCGGAGGG		
			AGC AA		
GAM2030	PLA2G2D	3'	GGAGGCTGAGGCAGGAGAATCA 25717	CCA	
			TGAT CCTGCCTCGGCCTCC		
			ACTA GGACGGAGTCGGAGG		
			AGA		
GAM2030	PLA2G2D	3'	GGCTGAGGCAGGCAGATCA 25718	CA	
			TGATC CCTGCCTCGGCC		
			ACTAG GGACGGAGTCGG		
			AC		
GAM2030	POLH	3'	GGGAGGCCAAGGCGGGCAGATC 22481	CA	C
	A		TGATC CCTGCCT GGCCTCCC		
			ACTAG GGGCGGA CCGGAGGG		
			AC A		
GAM2030	POLH	3'	GGGAGGCCGAGGCAGACAGATC 22482	CAC	
	A		TGATC CTGCCTCGGCCTCCC		

			ACTAG GACGGAGCCGGAGGG		
			ACA		
GAM2030	POLH	3'	GGGAGGCTAAGGCAGGAGAATC 22483	CCA	CG
	A		TGAT CCTGCCT GCCTCCC		
			ACTA GGACGGA CGGAGGG		
			AGA AT		
GAM2030	POLK	3'	GGGAGGCCGAATGGGCAGATCA 33101	CACC	___
			TGATC TGCC TCGGCCTCCC		
			ACTAG ACGG AGCCGGAGGG		
			___ GTA		
GAM2030	PPP1R12B	3'	GGAGGCCGAGGTGGACAGATCA 50392	CAC	TG
			TGATC C CCTCGGCCTCC		
			ACTAG G GGAGCCGGAGG		
			ACA GT		
GAM2030	PRKY	3'	GGGAGGCCAAGGCAGGCAGATC 12381	CA	C
	A		TGATC CCTGCCT GGCCTCCC		
			ACTAG GGACGGA CCGGAGGG		
			AC A		
GAM2030	PSD	5'	GGGAGGCCAGGCGGGCGGATCA 12440	A	C
			TGATCC CCTGCCT GGCCTCCC		
			ACTAGG GGGCGGA CCGGAGGG		
			C _		
GAM2030	PSMB2	3'	GGGAGGCCGAGGCGGGCGGATC 12476	A	
	A		TGATCC CCTGCCTCGGCCTCCC		
			ACTAGG GGGCGGAGCCGGAGGG		
			C		
GAM2030	PSMB9	3'	GGGAGGCCAAGGCAGGCGGATC 12507	A	C
	A		TGATCC CCTGCCT GGCCTCCC		
			ACTAGG GGACGGA CCGGAGGG		
			C A		
GAM2030	PSMB9	3'	GGGAGGCTGAGACAGAAGAATC 12508	CCAC	C
	A		TGAT CTG CTCGGCCTCCC		
			ACTA GAC GAGTCGGAGGG		
			AGAA A		
GAM2030	PSMD5	3'	GGGAGGCCAAGATGGGCAAATC 18561	CCA	GC C
	A		TGAT CCT CT GGCCTCCC		
			ACTA GGG GA CCGGAGGG		
			AAC TA A		
GAM2030	PTAFR	3'	GGGAGGCCGAGGTGGGCAGATC 8167	CA	TG
	AT		ATGATC CC CCTCGGCCTCCC		

			TACTAG GG GGAGCCGGAGGG		
			AC GT		
GAM2030	PTGIS	3'	GGGAGGCCGAGGTGGGCGGATC 8217	A	TG
	A		TGATCC CC CCTCGGCCTCCC		
			ACTAGG GG GGAGCCGGAGGG		
			C GT		
GAM2030	RAB3B	3'	GGGAGGCCGAGGCGGGTGGATC 12706		
	AT		ATGATCCACCTGCCTCGGCCTCCC		
			TACTAGGTGGGCGGAGCCGGAGGG		
GAM2030	RAB7L1	3'	GGGAGGCCAAGGCAGGCGGATC 15410	A	C
	A		TGATCC CCTGCCT GGCCTCCC		
			ACTAGG GGACGGA CCGGAGGG		
			C A		
GAM2030	RAB7L1	3'	GGGAGGCTGAGGCAGGAGAATC 15411	CCA	
	A		TGAT CCTGCCTCGGCCTCCC		
			ACTA GGACGGAGTCGGAGGG		
			AGA		
GAM2030	RAB7L1	3'	GGGAGGCTGAGGCAGGTGGATC 15412		
	G		TGATCCACCTGCCTCGGCCTCCC		
			GCTAGGTGGACGGAGTCGGAGGG		
GAM2030	RAD51L1	5'	GGGAGGCCGAAGCGGGCGGATC 56878	A	C
	A		TGATCC CCTGC TCGGCCTCCC		
			ACTAGG GGGCG AGCCGGAGGG		
			C A		
GAM2030	RBBP5	3'	GGGAGGCCAAGGCGGGTGGATC 18578		C
	A		TGATCCACCTGCCT GGCCTCCC		
			ACTAGGTGGGCGGA CCGGAGGG		
			A		
GAM2030	RBL1	3'	GGGAGGCCAAGGCGGGCAGATC 12788	CA	C
	A		TGATC CCTGCCT GGCCTCCC		
			ACTAG GGGCGGA CCGGAGGG		
			AC A		
GAM2030	RFC2	3'	GGGAGGCCGAGGCAGGTGGATC 12846		
	A		TGATCCACCTGCCTCGGCCTCCC		
			ACTAGGTGGACGGAGCCGGAGGG		
GAM2030	ROCK2	3'	GGGAGGCCAAGACGGGCGGATC 66622	A	C C
	A		TGATCC CCTG CT GGCCTCCC		

			ACTAGG GGGC GA CCGGAGGG	
			C A A	
GAM2030	SFRS2IP	5'	GGGAGGCCGAGGCAGGCAGATC 17544	CA
	A		TGATC CCTGCCTCGGCCTCCC	
			ACTAG GGACGGAGCCGGAGGG	
			AC	
GAM2030	SIM2	3'	GGGAGGCCAAGGTGGGCGGATC 24803	A TG C
	A		TGATCC CC CCT GGCCTCCC	
			ACTAGG GG GGA CCGGAGGG	
			C GT A	
GAM2030	SLC14A2	3'	GGGAGGCCGAGGCGGGTGGATC 24120	
	A		TGATCCACCTGCCTCGGCCTCCC	
			ACTAGGTGGGCGGAGCCGGAGGG	
GAM2030	SLC26A4	3'	GGGAGGCCGAGGCGGGTGGATC 6529	
	A		TGATCCACCTGCCTCGGCCTCCC	
			ACTAGGTGGGCGGAGCCGGAGGG	
GAM2030	SLC28A2	3'	GGGAGGCCGAGGCGGGCGGATC 16153	A
	G		TGATCC CCTGCCTCGGCCTCCC	
			GCTAGG GGGCGGAGCCGGAGGG	
			C	
GAM2030	SLC2A6	3'	GGGAGGCCAAAGCAGGTGGATT 34573	CTC
	A		TGATCCACCTGC GGCCTCCC	
			ATTAGGTGGACG CCGGAGGG	
			AAA	
GAM2030	SLC31A1	3'	AGGCTGAGGCAGGAGAATCA 10271	CCA
			TGAT CCTGCCTCGGCCT	
			ACTA GGACGGAGTCGGA	
			AGA	
GAM2030	SMG1	3'	GGGAGGCCGAGGCGGGCGGATC 31350	A
	AT		ATGATCC CCTGCCTCGGCCTCCC	
			TACTAGG GGGCGGAGCCGGAGGG	
			C	
GAM2030	SRGAP1	5'	GGAGGCTGAGGCAGGAGAATCA 72717	CCA
			TGAT CCTGCCTCGGCCTCC	
			ACTA GGACGGAGTCGGAGG	
			AGA	
GAM2030	SRGAP1	5'	GGGAGGCCAAGGCGGGTGGATT 72719	C
	A		TGATCCACCTGCCT GGCCTCCC	

			ATTAGGTGGGCGGA CCGAGGG		
			A		
GAM2030	SUDD	3'	GGGAGACCAAGGCGGGTGGATC 15159	C	C
	A		TGATCCACCTGCCT GG CTCCC		
			ACTAGGTGGGCGGA CC GAGGG		
			A A		
GAM2030	SULT2A1	3'	GGGAGGCCGAGACGGGCGGATC 72230	A	C
	A		TGATCC CCTG CTCGGCCTCCC		
			ACTAGG GGGC GAGCCGAGGG		
			C A		
GAM2030	SUV39H2	3'	GGAGGCTGAGGCAGGAGAATCA 45458	CCA	
			TGAT CCTGCCTCGGCCTCC		
			ACTA GGACGGAGTCGGAGG		
			AGA		
GAM2030	SWAP70	3'	GGGAGGCCGAGGCGGGTGGATC 71871		
	A		TGATCCACCTGCCTCGGCCTCCC		
			ACTAGGTGGGCGGAGCCGAGGG		
GAM2030	SWAP70	3'	GGGAGGCTGAGGCAGGAGAATC 71872	CCA	
	A		TGAT CCTGCCTCGGCCTCCC		
			ACTA GGACGGAGTCGGAGGG		
			AGA		
GAM2030	TACC1	3'	GGAAGGCCGAGGCAGGAGGATC 21877	A	—
	A		TGATCC CCTGCCTCGGCCT CC		
			ACTAGG GGACGGAGCCGGA GG		
			A A		
GAM2030	TBX1	3'	GGGAGGCTGAGGCAGGAGGATC 21139	A	
	A		TGATCC CCTGCCTCGGCCTCCC		
			ACTAGG GGACGGAGTCGGAGGG		
			A		
GAM2030	TBX6	3'	GGGAGGCTGAGGCGGGCAGATC 55816	CA	
	A		TGATC CCTGCCTCGGCCTCCC		
			ACTAG GGGCGGAGTCGGAGGG		
			AC		
GAM2030	TCF7	3'	GGCAGGCCGAGGCAGGTGGATC 13624		—
	A		TGATCCACCTGCCTCGGCCT CC		
			ACTAGGTGGACGGAGCCGGA GG		
			C		
GAM2030	TCTA	3'	GGGAGGCTGAGGCAGGCAGATC 42501	CA	
	A		TGATC CCTGCCTCGGCCTCCC		

			ACTAG GGACGGAGTCGGAGGG		
			AC		
GAM2030	TDG	5'	GGGAGGCCAAGGCAGGCGGACC 13647	A A	C
	A		TG TCC CCTGCCT GGCCTCCC		
			AC AGG GGACGGA CCGGAGGG		
			C C A		
GAM2030	TEM7	3'	GGGAGGCTGAGGCAGGCGGATC 40267	A	
	A		TGATCC CCTGCCTCGGCCTCCC		
			ACTAGG GGACGGAGTCGGAGGG		
			C		
GAM2030	TEP1	3'	GGAGGCCGGGCATGGTGGCTCA 24047	T _	T
			TGA CCACC TGCC CGGCCTCC		
			ACT GGTGG ACGG GCCGGAGG		
			C T _		
GAM2030	TEP1	3'	GGGAGGCCGAGGTGGGCAGATC 24048	CA	TG
	A		TGATC CC CCTCGGCCTCCC		
			ACTAG GG GGAGCCGGAGGG		
			AC GT		
GAM2030	TNFAIP6	3'	GGAAGGCCGAGGCAGAGGATC 60169	AC	_
			GATCC CTGCCTCGGCCT CC		
			CTAGG GACGGAGCCGGA GG		
			A_ A		
GAM2030	TNFRSF10A	3'	GGGAGGCTGAGGCGGGTGGATC 15238		
	A		TGATCCACCTGCCTCGGCCTCCC		
			ACTAGGTGGGCGGAGTCGGAGGG		
GAM2030	TNFRSF1B	3'	GGGAGGCTGAGGCGGGTGGATC 8398		
	A		TGATCCACCTGCCTCGGCCTCCC		
			ACTAGGTGGGCGGAGTCGGAGGG		
GAM2030	TNFSF14	3'	GGGAGGCCAAGGCAGGCGGATC 15081	A	C
	A		TGATCC CCTGCCT GGCCTCCC		
			ACTAGG GGACGGA CCGGAGGG		
			C A		
GAM2030	TNFSF15	3'	GGGAGGCCAAGGTGGGTGGATC 18868	TG	C
	AT		ATGATCCACC CCT GGCCTCCC		
			TACTAGGTGG GGA CCGGAGGG		
			GT A		
GAM2030	TRIM14	3'	GGGAGGCCGATGTGGGTGGATC 53776	TG	C
	A		TGATCCACC C TCGGCCTCCC		

			ACTAGGTGG G AGCCGGAGGG		
			GT T		
GAM2030	TRIM14	3'	GGGAGGCCAAGGTCGCCGAATC 29515	CCACCT	C
			GAT GCCT GGCCTCCC		
			CTA TGGA CCGGAGGG		
			AGCCGC A		
GAM2030	TRIM9	5'	GGGAGGCTAAGGCAGGCGGACC 31457	A A	CG
	A		TG TCC CCTGCCT GCCTCCC		
			AC AGG GGACGGA CGGAGGG		
			C C AT		
GAM2030	TRPM1	3'	GGGAGGCCAAGGCAGAAAGAT 11603	CAC	C
			ATC CTGCCT GGCCTCCC		
			TAG GACGGA CCGGAGGG		
			AAA A		
GAM2030	TSN	3'	GGGAGGCCGAGGCAGGGGGA 17303	A	
			TCC CCTGCCTCGGCCTCCC		
			AGG GGACGGAGCCGGAGGG		
			G		
GAM2030	TSNAX	3'	GGGAGGCCGAGGTAGGCAGATC 21159	CA	
	A		TGATC CCTGCCTCGGCCTCCC		
			ACTAG GGATGGAGCCGGAGGG		
			AC		
GAM2030	UBE2G2	3'	GGGAGACTGAGGCGGGCGGATC 65489	A	C
	AT		ATGATCC CCTGCCTCGG CTCCC		
			TACTAGG GGGCGGAGTC GAGGG		
			C A		
GAM2030	UBE2G2	3'	GGGAGGCCAAGGCAGGTAGATC 65491	C	C
	A		TGATC ACCTGCCT GGCCTCCC		
			ACTAG TGGACGGA CCGGAGGG		
			A A		
GAM2030	UPK1B	3'	GGGAGGCCGAGGTGGGCAGATC 23703	CA	TG
	A		TGATC CC CCTCGGCCTCCC		
			ACTAG GG GGAGCCGGAGGG		
			AC GT		
GAM2030	USP14	3'	GGGAGGCTGAGGCAGGTGGTTC 18936	T	
	A		TGA CCACCTGCCTCGGCCTCCC		
			ACT GGTGGACGGAGTCGGAGGG		
			T		
GAM2030	VDR	3'	GGGAGGTCGAGGTAGGTGGATC 6346		
	A		TGATCCACCTGCCTCGGCCTCCC		

ACTAGGTGGATGGAGCTGGAGGG

GAM2030 VHL	3'	GGAGGCTGAGGCAGGAGAATCA 6865	CCA
		TGAT CCTGCCTCGGCCTCC	
		ACTA GGACGGAGTCGGAGG	
		AGA	
GAM2030 VHL	3'	GGGAGGCCAGGGCAGGCAGATC 6867	CA TC
AT		ATGATC CCTGCC GGCCTCCC	
		TACTAG GGACGG CCGGAGGG	
		AC GA	
GAM2030 VHL	3'	GGGAGGCCTAGGCGGGTGGATC 6868	C
A		TGATCCACCTGCCT GGCCTCCC	
		ACTAGGTGGGCGGA CCGGAGGG	
		T	
GAM2030 VPS41	3'	GGAGGCTGAGGCAGGAGAATCA 27694	CCA
		TGAT CCTGCCTCGGCCTCC	
		ACTA GGACGGAGTCGGAGG	
		AGA	
GAM2030 VPS41	3'	GGGAGGCCTTGGCAGGTGGATC 27695	TC
A		TGATCCACCTGCC GGCCTCCC	
		ACTAGGTGGACGG CCGGAGGG	
		TT	
GAM2030 WIG1	3'	GGGAGGCCGAAGCAGGCGGATC 96104	A C
A		TGATCC CCTGC TCGGCCTCCC	
		ACTAGG GGACG AGCCGGAGGG	
		C A	
GAM2030 WW45	3'	GGGAGGCCGAGGTGGGTGGACC 41815	A TG
G		TG TCCACC CCTCGGCCTCCC	
		GC AGGTGG GGAGCCGGAGGG	
		C GT	
GAM2030 ZNF136	3'	GGGAGGCTGAGGCAGGAGGATC 60569	A
A		TGATCC CCTGCCTCGGCCTCCC	
		ACTAGG GGACGGAGTCGGAGGG	
		A	
GAM2030 ZNF264	3'	GAGACCACTAAGGCGGGTGGAT 14214	C__ C
CA		TGATCCACCTGCCT GG CTC	
		ACTAGGTGGGCGGA CC GAG	
		ATCA A	
GAM2030 ZNF36	3'	GGGAGGCCGAGGTGAGCGGATC 95584	AC _
A		TGATCC CT GCCTCGGCCTCCC	

			ACTAGG GA TGGAGCCGGAGGG	
			C_ G	
GAM2030	ZNF36	3'	GGGAGGCTGAGGCAGGAGAATC 95585	CCA
	A		TGAT CCTGCCTCGGCCTCCC	
			ACTA GGACGGAGTCGGAGGG	
			AGA	
GAM2030	ZNF74	3'	GGGAGGCCAAGGCAAGGGGATC 14263	A _ C
	A		TGATCC CCT GCCT GGCCTCCC	
			ACTAGG GGA CGGA CCGGAGGG	
			_ A A	
GAM2030	AF020591	3'	GAGGCCGAGGCAGGTGGATCA 27912	
			TGATCCACCTGCCTCGGCCTC	
			ACTAGGTGGACGGAGCCGGAG	
GAM2030	AKR1D1	3'	GGGAGGCCAAGGTGGGCAGATC 21133	CA TG C
	A		TGATC CC CCT GGCCTCCC	
			ACTAG GG GGA CCGGAGGG	
			AC GT A	
GAM2030	ALTE	3'	GGGAGGCCGAGGTGGGCAGATC 17581	CA TG
	A		TGATC CC CCTCGGCCTCCC	
			ACTAG GG GGAGCCGGAGGG	
			AC GT	
GAM2030	ALTE	3'	GGGAGGCCGAGGTGGGCAGATC 61005	CA TG
	A		TGATC CC CCTCGGCCTCCC	
			ACTAG GG GGAGCCGGAGGG	
			AC GT	
GAM2030	AP1GBP1	3'	GGGAGGGGAGGCAGGCAGAT 55446	CA GG
			ATC CCTGCCTC CCTCCC	
			TAG GGACGGAG GGAGGG	
			AC G_	
GAM2030	APXL2	3'	GGGAGGCCGAGGCGGGCGGATC 75681	A
	A		TGATCC CCTGCCTCGGCCTCCC	
			ACTAGG GGGCGGAGCCGGAGGG	
			C	
GAM2030	ARNTL2	3'	GGGAGGCCGAAGTGGGCGGATC 39853	A TG C
	A		TGATCC CC C TCGGCCTCCC	
			ACTAGG GG G AGCCGGAGGG	
			C GT A	
GAM2030	ARNTL2	3'	GGGAGGCTGAGACGGGCAGATC 39854	CA C
	A		TGATC CCTG CTCGGCCTCCC	

			ACTAG GGGC GAGTCGGAGGG		
			AC A		
GAM2030	ASAH1	3'	GGGAGGCCAAGGCGGGTGGATC 64319		C
	A		TGATCCACCTGCCT GGCCTCCC		
			ACTAGGTGGGCGGA CCGAGGG		
			A		
GAM2030	BANP	3'	GGGAGGCTGAGGCTGGTGGATC 66802		T
	A		TGATCCACC GCCTCGGCCTCCC		
			ACTAGGTGG CGGAGTCGGAGGG		
			T		
GAM2030	BFAR	3'	GGGTGAGGCAGGCGGATCA 61425	A	G
			TGATCC CCTGCCTCG CC		
			ACTAGG GGACGGAGT GG		
			C G		
GAM2030	BIA2	3'	GGGAGGCTGAGGCGGGTGGATC 71795		
	A		TGATCCACCTGCCTCGGCCTCCC		
			ACTAGGTGGGCGGAGTCGGAGGG		
GAM2030	BIRC1	3'	GGGAGGCTGAGGCGGGCGAATC 16994	CCA	
	AT		ATGAT CCTGCCTCGGCCTCCC		
			TACTA GGGCGGAGTCGGAGGG		
			AGC		
GAM2030	BLOV1	3'	GGGAGGCCAAGGCCAGCGGATC 76797	AC _ C	
	A		TGATCC CTG CCT GGCCTCCC		
			ACTAGG GAC GGA CCGGAGGG		
			C_ C A		
GAM2030	BLOV1	3'	GGGAGGCTGAGGCAGGAGAATC 76798	CCA	
	A		TGAT CCTGCCTCGGCCTCCC		
			ACTA GGACGGAGTCGGAGGG		
			AGA		
GAM2030	BPES	3'	AGTCCTGGAGGCAGGGAGATCA 43794	CA _ C	
			TGATC CCTGCCTC GG CT		
			ACTAG GGACGGAG CC GA		
			AG GT T		
GAM2030	C12orf2	3'	GGGAGGCCGAGGTGGGAGAATC 83684	CCA TG	
	A		TGAT CC CCTCGGCCTCCC		
			ACTA GG GGAGCCGGAGGG		
			AGA GT		
GAM2030	C1orf33	3'	GGAGGCTGAGGCAGGAGAATCA 32985	CCA	
			TGAT CCTGCCTCGGCCTCC		

		ACTA GGACGGAGTCGGAGG		
		AGA		
GAM2030	C1orf33 3'	GGGAAGCCGAGGTGGGCAGATC 32986	CA TG	C
	AT	ATGATC CC CCTCGGC TCCC		
		TACTAG GG GGAGCCG AGGG		
		AC GT A		
GAM2030	C20orf106 3'	GGGAGGCCGAGACGGGCAGATC 55908	CA	C
	A	TGATC CCTG CTCGGCCTCCC		
		ACTAG GGGC GAGCCGGAGGG		
		AC A		
GAM2030	C20orf106 3'	GGGAGGCTGAGGCAGGAGAATC 55909	CCA	
	A	TGAT CCTGCCTCGGCCTCCC		
		ACTA GGACGGAGTCGGAGGG		
		AGA		
GAM2030	C20orf106 3'	GGGAGGCTGAGGCGGGTGAATC 55910	C	
	A	TGAT CACCTGCCTCGGCCTCCC		
		ACTA GTGGGCGGAGTCGGAGGG		
		A		
GAM2030	C20orf175 3'	GGAGGCTGAGGCAGGAGAATCA 55926	CCA	
		TGAT CCTGCCTCGGCCTCC		
		ACTA GGACGGAGTCGGAGG		
		AGA		
GAM2030	C20orf175 3'	GGGAGGCCGAGGCAGGCGGATT 55927	A	
	A	TGATCC CCTGCCTCGGCCTCCC		
		ATTAGG GGACGGAGCCGGAGGG		
		C		
GAM2030	C20orf177 3'	GGGAGGCCGAGGCAGGCGGATC 62837	A	
	A	TGATCC CCTGCCTCGGCCTCCC		
		ACTAGG GGACGGAGCCGGAGGG		
		C		
GAM2030	C20orf183 3'	GGGAGGCCGAGGCGGGCGGATC 48535	A	
	A	TGATCC CCTGCCTCGGCCTCCC		
		ACTAGG GGGCGGAGCCGGAGGG		
		C		
GAM2030	C21orf108 3'	GGGAGGCCAAGGCGGGTGAATC 90117	C	C
	A	TGAT CACCTGCCT GGCCTCCC		
		ACTA GTGGGCGGA CCGGAGGG		
		A A		
GAM2030	C22orf19 3'	GGGAGGCCAAGGCGGGTGGATC 14825		C
	A	TGATCCACCTGCCT GGCCTCCC		

			ACTAGGTGGGCGGA CCGAGGG		
			A		
GAM2030	C22orf20	3'	GGAAGGCTGAGGCAGGAGAATC 48197	CCA	—
	A		TGAT CCTGCCTCGGCCT CC		
			ACTA GGACGGAGTCGGA GG		
			AGA A		
GAM2030	C22orf20	3'	GGGAGGCCAAGGTTGGCAGATC 48198	CA T C	
	A		TGATC CC GCCT GGCCTCCC		
			ACTAG GG TGA CCGAGGG		
			AC T A		
GAM2030	C2F	3'	GGGAGGCGGAGGCGGGTGGATC 22009	G	
	A		TGATCCACCTGCCTC GCCTCCC		
			ACTAGGTGGGCGGAG CGGAGGG		
			G		
GAM2030	C6.1A	3'	GGGAGGCAGGAGGATCA 44537	A GG	
			TGATCC CCTGCCTC CC		
			ACTAGG GGACGGAG GG		
			A —		
GAM2030	C6orf29	3'	GAGGCTGAGGCGGGCGGATCA 52458	A	
			TGATCC CCTGCCTCGGCCTC		
			ACTAGG GGGCGGAGTCGGAG		
			C		
GAM2030	C6orf29	3'	GAGGCTGAGGCGGGCGGATCA 48265	A	
			TGATCC CCTGCCTCGGCCTC		
			ACTAGG GGGCGGAGTCGGAG		
			C		
GAM2030	C6orf5	3'	GGGAGGCTGAGGCAGGAGAATC 31997	CCA	
	A		TGAT CCTGCCTCGGCCTCCC		
			ACTA GGACGGAGTCGGAGGG		
			AGA		
GAM2030	C6orf5	3'	GGGAGGCTGAGGCAGGCGGATC 31998	A	
	AT		ATGATCC CCTGCCTCGGCCTCCC		
			TACTAGG GGACGGAGTCGGAGGG		
			C		
GAM2030	C8orf2	3'	GGGAGGCCAAGGCAGGCGGATC 24155	A C	
	A		TGATCC CCTGCCT GGCCTCCC		
			ACTAGG GGACGGA CCGAGGG		
			C A		
GAM2030	CALN1	3'	GGGAGGCCAAGGCAGGTGGATC 49667	C	
	A		TGATCCACCTGCCT GGCCTCCC		

			ACTAGGTGGACGGA CCGGAGGG	
			A	
GAM2030	CAMKK2	5'	AGGCCAAGGCGGGTGGATCA 22615	C
			TGATCCACCTGCCT GGCCT	
			ACTAGGTGGGCGGA CCGGA	
			A	
GAM2030	CDT1	3'	GGGAGGCCAAGGTGGGCAGATC 78164	CA TG C
	A		TGATC CC CCT GGCCTCCC	
			ACTAG GG GGA CCGGAGGG	
			AC GT A	
GAM2030	cerk	3'	GGGAGGCCGAGGCGGGTGGATC 43168	
	A		TGATCCACCTGCCTCGGCCTCCC	
			ACTAGGTGGGCGGAGCCGGAGGG	
GAM2030	CFLAR	3'	GGGAGGCCAAGGAGGGCAGATC 15275	CA G C
	A		TGATC CCT CCT GGCCTCCC	
			ACTAG GGG GGA CCGGAGGG	
			AC A A	
GAM2030	CG012	3'	GGGAGGGTGAGGCAGGAGAATC 84163	CCA G
	A		TGAT CCTGCCTCG CCTCCC	
			ACTA GGACGGAGT GGAGGG	
			AGA G	
GAM2030	CNNM1	3'	GGAAGACCGAGGCGGGTGGATC 40124	C _
	A		TGATCCACCTGCCTCGG CT CC	
			ACTAGGTGGGCGGAGCC GA GG	
			A A	
GAM2030	COE2	3'	GGAAGACCGAGGTGGGCAGATC 64909	CA TG C _
	A		TGATC CC CTCGG CT CC	
			ACTAG GG GGAGCC GA GG	
			AC GT A A	
GAM2030	CPR2	3'	GGAGGCTGAGGCAGGTGAATCA 48835	C
			TGAT CACCTGCCTCGGCCTCC	
			ACTA GTGGACGGAGTCGGAGG	
			A	
GAM2030	CPR2	3'	GGGAGGCCAAGGCCCTCAGATC 48837	CACCT C
			GATC GCCT GGCCTCCC	
			CTAG CGGA CCGGAGGG	
			ACTCC A	
GAM2030	CRTAM	3'	GGGAGGCTGAGGTAGGCAGATC 39475	CA
	A		TGATC CCTGCCTCGGCCTCCC	

			ACTAG GGATGGAGTCGGAGGG	
			AC	
GAM2030	CSAD	3'	GGGAGGCCGAGGCGGGTGGATC 32583	
	A		TGATCCACCTGCCTCGGCCTCCC	
			ACTAGGTGGGCGGAGCCGGAGGG	
GAM2030	CYorf14	3'	GGGAGGCTGAGGTAGGCAGATC 38205	CA
	A		TGATC CCTGCCTCGGCCTCCC	
			ACTAG GGATGGAGTCGGAGGG	
			AC	
GAM2030	D21S2056E	3'	GGGAGGCCGAGGTGGCCAGATC 14869	CAC TG
	A		TGATC C CCTCGGCCTCCC	
			ACTAG G GGAGCCGGAGGG	
			ACC GT	
GAM2030	DCNP1	3'	GGGAGGCCCATGGTGGAGCA 56460	A _ CCTC
			TG TCCACC TG GGCCTCCC	
			AC AGGTGG AC CCGGAGGG	
			G T	
GAM2030	DDX34	3'	GGGAGGCCGAGGCGGGAGGATC 28673	A
	A		TGATCC CCTGCCTCGGCCTCCC	
			ACTAGG GGGCGGAGCCGGAGGG	
			A	
GAM2030	DDX34	3'	GGGAGGCCTAGGCGGGCAGATC 28674	CA C
	A		TGATC CCTGCCT GGCCTCCC	
			ACTAG GGGCGGA CCGGAGGG	
			AC T	
GAM2030	DEGS	3'	GGGAGGCCAAGGTGGGTGGATC 14803	TG C
	A		TGATCCACC CCT GGCCTCCC	
			ACTAGGTGG GGA CCGGAGGG	
			GT A	
GAM2030	DF	3'	GGGAGGCCGAGGTGGGAGGATC 10405	A TG
	AT		ATGATCC CC CCTCGGCCTCCC	
			TACTAGG GG GGAGCCGGAGGG	
			A GT	
GAM2030	DF	3'	GGGAGGCCGAGGTGGGAGGATC 76821	A TG
	AT		ATGATCC CC CCTCGGCCTCCC	
			TACTAGG GG GGAGCCGGAGGG	
			A GT	
GAM2030	DIS3	3'	GGGAGGACGAGGCGGGTGGATC 30921	G
	A		TGATCCACCTGCCTCG CCTCCC	

		ACTAGGTGGGCGGAGC GGAGGG		
		A		
GAM2030	DJ122O8.2 3'	GGAGGCTGTGGTAGGTGGATCA 40395		T
		TGATCCACCTGCC CGGCCTCC		
		ACTAGGTGGATGG GTCGGAGG		
		T		
GAM2030	DJ122O8.2 3'	GGGAGGCTGAGGCAGGAGAATC 40396		CCA
	A	TGAT CCTGCCTCGGCCTCCC		
		ACTA GGACGGAGTCGGAGGG		
		AGA		
GAM2030	DKFZP434C171 3'	GGGAGGCCGAGGTGGGTGGATC 32194		TG
	A	TGATCCACC CCTCGGCCTCCC		
		ACTAGGTGG GGAGCCGGAGGG		
		GT		
GAM2030	DKFZP434C1715 3'	GGGAGGCCAAGGCAGAAGGATC 87355	AC	C
	A	TGATCC CTGCCT GGCCTCCC		
		ACTAGG GACGGA CCGGAGGG		
		AA A		
GAM2030	DKFZp434E0519 3'	GGGAGGCCAAGGCAGGAGGATC 50996	A	C
	A	TGATCC CCTGCCT GGCCTCCC		
		ACTAGG GGACGGA CCGGAGGG		
		A A		
GAM2030	DKFZp434E0519 3'	GGGAGGCCGAGACAGGCAGATT 50997	CA	C
		GATC CCTG CTCGGCCTCCC		
		TTAG GGAC GAGCCGGAGGG		
		AC A		
GAM2030	DKFZp434E2220 5'	GGGAGGCCGAGGCGGGTGGATC 34714		
	AT	ATGATCCACCTGCCTCGGCCTCCC		
		TACTAGGTGGGCGGAGCCGGAGGG		
GAM2030	DKFZp434G171 3'	GGGAGGCCAAGGCAGGCAGATC 80245	CA	C
	A	TGATC CCTGCCT GGCCTCCC		
		ACTAG GGACGGA CCGGAGGG		
		AC A		
GAM2030	DKFZp434G171 3'	GGGAGGCCAAGGTGGGTGGATC 80246	TG	C
	A	TGATCCACC CCT GGCCTCCC		
		ACTAGGTGG GGA CCGGAGGG		
		GT A		
GAM2030	DKFZP434I1735 3'	GGAGGCCGAGGCAGGAAAATCG 89171	CCA	
		TGAT CCTGCCTCGGCCTCC		

		GCTA GGACGGAGCCGGAGG		
		AAA		
GAM2030	DKFZP434I2117 5'	GGAGGCCGACGCAGTCAT 49730	TCCAC	C
		ATGA CTGC TCGGCCTCC		
		TACT GACG AGCCGGAGG		
		_____ C		
GAM2030	DKFZP434K1421 3'	GAGGCTGAGGCAAGAAGATCA 50466	CACC	
		TGATC TGCCTCGGCCTC		
		ACTAG ACGGAGTCGGAG		
		AAGA		
GAM2030	DKFZP434K1421 3'	GGGAGGCCAAGGCAGAAGGAT 50467	AC	C
		ATCC CTGCCT GGCCTCCC		
		TAGG GACGGA CCGGAGGG		
		AA A		
GAM2030	DKFZP434N1511 3'	GGGAGGCCGAGGCGGGAGGATC 93062	A	
	AT	ATGATCC CCTGCCTCGGCCTCCC		
		TACTAGG GGGCGGAGCCGGAGGG		
		A		
GAM2030	DKFZP434P0721 3'	GGGAGGCTAAGGCAGGCGGATC 64464	A	CG
	A	TGATCC CCTGCCT GCCTCCC		
		ACTAGG GGACGGA CGGAGGG		
		C AT		
GAM2030	DKFZp547C176 3'	GGGAGCTGAGGCGGGCGGATCA 67803	A	C
		TGATCC CCTGCCTCGGC TCCC		
		ACTAGG GGGCGGAGTCG AGGG		
		C _		
GAM2030	DKFZp547G183 3'	GGGAGGCCAAGGTGAGCGGATC 38646	AC _	C
	A	TGATCC CT GCCT GGCCTCCC		
		ACTAGG GA TGGA CCGGAGGG		
		C_ G A		
GAM2030	DKFZp547G183 3'	GGGAGGCTGAGGCAGGAGAATC 38647	CCA	
	A	TGAT CCTGCCTCGGCCTCCC		
		ACTA GGACGGAGTCGGAGGG		
		AGA		
GAM2030	DKFZP564A022 3'	GGGAGGCTGAGGCGGGTAGATC 48974	C	
	A	TGATC ACCTGCCTCGGCCTCCC		
		ACTAG TGGGCGGAGTCGGAGGG		
		A		
GAM2030	DKFZP564B1023 3'	GGGAAGCCAAGGCAGGTGGATC 49366	C	C
	G	TGATCCACCTGCCT GGC TCCC		

		GCTAGGTGGACGGA CCG AGGG		
		A A		
GAM2030	DKFZP564B1023 3'	GGGAGGCCGAGGGGAGTGGATC 49367	_	G
	A	TGATCCAC CT CCTCGGCCTCCC		
		ACTAGGTG GG GGAGCCGGAGGG		
		A _		
GAM2030	DKFZp564K142 3'	GGGAGGCCAAGGCAGGCAGATC 50434	CA	C
	A	TGATC CCTGCCT GGCCTCCC		
		ACTAG GGACGGA CCGGAGGG		
		AC A		
GAM2030	DKFZP564M182 3'	GGGAGGCCGAGGCAGGCGGATC 78638	A	
	A	TGATCC CCTGCCTCGGCCTCCC		
		ACTAGG GGACGGAGCCGGAGGG		
		C		
GAM2030	DKFZP564M182 3'	GGGAGGCTGAAGCAGGAGAATC 78639	CCA	C
	A	TGAT CCTGC TCGCCTCCC		
		ACTA GGACG AGTCGGAGGG		
		AGA A		
GAM2030	DKFZp566H0824 3'	GGAGGCCAAGGCAGGTGGATCA 34490		C
	T	ATGATCCACCTGCCT GGCCTCC		
		TACTAGGTGGACGGA CCGGAGG		
		A		
GAM2030	DKFZP566J2046 3'	GGGAGGCCGAGGCGGGCGGCTC 49139	T A	
	A	TGA CC CCTGCCTCGGCCTCCC		
		ACT GG GGGCGGAGCCGGAGGG		
		C C		
GAM2030	DKFZP586C1324 3'	GGGAGGCCGAGGCAGGTGGATC 70359		
	A	TGATCCACCTGCCTCGGCCTCCC		
		ACTAGGTGGACGGAGCCGGAGGG		
GAM2030	DKFZP586D2223 3'	GGGAGGCCGCGGTGGGTGGATC 38295	TG T	
	A	TGATCCACC CC CGGCCTCCC		
		ACTAGGTGG GG GCCGGAGGG		
		GT C		
GAM2030	DKFZp727G131 3'	GGGAGACCGAGGTGGGCAGATC 59696	CA TG	C
	A	TGATC CC CCTCGG CTCCC		
		ACTAG GG GGAGCC GAGGG		
		AC GT A		
GAM2030	DRF1 3'	GGAGGCTGAGGCAGGAGAATCA 47752	CCA	
		TGAT CCTGCCTCGGCCTCC		

			ACTA GGACGGAGTCGGAGG		
			AGA		
GAM2030	DRF1	3'	GGGAGGCCAAGGCGGGTGGATC 47753	C	
	A		TGATCCACCTGCCT GGCCTCCC		
			ACTAGGTGGGCGGA CCGGAGGG		
			A		
GAM2030	ERAP140	3'	GGGAGGCCGAGGCAGGTGGATC 75705		
	A		TGATCCACCTGCCTCGGCCTCCC		
			ACTAGGTGGACGGAGCCGGAGGG		
GAM2030	FADS1	3'	GGGAGGTCCAGGCAGGAGGATC 26384	A	C
	A		TGATCC CCTGCCT GGCCTCCC		
			ACTAGG GGACGGA CTGGAGGG		
			A C		
GAM2030	FBXO26	3'	GGAGGCCGAGGTGGGAGGATCA 46630	A	TG
			TGATCC CC CCTCGGCCTCC		
			ACTAGG GG GGAGCCGGAGG		
			A GT		
GAM2030	FBXO27	3'	GGGAGGCTGAGGCAGGCGGATC 75012	A	
	A		TGATCC CCTGCCTCGGCCTCCC		
			ACTAGG GGACGGAGTCGGAGGG		
			C		
GAM2030	FBXO6	3'	GGGAGACCGAGGCAGGTGGATC 37996		C
	A		TGATCCACCTGCCTCGG CTCCC		
			ACTAGGTGGACGGAGCC GAGGG		
			A		
GAM2030	FBXO9	3'	GGGAGGCCAAGGCAGGAGGATT 54249	A	C
			GATCC CCTGCCT GGCCTCCC		
			TTAGG GGACGGA CCGGAGGG		
			A A		
GAM2030	FBXO9	3'	GGGAGGCTAAGACAGGCAGATC 54250	CA	C CG
	A		TGATC CCTG CT GCCTCCC		
			ACTAG GGAC GA CGGAGGG		
			AC A AT		
GAM2030	FKBP14	3'	GGGAGGCTGAGGCGGGCGGATC 36069	A	
	A		TGATCC CCTGCCTCGGCCTCCC		
			ACTAGG GGGCGGAGTCGGAGGG		
			C		
GAM2030	FKSG17	3'	GGAGGCTGAGGCAGGAGAATCA 50157	CCA	
			TGAT CCTGCCTCGGCCTCC		

			ACTA GGACGGAGTCGGAGG		
			AGA		
GAM2030	FKSG17	3'	GGGAGGCCAAGGCAGGCAGATC 50158	CA	C
	AT		ATGATC CCTGCCT GGCCTCCC		
			TACTAG GGACGGA CCGGAGGG		
			AC A		
GAM2030	FLJ10008	3'	GGGAGGCCGAGGCGGACGGATC 36192	AC	
	A		TGATCC CTGCCTCGGCCTCCC		
			ACTAGG GGCGGAGCCGGAGGG		
			CA		
GAM2030	FLJ10043	3'	GGGCTGAGGCAGGTGGATCA 36235		
			TGATCCACCTGCCTCGGCCT		
			ACTAGGTGGACGGAGTCGGG		
GAM2030	FLJ10058	3'	GGGAGGCTGAGGCAAGTGGATC 36263	C	
	A		TGATCCAC TGCCTCGGCCTCCC		
			ACTAGGTG ACGGAGTCGGAGGG		
			A		
GAM2030	FLJ10232	3'	GGAGGCTGAGGCAGGAGGATCA 36382	A	
	T		ATGATCC CCTGCCTCGGCCTCC		
			TACTAGG GGACGGAGTCGGAGG		
			A		
GAM2030	FLJ10244	3'	GGGAGGCCGAGGCGGGTGGATC 36403		
	A		TGATCCACCTGCCTCGGCCTCCC		
			ACTAGGTGGGCGGAGCCGGAGGG		
GAM2030	FLJ10244	3'	GGGAGGCTGAGGCAGGAGAATC 36404	CCA	
	A		TGAT CCTGCCTCGGCCTCCC		
			ACTA GGACGGAGTCGGAGGG		
			AGA		
GAM2030	FLJ10408	5'	GAGAAGTTCTGAAGATGGATCA 36583	C GCC	C____
	T		ATGATCCA CT TCGG CTC		
			TACTAGGT GA AGTC GAG		
			A ____ TTGAA		
GAM2030	FLJ10432	3'	GAGGCCGAGGTGCTACAGATC 39352	CACCT_	
			GATC GCCTCGGCCTC		
			CTAG TGGAGCCGGAG		
			ACATCG		
GAM2030	FLJ10460	3'	GGGAGGCTGAGGCGGGCAGATC 36621	CA	
	A		TGATC CCTGCCTCGGCCTCCC		

		ACTAG GGGCGGAGTCGGAGGG		
		AC		
GAM2030	FLJ10508	3' GGAAGGCCGAGCAAGGACCAT 36681	A ACC C	—
		ATG TCC TGC TCGGCCT CC		
		TAC AGG ACG AGCCGGA GG		
		C A__ _ A		
GAM2030	FLJ10547	3' GGGAGGCCAAGGTGAGTGGATC 36777	CT C	
	A	TGATCCAC GCCT GGCCTCCC		
		ACTAGGTG TGGA CCGGAGGG		
		AG A		
GAM2030	FLJ10613	3' GGGAGGCCGAGGTGGGCGGATC 39340	A TG	
	A	TGATCC CC CCTCGGCCTCCC		
		ACTAGG GG GGAGCCGGAGGG		
		C GT		
GAM2030	FLJ10650	3' GGGAGGCCGAGGTGGGCAGATC 36902	CA TG	
	A	TGATC CC CCTCGGCCTCCC		
		ACTAG GG GGAGCCGGAGGG		
		AC GT		
GAM2030	FLJ10704	3' GGGAGGCCGAGGCAGGTGGATC 36983		
	A	TGATCCACCTGCCTCGGCCTCCC		
		ACTAGGTGGACGGAGCCGGAGGG		
GAM2030	FLJ10781	3' GGGAGGCTGAGGCAGGTGATC 37173	C	
	A	TGATC ACCTGCCTCGGCCTCCC		
		ACTAG TGGACGGAGTCGGAGGG		
		C		
GAM2030	FLJ10811	3' GGGAGGCCAAGGCAGGAGGATC 37225	A C	
	A	TGATCC CCTGCCT GGCCTCCC		
		ACTAGG GGACGGA CCGGAGGG		
		A A		
GAM2030	FLJ10826	3' GGGAGGCCAAGGCAGGCGGATC 37248	A C	
	A	TGATCC CCTGCCT GGCCTCCC		
		ACTAGG GGACGGA CCGGAGGG		
		C A		
GAM2030	FLJ10830	3' GGGAGGCCAAGACAGGAGGATC 37266	A C C	
	A	TGATCC CCTG CT GGCCTCCC		
		ACTAGG GGAC GA CCGGAGGG		
		A A A		
GAM2030	FLJ10932	3' GGGAGGCCAAGGTGGGCAGATC 37429	CA TG C	
	A	TGATC CC CCT GGCCTCCC		

		ACTAG GG GGA CCGGAGGG		
		AC GT A		
GAM2030	FLJ10989	3' GGAGGCTGAGGCAGGAGAATCA 37504	CCA	
		TGAT CCTGCCTCGGCCTCC		
		ACTA GGACGGAGTCGGAGG		
		AGA		
GAM2030	FLJ10989	3' GGGAGGCCAAGGCGAGCGGATC 37505	ACC	C
	AT	ATGATCC TGCCT GGCCTCCC		
		TACTAGG GCGGA CCGGAGGG		
		CGA A		
GAM2030	FLJ11029	3' GGGAGGCTGAGGCAGGTGGATC 61634		
	A	TGATCCACCTGCCTCGGCCTCCC		
		ACTAGGTGGACGGAGTCGGAGGG		
GAM2030	FLJ11106	3' GGGAGGCCAAGGCGGGCGGATC 37625	A	C
	A	TGATCC CCTGCCT GGCCTCCC		
		ACTAGG GGGCGGA CCGGAGGG		
		C A		
GAM2030	FLJ11136	3' GGGAGGCCGAGGCCAGTGGATC 37668	CT	
	A	TGATCCAC GCCTCGGCCTCCC		
		ACTAGGTG CGGAGCCGGAGGG		
		AC		
GAM2030	FLJ11136	3' GGGAGGCTGAGGCAGGAGAATC 37669	CCA	
	A	TGAT CCTGCCTCGGCCTCCC		
		ACTA GGACGGAGTCGGAGGG		
		AGA		
GAM2030	FLJ11151	3' GGGAGGCTGAGACGGGCAGATC 68479	CA	C
	A	TGATC CCTG CTCGGCCTCCC		
		ACTAG GGGC GAGTCGGAGGG		
		AC A		
GAM2030	FLJ11267	3' GGGAGGCCAAGGTGGGTAAATT 39499	CC	TG C
	A	TGAT ACC CCT GGCCTCCC		
		ATTA TGG GGA CCGGAGGG		
		AA GT A		
GAM2030	FLJ11301	3' GGGAGGCTGAGGCAGGAGAATC 37808	CCA	
	A	TGAT CCTGCCTCGGCCTCCC		
		ACTA GGACGGAGTCGGAGGG		
		AGA		
GAM2030	FLJ11370	3' GGGAGGCCAAGGCAGGCAGATC 46966	CA	C
	A	TGATC CCTGCCT GGCCTCCC		

		ACTAG GGACGGA CCGGAGGG		
		AC A		
GAM2030	FLJ11370	3' GGGAGGCTGAGGCAGGAGAATC 46968	CCA	
	A	TGAT CCTGCCTCGGCCTCCC		
		ACTA GGACGGAGTCGGAGGG		
		AGA		
GAM2030	FLJ11637	3' GGGAGGCCGAGGCAGGCGGATC 46983	A	
	A	TGATCC CCTGCCTCGGCCTCCC		
		ACTAGG GGACGGAGCCGGAGGG		
		C		
GAM2030	FLJ11700	3' GGGAGGCCGAGGAGGGCAGATC 46565	CA G	
	A	TGATC CCT CCTCGGCCTCCC		
		ACTAG GGG GGAGCCGGAGGG		
		AC A		
GAM2030	FLJ11722	3' GGGAGGCCGAGGTGGGTGGATC 47004	TG	
	AT	ATGATCCACC CCTCGGCCTCCC		
		TACTAGGTGG GGAGCCGGAGGG		
		GT		
GAM2030	FLJ11722	3' GGGAGGTCGAGGCAGGTGGATC 47005		
	A	TGATCCACCTGCCTCGGCCTCCC		
		ACTAGGTGGACGGAGCTGGAGGG		
GAM2030	FLJ11726	3' GGGAGGCCGAGGCAGGTGGATC 47025		
	A	TGATCCACCTGCCTCGGCCTCCC		
		ACTAGGTGGACGGAGCCGGAGGG		
GAM2030	FLJ11996	3' AGGCTGAGGCGAGTGGATCA 47054	C	
		TGATCCAC TGCCTCGGCCT		
		ACTAGGTG GCGGAGTCGGA		
		A		
GAM2030	FLJ11996	3' GGGAGACCGAGGCATGAGAGTC 47067	CCACC C	
	A	TGAT TGCCTCGG CTCCC		
		ACTG ACGGAGCC GAGGG		
		AGAGT A		
GAM2030	FLJ11996	3' GGGAGACTGAGGCAGGCGGATC 47068	A C	
	A	TGATCC CCTGCCTCGG CTCCC		
		ACTAGG GGACGGAGTC GAGGG		
		C A		
GAM2030	FLJ12056	3' GGAAGGCCGAGGCAGGCGGATC 46821	A _	
	A	TGATCC CCTGCCTCGGCCT CC		

		ACTAGG GGACGGAGCCGGA GG		
		C A		
GAM2030	FLJ12078	3' CCGAGGCAGGCGGATCAT 47079	A	
		ATGATCC CCTGCCTCGG		
		TACTAGG GGACGGAGCC		
		C		
GAM2030	FLJ12078	3' GGGAGGCCGAGGCAGGCGGATC 47083	A	
	AT	ATGATCC CCTGCCTCGGCCTCCC		
		TACTAGG GGACGGAGCCGGAGGG		
		C		
GAM2030	FLJ12121	3' GGGAGGCCAAGGTGGGAGGATC 47091	A TG C	
	A	TGATCC CC CCT GGCCTCCC		
		ACTAGG GG GGA CCGGAGGG		
		A GT A		
GAM2030	FLJ12122	3' GGGAGGCCAAGGCTAGAGGATC 47094	ACCT C	
	G	TGATCC GCCT GGCCTCCC		
		GCTAGG CGGA CCGGAGGG		
		AGAT A		
GAM2030	FLJ12132	3' GGGAGGCCGAGGCAGGAGCATC 47103	CCA	
	G	TGAT CCTGCCTCGGCCTCCC		
		GCTA GGACGGAGCCGGAGGG		
		CGA		
GAM2030	FLJ12178	3' GGGAGCCTGAGGCAGGCGGATC 47829	A C	
	AT	ATGATCC CCTGCCTCGG CTCCC		
		TACTAGG GGACGGAGTC GAGGG		
		C C		
GAM2030	FLJ12190	3' GGGAGGCCAAGGCGGGTGAATC 47569	C C	
		GAT CACCTGCCT GGCCTCCC		
		CTA GTGGGCGGA CCGGAGGG		
		A A		
GAM2030	FLJ12298	3' GGGAGGCCAAGGCAGGCAGATC 50599	CA C	
	AT	ATGATC CCTGCCT GGCCTCCC		
		TACTAG GGACGGA CCGGAGGG		
		AC A		
GAM2030	FLJ12448	3' GAGGCCAAGGAGGTGGATCA 43477	G C	
		TGATCCACCT CCT GGCCTC		
		ACTAGGTGGA GGA CCGGAG		
		_ A		
GAM2030	FLJ12484	3' GAGATGTCAGGTGGACCAT 43174	A _ _	
		ATG TCCACCTG C CTC		

		TAC AGGTGGAC G GAG		
		C T TA		
GAM2030	FLJ12606	3' GGGAGGCCGAGGCGGGTGGATC 46069		
	A	TGATCCACCTGCCTCGGCCTCCC		
		ACTAGGTGGGCGGAGCCGGAGGG		
GAM2030	FLJ12618	3' GGGAAGCCAAGGCAGGTAGATT 46507	TG	C C C
	GT	A ATC ACCTGCCT GGC TCCC		
		T TAG TGGACGGA CCG AGGG		
		GT A A A		
GAM2030	FLJ12660	3' GGGAGGCTGAGGCAGGAGAATC 47898		CCA
	AT	ATGAT CCTGCCTCGGCCTCCC		
		TACTA GGACGGAGTCGGAGGG		
		AGA		
GAM2030	FLJ12666	3' GGGAGTCCGAGGCATGCGGATC 45071	ACC	C
	A	TGATCC TGCCTCGG CTCCC		
		ACTAGG ACGGAGCC GAGGG		
		CGT T		
GAM2030	FLJ12671	3' GGGAGGCCGAGGCGGGCGGATC 49110		A
	A	TGATCC CCTGCCTCGGCCTCCC		
		ACTAGG GGGCGGAGCCGGAGGG		
		C		
GAM2030	FLJ12921	3' GGGAGGCCGAGGCGGGCGGATC 46399		A
	A	TGATCC CCTGCCTCGGCCTCCC		
		ACTAGG GGGCGGAGCCGGAGGG		
		C		
GAM2030	FLJ12949	3' GGGAGGCCGAGGTGAAAGGATC 43726		ACC
	A	TGATCC TGCCTCGGCCTCCC		
		ACTAGG GTGGAGCCGGAGGG		
		AAA		
GAM2030	FLJ12985	3' GGGAGGCCAAGACAGGTAGATC 46798		C C C
	A	TGATC ACCTG CT GGCCTCCC		
		ACTAG TGGAC GA CCGGAGGG		
		A A A		
GAM2030	FLJ13117	3' GGGAGGCTGAGGCGGGTGGATC 43810		
	A	TGATCCACCTGCCTCGGCCTCCC		
		ACTAGGTGGGCGGAGTCGGAGGG		
GAM2030	FLJ13162	3' GGGAGGCCGAGGTGGGTGGATC 47187		TG
	A	TGATCCACC CTCGGCCTCCC		

		ACTAGGTGG GGAGCCGGAGGG	
		GT	
GAM2030	FLJ13193 3'	GGGAGGCTGAGACAGGTAGATC 50728	C C
	AT	ATGATC ACCTG CTCGGCCTCCC	
		TACTAG TGGAC GAGTCGGAGGG	
		A A	
GAM2030	FLJ13193 3'	GGGAGGCTGAGGCAGGAGAATC 50729	CCA
	A	TGAT CCTGCCTCGGCCTCCC	
		ACTA GGACGGAGTCGGAGGG	
		AGA	
GAM2030	FLJ13193 3'	GGGAGGCTGAGGCAGGAGAATC 50730	CCA
	A	TGAT CCTGCCTCGGCCTCCC	
		ACTA GGACGGAGTCGGAGGG	
		AGA	
GAM2030	FLJ13193 3'	GGGAGGTGGAGGCGGGTGGATC 50731	G
	A	TGATCCACCTGCCTC GCCTCCC	
		ACTAGGTGGGCGGAG TGGAGGG	
		G	
GAM2030	FLJ13305 3'	GGGAGGCCGAGACGGGTGGATC 91714	C
	A	TGATCCACCTG CTCGGCCTCCC	
		ACTAGGTGGGC GAGCCGGAGGG	
		A	
GAM2030	FLJ13390 3'	GGGAGGCCGAGGCAGGAAGATC 42839	CA
	AT	ATGATC CCTGCCTCGGCCTCCC	
		TACTAG GGACGGAGCCGGAGGG	
		AA	
GAM2030	FLJ13456 3'	GGGAGGCCGAGGCGGGCAGATC 66555	CA
	A	TGATC CCTGCCTCGGCCTCCC	
		ACTAG GGGCGGAGCCGGAGGG	
		AC	
GAM2030	FLJ13456 3'	GGGAGGCCGAGGTGGGTGGATC 66556	TG
	A	TGATCCACC CCTCGGCCTCCC	
		ACTAGGTGG GGAGCCGGAGGG	
		GT	
GAM2030	FLJ13611 3'	GGGAAGCTGAGGCAGGAGAATC 46867	CCA C
	A	TGAT CCTGCCTCGGC TCCC	
		ACTA GGACGGAGTCG AGGG	
		AGA A	
GAM2030	FLJ13621 3'	GGGAGGCCGAGGCGGGTGGATC 47225	
	A	TGATCCACCTGCCTCGGCCTCCC	

ACTAGGTGGGCGGAGCCGGAGGG

GAM2030	FLJ13769	3'	GGGAGGCCAAGGTGGGTAGATC	47260	C	TG	C
		AT	ATGATC ACC CCT GGCCTCCC				
			TACTAG TGG GGA CCGGAGGG				
			A GT A				
GAM2030	FLJ13769	3'	GGGAGGCCGAGCCAAGTGGATC	47261	C	C	
		A	TGATCCAC TG CTCGGCCTCCC				
			ACTAGGTG AC GAGCCGGAGGG				
			A C				
GAM2030	FLJ13848	3'	GGGAGGCTGAGGCAGGCGGGTC	45828	A		
		A	TGATCC CCTGCCTCGGCCTCCC				
			ACTGGG GGACGGAGTCGGAGGG				
			C				
GAM2030	FLJ13952	3'	GGGAGGCCAAGATGGGTGGATC	46015	GC	C	
		A	TGATCCACCT CT GGCCTCCC				
			ACTAGGTGGG GA CCGGAGGG				
			TA A				
GAM2030	FLJ13984	3'	GGGCTGAGGCAGGCAGATCG	45810	CA		
			TGATC CCTGCCTCGGCCT				
			GCTAG GGACGGAGTCGGG				
			AC				
GAM2030	FLJ14011	3'	GGGAGGCTGAGACAGGCGGATC	42319	A	C	
		A	TGATCC CCTG CTCGGCCTCCC				
			ACTAGG GGAC GAGTCGGAGGG				
			C A				
GAM2030	FLJ14100	3'	GGGAGGCTGAGGCGGGCGGATC	47338	A		
		A	TGATCC CCTGCCTCGGCCTCCC				
			ACTAGG GGGCGGAGTCGGAGGG				
			C				
GAM2030	FLJ14107	3'	GGGAGGCCAAGGCAGGCAGATC	47347	CA	C	
		A	TGATC CCTGCCT GGCCTCCC				
			ACTAG GGACGGA CCGGAGGG				
			AC A				
GAM2030	FLJ14117	3'	GGGAGGCCAAGGTGGGCGGATC	43230	A	TG	C
		AT	ATGATCC CC CCT GGCCTCCC				
			TACTAGG GG GGA CCGGAGGG				
			C GT A				
GAM2030	FLJ14117	3'	GGGAGGCCGAGGCAGGCGGATC	43231	A		
		A	TGATCC CCTGCCTCGGCCTCCC				

			ACTAGG GGACGGAGCCGGAGGG		
			C		
GAM2030	FLJ14117	3'	GGGATGCTGAGGCGGGCGGATC 43232	A	C
	A		TGATCC CCTGCCTCGGC TCCC		
			ACTAGG GGGCGGAGTCG AGGG		
			C T		
GAM2030	FLJ14129	3'	GGGAGCCTGGGGCAGGAGAATC 48809	CCA	C
	A		TGAT CCTGCCTCGG CTCCC		
			ACTA GGACGGGGTC GAGGG		
			AGA C		
GAM2030	FLJ14129	3'	GGGAGGCCGAGGCGGGCGGATC 48810	A	
	A		TGATCC CCTGCCTCGGCCTCCC		
			ACTAGG GGGCGGAGCCGGAGGG		
			C		
GAM2030	FLJ14225	3'	GGGAGGCCGAGGCGGGCGGATC 46387	A	
	AT		ATGATCC CCTGCCTCGGCCTCCC		
			TACTAGG GGGCGGAGCCGGAGGG		
			C		
GAM2030	FLJ14251	3'	GGGAGGCCAAGATGGGCGGATC 46487	A GC C	
	A		TGATCC CCT CT GGCTCCC		
			ACTAGG GGG GA CCGGAGGG		
			C TA A		
GAM2030	FLJ14251	3'	GGGAGGCTGAGGCAGGAGAATC 46488	CCA	
	A		TGAT CCTGCCTCGGCCTCCC		
			ACTA GGACGGAGTCGGAGGG		
			AGA		
GAM2030	FLJ14280	3'	GGGAGGCCGAGGCGGGCGGATC 46523	A	
	G		TGATCC CCTGCCTCGGCCTCCC		
			GCTAGG GGGCGGAGCCGGAGGG		
			C		
GAM2030	FLJ14326	3'	GGGAGGCCGAGGCAGGAAGATC 50778	CA	
	A		TGATC CCTGCCTCGGCCTCCC		
			ACTAG GGACGGAGCCGGAGGG		
			AA		
GAM2030	FLJ14326	3'	GGGAGGGTGAGGCGGGTGGATC 50779		G
	A		TGATCCACCTGCCTCG CCTCCC		
			ACTAGGTGGGCGGAGT GGAGGG		
			G		
GAM2030	FLJ14327	3'	GGGAGGCCGAGGCAGGTGGAAC 46686	A	
	A		TG TCCACCTGCCTCGGCCTCCC		

			AC AGGTGGACGGAGCCGGAGGG	
			A	
GAM2030	FLJ14345	3'	GGGAGGCCGAGGCAGGGGGATC 45660	A
	A		TGATCC CCTGCCTCGGCCTCCC	
			ACTAGG GGACGGAGCCGGAGGG	
			G	
GAM2030	FLJ14345	3'	GGGAGGCTGAGGCAGGAGAATC 45661	CCA
	A		TGAT CCTGCCTCGGCCTCCC	
			ACTA GGACGGAGTCGGAGGG	
			AGA	
GAM2030	FLJ14346	3'	GGAAGTCAAGGCAGGTGGATC 47368	C C
			GATCCACCTGCCT GGC TCCC	
			CTAGGTGGACGGA CTG AGGG	
			A A	
GAM2030	FLJ14346	3'	GGGAGGCCGAGGCGGGCGGATC 47369	A
			GATCC CCTGCCTCGGCCTCCC	
			CTAGG GGGCGGAGCCGGAGGG	
			C	
GAM2030	FLJ14397	3'	GGGAGACCGAGGCAGGCGGATC 52331	A C
	AT		ATGATCC CCTGCCTCGG CTCCC	
			TACTAGG GGACGGAGCC GAGGG	
			C A	
GAM2030	FLJ14397	3'	GGGAGGCTGAGGCAGGCGGATC 52332	A
	A		TGATCC CCTGCCTCGGCCTCCC	
			ACTAGG GGACGGAGTCGGAGGG	
			C	
GAM2030	FLJ14457	3'	GGGAGGCCGAGGCGGACAGATC 52410	CAC
	A		TGATC CTGCCTCGGCCTCCC	
			ACTAG GCGGAGCCGGAGGG	
			ACA	
GAM2030	FLJ14490	3'	GGAGTAGGCAGGTGGATC 52446	CGGC
			GATCCACCTGCCT CTCC	
			CTAGGTGGACGGA GAGG	
			T__	
GAM2030	FLJ14641	3'	GGGAGGCCGAGAAGGGTGGATC 52563	GC
	AT		ATGATCCACCT CTCGGCCTCCC	
			TACTAGGTGGG GAGCCGGAGGG	
			AA	
GAM2030	FLJ20004	3'	GGGAGGCCGAGGCGGGCAGATC 34762	CA
	A		TGATC CCTGCCTCGGCCTCCC	

		ACTAG GGGCGGAGCCGGAGGG	
		AC	
GAM2030	FLJ20004	3' GGAGGCTGAGGCAGGAGAATCA 97007	CCA
		TGAT CCTGCCTCGGCCTCC	
		ACTA GGACGGAGTCGGAGG	
		AGA	
GAM2030	FLJ20004	3' GGGAGGCCAAGATGGGCGGATC 97009	A GC C
	A	TGATCC CCT CT GGCCTCCC	
		ACTAGG GGG GA CCGGAGGG	
		C TA A	
GAM2030	FLJ20006	3' AGGCCGAGGAAGGTAGATCA 34777	C G
		TGATC ACCT CCTCGGCCT	
		ACTAG TGGA GGAGCCGGA	
		A A	
GAM2030	FLJ20006	3' GGGAGGCCAAGGAAGGCAGATC 34786	CA G C
	A	TGATC CCT CCT GGCCTCCC	
		ACTAG GGA GGA CCGGAGGG	
		AC A A	
GAM2030	FLJ20034	3' GAGATGCTGAGGCAGGTGGATC 34846	—
	AT	ATGATCCACCTGCCTCGGC CTC	
		TACTAGGTGGACGGAGTCG GAG	
		TA	
GAM2030	FLJ20045	3' GGGAGGCTGAGGTAGGTGGATC 34889	
	A	TGATCCACCTGCCTCGGCCTCCC	
		ACTAGGTGGATGGAGTCGGAGGG	
GAM2030	FLJ20055	3' GGAGGCCGAGGCTGGCAGATCA 34911	CA T
		TGATC CC GCCTCGGCCTCC	
		ACTAG GG CGGAGCCGGAGG	
		AC T	
GAM2030	FLJ20055	3' GGAGGCTGAGGCAAGAGAATCA 34912	CCACC
		TGAT TGCCTCGGCCTCC	
		ACTA ACGGAGTCGGAGG	
		AGAGA	
GAM2030	FLJ20059	3' GGGAGGCCGAGGTGGATAGATC 34928	CAC TG
	A	TGATC C CCTCGGCCTCCC	
		ACTAG G GGAGCCGGAGGG	
		ATA GT	
GAM2030	FLJ20059	3' GGGAGGCTGAGGCAGGCCAATC 34929	CCA
	A	TGAT CCTGCCTCGGCCTCCC	

		ACTA GGACGGAGTCGGAGGG		
		ACC		
GAM2030	FLJ20069	3' GGGAGGCTGAGGCAGGTGGATC 34956		
	A	TGATCCACCTGCCTCGGCCTCCC		
		ACTAGGTGGACGGAGTCGGAGGG		
GAM2030	FLJ20081	3' GGGAGGCCAACACAGGAGGATC 34991	A	CCTC
	A	TGATCC CCTG GGCCTCCC		
		ACTAGG GGAC CCGGAGGG		
		A ACAA		
GAM2030	FLJ20139	3' GGGAGGCTGAGGCAGGCGGATC 35121	A	
	G	TGATCC CCTGCCTCGGCCTCCC		
		GCTAGG GGACGGAGTCGGAGGG		
		C		
GAM2030	FLJ20211	3' GGGAGGCCGAGGTGGGCGGATC 35264	A	TG
	A	TGATCC CC CCTCGGCCTCCC		
		ACTAGG GG GGAGCCGGAGGG		
		C GT		
GAM2030	FLJ20280	3' GGGAGGCTGAAACAGGAGAATC 35332	CCA	CC
	A	TGAT CCTG TCGGCCTCCC		
		ACTA GGAC AGTCGGAGGG		
		AGA AA		
GAM2030	FLJ20306	3' AGGCCGGGTGCGGTGGCTCAT 35384	T	T _
		ATGA CCACC GC CTCGGCCT		
		TACT GGTGG CG GGGCCGGA		
		C _ T		
GAM2030	FLJ20306	3' GAGGCCGAAACAGGAGGATC 35395	A	CC
		GATCC CCTG TCGGCCTC		
		CTAGG GGAC AGCCGGAG		
		A AA		
GAM2030	FLJ20359	3' GGGAGGCCGAGGCAGGCGAATC 35519	CCA	
	A	TGAT CCTGCCTCGGCCTCCC		
		ACTA GGACGGAGCCGGAGGG		
		AGC		
GAM2030	FLJ20413	3' GGGAAGCTGAGGCGGGCGGATC 35596	A	C
	A	TGATCC CCTGCCTCGGC TCCC		
		ACTAGG GGGCGGAGTCG AGGG		
		C A		
GAM2030	FLJ20456	3' GGGAGGCTGAGGCAGGCGGATC 35665	A	
	A	TGATCC CCTGCCTCGGCCTCCC		

			ACTAGG GGACGGAGTCGGAGGG		
			C		
GAM2030	FLJ20464	3'	GGGAGGCTGAGGCAGGAGAATC 35697	CCA	
	A		TGAT CCTGCCTCGGCCTCCC		
			ACTA GGACGGAGTCGGAGGG		
			AGA		
GAM2030	FLJ20464	3'	GGGAGGCTGAGGCGGGCGGATC 35698	A	
	A		TGATCC CCTGCCTCGGCCTCCC		
			ACTAGG GGGCGGAGTCGGAGGG		
			C		
GAM2030	FLJ20464	3'	GGGAGGTCGAGGCAGGCGGATC 35699	A	
	A		TGATCC CCTGCCTCGGCCTCCC		
			ACTAGG GGACGGAGCTGGAGGG		
			C		
GAM2030	FLJ20546	3'	GGGAGGCCAGGCAGGCAGATC 35811	CA	C
	A		TGATC CCTGCCT GGCCTCCC		
			ACTAG GGACGGA CCGGAGGG		
			AC C		
GAM2030	FLJ20546	3'	GGGAGGTTGAGGCAGGAGAATC 35812	CCA	
	AT		ATGAT CCTGCCTCGGCCTCCC		
			TACTA GGACGGAGTTGGAGGG		
			AGA		
GAM2030	FLJ20694	3'	GGGAAGCTGAGGCAGGAGAATC 35978	CCA	C
	A		TGAT CCTGCCTCGGC TCCC		
			ACTA GGACGGAGTCG AGGG		
			AGA A		
GAM2030	FLJ20695	3'	GGGAGGCCAAGGTGGGTGAATC 35985	C	TG C
	A		TGAT CACC CCT GGCCTCCC		
			ACTA GTGG GGA CCGGAGGG		
			A GT A		
GAM2030	FLJ20700	3'	GGGAGGCCAAGGGGGCAGATCA 36014	CA	G C
			TGATC CCT CCT GGCCTCCC		
			ACTAG GGG GGA CCGGAGGG		
			AC _ A		
GAM2030	FLJ20700	3'	GGGAGGCCGAGGCGGGCAGATC 36015	CA	
	A		TGATC CCTGCCTCGGCCTCCC		
			ACTAG GGGCGGAGCCGGAGGG		
			AC		
GAM2030	FLJ20783	3'	GAGACCGAGGCGGGCGGATCA 36101	A	C
			TGATCC CCTGCCTCGG CTC		

			ACTAGG GGGCGGAGCC GAG		
			C A		
GAM2030	FLJ20825	3'	GGAAGGCTGAGGCGGGCAGATC 36147	CA	—
	AT		ATGATC CCTGCCTCGGCCT CC		
			TACTAG GGGCGGAGTCGGA GG		
			AC A		
GAM2030	FLJ20972	3'	GGGAGGCCAAGGTGGGCGGATC 47387	A TG C	
	A		TGATCC CC CCT GGCCTCCC		
			ACTAGG GG GGA CCGGAGGG		
			C GT A		
GAM2030	FLJ20972	3'	GGGAGGCTGAGGCAGGAGAATC 47388	CCA	
	A		TGAT CCTGCCTCGGCCTCCC		
			ACTA GGACGGAGTCGGAGGG		
			AGA		
GAM2030	FLJ21240	3'	GGGAGGCCGAGGCAGGCGGAGC 46266	A A	
	A		TG TCC CCTGCCTCGGCCTCCC		
			AC AGG GGACGGAGCCGGAGGG		
			G C		
GAM2030	FLJ21369	3'	GGGAGGCTGAAGCGGGTGGATC 46053	C	
	A		TGATCCACCTGC TCGGCCTCCC		
			ACTAGGTGGGCG AGTCGGAGGG		
			A		
GAM2030	FLJ21657	3'	GGGAGGCCGAGGCAGGCAGGTC 42802	CA	
	A		TGATC CCTGCCTCGGCCTCCC		
			ACTGG GGACGGAGCCGGAGGG		
			AC		
GAM2030	FLJ21687	3'	GGGAGGCCGAGGCTGGTGGATC 46301	T	
	A		TGATCCACC GCCTCGGCCTCCC		
			ACTAGGTGG CGGAGCCGGAGGG		
			T		
GAM2030	FLJ21777	3'	GGGAGGCCAAGGCGGGCAGATT 50844	CA C	
	A		TGATC CCTGCCT GGCCTCCC		
			ATTAG GGGCGGA CCGGAGGG		
			AC A		
GAM2030	FLJ21870	3'	GGGAGGCCGAGGCAGGTGGATC 43747		
	A		TGATCCACCTGCCTCGGCCTCCC		
			ACTAGGTGGACGGAGCCGGAGGG		
GAM2030	FLJ22009	3'	GGGAGGCTGAGGCAGGAGGATC 60919	A	
	A		TGATCC CCTGCCTCGGCCTCCC		

		ACTAGG GGACGGAGTCGGAGGG		
		A		
GAM2030	FLJ22054	3' GGGAGGCCCCAGACTGGCGGATC 96051	A	TGC C
	A	TGATCC CC CT GGCCTCCC		
		ACTAGG GG GA CCGGAGGG		
		C TCA C		
GAM2030	FLJ22167	3' GAGGCTGAGGCGGGTGGATCA 44873		
		TGATCCACCTGCCTCGGCCTC		
		ACTAGGTGGGCGGAGTCGGAG		
GAM2030	FLJ22389	3' GGGAGGTCAAGGCAGGAAGATC 46792	CA	C
	A	TGATC CCTGCCT GGCCTCCC		
		ACTAG GGACGGA CTGGAGGG		
		AA A		
GAM2030	FLJ22474	3' GGGAGGCCAAGGCGTGTGGATC 45616	C	C
	A	TGATCCAC TGCCT GGCCTCCC		
		ACTAGGTG GCGGA CCGGAGGG		
		T A		
GAM2030	FLJ22596	3' GGGAGGCCAAGGCAGGTGGATC 47643		C
	AT	ATGATCCACCTGCCT GGCCTCCC		
		TACTAGGTGGACGGA CCGGAGGG		
		A		
GAM2030	FLJ22692	3' GGGAGGCCGAGGCAGGCGGATC 47485	A	
	A	TGATCC CCTGCCTCGGCCTCCC		
		ACTAGG GGACGGAGCCGGAGGG		
		C		
GAM2030	FLJ22814	3' GGAAGGCCGAGGCGGGGGGATC 46726	A	—
	A	TGATCC CCTGCCTCGGCCT CC		
		ACTAGG GGGCGGAGCCGGA GG		
		G A		
GAM2030	FLJ22814	3' GGGAGGCCAAGGCGGGAGGATC 46728	A	C
	A	TGATCC CCTGCCT GGCCTCCC		
		ACTAGG GGGCGGA CCGGAGGG		
		A A		
GAM2030	FLJ22814	3' GGGAGGCTGAGGCAGGAGGATC 46729	A	
	A	TGATCC CCTGCCTCGGCCTCCC		
		ACTAGG GGACGGAGTCGGAGGG		
		A		
GAM2030	FLJ23040	3' GGGAGGCCACGGCAGGTGGATC 47988		TC
	AT	ATGATCCACCTGCC GGCCTCCC		

			TACTAGGTGGACGG CCGGAGGG	
			CA	
GAM2030	FLJ23042	3'	GGAGGCTGAGGCAGGAGAATCA 47946	CCA
			TGAT CCTGCCTCGGCCTCC	
			ACTA GGACGGAGTCGGAGG	
			AGA	
GAM2030	FLJ23042	3'	GGGAGGCCGAGGCGGGCGGATC 47947	A
	A		TGATCC CCTGCCTCGGCCTCCC	
			ACTAGG GGGCGGAGCCGGAGGG	
			C	
GAM2030	FLJ23112	3'	GGGAGGCCGAGGCGGGTGGATC 46813	
	A		TGATCCACCTGCCTCGGCCTCCC	
			ACTAGGTGGGCGGAGCCGGAGGG	
GAM2030	FLJ23120	3'	GGGAGGCTGAGGCGGGTGGATC 86329	
	A		TGATCCACCTGCCTCGGCCTCCC	
			ACTAGGTGGGCGGAGTCGGAGGG	
GAM2030	FLJ23235	3'	GGAGGCTGAGGCAGGAGAATCA 46881	CCA
			TGAT CCTGCCTCGGCCTCC	
			ACTA GGACGGAGTCGGAGG	
			AGA	
GAM2030	FLJ23499	3'	GGGAGGCCGAGGCAGGTGGATC 43139	
	A		TGATCCACCTGCCTCGGCCTCCC	
			ACTAGGTGGACGGAGCCGGAGGG	
GAM2030	FLJ23537	3'	GAGGCTGGGGCAGGAGAATCA 46543	CCA
			TGAT CCTGCCTCGGCCTC	
			ACTA GGACGGGGTCGGAG	
			AGA	
GAM2030	FLJ23537	3'	GGGAGGCCGGGACAGGTGGATC 46544	C
	A		TGATCCACCTG CTCGGCCTCCC	
			ACTAGGTGGAC GGGCCGGAGGG	
			A	
GAM2030	FLJ23556	3'	GGGAGGCTGAGGCAGAAGGATC 46446	AC
	A		TGATCC CTGCCTCGGCCTCCC	
			ACTAGG GACGGAGTCGGAGGG	
			AA	
GAM2030	FLJ23878	3'	GGGAGGCTGAGGCGGGCAGATC 59371	CA
	A		TGATC CCTGCCTCGGCCTCCC	

		ACTAG GGGCGGAGTCGGAGGG		
		AC		
GAM2030	FLJ25012	3' GGGAGGCCGAGGCAGGTGGATC 58712		
	AT	ATGATCCACCTGCCTCGGCCTCCC		
		TACTAGGTGGACGGAGCCGGAGGG		
GAM2030	FLJ31168	3' GGGAGGCTGAGGCAGGCAGATC 59183	CA	
	A	TGATC CCTGCCTCGGCCTCCC		
		ACTAG GGACGGAGTCGGAGGG		
		AC		
GAM2030	FLJ31455	3' GGGAGGCTGAGGCAGGAGAATC 59287	CCA	
	A	TGAT CCTGCCTCGGCCTCCC		
		ACTA GGACGGAGTCGGAGGG		
		AGA		
GAM2030	FLJ31737	3' GGGAGGCCGAGGTGGGTGGATC 59350	TG	
	A	TGATCCACC CCTCGGCCTCCC		
		ACTAGGTGG GGAGCCGGAGGG		
		GT		
GAM2030	FLJ31952	3' GGGAGGCTGAGGCAGGTGGATC 59049		
	A	TGATCCACCTGCCTCGGCCTCCC		
		ACTAGGTGGACGGAGTCGGAGGG		
GAM2030	FLJ32915	5' GGGAGGCCAAGGCGGGCAGATC 59434	CA	C
	A	TGATC CCTGCCT GGCCTCCC		
		ACTAG GGGCGGA CCGGAGGG		
		AC A		
GAM2030	FUSIP1	3' GGGAGGCCGAGGCGGGCGGATC 55042	A	
	A	TGATCC CCTGCCTCGGCCTCCC		
		ACTAGG GGGCGGAGCCGGAGGG		
		C		
GAM2030	GALNT6	3' GGGAGGCCAAGGCAGGTGGATC 24248		C
	A	TGATCCACCTGCCT GGCCTCCC		
		ACTAGGTGGACGGA CCGGAGGG		
		A		
GAM2030	GALNT6	3' GGGAGGCTGAGGCAGGAGAATC 24249	CCA	
	A	TGAT CCTGCCTCGGCCTCCC		
		ACTA GGACGGAGTCGGAGGG		
		AGA		
GAM2030	GLTP	3' GGGAGGCTGAGGCGGGTGGATC 33586		
	A	TGATCCACCTGCCTCGGCCTCCC		

ACTAGGTGGGCGGAGTCGGAGGG

GAM2030	GNB4	3'	GGGAGGCCAAGGTGGGCAGATC 41569	CA TG C
	A		TGATC CC CCT GGCCTCCC	
			ACTAG GG GGA CCGGAGGG	
			AC GT A	
GAM2030	GP5	3'	GGGACACCGAGGCAGGAGAATC 16877	CCA CC
	A		TGAT CCTGCCTCGG TCCC	
			ACTA GGACGGAGCC AGGG	
			AGA AC	
GAM2030	GTPBP5	3'	GGGAGGCCGAGGCTGGTGGATC 65978	T
	A		TGATCCACC GCCTCGGCCTCCC	
			ACTAGGTGG CGGAGCCGGAGGG	
			T	
GAM2030	HES2	3'	GGGAGGCCGAGGCGGGCAGATC 39377	CA
	A		TGATC CCTGCCTCGGCCTCCC	
			ACTAG GGGCGGAGCCGGAGGG	
			AC	
GAM2030	HRH4	3'	GGGAGGCCAAGGTGGGCGGATC 41543	A TG C
	AT		ATGATCC CC CCT GGCCTCCC	
			TACTAGG GG GGA CCGGAGGG	
			C GT A	
GAM2030	HSD17B7	3'	GGGAGGCCAAGGCAGAAGGATC 33483	AC C
	A		TGATCC CTGCCT GGCCTCCC	
			ACTAGG GACGGA CCGGAGGG	
			AA A	
GAM2030	HSH2	3'	GGGCCGAGGCAGGCAGATCG 52742	CA
			TGATC CCTGCCTCGGCCT	
			GCTAG GGACGGAGCCGGG	
			AC	
GAM2030	HSOBRGRP	3'	GGAAGGCCGGGGTGGATC 34463	GCCT _
			GATCCACCT CGGCCT CC	
			CTAGGTGGG GCCGGA GG	
			_____ A	
GAM2030	HSPC031	3'	GGGAGGCCAAGGCGGACGGATC 32749	AC C
	A		TGATCC CTGCCT GGCCTCCC	
			ACTAGG GGCGGA CCGGAGGG	
			CA A	
GAM2030	HSPC043	3'	GGGAGGCCAAGGCGGGCAGATC 68352	CA C
	A		TGATC CCTGCCT GGCCTCCC	

		ACTAG GGGCGGA CCGAGGG		
		AC A		
GAM2030	HT008	3'	GGAGACCATGGAAGAATCAT 60510	CCAC G TC C
		ATGAT CT CC GG CTCC		
		TACTA GA GG CC GAGG		
		A___ A TA A		
GAM2030	HYPK	3'	GGGAGGTTCGAGGCAGGTAGATC 33515	C
	A		TGATC ACCTGCCTCGGCCTCCC	
		ACTAG TGGACGGAGCTGGAGGG		
		A		
GAM2030	ICAM4	3'	GGGAGGCCGAGGCAGGAGAATC 42595	CCA
	G		TGAT CCTGCCTCGGCCTCCC	
		GCTA GGACGGAGCCGGAGGG		
		AGA		
GAM2030	ICAM4	3'	GGGAGGCCGAGGCAGGAGAATC 9544	CCA
	G		TGAT CCTGCCTCGGCCTCCC	
		GCTA GGACGGAGCCGGAGGG		
		AGA		
GAM2030	IL-23R	3'	GGGAGGCTGAGGCAGGAGAATC 59131	CCA
	A		TGAT CCTGCCTCGGCCTCCC	
		ACTA GGACGGAGTCGGAGGG		
		AGA		
GAM2030	IL10RB	3'	AGGTCGAGGCAGGCGGATCA 7123	A
		TGATCC CCTGCCTCGGCCT		
		ACTAGG GGACGGAGCTGGA		
		C		
GAM2030	IMAGE:4907098	3'	GGGAGGCTGAGGCAGGAGAATC 93326	CCA
	A		TGAT CCTGCCTCGGCCTCCC	
		ACTA GGACGGAGTCGGAGGG		
		AGA		
GAM2030	JAM1	3'	AGGCTGAGGCAGGCGGATCA 34219	A
		TGATCC CCTGCCTCGGCCT		
		ACTAGG GGACGGAGTCGGA		
		C		
GAM2030	JAM1	3'	AGGCTGAGGCAGGCGGATCA 58510	A
		TGATCC CCTGCCTCGGCCT		
		ACTAGG GGACGGAGTCGGA		
		C		
GAM2030	JAM1	3'	AGGCTGAGGCAGGCGGATCA 58538	A
		TGATCC CCTGCCTCGGCCT		

			ACTAGG GGACGGAGTCGGA		
			C		
GAM2030	JAM1	3'	AGGCTGAGGCAGGCGGATCA 58566	A	
			TGATCC CCTGCCTCGGCCT		
			ACTAGG GGACGGAGTCGGA		
			C		
GAM2030	JDD1	3'	GGGAGGCCAAGGTGGGAGGATC 63917	A TG C	
	A		TGATCC CC CCT GGCCTCCC		
			ACTAGG GG GGA CCGGAGGG		
			A GT A		
GAM2030	KALI	3'	GGGAGGCCAAGGGGGGAGATCA 54694	CA G C	
			TGATC CCT CCT GGCCTCCC		
			ACTAG GGG GGA CCGGAGGG		
			A_ G A		
GAM2030	KCNH6	3'	GGGAGGCCGAGGCGGGCGGATC 48574	A	
	A		TGATCC CCTGCCTCGGCCTCCC		
			ACTAGG GGGCGGAGCCGGAGGG		
			C		
GAM2030	KIAA0090	3'	GGGAGGCCAAGGCAGGCAGATC 89816	CA C	
	AT		ATGATC CCTGCCT GGCCTCCC		
			TACTAG GGACGGA CCGGAGGG		
			AC A		
GAM2030	KIAA0184	3'	GGGAGGCCGAGGCGAGCAGATC 65812	CACC	
	A		TGATC TGCCTCGGCCTCCC		
			ACTAG GCGGAGCCGGAGGG		
			ACGA		
GAM2030	KIAA0226	3'	GGGAGGCCAGTGCGGGCGGATC 64261	A _ C	
	AT		ATGATCC CCTGC CT GGCCTCCC		
			TACTAGG GGGCG GA CCGGAGGG		
			C T _		
GAM2030	KIAA0247	3'	GGGAGGCCGAGAGGCACAGACC 29074	A CACC _	
	A		TG TC TGCCTC GGCCTCCC		
			AC AG ACGGAG CCGGAGGG		
			C AC_ AG		
GAM2030	KIAA0252	3'	GGGAGGCCTAGGCGGGTGGATC 63458	C	
	A		TGATCCACCTGCCT GGCCTCCC		
			ACTAGGTGGGCGGA CCGGAGGG		
			T		
GAM2030	KIAA0266	3'	GGGAGGCCGAGATGGGTGGATC 41640	GC	
	AT		ATGATCCACCT CTCGGCCTCCC		

		TACTAGGTGGG GAGCCGGAGGG	
		TA	
GAM2030	KIAA0266	3' GGGAGGCCGAGATGGGTGGATC 41641	GC
	AT	ATGATCCACCT CTCGGCCTCCC	
		TACTAGGTGGG GAGCCGGAGGG	
		TA	
GAM2030	KIAA0321	5' GGCGGGGTGACGGATAG 63057 _ _ _	
		CTG CC TCGGCCTC CC	
		GAT GG AGCTGGGG GG	
		A C C	
GAM2030	KIAA0355	3' GGGAGGCCGAGGCAGGTGGATC 28708	
	A	TGATCCACCTGCCTCGGCCTCCC	
		ACTAGGTGGACGGAGCCGGAGGG	
GAM2030	KIAA0391	3' GGAGGCCGAAGTGGTGGCTCAT 28615	T T C
		ATGA CCACC GC TCGGCCTCC	
		TACT GGTGG TG AGCCGGAGG	
		C _ A	
GAM2030	KIAA0391	3' GGGAGGCCAAGACAGGAGGATC 28616	A C C
	A	TGATCC CCTG CT GGCCTCCC	
		ACTAGG GGAC GA CCGGAGGG	
		A A A	
GAM2030	KIAA0408	3' GGGAGGCCAAGGTGGGGGGATC 28800	A TG C
	A	TGATCC CC CCT GGCCTCCC	
		ACTAGG GG GGA CCGGAGGG	
		G GT A	
GAM2030	KIAA0431	3' GGGAGGCCAAAGCAGGACGATC 31550	CA CTC
	A	TGATC CCTGC GGCCTCCC	
		ACTAG GGACG CCGGAGGG	
		CA AAA	
GAM2030	KIAA0441	3' GGGAGGCCAAGGTGGGCGGATC 29638	A TG C
	A	TGATCC CC CCT GGCCTCCC	
		ACTAGG GG GGA CCGGAGGG	
		C GT A	
GAM2030	KIAA0441	3' GGGAGGCTGAGACAGGAGAATC 29639	CCA C
	A	TGAT CCTG CTCGGCCTCCC	
		ACTA GGAC GAGTCGGAGGG	
		AGA A	
GAM2030	KIAA0446	5' GGGAAGCCGAGGCGGGTGGATC 69454	C
	A	TGATCCACCTGCCTCGGC TCCC	

		ACTAGGTGGGCGGAGCCG AGGG	
		A	
GAM2030	KIAA0451	5' GGGAGGCCAAGACAGGAGGATC 29777	A C C
	A	TGATCC CCTG CT GGCCTCCC	
		ACTAGG GGAC GA CCGGAGGG	
		A A A	
GAM2030	KIAA0472	3' GGGAGGCTGAGGCAGGAGAATC 72358	CCA
	A	TGAT CCTGCCTCGGCCTCCC	
		ACTA GGACGGAGTCGGAGGG	
		AGA	
GAM2030	KIAA0472	3' GGGAGGCTGAGGCGGGCGGATC 72359	A
	A	TGATCC CCTGCCTCGGCCTCCC	
		ACTAGG GGGCGGAGTCGGAGGG	
		C	
GAM2030	KIAA0475	3' GGGAGGCTGAGGCAGGAGAATC 30121	CCA
	A	TGAT CCTGCCTCGGCCTCCC	
		ACTA GGACGGAGTCGGAGGG	
		AGA	
GAM2030	KIAA0475	3' GGGAGGCTGAGGCAGGCAGATC 30122	CA
	A	TGATC CCTGCCTCGGCCTCCC	
		ACTAG GGACGGAGTCGGAGGG	
		AC	
GAM2030	KIAA0547	3' GGAGGCTGAGGCAAGAGAATCA 29595	CCACC
		TGAT TGCCTCGGCCTCC	
		ACTA ACGGAGTCGGAGG	
		AGAGA	
GAM2030	KIAA0547	3' GGGAGGCCAAGACAGAAGGATC 29596	AC C C
	A	TGATCC CTG CT GGCCTCCC	
		ACTAGG GAC GA CCGGAGGG	
		AA A A	
GAM2030	KIAA0547	3' GGGAGGCCAAGGCTGGCAGATC 29597	CA T C
	A	TGATC CC GCCT GGCCTCCC	
		ACTAG GG CGGA CCGGAGGG	
		AC T A	
GAM2030	KIAA0547	3' GGGAGGCCAAGGTGGGCAGATC 29598	CA TG C
	A	TGATC CC CCT GGCCTCCC	
		ACTAG GG GGA CCGGAGGG	
		AC GT A	
GAM2030	KIAA0557	3' GGGAAGCTGAGGCAAGAGAATC 78570	CCACC C
	A	TGAT TGCCTCGGC TCCC	

		ACTA	ACGGAGTCG	AGGG	
		AGAGA	A		
GAM2030	KIAA0557	3'	GGGAGGCCGAGGCAGGTGGATC	78571	
	A		TGATCCACCTGCCTCGGCCTCCC		
			ACTAGGTGGACGGAGCCGGAGGG		
GAM2030	KIAA0563	3'	GGGAGGCCGAGGCGGGCGGATC	29886	A
	AT		ATGATCC CCTGCCTCGGCCTCCC		
			TACTAGG GGGCGGAGCCGGAGGG		
			C		
GAM2030	KIAA0565	3'	AGGCTGAGGCAGGAAGATCA	67430	CA
			TGATC CCTGCCTCGGCCT		
			ACTAG GGACGGAGTCGGA		
			AA		
GAM2030	KIAA0565	3'	GGGAGGCCAAGGTGGGTGGATC	67440	TG C
	A		TGATCCACC CCT GGCCTCCC		
			ACTAGGTGG GGA CCGGAGGG		
			GT A		
GAM2030	KIAA0596	3'	GGGAGGCCGAGGCGGGTGGATC	63495	
	A		TGATCCACCTGCCTCGGCCTCCC		
			ACTAGGTGGGCGGAGCCGGAGGG		
GAM2030	KIAA0618	3'	GGGAGGCCAAGGTGGGCAGATC	29856	CA TG C
	A		TGATC CC CCT GGCCTCCC		
			ACTAG GG GGA CCGGAGGG		
			AC GT A		
GAM2030	KIAA0628	3'	GGGAGGCCGAGGCGGGCGGATC	29534	A
	G		TGATCC CCTGCCTCGGCCTCCC		
			GCTAGG GGGCGGAGCCGGAGGG		
			C		
GAM2030	KIAA0643	3'	GGAGGCTGAGGCAGGAGAATCA	45979	CCA
			TGAT CCTGCCTCGGCCTCC		
			ACTA GGACGGAGTCGGAGG		
			AGA		
GAM2030	KIAA0694	3'	GGGAGGCCAAGACAGGCGGATC	72972	A C C
			GATCC CTG CT GGCCTCCC		
			CTAGG GGAC GA CCGGAGGG		
			C A A		
GAM2030	KIAA0794	3'	GGAAGGCCGGGCGCGGTGGCTC	81231	T _ T _
	AT		ATGA CCACC TGCC CGGCCT CC		

		TACT GGTGG GCGG GCCGGA GG	
		C C _ A	
GAM2030	KIAA0798	3' GGGAGGCCAAGGTGGGTGGATC 28451	TG C
	A	TGATCCACC CCT GGCCTCCC	
		ACTAGGTGG GGA CCGGAGGG	
		GT A	
GAM2030	KIAA0825	3' GGAGGCTGAGGCAGGAGAATCA 61686	CCA
		TGAT CCTGCCTCGGCCTCC	
		ACTA GGACGGAGTCGGAGG	
		AGA	
GAM2030	KIAA0825	3' GGGAGGCCAAAGTGGGAGATCA 61687	CA TG CTC
	T	ATGATC CC C GGCCTCCC	
		TACTAG GG G CCGGAGGG	
		A_ GT AAA	
GAM2030	KIAA0831	5' GGGAGGCCAAGACAGGTGGATC 30643	C C
	A	TGATCCACCTG CT GGCCTCCC	
		ACTAGGTGGAC GA CCGGAGGG	
		A A	
GAM2030	KIAA0831	3' GGGAGGCCGAGGCAGGCGGATC 30644	A
	A	TGATCC CCTGCCTCGGCCTCCC	
		ACTAGG GGACGGAGCCGGAGGG	
		C	
GAM2030	KIAA0872	3' GGAAGCTGAGGCAGGAGAATCA 30757	CCA C
		TGAT CCTGCCTCGGC TCC	
		ACTA GGACGGAGTCG AGG	
		AGA A	
GAM2030	KIAA0872	3' GGAAGGCCGAGGCGGGTGGGTC 30758	_
	A	TGATCCACCTGCCTCGGCCT CC	
		ACTGGGTGGGCGGAGCCGGA GG	
		A	
GAM2030	KIAA0872	3' GGGAGGCCGAGGCGGGCAGATC 30759	CA
	A	TGATC CCTGCCTCGGCCTCCC	
		ACTAG GGGCGGAGCCGGAGGG	
		AC	
GAM2030	KIAA0884	3' GGGAGGCCAAGGCAGGTGGATC 70754	CG
	A	TGATCCACCTGCCT GCCTCCC	
		ACTAGGTGGACGGA CGGAGGG	
		AA	
GAM2030	KIAA0889	3' AGGCTGAGGCAGGAGAATCA 31755	CCA
		TGAT CCTGCCTCGGCCT	

		ACTA GGACGGAGTCGGA	
		AGA	
GAM2030	KIAA0889	3' GGGAGGCCGAGGCGGGTGGATC 31780	
	A	TGATCCACCTGCCTCGGCCTCCC	
		ACTAGGTGGGCGGAGCCGGAGGG	
GAM2030	KIAA0892	3' GGGAGGCTGAGGCAGGAGGATC 71571	A
	A	TGATCC CCTGCCTCGGCCTCCC	
		ACTAGG GGACGGAGTCGGAGGG	
		A	
GAM2030	KIAA0894	3' GGAGGCCGGGCGCGGTGGCTCA 30336	T _ T
		TGA CCACC TGCC CGGCCTCC	
		ACT GGTGG GCGG GCCGGAGG	
		C C _	
GAM2030	KIAA0894	3' GGGAGGCCGAGGCAAGTGGATC 30338	C
	A	TGATCCAC TGCCTCGGCCTCCC	
		ACTAGGTG ACGGAGCCGGAGGG	
		A	
GAM2030	KIAA0907	3' GGAAGGCTGAGGCAGGAGAATC 30877	CCA _
	A	TGAT CCTGCCTCGGCCT CC	
		ACTA GGACGGAGTCGGA GG	
		AGA A	
GAM2030	KIAA0907	3' GGGAGGCCAAGGTGGGCGGAT 30879	A TG C
		ATCC CC CCT GGCCTCCC	
		TAGG GG GGA CCGGAGGG	
		C GT A	
GAM2030	KIAA0907	3' GGGAGGCCGAGGTGGGCAGATC 30880	CA TG
	A	TGATC CC CCTCGGCCTCCC	
		ACTAG GG GGAGCCGGAGGG	
		AC GT	
GAM2030	KIAA0953	3' GGGAGGCCAAGGCAGGTGGATC 67330	C
	A	TGATCCACCTGCCT GGCCTCCC	
		ACTAGGTGGACGGA CCGGAGGG	
		A	
GAM2030	KIAA0961	3' GGGAGGCCGGTGGGCAGATCAT 30405	CA TG TC
		ATGATC CC CC GGCCTCCC	
		TACTAG GG GG CCGGAGGG	
		AC GT _	
GAM2030	KIAA0981	3' GGGAGGCCTAGGCAGGCAGATC 62091	CA C
	A	TGATC CCTGCCT GGCCTCCC	

		ACTAG GGACGGA CCGGAGGG	
		AC T	
GAM2030 KIAA1032	3'	GGGAGACCGAGGCTGGCAGATC 66728	CA T C
A		TGATC CC GCCTCGG CTCCC	
		ACTAG GG CGGAGCC GAGGG	
		AC T A	
GAM2030 KIAA1086	3'	GAGGCCGAGGTGGGCAGATCG 71285	CA TG
		TGATC CC CCTCGGCCTC	
		GCTAG GG GGAGCCGGAG	
		AC GT	
GAM2030 KIAA1086	3'	GGGAGGCCAAGCTTGGTGGATC 71287	T_ CTC
G		TGATCCACC GC GGCCTCCC	
		GCTAGGTGG CG CCGGAGGG	
		TT AA_	
GAM2030 KIAA1117	3'	GGGAGGCCAAGGGAGAAGGATC 61772	AC G C
A		TGATCC CT CCT GGCCTCCC	
		ACTAGG GA GGA CCGGAGGG	
		AA G A	
GAM2030 KIAA1130	3'	AGGCCAAGACAGGTGGATCA 63076	C C
		TGATCCACCTG CT GGCCT	
		ACTAGGTGGAC GA CCGGA	
		A A	
GAM2030 KIAA1130	3'	GGAAGGCCAAGACAGGTGGATC 63096	C C _
A		TGATCCACCTG CT GGCCT CC	
		ACTAGGTGGAC GA CCGGA GG	
		A A A	
GAM2030 KIAA1160	3'	GGGAGGCCGAGGCGGGCGGGTC 40760	A
A		TGATCC CCTGCCTCGGCCTCCC	
		ACTGGG GGGCGGAGCCGGAGGG	
		C	
GAM2030 KIAA1160	3'	GGGAGGCTGAGGCAGGAGAATC 40761	CCA
A		TGAT CCTGCCTCGGCCTCCC	
		ACTA GGACGGAGTCGGAGGG	
		AGA	
GAM2030 KIAA1164	3'	GGGAGGCCAAGGTGGGCGGATC 70049	A TG C
AT		ATGATCC CC CCT GGCCTCCC	
		TACTAGG GG GGA CCGGAGGG	
		C GT A	
GAM2030 KIAA1164	3'	GGGAGGCCGAGGCAGGTGGATC 70050	
A		TGATCCACCTGCCTCGGCCTCCC	

ACTAGGTGGACGGAGCCGGAGGG

GAM2030 KIAA1191 3' GGGAGGCCAAGGTAGGTGGAT 40335 C
ATCCACCTGCCT GGCCTCCC
||||||| |||||
TAGGTGGATGGA CCGGAGGG

A

GAM2030 KIAA1202 3' GGGAGGCCGAGGCAGGTGGATC 72491
A TGATCCACCTGCCTCGGCCTCCC
|||||||
ACTAGGTGGACGGAGCCGGAGGG

GAM2030 KIAA1228 3' GGGAGGCCGAGGCGGGCGGAT 65677 A
ATCC CCTGCCTCGGCCTCCC
||| |||||
TAGG GGGCGGAGCCGGAGGG
C

GAM2030 KIAA1244 3' GGAGGCCGAGACAGGAGAATCG 72446 CCA C
TGAT CCTG CTCGGCCTCC
||| ||| |||||
GCTA GGAC GAGCCGGAGG
AGA A

GAM2030 KIAA1244 3' GGGAGGCCAAGGTGGGCAGAT 72447 CA TG C
ATC CC CCT GGCCTCCC
||| || ||| |||||
TAG GG GGA CCGGAGGG
AC GT A

GAM2030 KIAA1257 3' GGGAGGCCGAGGCGGGTGGATC 63406
A TGATCCACCTGCCTCGGCCTCCC
|||||||
ACTAGGTGGGCGGAGCCGGAGGG

GAM2030 KIAA1271 3' GGGAGGCCAAGGTGGGCAGATC 70143 CA TG C
G TGATC CC CCT GGCCTCCC
||||| || ||| |||||
GCTAG GG GGA CCGGAGGG
AC GT A

GAM2030 KIAA1277 3' GAGGCCAAGGCAGGCAGGTGGA 65078 C____
TCA TGATCCACCTGCCT GGCCTC
||||||| |||||
ACTAGGTGGACGGA CCGGAG
CGGAA

GAM2030 KIAA1328 3' GGAGGCTGAGGCAGGAGAATCA 62328 CCA
TGAT CCTGCCTCGGCCTCC
||| |||||
ACTA GGACGGAGTCGGAGG
AGA

GAM2030 KIAA1328 3' GGGAGGCCGAGGCAGCCGGATC 62329 AC
AT ATGATCC CTGCCTCGGCCTCCC
||||| |||||

			TACTAGG GACGGAGCCGGAGGG	
			CC	
GAM2030	KIAA1348	3'	GGGAGGCCGAGGCGGATGGATC 69125	C
	A		TGATCCA CTGCCTCGGCCTCCC	
			ACTAGGT GGCGGAGCCGGAGGG	
			A	
GAM2030	KIAA1348	3'	GGGAGGCTGAGGCAGGAAAATC 69126	CCA
	A		TGAT CCTGCCTCGGCCTCCC	
			ACTA GGACGGAGTCGGAGGG	
			AAA	
GAM2030	KIAA1364	3'	GGGAGGCCAAGGTGGGCACATC 64354	CCA TG C
	A		TGAT CC CCT GGCCTCCC	
			ACTA GG GGA CCGGAGGG	
			CAC GT A	
GAM2030	KIAA1404	3'	GGGAGGCCGAGGCAGGCGGATC 62692	A
	A		TGATCC CCTGCCTCGGCCTCCC	
			ACTAGG GGACGGAGCCGGAGGG	
			C	
GAM2030	KIAA1423	3'	GGGAGGCCAAGGTGGGAGGATC 62394	A TG C
	A		TGATCC CC CCT GGCCTCCC	
			ACTAGG GG GGA CCGGAGGG	
			A GT A	
GAM2030	KIAA1456	3'	GAGACTGAGGCAGGAGGATCA 67556	A C
			TGATCC CCTGCCTCGG CTC	
			ACTAGG GGACGGAGTC GAG	
			A A	
GAM2030	KIAA1456	3'	GGGAGGCCAAGGCAGAAGGATC 67561	AC C
	A		TGATCC CTGCCT GGCCTCCC	
			ACTAGG GACGGA CCGGAGGG	
			AA A	
GAM2030	KIAA1456	5'	GGGAGGCCGAGGCAGGCGGATC 67562	A
	A		TGATCC CCTGCCTCGGCCTCCC	
			ACTAGG GGACGGAGCCGGAGGG	
			C	
GAM2030	KIAA1473	3'	GGGAGGCTGAGGCAGGAGAATC 71211	CCA
	A		TGAT CCTGCCTCGGCCTCCC	
			ACTA GGACGGAGTCGGAGGG	
			AGA	
GAM2030	KIAA1559	3'	GGGAGGCCATGGCAGGTGGATC 73457	TC
	A		TGATCCACCTGCC GGCCTCCC	

		ACTAGGTGGACGG CCGGAGGG		
		TA		
GAM2030	KIAA1559	3' GGGAGGCTAAGGCAGGAGAATC 73458	CCA	CG
	A	TGAT CCTGCCT GCCTCCC		
		ACTA GGACGGA CGGAGGG		
		AGA AT		
GAM2030	KIAA1586	5' GGGAGGCCAAGGCTGGCAGATC 93940	CA T	C
	A	TGATC CC GCCT GGCCTCCC		
		ACTAG GG CGGA CCGGAGGG		
		AC T A		
GAM2030	KIAA1614	3' GGGAGGCCGAGGCGCCTGGATC 70667	CC	
	A	TGATCCA TGCCTCGGCCTCCC		
		ACTAGGT GCGGAGCCGGAGGG		
		CC		
GAM2030	KIAA1630	3' GGGAGGCCAAGGCTGGTGGATC 38656	T	C
	A	TGATCCACC GCCT GGCCTCCC		
		ACTAGGTGG CGGA CCGGAGGG		
		T A		
GAM2030	KIAA1641	3' GGGAGGCCAGTGCAGGTGGATC 81021	_	C
	A	TGATCCACCTGC CT GGCCTCCC		
		ACTAGGTGGACG GA CCGGAGGG		
		T _		
GAM2030	KIAA1649	3' GGAAGGCCGAGGCAGGCAGATC 51244	CA	_
	G	TGATC CCTGCCTCGGCCT CC		
		GCTAG GGACGGAGCCGGA GG		
		AC A		
GAM2030	KIAA1649	3' GGAGGCTGAGGCAGGAGAATCA 51245	CCA	
		TGAT CCTGCCTCGGCCTCC		
		ACTA GGACGGAGTCGGAGG		
		AGA		
GAM2030	KIAA1656	5' GGAGGCTGAGGCAGGAGAATCA 66375	CCA	
		TGAT CCTGCCTCGGCCTCC		
		ACTA GGACGGAGTCGGAGG		
		AGA		
GAM2030	KIAA1656	5' GGGAGGCCAGGTCAGGGGATC 66378	A _	C
	AT	ATGATCC CCTG CCT GGCCTCCC		
		TACTAGG GGAC GGA CCGGAGGG		
		_ T C		
GAM2030	KIAA1674	3' GGGAGGCCGAGGCGAGTGGATC 69346	C	
	A	TGATCCAC TGCCTCGGCCTCCC		

			ACTAGGTG GCGGAGCCGGAGGG		
			A		
GAM2030	KIAA1715	3'	GGGAGGCTGAGGCGGGCAGATC 68688	CA	
	AT		ATGATC CCTGCCTCGGCCTCCC		
			TACTAG GGGCGGAGTCGGAGGG		
			AC		
GAM2030	KIAA1724	3'	GGGAAGCCAAGGCAGGTGGATT 67618	C C	
			GATCCACCTGCCT GGC TCCC		
			TTAGGTGGACGGA CCG AGGG		
			A A		
GAM2030	KIAA1724	3'	GGGAGGCTGAGGCAGGAGAATC 67619	CCA	
	A		TGAT CCTGCCTCGGCCTCCC		
			ACTA GGACGGAGTCGGAGGG		
			AGA		
GAM2030	KIAA1751	3'	GGGAGGCCGAGGCAGGAGGATC 72162	A	
	A		TGATCC CCTGCCTCGGCCTCCC		
			ACTAGG GGACGGAGCCGGAGGG		
			A		
GAM2030	KIAA1829	3'	GGAGGGTGAGGCAGGAGAATCA 62648	CCA	G
			TGAT CCTGCCTCG CCTCC		
			ACTA GGACGGAGT GGAGG		
			AGA G		
GAM2030	KIAA1829	3'	GGGAGGCCGAGGTGGGCAGATC 62650	CA	TG
	A		TGATC CC CCTCGGCCTCCC		
			ACTAG GG GGAGCCGGAGGG		
			AC GT		
GAM2030	KIAA1841	3'	GGGAGGCCGAGGCGGGCAGATC 80854	CA	
	A		TGATC CCTGCCTCGGCCTCCC		
			ACTAG GGGCGGAGCCGGAGGG		
			AC		
GAM2030	KIAA1855	3'	GAGAGCAGAGACAGGTGGACCA 93954	A	C G _
			TG TCCACCTG CTC GC CTC		
			AC AGGTGGAC GAG CG GAG		
			C A A A		
GAM2030	KIAA1870	3'	GGGAGGCCAAGGCAGGCAGATC 52903	CA	C
	G		TGATC CCTGCCT GGCCTCCC		
			GCTAG GGACGGA CCGGAGGG		
			AC A		
GAM2030	KIAA1872	3'	AGGCCGAGGCAGGCGGATCA 63592	A	
			TGATCC CCTGCCTCGGCCT		

			ACTAGG GGACGGAGCCGGA		
			C		
GAM2030	KIAA1872	3'	GGGAGACCGAGACAGGTGGATC 63613	C	C
	A		TGATCCACCTG CTCGG CTCCC		
			ACTAGGTGGAC GAGCC GAGGG		
			A A		
GAM2030	KIAA1872	3'	GGGAGGCCGAGGCAGGCGGATC 63614	A	
	A		TGATCC CCTGCCTCGGCCTCCC		
			ACTAGG GGACGGAGCCGGAGGG		
			C		
GAM2030	KIAA1941	3'	GGAGGCCGGGCATGGTGGCTCA 75341	T	_ T
			TGA CCACC TGCC CGGCCTCC		
			ACT GGTGG ACGG GCCGGAGG		
			C T _		
GAM2030	KIAA1941	3'	GGGAGGCTGAGGCAGGAGAATC 75343	CCA	
	A		TGAT CCTGCCTCGGCCTCCC		
			ACTA GGACGGAGTCGGAGGG		
			AGA		
GAM2030	KIAA1948	3'	GGGAGGCCGAGGCAGGTGGATC 83305		
	GT		ATGATCCACCTGCCTCGGCCTCCC		
			TGCTAGGTGGACGGAGCCGGAGGG		
GAM2030	KIAA1951	3'	GGGAGACTGAGGCAGGAGGATC 74158	A	C
	A		TGATCC CCTGCCTCGG CTCCC		
			ACTAGG GGACGGAGTC GAGGG		
			A A		
GAM2030	KIAA1951	3'	GGGAGGCCGAGGCGGGCAGATC 74159	CA	
	A		TGATC CCTGCCTCGGCCTCCC		
			ACTAG GGGCGGAGCCGGAGGG		
			AC		
GAM2030	KIAA1951	3'	GGGAGGCTGAGGCAGGAGGATC 74160	A	
	A		TGATCC CCTGCCTCGGCCTCCC		
			ACTAGG GGACGGAGTCGGAGGG		
			A		
GAM2030	KIAA1958	3'	GGGAGGCCAAGGTGGGCAGATC 82785	CA TG	C
	A		TGATC CC CCT GGCCTCCC		
			ACTAG GG GGA CCGGAGGG		
			AC GT A		
GAM2030	KIAA1979	3'	AGGCTGAGACAGGTGGGCCA 89647	AT	C
			TG CCACCTG CTCGGCCT		

			AC GGTGGAC GAGTCGGA		
			CG A		
GAM2030	KLHL8	3'	GGGAGGCCGAGGTGGGTGGACC 63515	A	TG
	A		TG TCCACC CCTCGGCCTCCC		
			AC AGGTGG GGAGCCGGAGGG		
			C GT		
GAM2030	KR18	3'	GGGAGGCCAAGGCAAGCAGATC 53893	CACC	C
	A		TGATC TGCCT GGCCTCCC		
			ACTAG ACGGA CCGGAGGG		
			ACGA A		
GAM2030	KR18	3'	GGGAGGCTGAGGCAGGTGGATC 53894		
	A		TGATCCACCTGCCTCGGCCTCCC		
			ACTAGGTGGACGGAGTCGGAGGG		
GAM2030	LAP1B	3'	GGTCAGGCCAAGGCAGGTGGAT 65196	C	—
	CA		TGATCCACCTGCCT GGCCT CC		
			ACTAGGTGGACGGA CCGGA GG		
			A CT		
GAM2030	LHPP	5'	GAGATGCTGAGGCAGGTGGATC 42366		—
	A		TGATCCACCTGCCTCGGC CTC		
			ACTAGGTGGACGGAGTCG GAG		
			TA		
GAM2030	LIAS	3'	GGAGGCCAAGGCGGGTGGATCA 71166	C	
			TGATCCACCTGCCT GGCCTCC		
			ACTAGGTGGGCGGA CCGGAGG		
			A		
GAM2030	LIAS	3'	GGGAGGCTAAGGCAGGAGAATC 71167	CCA	CG
	A		TGAT CCTGCCT GCCTCCC		
			ACTA GGACGGA CCGAGGG		
			AGA AT		
GAM2030	LIM	3'	GGGAGGCCAAGACGGGCGGATC 22329	A	C C
	AT		ATGATCC CCTG CT GGCCTCCC		
			TACTAGG GGGC GA CCGGAGGG		
			C A A		
GAM2030	LIM	3'	GGGAGGCCAAGGTGGGTGGACC 22330	A	TG C
	A		TG TCCACC CCT GGCCTCCC		
			AC AGGTGG GGA CCGGAGGG		
			C GT A		
GAM2030	LRRFIP1	3'	GGGAGGCCAAGGCAGGTGGATC 17614		C
	A		TGATCCACCTGCCT GGCCTCCC		

			ACTAGGTGGACGGA CCGGAGGG		
			A		
GAM2030	LSR68	3'	GGGAGGCCGAGGCGGGTGGACC 38558	A	
	A		TG TCCACCTGCCTCGGCCTCCC		
			AC AGGTGGGCGGAGCCGGAGGG		
			C		
GAM2030	LYSAL1	3'	GGGAGGCCGAGGCGGGCGGATC 18125	A	
	AT		ATGATCC CCTGCCTCGGCCTCCC		
			TACTAGG GGGCGGAGCCGGAGGG		
			C		
GAM2030	MACF1	3'	GGGAGGCCAAGGCAGGCGGATC 53496	A	C
	A		TGATCC CCTGCCT GGCCTCCC		
			ACTAGG GGACGGA CCGGAGGG		
			C A		
GAM2030	MAWBP	3'	GAGGCCAAGGTGGGTGGATCA 42385	TG	C
			TGATCCACC CCT GGCCTC		
			ACTAGGTGG GGA CCGGAG		
			GT A		
GAM2030	MCAM	3'	GGGAGGCCGAGGCGGGCGGATC 22463	A	
	A		TGATCC CCTGCCTCGGCCTCCC		
			ACTAGG GGGCGGAGCCGGAGGG		
			C		
GAM2030	MED6	3'	GGAATGCCAAGGCAGGTGGATC 19613	C	C_
	A		TGATCCACCTGCCT GGC TCC		
			ACTAGGTGGACGGA CCG AGG		
			A TA		
GAM2030	MESDC2	3'	GGGAGGCCGAGGTGGGTGGATC 72920	TG	
	A		TGATCCACC CCTCGGCCTCCC		
			ACTAGGTGG GGAGCCGGAGGG		
			GT		
GAM2030	MGC10765	3'	GGAGGCTGAGGCAAGAGAATCA 44563	CCACC	
			TGAT TGCCTCGGCCTCC		
			ACTA ACGGAGTCGGAGG		
			AGAGA		
GAM2030	MGC10765	3'	GGGAGGCCGAGGTGGGTGGATC 44565	TG	
	A		TGATCCACC CCTCGGCCTCCC		
			ACTAGGTGG GGAGCCGGAGGG		
			GT		
GAM2030	MGC10814	3'	GGGAGGCCAAGGCGGGTGGGTC 52021	C	
	A		TGATCCACCTGCCT GGCCTCCC		

			ACTGGGTGGGCGGA CCGGAGGG		
			A		
GAM2030	MGC10814	5'	GGGAGGCCGAGGTGGGTGGATC 52022	TG	
	A		TGATCCACC CCTCGGCCTCCC		
			ACTAGGTGG GGAGCCGGAGGG		
			GT		
GAM2030	MGC10999	3'	GGGAGGCCAAGGCAGGAGGATT 51198	A	C
			GATCC CCTGCCT GGCCTCCC		
			TTAGG GGACGGA CCGGAGGG		
			A A		
GAM2030	MGC10999	3'	GGGAGGCTGAGGCGGGTGGATC 51199		
	AT		ATGATCCACCTGCCTCGGCCTCCC		
			TACTAGGTGGGCGGAGTCGGAGGG		
GAM2030	MGC11287	5'	GGGAGGCCGAGGCAGACGGATC 49620	AC	
	A		TGATCC CTGCCTCGGCCTCCC		
			ACTAGG GACGGAGCCGGAGGG		
			CA		
GAM2030	MGC11386	3'	GGGAGGCCGAAGTAAGCAGATC 53071	CACC	C
	A		TGATC TGC TCGGCCTCCC		
			ACTAG ATG AGCCGGAGGG		
			ACGA A		
GAM2030	MGC13017	3'	GGGAGGCCGAGGTGAGCAGATC 55576	CAC	_
	A		TGATC CT GCCTCGGCCTCCC		
			ACTAG GA TGGAGCCGGAGGG		
			AC_ G		
GAM2030	MGC13053	3'	GGGAGGCCGAGGCAGGCGGATC 52112	A	
	AT		ATGATCC CCTGCCTCGGCCTCCC		
			TACTAGG GGACGGAGCCGGAGGG		
			C		
GAM2030	MGC13053	3'	GGGAGGCTGAGGCAGGGGAATC 52113	_	A
	A		TGAT CC CCTGCCTCGGCCTCCC		
			ACTA GG GGACGGAGTCGGAGGG		
			A _		
GAM2030	MGC14126	3'	GGGAGGCTGAGGCGGGTGGATC 52941		
	A		TGATCCACCTGCCTCGGCCTCCC		
			ACTAGGTGGGCGGAGTCGGAGGG		
GAM2030	MGC14799	3'	GGGAGGCCGAGGCGGGCGGATC 51331	A	
	AT		ATGATCC CCTGCCTCGGCCTCCC		

		TACTAGG GGGCGGAGCCGGAGGG		
		C		
GAM2030	MGC14817	3' GGGAGGCCGAGGCAGGTGGATC 51338		
	A	TGATCCACCTGCCTCGGCCTCCC		
		ACTAGGTGGACGGAGCCGGAGGG		
GAM2030	MGC15397	3' GGGAGGCCGAGGCCGGTGATTC 55555	TC	T
	A	TGA CACC GCCTCGGCCTCCC		
		ACT GTGG CGGAGCCGGAGGG		
		TA C		
GAM2030	MGC15631	3' GAAGCTGAGGCAAGAGGATCA 52229	ACC	C
		TGATCC TGCCTCGGC TC		
		ACTAGG ACGGAGTCG AG		
		AGA A		
GAM2030	MGC16037	3' GGGAGGCCAATGCATGTGGATC 52893	C	CTC
	A	TGATCCAC TGC GGCCTCCC		
		ACTAGGTG ACG CCGGAGGG		
		T TAA		
GAM2030	MGC16142	3' GGGAGGCCAAGGTGGGAGGATC 52266	A	TG C
	A	TGATCC CC CCT GGCCTCCC		
		ACTAGG GG GGA CCGGAGGG		
		A GT A		
GAM2030	MGC16385	3' GGGAGGCCGAGACGGGCGGATC 59539	A	C
	A	TGATCC CCTG CTCGGCCTCCC		
		ACTAGG GGGC GAGCCGGAGGG		
		C A		
GAM2030	MGC16703	3' GGGAGGCCAAGGCAGGCAGATC 73495	CA	C
	A	TGATC CCTGCCT GGCCTCCC		
		ACTAG GGACGGA CCGGAGGG		
		AC A		
GAM2030	MGC20235	3' GGGAGGCCGAAGTGGGTGGATC 59556	TG	C
	G	TGATCCACC C TCGGCCTCCC		
		GCTAGGTGG G AGCCGGAGGG		
		GT A		
GAM2030	MGC20496	3' GGGAGGCCGAGGCAGGCAGATC 54530	CA	
	A	TGATC CCTGCCTCGGCCTCCC		
		ACTAG GGACGGAGCCGGAGGG		
		AC		
GAM2030	MGC21621	5' GGAGGCCTCGGCGGATCA 59440	ACCT	TC
		TGATCC GCC GGCCTCC		

		ACTAGG CGG CCGGAGG		
		_____ CT		
GAM2030	MGC23244	3' GGGAAGCCGAGGCGGGTGGAAAC 58836	A	C
	A	TG TCCACCTGCCTCGGC TCCC		
		AC AGGTGGGCGGAGCCG AGGG		
		A A		
GAM2030	MGC2396	3' GGGAGGCCAAGGTGGGAGGATC 54561	A TG	C
	A	TGATCC CC CCT GGCCTCCC		
		ACTAGG GG GGA CCGGAGGG		
		A GT A		
GAM2030	MGC2562	3' GGGAGGCCAAGGCAAGCAAATC 51446	CCACC	C
	A	TGAT TGCCT GGCCTCCC		
		ACTA ACGGA CCGGAGGG		
		AACGA A		
GAM2030	MGC2562	3' GGGAGGCCGAGGCGGGTGGATC 51447		
	A	TGATCCACCTGCCTCGGCCTCCC		
		ACTAGGTGGGCGGAGCCGGAGGG		
GAM2030	MGC2562	3' GGGAGGCCGAGGTGGGCAGATC 51448	CA TG	
	AT	ATGATC CC CCTCGGCCTCCC		
		TACTAG GG GGAGCCGGAGGG		
		AC GT		
GAM2030	MGC2663	3' GGGAGGCTGAGGCAAGTGAATC 44336	C C	
	A	TGAT CAC TGCCTCGGCCTCCC		
		ACTA GTG ACGGAGTCGGAGGG		
		A A		
GAM2030	MGC26641	3' GGAGTACGGAGCAGGTGGACCA 59324	A	CT GC
	T	ATG TCCACCTGC CG CTCC		
		TAC AGGTGGACG GC GAGG		
		C AG AT		
GAM2030	MGC2731	3' GGGAAGCCGAGGTGGGCGGATC 44163	A TG	C
	A	TGATCC CC CCTCGGC TCCC		
		ACTAGG GG GGAGCCG AGGG		
		C GT A		
GAM2030	MGC29762	3' GGGAGGCCAAGGCGGGTCAATC 59146	CC	C
	A	TGAT ACCTGCCT GGCCTCCC		
		ACTA TGGGCGGA CCGGAGGG		
		AC A		
GAM2030	MGC29891	3' AGGCAGAGGCAGGCGGATCA 58847	A	G
		TGATCC CCTGCCTC GCCT		

			ACTAGG GGACGGAG CGGA	
			C A	
GAM2030	MGC29891	3'	GGGAGGCCGAGGCGGGCGGATC 58866	A
	A		TGATCC CCTGCCTCGGCCTCCC	
			ACTAGG GGGCGGAGCCGGAGGG	
			C	
GAM2030	MGC29937	3'	GGAGGCTGAGGCAGGAGAATCA 58732	CCA
			TGAT CCTGCCTCGGCCTCC	
			ACTA GGACGGAGTCGGAGG	
			AGA	
GAM2030	MGC29937	3'	GGGAGGCCGTGGTGGGCGGATC 58733	A TG T
	A		TGATCC CC CC CGGCCTCCC	
			ACTAGG GG GG GCCGGAGGG	
			C GT T	
GAM2030	MGC3169	3'	GGGAGGCCGAGGCGGGCAGATC 44188	CA
	A		TGATC CCTGCCTCGGCCTCCC	
			ACTAG GGGCGGAGCCGGAGGG	
			AC	
GAM2030	MGC3169	3'	GGGAGGCTGAGGCAGGAGAATC 44189	CCA
	A		TGAT CCTGCCTCGGCCTCCC	
			ACTA GGACGGAGTCGGAGGG	
			AGA	
GAM2030	MGC3207	3'	GGGAGGCCGAGGCAGGTGGATC 63241	
	A		TGATCCACCTGCCTCGGCCTCCC	
			ACTAGGTGGACGGAGCCGGAGGG	
GAM2030	MGC39350	3'	GGGAGGCCAAGGCGGGCGGATC 59318	A C
	A		TGATCC CCTGCCT GGCCTCCC	
			ACTAGG GGGCGGA CCGGAGGG	
			C A	
GAM2030	MGC4248	3'	GGGAGGCCAAGGTGAGCAAGTC 51315	CCAC _ C
	A		TGAT CT GCCT GGCCTCCC	
			ACTG GA TGGG CCGGAGGG	
			AAC_ G A	
GAM2030	MGC4248	3'	GGGAGGCTGAGGCAGGAGAATC 51316	CCA
	A		TGAT CCTGCCTCGGCCTCCC	
			ACTA GGACGGAGTCGGAGGG	
			AGA	
GAM2030	MGC4342	3'	GGGAGGCCGAGCCTGAATC 44517	C CCT C
			GAT CA GC TCGGCCTCCC	

			CTA GT CG AGCCGGAGGG		
			A C__ _		
GAM2030	MGC4400	3'	GGGAGGCCAAGGCAGGAAGATC 52039	CA	C
	A		TGATC CCTGCCT GGCCTCCC		
			ACTAG GGACGGA CCGGAGGG		
			AA A		
GAM2030	MGC4562	3'	GGGAGGCTGAGGCGGGCGGATC 56742	A	
	A		TGATCC CCTGCCTCGGCCTCCC		
			ACTAGG GGGCGGAGTCGGAGGG		
			C		
GAM2030	MGC4663	3'	GGAGGCCGAGGCGGGCGGATCA 44788	A	
			TGATCC CCTGCCTCGGCCTCC		
			ACTAGG GGGCGGAGCCGGAGG		
			C		
GAM2030	MGC4840	3'	GGAAATCGAGGCGAGTGGATCA 72025	C	CC
			TGATCCAC TGCCTCGG TCC		
			ACTAGGTG GCGGAGCT AGG		
			A AA		
GAM2030	MGC4840	3'	GGGAGGTCGAGGTAGGCAGATC 72026	CA	
	A		TGATC CCTGCCTCGGCCTCCC		
			ACTAG GGATGGAGCTGGAGGG		
			AC		
GAM2030	MGC5254	3'	GGGAGGCCGAGGTGGGTGGATC 51388	TG	
	AT		ATGATCCACC CCTCGGCCTCCC		
			TACTAGGTGG GGAGCCGGAGGG		
			GT		
GAM2030	MGC5384	3'	GGGAGGCCAAGGCACATAGGTC 49091	CACC	C
	A		TGATC TGCCT GGCCTCCC		
			ACTGG ACGGA CCGGAGGG		
			ATAC A		
GAM2030	MGC5384	3'	GGGAGGCCGAGGCAGGCAGATC 49092	CA	
	A		TGATC CCTGCCTCGGCCTCCC		
			ACTAG GGACGGAGCCGGAGGG		
			AC		
GAM2030	MGC5457	3'	GGGAGGCTGAGGAAGGCAAATC 51941	CCA	G
	A		TGAT CCT CCTCGGCCTCCC		
			ACTA GGA GGAGTCGGAGGG		
			AAC A		
GAM2030	MGC9912	3'	GGGAGGCCGAGGTGGGAGGATC 55607	A	TG
	A		TGATCC CC CCTCGGCCTCCC		

			ACTAGG GG GGAGCCGGAGGG		
			A GT		
GAM2030	MOST2	5'	GAGGCTGAGGCAGGAGAATCA 40063	CCA	
			TGAT CCTGCCTCGGCCTC		
			ACTA GGACGGAGTCGGAG		
			AGA		
GAM2030	MOST2	5'	GGGAGGCCAAGGCAGGCAGATC 40068	CA	C
	A		TGATC CCTGCCT GGCCTCCC		
			ACTAG GGACGGA CCGGAGGG		
			AC A		
GAM2030	MRP63	3'	GAGGCCGGGTGCGGTGGCTCA 44046	T	T _
			TGA CCACC GC CTCGGCCTC		
			ACT GGTGG CG GGGCCGGAG		
			C _ T		
GAM2030	MRPL48	5'	AGGCCGAGGCGGGCGGATCA 32652	A	
			TGATCC CCTGCCTCGGCCT		
			ACTAGG GGGCGGAGCCGGA		
			C		
GAM2030	MRPL56	3'	GGAAGGCCGAGGTGGGTGGATC 52756	TG	_
	A		TGATCCACC CCTCGGCCT CC		
			ACTAGGTGG GGAGCCGGA GG		
			GT A		
GAM2030	MRPS10	3'	GGGAGGCCGAGGCAGGCGGATC 36821	A	
	A		TGATCC CCTGCCTCGGCCTCCC		
			ACTAGG GGACGGAGCCGGAGGG		
			C		
GAM2030	MRPS18B	3'	GGGAGGCTAAGGTAGGATCA 26754	ACC	CG
			TGATCC TGCCT GCCTCCC		
			ACTAGG ATGGA CGGAGGG		
			_ AT		
GAM2030	My015	3'	GGGAGGCCAAGCAGGCGGATC 67234	A	CTC
	A		TGATCC CCTGC GGCCTCCC		
			ACTAGG GGACG CCGGAGGG		
			C AAA		
GAM2030	MYO3B	3'	GGGAGGCCAAGATGGGCGGATC 58113	A	GC C
	AT		ATGATCC CCT CT GGCCTCCC		
			TACTAGG GGG GA CCGGAGGG		
			C TA A		
GAM2030	N4BP2	3'	GGGAGGCCGAGGTAGGTGGATC 36942		
	G		TGATCCACCTGCCTCGGCCTCCC		

GCTAGGTGGATGGAGCCGGAGGG

GAM2030	NBR2	3'	GGGAGGCCGAGGCAGGTGGTTC 20621	T
	AT		ATGA CCACCTGCCTCGGCCTCCC	
			TACT GGTGGACGGAGCCGGAGGG	
			T	
GAM2030	NMNAT	3'	GGGAGGCTGAGGCAGGAGAATC 43290	CCA
	A		TGAT CCTGCCTCGGCCTCCC	
			ACTA GGACGGAGTCGGAGGG	
			AGA	
GAM2030	NMT2	3'	GGGAGGCCAAGGTGGGCAGATC 17858	CA TG C
	AT		ATGATC CC CCT GGCCTCCC	
			TACTAG GG GGA CCGGAGGG	
			AC GT A	
GAM2030	NPTXR	3'	GAGGCCGGGCACGGTGGCTCA 55211	T _ T
			TGA CCACC TGCC CGGCCTC	
			ACT GGTGG ACGG GCCGGAG	
			C C _	
GAM2030	NPTXR	3'	GGGAGGCCGAGGCAGAAGAATC 55214	CCAC
			GAT CTGCCTCGGCCTCCC	
			CTA GACGGAGCCGGAGGG	
			AGAA	
GAM2030	NPTXR	3'	GGGAGGCTGAGACAGGCAGATC 55215	CA C
	A		TGATC CCTG CTCGGCCTCCC	
			ACTAG GGAC GAGTCGGAGGG	
			AC A	
GAM2030	NPTXR	3'	GAGGCCGGGCACGGTGGCTCA 27434	T _ T
			TGA CCACC TGCC CGGCCTC	
			ACT GGTGG ACGG GCCGGAG	
			C C _	
GAM2030	NPTXR	3'	GGGAGGCCGAGGCAGAAGAATC 27440	CCAC
			GAT CTGCCTCGGCCTCCC	
			CTA GACGGAGCCGGAGGG	
			AGAA	
GAM2030	NPTXR	3'	GGGAGGCTGAGACAGGCAGATC 27441	CA C
	A		TGATC CCTG CTCGGCCTCCC	
			ACTAG GGAC GAGTCGGAGGG	
			AC A	
GAM2030	OCLM	5'	GGGAGGCCGAGGTGGGTGGATC 42585	TG
	AT		ATGATCCACC CCTCGGCCTCCC	

			TACTAGGTGG GGAGCCGGAGGG		
			GT		
GAM2030	ORC6L	3'	GGGAGGCCAAGGTGGGTGGATC 27493	TG	C
	A		TGATCCACC CCT GGCCTCCC		
			ACTAGGTGG GGA CCGGAGGG		
			GT A		
GAM2030	p25	3'	AGGCCGAGGACGAGTGGTCA 23823	T	C _
			TGA CCAC TG CCTCGGCCT		
			ACT GGTG GC GGAGCCGGA		
			_ A A		
GAM2030	PAFAH2	3'	GGAGGCTGAAGCAGAAGAATCA 6505	CCAC	C
			TGAT CTGC TCGGCCTCC		
			ACTA GACG AGTCGGAGG		
			AGAA A		
GAM2030	PAFAH2	3'	GGGAGGCCAAGGCAGGCAGATC 6506	CA	C
	A		TGATC CCTGCCT GGCCTCCC		
			ACTAG GGACGGA CCGGAGGG		
			AC A		
GAM2030	PB1	3'	GGGAGGCCAAGATGGGTGGATT 37579	GC	C
	A		TGATCCACCT CT GGCCTCCC		
			ATTAGGTGGG GA CCGGAGGG		
			TA A		
GAM2030	PB1	3'	GGGAGGCCAAGGCGGGCAGATC 37580	CA	C
	A		TGATC CCTGCCT GGCCTCCC		
			ACTAG GGGCGGA CCGGAGGG		
			AC A		
GAM2030	PDCD7	3'	GGGAGGCCGAGGCGGGCCGATC 72608	CA	
	A		TGATC CCTGCCTCGGCCTCCC		
			ACTAG GGGCGGAGCCGGAGGG		
			CC		
GAM2030	phorbolin-1	3'	AGGCCAAGGCGGGTGGATCA 90203		C
			TGATCCACCTGCCT GGCCT		
			ACTAGGTGGGCGGA CCGGA		
			A		
GAM2030	PIWIL2	3'	GGGAGGCCGAGGCGGGTGGATC 36545		
	AT		ATGATCCACCTGCCTCGGCCTCCC		
			TACTAGGTGGGCGGAGCCGGAGGG		
GAM2030	PNPASE	3'	GGAGGCTGAGGCAGAAGAATCA 71440	CCAC	
			TGAT CTGCCTCGGCCTCC		

			ACTA GACGGAGTCGGAGG		
			AGAA		
GAM2030	PP591	5'	GGGAGGCTGAGGCAGGAGGATC 48148	A	
	A		TGATCC CCTGCCTCGGCCTCCC		
			ACTAGG GGACGGAGTCGGAGGG		
			A		
GAM2030	PPP1R3B	3'	GGGAGGCCGAGGCAGGTGGATC 45143		
	A		TGATCCACCTGCCTCGGCCTCCC		
			ACTAGGTGGACGGAGCCGGAGGG		
GAM2030	PPP1R3B	3'	GGGAGGCTGAGGCAGGAGAATC 45144	CCA	
	A		TGAT CCTGCCTCGGCCTCCC		
			ACTA GGACGGAGTCGGAGGG		
			AGA		
GAM2030	PRIC285	3'	GGGAAGCCGAGGCGGGCAGATC 62119	CA	C
	A		TGATC CCTGCCTCGGC TCCC		
			ACTAG GGGCGGAGCCG AGGG		
			AC A		
GAM2030	PRO0255	3'	GAGGCCGAGGCGGGCAGATCA 26968	CA	
			TGATC CCTGCCTCGGCCTC		
			ACTAG GGGCGGAGCCGGAG		
			AC		
GAM2030	PRO0478	3'	GGGAGGCCGAGGCGGGCAGATC 27033	CA	
	AT		ATGATC CCTGCCTCGGCCTCCC		
			TACTAG GGGCGGAGCCGGAGGG		
			AC		
GAM2030	PRO0628	3'	GGGAGGCCGAGGCTGGTGGATC 27063	T	
	A		TGATCCACC GCCTCGGCCTCCC		
			ACTAGGTGG CGGAGCCGGAGGG		
			T		
GAM2030	PRO1048	3'	GGGAGGCCGAGGCGGGCGGATC 38118	A	
	AT		ATGATCC CCTGCCTCGGCCTCCC		
			TACTAGG GGGCGGAGCCGGAGGG		
			C		
GAM2030	PRO2015	3'	GGGAGGCCGAGATGGGCAGAGC 38165	A CA GC	
	A		TG TC CCT CTCGGCCTCCC		
			AC AG GGG GAGCCGGAGGG		
			G AC TA		
GAM2030	PRO2198	5'	GGAGGCTGAGGCAGGAGAATCA 38409	CCA	
			TGAT CCTGCCTCGGCCTCC		

			ACTA GGACGGAGTCGGAGG	
			AGA	
GAM2030	PRO2198	5'	GGGAGGCCAAGGTGGGTGGATC 38410	TG C
	A		TGATCCACC CCT GGCCTCCC	
			ACTAGGTGG GGA CCGGAGGG	
			GT A	
GAM2030	PRO2730	3'	GGGAGGCCGAGGCGGGCGGATC 48186	A
	A		TGATCC CCTGCCTCGGCCTCCC	
			ACTAGG GGGCGGAGCCGGAGGG	
			C	
GAM2030	PRO2859	3'	GGGAGGCCGAGGTGGGCAGATC 38212	CA TG
	A		TGATC CC CCTCGGCCTCCC	
			ACTAG GG GGAGCCGGAGGG	
			AC GT	
GAM2030	PRO2859	3'	GGAGGCTGAAGCAGGAGAATCA 38210	CCA C
			TGAT CCTGC TCGGCCTCC	
			ACTA GGACG AGTCGGAGG	
			AGA A	
GAM2030	PRO2893	3'	GGGAGGCTGAGGCGGGCGGATC 38433	A
	AT		ATGATCC CCTGCCTCGGCCTCCC	
			TACTAGG GGGCGGAGTCGGAGGG	
			C	
GAM2030	PRO2949	3'	GGGAGGCCGAGACGGGCGGATC 38224	A C
	A		TGATCC CCTG CTCGGCCTCCC	
			ACTAGG GGGC GAGCCGGAGGG	
			C A	
GAM2030	PRO2964	3'	GGGAGGCTGAGGCTGGCGGATC 38262	A T
	AT		ATGATCC CC GCCTCGGCCTCCC	
			TACTAGG GG CGGAGTCGGAGGG	
			C T	
GAM2030	PRPF4	3'	GGGAGGCCGAGGTGGGTAGATC 17469	C TG
	G		TGATC ACC CCTCGGCCTCCC	
			GCTAG TGG GGAGCCGGAGGG	
			A GT	
GAM2030	PSR	3'	GGGAGGCCATGGCAGGTGGATC 65790	TC
	A		TGATCCACCTGCC GGCCTCCC	
			ACTAGGTGGACGG CCGGAGGG	
			TA	
GAM2030	PTK6	3'	GGGAGGCTGAGGCAGGTGGATC 21079	
	A		TGATCCACCTGCCTCGGCCTCCC	

ACTAGGTGGACGGAGTCGGAGGG

GAM2030 PTRF 3' GGGAGGCCGAGGTGGGCGGATC 64244 A TG
A TGATCC CC CCTCGGCCTCCC

||||| || |||||

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C GT

GAM2030 PXMP4 3' GGGAGGCTGAGGCAGGTGGATC 24335
A TGATCCACCTGCCTCGGCCTCCC

|||||

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GAM2030 RAB4B 5' GGGAGGCTGAGGCAGGCGGATC 32903 A
A TGATCC CCTGCCTCGGCCTCCC

|||||

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GAM2030 RAD51 3' GGGAGGCCGAGGCAGGTGGATC 56832
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|||||

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GAM2030 RAD51 3' GGGAGGCCGAGGCAGGTGGATC 12748
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GAM2030 RBPMS 3' GGGAGGCTGAGGCAGGCGGATC 23436 A
A TGATCC CCTGCCTCGGCCTCCC

|||||

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GAM2030 RES4-25 3' GGGAGGCCAAGGCAGGAAGATT 65270 CA C
GATC CCTGCCT GGCCTCCC

||| |||||

TTAG GGACGGA CCGGAGGG

AA A

GAM2030 RHOBTB3 3' GGGAGGCTGAGGCAAGTGGAT 30429 C
ATCCAC TGCCTCGGCCTCCC

|||||

TAGGTG ACGGAGTCGGAGGG

A

GAM2030 RNO2 3' GAGGCCGAGGCAGGTGGATCA 53938
TGATCCACCTGCCTCGGCCTC

|||||

ACTAGGTGGACGGAGCCGGAG

GAM2030 RNO2 5' GGGTTGAGGCGGGCAGATCA 53940 CA
TGATC CCTGCCTCGGCCT

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			ACTAG GGGCGGAGTTGGG	
			AC	
GAM2030	RoXaN	3'	GGAGGCCGAGATTAGAGAATCA 47295	CCAC C_
			TGAT CTG CTCGGCCTCC	
			ACTA GAT GAGCCGGAGG	
			AGA_ TA	
GAM2030	RoXaN	3'	GGGAGGCCAAGGCGGGTGGATC 47298	C
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			TACTAGGTGGGCGGA CCGGAGGG	
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GAM2030	RoXaN	3'	GGGAGGCCGAGGCGGGTGGATC 47299	
	A		TGATCCACCTGCCTCGGCCTCCC	
			ACTAGGTGGGCGGAGCCGGAGGG	
GAM2030	RoXaN	3'	GGGAGGCCGAGGTGGGTGATCA 47300	C TG
			TGATC ACC CCTCGGCCTCCC	
			ACTAG TGG GGAGCCGGAGGG	
			_ GT	
GAM2030	RoXaN	3'	GGGAGGCTGAGGCAGGAGAATC 47301	CCA
	A		TGAT CCTGCCTCGGCCTCCC	
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			AGA	
GAM2030	RPP14	3'	GGGAGGCTGCGGCAGGCGGATC 60223	A T
	A		TGATCC CCTGCC CGGCCTCCC	
			ACTAGG GGACGG GTCGGAGGG	
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GAM2030	RRP4	3'	GGGAGGCCAAGGCGGGCAGATC 27360	CA C
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			AC A	
GAM2030	SAMHD1	3'	GGGAGGCCAAGGTGGGCGGATC 61990	A TG C
	A		TGATCC CC CCT GGCCTCCC	
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			C GT A	
GAM2030	SC65	3'	GGGAGGCCAAGGTGGGTGGATC 22298	TG C
	A		TGATCCACC CCT GGCCTCCC	
			ACTAGGTGG GGA CCGGAGGG	
			GT A	
GAM2030	SCAND2	3'	GGGAGGCTGGGGCAGGAGAATC 54434	CCA
	A		TGAT CCTGCCTCGGCCTCCC	

			ACTA GGACGGGGTCGGAGGG		
			AGA		
GAM2030	SCIN	3'	GAGGATGAGGTAGGCGGATCA 53603	A	G
			TGATCC CCTGCCTCG CTC		
			ACTAGG GGATGGAGT GGAG		
			C A		
GAM2030	SCN12A	3'	GAGGCCAAGGCAGGTGGATCA 27082		C
			TGATCCACCTGCCT GGCCTC		
			ACTAGGTGGACGGA CCGGAG		
			A		
GAM2030	SCYA5	3'	GGGAGGCCAAGGTGGGTGGATC 12970	TG	C
	A		TGATCCACC CCT GGCCTCCC		
			ACTAGGTGG GGA CCGGAGGG		
			GT A		
GAM2030	SEMA3E	3'	GGGAGGCCGAGGCGGGTGGATC 25811		
	AT		ATGATCCACCTGCCTCGGCCTCCC		
			TACTAGGTGGGCGGAGCCGGAGGG		
GAM2030	SEMA3E	3'	TTGAAAGCAAGTGGATTA 25816	C	C_
			TGATCCAC TGC TCGG		
			ATTAGGTG ACG AGTT		
			A AA		
GAM2030	SEMA5A	3'	GGGAGGCCAAGGTGGGCGGATC 15595	A	TG C
	A		TGATCC CC CCT GGCCTCCC		
			ACTAGG GG GGA CCGGAGGG		
			C GT A		
GAM2030	SERF1B	3'	GGGAGACCAAGGCGGGTAGATC 43699	C	C C
			GATC ACCTGCCT GG CTCCC		
			CTAG TGGGCGGA CC GAGGG		
			A A A		
GAM2030	SGKL	3'	GGGAGGCCAAGGCAGGAGGATC 26060	A	C
	A		TGATCC CCTGCCT GGCCTCCC		
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			A A		
GAM2030	SGKL	3'	GGGAGGCCGAGGCAGGCAGATT 26061	CA	
	AT		ATGATC CCTGCCTCGGCCTCCC		
			TATTAG GGACGGAGCCGGAGGG		
			AC		
GAM2030	SGKL	3'	GGGAGGCTGAGGCGGGCAGATC 26062	CA	
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GAM2030	SIAT4A	3'	GGGAGGCCGAGGCGGGAGGATC 13140	A
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			A	
GAM2030	SMA3	3'	GGGAGGCTGAGGCAGGCGGATC 23261	A
	A		TGATCC CCTGCCTCGGCCTCCC	
			ACTAGG GGACGGAGTCGGAGGG	
			C	
GAM2030	SMAP-5	3'	GGGAGGCCGAGGCGGGCGGATC 48661	A
	A		TGATCC CCTGCCTCGGCCTCCC	
			ACTAGG GGGCGGAGCCGGAGGG	
			C	
GAM2030	SNAPC1	3'	GGGAGGCCGAGGTGGGCGGATC 13278	A TG
	A		TGATCC CC CCTCGGCCTCCC	
			ACTAGG GG GGAGCCGGAGGG	
			C GT	
GAM2030	Spir-2	3'	GGGAGGCCGAGGAGGGAGGATC 71157	A G
	A		TGATCC CCT CCTCGGCCTCCC	
			ACTAGG GGG GGAGCCGGAGGG	
			A A	
GAM2030	SPRY4	3'	GGGAGGCCAAGGTGGGTGGATC 49023	TG C
	A		TGATCCACC CCT GGCCTCCC	
			ACTAGGTGG GGA CCGGAGGG	
			GT A	
GAM2030	SPRY4	3'	GGGAGGCTGAGGCAGAAGAATC 49024	CCAC
	A		TGAT CTGCCTCGGCCTCCC	
			ACTA GACGGAGTCGGAGGG	
			AGAA	
GAM2030	SPRY4	3'	GGGAGGCTGAGGCAGGTGGATC 49025	
	A		TGATCCACCTGCCTCGGCCTCCC	
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GAM2030	SPTLC2	3'	GGGAGGCTGAGGCAGGTGGCTC 17999	T
	A		TGA CCACCTGCCTCGGCCTCCC	
			ACT GGTGGACGGAGTCGGAGGG	
			C	
GAM2030	SS18L1	3'	GGGAGGCCGAAGCGGGCGGATC 65957	A C
	A		TGATCC CCTGC TCGGCCTCCC	

			ACTAGG GGGCG AGCCGGAGGG	
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GAM2030	SUN1	3'	GGGAGGCTGAGGCGGGTGGATC 47915	
	A		TGATCCACCTGCCTCGGCCTCCC	
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GAM2030	SYAP1	3'	GGGAGGCCGAGGTGGGCAGATC 52474	CA TG
	A		TGATC CC CCTCGGCCTCCC	
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GAM2030	TACTILE	3'	GGGAGGCCGAGGTGGGTGGATC 20590	TG
	A		TGATCCACC CCTCGGCCTCCC	
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			GT	
GAM2030	TDP1	5'	GGGAGGCCGAGGCGGCTGAATC 37603	C C
	A		TGAT CA CTGCCTCGGCCTCCC	
			ACTA GT GGCGGAGCCGGAGGG	
			A C	
GAM2030	TRIAD3	3'	GGAGGCTGAGGCAGGAGAATCA 96135	CCA
			TGAT CCTGCCTCGGCCTCC	
			ACTA GGACGGAGTCGGAGG	
			AGA	
GAM2030	TRIM38	3'	AGGCTGAGGCAGGTGGATCA 22052	
			TGATCCACCTGCCTCGGCCT	
			ACTAGGTGGACGGAGTCGGA	
GAM2030	UBCE7IP5	3'	GGGAGGCCAAGGTGGGTGGATC 30848	TG C
	A		TGATCCACC CCT GGCCTCCC	
			ACTAGGTGG GGA CCGGAGGG	
			GT A	
GAM2030	ust3	3'	GGGAGGCTGAGGCGGGCAGATC 94856	CA
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			TACTAG GGGCGGAGTCGGAGGG	
			AC	
GAM2030	WBSCR21	3'	AGGCTGAGGCAGGAGAATCA 49294	CCA
			TGAT CCTGCCTCGGCCT	
			ACTA GGACGGAGTCGGA	
			AGA	
GAM2030	WBSCR23	5'	AGGCTGAGACAGGAGGATCA 47415	A C
			TGATCC CCTG CTCGGCCT	

			ACTAGG GGAC GAGTCGGA		
			A A		
GAM2030	WBSCR23	3'	GGGAGGCTGAGGCAGGAGGATC 47437	A	
	A		TGATCC CCTGCCTCGGCCTCCC		
			ACTAGG GGACGGAGTCGGAGGG		
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GAM2030	WBSCR23	3'	GGGAGGCTGAGGCAGGTGGATC 47438		
	A		TGATCCACCTGCCTCGGCCTCCC		
			ACTAGGTGGACGGAGTCGGAGGG		
GAM2030	WSB1	3'	GGGTGAGGCGGGCAAATCA 56977	CCA	G
			TGAT CCTGCCTCG CC		
			ACTA GGGCGGAGT GG		
			AAC G		
GAM2030	WSB1	3'	GGGTGAGGCGGGCAAATCA 56993	CCA	G
			TGAT CCTGCCTCG CC		
			ACTA GGGCGGAGT GG		
			AAC G		
GAM2030	ZAK	3'	GGGAGGCCAAGGCAGGAGGATT 56944	A	C
			GATCC CCTGCCT GGCCTCCC		
			TTAGG GGACGGA CCGGAGGG		
			A A		
GAM2030	ZAK	3'	GGGAGGCCAAGGTGGGCGGATC 56945	A TG	C
	A		TGATCC CC CCT GGCCTCCC		
			ACTAGG GG GGA CCGGAGGG		
			C GT A		
GAM2030	ZAK	3'	GGGAGGCTGAGGCAGGAGAATC 56946	CCA	
	A		TGAT CCTGCCTCGGCCTCCC		
			ACTA GGACGGAGTCGGAGGG		
			AGA		
GAM2030	ZFD25	3'	GGGAGGCCAAGGTGGGTGGATC 33113	TG	C
	A		TGATCCACC CCT GGCCTCCC		
			ACTAGGTGG GGA CCGGAGGG		
			GT A		
GAM2030	ZFP106	3'	GGAGGCCGGGCCTGGTGGCTCA 42731	T	T_ T
			TGA CCACC GCC CGGCCTCC		
			ACT GGTGG CGG GCCGGAGG		
			C TC _		
GAM2030	ZFP106	3'	GGAGGCTGAGACAGGAGAATCA 42732	CCA	C
			TGAT CCTG CTCGGCCTCC		

			ACTA GGAC GAGTCGGAGG	
			AGA A	
GAM2030	ZFP106	3'	GGGAGGCCGAGGCGGGTGGATC 42735	
	A		TGATCCACCTGCCTCGGCCTCCC	
			ACTAGGTGGGCGGAGCCGGAGGG	
GAM2030	ZFP106	3'	GGGAGGCTGAGGCAGGCAGATC 42736	CA
	A		TGATC CCTGCCTCGGCCTCCC	
			ACTAG GGACGGAGTCGGAGGG	
			AC	
GAM2030	ZNF197	3'	GAGGCCGAAGCGAGTGGATCA 23756	C C
			TGATCCAC TGC TCGGCCTC	
			ACTAGGTG GCG AGCCGGAG	
			A A	
GAM2030	ZNF297B	5'	GGAGGCTGAGGCTGGTGGATCA 26662	T
			TGATCCACC GCCTCGGCCTCC	
			ACTAGGTGG CGGAGTCGGAGG	
			T	
GAM2030	ZNF297B	5'	GGGAGGCCAAGGCAGGAGAATC 26664	CCA C
	G		TGAT CCTGCCT GGCCTCCC	
			GCTA GGACGGA CCGGAGGG	
			AGA A	
GAM2030	ZNF297B	3'	GGGAGGCCGAGATGGGTGGATC 26665	GC
	A		TGATCCACCT CTCGGCCTCCC	
			ACTAGGTGGG GAGCCGGAGGG	
			TA	
GAM2030	ZNF297B	3'	GGGAGGCCGAGGCAGGAGAATC 26666	CCA G
	A		TGAT CCTGCCTC GCCTCCC	
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			AGA G	
GAM2030	ZNF33A	3'	GGAGGCTGAGGCAGAAGAATCA 92999	CCAC
			TGAT CTGCCTCGGCCTCC	
			ACTA GACGGAGTCGGAGG	
			AGAA	
GAM2030	ZNF33A	3'	GGGAGGCTGAGGCGGGTGGATC 93000	
	A		TGATCCACCTGCCTCGGCCTCCC	
			ACTAGGTGGGCGGAGTCGGAGGG	
GAM2030	ZNF347	3'	GGAGGCTGAGGCAGGAGAATCA 51828	CCA
			TGAT CCTGCCTCGGCCTCC	

		ACTA GGACGGAGTCGGAGG		
		AGA		
GAM2030	ZNF347 3'	GGGAGTCCGAGGCAGGTGGATC 51829	C	
	A	TGATCCACCTGCCTCGG CTCCC		
		ACTAGGTGGACGGAGCC GAGGG		
		T		
GAM2030	LOC112687 3'	GGGAGGCTGAGGGAGGCGGATC 73238	A G	
	A	TGATCC CCT CTCGGCCTCCC		
		ACTAGG GGA GGAGTCGGAGGG		
		C G		
GAM2030	LOC115129 5'	GGAAGGCTGAGGCAGGAGAATC 73622	CCA	—
	AT	ATGAT CCTGCCTCGGCCT CC		
		TACTA GGACGGAGTCGGA GG		
		AGA A		
GAM2030	LOC115129 3'	GGCTGAGGCAGGAGAATCA 73624	CCA	
		TGAT CCTGCCTCGGCC		
		ACTA GGACGGAGTCGG		
		AGA		
GAM2030	LOC115129 5'	GGGAGGCTGAGGCAGGTGGATC 73625		
	A	TGATCCACCTGCCTCGGCCTCCC		
		ACTAGGTGGACGGAGTCGGAGGG		
GAM2030	LOC115196 3'	GGAGGCCGAGGCGGGTGGATCA 73659		
	T	ATGATCCACCTGCCTCGGCCTCC		
		TACTAGGTGGGCGGAGCCGGAGG		
GAM2030	LOC115861 3'	GGGAGGCCAAGGCGGGAGGATC 57417	A C	
	G	TGATCC CCTGCCT GGCCTCCC		
		GCTAGG GGGCGGA CCGAGGG		
		A A		
GAM2030	LOC116143 3'	GGGAGGCCGAGGCGGGTGGATC 74188		
	A	TGATCCACCTGCCTCGGCCTCCC		
		ACTAGGTGGGCGGAGCCGGAGGG		
GAM2030	LOC116143 3'	GGGAGGCTGAGGCAGGAGAATC 74189	CCA	
	A	TGAT CCTGCCTCGGCCTCCC		
		ACTA GGACGGAGTCGGAGGG		
		AGA		
GAM2030	LOC116143 3'	GGGAGGCTGAGGCGGGTGAATC 74190	C	
	A	TGAT CACCTGCCTCGGCCTCCC		

		ACTA GTGGGCGGAGTCGGAGGG		
		A		
GAM2030	LOC116228 3'	GGAGGCTGAGGCAGGAGAATCA 74229	CCA	
		TGAT CCTGCCTCGGCCTCC		
		ACTA GGACGGAGTCGGAGG		
		AGA		
GAM2030	LOC116228 3'	GGGAGGCCGAGGCAGTTGGATC 74230	C	
	A	TGATCCA CTGCCTCGGCCTCCC		
		ACTAGGT GACGGAGCCGGAGGG		
		T		
GAM2030	LOC116236 3'	GGGAGGCCGAGGTGGGTGGATC 74246	TG	
	A	TGATCCACC CCTCGGCCTCCC		
		ACTAGGTGG GGAGCCGGAGGG		
		GT		
GAM2030	LOC116349 3'	GGGAGGCCGAGGCAGGTAGATCA 74279	C	G
	T	ATGATC ACCTGCCTCG CCTCCC		
		TACTAG TGGACGGAGC GGAGGG		
		A _		
GAM2030	LOC118471 3'	GAGGCCGAGGCAGGCGGATCA 74353	A	
		TGATCC CCTGCCTCGGCCTC		
		ACTAGG GGACGGAGCCGGAG		
		C		
GAM2030	LOC119504 5'	GGGAGGCCAAGGCAGGTGGATC 74447	C	
	A	TGATCCACCTGCCT GGCCTCCC		
		ACTAGGTGGACGGA CCGGAGGG		
		A		
GAM2030	LOC121457 3'	GGGAGGCCGAGGTGGGCAGATC 74511	CA TG	
	A	TGATC CC CCTCGGCCTCCC		
		ACTAG GG GGAGCCGGAGGG		
		AC GT		
GAM2030	LOC122704 3'	GGGAGGCTGAGGCGGGCAGATC 74609	CA	
	A	TGATC CCTGCCTCGGCCTCCC		
		ACTAG GGGCGGAGTCGGAGGG		
		AC		
GAM2030	LOC124602 3'	GGGAAGTTGAGGTAGGCAGATC 74787	CA	C
	A	TGATC CCTGCCTCGGC TCCC		
		ACTAG GGATGGAGTTG AGGG		
		AC A		
GAM2030	LOC126282 3'	GAGGCTGAGGCGGGCGGATCA 74960	A	
		TGATCC CCTGCCTCGGCCTC		

		ACTAGG GGGCGGAGTCGGAG		
		C		
GAM2030	LOC126282 3'	GGGAGGCCGAGGCAGGAAGATT 74963	CA	
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		TTAG GGACGGAGCCGGAGGG		
		AA		
GAM2030	LOC126282 3'	GGGAGGCTGAGGCGGGCAGATC 74964	CA	
	A	TGATC CCTGCCTCGGCCTCCC		
		ACTAG GGGCGGAGTCGGAGGG		
		AC		
GAM2030	LOC126669 3'	GGGAGGCTGAGGCAGGCAGATC 75941	CA	
	A	TGATC CCTGCCTCGGCCTCCC		
		ACTAG GGACGGAGTCGGAGGG		
		AC		
GAM2030	LOC126669 3'	GGGAGGCTGAGGTAGGTGGATC 75942		
	A	TGATCCACCTGCCTCGGCCTCCC		
		ACTAGGTGGATGGAGTCGGAGGG		
GAM2030	LOC127262 3'	GGGAGGCTCAGGCAGACAAATC 76602	CCAC	C
	G	TGAT CTGCCT GGCCTCCC		
		GCTA GACGGA TCGGAGGG		
		AACA C		
GAM2030	LOC127294 3'	GGGAGGCCAAGGCGGGCAGATC 75146	CA	C
	A	TGATC CCTGCCT GGCCTCCC		
		ACTAG GGGCGGA CCGGAGGG		
		AC A		
GAM2030	LOC127428 3'	GGGAGGTCGAGGCAGGCAGATC 75162	CA	
	A	TGATC CCTGCCTCGGCCTCCC		
		ACTAG GGACGGAGCTGGAGGG		
		AC		
GAM2030	LOC130026 3'	GGGAGGCTGAGGCAGGCGGATC 57439	A	
	A	TGATCC CCTGCCTCGGCCTCCC		
		ACTAGG GGACGGAGTCGGAGGG		
		C		
GAM2030	LOC130535 3'	AGGCCGAGGCAGGTGGATCA 76642		
		TGATCCACCTGCCTCGGCCT		
		ACTAGGTGGACGGAGCCGGA		
GAM2030	LOC130535 3'	GGGAGGCCGAGGCAGGTGGATC 76653		
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GAM2030	LOC130589	3'	GGAAGGCCGAGGCAGGCGGATC	57934	A	—
	A		TGATCC CCTGCCTCGGCCT CC			
			ACTAGG GGACGGAGCCGGA GG			
			C A			
GAM2030	LOC131965	3'	GGGAGGCCGAGGTTGGGGGATC	75525	A	T
	AT		ATGATCC CC GCCTCGGCCTCCC			
			TACTAGG GG TGGAGCCGGAGGG			
			G T			
GAM2030	LOC132625	3'	GGGAGGCCAAAGCAGGAGGAT	76442	A	CTC
			ATCC CCTGC GGCCTCCC			
			TAGG GGACG CCGGAGGG			
			A AAA			
GAM2030	LOC134147	3'	GGGAGGCCAAAGTGGGTGGATC	57963	TG	CTC
	A		TGATCCACC C GGCCTCCC			
			ACTAGGTGG G CCGGAGGG			
			GT AAA			
GAM2030	LOC134147	3'	GGGAGGCCGAGGTGGGTGGATC	57964	TG	
	A		TGATCCACC CCTCGGCCTCCC			
			ACTAGGTGG GGAGCCGGAGGG			
			GT			
GAM2030	LOC135818	3'	GGAGGCTGAGGCAAGAGGATCA	75748	ACC	
			TGATCC TGCCTCGGCCTCC			
			ACTAGG ACGGAGTCGGAGG			
			AGA			
GAM2030	LOC137362	3'	GAGGCCGAGGCGGGTGGGTCA	75784		
			TGATCCACCTGCCTCGGCCTC			
			ACTGGGTGGGCGGAGCCGGAG			
GAM2030	LOC138241	3'	GGGAGGCCAAGGAGGGTGGATC	75834	G	C
	A		TGATCCACCT CCT GGCCTCCC			
			ACTAGGTGGG GGA CCGGAGGG			
			A A			
GAM2030	LOC138428	3'	GGGAGACTGAGGCAGGAGAATC	75860	CCA	C
	A		TGAT CCTGCCTCGG CTCCC			
			ACTA GGACGGAGTC GAGGG			
			AGA A			
GAM2030	LOC139422	3'	GGGAGGCCGAGGCAGGCGGATC	76353	A	
	AT		ATGATCC CCTGCCTCGGCCTCCC			

		TACTAGG GGACGGAGCCGGAGGG	
		C	
GAM2030	LOC142779 3'	GGGAGGCCGAGGTGGGCAGATC 76908	CA TG
	A	TGATC CC CCTCGGCCTCCC	
		ACTAG GG GGAGCCGGAGGG	
		AC GT	
GAM2030	LOC143196 3'	GGGAGGCCGAGGCGGGTGGATC 83804	
	A	TGATCCACCTGCCTCGGCCTCCC	
		ACTAGGTGGGCGGAGCCGGAGGG	
GAM2030	LOC143310 3'	GGGAGGCCGAGGTGGGCCGATC 77050	CA TG
	A	TGATC CC CCTCGGCCTCCC	
		ACTAG GG GGAGCCGGAGGG	
		CC GT	
GAM2030	LOC143465 3'	GGGAGGCTGAAGCAGGCAGATC 83876	CA C
	A	TGATC CCTGC TCGGCCTCCC	
		ACTAG GGACG AGTCGGAGGG	
		AC A	
GAM2030	LOC143888 3'	GGGAGGCTGAGGCAGGAGAATC 77173	CCA
	A	TGAT CCTGCCTCGGCCTCCC	
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		AGA	
GAM2030	LOC144289 3'	GGGAGGCTGAGGCAGGAGAATC 83959	CCA
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		TACTA GGACGGAGTCGGAGGG	
		AGA	
GAM2030	LOC144465 3'	GGAGGCTGAGGCAGGAGAATCA 77348	CCA
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		ACTA GGACGGAGTCGGAGG	
		AGA	
GAM2030	LOC144465 3'	GGGAGGTTGAGGCAGGAGAATC 77349	CCA
	A	TGAT CCTGCCTCGGCCTCCC	
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		AGA	
GAM2030	LOC144481 3'	GGGAGGCTGAGACAGGAGAATC 84021	CCA C
	A	TGAT CCTG CTCGGCCTCCC	
		ACTA GGAC GAGTCGGAGGG	
		AGA A	
GAM2030	LOC144481 3'	GGGAGGCTGAGGCAAGTGAAGC 84022	ATC C
	A	TG CAC TGCCTCGGCCTCCC	

		AC GTG ACGGAGTCGGAGGG		
		GAA A		
GAM2030	LOC144486 3'	GGGAGGCCAAGGCAGGTGGATC 84007	C	
	A	TGATCCACCTGCCT GGCCTCCC		
		ACTAGGTGGACGGA CCGGAGGG		
		A		
GAM2030	LOC144563 3'	GGGAGGCCGAGGCAGGCGGATC 77403	A	
	A	TGATCC CCTGCCTCGGCCTCCC		
		ACTAGG GGACGGAGCCGGAGGG		
		C		
GAM2030	LOC144817 3'	GGGAGGCTGAGGCGGGCGGATC 77520	A	
	A	TGATCC CCTGCCTCGGCCTCCC		
		ACTAGG GGGCGGAGTCGGAGGG		
		C		
GAM2030	LOC144845 3'	GGGAGGCCAAGGCGGGCAGATC 57461	CA	C
	A	TGATC CCTGCCT GGCCTCCC		
		ACTAG GGGCGGA CCGGAGGG		
		AC A		
GAM2030	LOC144845 3'	GGGAGGCTGAGGCAGGAAAATC 57462	CCA	
	A	TGAT CCTGCCTCGGCCTCCC		
		ACTA GGACGGAGTCGGAGGG		
		AAA		
GAM2030	LOC145082 5'	GGGAGGCTGAGGCAGGAGAATC 84192	CCA	
	AT	ATGAT CCTGCCTCGGCCTCCC		
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		AGA		
GAM2030	LOC145216 3'	GGAAGGCTGAGGCGGGCGGATC 84224	A	—
	A	TGATCC CCTGCCTCGGCCT CC		
		ACTAGG GGGCGGAGTCGGA GG		
		C A		
GAM2030	LOC145216 3'	GGAGGCTGAGGCAGGAGAATCA 84225	CCA	
		TGAT CCTGCCTCGGCCTCC		
		ACTA GGACGGAGTCGGAGG		
		AGA		
GAM2030	LOC145231 3'	GGCTGAGGCAGGCGAATTA 84252	CCA	
		TGAT CCTGCCTCGGCC		
		ATTA GGACGGAGTCGG		
		AGC		
GAM2030	LOC145231 3'	GGGAGGCTGAGGCGGGTGAATC 84255	C	
	AT	ATGAT CACCTGCCTCGGCCTCCC		

		TACTA GTGGGCGGAGTCGGAGGG		
		A		
GAM2030	LOC145299 3'	GGGAGGCCGAGGCGGGTGGATC 84278		
	AT	ATGATCCACCTGCCTCGGCCTCCC		
		TACTAGGTGGGCGGAGCCGGAGGG		
GAM2030	LOC145333 3'	GGGAGGCCGAGGCGGGCGGATC 84301	A	
	A	TGATCC CCTGCCTCGGCCTCCC		
		ACTAGG GGGCGGAGCCGGAGGG		
		C		
GAM2030	LOC145387 3'	GGGAGGCCAAGGC AAAAGGATT 84340	ACC	C
		GATCC TGCCT GGCCTCCC		
		TTAGG ACGGA CCGGAGGG		
		AAA A		
GAM2030	LOC145387 3'	GGGAGGCTGAGGCGGGCAGATC 84341	CA	
	A	TGATC CCTGCCTCGGCCTCCC		
		ACTAG GGGCGGAGTCGGAGGG		
		AC		
GAM2030	LOC145438 3'	GGGAGGCCGAGGCGGGCGGATC 84314	A	
	A	TGATCC CCTGCCTCGGCCTCCC		
		ACTAGG GGGCGGAGCCGGAGGG		
		C		
GAM2030	LOC145438 3'	GGGAGGCCGAGGTGACAGGATC 84315	ACC	
	GT	ATGATCC TGCCTCGGCCTCCC		
		TGCTAGG GTGGAGCCGGAGGG		
		ACA		
GAM2030	LOC145453 3'	GGGAGGCCAAGGCAGGTGGATC 77667		C
	A	TGATCCACCTGCCT GGCCTCCC		
		ACTAGGTGGACGGA CCGGAGGG		
		A		
GAM2030	LOC145482 3'	GGGAGGCAGAGGCGGGCAGATC 77746	CA	G
	A	TGATC CCTGCCTC GCCTCCC		
		ACTAG GGGCGGAG CGGAGGG		
		AC A		
GAM2030	LOC145483 3'	GGGAAGCTGAGGCAGGAGAATC 77756	CCA	C
	A	TGAT CCTGCCTCGGC TCCC		
		ACTA GGACGGAGTCG AGGG		
		AGA A		
GAM2030	LOC145483 3'	GGGAGGCTGAGGCAGGCAGATC 77757	CA	
	AT	ATGATC CCTGCCTCGGCCTCCC		

		TACTAG GGACGGAGTCGGAGGG		
		AC		
GAM2030	LOC145624 5'	GGAGGATGCATGTGGATCAT 84402	C	CTCGG
		ATGATCCAC TGC CCTCC		
		TACTAGGTG ACG GGAGG		
		T TA__		
GAM2030	LOC145663 3'	GGAAGGCCGAGGCAGGCGGATT 84427	A	_
		GATCC CCTGCCTCGGCCT CC		
		TTAGG GGACGGAGCCGGA GG		
		C A		
GAM2030	LOC145663 3'	GGGAGGCCGAGGCAGGCGGATC 84428	A	
	A	TGATCC CCTGCCTCGGCCTCCC		
		ACTAGG GGGCGGAGCCGGAGGG		
		C		
GAM2030	LOC145757 3'	GGGAGGCCAAGGCAGGTGGATC 77939	C	
	A	TGATCCACCTGCCT GGCCTCCC		
		ACTAGGTGGACGGA CCGGAGGG		
		A		
GAM2030	LOC145820 3'	GGGAGGCCTAGGCGGGCGGATC 77978	A	C
	A	TGATCC CCTGCCT GGCCTCCC		
		ACTAGG GGGCGGA CCGGAGGG		
		C T		
GAM2030	LOC145988 5'	GGGAGACCGAGGCAGGTGGATC 78069	C	
	A	TGATCCACCTGCCTCGG CTCCC		
		ACTAGGTGGACGGAGCC GAGGG		
		A		
GAM2030	LOC146159 3'	GGGAGGCTGAGGCAGGAGGATC 78179	A	
	A	TGATCC CCTGCCTCGGCCTCCC		
		ACTAGG GGACGGAGTCGGAGGG		
		A		
GAM2030	LOC146229 3'	GGGAGGCTGAGGCGGGTGGATC 78292		
	A	TGATCCACCTGCCTCGGCCTCCC		
		ACTAGGTGGGCGGAGTCGGAGGG		
GAM2030	LOC146332 3'	GGGAGGCCCAGGCAAGCAGATC 78359	CACC	C
	AT	ATGATC TGCCT GGCCTCCC		
		TACTAG ACGGA CCGGAGGG		
		ACGA C		
GAM2030	LOC146336 5'	GGGAGGCCGAGGCGGGTGGATC 78374		
	A	TGATCCACCTGCCTCGGCCTCCC		

ACTAGGTGGGCGGAGCCGGAGGG

GAM2030 LOC146452 3' GGAGGCCGAGGCAGAAAAATCA 78473 CCAC
TGAT CTGCCTCGGCCTCC
|||| |||||||||
ACTA GACGGAGCCGGAGG
AAAA

GAM2030 LOC146512 3' GGGTGAGGCAGAGGATCA 78501 AC G
TGATCC CTGCCTCG CC
|||| |||||| ||
ACTAGG GACGGAGT GG
A_ G

GAM2030 LOC146667 3' GGGAGGCCGAGGCGGTTGGATC 84714 C
A TGATCCA CTGCCTCGGCCTCCC
|||| |||||||||
ACTAGGT GGCGGAGCCGGAGGG
T

GAM2030 LOC146669 3' GGGAGGCCTCGAGGCAGGTGGA 78663 —
TCA TGATCCACCTGCCTC GGCCTCCC
|||| |||||||
ACTAGGTGGACGGAG CCGGAGGG
CT

GAM2030 LOC146713 3' AGGCCGAGGCAGGAGAATCA 84721 CCA
TGAT CCTGCCTCGGCCT
|||| |||||||||
ACTA GGACGGAGCCGGA
AGA

GAM2030 LOC146713 3' GGGAGGCCAAGGCGGGCGTATC 84735 CCA C
A TGAT CCTGCCT GGCCTCCC
|||| ||||| |||||
ACTA GGCGGA CCGGAGGG
TGC A

GAM2030 LOC146713 3' GGGAGGCCAAGGTGGGCAGATC 84736 CA TG C
A TGATC CC CCT GGCCTCCC
|||| || ||| |||||
ACTAG GG GGA CCGGAGGG
AC GT A

GAM2030 LOC146723 3' GGGAGGCCAAGGCGGACAGACC 78684 A CAC C
A TG TC CTGCCT GGCCTCCC
|| || ||||| |||||
AC AG GGCGGA CCGGAGGG
C ACA A

GAM2030 LOC146728 5' GGGAGGCCGAGGCAGGTACATC 84769 CC
A TGAT ACCTGCCTCGGCCTCCC
|||| |||||||||
ACTA TGGACGGAGCCGGAGGG
CA

GAM2030 LOC146728 5' GGGAGGCTGAGGCAAGAGAATC 84770 CCACC
AT ATGAT TGCCTCGGCCTCCC
|||| |||||||||

		TACTA ACGGAGTCGGAGGG AGAGA	
GAM2030	LOC146756 3'	GGGAGGCCGAGGCGGGCGGATC 84809 A TGATCC CCTGCCTCGGCCTCCC ACTAGG GGGCGGAGCCGGAGGG C	A
GAM2030	LOC146780 3'	GGGAGGCCAAGGCGGGTGGATC 84821 A TGATCCACCTGCCT GGCCTCCC ACTAGGTGGGCGGA CCGGAGGG A	C
GAM2030	LOC146901 3'	AGGCCGAGGTGGGAGAATCA 84889 TGAT CC CCTCGGCCT ACTA GG GGAGCCGGA AGA GT	CCA TG
GAM2030	LOC146901 3'	GGAAGGCCGAGGCAGGTGGATC 84906 A TGATCCACCTGCCTCGGCCT CC ACTAGGTGGACGGAGCCGGA GG A	—
GAM2030	LOC146923 3'	GGGAGGCCGAGGCGGGCGGATC 78803 A TGATCC CCTGCCTCGGCCTCCC ACTAGG GGGCGGAGCCGGAGGG C	A
GAM2030	LOC146975 5'	GGGAGGCCGAGGCAGGTGGATC 78829 A TGATCCACCTGCCTCGGCCTCCC ACTAGGTGGACGGAGCCGGAGGG	
GAM2030	LOC147057 3'	GGGAGGCCGAGGCAGGCGGATC 84989 A TGATCC CCTGCCTCGGCCTCCC ACTAGG GGACGGAGCCGGAGGG C	A
GAM2030	LOC147071 3'	GGGAGGCCGAGGCGGGCGGATC 73369 AT ATGATCC CCTGCCTCGGCCTCCC TACTAGG GGGCGGAGCCGGAGGG C	A
GAM2030	LOC147180 5'	GGGAGGCCGAGGCGGGCGGATC 85104 A TGATCC CCTGCCTCGGCCTCCC ACTAGG GGGCGGAGCCGGAGGG C	A
GAM2030	LOC147599 3'	GGGAGGCCGAGGCAGGTGGATC 85165 A TGATCCACCTGCCTCGGCCTCCC 	

ACTAGGTGGACGGAGCCGGAGGG

GAM2030	LOC147649 3'	GGGAGGCCGAGGGGGGGGGATC 79062	A	G
	A	TGATCC CCT CTCGGCCTCCC		
		ACTAGG GGG GGAGCCGGAGGG		
		G G		
GAM2030	LOC147660 3'	GGGAGGCCAAGGCACATAGGTC 79030	CACC	C
	A	TGATC TGCCT GGCCTCCC		
		ACTGG ACGGA CCGGAGGG		
		ATAC A		
GAM2030	LOC147660 3'	GGGAGGCCAAGGCAGGCAGAT 79031	CA	C
		ATC CTGCCT GGCCTCCC		
		TAG GGACGGA CCGGAGGG		
		AC A		
GAM2030	LOC147664 3'	GGGAGGCTGAGGCAGGCAGATC 79048	CA	
	A	TGATC CCTGCCTCGGCCTCCC		
		ACTAG GGACGGAGTCGGAGGG		
		AC		
GAM2030	LOC147700 3'	GGGAGGCCGAGGCGAGCAGATC 59885	CACC	
	A	TGATC TGCCTCGGCCTCCC		
		ACTAG GCGGAGCCGGAGGG		
		ACGA		
GAM2030	LOC147727 5'	GGGAGGCCGAGGCGGGCGGATC 79138	A	
	A	TGATCC CTGCCTCGGCCTCCC		
		ACTAGG GGGCGGAGCCGGAGGG		
		C		
GAM2030	LOC147990 3'	GGGAGGTCGAGGCGGGCAGATC 85226	CA	
	A	TGATC CTGCCTCGGCCTCCC		
		ACTAG GGGCGGAGCTGGAGGG		
		AC		
GAM2030	LOC148198 3'	GGGAGGCTGAGGCAGGAGAATC 71226	CCA	
	A	TGAT CTGCCTCGGCCTCCC		
		ACTA GGACGGAGTCGGAGGG		
		AGA		
GAM2030	LOC148206 3'	GGGAGGCAGAGGCAGGAGAATC 79465	CCA	G
	AT	ATGAT CTGCCTC GCCTCCC		
		TACTA GGACGGAG CGGAGGG		
		AGA A		
GAM2030	LOC148534 3'	AGGCCGGGCACGGTGGCTCAT 79628	T	_ T
		ATGA CCACC TGCC CGGCCT		

		TACT GGTGG ACGG GCCGGA	
		C C _	
GAM2030	LOC148534 3'	GGGAGGCCAAGGTGGGTCGATC 79639	C TG C
	A	TGATC ACC CCT GGCCTCCC	
		ACTAG TGG GGA CCGGAGGG	
		C GT A	
GAM2030	LOC148734 3'	GGGAGGCCGAGGTGGGCGGATC 79713	A TG
	A	TGATCC CC CCTCGGCCTCCC	
		ACTAGG GG GGAGCCGGAGGG	
		C GT	
GAM2030	LOC148756 3'	AGGCCGAGAAGAGATTA 85374	CAC GC
		TGATC CT CTCGGCCT	
		ATTAG GA GAGCCGGA	
		A_ A_	
GAM2030	LOC148758 5'	GGGAGGCCGAGGCGCCTGGATC 79725	CC
	A	TGATCCA TGCCTCGGCCTCCC	
		ACTAGGT GCGGAGCCGGAGGG	
		CC	
GAM2030	LOC148809 5'	GGGAGGCTGAGGCGGGTGGATC 79757	
	A	TGATCCACCTGCCTCGGCCTCCC	
		ACTAGGTGGGCGGAGTCGGAGGG	
GAM2030	LOC148823 3'	GGGAAGCCAAGACAGGTGGATC 59895	C C C
		GATCCACCTG CT GGC TCCC	
		CTAGGTGGAC GA CCG AGGG	
		A A A	
GAM2030	LOC148918 5'	GGGAGGCCAAGGCAGGCAGATC 79831	CA C
	A	TGATC CCTGCCT GGCCTCCC	
		ACTAG GGACGGA CCGGAGGG	
		AC A	
GAM2030	LOC148936 3'	GGAAGGCCGAGGCAGGAGGATC 85457	A _
	A	TGATCC CCTGCCTCGGCCT CC	
		ACTAGG GGACGGAGCCGGA GG	
		A A	
GAM2030	LOC148938 3'	GGGAGGCCGAGGCAGGAGGATC 85439	A
	A	TGATCC CCTGCCTCGGCCTCCC	
		ACTAGG GGACGGAGCCGGAGGG	
		A	
GAM2030	LOC149073 3'	GGGAGGCCAAGGCAGATGGAAC 85486	A C C
	A	TG TCCA CTGCCT GGCCTCCC	

		AC AGGT GACGGA CCGGAGGG		
		A A A		
GAM2030	LOC149113 5'	GGAAGGCTGAGGCACATGGACC 79915	A	CC
	A	TG TCCA TGCCTCGGCCT CC		
		AC AGGT ACGGAGTCGGA GG		
		C AC A		
GAM2030	LOC149113 3'	GGGAGGCCGAGGAGGGTGGATC 79916		G
	A	TGATCCACCT CCTCGGCCTCCC		
		ACTAGGTGGG GGAGCCGGAGGG		
		A		
GAM2030	LOC149175 3'	GGGAGGCCGAGATGGGCGGATC 79955	A	GC
	A	TGATCC CCT CTCGGCCTCCC		
		ACTAGG GGG GAGCCGGAGGG		
		C TA		
GAM2030	LOC149194 5'	GGGAGGCCAAGGCGGGTGGATC 79987		C
	A	TGATCCACCTGCCT GGCCTCCC		
		ACTAGGTGGGCGGA CCGGAGGG		
		A		
GAM2030	LOC149271 3'	GGGAGGCTGAGGCAGGAGAATC 80009		CCA
	A	TGAT CCTGCCTCGGCCTCCC		
		ACTA GGACGGAGTCGGAGGG		
		AGA		
GAM2030	LOC149319 3'	GGGAGGCCGAGGTGGGTGGATC 80074		TG
	A	TGATCCACC CCTCGGCCTCCC		
		ACTAGGTGG GGAGCCGGAGGG		
		GT		
GAM2030	LOC149460 3'	GGGAGGCCGAGGTGGGTAGAT 85612	C	TG
		ATC ACC CCTCGGCCTCCC		
		TAG TGG GGAGCCGGAGGG		
		A GT		
GAM2030	LOC149464 3'	GGGAGGCCAAGGTGGGTGGATC 85595		TG C
	A	TGATCCACC CCT GGCCTCCC		
		ACTAGGTGG GGA CCGGAGGG		
		GT A		
GAM2030	LOC149464 3'	GGGAGGCTGAGGCAGGAGAATC 85596		CCA
	A	TGAT CCTGCCTCGGCCTCCC		
		ACTA GGACGGAGTCGGAGGG		
		AGA		
GAM2030	LOC149628 3'	GGGAGGCCGAGGCAGGTGGATT 80280		
		GATCCACCTGCCTCGGCCTCCC		

TTAGGTGGACGGAGCCGGAGGG

GAM2030 LOC149710 3' GGGAGGCCGAGGTGGGTGGATC 80330 TG
A TGATCCACC CCTCGGCCTCCC

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ACTAGGTGG GGAGCCGGAGGG
GT

GAM2030 LOC149711 5' GGGAGGCTGAGGCAAGAGGATC 85854 ACC
A TGATCC TGCCTCGGCCTCCC

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ACTAGG ACGGAGTCGGAGGG
AGA

GAM2030 LOC150225 3' GAGGGTGAGCAGGTGGCCCA 86194 AT C G
TG CCACCTGC TCG CCTC

|| ||||||| ||| ||||
AC GGTGGACG AGT GGAG
CC _ G

GAM2030 LOC150343 3' GGGAGGCCGAGGCAGGTGGATC 80494
A TGATCCACCTGCCTCGGCCTCCC

|||||||||||||||||
ACTAGGTGGACGGAGCCGGAGGG

GAM2030 LOC150358 3' GGGAGGCCGAGGTGTGCAGATC 86099 _ CT
A TGATC CAC GCCTCGGCCTCCC

||||| ||| |||||||||
ACTAG GTG TGGAGCCGGAGGG
AC _

GAM2030 LOC150358 3' GGGAGGCCGAGTTGGGCGGATC 86100 A GC
A TGATCC CCT CTCGGCCTCCC

||||| ||| |||||||||
ACTAGG GGG GAGCCGGAGGG
C TT

GAM2030 LOC150372 3' GGGAGGCCGAGGCGGGTGGATC 80619
A TGATCCACCTGCCTCGGCCTCCC

|||||||||||||||||
ACTAGGTGGGCGGAGCCGGAGGG

GAM2030 LOC150465 3' GGGAGGCCAAGACAGGTAGACT 80683 GA C C C
GT AT TC ACCTG CT GGCCTCCC

|| || ||||| || |||||||
TG AG TGGAC GA CCGGAGGG
TC A A A

GAM2030 LOC150481 3' GGGAGGCCAAGGTGGGTGGATC 80711 TG C
A TGATCCACC CCT GGCCTCCC

||||||| ||| |||||||
ACTAGGTGG GGA CCGGAGGG
GT A

GAM2030 LOC150577 3' GGGAGGCCAAGGCAAGAGGATC 86257 ACC C
A TGATCC TGCCT GGCCTCCC

||||| ||||| |||||||

		ACTAGG ACGGA CCGGAGGG		
		AGA A		
GAM2030	LOC150622 3'	GGGAGGCCGAGGCAGGCGGATC 80766	A	
	A	TGATCC CCTGCCTCGGCCTCCC		
		ACTAGG GGACGGAGCCGGAGGG		
		C		
GAM2030	LOC150630 5'	GGGAGGCCAAGGCAGGAGGA 86304	A	C
		TCC CCTGCCT GGCCTCCC		
		AGG GGACGGA CCGGAGGG		
		A A		
GAM2030	LOC150630 3'	GGGAGGCCGAGGCAGGCAGATC 86305	CA	
	A	TGATC CCTGCCTCGGCCTCCC		
		ACTAG GGACGGAGCCGGAGGG		
		AC		
GAM2030	LOC150889 3'	GGGAGGCTGAGGCCGGTGGATC 80816	T	
	A	TGATCCACC GCCTCGGCCTCCC		
		ACTAGGTGG CGGAGTCGGAGGG		
		C		
GAM2030	LOC150935 3'	GGGAGGCCGAGGTGGGCGGATC 80835	A	TG
	A	TGATCC CC CCTCGGCCTCCC		
		ACTAGG GG GGAGCCGGAGGG		
		C GT		
GAM2030	LOC150998 3'	GGGAGGCCGAGAAGGGAGGATC 86362	A	GC
	A	TGATCC CCT CTCGGCCTCCC		
		ACTAGG GGG GAGCCGGAGGG		
		A AA		
GAM2030	LOC151056 5'	GGAGGCCGAGCTGAGGATC 80925	ACCT	C
		GATCC GC TCGGCCTCC		
		CTAGG CG AGCCGGAGG		
		AGT_ _		
GAM2030	LOC151068 3'	AGGCTGAGGCAGGCAGTTCA 86405	TCCA	
		TGA CCTGCCTCGGCCT		
		ACT GGACGGAGTCGGA		
		TGAC		
GAM2030	LOC151196 3'	GGAGGTTGAGGCAGGAGAATCA 86454	CCA	
		TGAT CCTGCCTCGGCCTCC		
		ACTA GGACGGAGTTGGAGG		
		AGA		
GAM2030	LOC151196 3'	GGGAGGCCGAGGCAGGTGGATC 86455		
	A	TGATCCACCTGCCTCGGCCTCCC		

ACTAGGTGGACGGAGCCGGAGGG

GAM2030	LOC151248	3'	GGGAGGCCAAGGCAGGCAGACC	80996	A CA	C
	A		TG TC CCTGCCT GGCCTCCC			
			AC AG GGACGGA CCGGAGGG			
			C AC A			
GAM2030	LOC151248	3'	GGGAGGCTGAGGCGGGTGGATC	80997		
	A		TGATCCACCTGCCTCGGCCTCCC			
			ACTAGGTGGGCGGAGTCGGAGGG			
GAM2030	LOC151429	3'	GGGAGGCCCAGGCCGGCGGATC	86540	A T	C
	A		TGATCC CC GCCT GGCCTCCC			
			ACTAGG GG CGGA CCGGAGGG			
			C C C			
GAM2030	LOC151429	3'	GGGAGGCCGAGGCGGGCAGAT	86542	CA	
			ATC CCTGCCTCGGCCTCCC			
			TAG GGGCGGAGCCGGAGGG			
			AC			
GAM2030	LOC151556	3'	GGGAGGCCGAGTCAGGTGGATC	81082		C
	A		TGATCCACCTG CTCGGCCTCCC			
			ACTAGGTGGAC GAGCCGGAGGG			
			T			
GAM2030	LOC151614	3'	GGGAGGCCAAGGCTGGTGGATC	81123	T	C
	A		TGATCCACC GCCT GGCCTCCC			
			ACTAGGTGG CGGA CCGGAGGG			
			T A			
GAM2030	LOC151632	3'	GGGAGGCCGGGGCAGGAGGATC	86648	A	
	A		TGATCC CCTGCCTCGGCCTCCC			
			ACTAGG GGACGGGGCCGGAGGG			
			A			
GAM2030	LOC151632	3'	GGGAGGCTGAGGCAGGAGAATC	86649	CCA	
	A		TGAT CCTGCCTCGGCCTCCC			
			ACTA GGACGGAGTCGGAGGG			
			AGA			
GAM2030	LOC151904	3'	GGGAGGCTGAGGCGGGTGGATC	81208		
	A		TGATCCACCTGCCTCGGCCTCCC			
			ACTAGGTGGGCGGAGTCGGAGGG			
GAM2030	LOC152271	3'	GGGAGGCCGAGGCAGGCAGATC	81363	CA	
	A		TGATC CCTGCCTCGGCCTCCC			

		ACTAG GGACGGAGCCGGAGGG		
		AC		
GAM2030	LOC152271 3'	GGGAGGCTGAGGCAGGAGAATC 81364	CCA	
	A	TGAT CCTGCCTCGGCCTCCC		
		ACTA GGACGGAGTCGGAGGG		
		AGA		
GAM2030	LOC152283 3'	GGGAAGCTGAGGCGAGCAGATC 86874	CACC	C
	A	TGATC TGCCTCGGC TCCC		
		ACTAG GCGGAGTCG AGGG		
		ACGA A		
GAM2030	LOC152313 3'	GGGAGGCTGAGGCGGGCAGATC 86852	CA	
	A	TGATC CCTGCCTCGGCCTCCC		
		ACTAG GGGCGGAGTCGGAGGG		
		AC		
GAM2030	LOC152426 3'	GGGAGGCCAAGGCAGGCGGATC 86900	A	C
	A	TGATCC CCTGCCT GGCCTCCC		
		ACTAGG GGACGGA CCGGAGGG		
		C A		
GAM2030	LOC152445 3'	GGAAGGCCGAGGTGGGTGGAT 86953	TG	_
		ATCCACC CCTCGGCCT CC		
		TAGGTGG GGAGCCGGA GG		
		GT A		
GAM2030	LOC152445 3'	GGGAGGCCAAGGCAGGCGGATC 86955	A	C
	A	TGATCC CCTGCCT GGCCTCCC		
		ACTAGG GGACGGA CCGGAGGG		
		C A		
GAM2030	LOC152453 3'	GGGAGGCCGAGGCGGGAGGATC 81477	A	
	A	TGATCC CCTGCCTCGGCCTCCC		
		ACTAGG GGGCGGAGCCGGAGGG		
		A		
GAM2030	LOC152698 5'	GAGAAGCTCAGAAGATGGATCA 61059	C GC C	_
	T	ATGATCCA CT CT GGC CTC		
		TACTAGGT GA GA TCG GAG		
		A A_ C AA		
GAM2030	LOC152804 3'	AGGCTGAGGCAGGAGAATCA 87068	CCA	
		TGAT CCTGCCTCGGCCT		
		ACTA GGACGGAGTCGGA		
		AGA		
GAM2030	LOC152804 3'	GGGAGGCCAACGTGGATGGATC 87086	C TG CTC	
	A	TGATCCA C C GGCCTCCC		

		ACTAGGT G G CCGGAGGG		
		A GT CAA		
GAM2030	LOC152860 3'	GGGAGGCAGAGGCGGGCGGATC 81581	A	G
	A	TGATCC CCTGCCTC GCCTCCC		
		ACTAGG GGGCGGAG CGGAGGG		
		C A		
GAM2030	LOC152897 3'	GGGAGGCCAAGGCTGGCAGATC 81609	CA T	C
	A	TGATC CC GCCT GGCCTCCC		
		ACTAG GG CGGA CCGGAGGG		
		AC T A		
GAM2030	LOC152926 3'	GGGAGGCCAAGGTGGGTAGATC 81632	C TG	C
	AT	ATGATC ACC CCT GGCCTCCC		
		TACTAG TGG GGA CCGGAGGG		
		A GT A		
GAM2030	LOC153146 3'	GGGAGGCCAAGGCAGGCATATC 87146	CCA	C
	A	TGAT CCTGCCT GGCCTCCC		
		ACTA GGACGGA CCGGAGGG		
		TAC A		
GAM2030	LOC153260 3'	AGGCTGAGGCGGGCAGATCA 81668	CA	
		TGATC CCTGCCTCGGCCT		
		ACTAG GGGCGGAGTCGGA		
		AC		
GAM2030	LOC153561 3'	GGGAGGCCAAGGCAGGCAGAT 81751	CA	C
		ATC CCTGCCT GGCCTCCC		
		TAG GGACGGA CCGGAGGG		
		AC A		
GAM2030	LOC153579 3'	GGGAGGCCGAGGCGGGTGGATC 81773		
	A	TGATCCACCTGCCTCGGCCTCCC		
		ACTAGGTGGGCGGAGCCGGAGGG		
GAM2030	LOC153642 3'	GGGAGGCTGAGGAAAGCAGATC 81788	CACCTG	
	A	TGATC CCTCGGCCTCCC		
		ACTAG GGAGTCGGAGGG		
		ACGAAA		
GAM2030	LOC153688 3'	GGGAGACCAAGGCGGGTGGATC 87324	C C	
	A	TGATCCACCTGCCT GG CTCCC		
		ACTAGGTGGGCGGA CC GAGGG		
		A A		
GAM2030	LOC154089 3'	GGGAGGTCGAGGCAGGTGGATC 81944		
	G	TGATCCACCTGCCTCGGCCTCCC		

GCTAGGTGGACGGAGCTGGAGGG

GAM2030	LOC154092	3'	GGGAGGCTGAAGCAGGAGGATC	87371	A	C	
	A		TGATCC CCTGC TCGGCCTCCC				
			ACTAGG GGACG AGTCGGAGGG				
			A A				
GAM2030	LOC154403	5'	GGAAGGCTGAGGCACATGGACC	81979	A	CC	—
	A		TG TCCA TGCCTCGGCCT CC				
			AC AGGT ACGGAGTCGGA GG				
			C AC A				
GAM2030	LOC154403	3'	GGGAGGCCGAGGAGGGTGGATC	81980		G	
	A		TGATCCACCT CCTCGGCCTCCC				
			ACTAGGTGGG GGAGCCGGAGGG				
			A				
GAM2030	LOC154739	5'	AGGCTGAGGCAGGAGAATCA	87429	CCA		
			TGAT CCTGCCTCGGCCT				
			ACTA GGACGGAGTCGGA				
			AGA				
GAM2030	LOC154791	3'	GGGAGGCCAAGGCAGGCGGATC	82054	A	C	
	A		TGATCC CCTGCCT GGCCTCCC				
			ACTAGG GGACGGA CCGGAGGG				
			C A				
GAM2030	LOC154877	3'	GGGAGGCTGAGGCAGGAGAATC	87562	CCA		
	A		TGAT CCTGCCTCGGCCTCCC				
			ACTA GGACGGAGTCGGAGGG				
			AGA				
GAM2030	LOC154881	3'	AGGCTGAGGCAGGAGGATCA	82068	A		
			TGATCC CCTGCCTCGGCCT				
			ACTAGG GGACGGAGTCGGA				
			A				
GAM2030	LOC154992	3'	GGGAGGCCGAGGAGGGTGGATC	82138		G	
	A		TGATCCACCT CCTCGGCCTCCC				
			ACTAGGTGGG GGAGCCGGAGGG				
			A				
GAM2030	LOC154992	3'	GGGAGGCTGAGGCAGAGAATCA	82139	CCAC		
			TGAT CTGCCTCGGCCTCCC				
			ACTA GACGGAGTCGGAGGG				
			AGA_				
GAM2030	LOC155006	3'	GGGAGGCCGAGGCAGGAGAATC	82174	CCA		
			GAT CCTGCCTCGGCCTCCC				

		CTA GGACGGAGCCGGAGGG	
		AGA	
GAM2030	LOC155072 3'	GGGAGGCTGAGGCGGGTGGATC 87669	
	A	TGATCCACCTGCCTCGGCCTCCC	
		ACTAGGTGGGCGGAGTCGGAGGG	
GAM2030	LOC155072 3'	GGGAGGCTGAGGTAGGTGGATC 87670	
	AT	ATGATCCACCTGCCTCGGCCTCCC	
		TACTAGGTGGATGGAGTCGGAGGG	
GAM2030	LOC155376 3'	GGGAGGCTAAGACAGGAGAATC 82248	CCA C CG
	A	TGAT CCTG CT GCCTCCC	
		ACTA GGAC GA CGGAGGG	
		AGA A AT	
GAM2030	LOC155438 3'	GGGAGGCCAAGGTGGGCAGATC 87685	CA TG C
	G	TGATC CC CCT GGCCTCCC	
		GCTAG GG GGA CCGGAGGG	
		AC GT A	
GAM2030	LOC157280 5'	GAGAACTCTGAAGATGGATCA 74344	C GCC C_____
	T	ATGATCCA CT TCGG CTC	
		TACTAGGT GA AGTC GAG	
		A ____ TCAAA	
GAM2030	LOC157292 5'	GGGAGGCTGAGGCGGGTGGATC 87700	
	A	TGATCCACCTGCCTCGGCCTCCC	
		ACTAGGTGGGCGGAGTCGGAGGG	
GAM2030	LOC157464 5'	GGGAGGCTGAGGCGGGTGAATC 87748	C
	A	TGAT CACCTGCCTCGGCCTCCC	
		ACTA GTGGGCGGAGTCGGAGGG	
		A	
GAM2030	LOC157657 3'	AGGCTGAGGCAGGCAGATCA 82429	CA
		TGATC CCTGCCTCGGCCT	
		ACTAG GGACGGAGTCGGA	
		AC	
GAM2030	LOC157657 3'	GGGAGGCTGAGGCAGGCAGATC 82436	CA
	A	TGATC CCTGCCTCGGCCTCCC	
		ACTAG GGACGGAGTCGGAGGG	
		AC	
GAM2030	LOC157983 3'	GGGAGGCCGAGGCGGGCGCATC 82541	CCA
	A	TGAT CCTGCCTCGGCCTCCC	

		ACTA GGGCGGAGCCGGAGGG CGC		
GAM2030	LOC157983 3'	GGGAGGCTGAGGCAGGGGAATC 82542	_	A
	A	TGAT CC CCTGCCTCGGCCTCCC 		
		ACTA GG GGACGGAGTCGGAGGG A _		
GAM2030	LOC158088 3'	GGGAGGCCGAGGTGGGTGGATC 87975	TG	
	A	TGATCCACC CCTCGGCCTCCC 		
		ACTAGGTGG GGAGCCGGAGGG GT		
GAM2030	LOC158160 3'	GGGAGGCCAAGGCAGAAGGATC 73473	AC	C
	A	TGATCC CTGCCT GGCCTCCC 		
		ACTAGG GACGGA CCGGAGGG AA A		
GAM2030	LOC158187 3'	GGGAGGCCGAGGTGGGTGGATC 87995	TG	
	A	TGATCCACC CCTCGGCCTCCC 		
		ACTAGGTGG GGAGCCGGAGGG GT		
GAM2030	LOC158191 3'	GGGAGGCCAAGGCGGGTGGATC 82680		C
	A	TGATCCACCTGCCT GGCCTCCC 		
		ACTAGGTGGGCGGA CCGGAGGG A		
GAM2030	LOC158288 5'	GGCGTGTAAGCAGGTGGTCA 88025	T	CT__ _
		TGA CCACCTGC CG GCC 		
		ACT GGTGGACG GT CGG _ AAAT G		
GAM2030	LOC158288 5'	GGGAGGCCAAGGCAGGGGGATC 88026	A	C
	A	TGATCC CCTGCCT GGCCTCCC 		
		ACTAGG GGACGGA CCGGAGGG G A		
GAM2030	LOC158288 3'	GGGAGGCCAAGGTGGGCAGATC 88027	CA TG	C
		GATC CC CCT GGCCTCCC 		
		CTAG GG GGA CCGGAGGG AC GT A		
GAM2030	LOC158292 5'	GGAGGCTGAGGCAGAAGAATCA 88050	CCAC	
		TGAT CTGCCTCGGCCTCC 		
		ACTA GACGGAGTCGGAGG AGAA		
GAM2030	LOC158292 5'	GGGAGGCCAAGGCGGGCGGATC 88053	A	C
	A	TGATCC CCTGCCT GGCCTCCC 		

		ACTAGG GGGCGGA CCGGAGGG	
		C A	
GAM2030	LOC158292 5'	GGGAGGCCGAGACAGGTGGATC 88054	C
	A	TGATCCACCTG CTCGGCCTCCC	
		ACTAGGTGGAC GAGCCGGAGGG	
		A	
GAM2030	LOC158337 3'	GGGAGGCCGAGGCGGGCAGATC 88111	CA
	A	TGATC CCTGCCTCGGCCTCCC	
		ACTAG GGGCGGAGCCGGAGGG	
		AC	
GAM2030	LOC158819 5'	GGGAGGCCAAGGCACAAGAATC 88282	CCACC C
	G	TGAT TGCCT GGCCTCCC	
		GCTA ACGGA CCGGAGGG	
		AGAAC A	
GAM2030	LOC158819 5'	GGGAGGCCCAGGCAGGCGGATC 88283	A C
	A	TGATCC CCTGCCT GGCCTCCC	
		ACTAGG GGACGGA CCGGAGGG	
		C C	
GAM2030	LOC158819 3'	GGGAGGCTGAGGCGGGTGGATC 88284	
	A	TGATCCACCTGCCTCGGCCTCCC	
		ACTAGGTGGGCGGAGTCGGAGGG	
GAM2030	LOC158987 3'	GGGAGGCCAAGGTGGGAGGATC 88329	A TG C
	A	TGATCC CC CCT GGCCTCCC	
		ACTAGG GG GGA CCGGAGGG	
		A GT A	
GAM2030	LOC158987 3'	GGGAGGCTGAGTCAGGCGGATC 88330	A C
	A	TGATCC CCTG CTCGGCCTCCC	
		ACTAGG GGAC GAGTCGGAGGG	
		C T	
GAM2030	LOC159036 3'	GGGAAGCCAAGGCGGGTGGATT 88349	C C
	A	TGATCCACCTGCCT GGC TCCC	
		ATTAGGTGGGCGGA CCG AGGG	
		A A	
GAM2030	LOC159053 3'	AGGCTGAGGCAGGAGAATCA 88362	CCA
		TGAT CCTGCCTCGGCCT	
		ACTA GGACGGAGTCGGA	
		AGA	
GAM2030	LOC159053 3'	GAGGCCGGGCGCAGTGGCTCA 88373	T C _
		TGA CCAC TGC CTCGGCCTC	

		ACT GGTG ACG GGGCCGGAG		
		C _ C		
GAM2030	LOC159053 3'	GGGAGGCCAAGGCGGGCAGATC 88375	CA	C
	A	TGATC CCTGCCT GGCCTCCC		
		ACTAG GGGCGGA CCGGAGGG		
		AC A		
GAM2030	LOC159053 3'	GGGAGGCCCAGGCAGGCGGGTC 88376	A	C
	AT	ATGATCC CCTGCCT GGCCTCCC		
		TACTGGG GGACGGA CCGGAGGG		
		C C		
GAM2030	LOC159110 3'	GGGAGGCCAAGACAGGTGCATC 82993	C	C C
	A	TGAT CACCTG CT GGCCTCCC		
		ACTA GTGGAC GA CCGGAGGG		
		C A A		
GAM2030	LOC159110 3'	GGGAGGCTGAGGCAGGTGAATC 82994	C	
	G	TGAT CACCTGCCTCGGCCTCCC		
		GCTA GTGGACGGAGTCGGAGGG		
		A		
GAM2030	LOC159116 3'	GGGAGGCCAAGACAGGTGCATC 82976	C	C C
	A	TGAT CACCTG CT GGCCTCCC		
		ACTA GTGGAC GA CCGGAGGG		
		C A A		
GAM2030	LOC159116 3'	GGGAGGCTGAGGCAGGTGAATC 82977	C	
	G	TGAT CACCTGCCTCGGCCTCCC		
		GCTA GTGGACGGAGTCGGAGGG		
		A		
GAM2030	LOC160646 3'	GGGAGGCCAAGTGCGGACATCA 83118	CCAC	_ C
		TGAT CTGC CT GGCCTCCC		
		ACTA GGCG GA CCGGAGGG		
		CA_ T A		
GAM2030	LOC161734 3'	AGGCAGAGGCTGATGGACCAT 88458	A	CCT G
		ATG TCCA GCCTC GCCT		
		TAC AGGT CGGAG CGGA		
		C AGT A		
GAM2030	LOC170395 3'	GGGAGGCCGAGGTGGGCAGATC 76873	CA	TG
	A	TGATC CC CCGGCCTCCC		
		ACTAG GG GGAGCCGGAGGG		
		AC GT		
GAM2030	LOC170395 3'	GGGAGGCTGAGGCAGGAGAATC 76874	CCA	
	A	TGAT CCTGCCTCGGCCTCCC		

		ACTA GGACGGAGTCGGAGGG AGA	
GAM2030	LOC196027 3'	GGGAGGCTAAGGCAGGTGGATC 88938 G TGATCCACCTGCCT GCCTCCC GCTAGGTGGACGGA CGGAGGG AT	CG
GAM2030	LOC196027 3'	GGGAGTCTGAGGCAAGGGGATC 88939 A TGATCC CCT GCCTCGG CTCCC ACTAGG GGA CGGAGTC GAGGG _ A T	A _ C
GAM2030	LOC196047 5'	GGGAGGTTAAGGCAGGCGGATC 91158 A TGATCC CCTGCCT GCCTCCC ACTAGG GGACGGA TGGAGGG C AT	A CG
GAM2030	LOC196528 3'	GGGAGGCTGAGGCAGAAGGATC 89108 A TGATCC CTGCCTCGGCCTCCC ACTAGG GACGGAGTCGGAGGG AA	AC
GAM2030	LOC196540 3'	GGAGGCTGAGGCAGGAGAATCA 91205 TGAT CCTGCCTCGGCCTCC ACTA GGACGGAGTCGGAGG AGA	CCA
GAM2030	LOC196540 3'	GGGAGGCCGAGGCAGGTGGATC 91207 A TGATCCACCTGCCTCGGCCTCCC ACTAGGTGGACGGAGCCGGAGGG	
GAM2030	LOC196761 3'	GGGAGGCCGCGGCGGGTGGATC 91120 A TGATCCACCTGCC CGGCCTCCC ACTAGGTGGGCGG GCCGGAGGG C	T
GAM2030	LOC197196 3'	GGGAGGCCGAGGTAGGCGGATC 91304 A TGATCC CCTGCCTCGGCCTCCC ACTAGG GGATGGAGCCGGAGGG C	A
GAM2030	LOC197196 3'	GGGAGGCTGAGGCAGGAGAATC 91305 A TGAT CCTGCCTCGGCCTCCC ACTA GGACGGAGTCGGAGGG AGA	CCA
GAM2030	LOC197201 3'	GGGAGGCCGAGGTAGGCGGATC 89287 A TGATCC CCTGCCTCGGCCTCCC 	A

		ACTAGG GGATGGAGCCGGAGGG	
		C	
GAM2030	LOC197319 3'	GGGAGGCCGAGGTGGGCGGATC 89324	A TG
	A	TGATCC CC CCTCGGCCTCCC	
		ACTAGG GG GGAGCCGGAGGG	
		C GT	
GAM2030	LOC197319 3'	GGGAGGCCGAGGTGGGTGGATC 89325	TG
	A	TGATCCACC CCTCGGCCTCCC	
		ACTAGGTGG GGAGCCGGAGGG	
		GT	
GAM2030	LOC197335 3'	GGGAGGCCAAGGCAGGTGGAT 89334	C
		ATCCACCTGCCT GGCCTCCC	
		TAGGTGGACGGA CCGGAGGG	
		A	
GAM2030	LOC199786 3'	GGGAGGCTGAGGCGGGCAGATC 89758	CA
	A	TGATC CCTGCCTCGGCCTCCC	
		ACTAG GGGCGGAGTCGGAGGG	
		AC	
GAM2030	LOC199858 3'	GGGAGGCTGAGGCGGGCGGATC 89799	A
	A	TGATCC CCTGCCTCGGCCTCCC	
		ACTAGG GGGCGGAGTCGGAGGG	
		C	
GAM2030	LOC200014 3'	GGAAAGCTGAGGCAGGTGGATC 89939	C_
	A	TGATCCACCTGCCTCGGC TCC	
		ACTAGGTGGACGGAGTCG AGG	
		AA	
GAM2030	LOC200282 3'	GGGAGGCCAAGACAGGAGGATC 90101	A C C
	A	TGATCC CCTG CT GGCCTCCC	
		ACTAGG GGAC GA CCGGAGGG	
		A A A	
GAM2030	LOC200317 3'	GGGAGGCCGAAGCAGGCAGATC 90227	CA C
	A	TGATC CCTGC TCGGCCTCCC	
		ACTAG GGACG AGCCGGAGGG	
		AC A	
GAM2030	LOC200728 3'	GGGAGGCCGAGGTGGGCAGATC 91686	CA TG
	AT	ATGATC CC CCTCGGCCTCCC	
		TACTAG GG GGAGCCGGAGGG	
		AC GT	
GAM2030	LOC200731 3'	GGGAGACCAAGGCAGGTGGATC 91699	C C
	A	TGATCCACCTGCCT GG CTCCC	

		ACTAGGTGGACGGA CC GAGGG	
		A A	
GAM2030	LOC200904 3'	GGGAGGCCGAGGCAGGCAGATC 91783	CA
	A	TGATC CCTGCCTCGGCCTCCC	
		ACTAG GGACGGAGCCGGAGGG	
		AC	
GAM2030	LOC200918 3'	AGGCTGAGGCAGGAGAATCA 90363	CCA
		TGAT CCTGCCTCGGCCT	
		ACTA GGACGGAGTCGGA	
		AGA	
GAM2030	LOC200940 3'	GGGAGGCTGAGGCAGGAGAATC 90394	CCA
	A	TGAT CCTGCCTCGGCCTCCC	
		ACTA GGACGGAGTCGGAGGG	
		AGA	
GAM2030	LOC200940 3'	GGGAGGCTGAGGCAGGCGGATC 90395	A
		GATCC CCTGCCTCGGCCTCCC	
		CTAGG GGACGGAGTCGGAGGG	
		C	
GAM2030	LOC201173 3'	GGGAGGCCGAGGCGGGCGGATC 88690	A
	AT	ATGATCC CCTGCCTCGGCCTCCC	
		TACTAGG GGGCGGAGCCGGAGGG	
		C	
GAM2030	LOC201220 3'	GGGAGGCCGAGGTGGGCGGATC 88723	A TG
	A	TGATCC CC CCTCGGCCTCCC	
		ACTAGG GG GGAGCCGGAGGG	
		C GT	
GAM2030	LOC201252 3'	GGGAAGCCGAGGTGGGCAGATC 89553	CA TG C
	A	TGATC CC CCTCGGC TCCC	
		ACTAG GG GGAGCCG AGGG	
		AC GT A	
GAM2030	LOC201627 3'	GGGAGGCCAAGGTGGACAGGTC 90457	CAC TG C
	A	TGATC C CCT GGCCTCCC	
		ACTGG G GGA CCGGAGGG	
		ACA GT A	
GAM2030	LOC201685 3'	GGGAGGCCGAGGCAGGCGGATC 91844	A
	A	TGATCC CCTGCCTCGGCCTCCC	
		ACTAGG GGACGGAGCCGGAGGG	
		C	
GAM2030	LOC201810 3'	GGGAGGCCGAGGCAGATGGATC 90503	C
	A	TGATCCA CTGCCTCGGCCTCCC	

		ACTAGGT GACGGAGCCGGAGGG		
		A		
GAM2030	LOC201868 5'	GGAAGGCTGAGGCACATGGACC 90528	A	CC _
	A	TG TCCA TGCCTCGGCCT CC		
		AC AGGT ACGGAGTCGGA GG		
		C AC A		
GAM2030	LOC201868 3'	GGGAGGCCGAGGAGGGTGGATC 90529		G
	AT	ATGATCCACCT CCTCGGCCTCCC		
		TACTAGGTGGG GGAGCCGGAGGG		
		A		
GAM2030	LOC201911 3'	GGGAGGCCGAGGCGGGCGGATC 91868	A	
	A	TGATCC CCTGCCTCGGCCTCCC		
		ACTAGG GGGCGGAGCCGGAGGG		
		C		
GAM2030	LOC201931 3'	GGGAGGCTGAGGCAGGAGGATC 90568	A	
	A	TGATCC CCTGCCTCGGCCTCCC		
		ACTAGG GGACGGAGTCGGAGGG		
		A		
GAM2030	LOC202020 3'	GGGAGGCCGAAGGGGGCGAATC 90602	CCA	G _
	A	TGAT CCT CCT CGGCCTCCC		
		ACTA GGG GGA GCCGGAGGG		
		AGC _ A		
GAM2030	LOC202038 3'	GGAAGGCCGAGGCGGGCGGATC 90623	A	_
	A	TGATCC CCTGCCTCGGCCT CC		
		ACTAGG GGGCGGAGCCGGA GG		
		C A		
GAM2030	LOC202052 3'	GGGAGGCTGTGGCAGGTGGATC 91901		T
	A	TGATCCACCTGCC CGGCCTCCC		
		ACTAGGTGGACGG GTCGGAGGG		
		T		
GAM2030	LOC202868 3'	GGGAGGCTGAGGCGGGTGGATC 92006		
	A	TGATCCACCTGCCTCGGCCTCCC		
		ACTAGGTGGGCGGAGTCGGAGGG		
GAM2030	LOC202868 3'	GGGAGGCTGAGGTAGGTGGATC 92007		
	AT	ATGATCCACCTGCCTCGGCCTCCC		
		TACTAGGTGGATGGAGTCGGAGGG		
GAM2030	LOC203025 3'	GAGGCCGAGGCGGGTGGGTCA 90746		
		TGATCCACCTGCCTCGGCCTC		

ACTGGGTGGGCGGAGCCGGAG

GAM2030 LOC203083 3' GAGGCCGAGGCAGGTGGATCA 92089
TGATCCACCTGCCTCGGCCTC
|||||
ACTAGGTGGACGGAGCCGGAG

GAM2030 LOC203083 3' GGGAGGCTGAGGCAGGAGAATC 92094 CCA
A TGAT CCTGCCTCGGCCTCCC
||| |||||
ACTA GGACGGAGTCGGAGGG
AGA

GAM2030 LOC203246 3' GGGAGGCCGAGGCGGGCGGATC 90836 A
A TGATCC CCTGCCTCGGCCTCCC
||||| |||||
ACTAGG GGGCGGAGCCGGAGGG
C

GAM2030 LOC203276 3' GGGAGGCCAAGGTGGACAGATC 92126 CAC TG C
A TGATC C CCT GGCCTCCC
|||| | ||| |||||
ACTAG G GGA CCGGAGGG
ACA GT A

GAM2030 LOC203276 3' GGGTGAGGCAGGAGAATCA 92127 CCA G
TGAT CCTGCCTCG CC
||| ||||| ||
ACTA GGACGGAGT GG
AGA G

GAM2030 LOC203289 3' GGGAGGCCGAGGCGGGCGCATC 90868 CCA
A TGAT CCTGCCTCGGCCTCCC
|||| |||||
ACTA GGGCGGAGCCGGAGGG
CGC

GAM2030 LOC203289 3' GGGAGGCTGAGGCAGGGGAATC 90869 _ A
A TGAT CC CCTGCCTCGGCCTCCC
|||| || |||||
ACTA GG GGACGGAGTCGGAGGG
A _

GAM2030 LOC203305 3' GGGAGGCCAAGGTGGGCAGATC 92179 CA TG C
A TGATC CC CCT GGCCTCCC
|||| || ||| |||||
ACTAG GG GGA CCGGAGGG
AC GT A

GAM2030 LOC203305 3' GGGTGAGGCAGGAGAATCA 92180 CCA G
TGAT CCTGCCTCG CC
||| ||||| ||
ACTA GGACGGAGT GG
AGA G

GAM2030 LOC203350 3' GGGTGGCCGAGGCAGGAAGATC 92244 CA T
A TGATC CCTGCCTCGGCC CCC
|||| ||||| |||

		ACTAG GGACGGAGCCGG GGG		
		AA T		
GAM2030	LOC203378 3'	GGAGACTGAGGCAGGAGAATCA 92293	CCA	C
		TGAT CCTGCCTCGG CTCC		
		ACTA GGACGGAGTC GAGG		
		AGA A		
GAM2030	LOC203378 3'	GGGAGGCTGAGGCAAGCGAATC 92294	CCACC	
		GAT TGCCTCGGCCTCCC		
		CTA ACGGAGTCGGAGGG		
		AGCGA		
GAM2030	LOC203397 3'	GGGAAGTTGAGGTAGGCAGATC 90900	CA	C
	A	TGATC CCTGCCTCGGC TCCC		
		ACTAG GGATGGAGTTG AGGG		
		AC A		
GAM2030	LOC219376 3'	GGGAGGCCAAGGTGGGAGATCG 95518	CA TG	C
		TGATC CC CCT GGCCTCCC		
		GCTAG GG GGA CCGGAGGG		
		A_ GT A		
GAM2030	LOC219376 3'	GGGAGGCTGGGGCAGGCGGATC 95519	A	
	A	TGATCC CCTGCCTCGGCCTCCC		
		ACTAGG GGACGGGGTCGGAGGG		
		C		
GAM2030	LOC219406 3'	GGCAGGCCGAGGCGGGCAGATC 95206	CA	_
	A	TGATC CCTGCCTCGGCCT CC		
		ACTAG GGGCGGAGCCGGA GG		
		AC C		
GAM2030	LOC219627 3'	GGGAGGCCAAGGCGGGCAGACC 93809	A CA	C
	AT	ATG TC CCTGCCT GGCCTCCC		
		TAC AG GGGCGGA CCGGAGGG		
		C AC A		
GAM2030	LOC219649 3'	GGGAGGCCGAAGCGGGTGGATC 94554		C
	A	TGATCCACCTGC TCGGCCTCCC		
		ACTAGGTGGGCG AGCCGGAGGG		
		A		
GAM2030	LOC219649 3'	GGGAGGCTGAGGCGGGTGGATC 94555		
	A	TGATCCACCTGCCTCGGCCTCCC		
		ACTAGGTGGGCGGAGTCGGAGGG		
GAM2030	LOC219673 3'	GGGAGGCCCAGGCGGGCGGATC 94627	A	C
	A	TGATCC CCTGCCT GGCCTCCC		

		ACTAGG GGGCGGA CCGGAGGG	
		C C	
GAM2030	LOC219722 5'	GGAGGCTGAAGCAGAAGAATCA 94683	CCAC C
		TGAT CTGC TCGGCCTCC	
		ACTA GACG AGTCGGAGG	
		AGAA A	
GAM2030	LOC219722 5'	GGGAGGCCGAGGTAGGCGGATC 94684	A
		GATCC CCTGCCTCGGCCTCCC	
		CTAGG GGATGGAGCCGGAGGG	
		C	
GAM2030	LOC219919 3'	GGGAGGCCGAGGCAGGCGGATC 94930	A
	A	TGATCC CCTGCCTCGGCCTCCC	
		ACTAGG GGACGGAGCCGGAGGG	
		C	
GAM2030	LOC219919 3'	GGGAGGCTGAGGCAGGAGAATC 94931	CCA
	A	TGAT CCTGCCTCGGCCTCCC	
		ACTA GGACGGAGTCGGAGGG	
		AGA	
GAM2030	LOC220064 3'	GGGAGCAGCGGCAGGTGGATC 95068	TCG C
		GATCCACCTGCC GC TCCC	
		CTAGGTGGACGG CG AGGG	
		CGA _	
GAM2030	LOC220370 3'	GGGAGGCCGAGGCGGGAAGATC 94402	CA
	A	TGATC CCTGCCTCGGCCTCCC	
		ACTAG GGGCGGAGCCGGAGGG	
		AA	
GAM2030	LOC220506 3'	GGAGGCCGAGGCAGGCGGATT 74519	A
		GATCC CCTGCCTCGGCCTCC	
		TTAGG GGACGGAGCCGGAGG	
		C	
GAM2030	LOC221042 3'	GAGAGCGAGGCGGGCAGATCA 94803	CA GC
		TGATC CCTGCCTCG CTC	
		ACTAG GGGCGGAGC GAG	
		AC GA	
GAM2030	LOC221178 3'	GGGAGGCCAAGGCAGGTGGATC 95172	C
	A	TGATCCACCTGCCT GGCCTCCC	
		ACTAGGTGGACGGA CCGGAGGG	
		A	
GAM2030	LOC221271 3'	GGGAGGCCGAGACGGGCAGATC 93523	CA C
	A	TGATC CTG CTCGGCCTCCC	

		ACTAG GGGC GAGCCGGAGGG	
		AC A	
GAM2030	LOC221271 3'	GGGAGGCCGAGGTGGGCGGATC 93524	A TG
	A	TGATCC CC CCTCGGCCTCCC	
		ACTAGG GG GGAGCCGGAGGG	
		C GT	
GAM2030	LOC221288 3'	GGGAGGCCGAGGTGGGCAGATC 95261	CA TG
	A	TGATC CC CCTCGGCCTCCC	
		ACTAG GG GGAGCCGGAGGG	
		AC GT	
GAM2030	LOC221410 3'	GGGAGGCCGAGGCAGGTAGATC 93698	C
	AT	ATGATC ACCTGCCTCGGCCTCCC	
		TACTAG TGGACGGAGCCGGAGGG	
		A	
GAM2030	LOC221474 3'	AGGCTGAGACAGGAGAATCA 93988	CCA C
		TGAT CCTG CTCGGCCT	
		ACTA GGAC GAGTCGGA	
		AGA A	
GAM2030	LOC221474 3'	GGGAGGCCGAGGTGGGCAGATC 93997	CA TG
	A	TGATC CC CCTCGGCCTCCC	
		ACTAG GG GGAGCCGGAGGG	
		AC GT	
GAM2030	LOC221477 3'	GGGAGGCTGAGGCAGGCAGATC 93775	CA
	A	TGATC CCTGCCTCGGCCTCCC	
		ACTAG GGACGGAGTCGGAGGG	
		AC	
GAM2030	LOC221490 3'	GGGAGGCCGAGGCGGGTGGATC 95307	
	A	TGATCCACCTGCCTCGGCCTCCC	
		ACTAGGTGGGCGGAGCCGGAGGG	
GAM2030	LOC221543 3'	GGGAGGCCGAGGCAGGTGGATC 95382	
	A	TGATCCACCTGCCTCGGCCTCCC	
		ACTAGGTGGACGGAGCCGGAGGG	
GAM2030	LOC221543 3'	GGGAGGCCGATGTGGGTGGATC 95383	TG C
	A	TGATCCACC C TCGGCCTCCC	
		ACTAGGTGG G AGCCGGAGGG	
		GT T	
GAM2030	LOC221585 3'	GGGAGGCCGAGACGGGCGGATC 95278	A C
	A	TGATCC CCTG CTCGGCCTCCC	

		ACTAGG GGGC GAGCCGGAGGG	
		C A	
GAM2030	LOC221766 3'	GGGAGGCCGAGGTGGGCAGATC 95422	CA TG
	A	TGATC CC CCTCGGCCTCCC	
		ACTAG GG GGAGCCGGAGGG	
		AC GT	
GAM2030	LOC221795 3'	GGGAGGCCGAGGCAGGCGGATC 94078	A
	A	TGATCC CCTGCCTCGGCCTCCC	
		ACTAGG GGACGGAGCCGGAGGG	
		C	
GAM2030	LOC221795 3'	GGGAGGCTGAGGCAGGAGAATC 94079	CCA
	A	TGAT CCTGCCTCGGCCTCCC	
		ACTA GGACGGAGTCGGAGGG	
		AGA	
GAM2030	LOC221931 3'	GGGAGGCCGAGGTGGGAAGATC 95632	CA TG
	AT	ATGATC CC CCTCGGCCTCCC	
		TACTAG GG GGAGCCGGAGGG	
		AA GT	
GAM2030	LOC221943 5'	GGGAGGCCAAGGCGGGTGGATC 95623	C
	A	TGATCCACCTGCCT GGCCTCCC	
		ACTAGGTGGGCGGA CCGGAGGG	
		A	
GAM2030	LOC221954 5'	GGGAGGCTGAGGCAGGCGGACA 95649	A A
		TG TCC CCTGCCTCGGCCTCCC	
		AC AGG GGACGGAGTCGGAGGG	
		- C	
GAM2030	LOC222066 3'	AGGCTGAGGCAGGAAAATCA 94312	CCA
		TGAT CCTGCCTCGGCCT	
		ACTA GGACGGAGTCGGA	
		AAA	
GAM2030	LOC222066 3'	GGGAGGCCGAGGCAGGCAGATC 94323	CA
	A	TGATC CCTGCCTCGGCCTCCC	
		ACTAG GGACGGAGCCGGAGGG	
		AC	
GAM2030	LOC222160 5'	GGGAGGCCGAGATGGGCGGATC 95787	A GC
	A	TGATCC CCT CTGGCCTCCC	
		ACTAGG GGG GAGCCGGAGGG	
		C TA	
GAM2030	LOC222182 3'	GGAGGCCAAGGCAGGTGGATCG 95856	C
		TGATCCACCTGCCT GGCCTCC	

GCTAGGTGGACGGA CCGGAGG
 A
 GAM2030 LOC222182 3' GGAGGCTGAGGCAGGAGAATCA 95857 CCA
 TGAT CCTGCCTCGGCCTCC
 ||| |||||
 ACTA GGACGGAGTCGGAGG
 AGA
 GAM2030 LOC222236 3' GGGAGGCCAAGGTGGGTGGGTC 95961 TG C
 A TGATCCACC CCT GGCCTCCC
 ||||| || |||||
 ACTGGGTGG GGA CCGGAGGG
 GT A
 GAM2030 LOC222865 3' GGGAGGCCGAGGCGGGTGGATC 94447
 A TGATCCACCTGCCTCGGCCTCCC
 |||||
 ACTAGGTGGGCGGAGCCGGAGGG

 GAM2030 LOC253216 5' GGGAGGCAGGTGGCCAT 96631 AT GG
 ATG CCACCTGCCTC CC
 || ||||| ||
 TAC GGTGGACGGAG GG
 C_ _
 GAM2030 LOC253532 3' GGGAGGCTAAGACAGGAGAATC 97737 CCA C CG
 A TGAT CCTG CT GCCTCCC
 ||| ||| || |||||
 ACTA GGAC GA CGGAGGG
 AGA A AT
 GAM2030 LOC253612 5' GGAGGCTGAGGCAAGAGAATCA 98553 CCACC
 TGAT TGCCTCGGCCTCC
 ||| |||||
 ACTA ACGGAGTCGGAGG
 AGAGA
 GAM2030 LOC253639 3' GAGGCTGAGGCAGGAGAATCA 97514 CCA
 TGAT CCTGCCTCGGCCTC
 ||| |||||
 ACTA GGACGGAGTCGGAG
 AGA
 GAM2030 LOC253639 3' GGGAGGCTGAGGCGGGTGGATC 97516
 AT ATGATCCACCTGCCTCGGCCTCCC
 |||||
 TACTAGGTGGGCGGAGTCGGAGGG

 GAM2030 LOC253664 3' GGGAGGCCGAGGCGGGTGGATC 96471
 G TGATCCACCTGCCTCGGCCTCCC
 |||||
 GCTAGGTGGGCGGAGCCGGAGGG

 GAM2030 LOC253840 3' GGAAGGCCGAGGTGGGTGGATC 97913 TG _
 A TGATCCACC CTCGGCCT CC
 ||||| ||||| ||

		ACTAGGTGG GGAGCCGGA GG	
		GT A	
GAM2030	LOC254041 5'	GGGAGGCCGAGGCAGGCAGATC 96557	CA
	A	TGATC CCTGCCTCGGCCTCCC	
		ACTAG GGACGGAGCCGGAGGG	
		AC	
GAM2030	LOC254045 3'	GGGAGGCTGAGACAGGAGAATC 98271	CCA C
	A	TGAT CCTG CTCGGCCTCCC	
		ACTA GGAC GAGTCGGAGGG	
		AGA A	
GAM2030	LOC254045 3'	GGGAGGCTGAGGCAAGTGAAGC 98272	ATC C
	A	TG CAC TGCCTCGGCCTCCC	
		AC GTG ACGGAGTCGGAGGG	
		GAA A	
GAM2030	LOC254176 3'	GAGGCCGAGGCAGGTGGATCA 99170	
		TGATCCACCTGCCTCGGCCTC	
		ACTAGGTGGACGGAGCCGGAG	
GAM2030	LOC254176 3'	GGGAGGCTGAGGCAGGAGAATC 99175	CCA
	A	TGAT CCTGCCTCGGCCTCCC	
		ACTA GGACGGAGTCGGAGGG	
		AGA	
GAM2030	LOC254243 3'	GGGAGGCCAAGGTGGGCAGATC 99265	CA TG C
	A	TGATC CC CCT GGCCTCCC	
		ACTAG GG GGA CCGGAGGG	
		AC GT A	
GAM2030	LOC254243 3'	GGGTGAGGCAGGAGAATCA 99266	CCA G
		TGAT CCTGCCTCG CC	
		ACTA GGACGGAGT GG	
		AGA G	
GAM2030	LOC254266 3'	GGGAGGCCGAGGCGGGCAGATC 99201	CA
	A	TGATC CCTGCCTCGGCCTCCC	
		ACTAG GGGCGGAGCCGGAGGG	
		AC	
GAM2030	LOC254351 3'	GGAAGGCCGAGTGTGGCAGATC 96692	CA T _ _
	G	TGATC CC GC CTCGGCCT CC	
		GCTAG GG TG GAGCCGGA GG	
		AC _ T A	
GAM2030	LOC254387 3'	GGGAGGCCAAGATCCACGGATC 96582	ACCTGC C
		GATCC CT GGCCTCCC	

		CTAGG	GA CCGGAGGG		
		CACCTA	A		
GAM2030	LOC254531 5'	GGGAGGCCAAGGCGGGTGGATC	96671	C	
	A	TGATCCACCTGCCT	GGCCTCCC		
		ACTAGGTGGGCGGA	CCGGAGGG		
		A			
GAM2030	LOC254808 3'	GGGAGGCCGAGGCGGGCGGATC	98808	A	
	A	TGATCC	CCTGCCTCGGCCTCCC		
		ACTAGG	GGGCGGAGCCGGAGGG		
		C			
GAM2030	LOC254875 3'	GGGAGGCTAAGACAGGAGAATC	97782	CCA	C CG
	A	TGAT	CCTG CT GCCTCCC		
		ACTA	GGAC GA CGGAGGG		
		AGA	A AT		
GAM2030	LOC255031 3'	GGGAGGCCGAGGCAGGAGGATC	99041	A	
	A	TGATCC	CCTGCCTCGGCCTCCC		
		ACTAGG	GGACGGAGCCGGAGGG		
		A			
GAM2030	LOC255042 3'	GGAGGCTGAGGCAGGAGAATCA	97048	CCA	
		TGAT	CCTGCCTCGGCCTCC		
		ACTA	GGACGGAGTCGGAGG		
		AGA			
GAM2030	LOC255042 3'	GGGAGGCCAAGGCAGGCAGATC	97050	CA	C
	AT	ATGATC	CCTGCCT GGCCTCCC		
		TACTAG	GGACGGA CCGGAGGG		
		AC	A		
GAM2030	LOC255042 3'	GGGAGGCCGAGGCAAGCAGATC	97051	CACC	
	A	TGATC	TGCCTCGGCCTCCC		
		ACTAG	ACGGAGCCGGAGGG		
		ACGA			
GAM2030	LOC255042 3'	GGGAGGCTGAGGCGGGTGGATC	97052		
	A	TGATCCACCTGCCTCGGCCTCCC			
		ACTAGGTGGGCGGAGTCGGAGGG			
GAM2030	LOC255177 3'	GGGAGGCTGAGGCAGGAGAATC	98397	CCA	
	A	TGAT	CCTGCCTCGGCCTCCC		
		ACTA	GGACGGAGTCGGAGGG		
		AGA			
GAM2030	LOC255185 3'	CGGGAGGCCAACGCCGAGGCGG	96830	A	III
	GCGGATCAT	ATGATCC	CCTGCCTC GGCCTCCC	G	

		TACTAGG GGGCGGAG CCGGAGGG C	
		C CCGCAA III	
GAM2030	LOC255193 3'	GGGAGGCCGAGGTGGGAAGATC 97105	CA TG
	A	TGATC CC CCTCGGCCTCCC	
		ACTAG GG GGAGCCGGAGGG	
		AA GT	
GAM2030	LOC255196 5'	GGGAGGCCGAGATGGGCGGATC 98963	A GC
		GATCC CCT CTCGGCCTCCC	
		CTAGG GGG GAGCCGGAGGG	
		C TA	
GAM2030	LOC255196 3'	GGGAGTCCGAGGCGAGTGAATC 98964	C C C
	A	TGAT CAC TGCCTCGG CTCCC	
		ACTA GTG GCGGAGCC GAGGG	
		A A T	
GAM2030	LOC255252 3'	GGGAGGCCAAGGCGGGTGGCTC 96709	T C
	A	TGA CCACCTGCCT GGCCTCCC	
		ACT GGTGGGCGGA CCGGAGGG	
		C A	
GAM2030	LOC255326 3'	GGGAGGCCCAGGCGGGCAGATC 98120	CA C
	A	TGATC CCTGCCT GGCCTCCC	
		ACTAG GGGCGGA CCGGAGGG	
		AC C	
GAM2030	LOC255328 3'	GGGAGGCTGAGGCAGGAGAATC 98345	CCA
	A	TGAT CCTGCCTCGGCCTCCC	
		ACTA GGACGGAGTCGGAGGG	
		AGA	
GAM2030	LOC255448 5'	GAGAACTCTGAAGATGGATCA 96304	C GCC C____
	T	ATGATCCA CT TCGG CTC	
		TACTAGGT GA AGTC GAG	
		A ____ TCAAA	
GAM2030	LOC255463 3'	GGGAGGCCAAGATGGGCAGATC 96542	CA GC C
	G	TGATC CCT CT GGCCTCCC	
		GCTAG GGG GA CCGGAGGG	
		AC TA A	
GAM2030	LOC255624 3'	GGGAGGCCAAGACAGGTAGATC 96165	C C C
	A	TGATC ACCTG CT GGCCTCCC	
		ACTAG TGGAC GA CCGGAGGG	
		A A A	
GAM2030	LOC255743 5'	GGGACCCAGCAGGTGGACA 97602	A CTC CC
		TG TCCACCTGC GG TCCC	

		AC AGGTGGACG CC AGGG	
		— AC —	
GAM2030	LOC255937 3'	GAGGCCGAGGCAGGCGGATCA 97683	A
		TGATCC CCTGCCTCGGCCTC	
		ACTAGG GGACGGAGCCGGAG	
		C	
GAM2030	LOC255971 3'	GGGAGGCCGAGGCGGGCGGATC 98313	A
	A	TGATCC CCTGCCTCGGCCTCCC	
		ACTAGG GGGCGGAGCCGGAGGG	
		C	
GAM2030	LOC256158 5'	GGAGGCCCGGGGCGGAGTCA 99503	CCAC —
		TGAT CTGCCTCGG CCTCC	
		ACTG GCGGGGCC GGAGG	
		A — C	
GAM2030	LOC256207 3'	AGGCTGAGGCAGGAAGATCA 96869	CA
		TGATC CCTGCCTCGGCCT	
		ACTAG GGACGGAGTCGGA	
		AA	
GAM2030	LOC256207 3'	GGGAGGCCAAGGTGGGTGGATC 96879	TG C
	A	TGATCCACC CCT GGCCTCCC	
		ACTAGGTGG GGA CCGGAGGG	
		GT A	
GAM2030	LOC256277 3'	GGGAGGCTGAAGCGGGTAGATC 96352	C C
	A	TGATC ACCTGC TCGGCCTCCC	
		ACTAG TGGGCG AGTCGGAGGG	
		A A	
GAM2030	LOC256515 3'	GGGAGGCCGAGGCAGGCGGATT 98215	A
	A	TGATCC CCTGCCTCGGCCTCCC	
		ATTAGG GGACGGAGCCGGAGGG	
		C	
GAM2030	LOC256515 3'	GGGAGGCTGAGGCAGGAGAATC 98216	CCA
	A	TGAT CCTGCCTCGGCCTCCC	
		ACTA GGACGGAGTCGGAGGG	
		AGA	
GAM2030	LOC256544 3'	GGGAGGCCGAGGCGGGCGCATC 97932	CCA
	A	TGAT CCTGCCTCGGCCTCCC	
		ACTA GGGCGGAGCCGGAGGG	
		CGC	
GAM2030	LOC256544 3'	GGGAGGCTGAGGCAGGGGAATC 97933	— A
	A	TGAT CC CCTGCCTCGGCCTCCC	

		ACTA GG GGACGGAGTCGGAGGG	
		A _	
GAM2030	LOC256594 3'	GGGAGGCCGAGGCAGGCGGATC 98865	A
	A	TGATCC CCTGCCTCGGCCTCCC	
		ACTAGG GGACGGAGCCGGAGGG	
		C	
GAM2030	LOC256594 3'	GGGAGGCTGAGGCAGGAGAATC 98866	CCA
	A	TGAT CCTGCCTCGGCCTCCC	
		ACTA GGACGGAGTCGGAGGG	
		AGA	
GAM2030	LOC256980 3'	GGGAGGCCGCGGCAGAAGGATC 96932	AC T
	A	TGATCC CTGCC CGGCCTCCC	
		ACTAGG GACGG GCCGGAGGG	
		AA C	
GAM2030	LOC257115 3'	GGGAGGCCGAGGCAGGTGGATC 98295	
	G	TGATCCACCTGCCTCGGCCTCCC	
		GCTAGGTGGACGGAGCCGGAGGG	
GAM2030	LOC257180 3'	GGGAGGCCGAGGCAGGTGGATC 97315	
	AT	ATGATCCACCTGCCTCGGCCTCCC	
		TACTAGGTGGACGGAGCCGGAGGG	
GAM2030	LOC257539 3'	GGGAGGCCGAGGAGGGCAGATC 99550	CA G
	A	TGATC CCT CCTCGGCCTCCC	
		ACTAG GGG GGAGCCGGAGGG	
		AC A	
GAM2030	LOC257578 3'	GGGAGGCCGAGGAGGGCAGATC 99662	CA G
	A	TGATC CCT CCTCGGCCTCCC	
		ACTAG GGG GGAGCCGGAGGG	
		AC A	
GAM2030	LOC257596 3'	GGGAGGCCGAGGCAGGTGGATC 99785	
	A	TGATCCACCTGCCTCGGCCTCCC	
		ACTAGGTGGACGGAGCCGGAGGG	
GAM2030	LOC257596 3'	GGGAGGCCGATGTGGGTGGATC 99786	TG C
	A	TGATCCACC C TCGGCCTCCC	
		ACTAGGTGG G AGCCGGAGGG	
		GT T	
GAM2030	LOC51122 3'	GGGAGGCCGAGGTGGGCAAATC 66199	CCA TG
	AT	ATGAT CC CCTCGGCCTCCC	

		TACTA GG GGAGCCGGAGGG	
		AAC GT	
GAM2030	LOC51145 3'	GGAGGCTGAGGCAGGAGAATCA 32925	CCA
		TGAT CCTGCCTCGGCCTCC	
		ACTA GGACGGAGTCGGAGG	
		AGA	
GAM2030	LOC51145 3'	GGGAGGCCGAGGCAGGTGGATC 32926	
	A	TGATCCACCTGCCTCGGCCTCCC	
		ACTAGGTGGACGGAGCCGGAGGG	
GAM2030	LOC51279 3'	GGGAGGCTGAGGCAGGAGAATC 33761	CCA
	A	TGAT CCTGCCTCGGCCTCCC	
		ACTA GGACGGAGTCGGAGGG	
		AGA	
GAM2030	LOC51336 3'	GGGAGGCCGAGGCAGGCGGATC 34073	A
	A	TGATCC CCTGCCTCGGCCTCCC	
		ACTAGG GGACGGAGCCGGAGGG	
		C	
GAM2030	LOC51336 3'	GGGAGGTTGAGGCAGGAGAATC 34074	CCA
	A	TGAT CCTGCCTCGGCCTCCC	
		ACTA GGACGGAGTTGGAGGG	
		AGA	
GAM2030	LOC51667 3'	CTGAAGACAGGATGGATCAT 32778	_ C _
		ATGATCCA CCTG CT CGG	
		TACTAGGT GGAC GA GTC	
		A A A	
GAM2030	LOC51759 3'	GGGAGGCCGAGGTGGGCGGATC 73171	A TG
	A	TGATCC CC CCTCGGCCTCCC	
		ACTAGG GG GGAGCCGGAGGG	
		C GT	
GAM2030	LOC54518 3'	GGGAGGCTGAGGCAGGAGGATC 39299	A
	A	TGATCC CCTGCCTCGGCCTCCC	
		ACTAGG GGACGGAGTCGGAGGG	
		A	
GAM2030	LOC55974 3'	AGGCCGGGCGCGGTGGCTCA 38740	T _ T
		TGA CCACC TGCC CGGCCT	
		ACT GGTGG GCGG GCCGGA	
		C C _	
GAM2030	LOC55974 3'	GGGAGGCCAAGGTGGGCGGATC 38748	A TG C
	G	TGATCC CC CCT GGCCTCCC	

		GCTAGG GG GGA CCGGAGGG		
		C GT A		
GAM2030	LOC57118 3'	GGGAGGCTGAGGCAGGAGAATC 40224	CCA	
	A	TGAT CCTGCCTCGGCCTCCC		
		ACTA GGACGGAGTCGGAGGG		
		AGA		
GAM2030	LOC63929 3'	GGGAGGTCCAGGCAGGTGGATC 42282	C	
		GATCCACCTGCCT GGCCTCCC		
		CTAGGTGGACGGA CTGGAGGG		
		C		
GAM2030	LOC85479 5'	GGGAGGCCGAGGCTGGCGGATC 53570	A T	
	A	TGATCC CC GCCTCGGCCTCCC		
		ACTAGG GG CGGAGCCGGAGGG		
		C T		
GAM2030	LOC89890 3'	GGGAGGCCGAGGCAGGTGGATC 61208		
	A	TGATCCACCTGCCTCGGCCTCCC		
		ACTAGGTGGACGGAGCCGGAGGG		
GAM2030	LOC90038 3'	GGGAGGCCAAGGTGGGCAGATC 61809	CA TG C	
	A	TGATC CC CCT GGCCTCCC		
		ACTAG GG GGA CCGGAGGG		
		AC GT A		
GAM2030	LOC90038 3'	GGGTGAGGCAGGAGAATCA 61810	CCA G	
		TGAT CCTGCCTCG CC		
		ACTA GGACGGAGT GG		
		AGA G		
GAM2030	LOC90072 3'	GGAAGGCCGAGGCGGGCAGATC 61959	CA	—
	A	TGATC CCTGCCTCGGCCT CC		
		ACTAG GGGCGGAGCCGGA GG		
		AC A		
GAM2030	LOC90092 3'	GGGAGGCCAAGGCAGGAAGAT 62070	CA C	
		ATC CCTGCCT GGCCTCCC		
		TAG GGACGGA CCGGAGGG		
		AA A		
GAM2030	LOC90092 3'	GGGAGGTCAAGGTAGGTGGATC 62071	C	
	A	TGATCCACCTGCCT GGCCTCCC		
		ACTAGGTGGATGGA CTGGAGGG		
		A		
GAM2030	LOC90141 3'	GGGAGGCCAAAGCAGGAGGATC 62306	A CTC	
	A	TGATCC CCTGC GGCCTCCC		

		ACTAGG GGACG CCGGAGGG	
		A AAA	
GAM2030	LOC90321 3'	GAGGCCGAGGCAAGAGGATT 62935	ACC
		GATCC TGCCTCGGCCTC	
		TTAGG ACGGAGCCGGAG	
		AGA	
GAM2030	LOC90321 3'	GGGAGGTTGAGGCAGGTGGATC 62937	
	A	TGATCCACCTGCCTCGGCCTCCC	
		ACTAGGTGGACGGAGTTGGAGGG	
GAM2030	LOC90333 3'	GAGGCAAAGACAGGTAGGTCA 62960	C C CG
		TGATC ACCTG CT GCCTC	
		ACTGG TGGAC GA CGGAG	
		A A AA	
GAM2030	LOC90509 3'	GGGAGGCCGAGACAGGCGGATC 63796	A C
	A	TGATCC CCTG CTCGGCCTCCC	
		ACTAGG GGAC GAGCCGGAGGG	
		C A	
GAM2030	LOC90589 3'	GGGAGGCCGAGGCAGGCGGACC 59775	A A
	A	TG TCC CCTGCCTCGGCCTCCC	
		AC AGG GGACGGAGCCGGAGGG	
		C C	
GAM2030	LOC90591 3'	AGGCTAAGGCAGGTGGATCA 64147	CG
		TGATCCACCTGCCT GCCT	
		ACTAGGTGGACGGA CGGA	
		AT	
GAM2030	LOC90591 3'	GGAGGCTGAGGCAGGAGAATCA 64175	CCA
		TGAT CCTGCCTCGGCCTCC	
		ACTA GGACGGAGTCGGAGG	
		AGA	
GAM2030	LOC90624 3'	GGGAGGCTGAGGCAGGAAAATC 64371	CCA
	A	TGAT CCTGCCTCGGCCTCCC	
		ACTA GGACGGAGTCGGAGGG	
		AAA	
GAM2030	LOC90624 3'	GGGAGGCTGAGGCGGGCAGATC 64372	CA
	A	TGATC CCTGCCTCGGCCTCCC	
		ACTAG GGGCGGAGTCGGAGGG	
		AC	
GAM2030	LOC90639 3'	GGAAGCTGAGGCAGGAGGATCA 64413	A C
		TGATCC CCTGCCTCGGC TCC	

		ACTAGG GGACGGAGTCG AGG		
		A A		
GAM2030	LOC90777 3'	GGGAGGCTGAGGCAGGAGGATC 64667	A	
	A	TGATCC CCTGCCTCGGCCTCCC		
		ACTAGG GGACGGAGTCGGAGGG		
		A		
GAM2030	LOC90784 5'	GGAGGCTGAGGCAGGAGAATCA 64698	CCA	
		TGAT CCTGCCTCGGCCTCC		
		ACTA GGACGGAGTCGGAGG		
		AGA		
GAM2030	LOC90785 3'	GGGAGGCTCAGGCAGGAGAATC 64717	CCA	C
	A	TGAT CCTGCCT GGCCTCCC		
		ACTA GGACGGA TCGGAGGG		
		AGA C		
GAM2030	LOC91035 3'	GGGAGGCTGAGGCAGGAGAATC 65302	CCA	
	A	TGAT CCTGCCTCGGCCTCCC		
		ACTA GGACGGAGTCGGAGGG		
		AGA		
GAM2030	LOC91056 3'	GAGGCTGCGGCGGGTGGATCA 96406		T
		TGATCCACCTGCC CGGCCTC		
		ACTAGGTGGGCGG GTCGGAG		
		C		
GAM2030	LOC91250 5'	GGGAGGCCAAGGCAGGAGAATC 65919	CCA	C
	G	TGAT CCTGCCT GGCCTCCC		
		GCTA GGACGGA CCGGAGGG		
		AGA A		
GAM2030	LOC91380 3'	GGAGGCTGAGGCAGGAGAATCA 66449	CCA	
		TGAT CCTGCCTCGGCCTCC		
		ACTA GGACGGAGTCGGAGG		
		AGA		
GAM2030	LOC91380 3'	GGGAGGTTGAGGCGGGTGGATC 66451		
	A	TGATCCACCTGCCTCGGCCTCCC		
		ACTAGGTGGGCGGAGTTGGAGGG		
GAM2030	LOC91442 3'	GGGAGGCCGAAGACAGCGGATC 66646	AC	C _
	AT	ATGATCC CTG CT CGGCCTCCC		
		TACTAGG GAC GA GCCGGAGGG		
		C_ A A		
GAM2030	LOC91442 3'	GGGAGGCCGAGGCATGAGAATC 66647	_ _	CC
	A	TGAT C CA TGCCTCGGCCTCCC		

		ACTA G GT ACGGAGCCGGAGGG	
		A A _	
GAM2030	LOC91574 3'	GGGAGGCCGAGGCGGGCGGATC 67113	A
	A	TGATCC CCTGCCTCGGCCTCCC	
		ACTAGG GGGCGGAGCCGGAGGG	
		C	
GAM2030	LOC91574 3'	GGGAGGCTAAGACAGGAAGATC 67114	CA C CG
	A	TGATC CCTG CT GCCTCCC	
		ACTAG GGAC GA CGGAGGG	
		AA A AT	
GAM2030	LOC91664 3'	GGGAGGCCAAGACCAATAGATC 67406	CACCTGC C
	A	TGATC CT GGCCTCCC	
		ACTAG GA CCGGAGGG	
		ATAACCA A	
GAM2030	LOC91750 3'	GGGAGGCCGAGGCAGGTGGATC 67656	
	AT	ATGATCCACCTGCCTCGGCCTCCC	
		TACTAGGTGGACGGAGCCGGAGGG	
GAM2030	LOC91948 3'	GGGAGGCCAAGGTGGGTGGATC 68238	TG C
	A	TGATCCACC CCT GGCCTCCC	
		ACTAGGTGG GGA CCGGAGGG	
		GT A	
GAM2030	LOC92078 3'	GGGAGGCCGAGGTGAGTGGATC 68607	CT
	A	TGATCCAC GCCTCGGCCTCCC	
		ACTAGGTG TGGAGCCGGAGGG	
		AG	
GAM2030	LOC92223 3'	GGGAGACTGAGGCAGGAGAATC 69052	CCA C
	A	TGAT CCTGCCTCGG CTCCC	
		ACTA GGACGGAGTC GAGGG	
		AGA A	
GAM2030	LOC92228 3'	GGGAGGCCGAGGCGGGGAGATC 69078	CA
	A	TGATC CCTGCCTCGGCCTCCC	
		ACTAG GGGCGGAGCCGGAGGG	
		AG	
GAM2030	LOC92231 3'	GGGAGGCTGTGGCGGGCGGATC 69092	A T
	A	TGATCC CCTGCC CGGCCTCCC	
		ACTAGG GGGCGG GTCGGAGGG	
		C T	
GAM2030	LOC92270 5'	GGGAGGCCAAGGGAGTGGATCA 69187	C G C
		TGATCCAC T CCT GGCCTCCC	

		ACTAGGTG A GGA CCGGAGGG	
		_ G A	
GAM2030	LOC92283 3'	GGGAGGCCGAGGCGGGCGGATC 69305	A
	A	TGATCC CCTGCCTCGGCCTCCC	
		ACTAGG GGGCGGAGCCGGAGGG	
		C	
GAM2030	LOC92299 3'	GGGAGGCCGAGGCAGGTGGAT 69372	
		ATCCACCTGCCTCGGCCTCCC	
		TAGGTGGACGGAGCCGGAGGG	
GAM2030	LOC92405 3'	GGAGGCCGAGGCAGGCGGATCA 69714	A
		TGATCC CCTGCCTCGGCCTCC	
		ACTAGG GGACGGAGCCGGAGG	
		C	
GAM2030	LOC92465 3'	GGGAGGCCAAGGTGGGTAGATC 69952	C TG C
	AT	ATGATC ACC CCT GGCCTCCC	
		TACTAG TGG GGA CCGGAGGG	
		A GT A	
GAM2030	LOC92465 5'	GGGAGGCTGAGGCAGGCGGATC 69953	A
	A	TGATCC CCTGCCTCGGCCTCCC	
		ACTAGG GGACGGAGTCGGAGGG	
		C	
GAM2030	LOC92465 5'	GGGAGGCTGTGGCAGGAAAATC 69954	CCA T
	A	TGAT CCTGCC CGGCCTCCC	
		ACTA GGACGG GTCGGAGGG	
		AAA T	
GAM2030	LOC92482 3'	GGGAGGCCAACGGGGGCGGATC 70023	A G TC_
	A	TGATCC CCT CC GGCCTCCC	
		ACTAGG GGG GG CCGGAGGG	
		C _ CAA	
GAM2030	LOC92499 5'	GGGAGGCCGAGGCAGGCAGATC 70108	CA
	A	TGATC CCTGCCTCGGCCTCCC	
		ACTAG GGACGGAGCCGGAGGG	
		AC	
GAM2030	LOC92573 5'	GGGAGGCCGAGGCAGGCAGATC 70377	CA
	A	TGATC CCTGCCTCGGCCTCCC	
		ACTAG GGACGGAGCCGGAGGG	
		AC	
GAM2030	LOC92661 5'	GGGAGGCCGAGGCAAGAGGGTC 70631	ACC
	AT	ATGATCC TGCCTCGGCCTCCC	

			TACTGGG ACGGAGCCGGAGGG	
			AGA	
GAM2030	LOC93132	5'	AGGCTGAGGCAGGAGAATCA 71976	CCA
			TGAT CCTGCCTCGGCCT	
			ACTA GGACGGAGTCGGA	
			AGA	
GAM2030	LOC93132	5'	GGGAGGCCAAGGCGGGTGGAT 71994	C
			ATCCACCTGCCT GGCCTCCC	
			TAGGTGGGCGGA CCGGAGGG	
			A	
GAM2030	LOC93132	5'	GGGAGGCTGAGGCAGGTGGATC 71995	
	A		TGATCCACCTGCCTCGGCCTCCC	
			ACTAGGTGGACGGAGTCGGAGGG	
GAM2030	LOC93613	3'	GGGAGGCCGAGGCGGGCAGATC 73077	CA
	A		TGATC CCTGCCTCGGCCTCCC	
			ACTAG GGGCGGAGCCGGAGGG	
			AC	
GAM2031	C1orf6	3'	CTCTCTGGACAGGAATTAACA 39694	G GC
			TGT GA CCTGTCCAGAGAG	
			ACA TT GGACAGGTCTCTC	
			A AA	
GAM2031	MYLK2	3'	CTCCCCAGACAGGGCTCCA 53584	CA__
			TGGAGCCCTGTC GAG	
			ACCTCGGGACAG CTC	
			ACCC	
GAM2031	PKIG	3'	CTCATGGAGCTCCACAGA 23926	A CCTG _
			TC TGTGGAGC TCCA GAG	
			AG ACACCTCG AGGT CTC	
			_ _ _ A	
GAM2031	STK6	3'	CTCCCTATTGAGAAAGCTCCAC 14587	C__ TCC A
	AT		ATGTGGAGC CTG AG GAG	
			TACACCTCG GAC TC CTC	
			AAA TTA C	
GAM2031	THBD	3'	CTCAGACAGAACCCCTACATGA 6276	AGCC_ CA
			TCATGTGG CTGTC GAG	
			AGTACATC GACAG CTC	
			CCCAA A_	
GAM2031	CNNM4	3'	CTCCCCAGTGGGCCACATGA 39863	A TGTCCA
			TCATGTGG GCCC GAG	

AGTACACC CGGG CTC
 _ TGACCC
 GAM2031 FLJ10352 3' CTCTCTGGACAAAGCATC 50471 _ CC
 GA GC TGTCCAGAGAG
 || || |||||
 CT CG ACAGGTCTCTC
 A AA
 GAM2031 FLJ10352 3' CTCTTAAGGAGCCTCACATGA 50472 GA _ GTCC
 TCATGTG GC CCT AGAG
 ||||| || ||| |||
 AGTACAC CG GGA TCTC
 TC A AT__
 GAM2031 FLJ21977 5' GGACAAAGCTCACATGA 50872 G CC
 TCATGTG AGC TGTCC
 ||||| ||| |||||
 AGTACAC TCG ACAGG
 _ AA
 GAM2031 KIAA0461 3' CTCTGGACAAAGGATCATACA 71395 _ G C_
 TGTG GA CC TGTCCAGAG
 ||| || || |||||
 ACAT CT GG ACAGGTCTC
 A A AA
 GAM2031 KIAA1130 3' CTCTGGGCTTCCTCCACATGG 63090 CCCT
 TCATGTGGAG GTCCAGAG
 ||||| |||||
 GGTACACCTC CGGGTCTC
 CTT_
 GAM2031 MGC10471 5' CTCTGCCAGGCTCCACAAGA 48765 A C TC
 TC TGTGGAGCC TG CAGAG
 || ||||| || |||||
 AG ACACCTCGG AC GTCTC
 A _ C_
 GAM2031 LOC146562 3' TCTCTGGACCCACGTGA 58255 AGCCCT
 TCATGTGG GTCCAGAGA
 ||||| |||||
 AGTGCACC CAGGTCTCT
 C____
 GAM2031 LOC148753 3' CTCCAACAGCCCCACATGG 85371 A CC CCA
 TCATGTGG GC TGT GAG
 ||||| || ||| |||
 GGTACACC CG ACA CTC
 C _ AC_
 GAM2031 LOC148946 3' CTCTAAGGAGGACCCTACATGA 85467 AG_ CTG AG
 TCATGTGG CC TCC AGAG
 ||||| || ||| |||
 AGTACATC GG AGG TCTC
 CCA _ AA
 GAM2031 LOC154739 5' TCTCTGGCCCTCCACTGA 87446 T CCCT T
 TCA GTGGAG G CCAGAGA
 || ||||| | |||||

AGT CACCTC C GGTCTCT
 _ C____
 GAM2031 LOC166341 3' CTCCCAGTGGGCCCCACATGA 83514 A TGTCCA
 TCATGTGG GCCC GAG
 ||||| ||| ||
 AGTACACC CGGG CTC
 C TGACC_
 GAM2031 LOC203276 3' TCTCTGGCCCTCCACTGA 92133 T CCCT T
 TCA GTGGAG G CCAGAGA
 ||| ||||| | |||||
 AGT CACCTC C GGTCTCT
 _ C____
 GAM2031 LOC203305 3' TCTCTGGCCCTCCACTGA 92186 T CCCT T
 TCA GTGGAG G CCAGAGA
 ||| ||||| | |||||
 AGT CACCTC C GGTCTCT
 _ C____
 GAM2031 LOC204084 5' CTCTCTGGACAGACTGACA 90996 GG CC
 TGT AG CTGTCCAGAGAG
 ||| || |||||
 ACA TC GACAGGTCTCTC
 G_ A_
 GAM2031 LOC254243 3' TCTCTGGCCCTCCACTGA 99272 T CCCT T
 TCA GTGGAG G CCAGAGA
 ||| ||||| | |||||
 AGT CACCTC C GGTCTCT
 _ C____
 GAM2031 LOC90038 3' TCTCTGGCCCTCCACTGA 61816 T CCCT T
 TCA GTGGAG G CCAGAGA
 ||| ||||| | |||||
 AGT CACCTC C GGTCTCT
 _ C____
 GAM2031 LOC91661 3' CTCCCCACCCCGGGCTCCAACA 57212 _ T__ CCA
 TGT GGAGCCC GT GAG
 ||| ||||| || |||
 ACA CCTCGGG CA CTC
 A CCC CCC
 GAM2031 LOC93444 5' CTCTCCAGACAGGGTACAACCTT 72825 T GGA CA
 GA TCA GT GCCCTGTC GAGAG
 ||| || ||||| |||||
 AGT CA TGGGACAG CTCTC
 T ACA AC
 GAM2032 BACH2 3' CTGTCAAGCAATGGATAAACAG 41782 C GGGA__
 CTCT AGAGTTGTT ATCCA GACAG
 ||||| ||||| |||||
 TCTCGACAA TAGGT CTGTC
 A AACGAA
 GAM2032 CHRNA1 3' CTGTCTCCCTGAAGAGTGAAC 5375 C____
 GTTCAT CAGGGAGACAG
 ||||| |||||

		CAAGTG GTCCCTCTGTC		
		AGAA		
GAM2032 HHIP	5'	CTGTCCCACCTAAACAACCTC 42753		CATCCAG A
		GAGTTGTT GG GACAG		
		CTCAACAA CC CTGTC		
		ATCCA__ _		
GAM2032 MME	3'	TCCCTATGGAGGAACAACCTCT 8034		A __
		AGAGTTGTTC TCCA GGGA		
		TCTCAACAAG AGGT CCCT		
		G AT		
GAM2032 MTCP1	5'	CTACATGGATAACAACCTCT 27242		C GGG
		AGAGTTGTT ATCCA AG		
		TCTCAACAA TAGGT TC		
		_ ACA		
GAM2032 NR1D1	3'	TGTCTCCCCACAACCCT 41672	A	TCATCCA
		AG GTTGT GGGAGACA		
		TC CAACA CCCTCTGT		
		C CC_____		
GAM2032 NR1I2	3'	TGTCTCCCTAGGGAATTC 15304	GTTCA _	
		GAGTT TCC AGGGAGACA		
		CTTAA GGG TCCCTCTGT		
		_____ A		
GAM2032 PCOLN3	3'	CTGCCCTGTTGCCAAACAACCTC 12411	_____ TC _	
		GAGTTGTT CA CAGGG AG		
		CTCAACAA GT GTCCC TC		
		ACC T_ G		
GAM2032 PFN2	3'	TGTCTTCATCAACAACCCT 54889	A	CATCCAG
		AG GTTGT GGAGACA		
		TC CAACAA CTTCTGT		
		C CTA_____		
GAM2032 PFN2	3'	TGTCTTCATCAACAACCCT 54890	A	CATCCAG
		AG GTTGT GGAGACA		
		TC CAACAA CTTCTGT		
		C CTA_____		
GAM2032 TNS	3'	CTGTCTCCCTAACTCAACTGCT 42950	_	TTCATCC
		AG AGTTG AGGGAGACAG		
		TC TCAAC TCCCTCTGTC		
		G TCAA_____		
GAM2032 FLJ10511	3'	CCCTAGAAAAACAACCTCT 36686	CA C	
		AGAGTTGTT TC AGGG		

TCTCAACAA AG TCCC
 AA A
 GAM2032 FLJ20195 3' CCCGATGAACACCTCT 35216 T CA
 AGAG TGTTTCATC GGG
 |||| ||||| ||
 TCTC ACAAGTAG CCC
 C _
 GAM2032 HAAO 3' TCCCTGCCAAACAACCTCT 60173 CATC
 AGAGTTGTT CAGGGA
 ||||| ||||
 TCTCAACAA GTCCCT
 ACC_
 GAM2032 KIAA0843 3' CTGAACAACCAGACAGACAACCT 30801 CA CA GAGA_
 CT AGAGTTGTT TC GG CAG
 ||||| || || ||
 TCTCAACAG AG CC GTC
 AC A_ AACAA
 GAM2032 KIAA1497 5' CTGTCCTTGTATGAGCAAC 68121 C GA
 GTTGTTTCAT CAGGGA CAG
 ||||| ||||| ||
 CAACGAGTA GTTCCT GTC
 T _
 GAM2032 KIAA1710 3' TCTCCATACATGAACAATCT 63181 G CCAG
 AGA TTGTTCAT GGAGA
 || ||||| ||||
 TCT AACAAGTA CCTCT
 _ CATA
 GAM2032 PDE7B 3' CTGCCGAAATGAGCAACTC 38949 CCA G
 GAGTTGTTCAT GG AG
 ||||| || ||
 CTCAACGAGTA CC TC
 AAG G
 GAM2032 SEC24B 3' CTGCATTGTTGGATGACAACCTC 21984 T G GA
 T AGAGTTGT CATCCAG GA CAG
 ||||| ||||| || ||
 TCTCAACA GTAGGTT TT GTC
 _ G AC
 GAM2032 LOC124753 5' CTGCCTCCCTGGCTTCCATCTC 74803 T TTCAT A
 GAG TG CCAGGGAG CAG
 || || ||||| ||
 CTC AC GGTCCCTC GTC
 T CTTC_ C
 GAM2032 LOC142948 3' CTACCGGGAGGAATGAATAACT 83777 _ A G
 C GAGTTGTTCA TCC GG AG
 ||||| || || ||
 CTCAATAAGT AGG CC TC
 AAGG G A
 GAM2032 LOC153914 5' CCACTAAAGTGAACAACCTC 81898 CC_ _
 GAGTTGTTCAT AG GG
 ||||| || ||

CTCAACAAGTG TC CC
 AAA A
 GAM2032 LOC219445 5' CTCCCTGGTTCAAACAATTC 93202 CAT_
 GAGTTGTT CCAGGGAG
 ||||| |||||
 CTTAACAA GGTCCCTC
 ACTT
 GAM2032 LOC219914 5' CCACTGGGAGGAACGAACAAC 94967 A____ _
 C GAGTTGTT TCCAG GG
 ||||| |||||
 CTCAACAAG GGGTC CC
 CAAGGA A
 GAM2033 ATP2B2 5' CAGCCATCACCCGGCAGC 9846 A _
 GCT CTGGGTGA GCTG
 || ||||| |||
 CGA GGCCCACT CGAC
 C AC
 GAM2033 BSCL2 5' GGACTACCGGCTTTACCCTCCC 51994 T____ T__ ACTA
 AGTAGCT AGCTACTGGG GAGC GG CC
 ||||| ||| || ||
 TCGATGACCC TTCG CC GG
 TCCCAT G__ ATCA
 GAM2033 IMPA2 5' AGTGTGTGCTCACCCACAGC 96944 AC _ G
 GCT TGGGTGAGC TG ACT
 || ||||| || |||
 CGA ACCCACTCG GT TGA
 C_ T G
 GAM2033 KCNE1L 3' AGTCCAGCTTCCAGTTGC 25388 T GT
 GC ACTGG GAGCTGGA
 || |||| |||||
 CG TGACC TTCGACCTGA
 T _
 GAM2033 KRTHA1 3' GGCAGCCAAGAACTCACCCAA 11237 AC C____ A A
 AGC GCT TGGGTGAG TGG CT CC
 || ||||| ||| |||
 CGA ACCCACTC ACC GA GG
 A_ AAAGA _ C
 GAM2033 MADH7 3' AGTATTGCTCACCCAGTGC 20922 T TGG
 GC ACTGGGTGAGC ACT
 || ||||| |||
 CG TGACCACTCG TGA
 _ TTA
 GAM2033 SQSTM1 3' GCTACCAGCAGCCCAGCACATA 15328 ____ GA T__ ACTA
 GCT AGCTA CTGGGT GC GG C
 |||| ||||| || || |
 TCGAT GACCCG CG CC G
 ACAC A_ A__ ATCA
 GAM2033 TPI1 3' AGCCCAGAAGCCAGTAACT 6294 C GAG A
 AG TACTGGGT CTGG CT
 || ||||| |||||

TC ATGACCCG GACC GA
 A AA_ C
 GAM2033 TRHDE 3' GGTATTCTCACCCAGTAG 26316 CTGG
 CTACTGGGTGAG ACT
 ||||| |||
 GATGACCCACTC TGG
 TTA_
 GAM2033 CAPN6 3' CAGCATTTACCCAGCAGC 27398 A ____
 GCT CTGGGTGA GCTG
 ||| ||||| |||
 CGA GACCCACT CGAC
 C TTA
 GAM2033 DT1P1A10 3' AGTTTCTGGGCCCACCCTAGCA 62246 A _ A ____
 GC GCT CT GGGTG GCT GGACT
 ||| || ||||| ||| |||||
 CGA GA CCCAC CGG TTTGA
 C T C GTC
 GAM2033 FLJ12700 3' GGCAGTCCACAGGCCTACAGCT 46657 AC GAGC A
 AGCT TGGGT TGGACT CC
 |||| ||||| ||||| ||
 TCGA ATCCG ACCTGA GG
 C_ GAC_ C
 GAM2033 FLJ32780 3' AGTCCTCTGGTCCCACAGCT 59297 AC _G CT
 AGCT TGGG T AG GGACT
 |||| ||||| || |||||
 TCGA ACCC G TC CCTGA
 C_ T G T_
 GAM2033 HRD1 3' CCTGTCTCACCCAGCAGC 70148 A _T
 GCT CTGGGTGAG C GG
 ||| ||||| || ||
 CGA GACCCACTC G CC
 C T T
 GAM2033 KIAA0356 3' GGTCTATGGGCCACCCAGTGC 66779 T A ____
 GC ACTGGGTG GCT GGACT
 || ||||| ||| |||||
 CG TGACCCAC CGG TCTGG
 _ C GTA
 GAM2033 KIAA0984 3' AGCTCACTCACCCACCAGCT 66137 AC C GA
 AGCT TGGGTGAG TG CT
 |||| ||||| || ||
 TCGA ACCCACTC AC GA
 CC _ TC
 GAM2033 KIAA1598 5' GTAGTCCAAGTGGGATATTAGC 37639 ____ G GAGC
 GCTA CT GGT TGGACTAC
 |||| || ||| |||||
 CGAT GG TCA ACCTGATG
 TATA G ____
 GAM2033 KIAA1681 3' AGTCCAAGTCCAGTAACT 61714 C GTGA _
 AG TACTGG GCT GGACT
 || ||||| ||| |||||

		TC ATGACC TGA CCTGA		
		A ____ A		
GAM2033	MGC17303	3' GGCAGTCAGATCCACCCAGTGC 58233	T	AG_ G A
		T AGC ACTGGGTG CTG ACT CC		
		TCG TGACCCAC GAC TGA GG		
		_ CTA _ C		
GAM2033	PDE4DIP	5' CCAGTGGTCACCCAGTAGC 97175	__ T__	
		GCTACTGGGTGA GC GG		
		CGATGACCCACT TG CC		
		GG A__		
GAM2033	SLC26A10	5' CCGGTAACCCAACAGTGGCT 56842	__ GA T__	
		AGCTACT GGGT GC GG		
		TCGGTGA CCCA TG CC		
		CAA A_ G__		
GAM2033	USP2	5' AGCCGGGACTCACCCGCAGCT 16108	AC __ A	
		AGCT TGGGTGAG CTGG CT		
		TCGA GCCCACTC GGCC GA		
		C_ AG _		
GAM2033	LOC143425	3' CTACTCACTCAGTAGCT 89013	C	
		AGCTACTGGGTGAG TGG		
		TCGATGACTCACTC ATC		
		-		
GAM2033	LOC145828	5' AGTCCCTCCCAGTGGCT 84537	TGAGCT	
		AGCTACTGGG GGACT		
		TCGGTGACCC CCTGA		
		TC__		
GAM2033	LOC151174	5' GGCCCGGCTCACCCACAGCT 86438	ACT A	
		AGCT GGGTGAGCTGG CT		
		TCGA CCCACTCGGCC GG		
		CAC C		
GAM2033	LOC158055	3' AGGCCTCCACCCAGTGCT 82576	T AGCT A	
		AGC ACTGGGTG GG CT		
		TCG TGACCCAC CC GA		
		_ CT_ G		
GAM2033	LOC158696	3' GTAGATCCACCAATAGCT 82861	C GTGAGC _	
		AGCTA TGG TGGA CTAC		
		TCGAT ACC ACCT GATG		
		A ____ A		
GAM2033	LOC196027	3' GGTTTTCACCCAGTAGTT 88940	CTG	
		AGCTACTGGGTGAG GACT		

TTGATGACCCACTT TTGG

GAM2033 LOC200812 5' CAGCCCATCCAGTATGCT 90301 _ A
AGC TACTGGGTG GCTG
||| ||||| |||
TCG ATGACCTAC CGAC
T C

GAM2033 LOC253836 5' CAGCGCTTCACCCAGTGC 99465 T _
GC ACTGGGTGA GCTG
|| ||||| |||
CG TGACCCACT CGAC
_ TCG

GAM2033 LOC256436 3' AGCCCAGAAGCCCAGTAACT 96247 C GAG A
AG TACTGGGT CTGG CT
|| ||||| ||| ||
TC ATGACCCG GACC GA
A AA_ C

GAM2033 LOC256492 5' TCCAGCTCAGTACAGCAGC 99434 A GG_
GCT CTG TGAGCTGGA
||| ||| |||||
CGA GAC ACTCGACCT
C ATG

GAM2033 LOC56181 3' GTCACCTCACTCAGCAGCT 97284 A CTG
AGCT CTGGGTGAG GAC
||| ||||| |||
TCGA GACTCACTC CTG
C A_

GAM2033 LOC92148 5' TCTACACACCCAGTACT 68888 C AGC
AG TACTGGGTG TGGA
|| ||||| |||
TC ATGACCCAC ATCT
_ AC_

GAM2034 SCAMP1 3' GCTAAATAAATATTCTCC 54500 T C
GGA AATATT ATTTAGC
||| ||||| |||||
CCT TTATAA TAAATCG
C A

GAM2034 SCAMP1 3' GCTAAATAAATATTCTCC 54501 T C
GGA AATATT ATTTAGC
||| ||||| |||||
CCT TTATAA TAAATCG
C A

GAM2034 NX-17 3' TGAATATCAGCCCCTAATA 40706 ATA_
TATTAGGG ATATTCA
||||| |||||
ATAATCCC TATAAGT
CGAC

GAM2034 LOC161589 3' GCTAAATGAATATTATCCCTAA 83159
TA TATTAGGGATAATATTCATTTAGC
|||||

ATAATCCCTATTATAAGTAAATCG

GAM2035 ARF5 3' CTCTGGGCACAGAGGGGTCCAC 9784 G ATT _
GTGGA CCCTCTGTGT CC GAG
||||| ||||| || |||
CACCT GGGAGACACG GG CTC
G _ T

GAM2035 BSG 3' CTTGGCCACAGAGGACTC 9955 C TATT
GAG CCTCTGTG CCGAG
||| ||||| |||||
CTC GGAGACAC GGTTC
A C _

GAM2035 BSG 3' CTTGGCCACAGAGGACTC 68406 C TATT
GAG CCTCTGTG CCGAG
||| ||||| |||||
CTC GGAGACAC GGTTC
A C _

GAM2035 DUSP2 3' CTCAGAGTTTCAGAAGCCCCCA 16628 A_ CC TGT C
C GTGG GC TCTG ATTC GAG
||||| || ||||| ||||| |||
CACCC CG AGAC TGAG CTC
CC A_ TT_ A

GAM2035 GNA11 5' CGGGGACTCCAGAGGGCTGCAC 76587 G T_ A
GTG AGCCCTCTG GT TTCCG
||| ||||| || |||||
CAC TCGGGAGAC CA GGGGC
G CT _

GAM2035 CDK5RAP3 5' CTCAAAGGCACAGAGGCCTCCA 48060 C ATTCC
C GTGGAG CCTCTGTGT GAG
||||| ||||| ||||| |||
CACCTC GGAGACACG CTC
C GAAA_

GAM2035 FACVL1 5' CTCGCTGGGACAGAGGGCCCCG 14673 A GTATTC
C GTGG GCCCTCTGT CGAG
||||| ||||| ||||| |||
CGCC CGGGAGACA GCTC
C GGGTC_

GAM2035 LOC150358 3' CGGGCACACAGAGGGCACCAC 86096 A AT
GTGG GCCCTCTGTGT TCCG
||||| ||||| ||||| |||||
CACCC CGGGAGACACA GGGC
A C _

GAM2035 LOC51026 3' CTCTTAATACACAGAGAACTCC 32685 CC CC
GGAG CTCTGTGTATT GAG
||||| ||||| ||||| |||
CCTC GAGACACATAA CTC
AA TT

GAM2036 ATP11A 3' CAAGCTCCTACAGGCTTGCTCT 77551 A _ A ATCA
CA TGA AG AAGCC TG AGCTTG
||| || ||||| || |||||

ACT TC TTCGG AC TCGAAC
 C G _ ATCC
 GAM2036 ZNF26 5' AGTTGGAATCACAGCTTCTTT 73337 CA CA__
 TA TGAAGAAGC TGAT AGCT
 ||||| ||| |||
 ATTTTCTTCG ACTA TTGA
 AC AAGG
 GAM2036 DKFZP564I0422 3' CTTATCATGGCCTCTCTCA 49513 A A C
 TGA AGA GCCATGAT AAG
 ||| ||| ||||| |||
 ACT TCT CGGTACTA TTC
 C C _
 GAM2036 EIF5 3' AAAGTTGATTTTCTTTC 10508 GCCAT C
 GAAAGAA GATCAAG TT
 ||||| ||||| ||
 CTTTCTT TTAGTTC AA
 _ A
 GAM2036 FLJ13231 3' CAAGTTTGCATAACCTACTTTC 43815 A CC_ AT
 A TGAAAG AG ATG CAAGCTTG
 ||||| || ||| |||||
 ACTTTC TC TAC GTTTGAAC
 A CAA _
 GAM2036 RPS6KB1 3' CAAGCTTGGTCAAACCTTTTCCC 13469 AA CCA
 A TG AGAAG TGATCAAGCTTG
 || ||||| |||||
 AC TTTTC ACTGGTTCGAAC
 CC AA_
 GAM2036 LOC148418 3' TGCATCATGGCCCCTTCA 79594 A AA _
 TGAA G GCCATGAT CA
 |||| | ||||| ||
 ACTT C CGGTACTA GT
 _CC C
 GAM2037 AMPH 3' GGTTTTTAAACCTTCATGA 9687 C_
 TCA AGGTTTAAAAACC
 ||| |||||
 AGT TCCAAATTTTGG
 ACT
 GAM2037 MPZ 3' GGTTTTTAAACAACCAAACAA 6752 CACAG_
 TTGT GTTTAAAAACC
 |||| |||||
 AACA CAAATTTTGG
 AACCAA
 GAM2037 PITX2 3' TTTTTCGCTTGCGAGCAAGGGA 6162 _ A TT
 TCCCTTG TC CAGGT AAAA
 ||||| || ||||| |||
 AGGGAAC AG GTTCG TTTT
 G C CT
 GAM2037 PLXNA1 3' GTTTGACATGACAAGG 72773 CAG TAA
 CCTTGTC GTT AAAC
 ||||| || |||

GGAACAGT CAG TTTG
 A__ __
 GAM2037 PPP1R12B 3' GTTTTCCTTGTGACAAG 50394 TTTA
 CTTGTCACAGG AAAAC
 ||||| ||||
 GAACAGTGTTT TTTG
 C__
 GAM2037 AND-1 3' GGTTTTTGTGTCATGTGCAAGG 24009 T GGTT
 CCTTG CACA TAAAAACC
 |||| ||| |||||
 GGAAC GTGT GTTTTTGG
 _ ACT_
 GAM2037 CECR7 5' GTTCTGTCCCATGACAAGG 80450 CA TT A
 CCTTGTC GG TA AAAC
 ||||| || |||||
 GGAACAGT CC GT TTTG
 A_ CT C
 GAM2037 DKFZp761P1010 3' TGGACCTGTGCAAAGGA 37945 C T
 TCC TTG CACAGGTTTA
 ||| ||| |||||
 AGG AAC GTGTCCAGGT
 A _
 GAM2037 FLJ11301 3' GGTCCTCCGACTCTAAACAAG 37809 CACA TAAA_
 GGA TCCCTTGT GGTT AACC
 ||||| ||| ||||
 AGGGAACA TCAG TTGG
 AATC CCTCC
 GAM2037 FLJ11320 3' TTTTGAACACAAGGGA 37832 CACAG
 TCCCTTGT GTTTAAAA
 ||||| |||||
 AGGGAACA CAAGTTTT

 GAM2037 FLJ13385 3' GTTTTTTAAACCTTAAAAAAGG 46284 GTCAC _
 CCTT AGGTTT AAAAAC
 ||| ||||| |||||
 GGAA TCCAAA TTTTG
 AAAAT A
 GAM2037 KIAA0227 5' GGCTTTTAAACCCGGAAGG 61351 G ACA A
 CCTT TC GGTTTAAAA CC
 ||| || ||||| ||
 GGAA GG CCAAATTTT GG
 G C__ C
 GAM2037 KIAA0546 3' AGCTTGTTTTCCACGGCAAGGG 71837 _____
 A TCCCTTGTC ACAGGTT
 ||||| |||||
 AGGGAACGG TGTTCA
 CACCTTT
 GAM2037 KIAA1078 3' TTTTAAACATGTACAAAGGG 65719 _ C G
 CCCTT GT ACA GTTTAAAAA
 |||| || ||| |||||

GGGAA CA TGT CAAATTTT
A _ A
GAM2037 KIAA1233 3' GGTTTAGTCTGTGAAAAAG 63758 G_ GT TAA
CTT TCACAG T AAACC
||| ||||| | ||||
GAA AGTGTC A TTTGG
AA TG____
GAM2037 KIAA1724 3' GGTTTCATGCCCTGTGACTAAG 67621 _ TTAA
CTT GTCACAGG AAACC
||| ||||| ||||
GAA CAGTGTCC TTTGG
T CGTAC
GAM2037 KIAA1795 3' GGCTTTTAAATTATAATAAGG 72617 CACAGG A
GA TCCCTTGT TTAAAA CC
||||| ||||| ||
AGGGAATA AAATTTT GG
ATATTA C
GAM2037 MAP 3' GGTTC AACCTGTGATAAAAGA 43368 CC TAA
TC TTGTCACAGGTT AACC
|| ||||| ||||
AG AATAGTGTCCAA TTGG
AA C____
GAM2037 MGC2454 3' TTTTGTGAGCCTGTAACAA 48286 C
TTGT ACAGGTTTAAAAA
||||| ||||| |||||
AACA TGTCCGAGTTTTT
A
GAM2037 SLC17A3 5' TTGAGTCCCACAGCAAGGGA 22792 CACA _
TCCCTTGT GG TTAA
||||| || ||||
AGGGAACG CC GAGTT
ACAC T
GAM2037 TLK2 3' GGTTTTTGCCATTGGACAA 23396 A GTT
TTGTC CAG TAAAAACC
||||| || |||||
AACAG GTT GTTTTTGG
_ ACC
GAM2037 TLK2 3' GGTTTTTGCCATTGGACAA 78809 A GTT
TTGTC CAG TAAAAACC
||||| || |||||
AACAG GTT GTTTTTGG
_ ACC
GAM2037 LOC146237 3' GACCTGCCAGACAAGGGA 84611 A____
TCCCTTGTC CAGGTT
||||| |||||
AGGGAACAG GTCCAG
ACC
GAM2037 LOC147976 5' GGTCTTTTGAATCACAAGGGA 79291 CACA _
TCCCTTGT GGTTTAAAA ACC
||||| ||||| |||||

		AGGGAACA CTAAGTTTT TGG		
		_____ C		
GAM2037	LOC150208 5'	GGTTTTTATGATAGTGCAAGG 86078	T	AGGTT
		CCTTG CAC TAAAAACC		
		GGAAC GTG ATTTTTGG		
		_ ATAGT		
GAM2037	LOC151103 3'	GGTTTTTGAATGTAACAAG 86412	C	GG
		CTTGT ACA TTAAAAACC		
		GAACA TGT AAGTTTTTGG		
		A _		
GAM2037	LOC200186 3'	TGAATTCTGCGCAAGGGA 91568	CA	_
		TCCCTTGT CAGG TTTA		
		AGGGAACG GTCT AAGT		
		C_ T		
GAM2037	LOC205011 5'	GGTCCTTAAACCTCGAAGACA 92331	AC__	AA
		TGTC AGGTTTAA ACC		
		ACAG TCCAAATT TGG		
		AAGC CC		
GAM2037	LOC220164 3'	GGCTTTTAAAGTTCTGACAGGG 93445	C G	A
		CCTTGTCAG TTTAAAA CC		
		GGGACAGT TT AAATTTT GG		
		C G C		
GAM2037	LOC253263 3'	TTTAAACTATGTACAAGGGA 98819	C	_
		TCCCTTGT ACA GGTTTAAA		
		AGGGAACA TGT TCAAATTT		
		_ A		
GAM2037	LOC83693 3'	GGTTTTTAAATGTGCATCAAG 49606	TCA	G
		CTTG CA GTTTAAAAACC		
		GAAC GT TAAATTTTTGG		
		TAC G		
GAM2037	LOC92335 3'	GTTTTGAGACACAAGGGA 69546	CACAGG	A
		TCCCTTGT TTTAAAA C		
		AGGGAACA GAGTTTT G		
		CA__ C		
GAM2038	CHRM1 3'	GCATCAGCAAGACAATGACA 96433	CCC	CTC_
		TGTTATTGTC TGC GC		
		ACAGTAACAG ACG CG		
		A_ ACTA		
GAM2038	COX15 3'	CAGGCTGATGGAGACAGTAACA 55279	C	TGCCTC
		TGTTATTGTC CC GCCTG		

ACAATGACAG GG CGGAC
 A TAGT__
 GAM2038 FLJ22056 3' AGGCCCTGGGGACAATACA 42830 T TGCCTC
 TGT ATTGTCCCC GCCT
 ||| ||||| |||
 ACA TAACAGGGG CGGA
 _ TCC__
 GAM2038 GDF11 3' CAGACGAGGCAGAGACAAAACA 20558 A CC C
 TGTT TTGTC CTGCCTCG CTG
 ||| |||| ||||| |||
 ACAA AACAG GACGGAGC GAC
 _ A_ A
 GAM2038 SNX11 3' CAGACGGGAACAGTAACA 26170 _ _
 TGTTATTGT CCC CTG
 ||||| ||| |||
 ACAATGACA GGG GAC
 A CA
 GAM2038 ZAK 3' CAGACACAGAGCAAGACAATAA 34099 CCC _ CGC_
 CA TGTTATTGTC TGC CT CTG
 ||||| ||| |||
 ACAATAACAG ACG GA GAC
 A_ A CACA
 GAM2038 LOC145622 3' CAGTAACGAACAGGGAACAGTA 77806 C CC C_
 ACA TGTTATTGT CCCTG TCG CTG
 ||||| |||| ||| |||
 ACAATGACA GGGAC AGC GAC
 A A_ AAT
 GAM2039 DPYSL3 3' GCTGTCCTTTGCCATCTCA 9127 A AT_
 TGAGA TGGCAA TAGT
 |||| ||||| |||
 ACTCT ACCGTTT GTCG
 _ CCT
 GAM2039 HMGN2 3' GATAAATTCTGCCATTTTCA 19807 A A
 TGAGAATGGCA AATT GTC
 ||||| |||| |||
 ACTTTTACCGT TTAA TAG
 C A
 GAM2039 IL1RAPL2 5' AGGCAGCATCTGCCATTCT 34273 AAATTA C
 AGAATGGCA GT GCCT
 ||||| || |||
 TCTTACCGT CG CGGA
 CTA__ A
 GAM2039 TPST2 3' GACAGATTTGCCATCCTC 14581 A A A
 GAG ATGGCAAA TT GTC
 ||| ||||| || |||
 CTC TACCGTTT AG CAG
 C _ A
 GAM2039 DKFZP434I092 3' GACTTGTGCCATTCTCA 68412 AAATT
 TGAGAATGGCA AGTC
 ||||| ||| |||

			ACTCTTACCGT	TCAG		
			GT__			
GAM2039	FLJ22283	5'	AGACGATGACTTGTCCATTCTC	50900	_	AATTA C
		A	TGAGAATGG CAA	GTCG CT		
			ACTCTTACC GTT	TAGC GA		
			T CAG__	A		
GAM2039	FLJ22969	3'	GCCGGTTCCTTGCCATTTC	69208	A	_ TA
			TGAGA TGGCAA	AAT GT		
			ACTTT ACCGTT	TTG CG		
			_	CC GC		
GAM2039	KIAA0426	3'	AGGCACTTGCCACCATTC	28919	A	CAAAATT C
			TG GAATGG	AGT GCCT		
			AC CTTACC	TCA CGGA		
			C	ACCGT__	_	
GAM2039	KIAA1190	3'	AGGCGACTAGGGCACCATACTC	71642	A	CAAAA
		A	TGAG ATGG	TTAGTCGCCT		
			ACTC TACC	GATCAGCGGA		
			A	ACGG__		
GAM2039	KIAA1715	3'	GCTTAAATTTTGCCTCCTCA	68687	AAT	_
			TGAG	GGCAAAATT AGT		
			ACTC	CCGTTTTAA TCG		
			CT_	AT		
GAM2039	KIAA1871	3'	GCAAATAATTTACCATTTTCA	61905	CA	GTC
			TGAGAATGG	AAATTA GC		
			ACTTTTACC	TTTAAT CG		
			A_	AAA		
GAM2039	PASK	3'	ACTGAGATCCTGACATTCTCA	31400	G	AAA__
			TGAGAATG	CA TTAGT		
			ACTCTTAC	GT AGTCA		
			A	CCTAG		
GAM2039	PCL1	3'	GATATTTTGCCATTATCA	33294	G	TA
			TGA	AATGGCAAAAT GTC		
			ACT	TTACCGTTTTA TAG		
			A	_		
GAM2039	ZNF317	5'	AGGCAAAGTGAAGTCCATTCTC	72472	AAA	C_
			GAGAATGGCA	TTAGT GCCT		
			CTCTTACCGT	AGTCA CGGA		
			C_	AA		
GAM2039	LOC133308	3'	GACACTTGCCATGTCTCA	75592	_	AATTA
			TGAGA	ATGGCAA GTC		

	ACTCT TACCGTT CAG		
	G CA__		
GAM2039 LOC145540 3'	GATAAATTCTGCCATTTTCA 77778	A	A
	TGAGAATGGCA AATT GTC		
	ACTTTTACCGT TTAA TAG		
	C A		
GAM2039 LOC148915 3'	GATAAATTCTGCCATTTTCA 79809	A	A
	TGAGAATGGCA AATT GTC		
	ACTTTTACCGT TTAA TAG		
	C A		
GAM2039 LOC150580 3'	GATAAATTCTACCATTTTCA 61067	CAA	A
	TGAGAATGG AATT GTC		
	ACTTTTACC TTAA TAG		
	ATC A		
GAM2039 LOC152212 3'	GATAAATTCTGCCATTTTCA 83711	A	A
	TGAGAATGGCA AATT GTC		
	ACTTTTACCGT TTAA TAG		
	C A		
GAM2039 LOC152267 3'	GATAAATTCTGCCATTTTCA 61035	A	A
	TGAGAATGGCA AATT GTC		
	ACTTTTACCGT TTAA TAG		
	C A		
GAM2039 LOC152343 3'	AGGCGAGTGCCACCATGCTCA 81417	A	CAAAAT G
	TGAG ATGG TA TCGCCT		
	ACTC TACC GT AGCGGA		
	G ACC__ G		
GAM2039 LOC88584 3'	GATAAATTCTGCCATTTTCA 61101	A	A
	TGAGAATGGCA AATT GTC		
	ACTTTTACCGT TTAA TAG		
	C A		
GAM2040 CDH12 3'	CTTATCATTTAAAGTGGTGTA 15777	CCCAA	GA
	TACACCACT GAA ATAAG		
	ATGTGGTGA TTT TATTC		
	AA__ AC		
GAM2040 GOCAP1 3'	ATTGTTCTTGGGAGCAGTGTA 43007	CA	G
	TACAC CTCCCAAGAA AAT		
	ATGTG GAGGGTTCTT TTA		
	AC G		
GAM2040 DKFZp434N2435 5'	CTTATTACTGTGGGGTGGT 98090	T	AGAAG
	ACCAC CCCA AATAAG		

		TGGTG GGGT TTATTC	
		_ GTCA_	
GAM2040	DKFZP564I122	3' CTTATTCTTCTCCCTCATGTGT 63877	CACTCCCA
	A	TACAC AGAAGAATAAG	
		ATGTG TCTTCTTATTC	
		TACTCCC_	
GAM2040	FLJ21791	3' CTTATTTGCAGAAAGTGGTGTA 62126	CCCAAGAA
		TACACCACT GAATAAG	
		ATGTGGTGA TTTATTC	
		AGACG__	
GAM2040	HMP19	3' CTTATTCTTTGTTAGGAAAATG 88860	CCAC CAA_
	TA	TACA TCC GAAGAATAAG	
		ATGT AGG TTTCTTATTC	
		AAA_ ATTG	
GAM2040	KIAA1719	3' TCTGTCTTGGGAGTGGTGTA 68742	_
		TACACCACTCCCAAGA AGA	
		ATGTGGTGAGGGTTCT TCT	
		G	
GAM2040	KIAA1853	3' TTTTCTTGAAGCAGTG 69929	CA C
		CAC CT CCAAGAAGAA	
		GTG GA GGTTCTTTT	
		AC A	
GAM2040	KIAA1877	3' CTTATTCTTCTGCCATGAGT 66748	CCA__
		ACTC AGAAGAATAAG	
		TGAG TCTTCTTATTC	
		TACCG	
GAM2040	KIAA1906	3' CTTATTCTTCTTGACTTTTGG 73571	CTCC_
		CCA CAAGAAGAATAAG	
		GGT GTTCTTCTTATTC	
		TTTCA	
GAM2040	OSBPL11	3' CTTAATTTCCCAAGAGTGGTG 43206	CCAA AA
		CACCACTC GAAG TAAG	
		GTGGTGAG CTTT ATTC	
		AACC A_	
GAM2040	YME1L1	3' TCATTCTTGATGTGGTGTA 58438	TCC _
		TACACCAC CAAGAA GA	
		ATGTGGTG GTTCTT CT	
		TA_ A	
GAM2040	ZNF262	3' CTTATTTTGTGTTGGGAGT 18723	A
		ACTCCCAAG AGAATAAG	

TGAGGGTTT TTTTATTC
 G
 GAM2040 LOC91960 3' TGTGGCTTGGAACGTGGTGTA 68294 TC_ AAGA
 TACACCAC CCAAG ATA
 ||||| ||| ||
 ATGTGGTG GGTTC TGT
 CAA GG_
 GAM2041 ACATN 5' GATGGCTCCCGGCTTCAG 17597 AGTG CA A
 TTGAAGCC GGG CCA TC
 ||||| || ||||
 GACTTCGG CCC GGT AG
 ____ TC C
 GAM2041 B3GALT2 3' GTGTCTCAGGCTCAA 15032 A AG
 TTGA GCC TGGGGCAC
 ||| || |||||
 AACT CGG ACTCTGTG
 - -
 GAM2041 CD164 3' GGA CTAGTGCAGAGGCTTTAA 21197 AGTGGG CAA
 TTGAAGCC GCAC TCC
 ||||| ||| ||
 AATTTCGG CGTG AGG
 AGA__ ATC
 GAM2041 HPS4 3' ATTGGTGCCACAAGCTTC 42226 CAG G
 GAAGC TG GGCACCAAT
 ||| || |||||
 CTTCG AC CCGTGGTTA
 A__ A
 GAM2041 SDPR 5' GACTGGTGCCCTGAGCTCCAA 17400 A CAG A
 TTG AGC TGGGGCACCA TC
 ||| || ||||| ||
 AAC TCG GTCCCGTGGT AG
 C A__ C
 GAM2041 C5orf6 3' GATTGGCTGTGCCAGCTTC 33954 CAG G _
 GAAGC TGG GCA CCAATC
 |||| ||| || |||||
 CTTCG ACC TGT GGTTAG
 ____ G C
 GAM2041 C8orf17 3' GGACCACACTGGCTGCAA 39998 A G CA
 TTG AGCCAGTG GG CC
 ||| ||||| || ||
 AAC TCGGTCAC CC GG
 G A A_
 GAM2041 CABP5 5' GACTGGTGCCCTGCGAGCTCCA 39562 A CA TG A
 TG AGC G GGGCACCA TC
 || ||| | ||||| ||
 AC TCG C CCCGTGGT AG
 C AG GT C
 GAM2041 FLJ13940 3' GGA CTGGTGCCCCACAGGCTTT 47309 A A
 AA TTGAAGCC GTGGGGCACCA TCC
 ||||| ||||| |||

AATTTTCGG CACCCCGTGGT AGG
 A C
 GAM2041 KCNMB2 3' ATTGGTGGACTGGTTTCAA 20684 GGGG
 TTGAAGCCAGT CACCAAT
 ||||| |||||
 AACTTTGGTCA GTGGTTA
 G__
 GAM2041 KIAA0530 3' GATTGGTGTATAGCTTTAA 71431 CAGTGGG
 TTGAAGC GCACCAATC
 ||||| |||||
 AATTTTCG TGTGGTTAG
 ATA__
 GAM2041 KIAA1522 3' GGATTGGCCTTCCTGTGCCTCA 65607 A _ TG AC
 A TTGA GC CAG GGGC CAATCC
 ||| || ||| |||||
 AACT CG GTC TCCG GTTAGG
 C T CT _
 GAM2041 KIAA1853 3' GGATGCCCACTAGTCCAA 69924 AA C _
 TTG GC AGTGGGGCA CC
 ||| || ||||| ||
 AAC TG TCACCCCGT GG
 C_ A A
 GAM2041 LOXL4 3' GATTGGTCTAAACTTCAA 50859 CCAG GGC
 TTGAAG TGG ACCAATC
 ||||| || |||||
 AACTTC ATC TGGTTAG
 AA__ _
 GAM2041 LSR7 5' GGACCGGCCCTGCCCCCGGCTT 38280 AGT _ AA
 CAA TTGAAGCC GGGGCA CC TCC
 ||||| ||||| || |||
 AACTTCGG CCCC GT GG AGG
 C_ CCC CC
 GAM2041 PLK 3' GGA CTGGTGCCCTCCTCACT 18525 CC TG A
 AG AG GGGCACCA TCC
 || || ||||| |||
 TC TC CCCGTGGT AGG
 AC CT C
 GAM2041 STK22D 3' GGTCCCCACTGGCCGCAA 50145 AA C
 TTG GCCAGTGGGG ACC
 ||| ||||| |||
 AAC CGGTCACCCC TGG
 GC _
 GAM2041 LOC124871 3' TGCTGCCCCACCAGCTTCAG 74818 CA C
 TTGAAGC GTGGGGCA CA
 ||||| ||||| ||
 GACTTCG CACCCCGT GT
 AC C
 GAM2041 LOC157349 3' GACTGGCTGCTGGCTCCGA 82341 A TG GGCA A
 TTG AGCCAG G CCA TC
 ||| ||||| | ||| ||

AGC TCGGTC C GGT AG
 C GT ____ C
 GAM2041 LOC222550 5' GGATCAATATCGTGCTGGCTT 96018 G CACCA
 AAGCCAGTG GG ATCC
 ||||| || |||
 TTCGGTCGT CT TAGG
 G ATAAC
 GAM2042 GEM 3' CAAATATAAGAAAGCTG 19150 CTAGC
 CAGCTT TTTATATTTG
 |||| | |||||
 GTCGAA GAATATAAAC
 A ____
 GAM2042 MBD4 3' ATAAAAATAAAAGCTGAC 15386 C GC
 GTCAGCTT TA TTTAT
 ||||| || ||||
 CAGTCGAA AT AAATA
 A AA
 GAM2042 STMN1 3' CAAATATTTTAGAAGCT 19912 CTTT
 AGCTTCTAG ATATTTG
 ||||| |||||
 TCGAAGATT TATAAAC
 T ____
 GAM2042 LOC158160 3' GTAAAGCCAGAGCTGAC 73474 T A
 GTCAGCT CT GCTTTAT
 ||||| || |||||
 CAGTCGA GA CGAAATG
 _ C
 GAM2042 LOC164971 5' GCAAACATAATCCAAGCTGAT 83348 CTAGCT A
 GTCAGCTT TTAT TTTGC
 ||||| || |||||
 TAGTCGAA AATA AAACG
 CCT ____ C
 GAM2042 LOC220549 5' GCAAATATTGAGCAAACACTGA 94508 CTTCTA T
 C GTCAG GCTT ATATTTGC
 |||| ||| |||||
 CAGTC CGAG TATAAACG
 ACAA_ T
 GAM2043 PODXL 3' TGTCCCCTCCCAATCCCCCA 19420 AAT TC TA
 TGGGGG TTGG AG GGACA
 |||| ||| || ||||
 ACCCCC AACC TC CCTGT
 CT_ C_ C_
 GAM2043 SYNGR3 3' TGCCCCTGCCAAGTTCCCCCA 16125 T TA A
 TGGGGGAATTTGG CAG GG CA
 ||||| ||| || ||
 ACCCCCTTGAACC GTC CC GT
 _ C_ _
 GAM2043 KIAA0152 3' TCCCATCGAAATTCCCCA 28982 A CAGTA
 TGGGGGA TTTGGT GGA
 ||||| |||| |||

ACCCCTT AAGCTA CCT
 A C____
 GAM2043 KIAA1894 3' TACCCTCCCAATTCCCCCA 74287 T TCA
 TGGGGGAATT GG GTA
 ||||| || ||
 ACCCCCTTAA CC CAT
 C TCC
 GAM2043 USP24 3' GTCCTACTGTTTCCCCTA 92793 TTTGGT
 TGGGGGAA CAGTAGGAC
 ||||| |||||
 ATCCCCTT GTCATCCTG
 T____
 GAM2043 LOC163944 5' TGCCCCACTCTTGCCATTTCCC 88424 TT C__ A A
 C GGGGAA TGGT AGT GG CA
 |||| ||| || ||
 CCCCTT ACCG TCA CC GT
 T_ TTC C C
 GAM2044 CROT 3' ACATATCATTAACACTGAGTG 41254 T A
 CACTC GTTTAATGA GTGT
 |||| ||||| ||||
 GTGAG CAAATTACT TACA
 T A
 GAM2044 EGFL3 3' GGACACTTCACGGGCCAGAG 63300 TTAA_
 CTCTG TGAAGTGTCC
 |||| |||||
 GAGAC ACTTCACAGG
 CCGGGC
 GAM2044 EGFL5 3' ACATTTATTAAACAGAAGT 87900 _ G
 ACT CTGTTTAATGAA TGT
 || ||||| ||||
 TGA GACAAATTATT ACA
 A _
 GAM2044 MS4A8B 3' GACAGAGATTTTAAACAGATGT 49587 C TGAAG_
 T AACA TCTGTTTAA TGTC
 |||| ||||| ||||
 TTGT AGACAAATT ACAG
 _ TTAGAG
 GAM2044 PLXNA2 3' ACACTTCGCAAAAACAGAG 48000 AA_
 CTCTGTTT TGAAGTGT
 ||||| |||||
 GAGACAAA GCTTCACA
 AAC
 GAM2044 PTGFRN 3' GATATTTAAACAGGTG 67768 T TGAA
 CAC CTGTTTAA GTGTC
 || ||||| ||||
 GTG GACAAATT TATAG
 _ _
 GAM2044 VHL 3' GGACACTTTGTAGAAAGTG 6863 CTG TG
 CACT TTAA AAGTGTCC
 |||| |||| |||||

			GTGA AGATT TTCACAGG			
			A__ GT			
GAM2044	BTN3A2	5'	GACACTCAAGGACAGA 23877	AA	A	
			TCTGTTT TGA GTGTC			
			AGACAGG ACT CACAG			
			A_ _			
GAM2044	BTN3A3	5'	GACACTCAAGGACAGA 23765	AA	A	
			TCTGTTT TGA GTGTC			
			AGACAGG ACT CACAG			
			A_ _			
GAM2044	DKFZp434G171	3'	GGACAAGTTAAACAGAATGT 80244	C		GAAG
			ACA TCTGTTTAAT TGTCC			
			TGT AGACAAATTG ACAGG			
			A A__			
GAM2044	DKFZp434K1210	3'	GACACTTGTGCACAGGTGT 34691	T	TTA	G
			ACAC CTGT AT AAGTGTC			
			TGTG GACA TG TTCACAG			
			_ CG_ _			
GAM2044	FBXO32	3'	GGACACTTCATTTGTAAATAG 55243			
			CTGTTTA ATGAAGTGTC			
			GATAAAT TACTTCACAGG			
			GTT			
GAM2044	HTCD37	3'	GACACTTCACTACTCCAGG 68301	TT_	A	
			TCTG TA TGAAGTGTC			
			GGAC AT ACTTCACAG			
			CTC C			
GAM2044	KIAA0748	3'	GACATGATAAACAGAAGT 29615	_		ATGAA
			ACT CTGTTTA GTGTC			
			TGA GACAAAT TACAG			
			A AG__			
GAM2044	MAP3K6	3'	GACAAAGCGTATTAAACAGA 17428			AAG__
			TCTGTTTAATG TGTC			
			AGACAAATTAT ACAG			
			GCGAA			
GAM2044	MGC10715	3'	GGACACTCAGGCACAGAGTG 44499	TTAA	A	
			CACTCTGT TGA GTGTCC			
			GTGAGACA ACT CACAGG			
			CGG_ _			
GAM2044	MYH10	3'	GGACACATATATTAAACAGATT 69672	C		AA_
	GTT		AACA TCTGTTTAATG GTGTCC			

			TTGT AGACAAATTAT CACAGG		
			T ATA		
GAM2044	NUDT13	3'	GACACTTCTATCAGCAGTGTT 63906	_	TTTAAT
			AACACT CTG GAAGTGTC		
			TTGTGA GAC CTTCACAG		
			C TAT__		
GAM2044	PCCX2	3'	GGACACTTCATTCCTTGCA 66586	TT__	
			TGT AATGAAGTGTCC		
			ACG TTA CTTT CACAGG		
			TTCC		
GAM2044	TEB4	3'	ACCTTGATTAAACAGAATGT 61281	C	G_ T
			ACA TCTGTTTAAT AAG GT		
			TGT AGACAAATTA TTC CA		
			A GG _		
GAM2044	TTY8	3'	GGACACTCCATTTTCTTGGA 51833	TTT_	A
			TCTG AATG AGTGTCC		
			AGGT TTAC TCACAGG		
			TCTT C		
GAM2044	LOC199775	3'	ACTACACTAAATCAGAGTGTT 89722	_	A A
			AACACTCTG TTTA TG AGT		
			TTGTGAGAC AAAT AC TCA		
			T C A		
GAM2044	LOC203197	3'	GGACACCCTTGGACAGA 90813	TGAA	
			TCTGTTTAA GTGTCC		
			AGACAGGTT CACAGG		
			CC__		
GAM2044	LOC204285	3'	GACCACTAACAGAGTG 91017	TAATGA	_
			CACTCTGTT AGTG TC		
			GTGAGACAA TCAC AG		
			_____ C		
GAM2044	LOC219513	5'	GGACGTCATCAAACAGAG 95988	A	AG
			CTCTGTTT ATGA TGTCC		
			GAGACAAA TACT GCAGG		
			C _		
GAM2044	LOC256221	5'	GGACACTTGTTTAAACAAG 96914	C T G	
			CT TGTT AAT AAGTGTCC		
			GA ACAA TTG TTCACAGG		
			_ T _		
GAM2045	KIAA1069	3'	TGACCTACATTCAACTGCAA 68535	_	C_
			TTGCAGTTGAA GT GTCG		

			AACGTCAACTT CA CAGT		
			A TC		
GAM2045	NICN1	3'	TGGCGACTTCATCTGCAA 51261	T	
			TTGCAG TGAAGTCGTCG		
			AACGTC ACTTCAGCGGT		
			T		
GAM2045	TEX27	3'	GCTGAACACCTGCAACTGCAA 41952	A TC CG	
			TTGCAGTTG AG GT TAGC		
			AACGTCAAC TC CA GTCG		
			G CA A_		
GAM2045	LOC142948	3'	TGGCCACCGGCCCAACTGCAG 83782	AA TC A	
			TTGCAGTTG GTCG GT GCCA		
			GACGTCAAC CGGC CA CGGT		
			C_ _ C		
GAM2045	LOC146488	5'	GCTACAACCGCTTCAACAACAA 71359	CA C C	
			TTG GTTGAAGT GT GTAGC		
			AAC CAACTTCG CA CATCG		
			AA C A		
GAM2045	LOC147080	3'	TGCACAACCTTCAGCCACAA 85053	CA C C	
			TTG GTTGAAGT GT GTA		
			AAC CGACTTCA CA CGT		
			AC A _		
GAM2045	LOC152845	5'	GCGGTGACCTCAGCTGCAA 60958	A GT	
			TTGCAGTTGA GTC CGT		
			AACGTCGACT CAG GCG		
			C TG		
GAM2045	LOC203052	3'	ACCACCATTTCAACTGCA 92073	C C	
			TGCAGTTGAAGT GT GT		
			ACGTCAACTTTA CA CA		
			C C		
GAM2045	LOC204084	5'	GGCCAGACCTCCAACCTGCAG 91000	A TC GTA	
			TTGCAGTTG AG GTC GCC		
			GACGTCAAC TC CAG CGG		
			C _ AC_		
GAM2046	ABCC1	3'	TCTGTGGACTGCAAGTCTTTGA 39606	A _ A	
	G		TTCA GAGG TTG TAGTTTATGGA		
			GAGT TTCT AAC GTCAGGTGTCT		
			_ G _		
GAM2046	ABH	3'	TCCAAACTCCCTGTTGGCTTTT 60464	TG TTTA_	
	T		AAGAGGT ATAG TGGA		

			TTTTTCG TGTC ACCT		
			GT CCTCAA		
GAM2046	ABR	3'	TGGATACAGCCTTTTGG 42010	ATA	
			TCAAGAGGTTG GTTTA		
			GGTTTTCCGAC TAGGT		
			A__		
GAM2046	ADAMTS1	3'	AGTGAGGATTATTAACCTCTGA 23748	A	ATGGA
	G		TTCA GAGGTTGATAGTTT		
			GAGT CTCCAATTATTAGG		
			AGTGAT		
GAM2046	ADAT1	5'	TTCATAAACTATACTGCCTTGT 24921	A	TG_
	GA		TCA GAGGT ATAGTTTATGGA		
			AGT TTCCG TATCAAATACTT		
			G TCA		
GAM2046	ADORA2A	5'	CTGTGAAAAAGCCCTTGGA 7277	A	GATAG
			TTCAAG GGTT TTTATGG		
			AGGTTC CCGA AAGTGTC		
			AA__		
GAM2046	AGPAT2	3'	TTATAAACACACTCTTGGA 22184	_	TGATA
			TTCAAGAG GT GTTTATGG		
			AGGTTCTC CA CAAATATT		
			A _____		
GAM2046	AGRN	3'	TTTGTAAACTTGTTGCTTTTGG 79589	TGAT	TG
	A		TCAAGAGGT AGTTTA GA		
			AGTTTTTCG TCAAAT TT		
			TTGT GT		
GAM2046	ALDH1B1	3'	CCATGGAATATTCCTTGGA 7319	AG	TGATAG
			TTCAAG GT TTTATGG		
			AGGTTC TA AGGTACC		
			CT TA__		
GAM2046	AMPD3	3'	CTGTGAATCTCCTCATGAA 6653	A	TT AGT
			TTCA GAGG GAT TTATGG		
			AAGT CTCC CTA AGTGTC		
			A T_ __		
GAM2046	APXL	3'	CTGTACTCAGCCTTTTGA 9714	TAGTT	
			TCAAGAGGTTGA TATGG		
			AGTTTTCCGACT ATGTC		
			C__		
GAM2046	APXL	3'	TGATAATTTATTAACCTTTTGG 9717	T	GGA
	A		TTCAAGAGGTTGATAG TTAT		

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AGGTTTTTCAATTATT AATA
      T  GT
GAM2046 ARSB  5' TTTATAAGCTTTTTTCTTATGA 5280    A  TT T
      A
      TTCA GAGG GA AGTTTATGGA
      ||| ||| || |||||
      AAGT TTCT TT TCGAATATTT
      A  TT _
GAM2046 ATF4  5' TCCGTGAGCGTCCATTTTGTGG 9811    A  T  A
      A
      TTCA GAGGT GAT GTTTATGGA
      ||| |||| || |||||
      AGGT TTTA CTG CGAGTGCCT
      G  C _
GAM2046 ATP11B 3' TTCATGAATATAAGGCTTCTAG 81128    A  GATA
      AA
      TTC AGAGGT GTTTATGGA
      || ||||| |||||
      AAG TCTTCGG TAAGTACTT
      A  AATA
GAM2046 ATP8B2 5' TCCTGCCTGTCAACCTCTTTGA 65849    _  TTTAT
      TCAA GAGGTTGATAG GGA
      ||| ||||| |||
      AGTT CTCCAAGTGTG CCT
      T  CGT__
GAM2046 B3GALT3 3' TCTGTAGACTAGAATTTCTT 53719    GA
      AAGAGGT TAGTTTATGGA
      ||||| |||||
      TTCTTTAA ATCAGATGTCT
      G_
GAM2046 BN51T 3' TTCATGGGCTATTATAGATGAA 88880    AGAGGT
      TTCA TGATAGTTTATGGA
      ||| |||||
      AAGT ATTATCGGGTACTT
      AGAT__
GAM2046 BSG 3' TCTGTGGCTTTCAGCCTCT 9959    T  T
      AGAGGTTGA AGTT ATGGA
      ||||| ||| |||
      TCTCCGACT TCGG TGTCT
      T  _
GAM2046 CALU 3' TCTGTGAATGCTAGCTCTCTTG 8697    _  ATA
      AA
      TTCAAGAG GTTG GTTTATGGA
      ||||| ||| |||||
      AAGTTCTC CGAT TAAGTGTCT
      T  CG_
GAM2046 CALU 3' AATTATTTGCCTTTTGAA 8693    T
      TTCAAGAGGT GATAGTT
      ||||| |||||
      AAGTTTTCCG TTATTAA
      T
GAM2046 CARD15 3' TTTGTAAATTGTCAGATGCT 42473    AGG  TG
      AG TTGATAGTTTA GA
      || ||||| ||

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			TC GACTGTAAAT TT		
			GTA GT		
GAM2046	CAV1	3'	TCTGTGGGCTGGCAGTCCT 10024	_ A	
			AGG TTG TAGTTTATGGA		
			TCC GAC GTCGGGTGTCT		
			T G		
GAM2046	CCND3	3'	GGCTTTGGCTTCTTGGA 10061	TG T	
			TTCAAGAGGT A AGTT		
			AGGTTCTTCG T TCGG		
			GT _		
GAM2046	CCR2	3'	TCTGATTCTGTCAATGTCTTGA 7224	G TTTAT	
	A		TTCAAGA GTTGATAG GGA		
			AAGTTCT TAACTGTC TCT		
			G TTAG _		
GAM2046	CCT2	3'	CCACGTGCTGTCGATCTTTGGA 22229	A TTA A	
			TTCA GAGGTTGATAGT TGG		
			AGGT TTCTAGCTGTCTG ACC		
			_ TGC C		
GAM2046	CD86	3'	TTTGTAAGTTCCTGGGCAACCT 23540	_ A _ _ TG	
			TTTTGA TCAAGA GGTTG TAG TTTA GA		
			AGTTTT CCAAC GTC GAAT TT		
			T GG CTT GT		
GAM2046	CEBPD	3'	CCGCTGCAGTTTCTTGG 97803	GG A TTAT	
			TCAAGA TTG TAGT GG		
			GGTTCT GAC GTCG CC		
			TT _ _		
GAM2046	CELSR3	3'	TCGTAGATGCCCCTCTCTGGG 9192	_ TTGATA	
			TTCA AGAGG GTTTATGGA		
			GGGT TCTCC TAGATGCTT		
			C CCG _		
GAM2046	CIT	3'	TCCATGAGAAATGGGCTTCTTG 70307	G AG	
	AG		TTCAAGAGGTT AT TTTATGGA		
			GAGTTCTTCGG TA GAGTACCT		
			G AA		
GAM2046	CKAP1	5'	TTCATGGCTTGCTTCAATCTTT 73904	T _	
	TGA		TCAAGAGGTTGA AGT TTATGGA		
			AGTTTTCTAACT TCG GGTACTT		
			_ TTC		
GAM2046	CLECSF6	5'	TCTGTGAACTGCGGTTTTT 72083	GG A	
			AGA TTG TAGTTTATGGA		

			TTT GGC GTCAAGTGTCT		
			TT _		
GAM2046	COL3A1	3'	TTCATTGATTAATCTCCTGGA 5399	A	AGTTT
			TTCA GAGGTTGAT ATGGA		
			AGGT CTCTAATTA TACTT		
			C GT__		
GAM2046	CPNE3	3'	AATAATTTACCTTTTGAA 15342	T	A
			TTCAAGAGGT GAT GTT		
			AAGTTTTCCA TTA TAA		
			T A		
GAM2046	CREB1	3'	TCTGTATGTGTTCAACATTTTT 16493	_	TAGTT
	GAA		TTCAAGAG GTTGA TATGGA		
			AAGTTTTT CAACT ATGTCT		
			A TGTGT		
GAM2046	CRSP8	3'	TTTATAAGCAATAAACCTTTTG 81861	G	A
			CAAGAGGTT AT GTTTATGGA		
			GTTTTCCAA TA CGAATATTT		
			A A		
GAM2046	CTBP2	3'	CCTTTATCAGTCCCTTGG 9002	A _	TTTAT
			TCAAG GG TTGATAG GG		
			GGTTC CC GACTATT CC		
			_ T T__		
GAM2046	CTMP	3'	TCCATCTTCTCAACTTTTT 54955	T_	TTT
			AAGAGGTTGA AG ATGGA		
			TTTTTCAACT TC TACCT		
			CT _		
GAM2046	CXADR	3'	TCTATGAAATGACTTCTT 9030		GATAG
			AAGAGGTT TTTATGGA		
			TTCTTCAG AAGTATCT		
			TA__		
GAM2046	CYFIP1	3'	CCGTAAACTATTTAGTGAG 67048		AGAGGTT
			TTCA GATAGTTTATGG		
			GAGT TTATCAAATGCC		
			GAT__		
GAM2046	CYP1B1	3'	TCCATGAGTTATCATGAATTTT 5449	GGT_	GT
			AAGA TGATA TTATGGA		
			TTTT ACTAT AGTACCT		
			AAGT TG		
GAM2046	DDB1	3'	TGTGAATTGTTAGTTTCTGAG 10402	A	GG
			TTCA GA TTGATAGTTTATG		

			GAGT CT GATTGTTAAGTGT		
			_ TT		
GAM2046	DDX26	3'	TGACATGCATTGTTGGCTATTT 25115	A TG T GA	
	GAA		TTCAAG GGT ATAGT TATG		
			AAGTTT TCG TGTTA GTAC		
			A GT C AGTC		
GAM2046	DPH2L1	3'	AACTATCAATTCTTGAG 9109	G	
			TTCAAGAG TTGATAGTT		
			GAGTTCTT AACTATCAA		
			-		
GAM2046	DR1	5'	CCGAGGGCGACTTTTTTGAG 60085	GATA TA	
			TTCAAGAGGTT GTT TGG		
			GAGTTTTTCAG CGG GCC		
			GA		
GAM2046	DXS1283E	3'	TTTATAAAACCATCGGATCTCT 71390	_ AG_	
			TGAG TTCAAGAGGTT GAT TTTATGGA		
			GAGTTCTCTAG CTA AAATATTT		
			G CCA		
GAM2046	EGR3	3'	TTTGTGGATGTTTTATTCTT 60304	T TA_ TG	
	GGA		TTCAAGAGGT GA GTTTA GA		
			AGGTTCTTTA TT TAGGT TT		
			T TTG GT		
GAM2046	EIF2AK3	3'	TTTGTTCCTTTGTTAGTCTCTTG 17904	GT TTT TG	
	AA		TTCAAGAG TGATAG A GA		
			AAGTTCTC ATTGTT T TT		
			TG TCT GT		
GAM2046	EIF4G2	5'	TCTATTAATATTATTCTTTTGA 9221	GT GTTT	
	A		TTCAAGAG TGATA ATGGA		
			AAGTTTTC ATTAT TATCT		
			TT AAT_		
GAM2046	EIF5A2	3'	GAGGTATACTGTCAATTTCTTGA 40205	T T GGA	
	A		TTCAAGAGGT GATAGT TAT		
			AAGTTCTTTA CTGTCA ATG		
			_ T GAGC		
GAM2046	EMR1	3'	TTCGTGCTCTGCAACTTCTT 10518	A TT	
			AAGAGGTTG TAG TATGGA		
			TTCTTCAAC GTC GTGCTT		
			_ TC		
GAM2046	ESR2	5'	TCCAGCTGCTGGCTTTTTTGA 9324	GA TTA	
			TTCAAGAGGTT TAGT TGGA		

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AGGTTTTTTCGG GTCG ACCT
TC ____
GAM2046 EXT2 3' TCCATGAGCTATTCCTCTTTGG 6384 _ TT
TCAA GAGG GATAGTTTATGGA
||||| ||| |||||
GGTT CTCC TTATCGAGTACCT
T ____
GAM2046 FANCE 5' TCCGTTCCCTCAGCCTCTGAG 41902 A TAGTTT
TTCA GAGGTTGA ATGGA
||||| |||
GAGT CTCCGACT TGCCT
_ CCCCT_
GAM2046 FECH 3' TGGGTACAAATTGTGTGGTTTC 5555 TT_ ATGGA
TTGAG TTCAAGAGG G ATAGTTT
||||| | |||||
GAGTTCTTT T TGTTAAA
GG G CATGGGTT
GAM2046 FGF13 3' TCAATGGTTCTATTGACTTTTT 54442 TG T_ GGA
G CAAGAGGT ATAG TTAT
||||| ||| |||
GTTTTTCA TATC GGTA
GT TT ACTT
GAM2046 FKRP 3' TCCATAGCCATCTACTCTCTTG 44440 _ T A T
AG TTCAAGAG GT GAT GTT ATGGA
||||| || ||| |||
GAGTTCTC CA CTA CGA TACCT
T T C _
GAM2046 FUT4 3' AAGTTGTCAGCTTTTTGA 10720 GT
TCAAGAGGTTGATA TT
||||| |||
AGTTTTTCGACTGT AA
TG
GAM2046 GABPB1 3' TTTATGAACTGTTTAACCCTGA 19139 A A _
A TTCA G GGTTGA TAGTTTATGGA
||||| ||| |||||
AAGT C CCAATT GTCAAGTATTT
_ _ T
GAM2046 GALNT3 3' TTTATAAATTACTATCTGTTGA 16830 G TGA
A TTCAA AGGT TAGTTTATGGA
||||| ||| |||||
AAGTT TCTA ATTAAATATTT
G TC_
GAM2046 GAS1 3' TCCGGAGCTTGACTTCTTGGA 10763 TG TA A
TTCAAGAGGT A GTTT TGGA
||||| | ||| |||
AGGTTCTTCA T CGAG GCCT
GT _ _
GAM2046 GAS1 3' TTTATAAATTGTATGCTTC 10765 TG
GAGGT ATAGTTTATGGA
||||| |||||

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			CTTCG TGTAAATATTT	
			TA	
GAM2046	GAS7	3'	TTTATGAGCTGTTAAGAATGAG 20865	AGAGG
			TTCA TTGATAGTTTATGGA	
			GAGT AATTGTCGAGTATTT	
			AAG__	
GAM2046	GASC1	3'	TGAGTTGTTGGCCTTTGTGAA 64899	_ TG GT
			TTCA AGAGGT ATA TTA	
			AAGT TTTCCG TGT AGT	
			G GT TG	
GAM2046	GLI2	3'	TCTATGAAGCCTAACTCTTGAG 48290	GTTGATAG
			TTCAAGAG TTTATGGA	
			GAGTTCTC AAGTATCT	
			AATCCG__	
GAM2046	GNAI1	3'	TCTGTAGACTAGAGTCTTG 10822	GGTTGA
			CAAGA TAGTTTATGGA	
			GTTCT ATCAGATGTCT	
			GAG__	
GAM2046	GOLGA4	3'	TTTATTCAGGTTGATCTGTTGA 60697	G TG AGTTT
	A		TTCAA AGGT AT ATGGA	
			AAGTT TCTA TG TATTT	
			G GT GACT_	
GAM2046	GPC5	3'	TCTATAAGTTATGGGGTAGATT 16770	GT__ G GT
	CTTGAG		TTCAAGAG T ATA TTATGGA	
			GAGTTCTT G TAT AATATCT	
			AGATGG G TG	
GAM2046	GPR4	5'	TCCATACATAACCTCCTTGAA 60583	_ ATAGTT
			TTCAAG AGGTTG TATGGA	
			AAGTTC TCCAAT ATACCT	
			C AC__	
GAM2046	GPR85	3'	TCTGTAAATCTTTAGCCTTGTTG 39107	A TA
	AA		TTCA GAGGTTGA GTTTATGGA	
			AAGT TTCCGATT TAAATGTCT	
			G TC	
GAM2046	HK1	5'	TGAGCATTGTTGATGCTCTTGA 5749	_ TG TTATGGA
	G		TTCAAGAG GT ATAGT	
			GAGTTCTC TA TGTTA	
			G GT CGAGT	
GAM2046	HMGCS2	3'	CCATGGAAAGCTTCCTGG 19811	A TGATAG
			TCA GAGGT TTTATGG	

GGT CTTCG AGGTACC
C AA____
GAM2046 IL12RB2 3' GGCTGTTAATCACTTGGA 9562 A
TTCAAG GGTGATAGTT
||||| |||||||
AGGTTC CTAATTGTCGG
A
GAM2046 IL1RAP 3' TCCATAGGTTTTAATATTTTGA 10987 G T TT
G TTCAAGA GTTGA AG TATGGA
||||| |||| || |||||
GAGTTTT TAATT TT ATACCT
A _ GG
GAM2046 ISG20 3' AGGCTTTCGGCTTTTTTG 11020 T
TCAAGAGGTTGA AGTTT
||||||||| |||||
GGTTTTTCGGCT TCGGA
T
GAM2046 ITGAM 3' TTCAATGTGACTTTAATTTTTT 72318 T TA__
GGA TTCAAGAGGTTGA AGTT TGGA
||||||||| ||| |||
AGGTTTTTTAATT TCAG ACTT
_ TGTA
GAM2046 ITPR1 3' CTATGAACTGTTAAATC 11071 GG
GA TTGATAGTTTATGG
|| |||||||||||
CT AATTGTCAAGTATC
A_
GAM2046 JAG1 3' TTTATATTTATTGACTCTTGAG 5816 G TG TT
TTCAAGAG T ATAG TATGGA
||||||| | ||| |||||
GAGTTCTC A TATT ATATTT
_ GT T_
GAM2046 KCNMB3 5' TCCAAATGTGAACTTTTTGAG 27716 G GTTTA
TTCAAGAGGTT ATA TGGA
||||||||| ||| |||
GAGTTTTTCAA TGT ACCT
G AA____
GAM2046 KL 3' TTCATACATTTGACTTCTAGAA 17745 A TG TAGTT
TTC AGAGGT A TATGGA
||| ||||| | |||||
AAG TCTTCA T ATACTT
A GT TAC__
GAM2046 MAP3K7 3' TTTATGACTCTAATATTAATCT 13520 GT____
CTT AAGAGGTTGATA TTATGGA
||||||||| |||||
TTCTCTAATTAT AGTATTT
AATCTC
GAM2046 MCM2 3' CCATAAGGATTCTTGG 68521 AG GATAG
TCAAG GTT TTTATGG
||||| ||| |||||||

		GGTTC TAG GAATACC	
		CT _____	
GAM2046	MEOX1	3' TCTGTAGGCTGCACATCTGAG 16956	A GGT A
		TTCA GA TG TAGTTTATGGA	
		GAGT CT AC GTCGGATGTCT	
		_ AC_ _	
GAM2046	MEOX1	3' TCTGTAGGCTGCACATCTGAG 16957	A GGT A
		TTCA GA TG TAGTTTATGGA	
		GAGT CT AC GTCGGATGTCT	
		_ AC_ _	
GAM2046	MFGE8	3' TCCATGGGCCCGCTGCCTCTTG 21010	TGATA
	G	TCAAGAGGT GTTTATGGA	
		GGTTCTCCG CGGGTACCT	
		TCGCC	
GAM2046	MGEA5	3' TTCATACAGTTCAGCCTCTAGA 25229	A TAGTT
	A	TTC AGAGGTTGA TATGGA	
		AAG TCTCCGACT ATACTT	
		A TGAC_	
GAM2046	MGEA5	3' TTTGTAGGACTTAATCTGTTGA 25230	G TAG TG
	A	TTCAA AGGTTGA TTTA GA	
		AAGTT TCTAATT GGAT TT	
		G CA_ GT	
GAM2046	MIPOL1	5' TCTGTGAGCTGCAAATCTTGGA 77589	GG A
		TTCAAGA TTG TAGTTTATGGA	
		AGGTTCT AAC GTCGAGTGTCT	
		A_ _	
GAM2046	MKKS	5' TTCATAAACATTGAACCTTTTGT 38753	_ A
	A	TCAAGAGGTT GAT GTTTATGGA	
		AGTTTTTCAA TTA CAAATACTT	
		G _	
GAM2046	MKKS	5' TTCATAGGTGTCCATCTTGGA 38754	GGTT G
		TTCAAGA GATA TTTATGGA	
		AGGTTCT CTGT GGATACTT	
		AC_ _	
GAM2046	MPP5	3' TCTGTTCTTAGATCTCTTGAA 42749	GAT TTT
		TTCAAGAGGTT AG ATGGA	
		AAGTTCTCTAG TC TGTCT	
		AT_ T_	
GAM2046	MTMR2	3' TCTGTAAACATAACCTTATTTG 32912	_ ATA
	AA	TTCAA GAGGTTG GTTTATGGA	

			AAGTT TTCCAAT CAAATGTCT		
			TA A__		
GAM2046	MTMR6	3'	ACAGCTTAGAATATTGATTTCT 95196	TG G	TGGA
			TGAA TTCAAGAGGT ATA TTTA		
			AAGTTCTTTA TAT AGAT		
			GT A TCGACAT		
GAM2046	N33	3'	TCTATAACCTCAGCTTTTT 23154	TA T	
			AAGAGGTTGA G TTATGGA		
			TTTTTCGACT C AATATCT		
			__C		
GAM2046	NEDD4	3'	TTTGTGAACCTATCTAAGCATGA 70548	AGAGGTT	TG
			G TTCA GATAGTTTA GA		
			GAGT CTATCAAGT TT		
			ACGAAT_ GT		
GAM2046	NEK2	3'	TTCAAATCTGTTAGCTTTGTGA 11769	A	TTTA
			A TTCA GAGGTTGATAG TGGA		
			AAGT TTTCGATTGTC ACTT		
			G TAA_		
GAM2046	NFE2L1	3'	TTTATAAATTATTTTCCTT 13637	TT	
			GAGG GATAGTTTATGGA		
			TTCC TTATTAAATATTT		
			TT		
GAM2046	NGFR	3'	TCCATGAGTTTTTCTCTTGGG 11803	TT TAG	
			TTCAAGAGG GA TTTATGGA		
			GGGTTCTCT TT GAGTACCT		
			TT T__		
GAM2046	NR2E3	3'	TCCATGGAGTTCTGATCTTT 33419	_ TAG	
			AGAGGTT GA TTTATGGA		
			TTTCTAG CT AGGTACCT		
			T TG_		
GAM2046	NRL	5'	TCCATGGAGCCTTCAGTCTCCT 21629	A GT TA _	
			GG TCA GAG TGA GTTT ATGGA		
			GGT CTC ACT CGAG TACCT		
			C TG TC G		
GAM2046	OAT	3'	TCTATGGATGTCATTATTTTGA 6058	GGT G	
			A TTCAAGA TGATA TTTATGGA		
			AAGTTTT ACTGT AGGTATCT		
			ATT _		
GAM2046	OGT	3'	TCCATGGATTGATTCAGTCTTC 14596	AG GT _	
			TGGA TTCA AG TGA TAGTTTATGGA		

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AGGT TC ACT GTTAGGTACCT
CT TG TA
GAM2046 OGT 3' TTTATAGGTTTTATAAACCACT 14599 A GAT__ TT
TGAG TTCAAG GGTT AG TATGGA
||||| ||| || |||||
GAGTTC CCAA TT ATATTT
A ATATT GG
GAM2046 PCDH9 5' TGAGCTGTCAGTTTCTGAA 83696 A GG
TTCA GA TTGATAGTTTA
|||| || |||||
AAGT CT GACTGTCGAGT
_ TT
GAM2046 PCTP 3' TCCATGGGTTGATGTCTCTGGA 41374 _ G TG AGT
TTCA AGA GT AT TTATGGA
|||| || || |||||
AGGT TCT TA TG GGTACCT
C G GT ____
GAM2046 PDE7A 3' AGCAACAATCTCTTGGA 66132 ATA
TTCAAGAGGTTG GTT
||||||| |||
AGGTTCTCTAAC CGA
AA_
GAM2046 PER2 3' TTCATGAGCCCGACCTCT 43365 ATA
AGAGGTTG GTTTATGGA
||||| |||||
TCTCCAGC CGAGTACTT
C__
GAM2046 PIP 3' TCTATAAAATAAACTTCTT 12136 GATAG
AAGAGGTT TTTATGGA
||||| |||||
TTCTTCAA AAATATCT
ATA__
GAM2046 PLA2G2D 3' CCATAAATCCTTCTTGGG 25712 TTGATA
TTCAAGAGG GTTTATGG
||||| |||||
GGGTTCTTC TAAATACC
C_____
GAM2046 PLAGL1 3' TACAATGTAATAATCTCTT 12153 A _ GGA
GAA TTCAAGAGGTTG TAGTT TAT
||||||| |||| |||
AAGTTCTCTAAT ATCAA GTA
_ T ACATT
GAM2046 PLOD3 3' TTCGTGGGCACAGGGCTTCTGG 8433 A GATA
G TC AGAGGTT GTTTATGGA
|| ||||| |||||
GG TCTTCGG CGGGTGCTT
G GACA
GAM2046 PMCHL1 3' TCTGATAATGTCAACTTTTGAA 49922 G GT _
TTCAAGAG TTGATA TTAT GGA
||||| ||||| ||| |||

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AAGTTTTTC AACTGT AATA TCT
 — — G
 GAM2046 POLQ 3' TCTATGAATTTGCCTTTTG 22735 TGAT
 CAAGAGGT AGTTTATGGA
 ||||| |||||
 GTTTTCCG TTAAGTATCT
 T—
 GAM2046 POLR2C 3' TGAGAAGTAACCTTTTGGA 12207 ATAG
 TTCAAGAGGTTG TTTA
 ||||| |||
 AGGTTTTCCAAT GAGT
 GAA—
 GAM2046 PPAT 3' GATTGTAACTTTTTGAA 12218
 TTCAAGAGGTTGATAGTT
 |||||
 AAGTTTTTCAATTGTTAG

 GAM2046 PPAT 3' GATTGTAACTTTTTGAA 12219
 TTCAAGAGGTTGATAGTT
 |||||
 AAGTTTTTCAATTGTTAG

 GAM2046 PRKCN 3' TTCGTAGATTGTCATCT 20565 T
 AGGT GATAGTTTATGGA
 ||| |||||
 TCTA CTGTTAGATGCTT

 GAM2046 PSG2 3' TTTATGAACATTTTTCTTGAG 49190 TT A
 TTCAAGAGG GAT GTTTATGGA
 ||||| || |||||
 GAGTTCTTT TTA CAAGTATTT
 T—
 GAM2046 PSG5 3' TTTATGAACATTTTTCTTGAG 12445 TTGAT
 TTCAAGAGG AGTTTATGGA
 ||||| |||||
 GAGTTCTTT TCAAGTATTT
 TTT—
 GAM2046 PTPN12 3' TTTGTAAATTATTTGCCCTGGA 12600 A A T TG
 G TTC AG GGT GATAGTTTA GA
 ||| || ||||| ||
 GAG TC CCG TTATTAAAT TT
 G— T GT
 GAM2046 PTPN2 3' TTTATAAGTATCTATTTAATCT 12583 —
 TTTG CAAGAGGTTGA TAG TTTATGGA
 ||||| || |||||
 GTTTTCTAATT ATC GAATATTT
 T TAT
 GAM2046 PXN 3' TTTATAAACTGCTGCTATTTGG 12677 A TGA
 A TTCAAG GGT TAGTTTATGGA
 ||||| || |||||

			AGGTTT TCG GTCAAATATTT	
			A TC_	
GAM2046	RAB5B	3'	TCCATGATTTGGCCTTGTGGA 12711	A TG TAGT
			TTCA GAGGT A TTATGGA	
			AGGT TTCCG T AGTACCT	
			G GT T__	
GAM2046	RABIF	3'	TTCATAGGCAAGACTTCTT 12733	GATA
			AAGAGGTT GTTTATGGA	
			TTCTTCAG CGGATACTT	
			AA__	
GAM2046	RAD23B	3'	TTTGTGAAATTAGCACTTTTGG 12740	_ AG TG
			TCAAGAG GTTGAT TTTA GA	
			GGTTTTTC CGATTA AAGT TT	
			A _ GT	
GAM2046	RBBP9	3'	TCTATAGAGTTAAACCTTTT 70701	GATAG
			AAGAGGTT TTTATGGA	
			TTTTCCAA AGATATCT	
			ATTG_	
GAM2046	RFXAP	3'	CCAGTTGTTGACCTTTGAG 6765	A TG GTTTA
			TTCA GAGGT ATA TGG	
			GAGT TTCCA TGT ACC	
			_ GT TG__	
GAM2046	RNF14	3'	TCTGGGTTTTGTTGGCTTTTTG 16275	TG TTTA
	AA		TTCAAGAGGT ATAG TGGA	
			AAGTTTTTCG TGTT GTCT	
			GT TTGG	
GAM2046	RPL4	3'	TCCATAAAGGTCAAATCATTTT 8266	GG__ AG
	GGA		TTCAAGA TTGAT TTTATGGA	
			AGGTTTT AACTG AAATACCT	
			ACTA G_	
GAM2046	SCN8A	3'	AATTGTCAGTTTCTTTGA 27213	_ GG
			TCAA GA TTGATAGTT	
			AGTT CT GACTGTAA	
			T TT	
GAM2046	SDHD	3'	TTCAATTTATCAATCTCTT 13001	TTTA
			AAGAGGTTGATAG TGGA	
			TTCTCTAACTATT ACTT	
			TA__	
GAM2046	SEL1L	3'	TTTATAAATTATTAATCTT 18608	
			GAGGTTGATAGTTTATGGA	

TTCTAATTATTAAATATTT

GAM2046 SEL1L 3' TTTGTGAGCTTTACTTCTTTGG 18611 _ TGAT TG
A TTCAA GAGGT AGTTTA GA
||||| ||||| ||
AGGTT CTTCA TCGAGT TT
T TT__ GT

GAM2046 SELE 3' TCCATGAGGCCAAACGTTTGA 6553 G GATAG
A TTCAAGA GTT TTTATGGA
||||| ||| |||||
AAGTTTT CAA GAGTACCT
G ACCG_

GAM2046 SERPINB9 3' CTATGTTTAGCTTTTTGAG 16017 TAGTT
TTCAAGAGGTTGA TATGG
||||||| ||||
GAGTTTTTCGATT GTATC
T____

GAM2046 SERPINB9 3' TCTATGCATTTATTGGCTCTTG 16035 G TG TT_
AA TTCAAGAG T ATAG TATGGA
||||||| | |||||
AAGTTCTC G TATT GTATCT
_GT TAC

GAM2046 SHOX 3' TCCATGTTCTGATTGGTTTTCT 6585 AG GG TG _ TT
GG TCA A T AT AG TATGGA
||| | | || || |||||
GGT T G TA TC GTACCT
CT TT GT G TT

GAM2046 SIAH2 3' TCCGTAAACCTTCAAAATTATT 18615 _ GG TA
TGG TCAA GA TTGA GTTTATGGA
|||| | |||| |||||
GGTT TT AACT CAAATGCCT
TA AA TC

GAM2046 SLC19A2 3' TTTATGAATGTGCATTTCTTGA 69554 T ATA
TCAAGAGGT G GTTTATGGA
||||||| | |||||
AGTTCTTTA C TAAGTATTT
_GTG

GAM2046 SLC3A2 5' TCCATGGAGCTACAGCCTCCTG 11527 A A _
AA TTCA GAGGTTG TAGTTT ATGGA
|||| ||||| ||||| |||||
AAGT CTCCGAC ATCGAG TACCT
C _ G

GAM2046 SMARCD1 3' TCTATAAGCTAGTTGATCTTGG 58187 GGTTGA
TCAAGA TAGTTTATGGA
||||| |||||
GGTTCT ATCGAATATCT
AGTTG_

GAM2046 SNX15 3' TCCATAAATAAAATTTGTTGGA 74131 G GATA
TTCAA AGGTT GTTTATGGA
||||| |||||

			AGGTT TTAA TAAATACCT		
			G AA__		
GAM2046	SOX11	3'	TTTGAAGCTTGTCTGCTTTGA 13324	A GT _ ATGGA	
	A		TTCA GAG TGATA GTTT		
			AAGT TTC GCTGT CGAA		
			_ TG T GTTT		
GAM2046	STX1A	3'	CCGTGTTGCCTTCTTGAA 17209	TT AGTTT	
			TTCAAGAGG GAT ATGG		
			AAGTTCTTC TTG TGCC		
			CG _____		
GAM2046	SURF5	3'	TTCAGTTTGTCTGCTCTTTGA 56922	_ GT TTTA	
			TCAA GAG TGATAG TGGA		
			AGTT CTC GCTGTT ACTT		
			T TG TG__		
GAM2046	SYCP1	3'	TTTGTAAGTTAGCCTTTGAA 13496	A AG TG	
			TTCA GAGGTTGAT TTTA GA		
			AAGT TTCCGATTG AAAT TT		
			_ _ GT		
GAM2046	TCF12	3'	TTTGTGAAGTTAGTGGACTTTT 13640	G _ TG	
	TGG		TCAAGAGGTT AT AGTTTA GA		
			GGTTTTTCAG TG TCAAGT TT		
			G AT GT		
GAM2046	TDGF1	3'	TCCATCGATCAGCCTCTCGAG 13663	A AGTTT	
			TTC AGAGGTTGAT ATGGA		
			GAG TCTCCGACTA TACCT		
			C GC__		
GAM2046	TRPC6	3'	TTTATAAACTGCTTTCTTGGA 17293	TTGA	
			TTCAAGAGG TAGTTTATGGA		
			AGGTTCTTT GTCAAATATTT		
			C__		
GAM2046	UQCRB	3'	TCCGTAAGTTACATCCTTATGG 21940	A T A GT	
	A		TTCA GAGG TG TA TTATGGA		
			AGGT TTCC AC AT AATGCCT		
			A T _ TG		
GAM2046	USH2A	3'	TCCATGAGAAAGTCATTTTGGA 24059	GGT AG_	
			TTCAAGA TGAT TTTATGGA		
			AGGTTTT ACTG GAGTACCT		
			_ AAA		
GAM2046	USP1	5'	TCTATAAATTAACCTTTGA 14022	GTTGA	
			TCAAGAG TAGTTTATGGA		

			AGTTCTC	ATTAAATATCT		
			A_____			
GAM2046	VAPA	3'	TCTGTTGCTGTTACCTCTTGAA	14547	T	TT
			TTCAAGAGGT GATAGT ATGGA			
			AAGTTCTCCA TTGTCG TGTCT			
			_____ T_			
GAM2046	VDLR	3'	TCTGTGACAAATGTTGACCTTT	70076	A	TG GT__
	GAG		TTCA GAGGT ATA TTATGGA			
			GAGT TTCCA TGT AGTGTCT			
			_____ GT AAAC			
GAM2046	XRCC4	5'	TCTGTGAAAGCGGGCGTTTTTG	14148	G	GATAG
	A		TTCAAGA GTT TTTATGGA			
			AGGTTTT CGG AAGTGTCT			
			G GCGA_			
GAM2046	YWHAG	3'	CACCAAAATTATTAATCCTCTT	25937	_____	A A
	GAG		TTCAAGAGG TTGATAGTTT TGG			
			GAGTTCTCC AATTATTAAC ACC			
			T _____ ACC			
GAM2046	ZHX1	3'	TTCATACTACTGTAACTTTTT	24290	T_	
			AAGAGGTTGATAGT TATGGA			
			TTTTTCAATTGTCA ATACTT			
			TC			
GAM2046	ZNF74	3'	TCCATAAACTATTATTTTC	14265	T	
			GAGG TGATAGTTTATGGA			
			CTTT ATTATCAAATACCT			
			T			
GAM2046	AD022	3'	TAAGAGATTATTGAGTTCTTGG	92648	G TG	ATGGA
			TCAAGAG T ATAGTTT			
			GGTTCTT A TATTAGA			
			G GT GAAT			
GAM2046	ADAM9	3'	CTATGAGTTATCATCTT	15105	T	GT
			GAGGT GATA TTATGG			
			TTCTA CTAT AGTATC			
			_____ TG			
GAM2046	AIG-1	3'	TGTAATAATGATGTCAATTTCA	32758	A	GT_ GGA
	TGAA		TTCA GAGGTTGATA TTAT			
			AAGT CTTTAACTGT AATA			
			A AGT ATGTT			
GAM2046	AKAP6	3'	TTCATTTTTTATGCTTCTTGAG	16255	TG	TTT
			TTCAAGAGGT ATAG ATGGA			

GAGTTCTTCG TATT TACTT
 — TTT
 GAM2046 ANKT 3' TTCATGTGCTATGATCTCTGAA 33462 A G T
 TTCA GAGGTT ATAGT TATGGA
 |||| ||||| |||| |||||
 AAGT CTCTAG TATCG GTACTT
 — — T
 GAM2046 ARPP-21 5' TCTATAGACTATTGTGAGCCT 33296 —
 AGGTT GATAGTTTATGGA
 |||| | ||||| |||||
 TCCGA TTATCAGATATCT
 GTG
 GAM2046 ASB16 5' AGGCTTTCAGTCTCTTGGA 55971 GT T
 TTCAAGAG TGA AGTTT
 ||||| || |||||
 AGGTTCTC ACT TCGGA
 TG T
 GAM2046 BAP29 3' TTTGTTATGTTAGCCTCTAGAA 61332 A GTTT TG
 TTC AGAGGTTGATA A GA
 || ||||| || | ||
 AAG TCTCCGATTGT T TT
 A AT__GT
 GAM2046 BY55 3' TCTAAATACTTGTTAACCTCTT 60065 _ TTA
 AAGAGGTTGATA GT TGGA
 ||||| || ||||
 TTCTCCAATTGT CA ATCT
 T TAA
 GAM2046 C16orf44 3' TCTGTAGACCAGCAGCAACTTC 45643 ATA__
 TT AAGAGGTTG GTTTATGGA
 ||||| |||||
 TTCTTCAAC CAGATGTCT
 GACGAC
 GAM2046 C1orf26 3' TCTGTGGGCTTGTCACTTTT 35068 T _
 AGAGGT GATA GTTTATGGA
 |||| |||| |||||
 TTTTCA CTGT CGGGTGTCT
 _ T
 GAM2046 C1orf9 3' TTTATAACTTTGTTAGGTTTTT 33163 G T_
 GAA TTCAAGAG TTGATAG TTATGGA
 ||||| ||||| |||||
 AAGTTTTT GATTGTT AATATTT
 G TC
 GAM2046 C20orf32 5' TCCATAGAATTTCAGTTTCTGAG 40140 A GG TAG
 TTCA GA TTGA TTTATGGA
 ||| || |||| |||||
 GAGT CT GACT AGATACCT
 _ TT TA_
 GAM2046 C20orf45 3' TCTGTAAATTATCCTTGTCTG 32644 A GTT_
 AA TTCA GAG GATAGTTTATGGA
 |||| || ||||| |||||

			AAGT CTT CTATTAAATGTCT		
			_ GTTC		
GAM2046	C20orf45	3'	TTCATAAATGAAACCCTTGA 32645	A	GATA
			TTCAAG GGTT GTTTATGGA		
			AGGTTC CCAA TAAATACTT		
			_ AG_		
GAM2046	C20orf48	3'	TCTGTGGACTTTTCATTTTTTT 46957	T	T
			AAGAGG TGA AGTTTATGGA		
			TTTTTT ACT TCAGGTGTCT		
			T T		
GAM2046	C21orf6	3'	TCTTGCCACTGTTGGCCTTTTG 34201	TG	TTAT
	A		TCAAGAGGT ATAGT GGA		
			AGTTTTCCG TGTCA TCT		
			GT CCGT		
GAM2046	C2orf6	3'	TCTATGTTTTTATTGTCTCTTG 37179	GTT	TT_
	AG		TTCAAGAG GATAG TATGGA		
			GAGTTCTC TTATT GTATCT		
			TG_ TTT		
GAM2046	C5orf7	3'	TCCCTATCCTGTGGCCTTTTG 64600	G	TT T
	A		TTCAAGAGGTT ATAG TA GGA		
			AGTTTTCCGG TGTC AT CCT		
			_ CT C		
GAM2046	C8orf6	3'	TCTGATATGTATTGGTTTCTTG 90784	GG TG	GTT _
	AA		TTCAAGA T ATA TAT GGA		
			AAGTTCT G TAT ATA TCT		
			TT GT GT_ G		
GAM2046	C9orf4	3'	TCATATAATTTTCAGCTTTTTTG 82768	TAGTT	A
	A		TTCAAGAGGTTGA TATGG		
			AGTTTTTCGACT ATACT		
			TTAAT		
GAM2046	CDW92	3'	TCCATGGAAGGAGAATCTTTTG 55431	GATAG	
	AA		TTCAAGAGGTT TTTATGGA		
			AAGTTTTCTAA AGGTACCT		
			GAGGA		
GAM2046	CHRNA6	3'	TTTGTGAACATTGTCATCCTTG 16099	A _	TG
	A		TCAAG GGT TGATAGTTTA GA		
			AGTTC CTA GTTATCAAGT TT		
			_ C GT		
GAM2046	CLDN7	3'	TCCATGTATAGTCCTCTTG 8964	TTGA	GTT
			TCAAGAGG TA TATGGA		

GGTTCTCC AT GTACCT
TG__ AT_
GAM2046 CLLD8 5' TTCATGGACTTGTCTTTTGG 50008 TTGAT
TCAAGAGG AGTTTATGGA
||||| |||||||
GGTTTTCT TCAGGTACTT
GT__
GAM2046 CNK2 3' TCTATAGGCTGTGGGTTTCATT 76492 ____ GG G
TTTGAA TTCAA GA TT ATAGTTTATGGA
|||| || || |||||||||
AAGTT CT GG TGTCGGATATCT
TTTA TT G
GAM2046 COASTER 3' TTGTGTTTTTAATTTCTTGA 32084 TAGTT TG
TCAAGAGGTTGA TA GA
||||||||| || ||
AGTTCTTTAATT GT TT
TTT__ GT
GAM2046 CPEB1 5' TCTGGTATGTAACTCTTGGA 48366 G GTTTA
TTCAAGAG TTGATA TGGA
||||| |||| |||
AGGTTCTC AATTGT GTCT
_ ATG_
GAM2046 CXYorf1 3' TCAGAAATTCTCAATTTTTTGA 82919 T A A
A TTCAAGAGGTTGA AGTTT TGG
||||||||| |||| |||
AAGTTTTTTAACT TTAAA ACT
C G
GAM2046 DC2 3' TCCGTAAGCTGAGAACTCTGGA 64921 A G GA
TTCA GAG TT TAGTTTATGGA
|||| ||| || |||||||||
AGGT CTC AG GTCGAATGCCT
_ A A_
GAM2046 DCTN4 3' AACTATTATAATCTCTTGAA 68393 ____
TTCAAGAGGT TGATAGTT
||||||||| |||||||
AAGTTCTCTA ATTATCAA
AT
GAM2046 DD96 3' TCTGTGAAATAAAGACTTTTTG 20465 GATAG
CAAGAGGTT TTTATGGA
||||||| |||||||
GTTTTTCAG AAGTGTCT
AAATA
GAM2046 DEPP 3' TCTGTGAGCTGTCAGTCT 23809 GT
AG TGATAGTTTATGGA
|| |||||||||||
TC ACTGTCGAGTGTCT
TG
GAM2046 DKFZP434B044 3' TCTATAAAAGTGCTTCATGAG 49724 A TGATAG
TTCA GAGGT TTTATGGA
|||| |||| |||||||

	GAGT CTTCG	AAATATCT		
	A	TGA__		
GAM2046	DKFZp434C0328	3' AATAGTCAAAC TTTTGAA	34547	_ A
		TTCAAGAGGTT GAT GTT		
		AAGTTTTTCAA CTG TAA		
		A A		
GAM2046	DKFZp434E2220	5' TTCAGTTTGTTAGTCTGTTGAA	34723	G GT TTTA
		TTCAA AG TGATAG TGGA		
		AAGTT TC ATTGTT ACTT		
		G TG TG__		
GAM2046	DKFZP434L1123	3' TTTATGGACTCTGACCTTTT	50494	GAT
		AAGAGGTT AGTTTATGGA		
		TTTTCCAG TCAGGTATTT		
		TC_		
GAM2046	DKFZp547I224	3' TCCAGGAGCTGGTTTTTTGAA	39964	GG TGA A
		TTCAAGA T TAGTTT TGGA		
		AAGTTTT G GTCGAG ACCT		
		TT__ G		
GAM2046	DKFZp547M072	3' TTTATAGACTATTAATTTTCTG	61718	AG
	A	TCA AGGTTGATAGTTTATGGA		
		AGT TTTAATTATCAGATATTT		
		CT		
GAM2046	DKFZP566B183	3' TCCATAAACATTTCTTTTC	31945	TT_ A
		GAGG GAT GTTTATGGA		
		CTTT TTA CAAATACCT		
		TCT _		
GAM2046	DKFZP566B183	3' TCTATAGGAGTGTTTAATTTCT	31946	TAG__
	TG	CAAGAGGTTGA TTTATGGA		
		GTTCTTTAATT GGATATCT		
		TGTGA		
GAM2046	DKFZp761B0514	3' CCAGAGGTGGCCTCTTGGA	51144	ATAGTTTA
		TTCAAGAGGTTG TGG		
		AGGTTCTCCGGT ACC		
		GGAG__		
GAM2046	DKFZp761D0614	3' TCTGTATTGTATTAATTTCTGG	88947	A GTT
	A	TTCA GAGGTTGATA TATGGA		
		AGGT CTTTAATTAT ATGTCT		
		_ GTT		
GAM2046	DKFZp761G0313	3' TCCATTTCTACTAACCTCTTG	66393	A TTT
	A	TTCAAGAGGTTG TAG ATGGA		

			AGGTTCTCCAAT ATC TACCT		
			C TT_		
GAM2046	DNAJC6	3'	TCTGTGGATGTCACGTATTTTG 29497	GGT_	G
	AA		TTCAAGA TGATA TTTATGGA		
			AAGTTTT ACTGT AGGTGTCT		
			ATGC _		
GAM2046	DNCLI2	3'	ACATGCTATCAGTTTTTTGG 21563	GG	TT GA
			TCAAGA TTGATAGT ATG		
			GGTTTT GACTATCG TAC		
			TT _ AC		
GAM2046	DVS27	3'	TCTGTATCACCTGACCTCTGGA 54227	A	GATAGTT
			TTCA GAGGTT TATGGA		
			AGGT CTCCAG ATGTCT		
			_ TCCACT_		
GAM2046	ELF2	3'	TAAGTCTGTCAGTTTCTT 23450	GG	_
			AAGA TTGATAG TTTA		
			TTCT GACTGTC GAAT		
			TT T		
GAM2046	EPN2	3'	TCCATAAGACACCTTTTGGG 31043		TGATAG
			TTCAAGAGGT TTTATGGA		
			GGGTTTTCCA GAATACCT		
			CA_____		
GAM2046	EPSIN	5'	CCCTCTGTGGCTTCTTGGA 26208	G	TTTAT
			TTCAAGAGGTT ATAG GG		
			AGGTTCTTCGG TGTC CC		
			_ TC_____		
GAM2046	ERp44	3'	TCCATAGTGGTATTTTTTTGGA 82605		TTG AGT
			TTCAAGAGG AT TTATGGA		
			AGGTTTTTT TG GATACCT		
			TA_ GT_		
GAM2046	FBXO22	3'	CTGTATTAGATCTTTTGAA 25145		GATAGTT
			TTCAAGAGGTT TATGG		
			AAGTTTTCTAG ATGTC		
			ATT_____		
GAM2046	FBXO3	3'	TCTGTGAAAAGACTTCTTG 54151		GATAG
			CAAGAGGTT TTTATGGA		
			GTTCTTCAG AAGTGTCT		
			AA_____		
GAM2046	FHX	3'	AGCATGGTTTTAGCTTCTTGGA 37918		TAGT GA
			TTCAAGAGGTTGA TTATG		

AGGTTCTTCGATT GGTAC
 TT__ GAC
 GAM2046 FLJ10097 3' ACTTTTTCTGTAAGCCTTTTGG 69034 G TTTAT A
 TCAAGAGGTT ATAG GG
 ||||| || ||
 GGTTTTCCGA TGTC TC
 A TTTT_ AT
 GAM2046 FLJ10376 3' TCTGTCTTACTATCTACTTCTT 36564 T TT_
 GAG TTCAAGAGGT GATAGT ATGGA
 ||||| |||| ||||
 GAGTTCTTCA CTATCA TGTCT
 T TTC
 GAM2046 FLJ10520 3' TCTACATTATCCATTTCTTGG 36711 T TTA
 TCAAGAGGT GATAGT TGGA
 ||||| |||| ||||
 GGTTCTTTA CTATTA ATCT
 C C__ A
 GAM2046 FLJ10520 3' TTTGTAAAAGCTAGCTTCTAGA 36716 A ATAG TG
 A TTC AGAGGTTG TTTA GA
 || ||||| |||| ||
 AAG TCTTCGAT AAAT TT
 A CGA_ GT
 GAM2046 FLJ10656 3' TTTATAAACTATGTACTCCTGG 36913 A GTTG
 TCA GAG ATAGTTTATGGA
 ||| || ||||| |||||
 GGT CTC TATCAAATATTT
 C ATG_
 GAM2046 FLJ10716 3' TCCATGAACTCATTTCCATTTG 37021 A TT _
 AG TTCAAG GG GAT AGTTTATGGA
 ||||| || || ||||| |||||
 GAGTTT CC TTA TCAAGTACCT
 A T_ C
 GAM2046 FLJ10718 3' TATTTAAATTGTTAATCCTTATG 37032 A TGGA
 AG TTCA GAGGTTGATAGTTTA
 |||| ||||| ||||| |||||
 GAGT TTCTAATTGTTAAAT
 A TTATT
 GAM2046 FLJ10895 3' TGGATTAATAATCTTTTGG 39360 A
 TCAAGAGGTTG TAGTTTA
 ||||| ||||| |||||
 GGTTTTCTAAT ATTAGGT
 A
 GAM2046 FLJ10898 3' TTCATAGATTATTCAGCCTTT 60144 _
 AGAGGTTGA TAGTTTATGGA
 ||||| ||||| ||||| |||||
 TTTCCGACT ATTAGATACTT
 T
 GAM2046 FLJ10989 3' GAGTGCGATTATTGGCTTCTGA 37502 A TG TATGGA
 G TTCA GAGGT ATAGTT
 |||| |||| |||||

GAGT CTTCG TATTAG
 _ GT CGTGAGT
 GAM2046 FLJ11151 3' TTTGTGAATTTATGTCCTTTTG 68484 TTGAT TG
 CAAGAGG AGTTTA GA
 ||||| ||||| ||
 GTTTTCC TTAAGT TT
 TGTAT GT
 GAM2046 FLJ11252 3' TTTATAAATATATTTTCATCCT 68221 T TA____
 TTTGAA TTCAAGAGG TGA GTTTATGGA
 ||||| || |||||
 AAGTTTTCC ACT TAAATATTT
 T TTTATA
 GAM2046 FLJ12294 3' TGGACTGTTATTTCTTGAA 47725 T
 TTCAAGAGGT GATAGTTTA
 ||||| |||||
 AAGTTCTTTA TTGTCAGGT
 _
 GAM2046 FLJ12505 3' TTCATGAAATAATCTCTTGAA 45720 ATAG
 TTCAAGAGGTTG TTTATGGA
 ||||| |||||
 AAGTTCTCTAAT AAGTACTT
 A____
 GAM2046 FLJ12529 3' TCCATAGGCTTTTCTTTTTTC 46090 TT_ T_
 GAGG GA AGTTTATGGA
 ||| || |||||
 CTTT CT TCGGATACCT
 TTT TT
 GAM2046 FLJ12643 3' TTCATATGACTAAATCTTTTGA 83674 GA _
 A TTCAAGAGGTT TAGTT TATGGA
 ||||| ||||| |||||
 AAGTTTTCTAA ATCAG ATACTT
 _ T
 GAM2046 FLJ12806 3' TTTATAGGCAGCACCTCTGAA 43394 A T ATA
 TTCA GAGGT G GTTTATGGA
 ||| ||||| | |||||
 AAGT CTCCA C CGGATATTT
 _ _ GA_
 GAM2046 FLJ13057 3' TTTATATACGTTGACCTTTTG 42707 TG A T
 CAAGAGGT AT GT TATGGA
 ||||| || |||||
 GTTTTCCA TG CA ATATTT
 GT _ T
 GAM2046 FLJ13057 3' TTTATGTATGTTGACCTTTTG 42708 TG GTT
 CAAGAGGT ATA TATGGA
 ||||| || |||||
 GTTTTCCA TGT GTATTT
 GT AT_
 GAM2046 FLJ13197 3' TTCATGATCATGGTTAACCTTT 45191 A AGT____
 GGAG TTC AGAGGTTGAT TTATGGA
 || ||||| |||||

GAG TTTCCAATTG AGTACTT
 G GTACT
 GAM2046 FLJ13204 3' TTTGTGTGCTCTTAACCTTCTG 45762 AG T T TG
 AG TTCA AGGTTGA AGT TA GA
 |||| ||||| || ||
 GAGT TCCAATT TCG GT TT
 CT C T GT
 GAM2046 FLJ14621 3' TCCATGCAACTGGATTTTTGGA 52542 GTTGA _
 TTCAAGAG TAGTT TATGGA
 ||||| |||| |||||
 AGGTTTT GTCAA GTACCT
 AG__ C
 GAM2046 FLJ14906 3' TCATTTATTGGACTTCTTGAA 52763 GA TT
 TTCAAGAGGTT TAGT ATGG
 ||||| |||| ||||
 AAGTTCTTCAG GTTA TACT
 _ TT
 GAM2046 FLJ20055 3' CTGTGAATGATTCTTGAA 34909 GTTGATA
 TTCAAGAG GTTTATGG
 ||||| |||||
 AAGTTCTT TAAGTGTC
 AG____
 GAM2046 FLJ20071 3' TCTGTGGTATTATCAATTCTTT 34961 AG _
 GAA TTCAAG GTTGATAGT TTATGGA
 |||| ||||| |||||
 AAGTTT TAACTATTA GGTGTCT
 CT T
 GAM2046 FLJ20093 3' TTTATATACTTCAACTTTCTGA 35041 AG T T
 A TTCA AGGTTGA AGT TATGGA
 |||| ||||| || |||||
 AAGT TTCAACT TCA ATATTT
 CT _ T
 GAM2046 FLJ20094 3' TCTGTGATGTCTTTTAACTTT 35045 T_ T__
 TTGGA TTCAAGAGGTTGA AG TTATGGA
 ||||| || |||||
 AGGTTTTTCAATT TC AGTGTCT
 TT TGT
 GAM2046 FLJ20097 5' TTCAACAAGCTTATCGACTTCT 35051 _ A_
 TGGA TTCAAGAGGTTGATA GTTT TGGA
 ||||| |||| ||||
 AGGTTCTTCAGCTAT CGAA ACTT
 T CA
 GAM2046 FLJ20152 5' TTTGTAAACACCAACTTTCTGA 39167 AG ATA TG
 G TTCA AGGTTG GTTTA GA
 |||| |||| |||| ||
 GAGT TTCAAC CAAAT TT
 CT CA_ GT
 GAM2046 FLJ20275 3' TTTGTGCACATGTTGATTTCTT 35311 TG _ T TG
 AAGAGGT ATA GT TA GA
 ||||| || || || ||

		TTCTTTA TGT CA GT TT	
		GT A C GT	
GAM2046	FLJ20628	3' TCCATAGATTGGCATT TTT 35913	TGA
		AGAGGT TAGTTTATGGA	
		TTTTTA GTTAGATACCT	
		CG_	
GAM2046	FLJ20628	3' TCCATAGATTTGTCTTTCTTC 35914	TT_ _
		GAGG GATAG TTTATGGA	
		CTTC CTGTT AGATACCT	
		TTT T	
GAM2046	FLJ20689	3' TCTATTATAATAATGGCTTCTT 35963	A GTTT_
	GG	TCAAGAGGTTG TA ATGGA	
		GGTTCTTCGGT AT TATCT	
		A AATAT	
GAM2046	FLJ20689	3' TCTATTATAATAATGGCTTCTT 35964	A GTTT_
	GG	TCAAGAGGTTG TA ATGGA	
		GGTTCTTCGGT AT TATCT	
		A AATAT	
GAM2046	FLJ20727	3' TCCAACGTGTGTTGACTCTTGG 36048	G TG GTTTA
	A	TTCAAGAG T ATA TGGA	
		AGGTTCTC A TGT ACCT	
		_GT GTGCA	
GAM2046	FLJ22029	3' AACTGTCAACTCTTGAA 46906	G
		TTCAAGAG TTGATAGTT	
		AAGTTCTC AACTGTCAA	
		-	
GAM2046	FLJ22029	3' TCATCAGATTAGCTGTTGACTT 46912	TG TA_ A
	TTTG	CAAGAGGT ATAGTT TGG	
		GTTTTTCA TGTCGA ACT	
		GT TTAG ACTT	
GAM2046	FLJ22601	5' TCATATATTGGTCTCTGAG 46110	A TT GTT
		TTCA GAGG GATA TATGG	
		GAGT CTCT TTAT ATACT	
		_ GG _	
GAM2046	FLJ22615	5' CTGTGGACGTGCCCTTGGA 69039	A TGATA
		TTCAAG GGT GTTTATGG	
		AGGTTC CCG CAGGTGTC	
		_ TG _	
GAM2046	FLJ22671	3' ACCATGATTGTCAGTTTCCTGA 46309	A GG T A
	G	TTCA GA TTGATAGTT ATGG	

GAGT CT GACTGTTAG TACC
 C TT _ AC
 GAM2046 FLJ22833 3' TGAATATTATCTCTTGAA 43410 T G
 TTCAAGAGGT GATA TTTA
 ||||| ||| |||
 AAGTTCTCTA TTAT AAGT

_ _
 GAM2046 FLJ23056 3' TTCAACTGGGACAACCTTTTGA 45023 A__ TATGGA
 A
 TTCAAGAGGTTG TAGTT
 ||||| |||
 AAGTTTTCCAAC GTCAA
 AGG CTT

GAM2046 FLJ23091 3' AGCTGTGGTTTCTTGGA 46663 GG G
 TTCAAGA TT ATAGTT
 ||||| || |||||
 AGGTTCT GG TGTCGA
 TT _

GAM2046 FLJ23251 3' TACCTGAATTGTTATACTTTTT 46100 _ T A
 GAA
 TTCAAGAGGT TGATAGTTTA GG
 ||||| ||||| ||
 AAGTTTTTCA ATTGTTAAGT CC
 T _ ATT

GAM2046 FLJ23516 3' TCTGTAAAATTAGTCTGTTGAA 44888 G GT AG
 TTCAA AG TGAT TTTATGGA
 ||||| || ||| |||||
 AAGTT TC ATTA AAATGTCT
 G TG _

GAM2046 FLJ25409 5' TCCCTATGTTAACTACTTGAG 58972 A GTTTAT
 TTCAAG GGTGATA GGA
 ||||| ||||| |||
 GAGTTC TCAATTGT CCT
 A ATC__

GAM2046 FLJ31101 3' TTTATAAATATGCTTCTTGAA 36173 TGATA
 TTCAAGAGGT GTTTATGGA
 ||||| |||||
 AAGTTCTTCG TAAATATTT
 TA__

GAM2046 FLJ31300 3' CTGTGGGTGGGCCTCTGAG 58930 A G AGT
 TTCA GAGGTT AT TTATGG
 ||| ||||| || |||||
 GAGT CTCCGG TG GGTGTC
 _ G _

GAM2046 FTSJ1 3' TTCATATTTGTACCTCTTGGA 25381 T TT
 TTCAAGAGGT GATAG TATGGA
 ||||| ||||| |||||
 AGGTTCTCCA CTGTT ATACTT
 _ T_

GAM2046 GDAP2 3' TTCATAGCAGCATCTCTTGAG 35128 T ATA T
 TTCAAGAGGT G GTT ATGGA
 ||||| || ||| |||||

			GAGTTCTCTA C CGA TACTT		
			_ GA _ _		
GAM2046	GGA2	3'	TCTGTGCCTTGT CAGCCTTTGA 57686	A	TT
	A		TTCA GAGGTTGATAG TATGGA		
			AAGT TTCCGACTGTT GTGTCT		
			_ CC		
GAM2046	GLUC	3'	TCCATAAGCTGTTTTTGCTT 40935	AGGTT	
			AAG GATAGTTTATGGA		
			TTC TTGTCTGAATACCT		
			GTTT_		
GAM2046	GR6	3'	TCTATGGATTGTATACCT 24751	TG	
			AGGT ATAGTTTATGGA		
			TCCA TGTTAGGTATCT		
			TA		
GAM2046	GT650	3'	CCATAATTTACCTTTTGG 54550	TGATAGT	
			TCAAGAGGT TTATGG		
			GGTTTTCCA AATACC		
			TTT_		
GAM2046	H-plk	5'	CTGTCATTGACTTTTTGAA 32382		
			TTCAAGAGGT TGATAG		
			AAGTTTTTCA ACTGTC		
			GTT		
GAM2046	H2AV	3'	TCTATTTATGTTTGACCTTTTG 25764	TG TA TT	
	GA		TTCAAGAGGT A GT ATGGA		
			AGGTTTTCCA T TA TATCT		
			GT TG TT		
GAM2046	HAPIP	3'	TCCGTATGTCACCTTCTTGAA 15469	T GTT	
			TTCAAGAGG TGATA TATGGA		
			AAGTTCTTT ACTGT ATGCCT		
			C _		
GAM2046	HCC-4	3'	TTTATGAAGAAAGACCTTTTG 57601	GATAG	
			CAAGAGGTT TTTATGGA		
			GTTTTCCAG AAGTATTT		
			AAAG_		
GAM2046	HCC8	3'	TCTATGAAAGTAAAGCTGTTTG 33694	A GATAG	
	AA		TTCAAG GGTT TTTATGGA		
			AAGTTT TCGA AAGTATCT		
			G AATGA		
GAM2046	HEI10	5'	TTTATGGACTCTCTTCAGCTTC 41300	A T_	
	TGGAG		TTC AGAGGTTGA AGTTTATGGA		

		GAG TCTTCGACT TCAGGTATTT	
		G TCTC	
GAM2046	HSPC019	3' TCTGTAA GTGGT GACTTTTTGA 26716	G AG
		G TTCAAGAGGTT AT TTTATGGA	
		GAGTTTTTCAG TG GAATGTCT	
		_ GT	
GAM2046	IR1899308	3' TCTGTGAGCACCGAGGCTTTTT 38528	GATA_
		GG TCAAGAGGTT GTTTATGGA	
		GGTTTTTCGG CGAGTGTCT	
		AGCCA	
GAM2046	KATNB1	3' CCAACTGTTGCTTCTTGG 20830	T TTA A
		TCAAGAGGT GATAGT TGG	
		GGTCTTCG TTGTCA ACC	
		- - -	
GAM2046	KCNMB2	3' GTGTTCTGAGTTGTCAGATCTC 20688	_ GT TGGA
		TTGAA TTCAAGAGGT TGATA TTA	
		AAGTTCTCTA ACTGT AGT	
		G TG CTTGTGT	
GAM2046	KCNQ5	3' TTTATAAGCCCGTTACCTTTT 39526	TGATA
		AAGAGGT GTTTATGGA	
		TTTTCCA CGAATATTT	
		TTGCC	
GAM2046	KHDRBS3	3' TCTATGAACAATCCCTTTT 22659	TT A
		AAGAGG GAT GTTTATGGA	
		TTTTCC CTA CAAGTATCT	
		_ A	
GAM2046	KIAA0089	3' GCCTTTCTGATCAATCTTTTGG 70509	AGTTTAT A
		TCAAGAGGTTGAT GG	
		GGTTTCTAACTA CC	
		GTCTTT_ GT	
GAM2046	KIAA0266	3' TCTGTAGATTGTTAGTTACTAG 41645	A A GT
		G TC AG G TGATAGTTTATGGA	
		GG TC T ATTGTTAGATGTCT	
		A A TG	
GAM2046	KIAA0317	3' TCTGTAAGCTTTTTCTTGAA 29748	TTGAT
		TTCAAGAGG AGTTTATGGA	
		AAGTTCTTT TCGAATGTCT	
		T_	
GAM2046	KIAA0318	3' TTTATGAAC TTTTCGCTTTTT 69532	T T
		AAGAGGT GA AGTTTATGGA	

		TTTTTCG CT TCAAGTATTT		
		_ T		
GAM2046	KIAA0319	3' TCTGTAGGCTGTGCGTTTGGA 29700	AG	TG
		TTCAAG GT ATAGTTTATGGA		
		AGGTTT CG TGTCGGATGTCT		
		G_ _		
GAM2046	KIAA0433	3' TTTATAAATGATTAGATTTTTG 31502	G	A
	AA	TTCAAGAG TTGAT GTTTATGGA		
		AAGTTTTT GATTA TAAATATTT		
		A G		
GAM2046	KIAA0663	3' TCTGCTGCTCTGTTAGCCTCTG 29790	A	TT _
	AA	TTCA GAGGTTGATAG TA TGGA		
		AAGT CTCCGATTGTC GT GTCT		
		_ TC C		
GAM2046	KIAA0729	3' TTTATAGGCTTAATTCTTGG 97414	GTTGAT	
		TCAAGAG AGTTTATGGA		
		GGTTCTT TCGGATATTT		
		AAT_		
GAM2046	KIAA0769	3' TCTTAACCTGTTGATCTATTTG 29759	_ TG T T	
	AG	TTCAAG AGGT ATAG TTA GGA		
		GAGTTT TCTA TGTC AAT TCT		
		A GT C _		
GAM2046	KIAA0773	3' ACATTTTATAACTTCTTGG 28718	A TTT	GA
		TCAAGAGGTTG TAG ATG		
		GGTTCTTCAAT ATT TAC		
		_ TT_ AT		
GAM2046	KIAA0776	3' TTTGTAAATTGGGTTCTTCATG 65451	A TTGA	TG
	GA	TTCA GAGG TAGTTTA GA		
		AGGT CTC GTTAAAT TT		
		A TTGG GT		
GAM2046	KIAA0826	3' TTCAAATGTTACCTTCTTGAA 83531	T	GTTTA
		TTCAAGAGG TGATA TGGA		
		AAGTTCTTC ATTGT ACTT		
		C AA_		
GAM2046	KIAA0836	3' TAAAGATTAATTTCTTGG 65169	AG	
		TCAAGAGGTTGAT TTTA		
		GGTTCTTTAATTA AAAT		
		G_		
GAM2046	KIAA0852	5' TCCATATGCCCACTCTCTTGGA 30766	GT ATA	T
		TTCAAGAG TG GT TATGGA		

AGGTTCTC AC CG ATACCT
 TC C__ T
 GAM2046 KIAA0854 3' TCTCAACTGCTCGGCCTCTTGG 30781 _ TATGGA
 TCAAGAGGTTGA TAGTT
 |||||
 GGTCTCCGGCT GTCAA
 C CTCT
 GAM2046 KIAA0870 3' TTTGTGTAGCTACTAACTTCTT 82385 A _ TG
 GG TCAAGAGGTTG TAGTT TA GA
 ||||| || ||
 GGTCTTCAAT ATCGA GT TT
 C T GT
 GAM2046 KIAA0893 3' AACTTCAGTTTTTTGAA 31061 GG T
 TTCAAGA TTGA AGTT
 ||||| ||||
 AAGTTTT GACT TCAA
 TT _
 GAM2046 KIAA0940 3' TGAAGTAGTCGATTTTTTTGAA 30535 _
 TTCAAGAGGTTGAT AGTTTA
 |||||
 AAGTTTTTAGCTG TCAAGT
 A
 GAM2046 KIAA0961 5' TCTGTGGACCCTGCTTCTGAA 30411 A TGATA
 TTCA GAGGT GTTTATGGA
 ||| |||||
 AAGT CTTCC CAGGTGTCT
 _ TCC__
 GAM2046 KIAA0981 3' TTTATAAATGTGAAGCTTTTTTG 62095 GATA
 A TCAAGAGGTT GTTTATGGA
 ||||| |||||
 AGTTTTTCGA TAAATATTT
 AGTG
 GAM2046 KIAA0999 3' TCCGTGTGCTGTTCTTTTGG 47966 GTT T
 TCAAGAG GATAGT TATGGA
 ||||| |||||
 GGTTTC TTGTCG GTGCCT
 _ T
 GAM2046 KIAA1025 3' TCCATAATCTGGGACTTTTT 64679 GA T
 AAGAGGTT TAG TTATGGA
 ||||| |||||
 TTTTTCAG GTC AATACCT
 G_ T
 GAM2046 KIAA1155 3' TCTATAAATTTGCCCTTTCTGG 62921 _ TTGAT
 A TTCA AGAGG AGTTTATGGA
 ||| ||||| |||||
 AGGT TTTCC TTAAATATCT
 C CGT__
 GAM2046 KIAA1155 3' TTTGTAGATTGACCTCTT 62922 GAT TG
 AAGAGGTT AGTTTA GA
 ||||| ||||| ||

		TTCTCCAG	TTAGAT	TT	
		___	GT		
GAM2046	KIAA1181	3'	TCCGTGGACCTCTACCTTCTGG	68914	AG T TA
	A		TTCA AGGT GA GTTTATGGA		
			AGGT TCCA CT CAGGTGCCT		
			CT T C_		
GAM2046	KIAA1199	3'	TTCACCTTTCCTGCAGCCTCTTG	72935	A TTTA_
	G		TCAAGAGGTTG TAG TGGA		
			GGTTCTCCGAC GTC ACTT		
			_ CTTTC		
GAM2046	KIAA1237	3'	AAAGTGTGCGCCTTTTTTGAA	81296	T G
			TTCAAGAGG TGATA TTT		
			AAGTTTTTC GCTGT AAA		
			C G		
GAM2046	KIAA1240	3'	TCTGTGAATTGTATGTATCTGA	67294	A GGTTG
	A		TTCA GA ATAGTTTATGGA		
			AAGT CT TGTTAAGTGTCT		
			_ ATGTA		
GAM2046	KIAA1244	3'	TTTGTAACCTTTGCCCTCCTTG	72452	_ TT T TG
	AG		TTCAAG AGG GA AGTTTA GA		
			GAGTTC TCC TT TCAAAT TT		
			C CG _ GT		
GAM2046	KIAA1266	3'	TTCATTTTCTCTGCCTTTTGG	66703	T TAGTTT
			TCAAGAGGT GA ATGGA		
			GGTTTTCCG CT TACTT		
			T CTTT_		
GAM2046	KIAA1317	5'	TTATACATTTTGATTTCTTGG	87217	TG T T A
			TCAAGAGGT A AGT TATGG		
			GGTTCTTTA T TTA ATATT		
			GT _ C C		
GAM2046	KIAA1371	3'	TCTGTAGCTGGCATGCCTCTTG	90478	_ A T
	GA		TTCAAGAGGT TG TAGTT ATGGA		
			AGGTTCTCCG AC GTCGA TGTCT		
			T G _		
GAM2046	KIAA1383	3'	TCCATGAATACTTATTTCTAGA	70343	A TGATA
	A		TTC AGAGGT GTTTATGGA		
			AAG TCTTTA TAAGTACCT		
			A TTCA_		
GAM2046	KIAA1430	3'	TTCATAATGGCATTAGTCTCTG	81652	A GT A _
	AG		TTCA GAG TGAT GT TTATGGA		

		GAGT CTC ATTA CG AATACTT		
		_ TG _ GT		
GAM2046	KIAA1434	3' TTTGTATCAAATGTCCTTTTGA 70215	_____	GTTTATGGA
	A	TTCAAGAGG TTGATA		
		AAGTTTTCC AACTAT		
		TGTA GTTT A		
GAM2046	KIAA1492	3' TCCAGTTGCATTTAATTTTTTG 65128		TA TTA
	AA	TTCAAGAGGTTGA GT TGGA		
		AAGTTTTTAATT CG ACCT		
		TA TTG		
GAM2046	KIAA1497	5' GAATGAACTTTTAATTTTTTG 68122		T GGA
	A	TTCAAGAGGTTGA AGTTTAT		
		AGGTTTTTAATT TCAAGTA		
		T AGG		
GAM2046	KIAA1497	5' TAACAATTATTAAGTTTTGTGA 68131	_	TATGGA
	G	TTCA AGAGGTTGATAGTT		
		GAGT TTTTCAATTATTAA		
		G CAAT		
GAM2046	KIAA1500	3' CCTGTATCAGCCTCATGGA 64807	A	GTTTAT
		TTCA GAGGTTGATA GG		
		AGGT CTCCGACTAT CC		
		A GT_____		
GAM2046	KIAA1546	3' GAATTATGGCTTTTTGAA 68498		G
		TTCAAGAGGTT ATAGTTT		
		AAGTTTTTCGG TATTAAG		
		-		
GAM2046	KIAA1554	3' CCTGAGCTGACAGCTTTTTGAA 96856		A T A
		TTCAAGAGGTTG TAGTTTA GG		
		AAGTTTTTCGAC GTCGAGT CC		
		A _ A		
GAM2046	KIAA1622	3' TAACTGTCAAGTTCTTGAG 55246		GGT
		TTCAAGA TGATAGTTTA		
		GAGTTCT ACTGTCAAAT		
		TG_		
GAM2046	KIAA1649	3' TCTATAAGCAGTCATCTTGG 51252		GGT A
		TCAAGA TGAT GTTTATGGA		
		GGTTCT ACTG CGAATATCT		
		_ A		
GAM2046	KIAA1649	3' TCTATAAGCAGTCATCTTGG 51253		GGT A
		TCAAGA TGAT GTTTATGGA		

GGTTCT ACTG CGAATATCT
 ____ A

GAM2046 KIAA1679 3' TTTATAATTCAGTCTTTTGAG 70721 GT TAGT
 TTCAAGAG TGA TTATGGA
 ||||| || |||||
 GAGTTTTC ACT AATATTT
 TG T____

GAM2046 KIAA1718 3' TTTATAAGCTATTAGCTTC 64979
 GAGGTTGATAGTTTATGGA
 |||||
 CTTGATTATCGAATATTT

GAM2046 KIAA1726 3' TCTGTAATGTTTCACCTTCTTGA 67835 T TAGT
 A TTCAAGAGGT GA TTATGGA
 ||||| || |||||
 AAGTTCTTCA CT AATGTCT
 _ TTGT

GAM2046 KIAA1737 3' TCTGTGGAGCTATAAGCCTCTT 67948 G _
 GGA TTCAAGAGGTT ATAGTTT ATGGA
 ||||| ||||| |||||
 AGGTTCTCCGA TATCGAG TGTCT
 A G

GAM2046 KIAA1858 3' TCTGTGGCCACTTGACTTCTTG 67724 TG TAGT
 CAAGAGGT A TTATGGA
 ||||| | |||||
 GTTCTTCA T GGTGTCT
 GT CACC

GAM2046 KIAA1871 3' CTATGTTAGGCTTTTTTGAA 61901 GATAGTT
 TTCAAGAGGTT TATGG
 ||||| |||||
 AAGTTTTTCGG GTATC
 ATT____

GAM2046 KIAA1887 3' TTTGTAAAGACAAGACCCTTGG 77281 A GATAG TG
 TCAAG GGTT TTTA GA
 |||| |||| |||| ||
 GGTC CCAG AAAT TT
 _ AACAG GT

GAM2046 KIAA1894 3' TCTGTGAACAGTCTTGACTTTT 74288 _ A
 TG CAAGAGGTT GAT GTTTATGGA
 ||||| || |||||
 GTTTTTTCAG CTG CAAGTGTCT
 TT A

GAM2046 KIAA1999 3' TCCTTTGTTGAGCCTTTTGAG 90634 _ TTTAT
 TTCAAGAGGTT GATAG GGA
 ||||| ||||| |||||
 GAGTTTTCCGA TTGTT CCT
 G T____

GAM2046 KR18 3' CCATGGTGCTTTCTTGGA 53888 GTTGAT _
 TTCAAGAG AGT TTATGG
 ||||| || |||||

			AGGTTCTT	TCG GGTACC	
			_____ T		
GAM2046	KRTAP1-3	3'	TTCATGAACGAATTATTTCTT	49044	TGATA
			AAGAGGT	GTTTATGGA	
			TTCTTTA	CAAGTACTT	
			TTAAG		
GAM2046	KRTAP3-2	3'	TTCATAGAAGAAAATTTCTTGG	50073	GATAG
			TCAAGAGGTT	TTTATGGA	
			GGTTCTTTAA	AGATACTT	
			AAGA_		
GAM2046	LBP-9	3'	TCCGTGTTTTAACTTTTTTGAG	28050	TAGTT
			TTCAAGAGGTTGA	TATGGA	
			GAGTTTTTCAATT	GTGCCT	
			TT__		
GAM2046	LIP8	5'	TCCGTGAACTTTTCCTCCTGGA	89527	A TTGAT
			TTCA GAGG	AGTTTATGGA	
			AGGT CTCC	TCAAGTGCCT	
			C TTT__		
GAM2046	LRMP	3'	TCGTAAATTAGTAACTTTT	21587	A
			AGAGGTTG	TAGTTTATGGA	
			TTTTCAAT	ATTAAATGCTT	
			G		
GAM2046	LRP15	5'	AGCTGCAGCCTTTTGAA	54753	A
			TTCAAGAGGTTG	TAGTT	
			AAGTTTTCCGAC	GTCGA	
			-		
GAM2046	LSM1	3'	GCCCAGAGGCTGTTGGCTCTTG	27840	G TG A A
	AA		TTCAAGAG T	ATAGTTT TGG	
			AAGTTCTC G	TGTCGGA ACC	
			_GT G CGT		
GAM2046	M96	3'	TCCATTGAGTCAGTTTTTTG	24759	GG AGTTT
			CAAGA TTGAT	ATGGA	
			GTTTT GACTG	TACCT	
			TT AGT__		
GAM2046	MAP2K5	5'	CCCCTTGTCACCTCTTGGA	12326	T TTTAT
			TTCAAGAGGT	GATAG GG	
			AGGTTCTCCA	CTGTT CC	
			_ CC__		
GAM2046	MARCKS	3'	TTTGTAAAACTGCAGTCATCTT	11416	_GT A _TG
	GGA		TTCAAGA G	TG TAGTTT A GA	

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AGGTTCT C AC GTCAAA T TT
A TG _ A GT
GAM2046 MDN1 3' TCTATAAAAACGATCCTTGG 63360 A ATAG
TCAAG GGTTG TTTATGGA
||||| ||||| |||||
GGTTC CTAGC AAATATCT
_ AA_
GAM2046 MDS025 3' TCCTGCTGTGGCTGTTGGCTTC 41829 TG TAT__
TT AAGAGGT ATAGTT GGA
||||| ||||| |||
TTCTTCG TGTCGG CCT
GT TGTCGT
GAM2046 MFN1 3' TTTGTAAACTATGCAACT 54323 _ TG
GGTTG ATAGTTTA GA
||||| ||||| ||
TCAAC TATCAAAT TT
G GT
GAM2046 MGC10902 3' GCCGTGATTGTCAGTTTCTTGA 48308 GG T A
G TTCAAGA TTGATAGTT ATGG
||||| ||||| |||||
GAGTTCT GACTGTTAG TGCC
TT _ GT
GAM2046 MGC11082 3' TTCGTGAACTAGTGATTGTGAA 52074 AGAG GA
TTCA GTT TAGTTTATGGA
||| ||| |||||
AAGT TAG ATCAAGTGCTT
GT_ TG
GAM2046 MGC11266 5' TCATGGGAAGGCCCTTGG 44490 A GATAG
TCAAG GGTT TTTATGG
||||| ||||| |||||
GGTTC CCGG GGGTACT
_ AA_
GAM2046 MGC14697 5' TCTTGTTCTGGTGACCTTTTGA 52207 GA TT T
A TTCAAGAGGT TAG TA GGA
||||| ||| ||| |||
AAGTTTTCCAG GTC GT TCT
TG TT _
GAM2046 MGC16063 5' TTTGTAATGTATTGGCCTTTT 54931 TG GT TG
AAGAGGT ATA TTA GA
||||| ||| ||| ||
TTTTCCG TAT AAT TT
GT GT GT
GAM2046 MGC16175 3' TCTGTAAGAAGAGGCTTTTGG 52280 GATAG
TCAAGAGGT TTTATGGA
||||| ||||| |||||
GGTTTTTCGG GAATGTCT
AGAA_
GAM2046 MGC16186 3' TCTTGTTTTATCAACGTTTTGG 51410 G TT T
A TTCAAGA GTTGATAG TA GGA
||||| ||||| ||| |||

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AGGTTTT CAACTATT GT TCT
 G TT _
 GAM2046 MGC16386 3' TCTGTGGCTCATGGCCTCT 55617 AT T
 AGAGGTTG AGTT ATGGA
 ||||| ||| |||||
 TCTCCGGT TCGG TGTCT
 AC _
 GAM2046 MGC19556 3' TCCATGCCAACATAACCTCT 54343 ATA _
 AGAGGTTG GTT TATGGA
 ||||| || |||||
 TCTCCAAT CAA GTACCT
 A__ CC
 GAM2046 MGC2560 3' ACAGAATGGATTATTGATTTTT 49567 TG GGA
 TGGA TTCAAGAGGT ATAGTTTAT
 ||||| |||||
 AGGTTTTTTA TATTAGGTA
 GT AGACAT
 GAM2046 MGC29898 3' TTTATAGATAGTTTGCCATTTT 59590 _ T A
 TTGG TCAAGA GGT GAT GTTTATGGA
 |||| | || |||||
 GGTCT CCG TTG TAGATATTT
 TTA T A
 GAM2046 MGC861 3' TCCATAAACATTCTCTGTTGAG 44132 G TT TA
 TTCAA AGG GA GTTTATGGA
 |||| | || |||||
 GAGTT TCT CT CAAATACCT
 G _ TA
 GAM2046 MIG 3' TCCAACCAGATTGTCAGCTCCT 11588 AG A_
 TGAG TTCAAG GTTGATAGTTT TGGA
 |||| ||||| |||
 GAGTTC CGACTGTTAGA ACCT
 CT CCA
 GAM2046 MS4A6E 3' TGAAGAACTATTGACTTCTTGG 58360 TG ATGGA
 TCAAGAGGT ATAGTTT
 ||||| |||||
 GGTTCTTCA TATCAAG
 GT AAGT
 GAM2046 MST4 3' TTTGTAAATTATCAAGCTTC 33743 _ TG
 GAGGTT GATAGTTTA GA
 |||| ||||| ||
 CTTCGA CTATTAAAT TT
 A GT
 GAM2046 MSTP028 3' CCTATGTGGGCTTTTTGG 50062 G GTTTAT
 TCAAGAGGTT ATA GG
 ||||| || ||
 GGTTTTTCGG TGT CC
 G AT____
 GAM2046 NECL1 3' TCCATAGGAACTGCCCTTGGA 41327 A TGATAG
 TTCAAG GGT TTTATGGA
 |||| | |||||

			AGGTTC CCG GGATACCT	
			_ TCAA_	
GAM2046	NEIL2	3'	TTGGTGACTGTTGATTTGTTGA 59572	G TG TATGGA
	A		TTCAA AGGT ATAGTT	
			AAGTT TTTA TGTCAG	
			G GT TGGTT	
GAM2046	NNT	3'	CTGTAGCAAAGCTCTTGGA 25628	G GATAGT
			TTCAAGAG TT TTATGG	
			AGGTTCTC AA GATGTC	
			G AC_	
GAM2046	NR4A3	3'	TCCATAAACAAAGTGCAATTTTT 23723	ATA_
	T		AAGAGGTTG GTTTATGGA	
			TTTTTTAAC CAAATACCT	
			GTGAA	
GAM2046	NRF	5'	TCTATTCAAATTGGCTTCTGAG 34508	A TG AGTTT
			TTCA GAGGT AT ATGGA	
			GAGT CTTCG TA TATCT	
			_ GT AACT_	
GAM2046	NSBP1	3'	TTTATAAACACAGCCTTT 48494	ATA
			AGAGGTTG GTTTATGGA	
			TTTCCGAC CAAATATTT	
			A_	
GAM2046	NYD-SP15	3'	TCTGTGGATTTGCCTGTTGG 48849	G TGAT
			TCAA AGGT AGTTTATGGA	
			GGTT TCCG TTAGGTGTCT	
			G T_	
GAM2046	OAZIN	5'	TTTATGACTTTTCGGCTTTGTGG 32440	A T T
	A		TTCA GAGGTTGA AGTT ATGGA	
			AGGT TTTCCGGCT TCAG TATTT	
			G T _	
GAM2046	OLIG1	3'	TTTGTAGACCAGCTGTTTGGA 97339	A ATA TG
			TTCAAG GGTTG GTTTA GA	
			AGGTTT TCGAC CAGAT TT	
			G _ GT	
GAM2046	ORMDL2	3'	TCCATAGCAGGAAGCCATTTGG 27195	A GATA T
			TCAAG GGTT GTT ATGGA	
			GGTTT CCGA CGA TACCT	
			A AGGA _	
GAM2046	OVCA2	3'	AACTATCAATTCTTGAG 55886	G
			TTCAAGAG TTGATAGTT	

GAGTTCTT AACTATCAA

GAM2046 P66 3' TTTGTAAAGATGCTTCTTGA 40746 TGATAG TG
TCAAGAGGT TTTA GA
||||||| ||| ||
AGTTCTTCG AAAT TT
TAG__ GT

GAM2046 PAK2 3' AAATTATTACTCTTTTGG 67136 GT
TCAAGAG TGATAGTTT
||||| |||||||
GGTTTTTC ATTATTA
TC

GAM2046 PAK6 3' TTTGTGAATTGTTTGCACCTTG 39812 AG T TG
CAAG GT GATAGTTTA GA
||| || ||||||| ||
GTTC CG TTGTTAAGT TT
A_ T GT

GAM2046 PI4KII 3' AGGCTATTAGGTTCTTGGGA 37947 G
TTCAAGAG TTGATAGTTT
||||| |||||||
AGGTTCTT GATTATCGGA
G

GAM2046 POU4F2 3' TCTGTAAATTATTAATTT 17115
AGGTTGATAGTTTATGGA
|||||||||||
TTTAATTATTAATGTCT

GAM2046 PRDM13 3' TGGAGGAAATTGTGCCTTTTGA 41514 TG ATGGA
A
TTCAAGAGGT ATAGTTT
||||||| |||||
AAGTTTTCCG TGTTAAA
__ GGAGGTG

GAM2046 PRKWNK2 3' TCCGTGGACGTCTATGCCTTT 92201 T__ A
AGAGGT GAT GTTTATGGA
||||| || |||||||
TTTCCG CTG CAGGTGCCT
TAT _

GAM2046 PSPH 3' GACTATTGATTTCCTGGA 17133 A TG
TTCA GAGGT ATAGTT
||| |||| |||||
AGGT CTTTA TATCAG
C GT

GAM2046 PTPRR 3' AGACCATCAATCTCTTGG 56449 A
TCAAGAGGTTGAT GTTT
||||||||| |||
GGTTCTCTAACTA CAGA
C

GAM2046 PTPRT 3' TCCATAGCTCTGCAGATTCTTG 56510 G A T_
GA
TTCAAGAG TTG TAG TTATGGA
||||||| ||| ||| |||||

AGGTTCTT GAC GTC GATACCT
 A _ TC
 GAM2046 RAB40A 5' TTTGTAAACATCTATCCCTTGG 82947 A TT_ A TG
 TCAAG GG GAT GTTTA GA
 ||||| || ||| ||||| ||
 GGTTC CC CTA CAAAT TT
 _ TAT _ GT
 GAM2046 RAB40B 3' TCTGTAAATCTACAGTTTTTTTG 23341 GG A _
 CAAGA TTG TAG TTTATGGA
 ||||| ||| ||| |||||
 GTTTT GAC ATC AAATGTCT
 TT _ T
 GAM2046 RBM14 3' TCTGTAGACTGTTGAGACT 21995 G_ TG
 AG T ATAGTTTATGGA
 || | |||||
 TC A TGTCAGATGTCT
 AG GT
 GAM2046 RENT2 3' TCTGACAATCTGTTAATTTCTT 32068 TTTAT_
 AAGAGGTTGATAG GGA
 ||||| ||||| |||
 TTCTTTAATTGTC TCT
 TAACAG
 GAM2046 RFX3 3' GTGCTGAACATTAACCTTTTTTG 57059 A TGGA
 A TTCAAGAGGTTGAT GTTTA
 ||||| ||||| |||||
 AGGTTTTTCAATTA CAAGT
 _ CGTGT
 GAM2046 RRN3 3' TTTGTGTTAACAGCTTTTTGA 37961 A TT TG
 TCAAGAGGTTG TAG TA GA
 ||||| ||| ||| ||
 AGTTTTTCGAC ATT GT TT
 A _ GT
 GAM2046 SEC15B 3' TTTATAAGCTACCAGTCTATGG 67268 AG GT A
 TCA AG TG TAGTTTATGGA
 ||| || ||| |||||
 GGT TC AC ATCGAATATTT
 A_ TG C
 GAM2046 SEF 3' ATCTGTAAAGGCAGCTGGCAGC 69995 A _____
 TTTTTGG TCAAGAGGTTG TAGT TTATGGA T
 ||||| ||||| ||||| |
 GGTTTTTCGAC GTCG AATGTCT A
 G ACGGA
 GAM2046 SEZ6 3' CCAACATCAGCCTCTTGG 74828 A TTA
 TCAAGAGGTTGAT GT TGG
 ||||| ||||| |||
 GGTTCTCCGACTA CA ACC
 _ _
 GAM2046 SGKLA 3' TTTATGTTCTATTTCATCTTTTG 26066 T TT
 TTCAAGAGGT GATAG TATGGA
 ||||| ||||| |||||

			AAGTTTTCTA TTATC GTATTT		
			C TT		
GAM2046	SGKL	3'	TTTGTGGATTATTTTCCTCTG 26067	A TT_	TG
	AA		TTCA GAGG GATAGTTTA GA		
			AAGT CTCC TTATTAGGT TT		
			_ TTT GT		
GAM2046	SLC11A2	3'	TTTATGAACTGATGTTCTCGTG 7054	A TTGA	
	AA		TTCA GAGG TAGTTTATGGA		
			AAGT CTCT GTCAAGTATTT		
			G TGTA		
GAM2046	SLC7A11	3'	TCTATGAGTCGCACAATTCTTG 27533	GT_ ATAG	
	AG		TTCAAGAG TG TTTATGGA		
			GAGTTCTT AC GAGTATCT		
			AAC GCT_		
GAM2046	SNAPC1	3'	TCTGTAGGTTATTTCTTGGA 13281	GGTT TT	
			TTCAAGA GATAG TATGGA		
			AGGTTCT TTATT ATGTCT		
			_____ GG		
GAM2046	SNAPC3	3'	CCATGGGCTAAATTTTGA 13283	GGTTGA	
			TCAAGA TAGTTTATGG		
			AGTTTT ATCGGGTACC		
			AA_____		
GAM2046	SPRY4	3'	TATTTTATTGGCCTTTTGAA 49030	TG TT	
			TTCAAGAGGT ATAG TA		
			AAGTTTTCCG TATT AT		
			GT TT		
GAM2046	SRP9	3'	TTGTAGTATCAGCTTGTTGAG 79935	G GT TG	
			TTCAA AGGTTGATA TTA GA		
			GAGTT TTCGACTAT GAT TT		
			G _ GT		
GAM2046	STK17A	3'	AGGTGTCAGCTTTTGAG 17666	G G	
			TTCAAGAG TTGATA TT		
			GAGTTTTC GACTGT GA		
			_ G		
GAM2046	SYT6	3'	TCCATGGAAGAGCCTTTGTGAG 79524	_ GATAG	
			TTCA AGAGGTT TTTATGGA		
			GAGT TTTCCGA AGGTACCT		
			G GA_____		
GAM2046	TBX4	3'	TCCAGTATTAACCTCTGTGG 38083	_ GTTTA	
			TCA AGAGGTTGATA TGGA		

GGT TCTCCAATTAT ACCT
G G____
GAM2046 TEB4 3' TTTGTGGACTTCTCTCTTTGGA 61288 _ TT T TG
TTCAA GAGG GA AGTTTA GA
||||| ||| || ||||| ||
AGGTT CTCT CT TCAGGT TT
T _ _ GT
GAM2046 TNFAIP3 3' TCCATGGACTGTGATTCTGAG 21910 A GTTG
TTCA GAG ATAGTTTATGGA
||||| ||| |||||
GAGT CTT TGTCAGGTACCT
_ AG_
GAM2046 TP53TG3 3' TCCGTGGGACATCTCTCTGGA 31731 A TT AG
TTCA GAGG GAT TTTATGGA
||||| ||| |||||
AGGT CTCT CTA GGGTGCCT
_ _ CA
GAM2046 TPD52 3' TCTATGAACTAGTCTACTTCTT 18673 T _
AAGAGGT GAT AGTTTATGGA
||||| ||| |||||
TTCTTCA CTG TCAAGTATCT
T A
GAM2046 TRAF3 5' CCACCGTCGGCTTCTGGAG 13848 A TA TTAT
TTC AGAGGTTGA GT GG
||| ||||| || ||
GAG TCTTCGGCT CA CC
G GC ____
GAM2046 TRPC3 3' TCCAAGAGACTATCAGTTCCTT 13860 AG A_
GG TCAAG GTTGATAGTTT TGGA
||||| ||||| |||
GGTTC TGACTATCAGA ACCT
CT GA
GAM2046 TSGA 3' TCAACTACTGTACAATTTCTTG 37975 _ TTA A
G TCAAGAGGTTG ATAGT TGG
||||||| ||| |||
GGTTCTTTAAC TGTC ACT
A TCA
GAM2046 TSPAN-3 3' TCTGCTGCTGTTGGCCTCTGGA 20371 A TG TTA
G TTC AGAGGT ATAGT TGGA
||| ||||| ||| |||
GAG TCTCCG TGTCG GTCT
G GT TC_
GAM2046 TTC4 3' TGGACAGTGGCCTCTTGAG 66910 ATA
TTCAAGAGGTTG GTTTA
||||||| |||
GAGTTCTCCGGT CAGGT
GA_
GAM2046 TU3A 3' TTTATGGACTGGCCCCTTTGAG 24187 A TTGA
TTCA GAGG TAGTTTATGGA
||||| ||| |||||

GAGT TTCC GTCAGGTATTT
 _ CCG_
 GAM2046 UBE3B 3' TTTAGCTAGTTTGATCTTTTGG 77450 TG__ TATGGA
 TCAAGAGGT A TAGTT
 ||||| | ||||
 GGTTTTCTA T ATCGA
 GT TG TTT
 GAM2046 UMP-CMPK 3' TCTGTGAGCAAACTTTTT 33312 GATA
 AAGAGGTT GTTTATGGA
 ||||| |||||
 TTTTCAA CGAGTGTCT
 AA_
 GAM2046 YAP1 3' TTTATAAACTTCTTTCTCTT 21469 TT T
 AAGAGG GA AGTTTATGGA
 |||| || |||||
 TTCTCT CT TCAAATATTT
 TT _
 GAM2046 YME1L1 3' TCTGTAATCCCAGCACTTTTGG 58441 _ ATAGT
 A TTCAAGAG GTTG TTATGGA
 ||||| || |||||
 AGGTTTTC CGAC AATGTCT
 A CCT_
 GAM2046 ZDHHC5 5' CCATGAGCTGTATCTTGA 93184 GGTTG
 TCAAGA ATAGTTTATGG
 |||| |||||
 AGTTCT TGTCGAGTACC
 A_
 GAM2046 ZNF220 3' TTTATAGACGGACTTCATTGAA 23162 _ GATA
 TTCAA GAGGTT GTTTATGGA
 |||| |||| |||||
 AAGTT CTTGAG CAGATATTT
 A G_
 GAM2046 ZNF323 3' TTTGTGAGCTGTGGGACTTT 48822 GT G TG
 AGAG T ATAGTTTA GA
 ||| | ||||| ||
 TTTC G TGTCGAGT TT
 AG G GT
 GAM2046 ZNF387 3' TTTATTTTTTATTAACCTCATG 28685 A TTT
 GA TTCA GAGGTTGATAG ATGGA
 ||| ||||| ||||
 AGGT CTCCAATTATT TATTT
 A TTT
 GAM2046 LOC112840 3' CCCATGATTGTAAGTTTCTTGA 55613 GG G T A
 G TTCAAGA TT ATAGTT ATGG
 ||||| || ||||| ||||
 GAGTTCT GA TGTTAG TACC
 TT A _ CC
 GAM2046 LOC112885 3' TCCTTTTGCCAATCTCTTGGA 57342 ATA TTAT
 TTCAAGAGGTTG GT GGA
 ||||| || |||

AGGTTCTCTAAC CG CCT
 ____ TTTT
 GAM2046 LOC113444 3' GGCTGTCAATCTCTGTGG 57364 _
 TCA AGAGGTTGATAGTT
 ||| |||||
 GGT TCTCTAACTGTCGG
 G
 GAM2046 LOC118738 3' TCCACACTGTCAGCTCCTTGG 76006 AG TTA
 TCAAG GTTGATAGT TGGA
 |||| ||||| |||
 GGTTT CGACTGTCA ACCT
 CT C_
 GAM2046 LOC122210 3' CTTATATTTTGTGCCCCTCTTG 74578 TT TT A
 G TCAAGAGG GATAG TATGG
 ||||| |||| ||||
 GGTTCTCC TTGTT ATATT
 CG TT CT
 GAM2046 LOC124152 3' TTTATGGTACATATTGATTGTC 74728 _ TG _ _
 TTGAA TTCAAGA GGT ATA GT TTATGGA
 ||||| ||| ||| |||||
 AAGTTCT TTA TAT CA GGTATTT
 G GT A T
 GAM2046 LOC129446 3' TTTATGAATTTGGATACCCTTT 76618 TTGAT_
 TGAG TTCAAGAGG AGTTTATGGA
 ||||| |||||
 GAGTTTTCC TTAAGTATTT
 CATAGGT
 GAM2046 LOC131744 5' TAGACACCAGCTTTTTTGAA 76391 ATA
 TTCAAGAGGTTG GTTTA
 ||||| ||||
 AAGTTTTTCGAC CAGAT
 CA_
 GAM2046 LOC131873 3' TTTGTAGGTTATCAGGTGACTT 76397 AGG_ TT TG
 GA TCAAG TTGATAG TA GA
 |||| ||||| || ||
 AGTTC GACTATT AT TT
 AGTG GG GT
 GAM2046 LOC132166 3' TTTGTA ACTATTGATTTCTGAA 75540 A TG T TG
 TTCA GAGGT ATAGTT A GA
 |||| |||| ||||| || ||
 AAGT CTTTA TATCAA T TT
 _ GT _ GT
 GAM2046 LOC142913 3' TCAGCACTGTCGTCTTCTTGGA 76934 T TTA
 TTCAAGAGG TGATAGT TGG
 ||||| ||||| |||
 AGGTTCTTC GCTGTCA ACT
 T CG_
 GAM2046 LOC142927 3' TCTGTGGGCTGGCGTCCT 76953 T A
 AGG TG TAGTTTATGGA
 ||| || |||||

	TCC GC GTCGGGTGTCT	
	T G	
GAM2046 LOC142955 3'	TTCATCTTTCAATCTTTTGA 76967	T TTT
	TCAAGAGGTTGA AG ATGGA	
	AGTTTTCTAACT TC TACTT	
	T _	
GAM2046 LOC144231 5'	TCTATGTCTGTTTCACTTTTTTG 83943	T_ TT
GA	TTCAAGAGGT GATAG TATGGA	
	AGGTTTTTCA TTGTC GTATCT	
	CT T_	
GAM2046 LOC144347 3'	CCATGGAGTGCCCTTGAA 77304	A TGAT G
	TTCAAG GGT A TTTATGG	
	AAGTTC CCG T AGGTACC	
	_ _ _ G	
GAM2046 LOC144453 3'	TTCATAGATTATTAGTTGTGGA 77330	AAGA GT
A	TTC G TGATAGTTTATGGA	
	AAG T ATTATTAGATACTT	
	GTG_ TG	
GAM2046 LOC145241 3'	TCCATGAATTATTACACTTT 63528	GT
	AGAG TGATAGTTTATGGA	
	TTTC ATTATTAAGTACCT	
	AC	
GAM2046 LOC145483 3'	TCCTCAGTGCTATTAATATTTT 77760	G TTAT_
GG	TCAAGA GTTGATAGT GGA	
	GGTTTT TAATTATCG CCT	
	A TGACT	
GAM2046 LOC145609 5'	TCTATGGATGCCTGCCTTGTGA 84371	A TGATA
G	TTCA GAGGT GTTTATGGA	
	GAGT TTCCG TAGGTATCT	
	G TCCG_	
GAM2046 LOC145871 5'	TCTGTGAGCACCGAGGCTTTTT 84553	GATA_
GG	TCAAGAGGTT GTTTATGGA	
	GGTTTTTCGG CGAGTGTCT	
	AGCCA	
GAM2046 LOC145945 5'	TTTATGAGTATAAACTCTTGAA 84575	GTTG G
	TTCAAGAG ATA TTTATGGA	
	AAGTTCTC TAT GAGTATTT	
	AAA_ _	
GAM2046 LOC146714 5'	TCCATGGAAACTGACATTTTTG 84753	_ GATAG
AG	TTCAAGAG GTT TTTATGGA	

GAGTTTTT CAG AGGTACCT
 A TCAA_
 GAM2046 LOC147040 5' TTCATCTCTTCTCTCAACCTTT 78839 T TTT_
 TGG TCAAGAGGTTGA AG ATGGA
 ||||| || ||||
 GGTTTTCCAAC TC TACTT
 C TTCTC
 GAM2046 LOC148195 5' CCATGCATGTCCTCTTGAG 85273 TTGATA T
 TTCAAGAGG GT TATGG
 ||||| || ||||
 GAGTTCTCC TA GTACC
 TG__ C
 GAM2046 LOC148195 5' TTCATAGAGCGCTGTTTCTTGA 85297 GGTT ____
 G TTCAAGA GATAGT TTATGGA
 ||||| ||||| |||||
 GAGTTCT TTGTCG GATACTT
 ____ CGA
 GAM2046 LOC148641 5' TCCATGGGGAAACCTTTGTGGA 79668 _ GATAG
 TTCA AGAGGTT TTTATGGA
 ||| ||||| |||||
 AGGT TTTCCAA GGGTACCT
 G AG__
 GAM2046 LOC148894 5' TCTGTATGTTTAACTCATGG 85424 A TAGTT
 TCA GAGGTTGA TATGGA
 ||| ||||| |||||
 GGT CTCTAATT ATGTCT
 A TTGT_
 GAM2046 LOC149386 5' TTCATGGCACAACCTTCTTGAA 85567 ATA T
 TTCAAGAGGTTG GTT ATGGA
 ||||| ||| |||||
 AAGTTCTTCAAC CGG TACTT
 A__ _
 GAM2046 LOC149401 5' TTCATAAGCATACCTTTT 80117 TGATA
 AAGAGGT GTTTATGGA
 ||||| |||||
 TTTTCCA CGAATACTT
 TA__
 GAM2046 LOC149401 5' TTGTACATTGTCAGTCTCTGTG 80118 _ GT T TG A
 G TCA AGAG TGATAGT TA G
 ||| ||| ||||| |||
 GGT TCTC ACTGTTA AT T
 G TG C GT
 GAM2046 LOC149420 3' TTCATAATCTCAGCTTTTTTGA 80159 _ TAGT
 A TTCAAGAG GTTGA TTATGGA
 ||||| ||||| |||||
 AAGTTTTT CGACT AATACTT
 T CT__
 GAM2046 LOC149703 3' TCCCAGGCTGTTGGTTTCTT 85825 GG TG AT
 AAGA T ATAGTTT GGA
 ||| | ||||| |||

	TTCT G TGTCGGA CCT		
	TT GT C_		
GAM2046 LOC149837 5'	TCTGATAGTATTTTAGCTTCTT 85908	TAGT _	
GAA	TTCAAGAGGTTGA TTAT GGA		
	AAGTTCTTCGATT GATA TCT		
	TTAT G		
GAM2046 LOC150150 3'	TCCATAGAATACCAGCTTCTGA 86013	A A G	
A	TTCA GAGGTTG TA TTTATGGA		
	AAGT CTTCGAC AT AGATACCT		
	_ C A		
GAM2046 LOC150157 3'	TCCAGGAGCTGGTTTTTTGAA 86027	GG TGA A	
	TTCAAGA T TAGTTT TGGA		
	AAGTTTT G GTCGAG ACCT		
	TT _ G		
GAM2046 LOC150225 5'	TTGTAAATCAATGTTTTTGGA 86210	G AGT TG	
	TTCAAGA GTTGAT TTA GA		
	AGGTTTT TAACTA AAT TT		
	G _ GT		
GAM2046 LOC150297 5'	CTGTCCTTGTGCCTCTTGGA 80627	T _	
	TTCAAGAGGT GATAG		
	AGGTTCTCCG CTGTC		
	TGTTT		
GAM2046 LOC150538 5'	TCTGTAACAGCACAGCTTCTGA 80741	A ATAGT	
G	TTCA GAGGTTG TTATGGA		
	GAGT CTTCGAC AATGTCT		
	_ ACGAC		
GAM2046 LOC150606 3'	CCAGTGTCTGCTTTTTTGAA 86267	T GTTTA	
	TTCAAGAGGT GATA TGG		
	AAGTTTTTCG CTGT ACC		
	T G _		
GAM2046 LOC151009 3'	CTATAAGGAGCTTTTTGA 86367	GATAG	
	TCAAGAGGTT TTTATGG		
	AGTTTTTCGA GAATATC		
	G _		
GAM2046 LOC151277 5'	TCTATGACATTGACTTTTTGAA 81007	TG A T	
	TTCAAGAGGT AT GTT ATGGA		
	AAGTTTTTCA TA CAG TATCT		
	GT _ _		
GAM2046 LOC151473 3'	TTCGTATCATTGGCCTCTT 81052	TG AGTT	
	AAGAGGT AT TATGGA		

	TTCTCCG TA ATGCTT GT CT__	
GAM2046 LOC151516 5'	TCTGTGGGTTTCTCTTGG 81069 TCAAGAGG GA AG TATGGA GGTTCTTC CT TT GTGTCT T_ _ GG	TT T TT
GAM2046 LOC151521 3'	TCTATGCTAACACTTTTGGAG 86625 TTCAAGAGGT G TAGT ATGGA GAGTTTTTCA C ATCG TATCT _ A _	T A TT
GAM2046 LOC151747 3'	TCCATAAAGGTCAAATCATTTT 81162 GGA TTCAAGA TTGAT TTTATGGA AGGTTTT AACTG AAATACCT ACTA G_	GG_ AG
GAM2046 LOC152426 5'	CCATGTTTGTCTCTTGA 86893 TTCAAGAGG ATAG TATGG AGGTTCTCC TGTT GTACC _ T_	TTG TT
GAM2046 LOC153642 3'	TAGATATTAGCTTTTTG 81792 CAAGAGGTTGATA TTTA GTTTTTCGATTAT AGAT	G
GAM2046 LOC153682 3'	TCTATAGGCTTAAACTATTTGA 87277 G TTCAAG GGTT AGTTTATGGA GAGTTT TCAA TCGGATATCT A AT_	A GAT
GAM2046 LOC154184 5'	TTTGTA AAAATTTATACTTCTTG 87388 AG TTCAAGAGGT TTTA GA GAGTTCTTCA AAAT TT TATTTA GT	TGATAG TG
GAM2046 LOC154214 3'	CTGTGAGTCACATCTTGAA 81959 TTCAAGA TGAT TTATGG AAGTTCT ACTG AGTGTC AC_ _	GGT AGT
GAM2046 LOC154214 5'	TCTGTTGACATTGGCTCTTGAA 81960 TTCAAGAG T AT GTT ATGGA AAGTTCTC G TA CAG TGTCT _ GT _ T	G TG A T
GAM2046 LOC154739 5'	TCCATGGGCTTGCTTTTTG 87445 CAAGAGGT AGTTTATGGA 	TGAT

	GTTTTTCG TCGGGTACCT	
	T____	
GAM2046 LOC157378 5'	TTCATAGGGTTTGGCTTTTTGG 82356	TG TAG
A	TTCAAGAGGT A TTTATGGA	
	AGGTTTTTCG T GGATACTT	
	GT TG_	
GAM2046 LOC157507 5'	TTCATACTATTTGTTTCTTGG 82380	TT TT
	TCAAGAGG GATAGT ATGGA	
	GGTTCTTT TTATCA TACTT	
	GT _	
GAM2046 LOC157798 5'	TCTGCCCGCATTGGCCTCCTGA 87866	A TG A TTA
A	TTCA GAGGT AT GT TGGA	
	AAGT CTCCG TA CG GTCT	
	C GT _ CCC	
GAM2046 LOC158014 5'	CCATAACCACTTTTTGAA 82557	TGATA T
	TTCAAGAGGT GTT ATGG	
	AAGTTTTCA CAA TACC	
	C____ _	
GAM2046 LOC158156 3'	TCCGCAAGCATCAGTTTTTTGA 82630	GG A A
A	TTCAAGA TTGAT GTTT TGGA	
	AAGTTTT GACTA CGAA GCCT	
	TT _ C	
GAM2046 LOC158158 3'	TCTGTAGGCTCCACCTCTGGG 82623	A T TA
	TC AGAGGT GA GTTTATGGA	
	GG TCTCCA CT CGGATGTCT	
	G C _	
GAM2046 LOC161734 3'	TCTGTAGGCTCCACCTCTGGG 88471	A T TA
	TC AGAGGT GA GTTTATGGA	
	GG TCTCCA CT CGGATGTCT	
	G C _	
GAM2046 LOC163231 5'	CTGTGGACTTGCCCTTGAA 83332	A TGAT
	TTCAAG GGT AGTTTATGG	
	AAGTTC CCG TCAGGTGTC	
	_ T____	
GAM2046 LOC163882 3'	TCCCTCCTGTTACCTCTTGG 83042	T TTTAT
	TCAAGAGGT GATAG GGA	
	GGTTCTCCA TTGTC CCT	
	C CTC__	
GAM2046 LOC169426 5'	TCTGCAGGCAGTGTTGGTTTCT 88628	GG TG _ AT
TGAA	TTCAAGA T ATA GTTT GGA	

	AAGTTCT G TGT CGGA TCT TT GT GA CG	
GAM2046 LOC196074 3'	GCATCATATTGGACTCTTGAA 88970 TTCAAGAG T ATA ATG AAGTTCTC G TAT TAC A GT AC__ GT	G TG GTTT GA
GAM2046 LOC196477 3'	AAAAAGATTATCTACCTTTTGG 89060 TCAAGAGGT GATAGTTT GGTTTTCCA CTATTAGA T AAAAT	T ATGGA
GAM2046 LOC196559 5'	TTTGTAAATCATTGTTGATCTCT 91212 TG CAAGAGGT ATAGT TTA GA GTTCTCTA TGTTA AAT TT GT CT GT	TG __ TG
GAM2046 LOC196792 3'	TTCATGAGCAATACTTCTT 88915 AAGAGGT GTTTATGGA TTCTTCA CGAGTACTT TAA__	TGATA
GAM2046 LOC196890 3'	TCCAGGAGCTGGTTTTTTTGAA 91228 TTCAAGA T TAGTTT TGGA AAGTTTT G GTCGAG ACCT TT__ G	GG TGA A
GAM2046 LOC197003 3'	TCCATACATTTTCAGTCCTCTTG 89216 GA TTCAAGAGG TTGA AGT TATGGA AGGTTCTCC GACT TTA ATACCT T _ C	_ T T
GAM2046 LOC199786 3'	TCCGCTTGCTGTGAGCCTTTTG 89768 G TCAAGAGGTT ATAGT TGGA GGTTTTCCGA TGTCG GCCT G TTC	G TTA
GAM2046 LOC199907 3'	TTTGTAACATAATTTCTTTTGA 89833 TCAAGAGG TAGTTTA GA AGTTTTCT ATCAAAT TT TTA_ GT	TTGA TG
GAM2046 LOC200093 3'	TCAGAAATTCTCAATTTTTTGA 63776 A TTCAAGAGGTTGA AGTTT TGG AAGTTTTTAACT TTAAA ACT C G	T A A
GAM2046 LOC200169 3'	TCTAGTTTTCTGTCAATTCCTT 91562 GAG TTCAAG GTTGATAG TGGA 	AG TTTA_

GAGTTT TAACTGTC ATCT
 CT TTTTG
 GAM2046 LOC200301 5' TCCTGTGGTTGATTTTTTGAG 90154 TG AGTTTAT
 TTCAAGAGGT AT GGA
 ||||| || ||
 GAGTTTTTTA TG CCT
 GT GTGT__
 GAM2046 LOC200399 5' TCTATGAATTCCGGGTAGGTTT 90242 GG TG ____
 CTTGAA TTCAAGA T AT AGTTTATGGA
 ||||| | || |||||
 AAGTTCT G TG TTAAGTATCT
 TT GA GGCC
 GAM2046 LOC200609 5' GGA CTATCATTTCTTGG 91667 T
 TCAAGAGGT GATAGTTT
 ||||| |||||
 GGTCTTTA CTATCAGG
 -
 GAM2046 LOC200942 3' TCTATAAATGGGGATCTCTGAA 90380 A GATA
 TTCA GAGGTT GTTTATGGA
 ||| ||||| |||||
 AAGT CTCTAG TAAATATCT
 - GGG_
 GAM2046 LOC201475 3' TTTGTAAAACTAAAGACTTTTT 89625 GA _TG
 GAA TTCAAGAGGTT TAGTTT A GA
 ||||| ||||| |||
 AAGTTTTTCAG ATCAAA T TT
 AA A GT
 GAM2046 LOC201725 3' GCTCTGTGCTATTACTTTTTGA 90475 T TT
 G TTCAAGAGGT GATAGT ATGGA
 ||||| ||||| |||||
 GAGTTTTTCA TTATCG TGTCT
 - _ CGG
 GAM2046 LOC201771 5' TCCGTAAAAAGTCTTTTTTGAA 70520 TTGATAG
 TTCAAGAGG TTTATGGA
 ||||| |||||
 AAGTTTTTC AAATGCCT
 TGAA__
 GAM2046 LOC201853 3' TCCAGGGGCTGGTTTTTTTGAA 90508 GG TGA TA
 TTCAAGA T TAGTT TGGA
 ||||| | |||| |||||
 AAGTTTT G GTCGG ACCT
 TT__ GG
 GAM2046 LOC202018 3' TTCATAAATTATTACAGCT 90612 ____
 GGTTG ATAGTTTATGGA
 |||| |||||
 TCGAC TATTAAATACTT
 AT
 GAM2046 LOC202134 3' TTTGTTTAATGCTCAGCTTTTT 91926 TA T_TG
 GGA TTCAAGAGGTTGA GTT A GA
 ||||| ||||| ||| | ||

	AGGTTTTTCGACT TAA T TT	
	CG TT GT	
GAM2046 LOC202347 3'	TAAATGATACTGTCATCCTCTT 91949	T _ GGA
GG	TCAAGAGG TGATAGT TTAT	
	GGTTCTCC ACTGTCA AGTA	
	T T AATT	
GAM2046 LOC202459 3'	TCCATAAGCTGAGAACTCTGGA 59932	A G GA
	TTCA GAG TT TAGTTTATGGA	
	AGGT CTC AG GTCGAATACCT	
	_ A A_	
GAM2046 LOC203069 5'	GAATTTTGATCTCTTGAG 90760	TG T
	TTCAAGAGGT A AGTTT	
	GAGTTCTCTA T TTAAG	
	GT _	
GAM2046 LOC203276 3'	TCCATGGGCTTGCTTTTTG 92132	TGAT
	CAAGAGGT AGTTTATGGA	
	GTTTTTCG TCGGGTACCT	
	T__	
GAM2046 LOC203305 3'	TCCATGGGCTTGCTTTTTG 92185	TGAT
	CAAGAGGT AGTTTATGGA	
	GTTTTTCG TCGGGTACCT	
	T__	
GAM2046 LOC203340 3'	CCATAAGTTGTTAGCTTTTGAA 90875	G GT A
	TTCAAGAG TTGATA TTATGG	
	AAGTTTTC GATTGT AATACC	
	_ TG C	
GAM2046 LOC203392 5'	TCCGTAGGCGCGCTCTCTGGAA 90910	A _ TGATA
	TTC AGAG GT GTTTATGGA	
	AAG TCTC CG CGGATGCCT	
	G T CG__	
GAM2046 LOC203411 3'	TCTGTAAGCACTAAACTTTTT 92314	GATA_
	AAGAGGTT GTTTATGGA	
	TTTTTCAA CGAATGTCT	
	AATCA	
GAM2046 LOC205327 3'	TTCATTATATCAGTCTTTTTGA 91073	_ GTTT
A	TTCAAGAGG TTGATA ATGGA	
	AAGTTTTTC GACTAT TACTT	
	T AT__	
GAM2046 LOC206795 5'	TAGGCTGTCAGCTCCTTGGA 92411	AG
	TTCAAG GTTGATAGTTTA	

	AGGTTC CGACTGTCGGAT	
	CT	
GAM2046 LOC219333 3'	TCTATAAATTATTGTA ACT 95189	___
	GGTT GATAGTTTATGGA	
	TCAA TTATTAAATATCT	
	TG	
GAM2046 LOC219653 3'	TCTGTAAGGATTGACCTGTTGG 92922	G TG AG
	TCAA AGGT AT TTTATGGA	
	GGTT TCCA TA GAATGTCT	
	G GT G_	
GAM2046 LOC220506 3'	TCCATCTTCTCAACTTTTT 74522	T_ TTT
	AAGAGGTTGA AG ATGGA	
	TTTTTCAACT TC TACCT	
	CT ___	
GAM2046 LOC221312 3'	TCCATGTTTCTGTTGGTATTTT 93559	GG TG TT_
	GGA TTCAAGA T ATAG TATGGA	
	AGGTTTT G TGTC GTACCT	
	AT GT TTT	
GAM2046 LOC221399 5'	TTCATAAATTACGTGTGCCTTT 95488	_ TGA_
	TTGGA TTCAAGA GGT TAGTTTATGGA	
	AGGTTTT CCG ATTAATACTT	
	T TGTGC	
GAM2046 LOC221415 5'	TCCGTGGTGGCCTCAGTCTTTT 95501	GT TAGT_
	GG TCAAGAG TGA TTATGGA	
	GGTTTTC ACT GGTGCCT	
	TG CCGGT	
GAM2046 LOC221479 3'	TTCAAATCTGTTTGTCTCTTGA 93847	TT TTTA
	A TTCAAGAGG GATAG TGGA	
	AAGTTCTCT TTGTC ACTT	
	GT TAA_	
GAM2046 LOC221601 5'	TTTGTA AAAATTTATACTTCTTG 95293	TGATAG TG
	AG TTCAAGAGGT TTTA GA	
	GAGTTCTTCA AAAT TT	
	TATTTA GT	
GAM2046 LOC221711 3'	TTCATAAAAATTAACCTTTTG 93828	AG
	CAAGAGGTTGAT TTTATGGA	
	GTTTTCCAATTA AAATACTT	
	A_	
GAM2046 LOC221752 3'	TAAGGGGTTAATCTTTTGAG 95425	AG
	TTCAAGAGGTTGAT TTTA	

	GAGTTTTCTAATTG GAAT	
	GG	
GAM2046 LOC221773 3'	TCTATGTGTATGTTGACTTTTT 92697	TG GTT_
	AAGAGGT ATA TATGGA	
	TTTTTCA TGT GTATCT	
	GT ATGT	
GAM2046 LOC222028 3'	TCCATGGGACGCCTTTCTGGA 95706	_ TGATAG
	TTCA AGAGGT TTTATGGA	
	AGGT TTTCCG GGGTACCT	
	C CA_____	
GAM2046 LOC253019 3'	TCTGCTGCTCTGTTGGCCTCTG 97112	A TG TT _
AA	TTCA GAGGT ATAG TA TGGA	
	AAGT CTCCG TGTC GT GTCT	
	_ GT TC C	
GAM2046 LOC253142 3'	TGAACTGGCCTTTTGAA 99227	TGA
	TTCAAGAGGT TAGTTA	
	AAGTTTTCCG GTCAAGT	

GAM2046 LOC253681 5'	TTCATCTCTTCTCTCAACCTTT 96844	T TTT_
TGG	TCAAGAGGTTGA AG ATGGA	
	GGTTTTCCAAC T TACTT	
	C TTCTC	
GAM2046 LOC253776 3'	TTTATGATGCTTTGACCTTTTG 99295	TG T _
G	TCAAGAGGT A AGT TTATGGA	
	GGTTTTCCA T TCG AGTATTT	
	GT _ T	
GAM2046 LOC253868 3'	TTCATATGTGTTTCAGCTTTGTG 97331	A TAGTT
AG	TTCA GAGGTTGA TATGGA	
	GAGT TTTCGACT ATACTT	
	G TGTGT	
GAM2046 LOC253921 3'	CCATGGCAAAC TTTCTTG 96508	GATAGT
	TCAAGAGGTT TTATGG	
	GGTTCTTCAA GGTACC	
	AC_____	
GAM2046 LOC253975 3'	TCTGCTGCTCTGTTGGCCTCTG 97688	A TG TT _
AA	TTCA GAGGT ATAG TA TGGA	
	AAGT CTCCG TGTC GT GTCT	
	_ GT TC C	
GAM2046 LOC254003 5'	TCCAGCCATCAGTTTCCTGAG 98028	A GG A TTA
	TTCA GA TTGAT GT TGGA	

GAGT CT GACTA CG ACCT
 C TT C ____
 GAM2046 LOC254128 3' TCTATAAACTAATGTCTTTGGA 97360 _ G TGA
 TTCAA GA GT TAGTTTATGGA
 ||||| || || |||||
 AGGTT CT TA ATCAAATATCT
 T G ____
 GAM2046 LOC254242 5' TCCATGCCTACCTGTGGTCTCT 98381 GT G TT____
 TGGA TTCAAGAG T ATAG TATGGA
 ||||| || |||||
 AGGTTCTC G TGTC GTACCT
 TG_ CATCC
 GAM2046 LOC254243 3' TCCATGGGCTTGCTTTTTG 99271 TGAT
 CAAGAGGT AGTTTATGGA
 ||||| |||||
 GTTTTTCG TCGGGTACCT
 T____
 GAM2046 LOC254672 3' TCTGATAATGTCAACTTTTGAA 96300 G GT _
 TTCAAGAG TTGATA TTAT GGA
 ||||| ||||| |||||
 AAGTTTTC AACTGT AATA TCT
 _ _ G
 GAM2046 LOC255196 3' TCTGTAAATTATCTTTTTC 98967 TT
 GAGG GATAGTTTATGGA
 ||||| |||||
 CTTT CTATTAAATGTCT
 TT
 GAM2046 LOC255975 5' TCTGTAGGCCACAGACTTCTT 97594 GATA
 AAGAGGTT GTTTATGGA
 ||||| |||||
 TTCTTCAG CGGATGTCT
 ACAC
 GAM2046 LOC256942 3' TCTATAAATTATCAGTCTGGGT 96187 AG_ GT
 G CA AG TGATAGTTTATGGA
 || || |||||
 GT TC ACTATTAAATATCT
 GGG TG
 GAM2046 LOC257319 3' ATCTATGGGTGATAGAAACAGC 97470 ____ AG
 TTTTGA TTTCAAGAGGTTG AT TTTATGGA T
 ||||| || ||||| |
 AAGTTTTTCGAC TA GGGTATCT A
 AAAGA GT
 GAM2046 LOC257319 3' TCTGTAAAGCATATTTACCTCT 97474 T _ _
 TGG TCAAGAGGT GATA GTTT ATGGA
 ||||| ||||| |||||
 GGTCTCCA TTAT CGAA TGTCT
 T A A
 GAM2046 LOC50999 3' GCCATCTAGCTTTTTGAA 32638 _ A
 TTCAAGAGGTT GAT GT
 ||||| ||||| |||||

AAGTTTTTCGA CTA CG
 T C
 GAM2046 LOC51026 3' TCCATAGGCATTTGCTTTTTAG 32688 _ T A
 AA TTC AAGAGGT GAT GTTTATGGA
 ||| ||||| ||| |||||
 AAG TTTTTCG TTA CGGATACCT
 A T _
 GAM2046 LOC51193 3' TCCATATTCTCTGATTTTCATGA 33371 A GAT TT
 A TTCA GAGGTT AG TATGGA
 |||| ||||| || |||||
 AAGT CTTTAG TC ATACCT
 A TC_ TT
 GAM2046 LOC51313 3' TTTATAGTACTCCTTGGCTCTT 33999 _ TG T_ _
 TTGAG TTCAAGAG GT A AGT TTATGGA
 ||||| || | ||| |||||
 GAGTTTTC CG T TCA GATATTT
 T GT CC T
 GAM2046 LOC51634 3' TTCATAAATATGGCTCTTGAA 32614 GTTGATA
 TTCAAGAG GTTTATGGA
 ||||| |||||
 AAGTTCTC TAAATACTT
 GGTA____
 GAM2046 LOC56270 3' TCTACATTGTCAGCTACTTGG 39510 A TTA
 TCAAG GGTTGATAGT TGGA
 |||| ||||| |||||
 GGTTT CCGACTGTTA ATCT
 A C____
 GAM2046 LOC57149 5' TCCCAGCTGTCAGTGCTTTTGG 40304 _ TAT
 A TTCAAGAG GTTGATAGTT GGA
 ||||| ||||| ||||| |||||
 AGGTTTTT TCGACTGTCGA CCT
 G C____
 GAM2046 LOC57149 5' TCGGAGGCTGTGAATCTTTTGG 40305 G A A
 A TTCAAGAGGTT ATAGTTT TGG
 ||||| ||||| ||||| |||||
 AGGTTTTCTAA TGTCGGA GCT
 G G
 GAM2046 LOC89231 3' TTTATAAATATTGTTGATCTTT 94304 _ TG _
 TTGAA TTCAAGA GGT ATA GTTTATGGA
 ||||| ||| ||| |||||
 AAGTTTT CTA TGT TAAATATTT
 T GT TA
 GAM2046 LOC89932 3' CCTGTGTCAGCCTTCTGAG 61457 AG GTTTAT
 TTCA AGGTTGATA GG
 |||| ||||| ||||| |||||
 GAGT TCCGACTGT CC
 CT GT____
 GAM2046 LOC90038 3' TCCATGGGCTTGCTTTTTG 61815 TGAT
 CAAGAGGT AGTTTATGGA
 ||||| |||||

		GTTTTTCG TCGGGTACCT	
		T___	
GAM2046	LOC90049 3'	TCCATAAAATTAACACCTTTT 61876	TGATAG_
		GGA TTCAAGAGGT TTTATGGA	
		AGGTTTTCCA AAATACCT	
		CAAATTA	
GAM2046	LOC90155 3'	TTTGTATCCATCAAGTTCTTGA 62370	G AGTT TG
		A TTCAAGAG TTGAT TA GA	
		AAGTTCTT AACTA AT TT	
		G CCT_ GT	
GAM2046	LOC90167 3'	TTCATGAATTAAATCAATTTCT 62374	A _
		AGAG TTC AGAGGTTGA TAGTTTATGGA	
		GAG TCTTTAACT ATTAAGTACTT	
		A AA	
GAM2046	LOC90170 5'	GCTAGTAAGTTATTCAGTCTCT 62379	GT _ GT GGA
		TGGA TTCAAGAG TGA TA TTAT	
		AGGTTCTC ACT AT AATG	
		TG T TG ATCGT	
GAM2046	LOC91040 3'	TCAGAAATTCTCAATTTTTTGA 65350	T A A
		A TTCAAGAGGTTGA AGTTT TGG	
		AAGTTTTTTAACT TTAAA ACT	
		C G	
GAM2046	LOC91263 3'	TCTATAGAACCCAGCCTCTAGA 66002	A ATAG
		A TTC AGAGGTTG TTTATGGA	
		AAG TCTCCGAC AGATATCT	
		A CCA_	
GAM2046	LOC91445 3'	TTCATAAGCTTCTTCCTCTGAA 61175	A TT T
		TTCA GAGG GA AGTTTATGGA	
		AAGT CTCC CT TCGAATACTT	
		_ TT _	
GAM2046	LOC91565 3'	AACATTTAACTTTTTGGA 67049	TA
		TTCAAGAGGTTGA GTT	
		AGGTTTTTCAATT CAA	
		TA	
GAM2046	LOC91947 3'	TCCATCTGTTGGTTTTGTGAG 68224	A GG TG TTT
		TTCA GA T ATAG ATGGA	
		GAGT TT G TGTC TACCT	
		G TT GT _	
GAM2046	LOC91947 3'	TTCAACTGTTTATTGACTTCTG 68226	A TG TTTA_
		AG TTCA GAGGT ATAG TGGA	

		GAGT CTTCA TATT ACTT	
		_ GT TGTCA	
GAM2046	LOC92573 5'	TCTGTAATCCCAGCTTCTTGG 70381	ATAGT
		TCAAGAGGTTG TTATGGA	
		GGTTCTTCGAC AATGTCT	
		CCT__	
GAM2046	LOC92606 3'	TTATGTGGCTGTTGGTTTTTTG 70529	GG TG _ A
	AG	TTCAAGA T ATAGTT TATGG	
		GAGTTTT G TGTCGG GTATT	
		TT GT T	
GAM2046	LOC93259 5'	TCCATGCTGGCAGCTTTTTG 72294	A TT
		CAAGAGGTTG TAGT ATGGA	
		GTTTTTCGAC GTCG TACCT	
		G _	
GAM2046	LOC93613 5'	TCTGTGAACCTGGGGCTCTTGG 73084	G GATA
		TCAAGAG TT GTTTATGGA	
		GGTTCTC GG CAAGTGTCT	
		G GTC_	
GAM2047	CCND2 3'	TCCCCAGCAAATCATCGGGCCA 10056	CCACA _ A
		TGGCCTGATGAT GC GG GA	
		ACCGGGCTACTA CG CC CT	
		AA__ A C	
GAM2047	GCN5L2 5'	CTCCGCTGCGGGGAGGCC 60529	GATGA A
		GGCCT TCC CAGCGGAG	
		CCGGA GGG GTCGCCTC	
		GG__ C	
GAM2047	GJA5 3'	CTGACCAGATCATCAGCCA 19164 C	CACAG
		TGGC TGATGATC CGG	
		ACCG ACTACTAG GTC	
		_ ACCA_	
GAM2047	HIVEP3 3'	TCCCCGCTGTGGTTGGCAGCCA 44702	C ATGAT A
		TGGC TG CCACAGCGG GA	
		ACCG AC GGTGTCGCC CT	
		_ GGTT_ C	
GAM2047	HOXD1 5'	CCGCCGGTATATTAGGCCA 44696	AT ACA
		TGGCCTGATG CC GCGG	
		ACCGGATTAT GG CGCC	
		AT C__	
GAM2047	SUFU 3'	CCTTGTGACCCATCAGGCCA 32934	ATC C
		TGGCCTGATG CACAG GG	

		ACCGGACTAC GTGTT CC		
		CCA _		
GAM2047	DKFZP586J1624 3'	CTCCGCCCAGTCACCATCAGGC 32043		ATCCACA_
	CA	TGGCCTGATG GCGGAG		
		ACCGGACTAC CGCCTC		
		CACTGACC		
GAM2047	KIAA1671 3'	CTTTGCTTATGAATCATCAGAC 66282	C	C C_
	C	GG CTGATGAT CA AGCGGAG		
		CC GACTACTA GT TCGTTTC		
		A A AT		
GAM2047	LOC159110 5'	TCTCCGCTGCCCCGGTCAACCA 82995	CCTGA	CA__
		TGG TGATC CAGCGGAGA		
		ACC ACTGG GTCGCCTCT		
		A__ CCCC		
GAM2047	LOC159116 5'	TCTCCGCTGCCCCGGTCAACCA 82978	CCTGA	CA__
		TGG TGATC CAGCGGAGA		
		ACC ACTGG GTCGCCTCT		
		A__ CCCC		
GAM2047	LOC165476 5'	CTCCGCTGCCTGCTCAGCCA 88550	C	TGATCCA
		TGGC TGA CAGCGGAG		
		ACCG ACT GTCGCCTC		
		_ CGTCC__		
GAM2047	LOC200032 5'	CTGACCAGATCATCAGCCA 85475	C	CACAG
		TGGC TGATGATC CGG		
		ACCG ACTACTAG GTC		
		_ ACCA_		
GAM2047	LOC219654 5'	CTCCGCTGCGGAGGGGGGCC 92932	GATGA	A
		GGCCT TCC CAGCGGAG		
		CCGGG AGG GTCGCCTC		
		GGG_ C		
GAM2047	LOC255862 3'	TCAAATGTAGACTATCAGGCCA 96115	A C	GCG
		TGGCCTGATG TC ACA GA		
		ACCGGACTAT AG TGT CT		
		C A AAA		
GAM2048	BAPX1 3'	ACCCTGGCAGTCCCAGGCAGCA 8643	C	_ ACT
		TGCTGCC TGGGAC CCA GGT		
		ACGACGG ACCCTG GGT CCA		
		_ AC C__		
GAM2048	BDKRB2 3'	ACCATCGGCAGTGCCAGGGCAG 7108	G	_ AAC
	CA	TGCTGCCCTGG AC CC TGGT		

ACGACGGGACC TG GG ACCA
 G AC CT_
 GAM2048 MUS81 5' ACCAACCCTTAGAGCAGCG 47818 C ACCCAAC
 TGCTGC CTGGG TGGT
 ||||| ||||| ||||
 GCGACG GATTC ACCA
 A ACCA____
 GAM2048 PIK3C2B 3' ACCGAAGCCACAGGGCAGCAT 12085 _ ACCCAAC
 ATGCTGCCCTG GG TGGT
 ||||| || ||||
 TACGACGGGAC CC GCCA
 A GAA____
 GAM2048 UBE2I 3' CCACTGGTTCAGACCCCAGGGC 13959 AC_____ AACT
 AGCAT ATGCTGCCCTGGG CC GG
 ||||| || ||
 TACGACGGGACCC GG CC
 CAGACT__T TCAA
 GAM2048 C5orf6 3' CAACTGGTAAAGCCCCAGGGCA 33948 C G_____ CAACT
 CCAT ATG TGCCCTGG ACC G
 ||| ||||| ||| |
 TAC ACGGGACC TGG C
 C CCGAAA__ TCAAC
 GAM2048 FLJ10619 3' ACCAGTTGGAATGGAGCA 36861 G CTGGGAC
 TGCT CC CCAACTGGT
 ||| || |||||
 ACGA GG GGTGACCA
 _ TAA____
 GAM2048 FLJ14708 3' ACCAGGGACTTGCCCCAGGGCA 52603 ACCCAA_
 GC GCTGCCCTGGG CTGGT
 ||||| ||||
 CGACGGGACCC GACCA
 CGTTCAGG
 GAM2048 FLJ20154 5' ACCAGTTGACCGAGCAGC 73300 CC GACC
 GCTGC TGG CAACTGGT
 |||| ||| |||||
 CGACG GCC GTTGACCA
 A_ A____
 GAM2048 FLJ22471 3' ACCAACCTTTCCAGGGCGGCA 47857 CCCAAC
 TGCTGCCCTGGGA TGGT
 ||||| ||||
 ACGGCGGGACCCT ACCA
 TTCCA_
 GAM2048 FLJ32861 3' CAACTGGTACCATCCAGGGCAA 59380 C G_____ CAACT
 CAT ATG TGCCCTGG ACC G
 ||| ||||| ||| |
 TAC ACGGGACC TGG C
 A TACCA__ TCAAC
 GAM2048 KIAA1068 3' ACCAGCCACTGCAGGCAGCAT 31683 C GGACCCAA
 ATGCTG CCTG CTGGT
 ||||| |||| ||||

			TACGAC GGAC	GACCA		
			_ GTCACC_			
GAM2048	OBSCN	3'	CGGAGGAGTCCCAGGACACA	71186	C C	_ AA
			TG TG CCTGGGAC CC CTG			
			AC AC GGACCCTG GG GGC			
			_ A A A_			
GAM2048	STOML1	3'	AGCTGGGGCCCAGGGCAGCAT	17862	A A	
			ATGCTGCCCTGGG CCCA CT			
			TACGACGGGACCC GGGT GA			
			G C			
GAM2048	LOC144319	3'	GTTTGGCCCCAGGGCAGCAT	83990	A C	
			ATGCTGCCCTGGG CC AAC			
			TACGACGGGACCC GG TTG			
			C T			
GAM2048	LOC196746	3'	CCACTGGTACTGACCCCGGGGC	88897	AC_____	AACT
			AGCA TGCTGCCCTGGG CC GG			
			ACGACGGGGCCC GG CC			
			CAGTCA__T TCAA			
GAM2048	LOC255193	5'	CCACTGGTCCGAACACCAGGGC	97101	GAC_____	AACT
			AGCA TGCTGCCCTGG CC GG			
			ACGACGGGACC GG CC			
			ACAAGCC__T TCAA			
GAM2048	LOC255631	5'	ACCAGTCAACTTGGGGCAGC	97965	TG ACCCA	
			GCTGCCC GG ACTGGT			
			CGACGGG TC TGACCA			
			GT AAC_			
GAM2048	LOC257081	3'	TGGGCTCCCAAGGCAGCAT	98595	C _	
			ATGCTGCC TGGGA CCCA			
			TACGACGG ACCCT GGGT			
			A C			
GAM2049	GPD1	3'	TCATGCCACCACATTTG	60398	C C	
			TAAATG GGTGGCAT GA			
			GTTTAC CCACCGTA CT			
			A _			
GAM2049	IL5RA	5'	TCGCATGGCCACCGCATTT	6906	AT__	
			AAATGCGGTGGC CGA			
			TTTACGCCACCG GCT			
			GTAC			
GAM2049	MYO1C	3'	TGCCGATGCCAAATATTTG	61873	CGG A	
			TAAATG TGGCATCG CA			

			GTTTAT ACCGTAGC GT		
			AA_ C		
GAM2049	C6orf37	3'	TGTCACACTGCATTTA 68097	GCATC	
			TAAATGCGGTG GACA		
			ATTTACGTCAC CTGT		
			A____		
GAM2049	DNAJC6	3'	TTGCAGAACCACCGCATT 29498	CA GA	
			AATGCGGTGG TC CAA		
			TTACGCCACC AG GTT		
			A_ AC		
GAM2049	FLJ11210	3'	GTCGATGTGCATGCTTTTA 60319	T GTG	
			TAAA GCG GCATCGAC		
			ATTT CGT TGTAGCTG		
			T ACG		
GAM2049	FLJ12476	3'	TCGATCTTCTGCATTTA 43270	T C	
			TAAATGCGG GG ATCGA		
			ATTTACGTC TC TAGCT		
			T _		
GAM2049	KIAA1034	3'	TCGATGGCATCCGCATTTG 63134	_ G	
			TAAATGCGG TG CATCGA		
			GTTTACGCC AC GTAGCT		
			T G		
GAM2049	KIAA1987	3'	TCATGTAAGTGCATTTA 89391	G C	
			TAAATGCGGT GCAT GA		
			ATTTACGTCA TGTA CT		
			A _		
GAM2049	MGC16063	3'	TGTCCTGGCCACTGCATT 54929	ATC	
			AATGCGGTGGC GACA		
			TTACGTCACCG CTGT		
			GTC		
GAM2049	LOC147949	3'	TGTCAGATGTCCACATTGCA 79279	— — —	
			TGCG GTGG CATC GACA		
			ACGT CACC GTAG CTGT		
			TA T A		
GAM2049	LOC150577	3'	GTCCTCACCGCATTTG 86258	CATC	
			TAAATGCGGTGG GAC		
			GTTTACGCCACT CTG		
			C____		
GAM2049	LOC158219	3'	TGTGTGTCACCACATTT 82694	C CG	
			AAATG GGTGGCAT ACA		

		TTTAC CCACTGTG TGT	
		A ____	
GAM2049	LOC202020 3'	TGTCTCACCACATTTA 90605	C CATC
		TAAATG GGTGG GACA	
		ATTTAC CCACT CTGT	
		A ____	
GAM2049	LOC90826 5'	TGTCGATGCAGGTTTATTTG 64788	CGGTG
		TAAATG GCATCGACA	
		GTTTAT CGTAGCTGT	
		TTGGA	
GAM2049	LOC93587 3'	TTGTCTTTACCTGCATTTA 73042	_ CATC
		TAAATGC GGTGG GACAA	
		ATTTACG CCATT CTGTT	
		T T__	
GAM2050	AKAP2 3'	CACAGGGATAAGAACAGAGG 24225	CGACCTT _
		CCTCTGTTC TCCC GTG	
		GGAGACAAG AGGG CAC	
		AAT__ A	
GAM2050	FGF1 3'	CACAGTTTAGAACAGAGG 53637	CG C TTCCC
		CCTCTGTTC A CT GTG	
		GGAGACAAG T GA CAC	
		AT T ____	
GAM2050	FGF1 3'	CACAGTTTAGAACAGAGG 53638	CG C TTCCC
		CCTCTGTTC A CT GTG	
		GGAGACAAG T GA CAC	
		AT T ____	
GAM2050	LNK 3'	GCACAGGAAAGGTACCCAGTAG 19647	_ TTCCG C
		CT CTG ACCTTTCC GTGC	
		GA GAC TGGAAAGG CACG	
		T CCA__ A	
GAM2050	ORM1 3'	CACAGCCTTGGATCAGGACAGA 7025	C _ TTTCCC
	G	CTCTGTTC GA CC GTG	
		GAGACAGG CT GG CAC	
		A A TTCCGA	
GAM2050	PRKCH 3'	GCACGAGAACCCAAAGGAATAG 21815	GACCT_ C
	AG	CTCTGTTCC TTC CGTGC	
		GAGATAAGG AAG GCACG	
		AAACCC A	
GAM2050	SAS 3'	GCACAATGGCAAAGCCAAACAG 21102	CCGAC _ C__
	AGG	CCTCTGTT CTTT CC GTGC	

			GGAGACAA	GAAA GG	CACG	
			ACC__	C TAA		
GAM2050	SDC2	5'	GCACGGGAAAAGGAGTCCGCGGA	67717	TCCGA	
	GG		CCTCTGT	CCTTTCCCGTGC		
			GGAGGCG	GGAAAGGGCACG		
			CCTGA			
GAM2050	STS	5'	CAGAAACCATGAACAGAGG	6240	CGACC	CCG
			CCTCTGTTC	TTTC TG		
			GGAGACAAG	AAAG AC		
			TACC_	__		
GAM2050	DKFZP566F2124	3'	CACAGAAAAAATGGAATAG	32215	ACC	CC
			CTGTTCCG	TTTC GTG		
			GATAAGGT	AAAG CAC		
			AAA	A_		
GAM2050	FLJ10415	3'	CACGGAAAAGGGAGCAGA	36585	GAC	C
			TCTGTTCC	CTTT CCGTG		
			AGACGAGG	GAAA GGCAC		
			__	A		
GAM2050	FLJ10648	3'	CACGGGAAGGAAGCAAAGG	36889	C	CCGAC
			CCT TGTT	CTTTCCCGTG		
			GGA ACGA	GGAAGGGCAC		
			A	A__		
GAM2050	FLJ11710	3'	CACAGGAGGGGCACAGAGG	46241	TCCGA	C
			CCTCTGT	CCTTTCC GTG		
			GGAGACA	GGGGAGG CAC		
			C__	A		
GAM2050	LOC143914	5'	GCACAGGCCCTCAGAATAGAGG	77110	C	CCTTT C
			CCTCTGTTC	GA CC GTGC		
			GGAGATAAG	CT GG CACG		
			A CCC_	A		
GAM2050	LOC219917	3'	CACGGAAGTCGCAGAACAG	93164	_	CTTTC
			CTGTTC	CGAC CCGTG		
			GACAAG	GCTG GGCAC		
			AC	AA__		
GAM2050	LOC222031	3'	CACAGAAAAGGCTGGGAAACGG	95671	TCTG	A CCC
			CC	TTCCG CCTTT GTG		
			GG	AGGGT GGAAA CAC		
			CAA_	C AGA		
GAM2050	LOC90957	3'	TGAGAGAAGTCAGAACAGAG	65091	C	C C
			CTCTGTTC	GAC TTTC CG		

			GAGACAAG CTG AGAG GT		
			A A A		
GAM2050	LOC93017	3'	CAATGAAAATGGAACAGAG 71702	ACC	CCG
			CTCTGTTCCG TTTC TG		
			GAGACAAGGT AAAG AC		
			A__ TA_		
GAM2051	AKAP1	3'	ACTATGGGTTCTCTTCGCAAA 14472	A CTT	C
			TTTGT GA GGAACCCA AGT		
			AAACG CT TCTTGGGT TCA		
			_ TC_ A		
GAM2051	AKAP1	3'	ACTATGGGTTCTCTTCGCAAA 58373	A CTT	C
			TTTGT GA GGAACCCA AGT		
			AAACG CT TCTTGGGT TCA		
			_ TC_ A		
GAM2051	EGF	3'	ACTATAGGTTTTGGTTCCACAA 10488	A C TG	CAC
			TTGT GA T GAACC AGT		
			AACA CT G TTTGG TCA		
			C T GT ATA		
GAM2051	EZH1	3'	GACTGTGGGTTCCAAATTAC 10551	AC	
			GTAG TTGGAACCCACAGTC		
			CATT AACCTTGGGTGTCAG		
			A_		
GAM2051	STAC	3'	GACTGTGGAGTAATAGCCACAA 13427	AGA TGGA _	
	A		TTTGT CT AC CCACAGTC		
			AAACA GA TG GGTGTCAG		
			CC_ TAA_ A		
GAM2051	CCR1	3'	GACTGTGGGCTCCATTC 8927	CT A	
			GA TGGA CCCACAGTC		
			CT ACCT GGGTGTGTCAG		
			T_ C		
GAM2051	FLJ10483	3'	GACTGTGGAAGAGATTACAAA 36652	A GGAAC	
			TTTGTAG CTT CCACAGTC		
			AAACATT GAG GGTGTCAG		
			A AA__		
GAM2051	KIAA1871	3'	ACTGTAAGAGTCTACAAA 61890	GGAACCC	
			TTTGTAGACTT ACAGT		
			AAACATCTGAG TGTCA		
			AA_____		
GAM2051	LOC150821	3'	GGGTTCCACATCCACAAA 60944	A CT	
			TTTGT GA TGGAACCC		

		AAACA CT ACCTTGGG	
		C AC	
GAM2051	LOC151057 3'	ACTGTGGGTACACCTATAAA 86379	ACT GA
		TTTGTAG TG ACCCACAGT	
		AAATATC AC TGGGTGTCA	
		C__ A_	
GAM2051	LOC157507 5'	ACTGTAAAAGTCTGCAAA 82377	GGAACCC
		TTTGTAGACTT ACAGT	
		AAACGTCTGAA TGTC A	
		AA_____	
GAM2051	LOC203339 5'	GGATTCCCAGTCTACAAA 92214	T C
		TTTGTAGACT GGAA CC	
		AAACATCTGA CCTT GG	
		C A	
GAM2051	LOC51030 3'	ACTGTAAATTAACCAATCTAC 32695	C AACCC__
	AAA	TTTGTAGA TTGG ACAGT	
		AAACATCT AACC TGTC A	
		_ AAATTAAA	
GAM2051	LOC90906 3'	GACTGTGGATCCCAAAC TTTGC 64951	C_ AAC
	A	TGTAGA TTGG CCACAGTC	
		ACGTTT AACC GGTGTCAG	
		CA CTA	
GAM2052	ACT 5'	GATCTTCAGATGGTGCTGGTG 40421	_ GGCAA
		CACTA CACCATT GGAGATC	
		GTGGT GTGGTAG CTTCTAG	
		C A_____	
GAM2052	AGRN 3'	GATTTTCTTGCCTGAGTGT 79586	_ TT
		ACAC CA GGCAAGGAGATC	
		TGTG GT CCGTTCTTTAG	
		A _____	
GAM2052	EGR2 5'	GATTTTTTTTTCTTGGTGTGTG 6375	_ TG C__
	TGGTG	CACTACAC CAT G AAGGAGATC	
		GTGGTGTG GTG T TTTTTTTAG	
		T GT CTT	
GAM2052	FPRL2 5'	GATCTAAGCTGGTGGTGTGG 60602	TG AAGG
		CTACACCAT GC AGATC	
		GGTGTGGTG CG TCTAG	
		GT AA_____	
GAM2052	IL22RA2 3'	GGTTTCCTTGCTTCCCTGTA 54773	CCATT
		TACA GGCAAGGAGATC	

			ATGT	TCG	TCCTTTGG	
			CCCT_			
GAM2052	MAD2L1	3'	GGTTTTTTTGTCAACATTGTGA	11418	C	CCA
		TG	CA TACA	TTGGCAAGGAGATC		
			GT GTGT	AACTGTTTTTTTGG		
			A	TAC		
GAM2052	MYB	3'	GGTTTTTTTGTATTGTTG	60283	C	T
			CA CA	TGGCAAGGAGATC		
			GT GT	ATTGTTTTTTTGG		
			T	T		
GAM2052	PBX2	3'	TTGTTGGTGGTGGTGGTG	11984	_	TG
			CACTAC	ACCAT	GCAA	
			GTGGTG	TGGTG	TGTT	
			G	GT		
GAM2052	PODXL	3'	GTCTTTTTGTCTGCAGTG	19419	A	CCATT
			CACT CA	GGCAAGGAGAT		
			GTGA GT	CTGTTTTTCTG		
			C	_____		
GAM2052	SOX11	3'	GATTTTTTTGTCAGTTTTGGT	13319	_____	
			ACCA	TTGGCAAGGAGATC		
			TGGT	GACTGTTTTTTTAG		
			TTT			
GAM2052	SURF4	3'	GATTTTTTTGCTTTATGTGG	53709	CCATT	
			CTACA	GGCAAGGAGATC		
			GGTGT	TCGTTTTTTTAG		
			ATT_			
GAM2052	TMPRSS3	3'	GATTTCTTTGTAGCATTTGGTG	44027	TTG_	
			CACCA	GCAAGGAGATC		
			GTGGT	TGTTTCTTTAG		
			TTACGA			
GAM2052	TNFAIP1	3'	GATTTTCTTGTCAGTTTCTGAG	41230	ACACC	
			CT	ATTGGCAAGGAGATC		
			GA	TGACTGTTCTTTTAG		
			GTCTT			
GAM2052	TSN	3'	GTCTTTTTGTAAGTGAGTG	17304	_	G
			CAC CATT	GCAAGGAGAT		
			GTG GTGA	TGTTTTTCTG		
			A	A		
GAM2052	WVOX	3'	GGTCTCTTTGCTTTCTGGTGGT	33491	TA	TT_
		G	CAC	CACCA	GGCAAGGAGATC	

GTG GTGGT TCGTTTCTCTGG
 _ CTT
 GAM2052 ZNF157 3' GATTTCCCTAATTAGTGGTGTG 14333 T CAA_
 TG CAC ACACCATTGG GGAGATC
 ||| ||||| |||||
 GTG TGTGGTGATT CCTTTAG
 _ AATC
 GAM2052 B7-H1 3' GGTCTTCTTGTTCATGTGAGTGT 27097 _ _
 G TACAC CAT TGGCAAGGAGATC
 ||||| ||| |||||
 GTGTG GTG ACTGTTCTTCTGG
 A T
 GAM2052 C5orf3 3' GATTTTTTTGTTTGAGTGT 38593 _ TT
 ACAC CA GGCAAGGAGATC
 ||||| || |||||
 TGTG GT TTGTTTTTTTAG
 A _
 GAM2052 COVA1 3' GTCTTTATTGTGTGTGGTG 73643 CATTG _
 CACTACAC GCAA GGAGAT
 ||||| ||| |||||
 GTGGTGTG TGTT TTTCTG
 _ A
 GAM2052 DKFZP434P0111 3' CCTGCCAGGGGTGTGGTG 67956 A A
 CACTACACC TTGGCA GG
 ||||| ||||| ||
 GTGGTGTGG GACCGT CC
 G _
 GAM2052 ERG-1 5' GATTTTCTTGCCATCTATG 42099 CCAT
 CA TGGCAAGGAGATC
 || |||||
 GT ACCGTTCTTTTAG
 ATCT
 GAM2052 KIAA0016 3' GTTTTTTTGTGGTGCAAGTG 29311 A ATTG
 CACT CACC GCAAGGAGAT
 ||| ||| |||||
 GTGA GTGG TGTTTTTTTG
 C _
 GAM2052 KIAA0410 3' GGTTTGGACATTTAAGGTGTAG 29427 AT__ G_ GAGATC
 TG CACTACACC TG CAAG
 ||||| || |||
 GTGATGTGG AC GTTT
 AATT AG GG
 GAM2052 KIAA1239 3' GTCTTTTGTCAAAGTGT 71848 CA
 ACAC TTGGCAAGGAGAT
 ||| |||||
 TGTG AACTGTTTTTCTG
 A_
 GAM2052 MDS006 3' GTCTCATGAGTGTGTGGTG 39984 CATTGG AG
 CACTACAC CA GAGAT
 ||||| || ||||

			GTGGTGTG	GT CTCTG	
			TGA__ A_		
GAM2052	P125	5'	GGTTTCCGGTCAGTGGTGTGGT	24208	AA
			ACTACACCATTGGC	GGAGATC	
			TGGTGTGGTGA	CTTTGG	
			G_		
GAM2052	PARG1	3'	GGTTTTTTTGTGTTGTTGTG	17869	C TT
			TACA CA	GGCAAGGAGATC	
			GTGT GT	TTGTTTTTTTGG	
			T TG		
GAM2052	Rabip4R	3'	GGTCTCCTGTGCTTGGTGTGTG	36277	T TT _
			CAC ACACCA	GGCA AGGAGATC	
			GTG TGTGGT	TCGT TCCTCTGG	
			_ _	G	
GAM2052	SE70-2	3'	GGTTTAAATGATAATGGTGTA	42347	G AG
			TACACCATTG CA	GAGATC	
			ATGTGGTAAT GT	TTTTGG	
			A AA		
GAM2052	TRIM11	3'	GGTTTCCTTGTCTCAAGGT	73192	ATT_ _
			ACC GG	CAAGGAGATC	
			TGG CC	GTTTCCTTGG	
			AACT T		
GAM2052	UNC5D	3'	GATTTACAGACCAAGGTGTGGT	56005	A CAAGG
	G		CACTACACC TTGG	AGATC	
			GTGGTGTGG AACC	TTTAG	
			_	AGACA	
GAM2052	LOC140112	5'	GGTTTCCTTGTGTTGGTGGCTGTA	76371	_ TG
			TACA CCAT	GCAAGGAGATC	
			ATGT GGTG	TGTTTCCTTTGG	
			C GT		
GAM2052	LOC143154	3'	GATTTTCCTTGTTATTATTG	76990	CCAT
			CA	TGGCAAGGAGATC	
			GT	ATTGTTTCCTTTAG	
			TATT		
GAM2052	LOC145453	3'	CTTGCCAATGGTGGAGTG	77660	A
			CACT CACCATTGGCAAG		
			GTGA GTGGTAACCGTTC		
			G		
GAM2052	LOC145858	5'	GGTTTTTTTGCCACTGCCGTTG	78004	T AC T
	TG		CAC AC CA	TGGCAAGGAGATC	

GTG TG GT ACCGTTTTTTTGG
 T CC C
 GAM2052 LOC146713 3' TTTTGGGTGGTGTGTG 84743 T GG
 CAC ACACCATT CAAGG
 ||| ||||| ||||
 GTG TGTGGTGG GTTTT

— —
 GAM2052 LOC158088 3' GTTTTCTTGCTGCTGTAG 87977 C TTG
 CTACA CA GCAAGGAGAT
 |||| || |||||
 GATGT GT CGTTCTTTTG
 C —

GAM2052 LOC196485 3' GGTTTTCTTGCTCCTGTGG 89076 T__
 CCAT GGCAAGGAGATC
 ||| |||||
 GGTG TCGTTCTTTTGG
 TCC

GAM2052 LOC202986 3' GGTTTTCTTGCTCCTGTGG 92070 T__
 CCAT GGCAAGGAGATC
 ||| |||||
 GGTG TCGTTCTTTTGG
 TCC

GAM2052 LOC221400 3' GGTCTCAGGTTGATGGTGGGGT 93912 TA TG AAG
 G CAC CACCAT GC GAGATC
 ||| |||| || ||||
 GTG GTGGTA TG CTCTGG
 GG GT GA_

GAM2052 LOC57805 5' GATCTCTTTTGAGGTGATGGTG 41287 _ A TG CA
 CACTA CACC T G AGGAGATC
 |||| ||| | | |||||
 GTGGT GTGG A T TTCTCTAG
 A _GT_

GAM2052 LOC90362 3' GTCTCCTTGAAGTGTTGTG 63116 C GG
 TACA CATT CAAGGAGAT
 |||| ||| |||||
 GTGT GTGA GTTCCTCTG
 T A_

GAM2052 LOC90841 3' GATTAGAAACCAGTGTGTGGT 64869 C CAAGG
 G CACTACAC ATTGG AGATC
 ||||| |||| ||||
 GTGGTGTG TGACC TTTAG
 _ AAAGA

GAM2053 FGF13 3' ACCAAGAAAATGTAAAAGACC 54441 CAGG ____
 GGTCTT GC TTCTTGGT
 |||| || |||||
 CCAGAA TG AAGAACCA
 AA__ TAA

GAM2053 INSRR 3' ACCCGTGGCCCTGAAGACGGTG 68987 G TCTT
 CACCG TCTTCAGGGCT GGT
 |||| ||||| |||

GTGGC AGAAGTCCCGG CCA
 _ TGC_
 GAM2053 LOXL3 3' ACCAAGAAACCCATGTCAGC 51865 CTT _ C
 GT CA GGG TTCTTGGT
 || ||| |||||
 CG GT CCC AAGAACCA
 ACT A A
 GAM2053 RAP1GA1 3' ACCTCTGCCCTGAAGACC 12767 TTCTT
 GGTCTTCAGGGC GGT
 ||||| |||
 CCAGAAGTCCCG CCA
 TCT_
 GAM2053 XRCC5 5' ACCAAAGCGCCTGAGGACCGG 41239 _ CT
 CCGGTCTTCAGG GCTT TGGT
 ||||| ||| |||
 GGCCAGGAGTCC CGAA ACCA
 G _
 GAM2053 EDG1 5' CCACCCCTGAAGCCAGTG 60049 C T CTTCT
 CAC GG CTTCAAGG TGG
 ||| || ||||| |||
 GTG CC GAAGTCCC ACC
 A _ C_
 GAM2053 KIAA0323 3' CCAAGAAGGGAAACGGTG 63947 GTC AGGG
 CACCG TTC CTTCTTGG
 |||| ||| |||||
 GTGGC AGG GAAGAACC
 AA_ _
 GAM2053 MGC15875 5' ACCAGCGCCCGAAGGCCG 53011 A TTC
 CCGTCTTC GGGC TTGGT
 ||||| ||| |||||
 GCCGGAAG CCCG GACCA
 _ C_
 GAM2053 NYD-SP21 3' ACCAAGAAGTCCAAACC 51860 CTTCA
 GGT GGGCTTCTTGGT
 ||| |||||
 CCA CCTGAAGAACCA
 AA_
 GAM2053 TTC2 3' CCAATGCCGAAGACCG 13876 AG TTC
 CCGTCTTC GGC TTGG
 ||||| ||| |||
 GCCAGAAG CCG AACC
 _ T_
 GAM2053 LOC199786 3' ACCAAGTTGCGGAGACCGGT 89730 AGG TT
 ACCGGTCTTC GC CTTGGT
 ||||| || |||||
 TGGCCAGAGG CG GAACCA
 _ TT
 GAM2053 LOC200030 3' ACCAAGAAGAGGAAGAAGACC 80119 AGGG_
 GGTCTTC CTTCTTGGT
 ||||| |||||

	CCAGAAG GAAGAACCA AAGGA	
GAM2053 LOC200030 3'	ACCAAGAAGAGGAAGAAGACC 80120	AGGG_
	GGTCTTC CTTCTTGGT 	
	CCAGAAG GAAGAACCA AAGGA	
GAM2053 LOC200030 3'	ACCAAGAAGTGGGAAGAAGACC 80121	AGG_
	GGTCTTC GCTTCTTGGT 	
	CCAGAAG TGAAGAACCA AAGG	
GAM2053 LOC200030 3'	ACCAAGAAGTGGGAAGAAGACC 80122	AGG_
	GGTCTTC GCTTCTTGGT 	
	CCAGAAG TGAAGAACCA AAGG	
GAM2053 LOC200030 3'	ACCAAGAAGTGGGAAGAAGACC 80123	AGG_
	GGTCTTC GCTTCTTGGT 	
	CCAGAAG TGAAGAACCA AAGG	
GAM2053 LOC204285 3'	ACCAAGAAGCTTCCAAACGAC 91009	TTCA__
	GTC GGGCTTCTTGGT 	
	CAG TTCGAAGAACCA CAAACC	
GAM2053 LOC51629 3'	ACCAAGAAGCCCTCAGCCTGGT 32604	T TC
G	CACCGG CT AGGGCTTCTTGGT 	
	GTGGTC GA TCCCGAAGAACCA C C_	
GAM2054 TEGT 5'	ACTGCTGCACGGACTCTGGA 65225	A C A
	TTCA AG CC TGCAGTAGT 	
	AGGT TC GG ACGTCGTCA C A C	
GAM2054 C21orf41 3'	ACAACTACGTGAGCTTGAAG 57169	A C GCA
	CTTC AAGC CAT GTAGTTGT 	
	GAAG TTCG GTG CATCAACA G A _	
GAM2054 DKFZP434I092 3'	ACAACTACTATCTAGGTTTGAA 68409	G CATGC
G	CTTCAAA CC AGTAGTTGT 	
	GAAGTTT GG TCATCAACA _ ATCTA	
GAM2054 DKFZp434O0515 3'	ACAACTGATAATAAGCTTTGAA 66507	CC GCAG
	TTCAAAGC AT TAGTTGT 	

AAGTTTCG TA GTCAACA
 AA ATA_
 GAM2054 FLJ13187 3' CAACTACAGTCTTTGAA 45161 CCCAT A
 TTCAAAG GC GTAGTTG
 ||||| || |||||
 AAGTTTC TG CATCAAC
 _____ A
 GAM2054 GMPPB 3' AGCTTCCTGTATGGGCCTCGAA 97433 AAA T_
 TTC GCCCATGCAG AGTT
 ||| ||||| |||||
 AAG CGGGTATGTC TCGA
 CTC CT
 GAM2054 KIAA0431 3' ACAACTGTCTTTAGCTTTGAAG 31544 CCA C _
 CTTCAAAGC TG AG TAGTTGT
 ||||| || |||||
 GAAGTTTCG AT TC GTCAACA
 _____ T T
 GAM2054 KIAA0461 3' CAGACAATGGACTTTGAAG 71392 C GCAGTAG
 CTTCAAAG CCAT TTG
 ||||| ||| |||
 GAAGTTTC GGTA GAC
 A ACA____
 GAM2054 LOC150157 5' ACAACTGCACCAGGCCCTGA 86016 AA CA CA
 TCA GCC TG GTAGTTGT
 ||| ||| || |||||
 AGT CGG AC CGTCAACA
 CC _ CA
 GAM2054 LOC196890 5' ACAACTGCACCAGGCCCTGA 91219 AA CA CA
 TCA GCC TG GTAGTTGT
 ||| ||| || |||||
 AGT CGG AC CGTCAACA
 CC _ CA
 GAM2054 LOC200058 3' ACAGTGGCATGGAGCTTTGAA 89955 _ AGTAG
 TTCAAAGC CCATGC TTGT
 ||||| ||||| |||||
 AAGTTTCG GGTACG GACA
 A GT____
 GAM2055 FMR2 3' TGGCAGGAGACTAATCAGA 10701 CCAC
 TCTGA TCTCCTGTCA
 ||||| |||||
 AGACT AGAGGACGGT
 AATC
 GAM2055 HSD17B1 5' GAGGACAGGAGAAGGTCAGA 6428 AC A
 TCTGACC TCTCCTGTC TC
 ||||| ||||| |||
 AGACTGG AGAGGACAG AG
 A_ G
 GAM2055 ITGA9 3' TGAAC TTTGGAGAGTGACAGA 11036 AC TG____
 TCTG CACTCTCC TCA
 ||||| ||||| |||

		AGAC GTGAGAGG AGT		
		A_ TTTCA		
GAM2055	RAD54B	3' GAGTATGGAGAGATGGTCAGA 25767	_	TGTCA
		TCTGACCA CTCTCC TC		
		AGACTGGT GAGAGG AG		
		A TATG_		
GAM2055	FLJ14775	3' CTGTGTAACAGGAGACAATCA 52679	CCAC	C TC
	GA	TCTGA TCTCCTGT A CAG		
		AGACT AGAGGACA T GTC		
		AACA A GT		
GAM2055	FLJ20420	3' TGGGTGGAGAGAGCCAGA 35612	ACCA	CTG
		TCTG CTCTC TCATCCA		
		AGAC GAGAG GGTGGGT		
		C_ A_		
GAM2055	FLJ31153	3' TGGAGAAGAGTGGTAAGA 58756	G	CCTG A
		TCT ACCACTCT TC TCCA		
		AGA TGGTGAGA AG AGGT		
		A _ _		
GAM2055	KIAA0247	3' GATGCAGGAGAATGGCCAG 29070	A C	T
		CTG CCA TCTCCTG CATC		
		GAC GGT AGAGGAC GTAG		
		C A _		
GAM2055	PGLYRP	5' CTGGACTTTGACAGTGGTCA 54669	CTCCT	_
		TGACCACT GTCA TCCAG		
		ACTGGTGA CAGT AGGTC		
		_ TTC		
GAM2055	LOC125488	5' TGAGCAAGGAGAGTGTCA 74874	C	_ _
		TGAC ACTCTCCT G TCA		
		ACTG TGAGAGGA C AGT		
		_ A G		
GAM2055	LOC127841	5' ATGGCAGGAGACAGTCAGA 75184	CAC	
		TCTGAC TCTCCTGTCAT		
		AGACTG AGAGGACGGTA		
		AC_		
GAM2055	LOC143310	3' GGCAGGAGAATGGCGAGA 77049	GA C	
		TCT CCA TCTCCTGTC		
		AGA GGT AGAGGACGG		
		GC A		
GAM2055	LOC151318	3' CTGGATGACAAATCGTCAGA 81029	CACTCTCC	
		TCTGAC TGTCATCCAG		

		AGACTG	ACAGTAGGTC		
		CTAA_____			
GAM2055	LOC158191	5'	CTGAATGAGGTCAGTGGTCG	82671	CT TG C
			TGACCACT CC TCAT CAG		
			GCTGGTGA GG AGTA GTC		
			CT _ A		
GAM2055	LOC221337	3'	TAGGCAGAAAGTGGTCAGA	93737	_ _
			TCTGACCACT CT CCTG		
			AGACTGGTGA GA GGAT		
			A C		
GAM2055	LOC253258	3'	CTGGAGTTTGGAGAGTGAGCAG	98229	AC TGTC A
			TCTG CACTCTCC TCCAG		
			AGAC GTGAGAGG AGGTC		
			GA TTTG_		
GAM2056	BRCA1	3'	GTTTGCCAGAAAACACCA	24573	AA GC
			TGG TTTTCTGG CGAAT		
			ACC AAAAGACC GTTTG		
			AC _		
GAM2056	EYA4	3'	TATTTGGAATAAAAATTCCA	15886	C GG
			TGGAATTTT TG CCGAATA		
			ACCTTAAAA AT GGTTTAT		
			_ AA		
GAM2056	MECP2	3'	ATTTGGCAGAAAATTACA	18385	G GG
			TG AATTTTCT GCCGAAT		
			AC TTAAAAGA CGGTTTA		
			A _		
GAM2056	ZFHX1B	3'	TTCGACTGAAAATTCCA	29608	T GC
			TGGAATTTTC GG CGAA		
			ACCTTAAAAG TC GCTT		
			_ A_		
GAM2056	CG012	3'	TGGCTACCCAGAAAATTTC A	84171	_____
			TGGAATTTTCTGG GCCG		
			ACTTTAAAAGACC CGGT		
			CAT		
GAM2056	HBXAP	3'	ATTTTTCCTAGAAAATTCCA	33880	A CC
			TGGA TTTTCTGGG GAAT		
			ACCT AAAAGATCC TTTA		
			C TT		
GAM2056	KIAA0997	3'	TCAACCCAAAAAGTTCCA	30889	C CC
			TGGAATTTT TGGG GA		

		ACCTTGAAA ACCC CT		
		A AA		
GAM2056 KIAA1014	3'	GTATTCTCCATAAAATTCCA 65961	C	CC
		TGGAATTTT TGGG GAATAC		
		ACCTTAAAA ACCT CTTATG		
		T _		
GAM2056 MAGEH1	3'	GTATTCGTTTAAAATTCC 26771	CT	C
		GGAATTTT GGGC GAATAC		
		CCTTAAAA TTTG CTTATG		
		T _ _		
GAM2056 PSK	5'	TATTCGGGGTTCAGACCCCA 32882	AATTT	_
		TGG TCTGGGCC GAATA		
		ACC AGACTTGG CTTAT		
		CC_ GG		
GAM2056 SDF1	3'	TATTCCTAGAACTTCCA 92520	T	CC
		TGGAA TTTCTGGG GAATA		
		ACCTT AAAGATCC CTTAT		
		C _		
GAM2056 TAO1	5'	TATTCGGGGTTCAGACCCCA 17720	AATTT	_
		TGG TCTGGGCC GAATA		
		ACC AGACTTGG CTTAT		
		CC_ GG		
GAM2056 VMP	3'	GTACCCGGCCACCAGAAAACCC 55765	AA	_ AA
C		GG TTTTCTGG GCCG TAC		
		CC AAAAGACC CGGC ATG		
		CC AC CC		
GAM2056 LOC126295	3'	GTATAATGCTCCAGAAAATTC 74975	_	CGA
		GAATTTTCTGG GC ATAC		
		CTTAAAAGACC CG TATG		
		T TAA		
GAM2056 LOC146184	5'	ATTCAACCAGAAAATTTCA 84596	GCC	
		TGGAATTTTCTGG GAAT		
		ACTTTAAAAGACC CTTA		
		AA_		
GAM2056 LOC150407	3'	GTATTCCAAGAAAATTTCA 80643	GGGCC	
		TGGAATTTTCT GAATAC		
		ACTTTAAAAGA CTTATG		
		AC_		
GAM2056 LOC154089	3'	TTGACTGAAAATTCCA 81948	T	GC
		TGGAATTTTC GG CGA		

ACCTTAAAAG TC GTT
 _ A_
 GAM2056 LOC221479 3' GTATGTACAGAAAATTC 93846 GG CGA
 GAATTTTCTG C ATAC
 ||||| | |||
 CTTAAAAGAC G TATG
 AT ____
 GAM2056 LOC91496 5' TTTGGCAGAAAATGCCA 66813 A GG
 TGG ATTTTCT GCCGAA
 || ||||| |||||
 ACC TAAAAGA CGGTTT
 G ____
 GAM2057 KIAA1706 3' AAGAACCCTCCTGTCCCCACGC 94363 T_ CC A C
 AG TTGCGTGG GC GA GGG TCTT
 ||||| || || |||||
 GACGCACC TG CT CCC AGAA
 CC TC _ A
 GAM2057 LOC149576 5' GGCCCAGGCACCACCCAA 80224 C CGAA
 TTG GTGGTGCC GGGCT
 || ||||| |||||
 AAC CACCACGG CCCGG
 C A____
 GAM2057 LOC200197 3' AAGAGCCCTCCGAGCCTCG 90010 T GC A
 CG GGT CCG AGGGCTCTT
 || ||| || |||||
 GC CCG GGC TCCCGAGAA
 T A_ C
 GAM2057 LOC255990 5' AGAGCCTGTGCCACACAA 97970 C T CCGAA
 TTG GTGG GC GGGCTCT
 || ||| || |||||
 AAC CACC CG TCCGAGA
 A _ TG____
 GAM2057 LOC256402 3' CCTTCAGGCACCACACAG 97543 C C
 TTG GTGGTGCC GAAGG
 || ||||| |||||
 GAC CACCACGG CTTCC
 A A
 GAM2058 AGTR1 5' GCGCGCCGCTAGCAGCTCTGC 7301 AAACCA G
 GCA GC TGGCGGCGCGC
 || || |||||
 CGT CG ATCGCCGCGCG
 CTCGA_ _
 GAM2058 AGTR1 5' GCGCGCCGCTAGCAGCTCTGC 24794 AAACCA G
 GCA GC TGGCGGCGCGC
 || || |||||
 CGT CG ATCGCCGCGCG
 CTCGA_ _
 GAM2058 AGTR1 5' GCGCGCCGCTAGCAGCTCTGC 49822 AAACCA G
 GCA GC TGGCGGCGCGC
 || || |||||

			CGT	CG	ATCGCCGCGCG		
			CTCGA_ _				
GAM2058	AGTR1	5'	GCGCGCCGCTAGCAGCTCTGC	17899	AAACCA	G	
			GCA	GC	TGGCGGCGCGC		
			CGT	CG	ATCGCCGCGCG		
			CTCGA_ _				
GAM2058	DNAH9	5'	GTCTGCCATGGTTTTACA	17411	C	GCG	C
			TG	AAAACCA	TGGCGG	GC	
			AC	TTTTGGT	ACCGTC	TG	
			A	_____	_____		
GAM2058	FBXL5	5'	GCGCGCCGCCTCTGCCCCGC	25136	AAAAC	CGT	
			GC	CAG	GGCGGCGCGC		
			CG	GTC	CCGCCGCGCG		
			CCCC_	T_			
GAM2058	FBXL5	5'	GCGCGCCGCCTCTGCCCCGC	54318	AAAAC	CGT	
			GC	CAG	GGCGGCGCGC		
			CG	GTC	CCGCCGCGCG		
			CCCC_	T_			
GAM2058	MAF	5'	CGCGCCGCCCTGCCTGCA	19309	AAACCA	T	
			TGCA	GCG	GGCGGCGCG		
			ACGT	CGT	CCGCCGCGC		
			C_____	C			
GAM2058	RAB26	5'	CGCGCCGCCCAACGGGCCTTGC	27601	AA	AGCGT	
	A		TGCAA	CC	GGCGGCGCG		
			ACGTT	GG	CCGCCGCGC		
			CC	GCAAC			
GAM2058	RPS18	5'	CGCCGCCGCTTGTGCTGCA	42881	AA	C	GT
			TGCA	AC	AGC	GGCGGCG	
			ACGT	TG	TCG	CCGCCG	
			CG	T	_____		
GAM2058	ABIN-2	5'	GCGCAGCTGCCGCGCTCTGCA	44460	AAACC		_____
			TGCA	AGCGTGGCGGC	GCGC		
			ACGT	TCGCGCCGTCG	CGCG		
			C_____	A			
GAM2058	ADAMTS18	5'	GCGCGCCGCCCGTGCGCT	58169	_____		
			AGCGT	GGCGGCGCGC			
			TCGCG	CCGCCGCGCG			
			TGC				
GAM2058	HBOA	3'	CTGCAGACGCTGGTTCTG	23930	A	G_	
			CA	AACCAGCGT	GCGG		

		GT TTGGTCGCA CGTC		
		C GA		
GAM2058	KIAA0649	5' GCGGAGCGCGCTGGCCCTGCA	29713	AAA G GG
		TGCA CCAGCGTG C CGC		
		ACGT GGTCGCGC G GCG		
		CCC _AG		
GAM2058	SPRY4	3' GCTGTGGCCACGCTGGTT	49019	G _
		AACCAGCGTGGC GC GC		
		TTGGTCGCACCG TG CG		
		G T		
GAM2058	URKL1	5' GCGCGCCGCCCGGCCAGGCCCG	35794	AAAA A_ GT
	CA	TGC CC GC GGCGGCGCGC		
		ACG GG CG CCGCCGCGCG		
		CCC_ AC GC		
GAM2058	LOC145813	5' GCCCAGCTGGTCTTG	84509	A CG
		CAA ACCAGCGTGG GC		
		GTT TGGTCGCACC CG		
		C _		
GAM2058	LOC148697	3' GCCACGCTGTGTCTTGCA	79677	A _
		TGCAA AC CAGCGTGGC		
		ACGTT TG GTCGCACCG		
		C T		
GAM2058	LOC205095	3' CGCCACCACTGGCTTCTGC	92383	A _ G G C
		GCA AA CCA C TGG GGCG		
		CGT TT GGT G ACC CCGC		
		C C _ _ A		
GAM2058	LOC221143	5' GCGCGCCGCCGAGGCGTTTTG	95215	CA G_
		CAAAAC GC TGGCGGCGCGC		
		GTTTTG CG GCCGCCGCGCG		
		_ GA		
GAM2058	LOC221296	3' GCGCGCCGCCACGCCCGG	93610	A_
		CC GCGTGGCGGCGCGC		
		GG CGCACCGCCGCGCG		
		CC		
GAM2058	LOC255391	5' GCGGGCACGCTGGTCTTGC	99457	A G GG
		GCAA ACCAGCGTG C CGC		
		CGTT TGGTCGCAC G GCG		
		C _ G_		
GAM2058	LOC255452	3' GCCGCCACGCGGGCTCCGCA	99395	AAAA A
		TGC CC GCGTGGCGGC		

		ACG GG CGCACCGCCG	
		CCTC G	
GAM2059	ALAD	5' CCCTAGGTTCCAACCAACTGA 5258	G C T ATGC
		TCAGT GG TGA GC AGGG	
		AGTCA CC ACCT TG TCCC	
		A A _ GA_	
GAM2059	CD22	3' CCCTGCCCCACCAGCCCACTGG 10101	A CAT
		TCAGTGGGCTGG TG GCAGGG	
		GGTCACCCGACC AC CGTCCC	
		_ CC_	
GAM2059	DNMT3L	5' CCCC AATCCCCCAGCCCCACTG 26284	_ ATGCA CA
	A	TCAGT GGGCTGG TG GGG	
		AGTCA CCCGACC AC CCC	
		C CCCTA _	
GAM2059	NDUFV3	5' CCAATAGCCCCAGCCCACTGA 41140	AT A CA
		TCAGTGGGCTGG GC TG GG	
		AGTCACCCGACC CG AT CC	
		C_ _ AA	
GAM2059	NKX3A	3' CCCTG GGGAGCCCACTG 21612	AT ATG_
	A	TCAGTGGGCTGG GC CAGGG	
		AGTCACCTGACC CG GTCCC	
		_ AGGG	
GAM2059	SPI1	5' CCCCACGACCGTCCAGCCCCTG 13352	T CA CA
	A	TCAG GGGCTGGATG TG GGG	
		AGTC CCCGACCTGC GC CCC	
		_ CA AC	
GAM2059	C20orf46	3' CCCACACGGGCAAGCAGCCAC 37734	GA A CA_
	TGA	TCAGTGGGCTG TGC TG GGG	
		AGTCACCCGAC ACG GC CCC	
		GA G ACA	
GAM2059	CAC-1	3' CCCCACCACCCAGCCCACTG 54295	A CA CA
		CAGTGGGCTGG TG TG GGG	
		GTCACCCGACC AC AC CCC	
		C C_ _	
GAM2059	CAMKK1	3' CCCTGCATGCACCCAGGGCCAC 51152	G_ A
		GTGG C TGG TGCATGCAGGG	
		CACC G ACC ACGTACGTCCC	
		G G C	
GAM2059	DKFZP434J037	5' CGCACAGCCTACTGA 48946	GATGCA A
		TCAGTGGGCTG TGC G	

	AGTCATCCGAC	ACG C	
	_____ C		
GAM2059 FLJ22795	3' CCCCATCTTCCAACCCACTGG	47632	C TGC CA
	TCAGTGGG TGGA ATG GGG		
	GGTCACCC ACCT TAC CCC		
	A TC_ _		
GAM2059 KIAA0552	5' CCCCATTTCCCCAGCCCAT	28989	ATGC CA
	GTGGGCTGG ATG GGG		
	TACCCGACC TAC CCC		
	CCTT _		
GAM2059 KIAA1884	3' CCGCAACATCCAGCCAC	73723	CA A
	GTGGGCTGGATG TGC GG		
	CACCCGACCTAC ACG CC		
	A_ _		
GAM2059 KR18	5' CCGGCTCCAGCCCACTGA	53890	ATGCAT A
	TCAGTGGGCTGG GC GG		
	AGTCACCCGACC CG CC		
	CT_ G		
GAM2059 PLAGL2	3' CCCC GCCCTCCAGCCAC	70956	TGCAT A
	GTGGGCTGGA GC GGG		
	CACCCGACCT CG CCC		
	CC_ C		
GAM2059 PP1628	3' CCCTGTTCCCAACCCCACTGA	48075	C_ ATGCAT
	TCAGTGGG TGG GCAGGG		
	AGTCACCC ACC TGTCCC		
	CA CCT_		
GAM2059 PTPN9	3' CCCTGCCTGCTCCCAGCCCACT	12596	AT T
	AGTGGGCTGG GCA GCAGGG		
	TCACCCGACC CGT CGTCCC		
	CT C		
GAM2059 LOC112476	3' CCCTGCACTTCTTCCAGCCC	59783	TGCA_
	GGGCTGGA TGCAGGG		
	CCCGACCT ACGTCCC		
	TCTTC		
GAM2059 LOC145717	3' CCCCATCTTCCAACCCACTGG	67371	C TGC CA
	TCAGTGGG TGGA ATG GGG		
	GGTCACCC ACCT TAC CCC		
	A TC_ _		
GAM2059 LOC151174	5' CCCACAGCTCAGCCCAT	86435	AT A CA
	GTGGGCTGG GC TG GG		

	TACCCGACT CG AC CC	
	— — AC	
GAM2059 LOC164714 5'	CCCCGTAGCCCAGCCCGC 88581	AT A A
	GTGGGCTGG GC TGC GGG	
	CGCCCGACC CG ATG CCC	
	— — C	
GAM2059 LOC220537 3'	CCCCATCTTCCAACCCACTGG 92421	C TGC CA
	TCAGTGGG TGGA ATG GGG	
	GGTCACCC ACCT TAC CCC	
	A TC_ —	
GAM2059 LOC253609 5'	CCCTGTCGGGCTCCAGCCAC 98564	T AT
	GTGGGCTGGA GC GCAGGG	
	CACCCGACCT CG TGTCCC	
	_ GC	
GAM2059 LOC57228 5'	CCCCAATTTTACAGCCCACTGA 40399	GATGCA CA
	TCAGTGGGCTG TG GGG	
	AGTCACCCGAC AC CCC	
	ATTTTA _	
GAM2059 LOC90249 5'	CCCCAAGTTCCAGCTCAC 62610	T A CA
	GTGGGCTGGA GC TG GGG	
	CACTCGACCT TG AC CCC	
	_ A _	
GAM2059 LOC90342 5'	CCCCAAGAGCATCCAGCCAC 63010	ATGCA
	GTGGGCTGGATGC GGG	
	CACCCGACCTACG CCC	
	AGAAC	
GAM2059 LOC90918 3'	CCACTGCACCCAGCCCACT 64999	ATGCA _
	AGTGGGCTGG TGCAG GG	
	TCACCCGACC ACGTC CC	
	C_ A	
GAM2060 CDH12 3'	CTTATCATTTAAAGTGGTGTA 15777	CCCAA GA
	TACACCACT GAA ATAAG	
	ATGTGGTGA TTT TATTC	
	AA_ AC	
GAM2060 GOCAP1 3'	ATTGTTCTTGGGAGCAGTGTA 43007	CA G
	TACAC CTCCCAAGAA AAT	
	ATGTG GAGGGTTCTT TTA	
	AC G	
GAM2060 DKFZp434N2435 5'	CTTATTACTGTGGGGTGGT 98090	T AGAAG
	ACCAC CCCA AATAAG	

		TGGTG GGGT TTATTC	
		_ GTCA_	
GAM2060	DKFZP564I122	3' CTTATTCTTCTCCCTCATGTGT 63877	CACTCCCA
	A	TACAC AGAAGAATAAG	
		ATGTG TCTTCTTATTC	
		TACTCCC_	
GAM2060	FLJ21791	3' CTTATTTGCAGAAAGTGGTGTA 62126	CCCAAGAA
		TACACCACT GAATAAG	
		ATGTGGTGA TTTATTC	
		AGACG__	
GAM2060	HMP19	3' CTTATTCTTTGTTAGGAAAATG 88860	CCAC CAA_
	TA	TACA TCC GAAGAATAAG	
		ATGT AGG TTTCTTATTC	
		AAA_ ATTG	
GAM2060	KIAA1719	3' TCTGTCTTGGGAGTGGTGTA 68742	_
		TACACCACTCCCAAGA AGA	
		ATGTGGTGAGGGTTCT TCT	
		G	
GAM2060	KIAA1853	3' TTTTCTTGAAGCAGTG 69929	CA C
		CAC CT CCAAGAAGAA	
		GTG GA GGTTCTTTT	
		AC A	
GAM2060	KIAA1877	3' CTTATTCTTCTGCCATGAGT 66748	CCA_
		ACTC AGAAGAATAAG	
		TGAG TCTTCTTATTC	
		TACCG	
GAM2060	KIAA1906	3' CTTATTCTTCTTGACTTTTGG 73571	CTCC_
		CCA CAAGAAGAATAAG	
		GGT GTTCTTCTTATTC	
		TTTCA	
GAM2060	OSBPL11	3' CTTAATTTCCCAAGAGTGGTG 43206	CCAA AA
		CACCACTC GAAG TAAG	
		GTGGTGAG CTTT ATTC	
		AACC A_	
GAM2060	YME1L1	3' TCATTCTTGATGTGGTGTA 58438	TCC _
		TACACCAC CAAGAA GA	
		ATGTGGTG GTTCTT CT	
		TA_ A	
GAM2060	ZNF262	3' CTTATTTTGTGGGAGT 18723	A
		ACTCCCAAG AGAATAAG	

		TGAGGGTTT TTTTATTC		
		G		
GAM2060	LOC91960	3' TGTGGCTTGGAACGTGGTGTA 68294	TC_	AAGA
		TACACCAC CCAAG ATA		
		ATGTGGTG GGTTT TGT		
		CAA GG_		
GAM2061	CHRM1	3' GCATCAGCAAGACAATGACA 96433	CCC	CTC_
		TGTTATTGTC TGC GC		
		ACAGTAACAG ACG CG		
		A_ ACTA		
GAM2061	COX15	3' CAGGCTGATGGAGACAGTAACA 55279	C	TGCCTC
		TGTTATTGTC CC GCCTG		
		ACAATGACAG GG CGGAC		
		A TAGT_		
GAM2061	FLJ22056	3' AGGCCCTGGGGACAATACA 42830	T	TGCCTC
		TGT ATTGTCCCC GCCT		
		ACA TAACAGGGG CGGA		
		_ TCC_		
GAM2061	GDF11	3' CAGACGAGGCAGAGACAAAACA 20558	A	CC C
		TGTT TTGTC CTGCCTCG CTG		
		ACAA AACAG GACGGAGC GAC		
		_ A_ A		
GAM2061	SNX11	3' CAGACGGAACAGTAACA 26170	_	_
		TGTTATTGT CCC CTG		
		ACAATGACA GGG GAC		
		A CA		
GAM2061	ZAK	3' CAGACACAGAGCAAGACAATAA 34099	CCC	_ CGC_
	CA	TGTTATTGTC TGC CT CTG		
		ACAATAACAG ACG GA GAC		
		A_ A CACA		
GAM2061	LOC145622	3' CAGTAACGAACAGGGAACAGTA 77806	C	CC C_
	ACA	TGTTATTGT CCCTG TCG CTG		
		ACAATGACA GGGAC AGC GAC		
		A A_ AAT		
GAM2062	HRH1	3' TCCCTTCTCAGAAACTTCT 7829	C	C C
		AG AGTT TCTGAGGAG GA		
		TC TCAA AGACTCTTC CT		
		T A C		
GAM2062	MEA	3' CTTCTCAGAGACCCACTTT 28275	CAGT	
		AAAG TCTCTGAGGAG		

TTTC AGAGACTCTTC
 ACCC
 GAM2062 NEDD4 3' CTCACAGAAAACTGTTT 70545 C_ AG
 AAGCAGTT TCTG GAG
 ||||| ||| ||
 TTTGTCAA AGAC CTC
 AA A_
 GAM2062 PCDH9 5' TTCCAGAGAATGCTCC 83698 A G A
 A AGCA TTCTCTG GGA
 | ||| ||||| ||
 C TCGT AAGAGAC CTT
 C _ _
 GAM2062 UBE4A 3' CTAAATTAGAGAACTGCT 17732 GG_
 AGCAGTTCTCTGA AG
 ||||| ||
 TCGTCAAGAGATT TC
 AAA
 GAM2062 BRD2 5' GCCCCAAAGAGACTGCTTT 18794 T GA A
 AAAGCAGT CTCT GG GC
 ||||| ||| ||
 TTTCGTCA GAGA CC CG
 _ AA C
 GAM2062 BRI3 3' CTCAATAAAGCACTGCTTT 31794 T C AG
 AAAGCAGT CT TG GAG
 ||||| || ||
 TTTCGTCA GA AT CTC
 C A AA
 GAM2062 FLJ20151 3' TCACTCCTTGACTTGCTCC 35147 A TTC TG C
 A AGCAG TC AGGAG GA
 | |||| || ||||| ||
 C TCGTT AG TCCTC CT
 C C_ GT A
 GAM2062 FLJ20507 3' CGCCCCCAGGCCACCTGCTCC 35736 A TTC_ A A
 A AGCAG TCTG GG GCG
 | |||| ||| || ||
 C TCGTC GGAC CC CGC
 C CACC _ C
 GAM2062 FLJ20507 3' CGCCCCCAGGCCACCTGCTCC 60842 A TTC_ A A
 A AGCAG TCTG GG GCG
 | |||| ||| || ||
 C TCGTC GGAC CC CGC
 C CACC _ C
 GAM2062 HDAC11 3' CGCCCCTTAGTGCTTT 46137 GTTCT A
 AAAGCA CTGAGG GCG
 ||||| ||||| ||
 TTTCGT GATTCC CGC
 _ C
 GAM2062 HSRNAFEV 3' TTCCCCAAGGAACTGCTCC 34455 A TC A
 A AGCAGTTC TG GGAG
 | ||||| || |||

		C TCGTCAAG AC CCTT	
		C GA C	
GAM2062 KIAA0022	3'	TCCAGAATGTAGAACTGCTTT 30287	C A_____
		AAAGCAGTT TCTG GGA	
		TTTCGTCAA AGAT CCT	
		_ GTAAGA	
GAM2062 KIAA1054	3'	TTCAGGGAAAGAAAGCTGCTT 68975	_____
		AAGCAGT TCTCTGAG	
		TTCGTCTG AGGGAAGT	
		AAAGAA	
GAM2062 KIAA1536	3'	ATTCTGTTCCTAAGAACTGCT 40875	C A _
T		AAGCAGTTCT TG GGAGC GAAT	
		TTTCGTCAAGA AT CCTTG CTTA	
		_ C T	
GAM2062 KIAA1615	3'	TCCAAATGAAGAGAACTCTTT 69287	C GA_____
		AAAG AGTTCTCT GGA	
		TTTC TCAAGAGA CCT	
		_ AGTAAA	
GAM2062 KIAA1813	5'	ATTCCTCCTCAGCCCTGTT 70822	TTCT C
		AGCAG CTGAGGAG GAAT	
		TTGTC GACTCCTC CTTA	
		CC_ A	
GAM2062 RHOBTB2	3'	GCAGCCCAGAGAACTCTCC 61602	A C A A_
		A AG AGTTCTCTG GG GC	
		C TC TCAAGAGAC CC CG	
		C _ _ GA	
GAM2062 SERHL	3'	CCTCAAAGAGGACTACTT 97350	C _
		AAG AGTTCTCT GAGG	
		TTC TCAGGAGA CTCC	
		A AA	
GAM2062 LOC151318	3'	TGCCCTGAAAAGCTGCTTT 81031	C TG A
		AAAGCAGTT TC AGG GCG	
		TTTCGTCAA AG TCC CGT	
		A _ _	
GAM2062 LOC158014	5'	TCTCAGAGCAACTGCTTT 82569	_
		AAAGCAGTT CTCTGAGG	
		TTTCGTCAA GAGACTCT	
		C	
GAM2062 LOC158376	3'	ATTCTGAAACCAAAGAGCTGCT 88134	C AGGAGC
T		AAGCAGTTCT TG GAAT	

		TTCGTCGAGA AC CTTA		
		A CAAAGT		
GAM2062	LOC158428 3'	ATTCTTTGCCAGAGAGCTGC 71081	A AGC_	
		GCAGTTCTCTG GG GAAT		
		CGTCGAGAGAC CC CTTA		
		_ GTTT		
GAM2062	LOC220431 5'	ATTCACCTCTTCAGAGACCACT 95993	CA T C_	
	T	AAG GT CTCTGAGGAG GAAT		
		TTC CA GAGACTTCTC CTTA		
		AC _ CA		
GAM2063	FGFRL1 3'	ATCCCCACTGCATTCTCCC 41908	AA__	
		GGGAGGAT TGGGGAT		
		CCCTCTTA ACCCCTA		
		CGTC		
GAM2063	GAGEB1 5'	ATCCGCAGCCAGTCCTCCCA 15034	AA__ G	
		TGGGAGGAT TG GGAT		
		ACCCTCCTG AC CCTA		
		ACCG G		
GAM2063	GSTT1 3'	ATCCCCACCCTGTCTTCC 73841	A__	
		GGAGGATA TGGGGAT		
		CCTTCTGT ACCCCTA		
		CCC		
GAM2063	HRH2 3'	CCCTCTTGCTTAATCCTCCCA 42509	_____ T	
		TGGGAGGAT AA GGGG		
		ACCCTCCTA TT TCCC		
		ATTCG C		
GAM2063	IER3 3'	ATCCGTGAGATCCTTCCA 54481	AA G	
		TGGGAGGAT TG GGAT		
		ACCTTCCTA GT CCTA		
		GA G		
GAM2063	IER3 3'	ATCCGTGAGATCCTTCCA 15319	AA G	
		TGGGAGGAT TG GGAT		
		ACCTTCCTA GT CCTA		
		GA G		
GAM2063	MUC4 5'	GTTCCCATTCCTCCA 37883	A TA	
		TGGG GGA ATGGGGAT		
		ACCC CCT TACCCTTG		
		_ _		
GAM2063	MUC4 5'	GTTCCCATTCCTCCA 57157	A TA	
		TGGG GGA ATGGGGAT		

ACCC CCT TACCCTTG

GAM2063 PIGK 3' TTTTGTATATCCTCCCA 67273 _ GG
TGGGAGGATA AT GGA
||||||| || |||
ACCCTCCTAT TG TTT
A TT

GAM2063 PSMB9 3' ATCTTTCACATCCTCTCA 12490 AAT
TGGGAGGAT GGGGAT
||||||| |||||
ACTCTCCTA TTTCTA
CAC

GAM2063 RGS5 3' ATCTACATATCTTCCCA 14621 A GG
TGGGAGGATA TG GAT
||||||| || |||
ACCCTTCTAT AC CTA
_ AT

GAM2063 RP42 3' ATCCTAGTTTATTCTCCCA 40565 TG_
TGGGAGGATAA GGGAT
||||||| |||||
ACCCTCTTATT TCCTA
TGA

GAM2063 SELL 3' ATCCTTTAAATCCTTCCA 7226 AAT
TGGGAGGAT GGGGAT
||||||| |||||
ACCTTCCTA TTCCTA
AAT

GAM2063 SORCS2 3' ATCCCGCAGGCTTCTCCCA 40796 TAA _
TGGGAGGA TG GGGAT
||||||| || |||||
ACCCTCTT AC CCCTA
CGG G

GAM2063 SPI1 3' CCCATTAACCTCCTCCCA 13351 _
TGGGAGGA TAATGGG
||||||| |||||
ACCCTCCT ATTACCC
CCA

GAM2063 TNFRSF11A 3' ATCCAAGTGATCCTCCCA 15188 A GG
TGGGAGGAT AT GGAT
||||||| || |||
ACCCTCCTA TG CCTA
G AA

GAM2063 TOMM22 3' ATCCCCACATTGTCTCA 40011 G AA
TGGGA GAT TGGGGAT
||||| ||| |||||
ACTCT TTA ACCCCTA
G C_

GAM2063 TTC3 5' ATCCCCCTTGCCCCCA 13881 A A T
TGGG GG TAA GGGGAT
||| || ||| |||||

			ACCC CC GTT CCCCTA		
			_ C C		
GAM2063	ABLM	3'	GTTCTCATCCTCTCCA	11325	_ TAA
			TGG GAGGA TGGGGAT		
			ACC CTCCT ACTCTTG		
			T _		
GAM2063	ABLM	3'	GTTCTCATCCTCTCCA	22985	_ TAA
			TGG GAGGA TGGGGAT		
			ACC CTCCT ACTCTTG		
			T _		
GAM2063	AMOTL1	3'	ATCCTTGGAATACCCCCA	74011	A _ AA
			TGGG GG AT TGGGGAT		
			ACCC CC TA GTTCCTA		
			_ A AG		
GAM2063	CDC14A	3'	ATCCTGATATCCTTCCA	14783	A G
			TGGGAGGATA T GGGAT		
			ACCTTCCTAT A TCCTA		
			_ G		
GAM2063	DKFZp434E0519	3'	ATCCCTCTGTCCTCCTA	50984	AT
			TGGGAGGATA GGGGAT		
			ATCCTCCTGT TCCCTA		
			C_		
GAM2063	DKFZP434L1435	3'	ATCCCCATCAGTTTTTCCT	93786	A_
			GGGAGGAT ATGGGGAT		
			TCCTTTTG TACCCCTA		
			AC		
GAM2063	DKFZP434L1435	3'	ATCCCCATCAGTTTTTCCT	99583	A_
			GGGAGGAT ATGGGGAT		
			TCCTTTTG TACCCCTA		
			AC		
GAM2063	DKFZP434L1435	3'	ATCCCCATCAGTTTTTCCT	99683	A_
			GGGAGGAT ATGGGGAT		
			TCCTTTTG TACCCCTA		
			AC		
GAM2063	DKFZP547E1010	3'	ATCCCTGTTGCCCCCA	67484	A A
			TGGG GG TAATGGGGAT		
			ACCC CC GTTGTCCCTA		
			_ _		
GAM2063	DKFZP547E1010	3'	ATCCCTGTTGCCCCCA	32173	A A
			TGGG GG TAATGGGGAT		

ACCC CC GTTGTCCCTA

GAM2063 DKFZp761G2113 3' ATTCCCATCCTTCCCA 70463 ATA
TGGGAGG ATGGGGAT
||||| |||||
ACCCTTC TACCCTTA

C__

GAM2063 DKFZp762K2015 3' ATCCCCCAGGTCCTCTCA 72888 AAT
TGGGAGGAT GGGGAT
||||| |||||
ACTCTCCTG CCCCTA

GAC

GAM2063 EFA6R 3' ATCGTTGATATCCTTCCA 31633 A G
TGGGAGGATA TGG GAT
||||| ||| |||
ACCTTCCTAT GTT CTA

A G

GAM2063 FLJ11767 3' ATCCCTGCAGTCCTTCCA 45058 AA
TGGGAGGAT TGGGGAT
||||| |||||
ACCTTCCTG GTCCCTA

AC

GAM2063 FLJ12681 3' ATCTCCCATCCATCCCA 43182 _ AAT
TGGGA GGAT GGGGAT
|||| ||| |||||
ACCCT CCTA CCTCTA

A C__

GAM2063 FLJ13612 3' ATGTTCTTATCCCCCA 48085 A T G
TGGG GGATAA GGG AT
||| ||||| ||| ||
ACCC CCTATT CTT TA

_ _ G

GAM2063 FLJ14596 3' ATCGTCTTTTCTCCTCCCA 52510 T T_ G
TGGGAGGA AA GG GAT
||||| || ||| |||
ACCCTCCT TT CT CTA

C TT G

GAM2063 FLJ22596 5' ATCCCCATCTCATCTCA 47642 G TA
TGGGA GA ATGGGGAT
|||| || |||||
ACTCT CT TACCCCTA

A C_

GAM2063 FLJ32658 3' ATCCCCATTGTTAGTCCA 59076 AG
TGGG GATAATGGGGAT
||| |||||
ACCT TTGTTACCCCTA

GA

GAM2063 KIAA0280 3' ATCCTGTATTCTCCCA 93287 ATG
TGGGAGGATA GGGAT
||||| |||||

		ACCCTCTTAT TCCTA		
		G__		
GAM2063	KIAA0682	3' ATCCCCAGGCTTCTCTCA	33006	TAA
		TGGGAGGA TGGGGAT		
		ACTCTCTT ACCCCTA		
		CGG		
GAM2063	KIAA1069	3' ATGTTCTTATCCCACCCA	68527	A_ T G
		TGGG GGATAA GGG AT		
		ACCC CCTATT CTT TA		
		AC _ G		
GAM2063	KIAA1300	5' ATGCTTATTCTCTCCA	63523	TA G
		TGGGAGGA ATGGG AT		
		ACCCTCCT TATTC TA		
		_ G		
GAM2063	KIAA1388	5' CCCTGTTTCATCTTCCA	95226	_
		TGGGAGGAT AATGGGG		
		ACCCTTCTA TTGTCCC		
		CT		
GAM2063	KIAA1822	3' ATCCCCATCCCTGCTCA	68179	_ ATA
		TGGG AGG ATGGGGAT		
		ACTC TCC TACCCCTA		
		G C_		
GAM2063	MGC1127	3' ATCCCCATTCCAATTCCA	54330	_ TA
		TGGGA GGA ATGGGGAT		
		ACCTT CCT TACCCCTA		
		AA _		
GAM2063	MGC2865	3' ATCCCCGCCGTCCTTCCA	51456	AA
		TGGGAGGAT TGGGGAT		
		ACCTTCCTG GCCCCTA		
		CC		
GAM2063	SNAP29	3' ATTCTTTCATCCTCCA	17711	AAT
		TGGGAGGAT GGGGAT		
		ACCCTCCTA TTCTTA		
		CT_		
GAM2063	SYT6	5' ATCCCTCCTTATTCCCCCA	79516	A T_
		TGGG GGATAA G GGGAT		
		ACCC CTTATT C CCCTA		
		C C T		
GAM2063	TRF4-2	3' ATCCTTGGAGTCCTCTCA	42610	AA
		TGGGAGGAT TGGGGAT		

		ACTCTCCTG GTTCCTA	
		AG	
GAM2063	ZIN	3' ATCCCCCATCCTCCCA	26390 AAT
		TGGGAGGAT GGGGAT	
		ACCCTCCTA CCCCTA	
		C__	
GAM2063	LOC145333	5' ATCTTCACATTCTCCCA	84289 AA
		TGGGAGGAT TGGGGAT	
		ACCCTCTTA ACTTCTA	
		C_	
GAM2063	LOC145678	5' ATCCCCAGGCCTCTCCTCCTA	84431 TAA__
		TGGGAGGA TGGGGAT	
		ATCCTCCT ACCCCTA	
		CTCCGG	
GAM2063	LOC146315	5' ATCCGTGAGATCTTCCCA	61556 AA G
		TGGGAGGAT TG GGAT	
		ACCCTTCTA GT CCTA	
		GA G	
GAM2063	LOC149372	3' ATCCCCATTTCTCCTCCC	80100 T_
		GGGAGGA AATGGGGAT	
		CCCTCCT TTACCCCTA	
		CT	
GAM2063	LOC149670	3' TATCCCCAGTTCCTCCT	80309 TAA ____
		GGGAGGA TGGGGAT A	
		TCCTCCT ACCCCTA T	
		TG_ ____	
GAM2063	LOC150051	3' ATTTTTGTAAACCTCCCA	85952 A GG
		TGGGAGG TAAT GGAT	
		ACCCTCC ATTG TTTA	
		A TT	
GAM2063	LOC150577	3' TATCCCCACTATCCCAAACTC	86259 _____ A ____
	CT	GGGA GGATA TGGGGAT A	
		TCCT CCTAT ACCCCTA T	
		CAAAAC C ____	
GAM2063	LOC154007	3' ATCTGTGTTTTCTCCTCCCA	81923 T G
		TGGGAGGA AATG GGAT	
		ACCCTCCT TTGT TCTA	
		T G	
GAM2063	LOC197342	3' ATTCTTGGCCTCCTCCCA	89351 TAA
		TGGGAGGA TGGGGAT	

		ACCCTCCT GTTCTTA		
		CCG		
GAM2063	LOC220895 3'	ATCCCTGGGTCTTCCCA	92490	AAT
		TGGGAGGAT GGGGAT		
		ACCCTTCTG TCCCTA		
		GG_		
GAM2063	LOC221103 3'	ATCCTCATCCCTTCCA	94870	ATA
		TGGGAGG ATGGGGAT		
		ACCTTCC TACTCCTA		
		C_		
GAM2063	LOC51008 3'	ATTCCCACTCCTCCCA	32528	TAA
		TGGGAGGA TGGGGAT		
		ACCCTCCT ACCCTTA		
		C_		
GAM2063	LOC81558 3'	ATCCCCCATCCTCTCA	48679	AAT
		TGGGAGGAT GGGGAT		
		ACTCTCCTA CCCCTA		
		C_		
GAM2063	LOC90408 5'	ATCCTCCTGCCTTATCCTCCCA	63338	T_____
		TGGGAGGATAA GGGGAT		
		ACCCTCCTATT CTCCTA		
		CCGTC		
GAM2063	LOC91373 3'	ATCCCCATTGGTTTCCCA	66407	A
		TGGGAGG TAATGGGGAT		
		ACCCTTT GTTACCCCTA		
		G		
GAM2064	GPD1 3'	TCATGCCACCACATTTG	60398	C C
		TAAATG GGTGGCAT GA		
		GTTTAC CCACCGTA CT		
		A _		
GAM2064	IL5RA 5'	TCGCATGGCCACCGCATTT	6906	AT__
		AAATGCGGTGGC CGA		
		TTTACGCCACCG GCT		
		GTAC		
GAM2064	MYO1C 3'	TGCCGATGCCAAATATTTG	61873	CGG A
		TAAATG TGGCATCG CA		
		GTTTAT ACCGTAGC GT		
		AA_ C		
GAM2064	C6orf37 3'	TGTCACACTGCATTTA	68097	GCATC
		TAAATGCGGTG GACA		

		ATTACGTCAC	CTGT		
		A_____			
GAM2064	DNAJC6	3'	TTGCAGAACCACCGCATT	29498	CA GA
			AATGCGGTGG TC CAA		
			TTACGCCACC AG GTT		
			A_ AC		
GAM2064	FLJ11210	3'	GTCGATGTGCATGCTTTTA	60319	T GTG
			TAAA GCG GCATCGAC		
			ATTT CGT TGTAGCTG		
			T ACG		
GAM2064	FLJ12476	3'	TCGATCTTCTGCATTTA	43270	T C
			TAAATGCGG GG ATCGA		
			ATTTACGTC TC TAGCT		
			T _		
GAM2064	KIAA1034	3'	TCGATGGCATCCGCATTTG	63134	_ G
			TAAATGCGG TG CATCGA		
			GTTTACGCC AC GTAGCT		
			T G		
GAM2064	KIAA1987	3'	TCATGTAAGTGCATTTA	89391	G C
			TAAATGCGGT GCAT GA		
			ATTTACGTCA TGTA CT		
			A _		
GAM2064	MGC16063	3'	TGTCCTGGCCACTGCATT	54929	ATC
			AATGCGGTGGC GACA		
			TTACGTCACCG CTGT		
			GTC		
GAM2064	LOC147949	3'	TGTCAGATGTCCACATTGCA	79279	_ _ _
			TGCG GTGG CATC GACA		
			ACGT CACC GTAG CTGT		
			TA T A		
GAM2064	LOC150577	3'	GTCCTCACCGCATTTG	86258	CATC
			TAAATGCGGTGG GAC		
			GTTTACGCCACT CTG		
			C_____		
GAM2064	LOC158219	3'	TGTGTGTCACCACATTT	82694	C CG
			AAATG GGTGGCAT ACA		
			TTTAC CCACTGTG TGT		
			A _		
GAM2064	LOC202020	3'	TGTCTCACACATTTA	90605	C CATC
			TAAATG GGTGG GACA		

		ATTTAC CCACT CTGT		
		A _		
GAM2064	LOC90826	5' TGTCGATGCAGGTTTATTTG	64788	CGGTG
		TAAATG GCATCGACA		
		GTTTAT CGTAGCTGT		
		TTGGA		
GAM2064	LOC93587	3' TTGTCTTTACCTGCATTTA	73042	_ CATC
		TAAATGC GGTGG GACAA		
		ATTTACG CCATT CTGTT		
		T T _		
GAM2065	DLEC1	3' CATCTGGCCCTCCCTTG	24716	A A C
		CAAGG AGGGC GG GTG		
		GTTCC TCCCG TC TAC		
		C G _		
GAM2065	DLEC1	3' CATCTGGCCCTCCCTTG	24728	A A C
		CAAGG AGGGC GG GTG		
		GTTCC TCCCG TC TAC		
		C G _		
GAM2065	PIP5K1A	3' TATCCCACCCTGCCTTGATA	14520	A CA C
		TATCAAGG AGGG GG GTG		
		ATAGTTCC TCCC CC TAT		
		G A_ C		
GAM2065	SOX11	3' ACCCACCCTTGGTA	13308	AA CA C
		TATCAAGG GGG GG GT		
		ATGGTTCC CCC CC CA		
		CC A_ _		
GAM2065	CHL1	3' TGTTACCTTTCCTCAATA	22768	CA CA
		TAT AGGAAGGG GGCG		
		ATA TCCTTTCC TTGT		
		AC A_		
GAM2065	EPB41L1	3' CATTCTGCCCTTCCCTGA	71104	A C
		TCA GGAAGGGCAGG GTG		
		AGT CCTTCCCGTCT TAC		
		C _		
GAM2065	FLJ00060	3' CATACCCCTGCCCTCCTCTGA	61741	_ A CGTG
		TCA AGGA GGGCAGG ATG		
		AGT TCCT CCCGTCC TAC		
		C _ CCCA		
GAM2065	FLJ10898	5' CACCACAGCCCTTTCTCAATA	60126	CA AGGC
		TAT AGGAAGGGC GTG		

		ATA TCTTTCCCG CAC		
		AC ACAC		
GAM2065	FLJ22557	3' ATCATCCCATCCTTAATA	45581	C A CAGGC
		TAT AAGGA GGG GTGAT		
		ATA TTCCT CCC TACTA		
		A A _____		
GAM2065	KIAA0574	3' CATCCCCTGCCCTCCCCTGA	69808	A A CGT
		TCA GG AGGGCAGG GATG		
		AGT CC TCCCGTCC CTAC		
		C C C__		
GAM2065	KIAA0632	3' CACCTCAGAAACCCTTCCTTGA	32071	CA__ C
		TCAAGGAAGGG GG GTG		
		AGTTCCTTCCC CT CAC		
		AAAGA C		
GAM2065	KIAA1045	3' CATCACATGTCCTTCC	71599	GGC
		GGAAGGGCA GTGATG		
		CCTTCCTGT CACTAC		
		A__		
GAM2065	KIAA1354	5' CAGTGACTGCCTTCCCTTGATA	61572	A G _
		TATCAAGG AGGGCAG CG TG		
		ATAGTTCC TTCCGTC GT AC		
		C A G		
GAM2065	MGC20460	5' CACCGCCTCCTACCCTTCTT	54901	C__ _
		AGGAAGGG AGGCG TG		
		TTCTTCCC TCCGC AC		
		ATCC C		
GAM2065	LOC158476	3' CACGCCCGCCCCCCCCATTGA	88186	_ AA_ A
		TCAA GG GGGC GGC GTG		
		AGTT CC CCG CCGCAC		
		A CCC C		
GAM2065	LOC90459	3' CACACCCGCTAATTTTGT	63550	A_ A C
		CAAGGA GGGC GG GTG		
		GTTTTT TCCG CC CAC		
		AA C A		
GAM2066	PIP5K1A	3' TATCCACCCCTGCCTTGATA	14520	A CA C
		TATCAAGG AGGG GG GTG		
		ATAGTTCC TCCC CC TAT		
		G A_ C		
GAM2066	SOX11	3' ACCCACCCCCCCTTGGTA	13308	AA CA C
		TATCAAGG GGG GG GT		

ATGGTTCC CCC CC CA
 CC A_ _
 GAM2066 CHL1 3' TGTTACCTTTCCTCAATA 22768 CA CA
 TAT AGGAAGGG GGCG
 ||| ||||| |||
 ATA TCCTTTCC TTGT
 AC A_
 GAM2066 EPB41L1 3' CATTCTGCCCTTCCCTGA 71104 A C
 TCA GGAAGGGCAGG GTG
 ||| ||||| |||
 AGT CCTTCCCGTCT TAC
 C _
 GAM2066 FLJ00060 3' CATACCCCTGCCCTCCTCTGA 61741 _ A CGTG
 TCA AGGA GGGCAGG ATG
 ||| ||| ||||| |||
 AGT TCCT CCCGTCC TAC
 C _ CCCA
 GAM2066 FLJ10898 5' CACCACAGCCCTTTCTCAATA 60126 CA AGGC
 TAT AGGAAGGGC GTG
 ||| ||||| |||
 ATA TCTTTCCCG CAC
 AC ACAC
 GAM2066 FLJ22557 3' ATCATCCCATCCTTAATA 45581 C A CAGGC
 TAT AAGGA GGG GTGAT
 ||| ||||| ||| |||||
 ATA TTCCT CCC TACTA
 A A _
 GAM2066 KIAA0574 3' CATCCCCTGCCCTCCCCTGA 69808 A A CGT
 TCA GG AGGGCAGG GATG
 ||| || ||||| |||
 AGT CC TCCCGTCC CTAC
 C C C_
 GAM2066 KIAA0632 3' CACCTCAGAAACCCTTCCTTGA 32071 CA_ C
 TCAAGGAAGGG GG GTG
 ||||| ||| |||
 AGTTCCTTCCC CT CAC
 AAAGA C
 GAM2066 KIAA1354 5' CAGTGA CTGCCTTCCCTTGATA 61572 A G _
 TATCAAGG AGGGCAG CG TG
 ||||| ||||| ||| |||
 ATAGTTCC TTCCGTC GT AC
 C A G
 GAM2066 MGC20460 5' CACCGCCTCCTACCCTTCTT 54901 C_ _
 AGGAAGGG AGGCG TG
 ||||| ||| |||
 TTCTTCCC TCCGC AC
 ATCC C
 GAM2066 LOC158476 3' CACGCCCCGCCCCCCCCATTGA 88186 _ AA_ A
 TCAA GG GGGC GGCGTG
 ||| || ||| |||||

AGTT CC CCCG CCGCAC
 A CCC C
 GAM2066 LOC90459 3' CACACCCGCTAATTTTGG 63550 A_ A C
 CAAGGA GGGC GG GTG
 ||||| ||| || |||
 GTTTTT TCCG CC CAC
 AA C A
 GAM2067 SCAMP1 3' GCTAAATAAATATTCTCC 18014 T C
 GGA AATATT ATTTAGC
 ||| ||||| |||||
 CCT TTATAA TAAATCG
 C A
 GAM2067 SCAMP1 3' GCTAAATAAATATTCTCC 54500 T C
 GGA AATATT ATTTAGC
 ||| ||||| |||||
 CCT TTATAA TAAATCG
 C A
 GAM2067 NX-17 3' TGAATATCAGCCCCTAATA 40706 ATA_
 TATTAGGG ATATTCA
 ||||| |||||
 ATAATCCC TATAAGT
 CGAC
 GAM2067 LOC161589 3' GCTAAATGAATATTATCCCTAA 83159
 TA TATTAGGGATAATATTCATTTAGC
 |||||
 ATAATCCCTATTATAAGTAAATCG
 GAM2068 SCAMP1 3' GCTAAATAAATATTCTCC 18014 T C
 GGA AATATT ATTTAGC
 ||| ||||| |||||
 CCT TTATAA TAAATCG
 C A
 GAM2068 SCAMP1 3' GCTAAATAAATATTCTCC 54500 T C
 GGA AATATT ATTTAGC
 ||| ||||| |||||
 CCT TTATAA TAAATCG
 C A
 GAM2068 NX-17 3' TGAATATCAGCCCCTAATA 40706 ATA_
 TATTAGGG ATATTCA
 ||||| |||||
 ATAATCCC TATAAGT
 CGAC
 GAM2068 LOC161589 3' GCTAAATGAATATTATCCCTAA 83159
 TA TATTAGGGATAATATTCATTTAGC
 |||||
 ATAATCCCTATTATAAGTAAATCG
 GAM2069 GALE 3' CACAGGGTCCAAGAGTTCATCA 63859 _ CTCA C
 TGA GAACTC TG ACCCTGTG
 ||| ||||| ||| |||||

			ACT CTTGAG AC TGGGACAC		
			A A__ C		
GAM2069	LRR2	3'	CACACTGATAAGGAGTTC 44736	C G CCC	
			GAACCTCT AT CA TGTG		
			CTTGAGGA TA GT ACAC		
			A _ C__		
GAM2069	SLC7A4	3'	ACAGGCTGGGGAGTCCTCA 65817	A TGCAC	
			TGAG ACTCCTCA CCTGT		
			ACTC TGAGGGGT GGACA		
			C C__		
GAM2069	TMEM2	3'	ACAGGGTGCATGCGTCTC 26334	ACTCCT	
			GAGA CATGCACCCTGT		
			CTCT GTACGTGGGACA		
			GC__		
GAM2069	AD022	3'	CACAAAGCCTGTCAGAGTTTTC 92647	CT_ T ACCC	
	A		TGAGAACTC CA GC TGTG		
			ACTTTTGAG GT CG ACAC		
			ACT C AA__		
GAM2069	DCNP1	3'	ACAGAGAGACAGTTCTCA 56454	C_ ATGCACC	
			TGAGAACT CTC CTGT		
			ACTCTTGA GAG GACA		
			CA A__		
GAM2069	FLJ13102	3'	CACAGAATTTTCAGGGAAGAGTT 46526	C A_ CACC_	
	CTC		GAGAACTC TC TG CTGTG		
			CTCTTGAG AG AC GACAC		
			A GG TTAA		
GAM2069	KIAA0172	3'	CACAAAGTGGTGTCTGGTTCTC 65594	CCT G CC	
	A		TGAGAACT CAT CAC TGTG		
			ACTCTTGG GTG GTG ACAC		
			TCT _ AA		
GAM2069	KIAA0992	5'	CACAGAGTGCATGAAGACCGTT 32715	_ C C	
	C		GAAC TC TCATGCAC CTGTG		
			CTTG AG AGTACGTG GACAC		
			CC A A		
GAM2069	KIAA1940	3'	CACAGCCAGTGAGGAGCTGTCA 80776	GAA GCACC	
			TGA CTCCTCAT CTGTG		
			ACT GAGGAGTG GACAC		
			GTC ACC__		
GAM2069	LOC123242	5'	CACACGAAGTGGAGTCCTCA 76109	A TGCACCC	
			TGAG ACTCCTCA TGTG		

			ACTC TGAGGAGT	ACAC		
			C CAAGC__			
GAM2069	LOC153682	5'	CACAAGGGCAATATGAGGGCCC	87268	AA T	CA_ _
			TCA TGAG C CCTCATG CCCT GTG			
			ACTC G GGAGTAT GGGA CAC			
			CC_ AAC A			
GAM2069	LOC196955	5'	CACACGAACTGAGGAGTCCTCA	77862	A	TGCACCC
			TGAG ACTCCTCA TGTG			
			ACTC TGAGGAGT ACAC			
			C CAAGC__			
GAM2070	DLEC1	3'	CATCTGGCCCTCCCTTG	24717	A A C	
			CAAGG AGGGC GG GTG			
			GTTCC TCCCG TC TAC			
			C G _			
GAM2070	DLEC1	3'	CATCTGGCCCTCCCTTG	96278	A A C	
			CAAGG AGGGC GG GTG			
			GTTCC TCCCG TC TAC			
			C G _			
GAM2070	PIP5K1A	3'	TATCCCACCCTGCCTTGATA	14520	A CA C	
			TATCAAGG AGGG GG GTG			
			ATAGTTCC TCCC CC TAT			
			G A_ C			
GAM2070	SOX11	3'	ACCCACCCCCCTTG GTA	13308	AA CA C	
			TATCAAGG GGG GG GT			
			ATGGTTCC CCC CC CA			
			CC A_ _			
GAM2070	CHL1	3'	TGTTACCTTTCCTCAATA	22768	CA CA	
			TAT AGGAAGGG GGCG			
			ATA TCCTTTCC TTGT			
			AC A_			
GAM2070	EPB41L1	3'	CATTCTGCCCTTCCCTGA	71104	A C	
			TCA GGAAGGGCAGG GTG			
			AGT CCTTCCCGTCT TAC			
			C _			
GAM2070	FLJ00060	3'	CATACCCCCTGCCCTCCTCTGA	61741	_ A CGTG	
			TCA AGGA GGGCAGG ATG			
			AGT TCCT CCCGTCC TAC			
			C _ CCCA			
GAM2070	FLJ10898	5'	CACCACAGCCCTTTCTCAATA	60126	CA AGGC	
			TAT AGGAAGGGC GTG			

ATA TCTTTCCCG CAC
 AC ACAC
 GAM2070 FLJ22557 3' ATCATCCCATCCTTAATA 45581 C A CAGGC
 TAT AAGGA GGG GTGAT
 ||| ||||| ||| |||||
 ATA TTCCT CCC TACTA
 A A ____
 GAM2070 KIAA0574 3' CATCCCCTGCCCTCCCCTGA 69808 A A CGT
 TCA GG AGGGCAGG GATG
 ||| || ||||| |||
 AGT CC TCCCGTCC CTAC
 C C C__
 GAM2070 KIAA0632 3' CACCTCAGAAACCCTTCCTTGA 32071 CA__ C
 TCAAGGAAGGG GG GTG
 ||||| ||| |||
 AGTTCCTTCCC CT CAC
 AAAGA C
 GAM2070 KIAA1045 3' CATCACATGTCCTTCC 71599 GGC
 GGAAGGGCA GTGATG
 ||||| |||||
 CCTTCCTGT CACTAC
 A__
 GAM2070 KIAA1354 5' CAGTGACTGCCTTCCCTTGATA 61572 A G _
 TATCAAGG AGGGCAG CG TG
 ||||| ||||| || ||
 ATAGTTCC TTCCGTC GT AC
 C A G
 GAM2070 MGC20460 5' CACCGCCTCCTACCCTTCTT 54901 C__ _
 AGGAAGGG AGGCG TG
 ||||| ||||| ||
 TTCTTCCC TCCGC AC
 ATCC C
 GAM2070 LOC158476 3' CACGCCCGCCCCCCCCATTGA 88186 _ AA_ A
 TCAA GG GGGC GGC GTG
 ||| || ||| |||||
 AGTT CC CCG CCGCAC
 A CCC C
 GAM2070 LOC90459 3' CACACCCGCTAATTTTGT 63550 A_ A C
 CAAGGA GGGC GG GTG
 ||||| ||| || |||
 GTTTTT TCCG CC CAC
 AA C A
 GAM2071 SCAMP1 3' GCTAAATAAATATTCTCC 54500 T C
 GGA AATATT ATTTAGC
 ||| ||||| |||||
 CCT TTATAA TAAATCG
 C A
 GAM2071 SCAMP1 3' GCTAAATAAATATTCTCC 54501 T C
 GGA AATATT ATTTAGC
 ||| ||||| |||||

CCT TTATAA TAAATCG
 C A
 GAM2071 NX-17 3' TGAATATCAGCCCCTAATA 40706 ATA_
 TATTAGGG ATATTCA
 ||||| |||||
 ATAATCCC TATAAGT
 CGAC
 GAM2071 LOC161589 3' GCTAAATGAATATTATCCCTAA 83159
 TA TATTAGGGATAATATTCATTTAGC
 |||||
 ATAATCCCTATTATAAGTAAATCG

 GAM2072 DBN1 3' TCAGATATTTTGCACGAATTTT 16560 A CT_ C
 A TGAAATTC TGCAAG TC GA
 ||||| ||||| ||
 ATTTTAAG ACGTTT AG CT
 C TAT A
 GAM2072 DBN1 3' TCAGATATTTTGCACGAATTTT 56021 A CT_ C
 A TGAAATTC TGCAAG TC GA
 ||||| ||||| ||
 ATTTTAAG ACGTTT AG CT
 C TAT A
 GAM2072 KCNJ5 5' TCGGAAGCTCCGATCTCA 7979 A CATGCA
 TGA ATT AGCTTCCGA
 ||| |||||
 ACT TAG TCGAAGGCT
 C CC____
 GAM2072 PTPRA 5' TCAGAAGCTTGCCAGTTTTTCA 55952 TTCAT C
 TGAAA GCAAGCTTC GA
 |||| ||||| ||
 ACTTT CGTTCGAAG CT
 TTGAC A
 GAM2072 ZNF175 3' TCAGAAGCATTTTGGATTTTCAG 24085 TGCAA C
 A TCTGAAATTCA GCTTC GA
 ||||| ||||| ||
 AGACTTTAGGT CGAAG CT
 TTTA_ A
 GAM2072 DEGS 3' TCAGAAGCTCCCCTGGCACAAT 14804 CA A_____ C
 TTCAGA TCTGAAATT TGC AGCTTC GA
 ||||| ||||| ||
 AGACTTTAA ACG TCGAAG CT
 C_ GTCCCC A
 GAM2072 FLJ10702 3' AAGCGTTCATGAATTTAGA 36967 A CAA
 TCTGAA TTCATG GCTT
 ||||| ||||| ||
 AGATTT AAGTAC CGAA
 _ TTG
 GAM2072 FLJ12704 5' CTTGCATTACATGTATTTTCA 47168 T _____
 TCTGAAAT CA TGCAAG
 ||||| |||||

AGACTTTA GT ACGTTC
 T ACATT
 GAM2072 FLJ22833 3' TCAGAAAGTGCCAAATTTTCAG 43409 CAT AA C
 CTGAAATT GC GCTTC GA
 ||||| || |||||
 GACTTTAA CG TGAAG CT
 AC_ _ A
 GAM2072 RAD52B 3' GAAGCTTGCTATTCAGA 89600 ATTCAT
 TCTGAA GCAAGCTTC
 ||||| |||||
 AGACTT CGTTCGAAG
 AT____
 GAM2072 LOC116064 3' AAGTTTTGCATGAATCACA 74103 AA _
 TG ATTCATGCAAG CTT
 || ||||| |||||
 AC TAAGTACGTTT GAA
 AC T
 GAM2072 LOC148823 3' GAAGTGTTTTGGATTTCAGA 59892 TGCAA
 TCTGAAATTCA GCTTC
 ||||| |||||
 AGACTTTAGGT TGAAG
 TTTG_
 GAM2072 LOC256107 5' TGGATGCATGGACTTCAGA 98599 A AGCT
 TCTGAA TTCATGCA TCCG
 ||||| ||||| |||||
 AGACTT AGGTACGT AGGT
 C ____
 GAM2073 CAPN10 3' AGGCCATCCATTACACAGC 43858 CA AGC C
 GC TGAA TG ATGGCCT
 || |||| || |||||
 CG ACTT AC TACCGGA
 AC _ C
 GAM2073 CAPN10 3' AGGCCATCCATTACACAGC 43861 CA AGC C
 GC TGAA TG ATGGCCT
 || |||| || |||||
 CG ACTT AC TACCGGA
 AC _ C
 GAM2073 CAPN10 3' AGGCCATCCATTACACAGC 43864 CA AGC C
 GC TGAA TG ATGGCCT
 || |||| || |||||
 CG ACTT AC TACCGGA
 AC _ C
 GAM2073 CAPN10 3' AGGCCATCCATTACACAGC 43867 CA AGC C
 GC TGAA TG ATGGCCT
 || |||| || |||||
 CG ACTT AC TACCGGA
 AC _ C
 GAM2073 MAPK14 3' CAGGCAGCCTTCATAGGC 58125 _ A A
 GCC ATGAA GCTGC TG
 || |||| ||||| ||

			CGG TACTT CGACG AC			
			A C G			
GAM2073	MAPK14	3'	CAGGCAGCCTTCATAGGC 58131	_	A	A
			GCC ATGAA GCTGC TG			
			CGG TACTT CGACG AC			
			A C G			
GAM2073	MAPK14	3'	CAGGCAGCCTTCATAGGC 8976	_	A	A
			GCC ATGAA GCTGC TG			
			CGG TACTT CGACG AC			
			A C G			
GAM2073	OPRD1	3'	CAGGCCATCCGGCCCCCAGACG 8068	CA_	AAA	C
	C		GC TG GCTG ATGGCCTG			
			CG AC CGGC TACCGGAC			
			CAG CCC C			
GAM2073	PET112L	3'	GCCACAGCTATGGCGT 17080	GAA	CA	
			ACGCCAT AGCTG TGGC			
			TGCGGTA TCGAC ACCG			
			— —			
GAM2073	SCML2	3'	GCTTATAAGCTTTTCATGAAGT 21427	GC	GCAT	
			AC CATGAAAGCT GGC			
			TG GTACTTTCGA TCG			
			AA ATAT			
GAM2073	DOCK2	3'	TAGGCACAGCTTTCAT 71401	CATG		
			ATGAAAGCTG GCCTG			
			TACTTTCGAC CGGAT			
			A_			
GAM2073	HTF9C	5'	CAGGCGGCCCCCATGGCGT 42993	AAA	A	
			ACGCCATG GCTGC TG			
			TGCGGTAC CGGCG AC			
			CCC G			
GAM2073	KIAA0237	3'	GCCAGTCCTCCCATGGTCA 29225	C	AA CT A	
			A GCCATG AG GC TGGC			
			A TGGTAC TC TG ACCG			
			C CC C_ _			
GAM2073	KIAA1940	3'	CAGCACACCCAGCTCCCATGGC 80777	AA	CA GC	
	GT		ACGCCATG AGCTG TG CTG			
			TGCGGTAC TCGAC AC GAC			
			CC CC AC			
GAM2073	MGC23280	3'	CAGGCCAGGATGCTTGCCATGG 59053	A_	TGCA	
	C		GCCATG AAGC TGGCCTG			

		CGGTAC TTCG ACCGGAC		
		CG TAGG		
GAM2073	MGC23937	3' CAGGCCATTATGTTTTTCATGG 59599		_ TGC
		C GCCATGAAAG C ATGGCCTG		
		CGGTACTTTT G TACCGGAC		
		T TAT		
GAM2073	NICE-3	3' CAGATGTGTTGCAGCTTTCCTG 31882	T	TG _
		CA GAAAGCTGCA GC CTG		
		GT CTTTCGACGT TG GAC		
		C TG TA		
GAM2073	PRDM12	3' CAGGCCACGCAGCTGGTGCGGC 41510	AT AA	A
		GCC G AGCTGC TGGCCTG		
		CGG T TCGACG ACCGGAC		
		CG GG C		
GAM2073	TA-PP2C	3' CAGACCCAAGCTTCCATGGGT 58404	G A	GCAT C
		AC CCATG AAGCT GG CTG		
		TG GGTAC TTCGA CC GAC		
		_ C AC_ A		
GAM2073	LOC148229	5' GCCATCGCCCATGGTGT 79489	AAA T C	
		ACGCCATG GC G ATGGC		
		TGTGGTAC CG C TACCG		
		C_ _ _		
GAM2073	LOC152580	5' CAGAGCCACAGCTTTCCTCCAGC 86983	CAT	CA _
		GC GAAAGCTG TGGC CTG		
		CG CTTTCGAC ACCG GAC		
		ACC _ A		
GAM2073	LOC155054	3' CAGGCCATGCAGCAGTCACGC 82202	CA AA	
		GC TGA GCTGCATGGCCTG		
		CG ACT CGACGTACCGGAC		
		C_ GA		
GAM2073	LOC158363	3' CAGGCTTAGGCTTTCATG 88114	GCAT	
		CATGAAAGCT GGCCTG		
		GTACTTTCGG TCGGAC		
		AT_		
GAM2073	LOC90288	3' CAGACCTTTGCTCTCATGGTG 62776	A TGCAT C	
		CGCCATGA AGC GG CTG		
		GTGGTACT TCG CC GAC		
		C TTT_ A		
GAM2074	ABCE1	5' GGGGATCGTTTTCTCCAGA 60261	C CTG	
		TCTGGAGAAA TG CCTC		

			AGACCTCTTT GC GGGG		
			T TA_		
GAM2074 AKAP13	3'	TGAGGCAGCTGCCTCCTGA	91257	T	AAACT
		TC GGAG GCTGCCTCA			
		AG CCTC CGACGGAGT			
		T CGT_			
GAM2074 ALOX12B	5'	GGGCAGCAGCTTTTCCAGA	8537		A
		TCTGGAGAA CTGCTGCCT			
		AGACCTTTT GACGACGGG			
		C			
GAM2074 BCL7A	3'	GAGGCGGCGTTACCTCCAGA	40984	A_	T
		TCTGGAG AAC GCTGCCTC			
		AGACCTC TTG CGGCGGAG			
		CA _			
GAM2074 CLDN3	3'	TGGGGCAGCTTCCCCAG	8961	A	ACT
		CTGG GAA GCTGCCTCA			
		GACC CTT CGACGGGGT			
		C _			
GAM2074 CUTL1	3'	GAGCCCCAGTCTCTTCAGA	10348	A	CT C
		TCTGGAGA ACTG GC TC			
		AGACTTCT TGAC CG AG			
		C CC _			
GAM2074 EFNA1	3'	TGGGGCAGCACTCCCCAGA	16666	A	AAC
		TCTGG GA TGCTGCCTCA			
		AGACC CT ACGACGGGGT			
		C C_			
GAM2074 EGR1	3'	TGAGCTTCGGTTCTCCAGA	10493	A	CT C
		TCTGGAGAA CTG GC TCA			
		AGACCTCTT GGC CG AGT			
		_ TT _			
GAM2074 FLT1	3'	TGAGGAGAGTTTTCTCCA	10664	_	G G
		TGGAGAAA CT CT CCTCA			
		ACCTCTTT GA GA GGAGT			
		T _ _			
GAM2074 FRK	5'	AGCCGGTAAGTCTCTCCAGG	10715	A	_ C
		TCTGGAGA ACT GCTG CT			
		GGACCTCT TGA TGGC GA			
		C A C			
GAM2074 GAB2	3'	GAGGCAGCATCTCCAGA	25458		AAC
		TCTGGAGA TGCTGCCTC			

AGACCTCT ACGACGGAG

GAM2074 GPC6 5' AGGCAGCAGCCTTCCCAG 20329 A A_
CTGG GAA CTGCTGCCT
||||| ||| |||||
GACC CTT GACGACGGA
_ CC

GAM2074 GUCA2B 3' TGAGGCAGCCCAGCTCCTGA 24020 T AAAC
TC GGAG GCTGCCTCA
|| ||| |||||
AG CCTC CGACGGAGT
T GACC_

GAM2074 IL8RA 3' TGAGGCAGGCACTGCCA 7153 _ AAAC _
TGG AG TGC TGCCTCA
||| || ||| |||||
ACC TC ACG ACGGAGT
G _ G

GAM2074 MADH6 5' AGGCAGGGCTTTCCAGA 19972 AA TG
TCTGGAGA C CTGCCT
||||| | |||||
AGACCTTT G GACGGA
CG _

GAM2074 MGAM 3' GGGGCAGTTTCTCCAGG 72812 G
TCTGGAGAAACTGCT CC
||||||| |||
GGACCTCTTTGACGG GG

GAM2074 MYO7A 3' GAGGCAGCAGTGGGTTTCAGG 6032 GAA
TCTGGA ACTGCTGCCTC
||||| |||||
GGA CTT TGACGACGGAG
GGG

GAM2074 NEUROD2 3' AGGAGTGCTTCTCCAGG 21592 ACT G
TCTGGAGAA GCT CCT
||||| ||| |||
GGACCTCTT TGA GGA
CG_ _

GAM2074 NPY2R 3' TGAACAGAAATTTCTCCAGG 8067 CTG CC
TCTGGAGAAA CTG TCA
||||| ||| |||
GGACCTCTTT GAC AGT
AAA A_

GAM2074 OXTR 3' TGAATAGACATTTCTCCA 8083 C _ CC
TGGAGAAA TG CTG TCA
||||| ||| |||
ACCTCTTT AC GAT AGT
_ A A_

GAM2074 PPP2R4 3' TGAGGCATGTCTTTCCAGA 61184 A TGC
TCTGGAGA AC TGCCTCA
||||| || |||||

AGACCTTT TG ACGGAGT
 C T__
 GAM2074 REV3L 5' TGAGGAAGATTTCTCTCA 12825 _ CTG G
 TG GAGAAA CT CCTCA
 || ||||| || |||||
 AC CTCTTT GA GGAGT
 T A__ A
 GAM2074 RXRA 3' TGAGGCAGCAGCCTTC 12925 AAA
 GGAG CTGCTGCCTCA
 |||| |||||
 CTTC GACGACGGAGT
 C__
 GAM2074 SURF5 3' TGAGGCAGCATTTCCTCCA 56919 A C
 TGGAG AA TGCTGCCTCA
 |||| || |||||
 ACCTC TT ACGACGGAGT
 C T
 GAM2074 VANGL2 3' TGAGACATCGGACTCTCCGGA 72095 AA C C
 TCTGGAGA CTG TG CTCA
 ||||| || || |||||
 AGGCCTCT GGC AC GAGT
 CA T A
 GAM2074 WARS 3' GAGGCAGCAGCCCTCGAGG 67865 G AAA
 TCT GAG CTGCTGCCTC
 ||| || |||||
 GGA CTC GACGACGGAG
 G CC_
 GAM2074 ZNF45 5' GACTTGGCACTTCTCCAGA 14250 AC CC
 TCTGGAGAA TGCTG TC
 ||||| |||| ||
 AGACCTCTT ACGGT AG
 C_ TC
 GAM2074 BLR1 3' TGAGGCAGGGAAGTCCCCAGG 53119 A AA_ G
 TCTGG GA CT CTGCCTCA
 |||| || || |||||
 GGACC CT GG GACGGAGT
 C GAA _
 GAM2074 C20orf150 3' TGAAGCCGAGCTCCTCCAGA 66017 AA ACT _ C
 TCTGGAG GCT GC TCA
 ||||| || || |||||
 AGACCTC CGA CG AGT
 CT__ GC A
 GAM2074 C20orf4 3' GGGCAGCAATCTCTCCAGG 31948 AAC
 TCTGGAGA TGCTGCCT
 ||||| |||||
 GGACCTCT ACGACGGG
 CTA
 GAM2074 C20orf7 3' TGAATATGCACCTTCTCCAGA 44383 AC TGCC
 TCTGGAGAA TGC TCA
 ||||| || ||

			AGACCTCTT ACG AGT		
			CC TATA		
GAM2074	C6orf26	3'	AGAAAGCAGCTTTCTCCA 48268	_	GC
			TGGAGAAA CTGCT CT		
			ACCTCTTT GACGA GA		
			C AA		
GAM2074	CASKIN1	3'	TGAGGCGGATTTCCCCAGA 40784	A	CTG
			TCTGG GAAA CTGCCTCA		
			AGACC CTTT GGCGGAGT		
			C A__		
GAM2074	CCR8	3'	TGAGGCAGATGCCTCTAGA 19041	AA	ACTG
			TCTGGAG CTGCCTCA		
			AGATCTC GACGGAGT		
			CGTA__		
GAM2074	CPGL2	5'	GAAGCCGCTTTGTTCTCCAGA 74884	ACT_	T C
			TCTGGAGAA GC GC TC		
			AGACCTCTT CG CG AG		
			GTTT C A		
GAM2074	CSRP2BP	5'	TGAAGCAGCAGTGGGACCAG 70657	AGAA	C
			CTGG ACTGCTGC TCA		
			GACC TGACGACG AGT		
			AGGG A		
GAM2074	DGKD	3'	TGAAACAACACTTTCTCCAG 60113	C C	CC
			CTGGAGAAA TG TG TCA		
			GACCTCTTT AC AC AGT		
			C A AA		
GAM2074	DKFZP434A043	3'	TGAGGTAGTAATTTCTCAGA 31823	GA	C
			TCTG GAAA TGCTGCCTCA		
			AGAC CTTT ATGATGGAGT		
			TC A		
GAM2074	DKFZP434P0111	3'	TGAGGGTGTCTTTCCAGA 67963	A T	TG
			TCTGGAGA AC GC CCTCA		
			AGACCTTT TG TG GGAGT		
			C _ _		
GAM2074	DKFZP586M1120	3'	TGAGGCAGCAGCTCCCAG 49287	A	AA
			CTGG GA CTGCTGCCTCA		
			GACC CT GACGACGGAGT		
			_ C_		
GAM2074	ERG-1	3'	TGAGACATGTTTCTCCAGG 42102	TGC	C
			TCTGGAGAAAC TG CTCA		

			GGACCTCTTTG AC GAGT		
			T__ A		
GAM2074	FASTK	3'	TGAGGCAGAAGCTCCAGG	22969	AAACTG
			TCTGGAG CTGCCTCA		
			GGACCTC GACGGAGT		
			GAA__		
GAM2074	FLJ14855	5'	GGTCCCAGTTTTCCAGA	53766	A CT_
			TCTGGAGAA CTG GCC		
			AGACCTTTT GAC TGG		
			_ CCT		
GAM2074	FLJ20249	3'	TGAGGAGTCCCTCCCAGA	80223	A AACT G
			TCTGG GA GCT CCTCA		
			AGACC CT TGA GGAGT		
			_ CCC_ _		
GAM2074	FLJ20730	3'	TGAAGAAGCAGTTTCTCAGA	36053	G GCC
			TCTG AGAAACTGCT TCA		
			AGAC TCTTTGACGA AGT		
			_ AGA		
GAM2074	FLJ21007	5'	TGAAGCTTGACACAAGCTCTCCA	48648	AAC__ T_ C
			GA TCTGGAGA TGC GC TCA		
			AGACCTCT ACG CG AGT		
			CGAAC TT A		
GAM2074	GPT2	3'	TGAGGCAGCAGCCTCTA	56772	AAA
			TGGAG CTGCTGCCTCA		
			ATCTC GACGACGGAGT		
			C__		
GAM2074	KIAA0542	3'	GGGGCAGCTCCTCCAGG	66665	AAACT
			TCTGGAG GCTGCCTC		
			GGACCTC CGACGGGG		
			CT__		
GAM2074	KIAA0652	3'	TGAGGCAGCAATCTTTGG	29125	TG AAC
			C GAGA TGCTGCCTCA		
			G TTCT ACGACGGAGT		
			GT A__		
GAM2074	KIAA1030	3'	GAGGCAGCAGTGAGCCGAGA	94981	_ AGAA
			TCT GG ACTGCTGCCTC		
			AGA CC TGACGACGGAG		
			G GAG_		
GAM2074	KIAA1086	3'	TGAGGCAGGGGGTCCCCA	71291	A AA G
			TGG GA CT CTGCCTCA		

	ACC CT GG GACGGAGT	
	C GG _	
GAM2074 KIAA1322	3' TGAGATAGTTTTTCCAGA 73118	CTGC
	TCTGGAGAACTG CTCA	
	AGACCTTTTGTAT GAGT	
	A__	
GAM2074 KIAA1634	3' GCATCAGTCTCTTCTCCAGA 64124	__ C
	TCTGGAGAA ACTG TGC	
	AGACCTCTT TGAC ACG	
	CTC T	
GAM2074 KIAA1638	3' TGAAACAACGGTGACCTCTCCA 47824	A__ C CC
	GG TCTGGAGA ACTG TG TCA	
	GGACCTCT TGGC AC AGT	
	CCAG A AA	
GAM2074 KIAA1771	5' GGGTTACCAGACCTCTCCAGA 79866	AA_ CT_
	TCTGGAGA CTG GCCT	
	AGACCTCT GAC TGGG	
	CCA CAT	
GAM2074 KIAA1894	3' GAGGCAACCTTTGCCTTCTTCA 74285	ACT _____
	GA TCTGGAGAA GC TGCCTC	
	AGACTTCTT CG ACGGAG	
	C__ TTTCCA	
GAM2074 KIAA1937	3' GAGGCAGTGTCCCCCAGG 74071	AGAA T
	TCTGG AC GCTGCCTC	
	GGACC TG TGACGGAG	
	CCC_ _	
GAM2074 KIAA1985	3' TGA AAAAGCACTTTCTCCA 45018	C GCC
	TGGAGAAA TGCT TCA	
	ACCTCTTT ACGA AGT	
	C AA_	
GAM2074 LCHN	3' TGAGATGCTTTTCTCCAGA 87480	CT TGC
	TCTGGAGAAA GC CTCA	
	AGACCTCTTT CG GAGT	
	_ TA_	
GAM2074 MGC13007	3' CAGTTCAGTTATCTCCAGA 51277	_ _
	TCTGGAGA AACTG CTG	
	AGACCTCT TTGAC GAC	
	A TT	
GAM2074 MGC16385	5' TGAAGCAGCAGCTGGGCTAGG 59543	AGAAA C
	TCTGG CTGCTGC TCA	

		GGATC GACGACG AGT	
		GGGTC A	
GAM2074	MGC26914	3' TGAATAGACATTTCTCCA 59332	C _ CC
		TGGAGAAA TG CTG TCA	
		ACCTCTTT AC GAT AGT	
		_ A A_	
GAM2074	PPP1R13B	3' TGAGGCCCTTTCTCCAG 31660	CTGCT
		CTGGAGAAA GCCTCA	
		GACCTCTTT CGGAGT	
		CC__	
GAM2074	PSKH1	3' AGGCTCCAGCCTCTCCAGA 68791	AA CT
		TCTGGAGA CTG GCCT	
		AGACCTCT GAC CGGA	
		CC CT	
GAM2074	SPAF	3' TGAAGCGATTTCTTTTCCAGA 83521	CTGC_ C
		TCTGGAGAAA TGC TCA	
		AGACCTTTTT GCG AGT	
		CTTTA A	
GAM2074	SUN1	3' TGAGTTTCCCAGTTTCTACAGA 47926	G CTGC_
		TCTG AGAACTG CTCA	
		AGAC TCTTTGAC GAGT	
		A CCTTT	
GAM2074	USP24	3' TGAAAATGCTGTGTTCTCCAGA 92795	_ T TGCC
		TCTGGAGAA AC GC TCA	
		AGACCTCTT TG CG AGT	
		G T TAAA	
GAM2074	LOC123096	3' TGAGGCAGACACTCCAG 74654	AAAC _
		CTGGAG TG CTGCCTCA	
		GACCTC AC GACGGAGT	
		__ A	
GAM2074	LOC129831	5' TGAGACAGCAGCGGTGGCAGA 75398	GAGAA _
		TCTG ACTGCTGC CTCA	
		AGAC TGGCGACG GAGT	
		GG__ ACA	
GAM2074	LOC134637	3' TGAGAACACCTTCTCCAGG 75693	AC CTGC
		TCTGGAGAA TG CTCA	
		GGACCTCTT AC GAGT	
		CC AA__	
GAM2074	LOC146420	3' TGAACCTCCAGATTCTCCAGA 84653	A CTGCC
		TCTGGAGAA CTG TCA	

	AGACCTCTT GAC AGT	
	A CTTCA	
GAM2074 LOC147711 5'	TGAGCAGGCAAGTCTCTTCAGA 79117	A _ GC
	TCTGGAGA ACT GCT CTCA	
	AGACTTCT TGA CGG GAGT	
	C A AC	
GAM2074 LOC148753 3'	TGAGACTCCATTTTCTCCAGG 85373	C CTGC
	TCTGGAGAAA TG CTCA	
	GGACCTCTTT AC GAGT	
	T CTCA	
GAM2074 LOC150290 3'	TGAGGCAGATGGTGCCCAGA 80592	AGAA _
	TCTGG ACTG CTGCCTCA	
	AGACC TGGT GACGGAGT	
	CG_ A	
GAM2074 LOC153218 5'	TGAAATAGAACTTTTCCAGA 81658	ACTG CC
	TCTGGAGAA CTG TCA	
	AGACCTTTT GAT AGT	
	CAA_ AA	
GAM2074 LOC157570 5'	TGAGGCTTTTTCTTCAGA 82397	CTGCT
	TCTGGAGAAA GCCTCA	
	AGACTTCTTT CGGAGT	
	TT__	
GAM2074 LOC197259 5'	TGAGGCAGTGGCCTCCGGA 89304	AAA TG
	TCTGGAG C CTGCCTCA	
	AGGCCTC G GACGGAGT	
	C_ GT	
GAM2074 LOC199923 3'	TGAGTTAGCCAGTTTCTTCAGA 89879	_ C
	TCTGGAGAAACTG CTG CTCA	
	AGACTTCTTTGAC GAT GAGT	
	C T	
GAM2074 LOC200940 3'	TGAGGCAGGCGGATCTCCTGA 90398	T AA _
	TC GGAGA CTGC TGCCTCA	
	AG CCTCT GGCG ACGGAGT	
	T A_ G	
GAM2074 LOC205327 3'	AGTCAATGTTTCTCCAGA 91067	TGC C
	TCTGGAGAAAC TG CT	
	AGACCTCTTTG AC GA	
	TA_ T	
GAM2074 LOC221288 3'	TGAAGCAGCAGTATCTAGA 95264	GAA C
	TCTGGA ACTGCTGC TCA	

	AGATCT TGACGACG AGT	
	A__ A	
GAM2074 LOC253254 5'	TGAGAAGAACTTCTTCAGA 98908	ACTG GC
	TCTGGAGAA CT CTCA	
	AGACTTCTT GA GAGT	
	CAA_ A_	
GAM2074 LOC256789 3'	TGAGGCTGTACTCTCTAGA 99312	AAC T
	TCTGGAGA TGC GCCTCA	
	AGATCTCT ATG CGGAGT	
	C__ T	
GAM2074 LOC257336 5'	GGGCCCTAGTCCTCCAGA 97900	AA CT
	TCTGGAG ACTG GCCT	
	AGACCTC TGAT CGGG	
	C_ CC	
GAM2074 LOC91923 5'	AGAGTTCCAGTTTCTCCA 68169	CT _
	TGGAGAACTG GC CT	
	ACCTCTTTGAC TG GA	
	CT A	
GAM2074 LOC92876 5'	AGAGTTCCAGTTTCTCCA 71346	CT _
	TGGAGAACTG GC CT	
	ACCTCTTTGAC TG GA	
	CT A	
GAM2074 LOC93496 3'	TGAAACAGACTTACACTTCTTC 72863	ACTG____ CC
AGA	TCTGGAGAA CTG TCA	
	AGACTTCTT GAC AGT	
	CACATTCA AA	
GAM2075 ANKTM1 3'	CCACCCTTCTTGCTGTCC 24697	CC A
	GGACAGCGAGG AGG TGG	
	CCTGTCGTTCT TCC ACC	
	_ C	
GAM2075 ATP1A2 3'	TCCATTTCCCACTTCCAC 7370	C CGA CCA
	GTGGA AG GG GGATGGA	
	CACCT TC CC TTTACCT	
	_ AC_ _	
GAM2075 B3GAT1 3'	CCACGGCCCCACTGTCCAC 38451	CGA AGGA
	GTGGACAG GGCC TGG	
	CACCTGTC CCGG ACC	
	ACC C__	
GAM2075 B3GAT1 3'	CCACGGCCCCACTGTCCAC 55051	CGA AGGA
	GTGGACAG GGCC TGG	

CACCTGTC CCGG ACC
ACC C____
GAM2075 COL1A1 3' CTCCATCCCAACCTGGCTCCC 5395 AC G CCA
GG AGC AGG GGATGGAG
|| ||| ||| |||||
CC TCG TCC CCTACCTC
C_ G AAC
GAM2075 DAAM2 3' CTCCATCCTGTCTACTAATCCA 93901 CAGCG C
C GTGGA AGGC AGGATGGAG
|||| | ||| |||||
CACCT TCTG TCCTACCTC
AATCA _
GAM2075 EGFR 3' CTCCATCCCAACAGCCATGCCC 19085 ACA A CA____
GC GTGG GCG GGC GGATGGAG
|||| ||| ||| |||||
CGCC CGT CCG CCTACCTC
_ A ACAAC
GAM2075 ELAVL3 3' CCACCCCAGGCTGGGCTGTTCA 9224 GA A_ A
C GTGGACAGC GGCC GG TGG
||||||| ||| || |||
CACTTGTCG TCGG CC ACC
GG AC C
GAM2075 ELAVL3 3' CCATCCTCCTGCCCCAC 9225 ACA G CC
GTGG GC AGG AGGATGG
|||| || ||| |||||
CACC CG TCC TCCTACC
CC_ _ _
GAM2075 EN1 3' CCACCGCCTCGCTGCC 9247 A CA A
GG CAGCGAGGC GG TGG
|| ||||| || |||
CC GTCGCTCCG CC ACC
_ _ _
GAM2075 KLHL1 5' CCCC GGCCCCGCTGTCC 40870 A A AT
GGACAGCG GGCC GG GG
|||||| ||| || ||
CCTGTGCG CCGG CC CC
C G _
GAM2075 LGI1 3' TCCATCCTTA ACTGTCCA 18735 CGAGGCC
TGGACAG AGGATGGA
||||| |||||
ACCTGTC TCCTACCT
AAT____
GAM2075 LOXL1 5' TCCTGAGAGCCTCTGTCCAC 60822 C ____
GTGGACAG GAGGC CAGGA
|||||| ||| |||
CACCTGTC CTCCG GTCCT
T AGA
GAM2075 MUC5B 3' CTCCATCCCCATGCTCTGTCCA 67398 CGA CA____
C GTGGACAG GGC GGATGGAG
|||||| ||| |||||

			CACCTGTC TCG CCTACCTC	
			____ TACC	
GAM2075 NXF5	3'	TCCATCCCAGTGTCCAC	53090	G GAGGCCA
		GTGGACA C	GGATGGA	
		CACCTGT G	CCTACCT	
		_ AC _		
GAM2075 NXF5	3'	TCCATCCCAGTGTCCAC	53690	G GAGGCCA
		GTGGACA C	GGATGGA	
		CACCTGT G	CCTACCT	
		_ AC _		
GAM2075 NXF5	3'	TCCATCCCAGTGTCCAC	53693	G GAGGCCA
		GTGGACA C	GGATGGA	
		CACCTGT G	CCTACCT	
		_ AC _		
GAM2075 NXF5	3'	TCCATCCCAGTGTCCAC	53695	G GAGGCCA
		GTGGACA C	GGATGGA	
		CACCTGT G	CCTACCT	
		_ AC _		
GAM2075 NXF5	3'	TCCATCCCAGTGTCCAC	53697	G GAGGCCA
		GTGGACA C	GGATGGA	
		CACCTGT G	CCTACCT	
		_ AC _		
GAM2075 PDE4A	3'	CCATCCTGGCCGCACCCC	21679	ACA GA
		GG GC GGCCAGGATGG		
		CC CG CCGGTCCTACC		
		CCA _		
GAM2075 PTPN1	3'	CTCCACCTCCACCCACTGTCCG	12577	CGA CC_ A
C		GTGGACAG GG AGG TGGAG		
		CGCCTGTC CC TCC ACCTC		
		AC_ ACC _		
GAM2075 SARDH	3'	CCATCCCATGCTGTCCAT	24017	A CCAG
		GTGGACAGCG GG GATGG		
		TACCTGTCGT CC CTACC		
		A _		
GAM2075 SF3B3	3'	CCACCACCATCACTGCCAC	25783	A C _ CCA A
		GTGG CAG GA GG GG TGG		
		CACC GTC CT CC CC ACC		
		_ A A A _		
GAM2075 SLC20A2	3'	TCCATCCCACACTGTTCAC	23120	CGAGGCCA
		GTGGACAG GGATGGA		

		CACTTGTC	CCTACCT		
		ACAC_____			
GAM2075	SLC9A3R2	3'	CCATCCTGCCCTGCCAC	62099	A CGA C
			GTGG CAG GGC AGGATGG		
			CACC GTC CCG TCCTACC		
			C C_ _		
GAM2075	SOST	3'	CCCCTTGACCTCGCTGCCCAT	48223	A C_ AT
			GTGG CAGCGAGG CAGG GG		
			TACC GTCGCTCC GTTC CC		
			C AC C_		
GAM2075	SOX13	3'	CTCCATCCTCAAAGCCCCAC	20279	ACA GAGGCC
			GTGG GC AGGATGGAG		
			CACC CG TCCTACCTC		
			CC_ AAAC_		
GAM2075	SURF5	3'	CCGCAGGCCTCCTGTCCAC	23124	C AGGA
			GTGGACAG GAGGCC TGG		
			CACCTGTC CTCCGG GCC		
			_ AC_		
GAM2075	SYNGR1	3'	CCATCCTGGGCCCCAC	17498	ACAGCGA _
			GTGG GGCC AGGATGG		
			CACC CCGG TCCTACC		
			C_____ G		
GAM2075	WNT5A	5'	CCCCGGGGCCTCGCCCCCAC	14119	ACA A_ AT
			GTGG GCGAGGCC GG GG		
			CACC CGCTCCGG CC CC		
			CCC GG _		
GAM2075	ARTN	5'	CCCAGCCCTCGCTGCCAC	55113	A _ CA
			GTGG CAGCGAGG C GG		
			CACC GTCGCTCC G CC		
			_ C AC		
GAM2075	ATPW	5'	CTCCATCCCGGCCCCAGCCCA	32258	ACA GA_ A
			TGG GC GGCC GGATGGAG		
			ACC CG CCGG CCTACCTC		
			_ ACC C		
GAM2075	C22orf4	3'	CCGCAGCTGGCCTCACTGTCC	61270	C GA_
			GGACAG GAGGCCAG TGG		
			CCTGTC CTCCGGTC GCC		
			A GAC		
GAM2075	C5orf4	3'	CCATCCTGGCCTCCTCTC	33426	C C
			GA AG GAGGCCAGGATGG		

		CT TC CTCCGGTCCTACC	
		C _	
GAM2075	C5orf4	3' CCATCCTGGCCTCCTCTC	51488 C C
		GA AG GAGGCCAGGATGG	
		CT TC CTCCGGTCCTACC	
		C _	
GAM2075	C8orf14	5' TTTCATTAGCCTGGCTGTCCAC	55083 G CAG
		GTGGACAGC AGGC GATGGAG	
		CACCTGTCG TCCG TTACTTT	
		G A__	
GAM2075	DKFZp547H236	5' CCTGGCCTCCTGCCCAC	79245 A C
		GTGG CAG GAGGCCAGG	
		CACC GTC CTCCGGTCC	
		C _	
GAM2075	FLJ10292	3' TCCATCCCCACTATCTAC	36434 C CGA CCA
		GTGGA AG GG GGATGGA	
		CATCT TC CC CCTACCT	
		A A__ __	
GAM2075	FLJ21977	3' TCCATCCTAGCCCCAC	50875 ACAGCGA C
		GTGG GGC AGGATGGA	
		CACC CCG TCCTACCT	
		C_____ A	
GAM2075	FLJ22471	3' CCACCCCGCGCTGTCCAT	47859 A CCA A
		GTGGACAGCG GG GG TGG	
		TACCTGTCGC CC CC ACC	
		G ____ _	
GAM2075	JAM1	3' CTCCATCTACCACCATCCAC	34225 CAGCGA CCA
		GTGGA GG GGATGGAG	
		CACCT CC TCTACCTC	
		ACCA__ A__	
GAM2075	JAM1	3' CTCCATCTACCACCATCCAC	58514 CAGCGA CCA
		GTGGA GG GGATGGAG	
		CACCT CC TCTACCTC	
		ACCA__ A__	
GAM2075	JAM1	3' CTCCATCTACCACCATCCAC	58542 CAGCGA CCA
		GTGGA GG GGATGGAG	
		CACCT CC TCTACCTC	
		ACCA__ A__	
GAM2075	JAM1	3' CTCCATCTACCACCATCCAC	58570 CAGCGA CCA
		GTGGA GG GGATGGAG	

CACCT CC TCTACCTC
ACCA__ A__
GAM2075 KIAA0523 5' CCTGGCCTCACTCCCAC 68356 AC C
GTGG AG GAGGCCAGG
|||| || |||||
CACC TC CTCCGGTCC
C_ A
GAM2075 KIAA0544 3' CCACGGCCTCGCCACCAC 71459 ACA AGGA
GTGG GCGAGGCC TGG
|||| ||||| ||
CACC CGCTCCGG ACC
AC_ C__
GAM2075 KIAA1029 3' CTCCATCCCAGTTCAGACTGTC 24426 CGA_ CA
CA TGGACAG GGC GGATGGAG
||||| || |||||
ACCTGTC TTG CCTACCTC
AGAC AC
GAM2075 KIAA1199 3' CCACCCTAGCCCTTGCTGCCAC 72929 A _C A
GTGG CAGCGAGG C AGG TGG
|||| ||||| || ||
CACC GTCGTTCC G TCC ACC
_ C A C
GAM2075 KIAA1453 3' CCACCCCACATTGCTGTCCA 47660 GGCCA A
TGGACAGCGA GG TGG
||||||| || ||
ACCTGTCGTT CC ACC
ACAC_ C
GAM2075 MAP 3' CCACCCCCGCATGCGTCTGTCC 43366 _ AG_ CA A
AC GTGGACAG CG GC GG TGG
||||||| || || ||
CACCTGTC GC CG CC ACC
T GTA CC C
GAM2075 MGC23244 3' CCATCCTGAGACCCCGTCC 58829 AGC A C__
GGAC G GG CAGGATGG
|||| || |||||
CCTG C CC GTCCTACC
__ C AGA
GAM2075 MGC3036 3' CAGGTGGCCTCGCTGCC 43981 A GGA
GG CAGCGAGGCCA TG
|| ||||| ||
CC GTCGCTCCGGT AC
_ GG_
GAM2075 moblak 3' CTCCACCCTCACTCCATCCAC 56397 CAGC GCC A
GTGGA GAG AGG TGGAG
|||| || || |||||
CACCT CTC TCC ACCTC
AC__ AC_ C
GAM2075 NUDE1 5' CCGCGTTGGCCTCGCCGCC 35053 ACA GA
GG GCGAGGCCAG TGG
|| ||||| ||

CC CGCTCCGGTT GCC
 GC_ GC
 GAM2075 PTPRN2 3' TCCATCCCGCCCTTCCCAC 56446 AC CGA CA
 GTGG AG GGC GGATGGA
 |||| || ||| |||||
 CACC TC CCG CCTACCT
 CT _ C_
 GAM2075 PTPRN2 3' TCCATCCCGCCCTTCCCAC 56447 AC CGA CA
 GTGG AG GGC GGATGGA
 |||| || ||| |||||
 CACC TC CCG CCTACCT
 CT _ C_
 GAM2075 SCYA22 3' CTCCATCCCTGTGGCTGTC 92590 GAG CA
 GACAGC GC GGATGGAG
 ||||| || |||||
 CTGTCTG TG CCTACCTC
 G_ TC
 GAM2075 UBP1 3' CTCCATCTCTGACCACCCCCAC 27991 ACAGCGA C _
 GTGG GG CAG GATGGAG
 ||| ||| |||||
 CACC CC GTC CTACCTC
 CCCA_ A T
 GAM2075 LOC115129 3' CCAGTTCCCCTCCATCCAC 73613 CAGC CCA _
 GTGGA GAGG GGA TGG
 |||| ||| ||| |||
 CACCT CTCC CCT ACC
 AC_ _ TG
 GAM2075 LOC116113 3' CTCCACCCCTCCTCCATCCAC 93836 CAGC CCA A
 GTGGA GAGG GG TGGAG
 |||| ||| |||||
 CACCT CTCC CC ACCTC
 AC_ TC_ C
 GAM2075 LOC148760 3' CTCCATCCCAACCCCTGCACCA 85363 ACA A CCA_
 C GTGG GCG GG GGATGGAG
 ||| ||| || |||||
 CACC CGT CC CCTACCTC
 A_ C CAAC
 GAM2075 LOC150848 5' CCATTCCCCTTCCAC 86318 C CGA CCA
 GTGGA AG GG GGATGG
 ||||| || || |||||
 CACCT TC CC CTTACC
 _ A_ _
 GAM2075 LOC152897 5' CCATCCTGGCTGCTGATCCA 81604 _ GA
 TGGA CAGC GGCCAGGATGG
 ||| ||| |||||
 ACCT GTCG TCGGTCCTACC
 A _
 GAM2075 LOC153577 5' CTCCATCTGTTCTCCACCTAC 87237 AC C_ GC G
 CCAC GTGG AG GAG CAG ATGGAG
 |||| || ||| ||| |||||

	CACC TC CTC GTC TACCTC		
	CA CACC TT _		
GAM2075 LOC157349 3'	CCATCCCGTTCTGTCC 82331	CGA CA	
	GGACAG GGC GGATGG		
	CCTGTC TTG CCTACC		
	_ C _		
GAM2075 LOC197342 3'	CTCCAGCCTGGCCTCACTGTCC 89363	C A	
	GGACAG GAGGCCAGG TGGAG		
	CCTGTC CTCCGGTCC ACCTC		
	A G		
GAM2075 LOC221466 3'	CTCCACCCCAGCCTCTGTTCCC 95313	AC _ CA A	
CAT	GTGG AGC GAGGC GG TGGAG		
	TACC TTG CTCCG CC ACCTC		
	CC T AC C		
GAM2075 LOC221543 5'	CTTCGGTAACCTCACTGTCTAC 95376	C CCAGGA	
	GTGGACAG GAGG TGGAG		
	CATCTGTC CTCC GCTTC		
	A AATG_		
GAM2075 LOC256866 5'	CTTGGCCTCACCGTCTAC 98013	AGC	
	GTGGAC GAGGCCAGG		
	CATCTG CTCCGGTTC		
	CCA		
GAM2075 LOC257490 5'	CCACCCCAGGTGTCCTGTCCAT 99559	C G A_ A	
	GTGGACAG GA GCC GG TGG		
	TACCTGTC CT TGG CC ACC		
	_ G AC C		
GAM2075 LOC257596 5'	CTTCGGTAACCTCACTGTCTAC 99779	C CCAGGA	
	GTGGACAG GAGG TGGAG		
	CATCTGTC CTCC GCTTC		
	A AATG_		
GAM2075 LOC58512 3'	CTCCATCCTCAGCCCTCTGCCC 65283	A CGA C_	
AC	GTGG CAG GGC AGGATGGAG		
	CACC GTC CCG TCCTACCTC		
	C TC_ AC		
GAM2075 LOC90522 3'	CTCCATCCCATGTCCCGCCCA 63854	ACA A CA_	
	TGG GCG GGC GGATGGAG		
	ACC CGC CTG CCTACCTC		
	_ C TAC		
GAM2075 LOC90784 5'	CTCCACCCCACCTCCGTCCA 64695	AGC CCA A	
	TGGAC GAGG GG TGGAG		

ACCTG CTTC CC ACCTC
 C__ AC_ C
 GAM2075 LOC92979 3' CATTGTCTGGCCTCACTGCCCA 57252 A C ____
 C GTGG CAG GAGGCCAG GATG
 |||| || |||| ||||
 CACC GTC CTCCGGTC TTAC
 C A TG
 GAM2076 ELF3 3' TGACCTTGACCTTGACCAA 16685 T GAT AAA
 TTGGT CAAGG GG GTCA
 |||| |||| || ||||
 AACCA GTTCC TC CAGT
 _ AGT ____
 GAM2076 JAK2 3' TGACCTTCATTCTGAGACCAA 18318 CAA AA
 TTGGTT GGGATGGA GTCA
 |||| |||| |||| ||||
 AACCAG TCTTACTT CAGT
 AG_ C_
 GAM2076 SLC10A2 5' ACTCTCTGTCTTGACCAA 6590 CAA A
 TTGGTT GGGATGGA AGT
 |||| |||| |||| ||||
 AACCAG TTCTGTCT TCA
 ____ C
 GAM2076 FLJ10803 3' GTGACTTTCAGTTAAAGCCAA 37205 CAAGG G
 TTGGTT GAT GAAAGTCAC
 |||| || |||| |||| ||||
 AACCGA TTG CTTTCAGTG
 AA__ A
 GAM2076 KIAA1958 5' GTGACTTTGAACCCCAAACC 82788 CAA ATGG
 GGTT GGG AAAGTCAC
 |||| || |||| |||| ||||
 CCAA CCC TTTCAGTG
 A__ CAAG
 GAM2076 MARCKS 3' ACTTTCACCTGCCCCA 11411 TTCA A
 TGG AGGG TGGAAAGT
 || |||| |||| |||| ||||
 ACC TCCC ACCTTTCA
 CG__ _
 GAM2076 TUB 5' GTGGGACCATCCCTTAAACC 13898 C AAAG
 GGTT AAGGGATGG TCAC
 |||| |||| |||| |||| ||||
 CCAA TTCCCTACC GGTG
 A AG__
 GAM2076 LOC80298 3' ACTTTTACCTTGAACCA 48062 GATG
 TGGTTCAAGG GAAAGT
 |||| |||| |||| |||| ||||
 ACCAAGTTCC TTTTCA
 A__
 GAM2077 CDH12 3' CTTATCATTTAAAGTGGTGTA 15777 CCCAA GA
 TACACCACT GAA ATAAG
 |||| |||| |||| |||| ||||

ATGTGGTGA TTT TATTC
 AA__ AC
 GAM2077 GOCAP1 3' ATTGTTCTTGGGAGCAGTGTA 43007 CA G
 TACAC CTCCCAAGAA AAT
 |||| ||||| ||
 ATGTG GAGGGTTCTT TTA
 AC G
 GAM2077 DKFZp434N2435 5' CTTATTACTGTGGGGTGGT 98090 T AGAAG
 ACCAC CCCA AATAAG
 |||| || ||||
 TGGTG GGGT TTATTC
 _ GTCA_
 GAM2077 DKFZP564I122 3' CTTATTCTTCTCCCTCATGTGT 63877 CACTCCCA
 A TACAC AGAAGAATAAG
 |||| |||||
 ATGTG TCTTCTTATTC
 TACTCCC_
 GAM2077 FLJ21791 3' CTTATTTGCAGAAGTGGTGTA 62126 CCCAAGAA
 TACACCACT GAATAAG
 ||||| ||||
 ATGTGGTGA TTTATTC
 AGACG_
 GAM2077 HMP19 3' CTTATTCTTTGTTAGGAAAATG 88860 CCAC CAA_
 TA TACA TCC GAAGAATAAG
 ||| || |||||
 ATGT AGG TTTCTTATTC
 AAA_ ATTG
 GAM2077 KIAA1719 3' TCTGTCTTGGGAGTGGTGTA 68742 _
 TACACCACTCCCAAGA AGA
 ||||| |||||
 ATGTGGTGAGGGTTCT TCT
 G
 GAM2077 KIAA1853 3' TTTTCTTGGAAGCAGTG 69929 CA C
 CAC CT CCAAGAAGAA
 || |||||
 GTG GA GGTTCTTTT
 AC A
 GAM2077 KIAA1877 3' CTTATTCTTCTGCCATGAGT 66748 CCA_
 ACTC AGAAGAATAAG
 ||| |||||
 TGAG TCTTCTTATTC
 TACCG
 GAM2077 KIAA1906 3' CTTATTCTTCTTGACTTTTGG 73571 CTCC_
 CCA CAAGAAGAATAAG
 || |||||
 GGT GTTCTTCTTATTC
 TTTCA
 GAM2077 OSBPL11 3' CTTAATTTCCCAAGAGTGGTG 43206 CCAA AA
 CACCACTC GAAG TAAG
 ||||| ||| |||

		GTGGTGAG CTTT ATTC		
		AACC A_		
GAM2077	YME1L1	3' TCATTCTTGATGTGGTGTA 58438	TCC	_
		TACACCAC CAAGAA GA		
		ATGTGGTG GTTCTT CT		
		TA_ A		
GAM2077	ZNF262	3' CTTATTTTGTGGGAGT 18723	A	
		ACTCCCAAG AGAATAAG		
		TGAGGGTTT TTTTATTC		
		G		
GAM2077	LOC91960	3' TGTGGCTTGAACGTGGTGTA 68294	TC_	AAGA
		TACACCAC CCAAG ATA		
		ATGTGGTG GGTTT TGT		
		CAA GG_		
GAM2078	BCL11A	3' ATGTGATTAAACAAACAAACA 43463	GC	CA_
	A	TTGTTTG TTGTTTAA GCAT		
		AACAAAC AACAAATT TGTA		
		A_ TAG		
GAM2078	CALB1	3' TATGTATAACAAGCCAAACA 18210	TAACA	
		TGTTTGGCTTGTT GCATA		
		ACAAACCGAACAA TGTAT		
		TA_		
GAM2078	DDEF1	3' TATGCTGTTCTACAAGCAAACA 60306	G	TT
	A	TTGTTTG CTTGT AACAGCATA		
		AACAAAC GAACA TTGTCGTAT		
		_ TC		
GAM2078	SEC15L	3' TTGTGGAAACAAGCCAAAC 72730	A_	
		GTTTGGCTTGTTT ACAG		
		CAAACCGAACAAA TGTT		
		GG		
GAM2078	LOC153470	5' TATGCAGACGACAAACCAGACA 81700	C	TAACA
	A	TTGTTTG TTGTT GCATA		
		AACAGACC AACAG CGTAT		
		A CAGA_		
GAM2078	LOC221296	3' TTGTAAGCCAAGCAA 93621	GTTTA	
		TTGTTTGCTT ACAG		
		AACGAACCGAA TGTT		

GAM2079	ADAM20	5' AGCTCCACCAGGACACAGATCC 15101	TAC	GA
		GG CTGTGTCCTGG GAGCT		

CC GACACAGGACC CTCGA
 TA_ AC
 GAM2079 HIP1 3' CTCTCCCAAAGGGCACACC 19253 ACCT _
 GGT GTGTCCT GGGAGAG
 ||| ||||| |||||
 CCA CACGGGA CCCTCTC
 _ AA
 GAM2079 KCNA6 3' TCCAGGACCAAATACCT 11144 CC T
 AGGTA TG GTCCTGGG
 |||| | |||||
 TCCAT AC CAGGACCT
 AA _
 GAM2079 KCNK4 3' CTCTCCAGCGCGAGAGACC 33982 AC G C
 GGT CT TGT CTGGGAGAG
 ||| || |||||
 CCA GA GCG GACCCTCTC
 GA _ C
 GAM2079 LZTS1 3' GCTCTCCCAGTGAACCTCCT 41034 TACCTGTG _
 AGG TC CTGGGAGAGC
 ||| || |||||
 TCC AG GACCCTCTCG
 TCA_ T
 GAM2079 MUCDHL 3' CCTCCAGGGACCCT 49203 TACCT G A
 AGG GT TCCTGGGAG G
 ||| || ||||| |
 TCC CA GGGACCCTC C
 _ C
 GAM2079 MUCDHL 3' CCTCCAGGGACCCT 88639 TACCT G A
 AGG GT TCCTGGGAG G
 ||| || ||||| |
 TCC CA GGGACCCTC C
 _ C
 GAM2079 SERPINH2 3' AGCCCCTGGGACCAGGCACC 8784 A T TG AGA
 GGT CCTG GTCC GG GCT
 ||| ||| ||| || |||
 CCA GGAC CAGG CC CGA
 C _ GT C_
 GAM2079 SOX12 3' CTCTCCCAAGTGGCATAGCCC 23684 TAC _ _
 GG CTGTGTC CT GGGAGAG
 || ||||| || |||||
 CC GATACGG GA CCCTCTC
 C_ T A
 GAM2079 DKFZp762P2111 3' CTCTCCCAGCAGGGTCCT 87631 TA TGTC
 AGG CCTG CTGGGAGAG
 ||| ||| |||||
 TCC GGAC GACCCTCTC
 TG _
 GAM2079 FLJ23510 5' CCAGACACACAAGTACCT 45624 C C_
 AGGTAC TGTGT CTGG
 ||||| ||||| |||

TCCATG ACACA GACC
 A CA
 GAM2079 KIAA0057 3' CTCTCCCAGCCAGTGGTCCT 25411 T TG TC
 AGG ACC TG CTGGGAGAG
 ||| ||| || |||||
 TCC TGG AC GACCCTCTC
 _ TG C_
 GAM2079 KIAA0084 3' AGCCCTCCCAGGGCCAGGTTCC 68704 T T A
 T AGG ACCTG GTCCTGGGAG GCT
 ||| ||||| ||||| |||
 TCC TGGAC CGGGACCCTC CGA
 T _ C
 GAM2079 KIAA0872 3' CCCAGGACACAGCACCT 30748 AC
 AGGT CTGTGTCCTGGG
 ||| |||||
 TCCA GACACAGGACCC
 C_
 GAM2079 KIAA0940 3' AGCCCCTGGGTAACACAGGTCC 30530 T _ TG AGA
 T AGG ACCTGTGT CC GG GCT
 ||| ||||| || |||
 TCC TGGACACA GG CC CGA
 _ AT GT C_
 GAM2079 KIAA1297 3' AGCTCTCCCAGGCCTGAGGGTA 72626 GTGT_
 CC GGTACCT CCTGGGAGAGCT
 ||||| |||||
 CCATGGG GGACCCTCTCGA
 AGTCC
 GAM2079 KIAA1674 3' AGCACGCAAGACACAGGTACC 69328 C GGAGA
 GGTACCTGTGTC TG GCT
 ||||| || |||
 CCATGGACACAG AC CGA
 A GCA_
 GAM2079 MAFB 3' GCCCTGAGACACAGGCCCT 19591 TA CT AGA
 AGG CCTGTGTC GGG GC
 ||| ||||| ||| ||
 TCC GGACACAG TCC CG
 C_ AG _
 GAM2079 OSBPL5 3' AGCCCTCCCTCCCAGGCACC 73061 A TGTCTT A
 GGT CCTG GGGAG GCT
 ||| ||| ||||| |||
 CCA GGAC CCCTC CGA
 C CCT_ C
 GAM2079 p25 3' CTCTCCCAAATGGCTCAGCCT 23831 TAC T C_
 AGG CTG GTC TGGGAGAG
 ||| ||| ||| |||||
 TCC GAC CGG ACCCTCTC
 _ T TAAA
 GAM2079 LOC147958 5' CTCCCAGGGCACAAACC 88521 ACC
 GGT TGTGTCCTGGGAG
 ||| |||||

		CCA ACACGGGACCCTC	
		A__	
GAM2079	LOC148696 5'	AGCCCTCCAGGGATTGCAGTC 85343	TAC __ A
	CT	AGG CTGTG TCCTGGGAG GCT	
		TCC GACGT GGGACCCTC CGA	
		T__ TA C	
GAM2079	LOC149372 5'	AGCTCTCCTTCACAGACACCT 80098	AC TCCT
		AGGT CTGTG GGGAGAGCT	
		TCCA GACAC TCCTCTCGA	
		CA T__	
GAM2079	LOC220018 5'	AGCCCCCTGTGGGCACAGACAC 95026	AC T__ AGA
	C	GGT CTGTGTCC GGG GCT	
		CCA GACACGGG CCC CGA	
		CA TGT C__	
GAM2079	LOC222029 5'	TCCAGGGCACAGACACC 95693	AC
		GGT CTGTGTCCTGGGA	
		CCA GACACGGGACCCT	
		CA	
GAM2079	LOC91355 5'	AGCCCCCCCAGGCACGGTCCT 66302	T T T AGA
		AGG ACC GTG CCTGGG GCT	
		TCC TGG CAC GGACCC CGA	
		_ _ _ CCC	
GAM2080	ADAT1 3'	GCATGGTGGCGCACACCTGTAA 24918	AGG AAC
	T	ATTACAGGTGTG CAC GC	
		TAATGTCCACAC GTG CG	
		GCG GTA	
GAM2080	AICDA 3'	GCGTGGTGGCTCACGCCTGTAA 40695	G A
	T	ATTACAGGTGTGAG CAC ACGC	
		TAATGTCCGCACTC GTG TGCG	
		G G	
GAM2080	ALDH3B1 3'	CCAACGCGCGGCTCACACCTGT 93153	_____ ACAAC
	AAT	ATTACAGGTGTGAG GC G	
		TAATGTCCCACTC CG C	
		GGCG__ CAACA	
GAM2080	ATM 3'	CCAACGCGCGGCTCACGCCTGT 5293	_____ ACAAC
	AAT	ATTACAGGTGTGAG GC G	
		TAATGTCCGCACTC CG C	
		GGCG__ CAACA	
GAM2080	ATM 3'	CCAACGCGCGGCTCACGCCTGT 57132	_____ ACAAC
	AAT	ATTACAGGTGTGAG GC G	

			TAATGTCCGCACTC	CG	C	
			GGCG	CAACA		
GAM2080	ATM	3'	GCAGCTCACACCTATAAT	57145	C	_____
			ATTA AGGTGTGAG	GC		
			TAAT TCCACACTC	CG		
			A	GA		
GAM2080	BHMT2	3'	GCGAAGTGACTCACACCTGCAA	34737	A	G AA
	T		ATT CAGGTGTGAG	CAC	CGC	
			TAA GTCCACACTC	GTG	GCG	
			C	A	AA	
GAM2080	BRCA1	3'	GCATGGTGGCTCACGCCTGTAA	24447		G AAC
	T		ATTACAGGTGTGAG	CAC	GC	
			TAATGTCCGCACTC	GTG	CG	
			G	GTA		
GAM2080	BRCA1	3'	GCATGGTGGCTCACGCCTGTAA	24459		G AAC
	T		ATTACAGGTGTGAG	CAC	GC	
			TAATGTCCGCACTC	GTG	CG	
			G	GTA		
GAM2080	BRCA1	3'	GCATGGTGGCTCACGCCTGTAA	24470		G AAC
	T		ATTACAGGTGTGAG	CAC	GC	
			TAATGTCCGCACTC	GTG	CG	
			G	GTA		
GAM2080	BRCA1	3'	GCATGGTGGCTCACGCCTGTAA	24479		G AAC
	T		ATTACAGGTGTGAG	CAC	GC	
			TAATGTCCGCACTC	GTG	CG	
			G	GTA		
GAM2080	BRCA1	3'	GCATGGTGGCTCACGCCTGTAA	24487		G AAC
	T		ATTACAGGTGTGAG	CAC	GC	
			TAATGTCCGCACTC	GTG	CG	
			G	GTA		
GAM2080	BRCA1	3'	GCATGGTGGCTCACGCCTGTAA	24495		G AAC
	T		ATTACAGGTGTGAG	CAC	GC	
			TAATGTCCGCACTC	GTG	CG	
			G	GTA		
GAM2080	BRCA1	3'	GCATGGTGGCTCACGCCTGTAA	24504		G AAC
	T		ATTACAGGTGTGAG	CAC	GC	
			TAATGTCCGCACTC	GTG	CG	
			G	GTA		
GAM2080	BRCA1	3'	GCATGGTGGCTCACGCCTGTAA	24514		G AAC
	T		ATTACAGGTGTGAG	CAC	GC	

			TAATGTCCGCACTC GTG CG	
			G GTA	
GAM2080	BRCA1	3'	GCATGGTGGCTCACGCCTGTAA 24522	G AAC
	T		ATTACAGGTGTGAG CAC GC	
			TAATGTCCGCACTC GTG CG	
			G GTA	
GAM2080	BRCA1	3'	GCATGGTGGCTCACGCCTGTAA 24530	G AAC
	T		ATTACAGGTGTGAG CAC GC	
			TAATGTCCGCACTC GTG CG	
			G GTA	
GAM2080	BRCA1	3'	GCATGGTGGCTCACGCCTGTAA 24566	G AAC
	T		ATTACAGGTGTGAG CAC GC	
			TAATGTCCGCACTC GTG CG	
			G GTA	
GAM2080	C1orf1	3'	GCGGTGGCTTACACCTGTAAT 8679	G AA
			ATTACAGGTGTGAG CAC CGC	
			TAATGTCCACATTC GTG GCG	
			G _	
GAM2080	C21orf5	3'	GCGGTGGCTCACACCTGTAAT 18885	G AA
			ATTACAGGTGTGAG CAC CGC	
			TAATGTCCCACTC GTG GCG	
			G _	
GAM2080	C5R1	3'	GTGGCTCACGCCTGTAAT 9975	G
			ATTACAGGTGTGAG CAC	
			TAATGTCCGCACTC GTG	
			G	
GAM2080	CASP6	3'	GCGTGGTTACTCACACCTGTAA 8733	GC A
	T		ATTACAGGTGTGAG AC ACGC	
			TAATGTCCCACTC TG TGCG	
			AT G	
GAM2080	CASP6	3'	GCGTGGTTACTCACACCTGTAA 53364	GC A
	T		ATTACAGGTGTGAG AC ACGC	
			TAATGTCCCACTC TG TGCG	
			AT G	
GAM2080	CHRNA5	3'	GCACGGTGGCTCACACCTGTAA 60466	G AAC
	T		ATTACAGGTGTGAG CAC GC	
			TAATGTCCCACTC GTG CG	
			G GCA	
GAM2080	COG7	3'	GTGGCTCACGCCTGTAAT 68258	G
			ATTACAGGTGTGAG CAC	

			TAATGTCCGCACTC GTG		
			G		
GAM2080	CORO2A	3'	GCGCAGTGGCTCACGCCTGTAA 54496	G	AA
	TT		AATTACAGGTGTGAG CAC CGC		
			TTAATGTCCGCACTC GTG GCG		
			G AC		
GAM2080	CORO2A	3'	GCGCAGTGGCTCACGCCTGTAA 14103	G	AA
	TT		AATTACAGGTGTGAG CAC CGC		
			TTAATGTCCGCACTC GTG GCG		
			G AC		
GAM2080	CPM	3'	GTGGCTCACACCTTGTAAT 60410	G	
			ATTACA GGTGTGAG CAC		
			TAATGT CCACACTC GTG		
			T G		
GAM2080	CRACC	3'	GCATGGTGGCTCACACCTGTAA 41312	G	AAC
	T		ATTACAGGTGTGAG CAC GC		
			TAATGTCCACACTC GTG CG		
			G GTA		
GAM2080	CRSP9	3'	GTGGCTCACACTTATAAT 16226	C	G
			ATTA AGGTGTGAG CAC		
			TAAT TTCACACTC GTG		
			A G		
GAM2080	CTMP	3'	GCGCTGTGGCTCACACCTGTAA 54951	G	A
	T		ATTACAGGTGTGAG CACA CGC		
			TAATGTCCACACTC GTGT GCG		
			G C		
GAM2080	CTSS	3'	GCACGGTGGCTCACGCCTGTAA 15819	G	AAC
	T		ATTACAGGTGTGAG CAC GC		
			TAATGTCCGCACTC GTG CG		
			G GCA		
GAM2080	CYP3A4	3'	GTGGCTCACGCCTGTAA 34365	G	
			ATTACAGGTGTGAG CAC		
			TAATGTCCGCACTC GTG		
			G		
GAM2080	CYP4F3	3'	GCACGGTAGCTCACACCTGTAA 8010	GC	AAC
	T		ATTACAGGTGTGAG AC GC		
			TAATGTCCACACTC TG CG		
			GA GCA		
GAM2080	DBT	3'	GCATGGTGGCTCACGCCTGTAA 10375	G	AAC
	T		ATTACAGGTGTGAG CAC GC		

			TAATGTCCGCACTC GTG CG		
			G GTA		
GAM2080	DFFA	3'	GCGCAGTGGCTCACGCCTGTAA 16595	G	AA
	T		ATTACAGGTGTGAG CAC CGC		
			TAATGTCCGCACTC GTG GCG		
			G AC		
GAM2080	DHFR	3'	GCATTGTGGCGCACACCTGTA 7650	AGG	C
			TACAGGTGTG CACAA GC		
			ATGTCCACAC GTGTT CG		
			GCG A		
GAM2080	DHFR	3'	GTGGCTCACACCTGTAAT 7654	G	
			ATTACAGGTGTGAG CAC		
			TAATGTCCCACTC GTG		
			G		
GAM2080	DMC1	3'	GCGTGGTGGCTCACACCTGTAA 23945	G	A
	T		ATTACAGGTGTGAG CAC ACGC		
			TAATGTCCCACTC GTG TGCG		
			G G		
GAM2080	EFG2	5'	GCATGGTGGCTCACGCCTGTAA 51482	G	AAC
	T		ATTACAGGTGTGAG CAC GC		
			TAATGTCCGCACTC GTG CG		
			G GTA		
GAM2080	EGFL5	3'	GCGGTGGCTCACGCCTGTAAT 87915	G	AA
			ATTACAGGTGTGAG CAC CGC		
			TAATGTCCGCACTC GTG GCG		
			G		
GAM2080	EHHADH	3'	GTGGCTCACACCTGTAAT 10501	G	
			ATTACAGGTGTGAG CAC		
			TAATGTCCCACTC GTG		
			G		
GAM2080	F2R	3'	GCGCGGTGGCTCACGCCTGTAA 10570	G	AA
	T		ATTACAGGTGTGAG CAC CGC		
			TAATGTCCGCACTC GTG GCG		
			G GC		
GAM2080	F2RL3	3'	GCGGCTCACACCTGCAAT 15518	A	_____
			ATT CAGGTGTGAG GC		
			TAA GTCCCACTC CG		
			C GG_____		
GAM2080	F2RL3	3'	GTGGCTCACGCCTATAAT 15524	C	G
			ATTA AGGTGTGAG CAC		

			TAAT TCCGCACTC GTG		
			A G		
GAM2080	FANCC	3'	GTGGCTCACACCTGTGAT 71048	G	
			ATTACAGGTGTGAG CAC		
			TAGTGTCCCACTC GTG		
			G		
GAM2080	FANCD2	3'	GCGGTGGCTCACACCTGTAAT 53530	G AA	
			ATTACAGGTGTGAG CAC CGC		
			TAATGTCCCACTC GTG GCG		
			G _		
GAM2080	FCMD	3'	GTGGCTCACACCTGTAAT 23043	G	
			ATTACAGGTGTGAG CAC		
			TAATGTCCCACTC GTG		
			G		
GAM2080	FKRP	3'	GCGGGGGCTCACGCCTGTAAT 44437	G ACAA	
			ATTACAGGTGTGAG C CGC		
			TAATGTCCGCACTC G GCG		
			GGG		
GAM2080	FUT3	3'	GCGCTGTGGCTCACGCCTGTAA 5623	G A	
	TT		AATTACAGGTGTGAG CACA CGC		
			TTAATGTCCGCACTC GTGT GCG		
			G C		
GAM2080	FUT6	3'	GCGGTGGCTCACACCTGTAAT 5640	G AA	
			ATTACAGGTGTGAG CAC CGC		
			TAATGTCCCACTC GTG GCG		
			G _		
GAM2080	GAS7	3'	GCACGGTGGCTCACGCCTGTAA 20851	G AAC	
	T		ATTACAGGTGTGAG CAC GC		
			TAATGTCCGCACTC GTG CG		
			G GCA		
GAM2080	GNE	3'	GTGGCTCACGCCTGTAAT 19678	G	
			ATTACAGGTGTGAG CAC		
			TAATGTCCGCACTC GTG		
			G		
GAM2080	GRAF	3'	GTGGCTCACGCCTATAAT 31245	C G	
			ATTA AGGTGTGAG CAC		
			TAAT TCCGCACTC GTG		
			A G		
GAM2080	GRM6	3'	GCATGGTGGCTCACACCTGTAA 7767	G AAC	
	T		ATTACAGGTGTGAG CAC GC		

		TAATGTCCCACTC GTG CG	
		G GTA	
GAM2080 HFE	3'	GCACGGTGGCTCACGCCTGTAA 6399	G AAC
T		ATTACAGGTGTGAG CAC GC	
		TAATGTCCGCACTC GTG CG	
		G GCA	
GAM2080 HIP1	3'	GTGGCTCACGCCTGTAAT 19263	G
		ATTACAGGTGTGAG CAC	
		TAATGTCCGCACTC GTG	
		G	
GAM2080 HUNK	3'	GCGGCTCACACCTGTAAT 28186	_____
		ATTACAGGTGTGAG GC	
		TAATGTCCCACTC CG	
		GG_____	
GAM2080 IFNAR1	3'	GCACGGTGGCTCACACCTGTAA 7140	G AAC
T		ATTACAGGTGTGAG CAC GC	
		TAATGTCCCACTC GTG CG	
		G GCA	
GAM2080 IL10	3'	GCGCGGTGGCTCACGCCTGTAA 6927	G AA
T		ATTACAGGTGTGAG CAC CGC	
		TAATGTCCGCACTC GTG GCG	
		G GC	
GAM2080 IL11	3'	GCATGGTGGCTCACGCCTGTAA 7186	G AAC
T		ATTACAGGTGTGAG CAC GC	
		TAATGTCCGCACTC GTG CG	
		G GTA	
GAM2080 IL17R	3'	GCACGGTGGCTCACGCCTGTAA 27556	G AAC
T		ATTACAGGTGTGAG CAC GC	
		TAATGTCCGCACTC GTG CG	
		G GCA	
GAM2080 IL18	3'	GCGCAGTGGCTCACGCCTGTAA 9594	G AA
T		ATTACAGGTGTGAG CAC CGC	
		TAATGTCCGCACTC GTG GCG	
		G AC	
GAM2080 IRAK1	3'	GCGGTGGCTCACGCCTGTAAT 9613	G AA
		ATTACAGGTGTGAG CAC CGC	
		TAATGTCCGCACTC GTG GCG	
		G _	
GAM2080 ITCH	3'	GCATGGTGGCTCATACCTGTAA 49754	G AAC
T		ATTACAGGTGTGAG CAC GC	

		TAATGTCCATACTC GTG CG	
		G GTA	
GAM2080 JRK	3'	GTGGCTCACGCCTGTAAT 87833	G
		ATTACAGGTGTGAG CAC	
		TAATGTCCGCACTC GTG	
		G	
GAM2080 KAI1	3'	GCGCGGTGCTCACGCCTGTAAT 11125	G AA
		ATTACAGGTGTGAG CAC CGC	
		TAATGTCCGCACTC GTG GCG	
		GC	
GAM2080 KIF1B	3'	GTGGCTCACGCCTGTAAT 31270	G
		ATTACAGGTGTGAG CAC	
		TAATGTCCGCACTC GTG	
		G	
GAM2080 KLF8	5'	GCGGCTCACACCTGTAAT 24373	_____
		ATTACAGGTGTGAG GC	
		TAATGTCCACACTC CG	
		GG_____	
GAM2080 LAMP2	3'	CCAACGCGCGGCTCACGCCTGT 26569	_____ ACAAC
AAT		ATTACAGGTGTGAG GC G	
		TAATGTCCGCACTC CG C	
		GGCG_____ CAACA	
GAM2080 LDLR	3'	GCAGTGGCCTCACGCCTGTAAT 6737	A AC
		ATTACAGGTGTGAGGC CA GC	
		TAATGTCCGCACTCCG GT CG	
		GA	
GAM2080 LDLR	3'	GTGCCTCACGCCTGTAAT 6742	
		ATTACAGGTGTGAGGCAC	
		TAATGTCCGCACTCCGTG	
GAM2080 LEP	3'	GCGGTGGCTCACGCCTGTAAT 5864	G AA
		ATTACAGGTGTGAG CAC CGC	
		TAATGTCCGCACTC GTG GCG	
		G	
GAM2080 LILRB1	3'	GCACGGTGGCTCACGCCTGTAA 22873	G AAC
TT		AATTACAGGTGTGAG CAC GC	
		TTAATGTCCGCACTC GTG CG	
		G GCA	
GAM2080 LRRC2	3'	GCACGGTGGCTCACACCTATAA 44748	C G AAC
T		ATTA AGGTGTGAG CAC GC	

		TAAT TCCCACTC GTG CG		
		A G GCA		
GAM2080 LRRC2	3'	GCGCGGTGACTCACGCCTATAA 44750	C	G AA
T		ATTA AGGTGTGAG CAC CGC		
		TAAT TCCGCACTC GTG GCG		
		A A GC		
GAM2080 LRRC2	3'	GCGGCTCACACCTGTAAT 44751	_____	
		ATTACAGGTGTGAG GC		
		TAATGTCCCACTC CG		
		GG_____		
GAM2080 LUZP1	3'	GCGTGGTGGCTCACACCTGTAA 54401		G A
T		ATTACAGGTGTGAG CAC ACGC		
		TAATGTCCCACTC GTG TGCG		
		G G		
GAM2080 MAFF	3'	GCGCGGTGGCTCACATCTGTAA 25581		G AA
T		ATTACAGGTGTGAG CAC CGC		
		TAATGTCTACACTC GTG GCG		
		G GC		
GAM2080 MCM4	3'	GCGCGGTGGCTCACACCTGTAA 62578		G AA
T		ATTACAGGTGTGAG CAC CGC		
		TAATGTCCCACTC GTG GCG		
		G GC		
GAM2080 MLLT4	3'	GCGCAGTGGCTCACACCTGTAA 72900		G AA
T		ATTACAGGTGTGAG CAC CGC		
		TAATGTCCCACTC GTG GCG		
		G AC		
GAM2080 MOG	3'	GCGGTGGCTCACGCCTGTAAT 11673		G AA
		ATTACAGGTGTGAG CAC CGC		
		TAATGTCCGCACTC GTG GCG		
		G _		
GAM2080 MS4A1	3'	GCGGAGGCTCACGCCTGTAAT 5549		G ACAA
		ATTACAGGTGTGAG C CGC		
		TAATGTCCGCACTC G GCG		
		_ GAG _		
GAM2080 MYO1B	3'	GCGTGGTGGCTCACACCTATAA 25245	C	G A
T		ATTA AGGTGTGAG CAC ACGC		
		TAAT TCCCACTC GTG TGCG		
		A G G		
GAM2080 MYO1C	3'	GCATGGTGGCTCACGCCTGTAA 61864		G AAC
		TTACAGGTGTGAG CAC GC		

		AATGTCCGCACTC GTG CG	
		G GTA	
GAM2080 NFKBIL2	3'	GCGCGGTGGCTCACGCCTGTAA 26452	G AA
T		ATTACAGGTGTGAG CAC CGC	
		TAATGTCCGCACTC GTG GCG	
		G GC	
GAM2080 NPHP1	3'	GCGCGGTGGCTCACGCCTGTAA 63145	G AA
T		ATTACAGGTGTGAG CAC CGC	
		TAATGTCCGCACTC GTG GCG	
		G GC	
GAM2080 NPHS1	3'	GCGGTGACTCACGCCTATAAT 17372	C G AA
		ATTA AGGTGTGAG CAC CGC	
		TAAT TCCGCACTC GTG GCG	
		A A _	
GAM2080 NT5C2	3'	CCAACGCGCGGCTCACGCCTGT 25258	_____ ACAAC
AAT		ATTACAGGTGTGAG GC G	
		TAATGTCCGCACTC CG C	
		GGCG_ CAACA	
GAM2080 NUP62	3'	GCGCAGTGGCTACCCCTGTAA 33785	T G AA
T		ATTACAGG GTGAG CAC CGC	
		TAATGTCC CACTC GTG GCG	
		C G AC	
GAM2080 OASL	3'	CGTGGTAGCTCACACCTGTAAT 14955	GC A
		ATTACAGGTGTGAG AC ACG	
		TAATGTCCCACTC TG TGC	
		GA G	
GAM2080 OPA3	3'	GCGGTGGCTCACGCCTGTAAT 47846	G AA
		ATTACAGGTGTGAG CAC CGC	
		TAATGTCCGCACTC GTG GCG	
		G _	
GAM2080 PA2G4	3'	GCGCGGTGGCTCACGCCTGTAA 71829	G AA
T		ATTACAGGTGTGAG CAC CGC	
		TAATGTCCGCACTC GTG GCG	
		G GC	
GAM2080 PCDH11X	3'	GCGCGGTGGCTCACGCCTGTAA 53129	G AA
T		ATTACAGGTGTGAG CAC CGC	
		TAATGTCCGCACTC GTG GCG	
		G GC	
GAM2080 PCDH11X	3'	GCGGCTCACACCTGTAAT 53130	_____
		ATTACAGGTGTGAG GC	

		TAATGTCCCACTC CG	
		GG__	
GAM2080	PCDH11Y 3'	GCGCGGTGGCTCACGCCTGTAA 53163	G AA
	TT	AATTACAGGTGTGAG CAC CGC	
		TTAATGTCCGCACTC GTG GCG	
		G GC	
GAM2080	PCDH11Y 3'	GCGCGGTGGCTCACGCCTGTAA 53182	G AA
	TT	AATTACAGGTGTGAG CAC CGC	
		TTAATGTCCGCACTC GTG GCG	
		G GC	
GAM2080	PKD2 3'	CCAACGCACGGCTCACGCCTGT 60717	_____ ACAAC
	AAT	ATTACAGGTGTGAG GC G	
		TAATGTCCGCACTC CG C	
		GGCA__ CAACA	
GAM2080	PSMB9 3'	GCACGGTGGCTCACGCCTGTAA 12504	G AAC
	T	ATTACAGGTGTGAG CAC GC	
		TAATGTCCGCACTC GTG CG	
		G GCA	
GAM2080	PSMB9 3'	GCGGTGGCTCACACCTATAAT 12506 C	G AA
		ATTA AGGTGTGAG CAC CGC	
		TAAT TCCCACTC GTG GCG	
		A G _	
GAM2080	PTAFR 3'	GCGCAGTGGCTCACACCTGTAA 8166	G AA
	T	ATTACAGGTGTGAG CAC CGC	
		TAATGTCCCACTC GTG GCG	
		G AC	
GAM2080	PTER 5'	GCGTTGTACCCGAGTTACCTGT 48409	___ A C
	AGT	ATTACAGGTG TG GG ACAACGC	
		TGATGTCCAT GC CC TGTTGCG	
		TGA _ A	
GAM2080	RAB3B 3'	GCGCGGTGGCTCACGCCTGTAA 12704	G AA
	T	ATTACAGGTGTGAG CAC CGC	
		TAATGTCCGCACTC GTG GCG	
		G GC	
GAM2080	RAB7L1 3'	GCGTGGTGGCTCACACCTGTAA 15408	G A
	T	ATTACAGGTGTGAG CAC ACGC	
		TAATGTCCCACTC GTG TGCG	
		G G	
GAM2080	RFC2 3'	GCGCGGTAGTCACGCCTGTAAT 12842	GGC AA
		ATTACAGGTGTGA AC CGC	

			TAATGTCCGCACT TG GCG	
			GA_ GC	
GAM2080	SIM2	3'	GCGGCTCACACCTGTAAT 24802	_____
			ATTACAGGTGTGAG GC	
			TAATGTCCCACTC CG	
			GG__	
GAM2080	SLC14A2	3'	GCACGGTGGCTCACGCCTGTAA 24119	G AAC
	T		ATTACAGGTGTGAG CAC GC	
			TAATGTCCGCACTC GTG CG	
			G GCA	
GAM2080	SLC2A3	3'	GCGGTGGCTCACGCCTGTAAT 23641	G AA
			ATTACAGGTGTGAG CAC CGC	
			TAATGTCCGCACTC GTG GCG	
			G _	
GAM2080	SLC2A6	3'	GTGGCTCACGCCTGTAAT 34575	G
			ATTACAGGTGTGAG CAC	
			TAATGTCCGCACTC GTG	
			G	
GAM2080	SMG1	3'	GTGGCTCACGCCTGTAAT 31351	G
			ATTACAGGTGTGAG CAC	
			TAATGTCCGCACTC GTG	
			G	
GAM2080	SRGAP1	5'	GTGACTCACGCCTGTAAT 72720	G
			ATTACAGGTGTGAG CAC	
			TAATGTCCGCACTC GTG	
			A	
GAM2080	STAT3	3'	GCATGGTGGCTCACGCCTGTAA 13438	G AAC
	T		ATTACAGGTGTGAG CAC GC	
			TAATGTCCGCACTC GTG CG	
			G GTA	
GAM2080	STAT3	3'	GCATGGTGGCTCACGCCTGTAA 58379	G AAC
	T		ATTACAGGTGTGAG CAC GC	
			TAATGTCCGCACTC GTG CG	
			G GTA	
GAM2080	SWAP70	3'	GCGTGGTGGCTCACGCCTGTAA 71869	G A
	T		ATTACAGGTGTGAG CAC ACGC	
			TAATGTCCGCACTC GTG TGCG	
			G G	
GAM2080	TCTA	3'	GCATGGTGGCTCACGCCTGTAA 42498	G AAC
	T		ATTACAGGTGTGAG CAC GC	

			TAATGTCCGCACTC GTG CG	
			G GTA	
GAM2080	TEM7	3'	GTGGCTCACGCCTGTAAT 40268	G
			ATTACAGGTGTGAG CAC	
			TAATGTCCGCACTC GTG	
			G	
GAM2080	TGFB1	3'	GCGGGGTGCTCACGCCTGTAAT 7257	G AA
			ATTACAGGTGTGAG CAC CGC	
			TAATGTCCGCACTC GTG GCG	
			- GG	
GAM2080	TM7SF3	3'	GTGGCTCACACCTGTAAT 60394	G
			ATTACAGGTGTGAG CAC	
			TAATGTCCCACTC GTG	
			G	
GAM2080	TNFAIP6	3'	GCGCAGTGGCTCACTCCTGTAA 60168	T G AA
	T		ATTACAGG GTGAG CAC CGC	
			TAATGTCC CACTC GTG GCG	
			T G AC	
GAM2080	TNFSF10	3'	GTGGCTCACACCTGTAAT 15093	G
			ATTACAGGTGTGAG CAC	
			TAATGTCCCACTC GTG	
			G	
GAM2080	TNFSF15	3'	GCGCAGTGGCTCACACCTGTAA 18867	G AA
	T		ATTACAGGTGTGAG CAC CGC	
			TAATGTCCCACTC GTG GCG	
			G AC	
GAM2080	TRIM14	3'	GCGCGGTGGCTCACGCCTGTAA 53774	G AA
	T		ATTACAGGTGTGAG CAC CGC	
			TAATGTCCGCACTC GTG GCG	
			G GC	
GAM2080	TSN	3'	GCGTGGTGGCTCACACCTGTAA 17301	G A
	T		ATTACAGGTGTGAG CAC ACGC	
			TAATGTCCCACTC GTG TGCG	
			G G	
GAM2080	TSNAX	3'	GCGTGGTGGCTCACGCCTGTAA 21158	G A
	T		ATTACAGGTGTGAG CAC ACGC	
			TAATGTCCGCACTC GTG TGCG	
			G G	
GAM2080	UC28	3'	GCACGGTGGCTCACGCCTGTAA 41587	G AAC
	T		ATTACAGGTGTGAG CAC GC	

		TAATGTCCGCACTC GTG CG	
		G GCA	
GAM2080	USP14	3' GCACGGTGGCTCACGCCTGTAA 18934	G AAC
	T	ATTACAGGTGTGAG CAC GC	
		TAATGTCCGCACTC GTG CG	
		G GCA	
GAM2080	VDR	3' GCGCGGTGGCTCACGCCTGTAA 6345	G AA
	T	ATTACAGGTGTGAG CAC CGC	
		TAATGTCCGCACTC GTG GCG	
		G GC	
GAM2080	VPS41	3' GCATGGTGGCTCACGCCCGTAA 27693	A G AAC
	T	ATTAC GGTGTGAG CAC GC	
		TAATG CCGCACTC GTG CG	
		C G GTA	
GAM2080	WIG1	3' GCGCGGTGGCTCACGCCTGTAA 96102	G AA
	T	ATTACAGGTGTGAG CAC CGC	
		TAATGTCCGCACTC GTG GCG	
		G GC	
GAM2080	WSX1	3' GTGGCTCACGCCTGTAAT 17916	G
		ATTACAGGTGTGAG CAC	
		TAATGTCCGCACTC GTG	
		G	
GAM2080	WW45	3' GCGTGGTGGCTCACTCCTGTAA 41813	T G A
	T	ATTACAGG GTGAG CAC ACGC	
		TAATGTCC CACTC GTG TGCG	
		T G G	
GAM2080	XT3	3' GCACGGTGGCTCACGCCTGTAA 39915	G AAC
	T	ATTACAGGTGTGAG CAC GC	
		TAATGTCCGCACTC GTG CG	
		G GCA	
GAM2080	ZNF136	3' GCGGCTCACACCTGTAAT 60568	_____
		ATTACAGGTGTGAG GC	
		TAATGTCCCACTC CG	
		GG_____	
GAM2080	ZNF137	3' GCGGTGGCTCACACCTGTAAT 14311	G AA
		ATTACAGGTGTGAG CAC CGC	
		TAATGTCCCACTC GTG GCG	
		G _	
GAM2080	ZNF255	5' TTGTACCCAACTTGTAG 20500	G A C
		TTACAGGT TG GG ACAA	

			GATGTTCA AC CC TGTT	
			— — A	
GAM2080	ZNF36	3'	GCGGTGGCTCACGCCTGTAAT 95582	G AA
			ATTACAGGTGTGAG CAC CGC	
			TAATGTCCGCACTC GTG GCG	
			G —	
GAM2080	AF020591	3'	GCACGGTACCTCACACCTGTAA 27914	C AAC
	T		ATTACAGGTGTGAGG AC GC	
			TAATGTCCCACTCC TG CG	
			A GCA	
GAM2080	AP1GBP1	3'	GCGCGGTGGCTCACACCTGTAA 55445	G AA
	T		ATTACAGGTGTGAG CAC CGC	
			TAATGTCCCACTC GTG GCG	
			G GC	
GAM2080	APOF	3'	GCGGTGGCTCACGCCTGTAAT 9693	G AA
			ATTACAGGTGTGAG CAC CGC	
			TAATGTCCGCACTC GTG GCG	
			G —	
GAM2080	APXL2	3'	GCGCGGTGGCTCACGCCTGTAA 75680	G AA
	T		ATTACAGGTGTGAG CAC CGC	
			TAATGTCCGCACTC GTG GCG	
			G GC	
GAM2080	ARNTL2	3'	CGTGGTGCTCACGCCTGTAAT 39846	G A
			ATTACAGGTGTGAG CAC ACG	
			TAATGTCCGCACTC GTG TGC	
			— G	
GAM2080	ASAH1	3'	GCGGTGGCTCACGCCTGTAAT 64317	G AA
			ATTACAGGTGTGAG CAC CGC	
			TAATGTCCGCACTC GTG GCG	
			G —	
GAM2080	BIA2	3'	GTGGCTCACGCCTGTAAT 71796	G
			ATTACAGGTGTGAG CAC	
			TAATGTCCGCACTC GTG	
			G	
GAM2080	BIRC1	3'	GCGGTGGCTCACACCTGTAAT 16992	G AA
			ATTACAGGTGTGAG CAC CGC	
			TAATGTCCCACTC GTG GCG	
			G —	
GAM2080	BLOV1	3'	GCACGGTGGCTCACGCCTGTAA 76796	G AAC
	T		ATTACAGGTGTGAG CAC GC	

		TAATGTCCGCACTC GTG CG	
		G GCA	
GAM2080	C12orf2 3'	GCATGGTGGCTCACGCCTGTAA 83683	G AAC
	T	ATTACAGGTGTGAG CAC GC	
		TAATGTCCGCACTC GTG CG	
		G GTA	
GAM2080	C13orf1 3'	GCGCGGTGGCTCACACCTGTAA 40365	G AA
	T	ATTACAGGTGTGAG CAC CGC	
		TAATGTCCCACTC GTG GCG	
		G GC	
GAM2080	C20orf106 3'	GCGCGGTGGCTCACCCCTGTAA 55906	T G AA
	T	ATTACAGG GTGAG CAC CGC	
		TAATGTCC CACTC GTG GCG	
		C G GC	
GAM2080	C20orf108 3'	GCGGTGGCTCACGCCTGTAAT 55882	G AA
		ATTACAGGTGTGAG CAC CGC	
		TAATGTCCGCACTC GTG GCG	
		G _	
GAM2080	C20orf142 3'	GCATGGTGGCTCACACCTGTAA 75284	G AAC
	T	ATTACAGGTGTGAG CAC GC	
		TAATGTCCCACTC GTG CG	
		G GTA	
GAM2080	C20orf142 3'	GCGGCTCACACCTATAAT 75285 C	_____
		ATTA AGGTGTGAG GC	
		TAAT TCCCACTC CG	
		A GG_	
GAM2080	C20orf172 3'	GCGCAATGGCTCACGCCTGTAA 46766	G CAA
	T	ATTACAGGTGTGAG CA CGC	
		TAATGTCCGCACTC GT GCG	
		G AAC	
GAM2080	C20orf175 3'	GTGGCTCACGCCTGTAAT 55928	G
		ATTACAGGTGTGAG CAC	
		TAATGTCCGCACTC GTG	
		G	
GAM2080	C20orf177 3'	GCGTGGTGGCTCACGCCTGTAA 62835	G A
	T	ATTACAGGTGTGAG CAC ACGC	
		TAATGTCCGCACTC GTG TGCG	
		G G	
GAM2080	C20orf183 3'	GTGGCTCACGCCTGTAAT 48536	G
		ATTACAGGTGTGAG CAC	

		TAATGTCCGCACTC GTG	
		G	
GAM2080	C20orf29 3'	GCGCGGTGGCTCACGCCTGTAA 37711	G AA
	T	ATTACAGGTGTGAG CAC CGC	
		TAATGTCCGCACTC GTG GCG	
		G GC	
GAM2080	C21orf108 3'	GCATGGTAGCGCACACCTGTAA 90116	AG _ AAC
	TT	AATTACAGGTGTG GC AC GC	
		TTAATGTCCACAC CG TG CG	
		G_ A GTA	
GAM2080	C2F 3'	GCACGGTGGCTCACGCCTGTAA 22008	G AAC
	T	ATTACAGGTGTGAG CAC GC	
		TAATGTCCGCACTC GTG CG	
		G GCA	
GAM2080	C6orf29 3'	GCGCCGTGGCTCACGCCTGTAA 48266	G AA
	T	ATTACAGGTGTGAG CAC CGC	
		TAATGTCCGCACTC GTG GCG	
		G CC	
GAM2080	C6orf29 3'	GCGCCGTGGCTCACGCCTGTAA 52459	G AA
	T	ATTACAGGTGTGAG CAC CGC	
		TAATGTCCGCACTC GTG GCG	
		G CC	
GAM2080	C6orf5 3'	GCGCAGTGGCTCACACCTGTAA 31995	G AA
	T	ATTACAGGTGTGAG CAC CGC	
		TAATGTCCCACTC GTG GCG	
		G AC	
GAM2080	C8orf2 3'	GCGCGGTGGCTCACACCTGTAA 24153	G AA
	T	ATTACAGGTGTGAG CAC CGC	
		TAATGTCCCACTC GTG GCG	
		G GC	
GAM2080	CALN1 3'	GCGGTGGCTCACACCTATAAT 49664	C G AA
		ATTA AGGTGTGAG CAC CGC	
		TAAT TCCCACTC GTG GCG	
		A G _	
GAM2080	CAMKK2 5'	GCGCGGTGACTCACACCTGTAA 22624	G AA
	T	ATTACAGGTGTGAG CAC CGC	
		TAATGTCCCACTC GTG GCG	
		A GC	
GAM2080	CBCIP2 3'	GCGCAGTGACTCACGCCTGTAA 52659	G AA
	T	ATTACAGGTGTGAG CAC CGC	

			TAATGTCCGCACTC GTG GCG	
			A AC	
GAM2080	CCR6	3'	GCATGGTGGCTCACACCTGTAA 49404	G AAC
	T		ATTACAGGTGTGAG CAC GC	
			TAATGTCCCACTC GTG CG	
			G GTA	
GAM2080	CCR6	3'	GCATGGTGGCTCACACCTGTAA 16443	G AAC
	T		ATTACAGGTGTGAG CAC GC	
			TAATGTCCCACTC GTG CG	
			G GTA	
GAM2080	cerk	3'	GCGCGGTGGCTCACGCCTGTAA 43167	G AA
	T		ATTACAGGTGTGAG CAC CGC	
			TAATGTCCGCACTC GTG GCG	
			G GC	
GAM2080	CFLAR	3'	GCGTAGTGGCTCACACCTGTAA 15274	G A
	T		ATTACAGGTGTGAG CAC ACGC	
			TAATGTCCCACTC GTG TGCG	
			G A	
GAM2080	CHST3	3'	GCGGTGGCTCATACCTGTAAT 16239	G AA
			ATTACAGGTGTGAG CAC CGC	
			TAATGTCCATACTC GTG GCG	
			G _	
GAM2080	CNNM1	3'	GCGCGGTGGCTCACACCTGTAA 40123	G AA
	T		ATTACAGGTGTGAG CAC CGC	
			TAATGTCCCACTC GTG GCG	
			G GC	
GAM2080	CSAD	3'	GTGGCTCACGCCTGTAAT 32584	G
			ATTACAGGTGTGAG CAC	
			TAATGTCCGCACTC GTG	
			G	
GAM2080	D21S2056E	3'	GTGGCTCACACCTGTAAT 14871	G
			ATTACAGGTGTGAG CAC	
			TAATGTCCCACTC GTG	
			G	
GAM2080	DCOHN	3'	GCACGGTGGCTCACGCCTGTAA 50527	G AAC
	T		ATTACAGGTGTGAG CAC GC	
			TAATGTCCGCACTC GTG CG	
			G GCA	
GAM2080	dJ383J4.3	3'	GCGGCTCACACCTGTAATT 67494	_____
			AATTACAGGTGTGAG GC	

	TTAATGTCCCACTC CG		
	GG__		
GAM2080 DKFZP434B168 3'	GCGTGGTTGCTCACGCCTGTAA 31869	G	CA_
T	ATTACAGGTGTGAG CA ACGC		
	TAATGTCCGCACTC GT TGCG		
	_ TGG		
GAM2080 DKFZP434C171 3'	GTGGCTCACGCCTGTAAT 32198	G	
	ATTACAGGTGTGAG CAC		
	TAATGTCCGCACTC GTG		
	G		
GAM2080 DKFZp434E0519 3'	GCATGGTGGCTCACACTTATAA 50992	C	G AAC
T	ATTA AGGTGTGAG CAC GC		
	TAAT TTCACACTC GTG CG		
	A G GTA		
GAM2080 DKFZp434E0519 3'	GCGGTGGCTCACACCTATAAT 50993	C	G AA
	ATTA AGGTGTGAG CAC CGC		
	TAAT TCCCACTC GTG GCG		
	A G _		
GAM2080 DKFZp547C176 3'	GCGCAGTGGCTCACACCTGTAA 67802	G	AA
T	ATTACAGGTGTGAG CAC CGC		
	TAATGTCCCACTC GTG GCG		
	G AC		
GAM2080 DKFZp547G183 3'	GCGCGGTGGCTCACGCCTGTAA 38645	G	AA
TT	AATTACAGGTGTGAG CAC CGC		
	TTAATGTCCGCACTC GTG GCG		
	G GC		
GAM2080 DKFZp547I094 3'	GCGTGGTGGCTCACACCTGTAA 50564	G	A
T	ATTACAGGTGTGAG CAC ACGC		
	TAATGTCCCACTC GTG TGCG		
	G G		
GAM2080 DKFZP564M182 3'	GCGGTGGCTCACGCCTGTAAT 78634	G	AA
	ATTACAGGTGTGAG CAC CGC		
	TAATGTCCGCACTC GTG GCG		
	G _		
GAM2080 DKFZP564M182 3'	GCGTGGTGGCTCATCTGTAA 78635	G	A
T	ATTACAGGTGTGAG CAC ACGC		
	TAATGTCTACACTC GTG TGCG		
	G G		
GAM2080 DKFZP566J2046 3'	CGCGGTGGCTCACGCCTGTAA 49137	G	AA
	ATTACAGGTGTGAG CAC CG		

		TAATGTCCGCACTC GTG GC	
		G GC	
GAM2080	DKFZP586D2223 3'	GCGCCGTGGCTCACACCTGTAA 38293	G AA
	T	ATTACAGGTGTGAG CAC CGC	
		TAATGTCCCACTC GTG GCG	
		G CC	
GAM2080	DKFZP586D2223 3'	TGGCTCACACCTGTAATT 38299	G
		AATTACAGGTGTGAG CA	
		TTAATGTCCCACTC GT	
		G	
GAM2080	DKFZP586M1120 3'	GTGGCTCACGCCTGTAAT 49284	G
		ATTACAGGTGTGAG CAC	
		TAATGTCCGCACTC GTG	
		G	
GAM2080	DKFZp761J139 5'	GCGCGGTGGCTCACGCCTGTAA 51107	G AA
	T	ATTACAGGTGTGAG CAC CGC	
		TAATGTCCGCACTC GTG GCG	
		G GC	
GAM2080	DRF1 3'	GCGAGGTGGCTCACACCTGTAA 47751	G AA
	T	ATTACAGGTGTGAG CAC CGC	
		TAATGTCCCACTC GTG GCG	
		G GA	
GAM2080	FBXO27 3'	GCAGGGTGGCTCACACCTGTAA 75011	G AAC
	T	ATTACAGGTGTGAG CAC GC	
		TAATGTCCCACTC GTG CG	
		G GGA	
GAM2080	FBXO6 3'	GCACTGTGGCTCACGCCTGTAA 37994	G AC
	T	ATTACAGGTGTGAG CACA GC	
		TAATGTCCGCACTC GTGT CG	
		G CA	
GAM2080	FBXO9 3'	GCGACTCACACCTATAAT 54248 C	_____
		ATTA AGGTGTGAG GC	
		TAAT TCCCACTC CG	
		A AG_____	
GAM2080	FKSG17 3'	GCATGGTGGTGCACACCTGTAA 50156	AGG AAC
	T	ATTACAGGTGTG CAC GC	
		TAATGTCCACAC GTG CG	
		GTG GTA	
GAM2080	FLJ10043 3'	GTGCCTCACACCTGTAAT 36236	
		ATTACAGGTGTGAGGCAC	

TAATGTCCACACTCCGTG

GAM2080	FLJ10139	3'	GCGGCTCACACCTATAAT	36316	C	_____
			ATTA AGGTGTGAG	GC		
			TAAT TCCACACTC	CG		
			A	GG_____		
GAM2080	FLJ10460	3'	GCACGGTGGCTCACGCCTGTAA	36617	G	AAC
	T		ATTACAGGTGTGAG CAC	GC		
			TAATGTCCGCACTC GTG	CG		
			G	GCA		
GAM2080	FLJ10460	3'	GCGCAGTGGCTCACACCTGTAA	36619	G	AA
	T		ATTACAGGTGTGAG CAC	CGC		
			TAATGTCCACACTC GTG	GCG		
			G	AC		
GAM2080	FLJ10460	3'	GCGGCTCACACCTGTAA	36620	_____	
			ATTACAGGTGTGAG	GC		
			TAATGTCCACACTC	CG		
			GG_____			
GAM2080	FLJ10547	3'	GTGGCTCACACCTGTAA	36778	G	
			ATTACAGGTGTGAG CAC			
			TAATGTCCACACTC GTG			
			G			
GAM2080	FLJ10607	3'	GTGGCTCACGCCTGTAA	77642	G	
			ATTACAGGTGTGAG CAC			
			TAATGTCCGCACTC GTG			
			G			
GAM2080	FLJ10650	3'	GCGGCTCACACCTGTAA	36901	_____	
			ATTACAGGTGTGAG	GC		
			TAATGTCCACACTC	CG		
			GG_____			
GAM2080	FLJ10704	3'	GCGTGGTGGCTCACACCTGTAA	36981	G	A
	T		ATTACAGGTGTGAG CAC	ACGC		
			TAATGTCCACACTC GTG	TGCG		
			G	G		
GAM2080	FLJ10781	3'	GCACGGTGGCTCACGCCTGTAA	37171	G	AAC
	T		ATTACAGGTGTGAG CAC	GC		
			TAATGTCCGCACTC GTG	CG		
			G	GCA		
GAM2080	FLJ10803	3'	GCACGGTGGCTCACACCTGTAA	37204	G	AAC
	T		ATTACAGGTGTGAG CAC	GC		

		TAATGTCCCACTC GTG CG		
		G GCA		
GAM2080	FLJ10803	3' GTGGCTCACACCGGTAAT 37206	A	G
		ATTAC GGTGTGAG CAC		
		TAATG CCACACTC GTG		
		G G		
GAM2080	FLJ10826	3' GCATGGTGGCTCACGCCTGTAA 37247		G AAC
	T	ATTACAGGTGTGAG CAC GC		
		TAATGTCCGCACTC GTG CG		
		G GTA		
GAM2080	FLJ10989	3' GTGGCTCACACCTGTAA 37506		G
		ATTACAGGTGTGAG CAC		
		TAATGTCCCACTC GTG		
		G		
GAM2080	FLJ11029	3' GTGGCTCACACCTGTAA 61635		G
		ATTACAGGTGTGAG CAC		
		TAATGTCCCACTC GTG		
		G		
GAM2080	FLJ11136	3' GCGCTGTGGCTCACGCCTGTAA 37667		G A
	T	ATTACAGGTGTGAG CACA CGC		
		TAATGTCCGCACTC GTGT GCG		
		G C		
GAM2080	FLJ11149	3' GCAGTTGCTCACACCGGTAAT 37686	A	GCA _
		ATTAC GGTGTGAG CAAC GC		
		TAATG CCACACTC GTTG CG		
		G _ A		
GAM2080	FLJ11151	3' TGCTGGTGCACACCTGTAA 68483		A__
		ATTACAGGTGTG GGCA		
		TAATGTCCACAC TCGT		
		GTGG		
GAM2080	FLJ11370	3' GTGGCTCATACCTGTAA 46969		G
		ATTACAGGTGTGAG CAC		
		TAATGTCCATACTC GTG		
		G		
GAM2080	FLJ11637	3' GCGCGGTGGCTCACGCCTGTAA 46982		G AA
	T	ATTACAGGTGTGAG CAC CGC		
		TAATGTCCGCACTC GTG GCG		
		G GC		
GAM2080	FLJ11700	3' GCGGCTCACACCTGTAA 46563		_____
		ATTACAGGTGTGAG GC		

	TAATGTCCCACTC	CG	
	GG____		
GAM2080 FLJ11726	3' GTGGCTCACACCTGTAAT	47029	G
	ATTACAGGTGTGAG	CAC	
	TAATGTCCCACTC	GTG	
	G		
GAM2080 FLJ11800	3' CCAACGCGCAGCTCACACTTGT	47037	_____ ACAAC
	AAT	ATTACAGGTGTGAG	GC G
	TAATGTTCACTC	CG C	
	GACG____	CAACA	
GAM2080 FLJ11996	3' GCGGCTCACACCTGTAATT	47065	_____
	AATTACAGGTGTGAG	GC	
	TTAATGTCCCACTC	CG	
	GG____		
GAM2080 FLJ12078	3' GCACGGTGGCTCACGCCTGTAA	47082	G AAC
	T	ATTACAGGTGTGAG	CAC GC
	TAATGTCCGCACTC	GTG CG	
	G	GCA	
GAM2080 FLJ12294	5' CCAACGCGCAGCTCACACCTGT	47713	_____ ACAAC
	AA	TTACAGGTGTGAG	GC G
	AATGTCCCACTC	CG C	
	GACG____	CAACA	
GAM2080 FLJ12294	3' GCGCGGTGGCTCACGCCTGTAA	47716	G AA
	T	ATTACAGGTGTGAG	CAC CGC
	TAATGTCCGCACTC	GTG GCG	
	G	GC	
GAM2080 FLJ12363	3' GCGCAGTGGCTCACACCTGTAA	50637	G AA
	T	ATTACAGGTGTGAG	CAC CGC
	TAATGTCCCACTC	GTG GCG	
	G	AC	
GAM2080 FLJ12409	3' GCACGGTGGCTCACACCTGTAA	47772	G AAC
		TTACAGGTGTGAG	CAC GC
	AATGTCCCACTC	GTG CG	
	G	GCA	
GAM2080 FLJ12547	3' GCGCGGTGGCTCACGCCTGTAA	47134	G AA
	T	ATTACAGGTGTGAG	CAC CGC
	TAATGTCCGCACTC	GTG GCG	
	G	GC	
GAM2080 FLJ12660	3' GCGTGGTGGCTCACGCCTGTAA	47897	G A
	T	ATTACAGGTGTGAG	CAC ACGC

		TAATGTCCGCACTC GTG TGCG	
		G G	
GAM2080	FLJ12666 3'	GCGCAGTGGCTCACGCCTGTAA 45070	G AA
	T	ATTACAGGTGTGAG CAC CGC	
		TAATGTCCGCACTC GTG GCG	
		G AC	
GAM2080	FLJ12985 3'	GCGGTGGCTCACACCTGTAAT 46797	G AA
		ATTACAGGTGTGAG CAC CGC	
		TAATGTCCCACTC GTG GCG	
		G _	
GAM2080	FLJ13162 3'	GCGCAGTGGCTCACGCCTGTAA 47186	G AA
	T	ATTACAGGTGTGAG CAC CGC	
		TAATGTCCGCACTC GTG GCG	
		G AC	
GAM2080	FLJ13193 3'	GCACGGTGGCTCACGCCTGTAA 50724	G AAC
	T	ATTACAGGTGTGAG CAC GC	
		TAATGTCCGCACTC GTG CG	
		G GCA	
GAM2080	FLJ13193 3'	GCGCGGTGGCTCACACCTGTAA 50725	G AA
	T	ATTACAGGTGTGAG CAC CGC	
		TAATGTCCCACTC GTG GCG	
		G GC	
GAM2080	FLJ13193 3'	GCGTAGTGGCGCACACCTGCAA 50726	A AGG A
	T	ATT CAGGTGTG CAC ACGC	
		TAA GTCCACAC GTG TGCG	
		C GCG A	
GAM2080	FLJ13330 3'	GTGGCTCACACCTGTAAT 47667	G
		ATTACAGGTGTGAG CAC	
		TAATGTCCCACTC GTG	
		G	
GAM2080	FLJ13448 3'	GCGTGGTGGCACACACCTGTAA 47882	AG _ A
	T	ATTACAGGTGTG GC AC ACGC	
		TAATGTCCACAC CG TG TGCG	
		A_ G G	
GAM2080	FLJ13448 3'	GTGGCTCACACCTGTAAT 47884	G
		ATTACAGGTGTGAG CAC	
		TAATGTCCCACTC GTG	
		G	
GAM2080	FLJ13456 3'	GCGCGGTGGCTCACGCCTGTAA 66551	G AA
	T	ATTACAGGTGTGAG CAC CGC	

	TAATGTCCGCACTC GTG GCG	
	G GC	
GAM2080 FLJ13544 3'	GCGGTGGCTCACACCTGT 47207	G AA
	ACAGGTGTGAG CAC CGC	
	TGTCCCACTC GTG GCG	
	G _	
GAM2080 FLJ13614 3'	GTGGCTCACACCTGTAAT 58201	G
	ATTACAGGTGTGAG CAC	
	TAATGTCCCACTC GTG	
	G	
GAM2080 FLJ13659 3'	GCGGTGGCTCACACCTGTAAT 48034	G AA
	ATTACAGGTGTGAG CAC CGC	
	TAATGTCCCACTC GTG GCG	
	G _	
GAM2080 FLJ13769 3'	GCGTGGTGGCTCACGCCTGTAA 47256	G A
T	ATTACAGGTGTGAG CAC ACGC	
	TAATGTCCGCACTC GTG TGCG	
	G G	
GAM2080 FLJ13848 3'	GCGGTGGCTTACACCTGTAAT 45824	G AA
	ATTACAGGTGTGAG CAC CGC	
	TAATGTCCACATTC GTG GCG	
	G _	
GAM2080 FLJ14011 3'	GCGCAGTGGCTTACACCTGTAA 42317	G AA
	TTACAGGTGTGAG CAC CGC	
	AATGTCCACATTC GTG GCG	
	G AC	
GAM2080 FLJ14100 3'	GCGCAGTGGCTCACGCCTGTAA 47335	G AA
T	ATTACAGGTGTGAG CAC CGC	
	TAATGTCCGCACTC GTG GCG	
	G AC	
GAM2080 FLJ14117 3'	GCGGTGGCTCACACTTGTAAT 43227	G AA
	ATTACAGGTGTGAG CAC CGC	
	TAATGTTCACTC GTG GCG	
	G _	
GAM2080 FLJ14117 3'	GCGTGGTGGCTCACACTTGTAAT 43228	G A
T	ATTACAGGTGTGAG CAC ACGC	
	TAATGTTCACTC GTG TGCG	
	G G	
GAM2080 FLJ14117 3'	GCGTGGTGGCTCACGCCTGTAA 43229	G A
T	ATTACAGGTGTGAG CAC ACGC	

		TAATGTCCGCACTC GTG TGCG		
		G G		
GAM2080	FLJ14225	3' GCGCGGTGGCTCACGCCTGTAA 46386	G	AA
	T	ATTACAGGTGTGAG CAC CGC		
		TAATGTCCGCACTC GTG GCG		
		G GC		
GAM2080	FLJ14251	3' GTGGCTCACACCTGTAAT 46489	G	
		ATTACAGGTGTGAG CAC		
		TAATGTCCCACTC GTG		
		G		
GAM2080	FLJ14326	3' GTGGCTCACGCCTGTAAT 50781	G	
		ATTACAGGTGTGAG CAC		
		TAATGTCCGCACTC GTG		
		G		
GAM2080	FLJ14327	3' GCGCAGTGGCTCACATCTGTAA 46684	G	AA
	T	ATTACAGGTGTGAG CAC CGC		
		TAATGTCTACACTC GTG GCG		
		G AC		
GAM2080	FLJ14345	3' GCGTGGTGGCTCACGCCTGTAA 45659	G	A
	T	ATTACAGGTGTGAG CAC ACGC		
		TAATGTCCGCACTC GTG TGCG		
		G G		
GAM2080	FLJ14346	3' GCGCGGTGGCTCACGCCTGTAA 47366	G	AA
	T	ATTACAGGTGTGAG CAC CGC		
		TAATGTCCGCACTC GTG GCG		
		G GC		
GAM2080	FLJ14346	3' GCGGCTCACACCTGTAAT 47367	_____	
		ATTACAGGTGTGAG GC		
		TAATGTCCCACTC CG		
		GG_____		
GAM2080	FLJ14397	3' GCATGGTGGCTCACACCTATAA 52329	C	G AAC
	T	ATTA AGGTGTGAG CAC GC		
		TAAT TCCCACTC GTG CG		
		A G GTA		
GAM2080	FLJ14457	3' GCGCGGTGGCTCACGCCTGTAA 52408	G	AA
		TTACAGGTGTGAG CAC CGC		
		AATGTCCGCACTC GTG GCG		
		G GC		
GAM2080	FLJ14466	3' GCATGGTGGCTCACGCCTGTAA 52429	G	AAC
	T	ATTACAGGTGTGAG CAC GC		

		TAATGTCCGCACTC GTG CG		
		G GTA		
GAM2080	FLJ14621	3' GCACGGTGGCTCACGCCTGTAA 52538	G	AAC
	T	ATTACAGGTGTGAG CAC GC		
		TAATGTCCGCACTC GTG CG		
		G GCA		
GAM2080	FLJ14641	3' GTGGCTCACACCTGTAAT 52565	G	
		ATTACAGGTGTGAG CAC		
		TAATGTCCCACTC GTG		
		G		
GAM2080	FLJ14642	3' TGTGGCTCACACCTGTAAT 52583	G	
		ATTACAGGTGTGAG CACA		
		TAATGTCCCACTC GTGT		
		G		
GAM2080	FLJ20004	3' GCACGGTGGCTCACGCCTGTAA 97006	G	AAC
	T	ATTACAGGTGTGAG CAC GC		
		TAATGTCCGCACTC GTG CG		
		G GCA		
GAM2080	FLJ20006	3' GCACGGTGGCTCACGCCTGTAA 34785	G	AAC
	T	ATTACAGGTGTGAG CAC GC		
		TAATGTCCGCACTC GTG CG		
		G GCA		
GAM2080	FLJ20013	3' GCGCGGTGACTCACACCTGTAA 34798	G	AA
	T	ATTACAGGTGTGAG CAC CGC		
		TAATGTCCCACTC GTG GCG		
		A GC		
GAM2080	FLJ20013	3' GTGGCTCACACCTGTAAT 34801	G	
		ATTACAGGTGTGAG CAC		
		TAATGTCCCACTC GTG		
		G		
GAM2080	FLJ20034	3' GCATGGTGGCTCACGCCTGTAA 34848	G	AAC
	T	ATTACAGGTGTGAG CAC GC		
		TAATGTCCGCACTC GTG CG		
		G GTA		
GAM2080	FLJ20045	3' GCGCAGTGGCTCACACCTCTAA 34887	C	G AA
	T	ATTA AGGTGTGAG CAC CGC		
		TAAT TCCCACTC GTG GCG		
		C G AC		
GAM2080	FLJ20055	3' GTGGCTCACGCCTGTAAT 34913	G	
		ATTACAGGTGTGAG CAC		

		TAATGTCCGCACTC GTG		
		G		
GAM2080	FLJ20139	3' GCGGTGACTCGCACCTGTAAT 35119	G	AA
		ATTACAGGTGTGAG CAC CGC		
		TAATGTCCACGCTC GTG GCG		
		A _		
GAM2080	FLJ20139	3' GCGTGGTGGTTCACACCTGTAA 35120	G	A
	T	ATTACAGGTGTGAG CAC ACGC		
		TAATGTCCACACTT GTG TGCG		
		G G		
GAM2080	FLJ20174	3' GTGGCTCACGCCTGTAAT 35194	G	
		ATTACAGGTGTGAG CAC		
		TAATGTCCGCACTC GTG		
		G		
GAM2080	FLJ20211	3' GTGGCTCACGCCTGTAAT 35265	G	
		ATTACAGGTGTGAG CAC		
		TAATGTCCGCACTC GTG		
		G		
GAM2080	FLJ20280	3' GCATGGTGGCTCACACCTGTAA 35330	G	AAC
	T	ATTACAGGTGTGAG CAC GC		
		TAATGTCCCACTC GTG CG		
		G GTA		
GAM2080	FLJ20340	3' GCGCGGTGGCTCACACCCGTAA 35458	A	G AA
	T	ATTAC GGTGTGAG CAC CGC		
		TAATG CCACACTC GTG GCG		
		C G GC		
GAM2080	FLJ20700	3' GCATGGTGGCTCACGCCTGTAA 36009	G	AAC
		TTACAGGTGTGAG CAC GC		
		AATGTCCGCACTC GTG CG		
		G GTA		
GAM2080	FLJ20783	3' GCGCGGTGGCTCACGCCTGTAA 36102	G	AA
	T	ATTACAGGTGTGAG CAC CGC		
		TAATGTCCGCACTC GTG GCG		
		G GC		
GAM2080	FLJ20808	3' GTGGCTCACACCCATAAT 36121 CA	G	
		ATTA GGTGTGAG CAC		
		TAAT CCACACTC GTG		
		AC G		
GAM2080	FLJ20825	3' GCACGGTGGCTCACGCCTGTAA 36145	G	AAC
	T	ATTACAGGTGTGAG CAC GC		

	TAATGTCCGCACTC GTG CG	
	G GCA	
GAM2080 FLJ21657 3'	CGTGGTGGCTCACGCCTGTAAT 42797	G A
	ATTACAGGTGTGAG CAC ACG	
	TAATGTCCGCACTC GTG TGC	
	G G	
GAM2080 FLJ21687 3'	GCGTGGTGGCTCACGCCTGTAA 46300	G A
T	ATTACAGGTGTGAG CAC ACGC	
	TAATGTCCGCACTC GTG TGCG	
	G G	
GAM2080 FLJ22054 3'	GCGTGGTGGCTCACACCTGTAA 96049	G A
T	ATTACAGGTGTGAG CAC ACGC	
	TAATGTCCCACTC GTG TGCG	
	G G	
GAM2080 FLJ22692 3'	GCGCAGTGGCTCACGCCTGTAA 47484	G AA
T	ATTACAGGTGTGAG CAC CGC	
	TAATGTCCGCACTC GTG GCG	
	G AC	
GAM2080 FLJ22814 3'	GCGGTGGCTCACGCCTGTAAT 46725	G AA
	ATTACAGGTGTGAG CAC CGC	
	TAATGTCCGCACTC GTG GCG	
	G _	
GAM2080 FLJ23499 3'	GCATGGTGGCTCACGCCTGTAA 43137	G AAC
T	ATTACAGGTGTGAG CAC GC	
	TAATGTCCGCACTC GTG CG	
	G GTA	
GAM2080 FLJ25012 3'	GCGCAGTGGCTCACGCCTGTAA 58711	G AA
T	ATTACAGGTGTGAG CAC CGC	
	TAATGTCCGCACTC GTG GCG	
	G AC	
GAM2080 FLJ30092 3'	GCGTGGGGCTCACACCTGTAAT 59340	G ACA
	ATTACAGGTGTGAG C ACGC	
	TAATGTCCCACTC G TGCG	
	_ GGG	
GAM2080 FLJ30681 3'	GTGTTGGCACACACCTGTAAT 93438	AG A
	ATTACAGGTGTG GC CAACGC	
	TAATGTCCACAC CG GTTGTG	
	A_ _	
GAM2080 FLJ31168 3'	GCATGGTGGCTCACACCTGTAA 59182	G AAC
T	ATTACAGGTGTGAG CAC GC	

		TAATGTCCCACTC GTG CG	
		G GTA	
GAM2080	FLJ31455 3'	GTGGCTCACGCCTGTAAT 59289	G
		ATTACAGGTGTGAG CAC	
		TAATGTCCGCACTC GTG	
		G	
GAM2080	FLJ31952 3'	GCACGGTGGCTCACACCTGTAA 59048	G AAC
	T	ATTACAGGTGTGAG CAC GC	
		TAATGTCCCACTC GTG CG	
		G GCA	
GAM2080	FUSIP1 3'	GCGTGGTGGCTCACACCTGTAA 55041	G A
	T	ATTACAGGTGTGAG CAC ACGC	
		TAATGTCCCACTC GTG TGCG	
		G G	
GAM2080	GALNT6 3'	GTGGCTCACACCTGTAAT 24250	G
		ATTACAGGTGTGAG CAC	
		TAATGTCCCACTC GTG	
		G	
GAM2080	GCN2 3'	GTGGCTCACACCTTTAAT 63438	C G
		ATTA AGGTGTGAG CAC	
		TAAT TCCCACTC GTG	
		T G	
GAM2080	GLTP 3'	GTGGCTCACGCCTGTAAT 33587	G
		ATTACAGGTGTGAG CAC	
		TAATGTCCGCACTC GTG	
		G	
GAM2080	GP5 3'	CCAACGCACAGCTCACGCCTGT 16867	_____ ACAAC
	AAT	ATTACAGGTGTGAG GC G	
		TAATGTCCGCACTC CG C	
		GACA__ CAACA	
GAM2080	HES2 3'	GCGCGGTGGCTCACGCCTGTAA 39375	G AA
	T	ATTACAGGTGTGAG CAC CGC	
		TAATGTCCGCACTC GTG GCG	
		G GC	
GAM2080	HIC 3'	GCACGGTGGCTTACACCTGTAA 68049	G AAC
		TTACAGGTGTGAG CAC GC	
		AATGTCCACATTC GTG CG	
		G GCA	
GAM2080	HSA250303 3'	CGCAGTGGCTCACGCCTGTAA 38021	G AA
	T	AATTACAGGTGTGAG CAC CG	

			TTAATGTCCGCACTC GTG GC		
			G AC		
GAM2080	HSC3	3'	GTGGCTCACACCTGTAAT 59733	G	
			ATTACAGGTGTGAG CAC		
			TAATGTCCCACTC GTG		
			G		
GAM2080	HSMPP8	3'	GCGTGGTGGCTCACACCTATAA 95137	C	G A
	T		ATTA AGGTGTGAG CAC ACGC		
			TAAT TCCCACTC GTG TGCG		
			A G G		
GAM2080	INE1	3'	GCGGTGGCTCACGCCTGTAAT 14759	G	AA
			ATTACAGGTGTGAG CAC CGC		
			TAATGTCCGCACTC GTG GCG		
			G _		
GAM2080	JAM1	3'	GCGCAGTGGCTCACGCCTATAA 58517	C	G AA
	T		ATTA AGGTGTGAG CAC CGC		
			TAAT TCCGCACTC GTG GCG		
			A G AC		
GAM2080	JAM1	3'	GCGCAGTGGCTCACGCCTATAA 58545	C	G AA
	T		ATTA AGGTGTGAG CAC CGC		
			TAAT TCCGCACTC GTG GCG		
			A G AC		
GAM2080	JAM1	3'	GCGCAGTGGCTCACGCCTATAA 58574	C	G AA
	T		ATTA AGGTGTGAG CAC CGC		
			TAAT TCCGCACTC GTG GCG		
			A G AC		
GAM2080	JAM1	3'	GCGCAGTGGCTCACGCCTATAA 34231	C	G AA
	T		ATTA AGGTGTGAG CAC CGC		
			TAAT TCCGCACTC GTG GCG		
			A G AC		
GAM2080	KALI	3'	GCA TGGTGGCTCACACCTGTAA 54693	G	AAC
	T		ATTACAGGTGTGAG CAC GC		
			TAATGTCCCACTC GTG CG		
			G GTA		
GAM2080	KATII	3'	GCA TGGTGC GTCACACCTATAA 33165	C	G AAC
	T		ATTA AGGTGTGA GCAC GC		
			TAAT TCCCACT CGTG CG		
			A G GTA		
GAM2080	KIAA0042	3'	GTGGCTCACGCCTGTAAT 30238	G	
			ATTACAGGTGTGAG CAC		

		TAATGTCCGCACTC GTG	
		G	
GAM2080 KIAA0159	3'	GCACTGTGGCTCACGCCTGTAA 30142	G AC
	T	ATTACAGGTGTGAG CACA GC	
		TAATGTCCGCACTC GTGT CG	
		G CA	
GAM2080 KIAA0184	3'	GTGGCTTACACCTGTAAT 65813	G
		ATTACAGGTGTGAG CAC	
		TAATGTCCACATTC GTG	
		G	
GAM2080 KIAA0191	5'	GCGTCGCGCGCGCCTGTAG 66512	AG ACA
		TTACAGGTGTG GC ACGC	
		GATGTCCGCGC CG TGCG	
		G_ C__	
GAM2080 KIAA0226	3'	GTGGCTCACACCTGTAAT 64263	G
		ATTACAGGTGTGAG CAC	
		TAATGTCCCACTC GTG	
		G	
GAM2080 KIAA0355	3'	GCGTGGTGGCTCACGCCTGTAA 28707	G A
	T	ATTACAGGTGTGAG CAC ACGC	
		TAATGTCCGCACTC GTG TGCG	
		G G	
GAM2080 KIAA0408	3'	GCATTGTGGTGGTCACCTGTAG 28799	TGAGG C
	T	ATTACAGGTG CACAA GC	
		TGATGTCCAC GTGTT CG	
		TGGTG A	
GAM2080 KIAA0445	5'	GCGCAGTGGCTCACGCCTGTAA 28638	G AA
	T	ATTACAGGTGTGAG CAC CGC	
		TAATGTCCGCACTC GTG GCG	
		G AC	
GAM2080 KIAA0472	3'	GCATGGTGGCTCACGCCTGTAA 72356	G AAC
	T	ATTACAGGTGTGAG CAC GC	
		TAATGTCCGCACTC GTG CG	
		G GTA	
GAM2080 KIAA0547	3'	GCATGGTGGCTCACGCCTATAA 29594	C G AAC
	TT	AATTA AGGTGTGAG CAC GC	
		TTAAT TCCGCACTC GTG CG	
		A G GTA	
GAM2080 KIAA0635	3'	GTGGCTCACGCCTGTAAT 28418	G
		ATTACAGGTGTGAG CAC	

		TAATGTCCGCACTC GTG	
		G	
GAM2080 KIAA0694	3'	GCATGGTAGCTCACGCCTGTAA 72970	GC AAC
	T	ATTACAGGTGTGAG AC GC	
		TAATGTCCGCACTC TG CG	
		GA GTA	
GAM2080 KIAA0752	3'	GTGGCTCACGCCTGTAAT 67634	G
		ATTACAGGTGTGAG CAC	
		TAATGTCCGCACTC GTG	
		G	
GAM2080 KIAA0825	3'	GCATGGTGGCTCACGCCTGTAA 61685	G AAC
	T	ATTACAGGTGTGAG CAC GC	
		TAATGTCCGCACTC GTG CG	
		G GTA	
GAM2080 KIAA0831	3'	GCGCGGTGGCTCACGCCTGTAA 30641	G AA
	T	ATTACAGGTGTGAG CAC CGC	
		TAATGTCCGCACTC GTG GCG	
		G GC	
GAM2080 KIAA0864	3'	GCGCTGCTTTTACCTGTA 63941	T CAA
		TACAGGTG GAGGCA CGC	
		ATGTCCAC TTTCGT GCG	
		T C__	
GAM2080 KIAA0872	3'	CGGAGGCTCACGCCTGTAAT 30751	G ACAA
		ATTACAGGTGTGAG C CG	
		TAATGTCCGCACTC G GC	
		GAG	
GAM2080 KIAA0894	3'	GCGCGGTGGCTCACGCCTGTAA 30335	G AA
	T	ATTACAGGTGTGAG CAC CGC	
		TAATGTCCGCACTC GTG GCG	
		G GC	
GAM2080 KIAA0907	3'	GCACGGTGGCTCACGCCTGTAA 30875	G AAC
	T	ATTACAGGTGTGAG CAC GC	
		TAATGTCCGCACTC GTG CG	
		G GCA	
GAM2080 KIAA0907	3'	GCGCAGTGGCTCACGCCTGTAA 30876	G AA
	T	ATTACAGGTGTGAG CAC CGC	
		TAATGTCCGCACTC GTG GCG	
		G AC	
GAM2080 KIAA0930	3'	GCGCAGTGGCTCACGCCTGTAA 71070	G AA
	T	ATTACAGGTGTGAG CAC CGC	

		TAATGTCCGCACTC GTG GCG		
		G AC		
GAM2080	KIAA0981	3' GCGGTGGCTCACGCCTATAAT 62090	C	G AA
		ATTA AGGTGTGAG CAC CGC		
		TAAT TCCGCACTC GTG GCG		
		A G _		
GAM2080	KIAA1001	3' GCGCAGTGGCTCACACCTGTAG 31009		G AA
	T	ATTACAGGTGTGAG CAC CGC		
		TGATGTCCCACTC GTG GCG		
		G AC		
GAM2080	KIAA1056	3' GCGTGGTGGCTCACGCCTGTAA 30315		G A
	T	ATTACAGGTGTGAG CAC ACGC		
		TAATGTCCGCACTC GTG TGCG		
		G G		
GAM2080	KIAA1086	3' GCATGGTGGCTCACACCTATAA 71286	C	G AAC
	T	ATTA AGGTGTGAG CAC GC		
		TAAT TCCCACTC GTG CG		
		A G GTA		
GAM2080	KIAA1160	3' GCGCAGTGGCTCACGCCTGTAA 40759		G AA
		TTACAGGTGTGAG CAC CGC		
		AATGTCCGCACTC GTG GCG		
		G AC		
GAM2080	KIAA1164	3' GCGCAGTGGCTCACGCCTGTAA 70047		G AA
	T	ATTACAGGTGTGAG CAC CGC		
		TAATGTCCGCACTC GTG GCG		
		G AC		
GAM2080	KIAA1191	3' GCGTGGTGGCTCACGCCTGTAA 40334		G A
	T	ATTACAGGTGTGAG CAC ACGC		
		TAATGTCCGCACTC GTG TGCG		
		G G		
GAM2080	KIAA1228	3' GCGGTGGCTCACGCCTGTAAT 65676		G AA
		ATTACAGGTGTGAG CAC CGC		
		TAATGTCCGCACTC GTG GCG		
		G _		
GAM2080	KIAA1244	3' GCACGGTGGCTCACGCCTGTAA 72445		G AAC
	T	ATTACAGGTGTGAG CAC GC		
		TAATGTCCGCACTC GTG CG		
		G GCA		
GAM2080	KIAA1271	3' GCGCAGTGGCTCACGCCTGTAA 70141		G AA
	T	ATTACAGGTGTGAG CAC CGC		

		TAATGTCCGCACTC GTG GCG	
		G AC	
GAM2080 KIAA1276	3'	CCAACGCGCAGCTCACGCCTGT 67028	_____ ACAAC
	AAT	ATTACAGGTGTGAG GC G	
		TAATGTCCGCACTC CG C	
		GACG__ CAACA	
GAM2080 KIAA1328	3'	GCGCGGTGGCTTACACCTGTAA 62325	G AA
	T	ATTACAGGTGTGAG CAC CGC	
		TAATGTCCACATTC GTG GCG	
		G GC	
GAM2080 KIAA1364	3'	GCATGGTGGTGCACACCTGTAA 64351	AGG AAC
	T	ATTACAGGTGTG CAC GC	
		TAATGTCCACAC GTG CG	
		GTG GTA	
GAM2080 KIAA1404	3'	GCGTTATGGCGGGCGCCTGTAA 62691	GAG AC_
	T	ATTACAGGTGT GC AACGC	
		TAATGTCCGCG CG TTGCG	
		GG_ GTA	
GAM2080 KIAA1423	3'	GTGGCTCACATCTGTAAT 62395	G
		ATTACAGGTGTGAG CAC	
		TAATGTCTACACTC GTG	
		G	
GAM2080 KIAA1473	3'	GCACGGTGGCTCACGCCTGTAA 71210	G AAC
	T	ATTACAGGTGTGAG CAC GC	
		TAATGTCCGCACTC GTG CG	
		G GCA	
GAM2080 KIAA1486	3'	GCGTGGTGGCTCACGCCTGTAA 67976	G A
	T	ATTACAGGTGTGAG CAC ACGC	
		TAATGTCCGCACTC GTG TGCG	
		G G	
GAM2080 KIAA1508	3'	GCGCAGTGGCTCACACCTTTAA 62554	C G AA
	T	ATTA AGGTGTGAG CAC CGC	
		TAAT TCCACACTC GTG GCG	
		T G AC	
GAM2080 KIAA1586	5'	GCATGGTGGCTCACACCTGTAA 93939	G AAC
	T	ATTACAGGTGTGAG CAC GC	
		TAATGTCCACACTC GTG CG	
		G GTA	
GAM2080 KIAA1656	5'	GCGCGGTGGCTCACGCCTGTAA 66371	G AA
	T	ATTACAGGTGTGAG CAC CGC	

		TAATGTCCGCACTC GTG GCG	
		G GC	
GAM2080 KIAA1821	3'	GCATGGTGGCTCACGCCTGTAA 72268	G AAC
	T	ATTACAGGTGTGAG CAC GC	
		TAATGTCCGCACTC GTG CG	
		G GTA	
GAM2080 KIAA1829	3'	GCGGTGGCTCACGCCTGTAAT 62646	G AA
		ATTACAGGTGTGAG CAC CGC	
		TAATGTCCGCACTC GTG GCG	
		G _	
GAM2080 KIAA1872	3'	GTGGCTCACGCCTATAAT 63617 C	G
		ATTA AGGTGTGAG CAC	
		TAAT TCCGCACTC GTG	
		A G	
GAM2080 KIAA1941	3'	GCATGGTGGCTCACACCTGTAA 75339	G AAC
	T	ATTACAGGTGTGAG CAC GC	
		TAATGTCCACACTC GTG CG	
		G GTA	
GAM2080 KIAA1951	3'	GCGTGGTGGCTCACGCCTGTAA 74157	G A
	T	ATTACAGGTGTGAG CAC ACGC	
		TAATGTCCGCACTC GTG TGCG	
		G G	
GAM2080 KIAA1954	3'	GTGTCTCACACCTGTAAT 78228	
		ATTACAGGTGTGAGGCAC	
		TAATGTCCACACTCTGTG	
GAM2080 KIAA1958	3'	GTGGCTCACGCCTATAAT 82791 C	G
		ATTA AGGTGTGAG CAC	
		TAAT TCCGCACTC GTG	
		A G	
GAM2080 KLHL6	3'	CCAACGCGCGGCTCACGCCTGT 56168	_____ ACAAC
	AAT	ATTACAGGTGTGAG GC G	
		TAATGTCCGCACTC CG C	
		GGCG_ CAACA	
GAM2080 KR18	3'	GCACGGTGGCTCACACCTGTAA 53891	G AAC
	T	ATTACAGGTGTGAG CAC GC	
		TAATGTCCACACTC GTG CG	
		G GCA	
GAM2080 KR18	3'	GCGCGGTGGCTCACACCTGTGA 53892	G AA
	T	ATTACAGGTGTGAG CAC CGC	

			TAGTGTCCACACTC GTG GCG G GC	
GAM2080 KREMEN	3'	GCATGGTGGCACACACCTGTAA 50234		AG _ AAC
T		ATTACAGGTGTG GC AC GC TAATGTCCACAC CG TG CG A_ G GTA		
GAM2080 LIAS	3'	GTGGCTCACGCCTGTAAT 71168	G	
		ATTACAGGTGTGAG CAC TAATGTCCGCACTC GTG G		
GAM2080 LIM	3'	GCGCGGTGGCTCACGCCTGTAA 22328	G	AA
T		ATTACAGGTGTGAG CAC CGC TAATGTCCGCACTC GTG GCG G GC		
GAM2080 LRG	3'	GCGGGGGCTCACGCCTGTAAT 54823	G	ACAA
		ATTACAGGTGTGAG C CGC TAATGTCCGCACTC G GCG _GGG_		
GAM2080 LYSAL1	3'	GCGCGGTGGCTCACGCCTGTAA 18124	G	AA
T		ATTACAGGTGTGAG CAC CGC TAATGTCCGCACTC GTG GCG G GC		
GAM2080 MACF1	3'	CCAACGCGCAGCTCACACCTGT 53494		_____ ACAAC
AAT		ATTACAGGTGTGAG GC G TAATGTCCACACTC CG C GACG__ CAACA		
GAM2080 MESDC2	3'	GTGGCTCACGCCTGTAAT 72922	G	
		ATTACAGGTGTGAG CAC TAATGTCCGCACTC GTG G		
GAM2080 MGC10814	3'	GCACGGTGGCTCACACCTGTAA 52019	G	AAC
T		ATTACAGGTGTGAG CAC GC TAATGTCCACACTC GTG CG G GCA		
GAM2080 MGC11386	3'	GCGCAGTGGCTCACGCCTATAA 53068	C	G AA
T		ATTA AGGTGTGAG CAC CGC TAAT TCCGCACTC GTG GCG A G AC		
GAM2080 MGC12972	3'	GCGCAGTGGCTCCCACCTGTAA 52054	T	G AA
T		ATTACAGGTG GAG CAC CGC 		

		TAATGTCCAC CTC GTG GCG	
		C G AC	
GAM2080	MGC13053	3' GCACGGTGGCTCACGCCTGTAA 52109	G AAC
	T	ATTACAGGTGTGAG CAC GC	
		TAATGTCCGCACTC GTG CG	
		G GCA	
GAM2080	MGC14126	3' GCGGTGGCTCACGCCTGTAAT 52939	G AA
		ATTACAGGTGTGAG CAC CGC	
		TAATGTCCGCACTC GTG GCG	
		G —	
GAM2080	MGC14407	3' GTGGCTCACACCTGTAAT 52976	G
		ATTACAGGTGTGAG CAC	
		TAATGTCCACACTC GTG	
		G	
GAM2080	MGC14817	3' GCATGGTGGCTCACACCTGTAA 51337	G AAC
	T	ATTACAGGTGTGAG CAC GC	
		TAATGTCCACACTC GTG CG	
		G GTA	
GAM2080	MGC15397	3' GCGCGGTGGCTCACGCCTGTAA 55553	G AA
	T	ATTACAGGTGTGAG CAC CGC	
		TAATGTCCGCACTC GTG GCG	
		G GC	
GAM2080	MGC16385	3' GCGCGGTGGCTCACGCCTGTAA 59538	G AA
	T	ATTACAGGTGTGAG CAC CGC	
		TAATGTCCGCACTC GTG GCG	
		G GC	
GAM2080	MGC20235	3' GCGCAGTGGCTTACACCTGTAA 59555	G AA
	T	ATTACAGGTGTGAG CAC CGC	
		TAATGTCCACATTC GTG GCG	
		G AC	
GAM2080	MGC23244	3' GTGGCTCACGCCTGTAAT 58837	G
		ATTACAGGTGTGAG CAC	
		TAATGTCCGCACTC GTG	
		G	
GAM2080	MGC2562	3' GCACGGTGGCTCACACCTGTAA 51443	G AAC
	T	ATTACAGGTGTGAG CAC GC	
		TAATGTCCACACTC GTG CG	
		G GCA	
GAM2080	MGC2562	3' GCATGGTGA CTCATACCTGTAA 51444	G AAC
	T	ATTACAGGTGTGAG CAC GC	

		TAATGTCCATACTC GTG CG		
		A GTA		
GAM2080	MGC2562	3' GCGGTGGCTCACGCCTATAAT 51445	C	G AA
		ATTA AGGTGTGAG CAC CGC		
		TAAT TCCGCACTC GTG GCG		
		A G _		
GAM2080	MGC29762	3' GCGCAGTGGCTCACACCTGTAA 59145		G AA
	T	ATTACAGGTGTGAG CAC CGC		
		TAATGTCCCACTC GTG GCG		
		G AC		
GAM2080	MGC29891	3' CCAACGCGCGGCTCACGCCTGT 58855		_____ ACAAC
	AAT	ATTACAGGTGTGAG GC G		
		TAATGTCCGCACTC CG C		
		GGCG_ CAACA		
GAM2080	MGC29891	3' GCGGCTCACACCTGTAAT 58864		_____
		ATTACAGGTGTGAG GC		
		TAATGTCCCACTC CG		
		GG_		
GAM2080	MGC3207	3' GCGCAGTGGCTCACACCTGTAA 63240		G AA
	T	ATTACAGGTGTGAG CAC CGC		
		TAATGTCCCACTC GTG GCG		
		G AC		
GAM2080	MGC39350	3' GCGGCTCACACCTGTAAT 59317		_____
		ATTACAGGTGTGAG GC		
		TAATGTCCCACTC CG		
		GG_		
GAM2080	MGC4248	3' GTGGCTCACACCTGTAAT 51317		G
		ATTACAGGTGTGAG CAC		
		TAATGTCCCACTC GTG		
		G		
GAM2080	MGC4400	3' GTGGCTCACACCTGTAAT 52040		G
		ATTACAGGTGTGAG CAC		
		TAATGTCCCACTC GTG		
		G		
GAM2080	MGC4562	3' GCACGGTGGCTCACGCCTGTAA 56741		G AAC
		TTACAGGTGTGAG CAC GC		
		AATGTCCGCACTC GTG CG		
		G GCA		
GAM2080	MGC4663	3' GCGCGGTGGCTCACGCCTATAA 44787	C	G AA
	T	ATTA AGGTGTGAG CAC CGC		

		TAAT TCCGCACTC GTG GCG		
		A G GC		
GAM2080	MGC4840	3' GCGTGATGGCTCACACCTGTAA 72024		G CA
	TT	AATTACAGGTGTGAG CA ACGC		
		TTAATGTCCCACTC GT TGCG		
		G AG		
GAM2080	MGC5254	3' GTGGCTCACGCCTGTAAT 51389		G
		ATTACAGGTGTGAG CAC		
		TAATGTCCGCACTC GTG		
		G		
GAM2080	MGC5457	3' GCGCGGTGGCTCACACCTTAAT 51940	C	G AA
		ATTA AGGTGTGAG CAC CGC		
		TAAT TCCCACTC GTG GCG		
		— G GC		
GAM2080	MKRN4	3' GCGCGGTGGCTCACGCCTGTAA 48466		G AA
	T	ATTACAGGTGTGAG CAC CGC		
		TAATGTCCGCACTC GTG GCG		
		G GC		
GAM2080	MOST2	5' GCGTCATGGCTCACACCTGTAA 40067		G CA
	T	ATTACAGGTGTGAG CA ACGC		
		TAATGTCCCACTC GT TGCG		
		G AC		
GAM2080	MRP63	3' GCGGTGGCTCACGCCTGTAAT 44048		G AA
		ATTACAGGTGTGAG CAC CGC		
		TAATGTCCGCACTC GTG GCG		
		G —		
GAM2080	MRPL56	3' GTGGCTCACGCCTGTAAT 52757		G
		ATTACAGGTGTGAG CAC		
		TAATGTCCGCACTC GTG		
		G		
GAM2080	MRPS10	3' GCACGGTGGCTCACGCCTGTAA 36820		G AAC
	T	ATTACAGGTGTGAG CAC GC		
		TAATGTCCGCACTC GTG CG		
		G GCA		
GAM2080	MRPS18B	3' GCGTGGTGGCTCACTCCTGTAA 26752	T	G A
	T	ATTACAGG GTGAG CAC ACGC		
		TAATGTCC CACTC GTG TGCG		
		T G G		
GAM2080	My015	3' GCGGTGGCTCACCCCTGTAAT 67231	T	G AA
		ATTACAGG GTGAG CAC CGC		

		TAATGTCC CACTC GTG GCG	
		C G _	
GAM2080 NMNAT	3'	GCGGCTCACACCTGTAAT 43289	_____
		ATTACAGGTGTGAG GC	
		TAATGTCCCACTC CG	
		GG_	
GAM2080 NMT2	3'	GCGTGGTGGCTCACGCCTGTAA 17857	G A
T		ATTACAGGTGTGAG CAC ACGC	
		TAATGTCCGCACTC GTG TGCG	
		G G	
GAM2080 NPTXR	3'	GCACGGTGGCTCACGCCTGTAA 55212	G AAC
T		ATTACAGGTGTGAG CAC GC	
		TAATGTCCGCACTC GTG CG	
		G GCA	
GAM2080 NPTXR	3'	GCACGGTGGCTCACGCCTGTAA 27436	G AAC
T		ATTACAGGTGTGAG CAC GC	
		TAATGTCCGCACTC GTG CG	
		G GCA	
GAM2080 ORC6L	3'	GCGCAGTGGCTCACGCCTGTAA 27492	G AA
T		ATTACAGGTGTGAG CAC CGC	
		TAATGTCCGCACTC GTG GCG	
		G AC	
GAM2080 PB1	3'	GCGCGGTGGCTCACACCTGTAA 37578	G AA
T		ATTACAGGTGTGAG CAC CGC	
		TAATGTCCCACTC GTG GCG	
		G GC	
GAM2080 PDCD7	3'	GTGGCTCACGCCTGTAAT 72609	G
		ATTACAGGTGTGAG CAC	
		TAATGTCCGCACTC GTG	
		G	
GAM2080 phorbolin-1	3'	GCGCGGTGGCTCACGCCTGTAA 90211	G AA
T		ATTACAGGTGTGAG CAC CGC	
		TAATGTCCGCACTC GTG GCG	
		G GC	
GAM2080 PILR(ALPHA)	3'	TGGCGCACACCTGTAAT 26482	AG A
		ATTACAGGTGTG GC CA	
		TAATGTCCACAC CG GT	
		G_ _	
GAM2080 POLYDOM	3'	GTGGCTCACGCCTGTAAT 44689	G
		ATTACAGGTGTGAG CAC	

		TAATGTCCGCACTC GTG		
		G		
GAM2080	PP591	5' GCGTGGTGGCTCACACCTATAA 48147	C	G A
	TT	AATTA AGGTGTGAG CAC ACGC		
		TTAAT TCCCACTC GTG TGCG		
		A G G		
GAM2080	PRIC285	3' GCGTGGTGGCTCACGCCCATAA 62118	CA	G A
	T	ATTA GGTGTGAG CAC ACGC		
		TAAT CCGCACTC GTG TGCG		
		AC G G		
GAM2080	PRO0255	3' GCACTGTGGCTCACGCCTGTAA 26970		G AC
	T	ATTACAGGTGTGAG CACA GC		
		TAATGTCCGCACTC GTGT CG		
		G CA		
GAM2080	PRO0478	3' GCAGCTCACACCTGTAAT 27031	_____	
		ATTACAGGTGTGAG GC		
		TAATGTCCCACTC CG		
		GA_____		
GAM2080	PRO0478	5' GCGGCTCACACCTGTAAT 27032	_____	
		ATTACAGGTGTGAG GC		
		TAATGTCCCACTC CG		
		GG_____		
GAM2080	PRO0618	3' GCGCAGTGA CTACGCCTGTAA 27054		G AA
	T	ATTACAGGTGTGAG CAC CGC		
		TAATGTCCGCACTC GTG GCG		
		A AC		
GAM2080	PRO1048	5' GCATGGTGA CTACATCTGTAA 38115		G AAC
	T	ATTACAGGTGTGAG CAC GC		
		TAATGTCTACACTC GTG CG		
		A GTA		
GAM2080	PRO1048	3' GCGCGGTGGCTCACACCTGTAA 38116		G AA
	T	ATTACAGGTGTGAG CAC CGC		
		TAATGTCCCACTC GTG GCG		
		G GC		
GAM2080	PRO2015	3' GCGTGGTGGCTCACGCCTGTAA 38163		G A
	T	ATTACAGGTGTGAG CAC ACGC		
		TAATGTCCGCACTC GTG TGCG		
		G G		
GAM2080	PRO2198	5' GCGATGGCTCACGCCTGTAAT 38408		G CAA
		ATTACAGGTGTGAG CA CGC		

			TAATGTCCGCACTC GT GCG		
			G A__		
GAM2080	PRO2730	3'	GCGCGGTGGCTCACACCTGTAA 48184	G	AA
	T		ATTACAGGTGTGAG CAC CGC		
			TAATGTCCCACTC GTG GCG		
			G GC		
GAM2080	PRO2964	3'	GCGCGGTGGCTCACGCCTGTAA 38260	G	AA
	T		ATTACAGGTGTGAG CAC CGC		
			TAATGTCCGCACTC GTG GCG		
			G GC		
GAM2080	PRPF4	3'	GCGTGGTGGCTCACGCCTGTAA 17468	G	A
	T		ATTACAGGTGTGAG CAC ACGC		
			TAATGTCCGCACTC GTG TGCG		
			G G		
GAM2080	PSR	3'	GCGCCGTAGCTCACCCCTGTAA 65789	T	GC AA
	T		ATTACAGG GTGAG AC CGC		
			TAATGTCC CACTC TG GCG		
			C GA CC		
GAM2080	PSR	3'	GTGGCTCACACCTGTAAT 65792	G	
			ATTACAGGTGTGAG CAC		
			TAATGTCCCACTC GTG		
			G		
GAM2080	PTP4A1	3'	GTGCCTCACACCTGAATT 14410	A	
			AATT CAGGTGTGAGGCAC		
			TTAA GTCCCACTCCGTG		
			—		
GAM2080	PXMP4	3'	GCACTGTGGCTCACTCCTGTAA 24334	T	G AC
	T		ATTACAGG GTGAG CACA GC		
			TAATGTCC CACTC GTGT CG		
			T G CA		
GAM2080	RoXaN	3'	GCGCGGTGGCTCACACCTATAA 47294	C	G AA
	T		ATTA AGGTGTGAG CAC CGC		
			TAAT TCCCACTC GTG GCG		
			A G GC		
GAM2080	RRP4	3'	GCACGGTGGCTCACGCCTATAA 27357	C	G AAC
	T		ATTA AGGTGTGAG CAC GC		
			TAAT TCCGCACTC GTG CG		
			A G GCA		
GAM2080	S164	3'	TTGTGAGATCTGTAATT 61433	GTGAGG	
			AATTACAGGT CACAA		

			TTAATGTCTA GTGTT		
			GA_____		
GAM2080	SAC2	3'	GTGGCTCACACCTATAAT 30727	C	G
			ATTA AGGTGTGAG CAC		
			TAAT TCCCACTC GTG		
			A G		
GAM2080	SC65	3'	GCACGGTGGCTCACGCCTGTAA 22294	G	AAC
	T		ATTACAGGTGTGAG CAC GC		
			TAATGTCCGCACTC GTG CG		
			G GCA		
GAM2080	SC65	3'	GCATGGTGGCACACACCTGTAA 22295	AG	_ AAC
	T		ATTACAGGTGTG GC AC GC		
			TAATGTCCACAC CG TG CG		
			A_ G GTA		
GAM2080	SC65	3'	GCGGTGGCTCACACCTGTAAT 22296	G	AA
			ATTACAGGTGTGAG CAC CGC		
			TAATGTCCCACTC GTG GCG		
			G _		
GAM2080	SCIN	3'	GCGCGGTGGCTCACACCTGTAA 53604	G	AA
	T		ATTACAGGTGTGAG CAC CGC		
			TAATGTCCCACTC GTG GCG		
			G GC		
GAM2080	SCYA5	3'	GCGTGGTGGCCACGCCTGTAA 12969	A	_ A
	T		ATTACAGGTGTG GGC AC ACGC		
			TAATGTCCGCAC CCG TG TGCG		
			_ G G		
GAM2080	SEMA3E	3'	GCGCGGTGGCTCACGCCTGTAA 25810	G	AA
	T		ATTACAGGTGTGAG CAC CGC		
			TAATGTCCGCACTC GTG GCG		
			G GC		
GAM2080	SIAT4A	3'	GTGGCTCACACCTGTAAT 13141	G	
			ATTACAGGTGTGAG CAC		
			TAATGTCCCACTC GTG		
			G		
GAM2080	SLC19A3	3'	TGTGGCTCACACCTGTAAT 48255	G	
			ATTACAGGTGTGAG CACA		
			TAATGTCCCACTC GTGT		
			G		
GAM2080	SLC19A3	3'	GTGGCTCACTCCTGTAAT 48248	T	G
			ATTACAGG GTGAG CAC		

			TAATGTCC CACTC GTG	
			T G	
GAM2080	SMAP-5	3'	GCGTGGTAGCTCACGCCTGTAA 48660	GC A
	T		ATTACAGGTGTGAG AC ACGC	
			TAATGTCCGCACTC TG TGCG	
			GA G	
GAM2080	SPTLC2	3'	GCGGTGGCTCACACCTGTAAT 17996	G AA
			ATTACAGGTGTGAG CAC CGC	
			TAATGTCCCACTC GTG GCG	
			G _	
GAM2080	TACTILE	3'	GCGCAGTGGCTCACGCCTGTAA 20588	G AA
	T		ATTACAGGTGTGAG CAC CGC	
			TAATGTCCGCACTC GTG GCG	
			G AC	
GAM2080	TIP47	3'	GCGGTGGCTCACACCTGTAAT 20605	G AA
			ATTACAGGTGTGAG CAC CGC	
			TAATGTCCCACTC GTG GCG	
			G _	
GAM2080	TRIM38	3'	GCATGGTGGCTCACGCCTGTAA 22056	G AAC
	T		ATTACAGGTGTGAG CAC GC	
			TAATGTCCGCACTC GTG CG	
			G GTA	
GAM2080	UBF-fl	3'	GCGCAGTGGCTCACACCTGTAA 52626	G AA
	T		ATTACAGGTGTGAG CAC CGC	
			TAATGTCCCACTC GTG GCG	
			G AC	
GAM2080	ust3	3'	GCGGTGGCTCACGCCTGTAA 94855	G AA
			ATTACAGGTGTGAG CAC CGC	
			TAATGTCCGCACTC GTG GCG	
			G _	
GAM2080	WBSCR21	3'	GCGTGGTGGTGACACCTGTAA 49304	AGG A
	T		ATTACAGGTGTG CAC ACGC	
			TAATGTCCACAC GTG TGCG	
			GTG G	
GAM2080	WBSCR22	3'	GCGTGGTGGCTCACACCTGTAA 34469	G A
	T		ATTACAGGTGTGAG CAC ACGC	
			TAATGTCCCACTC GTG TGCG	
			G G	
GAM2080	YME1L1	3'	GCGCGGTTGCTCACGCCTGTAA 58435	G _ AA
	T		ATTACAGGTGTGAG CA C CGC	

		TAATGTCCGCACTC GT G GCG	
		_ T GC	
GAM2080	YME1L1	3' GCGCGGTTGCTCACGCCTGTAA 27322	G _ AA
	T	ATTACAGGTGTGAG CA C CGC	
		TAATGTCCGCACTC GT G GCG	
		_ T GC	
GAM2080	ZAK	3' GCACGGTGGCTCACGCCTGTAA 56942	G AAC
	T	ATTACAGGTGTGAG CAC GC	
		TAATGTCCGCACTC GTG CG	
		G GCA	
GAM2080	ZFP106	3' GCGGCTCACACCTGTAAT 42729	_____
		ATTACAGGTGTGAG GC	
		TAATGTCCACACTC CG	
		GG_____	
GAM2080	ZFP106	3' GCGTGGTGGCTCACGCCTGTAA 42730	G A
	T	ATTACAGGTGTGAG CAC ACGC	
		TAATGTCCGCACTC GTG TGCG	
		G G	
GAM2080	ZNF297B	3' GCATGGTGGCTCACGCCTGTAA 26659	G AAC
	T	ATTACAGGTGTGAG CAC GC	
		TAATGTCCGCACTC GTG CG	
		G GTA	
GAM2080	ZNF297B	3' GCGTGGTGGCGCACACCTGTAA 26660	AGG A
	T	ATTACAGGTGTG CAC ACGC	
		TAATGTCCACAC GTG TGCG	
		GCG G	
GAM2080	ZNF297B	5' GCGTGGTGGCTCACACCTGTAA 26661	G A
	T	ATTACAGGTGTGAG CAC ACGC	
		TAATGTCCCACTC GTG TGCG	
		G G	
GAM2080	LOC115129	3' GCAAGGTGGCTCACACCTATAA 73620	C G AAC
	T	ATTA AGGTGTGAG CAC GC	
		TAAT TCCCACTC GTG CG	
		A G GAA	
GAM2080	LOC115129	5' GCACGGTGGCTCACGCCTATAA 73621	C G AAC
	T	ATTA AGGTGTGAG CAC GC	
		TAAT TCCGCACTC GTG CG	
		A G GCA	
GAM2080	LOC115273	3' GCATGGTGGCTCACGCCTGTAA 73753	G AAC
	T	ATTACAGGTGTGAG CAC GC	

		TAATGTCCGCACTC GTG CG	
		G GTA	
GAM2080	LOC116143 3'	GCACGGTGGCTCACTCCTGTAA 74185	T G AAC
	T	ATTACAGG GTGAG CAC GC	
		TAATGTCC CACTC GTG CG	
		T G GCA	
GAM2080	LOC116143 3'	GCGTGGTAGCTCACGCCTGTAA 74187	GC A
	TT	AATTACAGGTGTGAG AC ACGC	
		TTAATGTCCGCACTC TG TGCG	
		GA G	
GAM2080	LOC116228 3'	GCACGGTGGCTCATACCTGTAA 74228	G AAC
	T	ATTACAGGTGTGAG CAC GC	
		TAATGTCCATACTC GTG CG	
		G GCA	
GAM2080	LOC116349 3'	GCGCCGTGGCTCACGCCTGTAA 74277	G AA
	T	ATTACAGGTGTGAG CAC CGC	
		TAATGTCCGCACTC GTG GCG	
		G CC	
GAM2080	LOC119504 5'	GTGGCTCACGCCTGTAAT 74448	G
		ATTACAGGTGTGAG CAC	
		TAATGTCCGCACTC GTG	
		G	
GAM2080	LOC121457 3'	GCGCAGTGGCTCACACCTGTAA 74510	G AA
	T	ATTACAGGTGTGAG CAC CGC	
		TAATGTCCCACTC GTG GCG	
		G AC	
GAM2080	LOC122704 3'	GCGGTGGCTCACGCCTGTAAT 74608	G AA
		ATTACAGGTGTGAG CAC CGC	
		TAATGTCCGCACTC GTG GCG	
		G _	
GAM2080	LOC122970 3'	GTGGCTCACACCTGTAAT 74643	G
		ATTACAGGTGTGAG CAC	
		TAATGTCCCACTC GTG	
		G	
GAM2080	LOC124602 3'	GTGACTCACACCTGTAAT 74789	G
		ATTACAGGTGTGAG CAC	
		TAATGTCCCACTC GTG	
		A	
GAM2080	LOC126282 3'	GCGCGGTGGCTCACGCCTGTAA 74961	G AA
	T	ATTACAGGTGTGAG CAC CGC	

		TAATGTCCGCACTC GTG GCG	
		G GC	
GAM2080	LOC126282 3'	GCGTGGTGGCTCACACCTGTAA 74962	G A
	T	ATTACAGGTGTGAG CAC ACGC	
		TAATGTCCCACTC GTG TGCG	
		G G	
GAM2080	LOC130535 3'	GCACGGTGACTCACACTTGTAA 76652	G AAC
	T	ATTACAGGTGTGAG CAC GC	
		TAATGTTCACTC GTG CG	
		A GCA	
GAM2080	LOC130589 3'	GCACGGTGGCTCACGCCTGTAA 57933	G AAC
	T	ATTACAGGTGTGAG CAC GC	
		TAATGTCCGCACTC GTG CG	
		G GCA	
GAM2080	LOC130951 3'	GTGGCTCACACCTGTAAT 57944	G
		ATTACAGGTGTGAG CAC	
		TAATGTCCCACTC GTG	
		G	
GAM2080	LOC134147 3'	GCGGTGGCTCACGCCTGTAAT 57962	G AA
		ATTACAGGTGTGAG CAC CGC	
		TAATGTCCGCACTC GTG GCG	
		G _	
GAM2080	LOC138241 3'	GTGGCTCACGCCTGTAAT 75837	G
		ATTACAGGTGTGAG CAC	
		TAATGTCCGCACTC GTG	
		G	
GAM2080	LOC138428 3'	GTGGCTCACACCTATAAT 75861	C G
		ATTA AGGTGTGAG CAC	
		TAAT TCCCACTC GTG	
		A G	
GAM2080	LOC139422 3'	GCGGTGGCTCACACCTGTAAT 76351	G AA
		ATTACAGGTGTGAG CAC CGC	
		TAATGTCCCACTC GTG GCG	
		G _	
GAM2080	LOC143310 3'	GCACGGTGGCTCACGCCTGTAA 77047	G AAC
	T	ATTACAGGTGTGAG CAC GC	
		TAATGTCCGCACTC GTG CG	
		G GCA	
GAM2080	LOC143465 3'	GCGGCTCACACCTGTAAT 83874	_____
		ATTACAGGTGTGAG GC	

	TAATGTCCCACTC CG	
	GG__	
GAM2080 LOC143888 3'	GTGGCTCACGCCTGTAAT 77174	G
	ATTACAGGTGTGAG CAC	
	TAATGTCCGCACTC GTG	
	G	
GAM2080 LOC144289 3'	GTGTCTCACATCTGTAAT 83961	
	ATTACAGGTGTGAGGCAC	
	TAATGTCTACACTCTGTG	
GAM2080 LOC144486 3'	GCGGTGGCTCACGCCTGTAAT 84006	G AA
	ATTACAGGTGTGAG CAC CGC	
	TAATGTCCGCACTC GTG GCG	
	G _	
GAM2080 LOC144563 3'	GCGTGGTGGCTCACACCTGTGA 77398	G A
T	ATTACAGGTGTGAG CAC ACGC	
	TAGTGTCCCACTC GTG TGCG	
	G G	
GAM2080 LOC144583 3'	GTGGCTCACACCTGTAAT 77421	G
	ATTACAGGTGTGAG CAC	
	TAATGTCCCACTC GTG	
	G	
GAM2080 LOC144817 3'	CCAACGCACGGCTCACTCCTGT 77510	T _____ ACAAC
AAT	ATTACAGG GTGAG GC G	
	TAATGTCC CACTC CG C	
	T GGCA__ CAACA	
GAM2080 LOC144817 3'	GCATGGTGGCGCACACCTGTAA 77517	AGG AAC
T	ATTACAGGTGTG CAC GC	
	TAATGTCCACAC GTG CG	
	GCG GTA	
GAM2080 LOC144817 3'	GCGCAGTGGCTCACGCCTGTAA 77518	G AA
T	ATTACAGGTGTGAG CAC CGC	
	TAATGTCCGCACTC GTG GCG	
	G AC	
GAM2080 LOC144845 3'	CCAACGCGCGGCTCACTCCTGT 57457	T _____ ACAAC
AAT	ATTACAGG GTGAG GC G	
	TAATGTCC CACTC CG C	
	T GGCG__ CAACA	
GAM2080 LOC145216 3'	GCGGTGGCTCACGCCTGTAAT 84223	G AA
	ATTACAGGTGTGAG CAC CGC	

		TAATGTCCGCACTC GTG GCG		
		G _		
GAM2080	LOC145299 3'	GCGCGGTGGCTCACGCCTGTAA 84277	G	AA
	T	ATTACAGGTGTGAG CAC CGC		
		TAATGTCCGCACTC GTG GCG		
		G GC		
GAM2080	LOC145333 3'	GCGCGGTGGCTCACGCCTGTAA 84300	G	AA
	T	ATTACAGGTGTGAG CAC CGC		
		TAATGTCCGCACTC GTG GCG		
		G GC		
GAM2080	LOC145387 3'	GTGGCTTACACCTGTAAT 84343	G	
		ATTACAGGTGTGAG CAC		
		TAATGTCCACATTC GTG		
		G		
GAM2080	LOC145438 3'	GCGGTGGCTCACGCCTGTAAT 84313	G	AA
		ATTACAGGTGTGAG CAC CGC		
		TAATGTCCGCACTC GTG GCG		
		G _		
GAM2080	LOC145453 3'	GTGGCTCACACCTGTAAT 77668	G	
		ATTACAGGTGTGAG CAC		
		TAATGTCCCACTC GTG		
		G		
GAM2080	LOC145483 3'	GCGCAGTGGCTCACGCCTGTAA 77755	G	AA
	T	ATTACAGGTGTGAG CAC CGC		
		TAATGTCCGCACTC GTG GCG		
		G AC		
GAM2080	LOC145662 3'	GCGCGGTGGCTCACGCCTGCAA 77836	A	G AA
	T	ATT CAGGTGTGAG CAC CGC		
		TAA GTCCGCACTC GTG GCG		
		C G GC		
GAM2080	LOC145663 3'	GTGGCTCACGCCTGTAAT 84429	G	
		ATTACAGGTGTGAG CAC		
		TAATGTCCGCACTC GTG		
		G		
GAM2080	LOC145988 5'	GTGGCTCACGCCTGTAAT 78071	G	
		ATTACAGGTGTGAG CAC		
		TAATGTCCGCACTC GTG		
		G		
GAM2080	LOC146272 5'	GTGGCTCACACCTGTAAT 78330	G	
		ATTACAGGTGTGAG CAC		

		TAATGTCCCACTC GTG		
		G		
GAM2080	LOC146332 3'	GCGCAGTGGCTCACGCCTGTAA 78357	G	AA
	T	ATTACAGGTGTGAG CAC CGC		
		TAATGTCCGCACTC GTG GCG		
		G AC		
GAM2080	LOC146540 3'	GCACGGTGGCTCACACCTGTGA 78528	G	AAC
	T	ATTACAGGTGTGAG CAC GC		
		TAGTGTCCCACTC GTG CG		
		G GCA		
GAM2080	LOC146540 3'	GTGGCTCACACCTGTAAT 78529	G	
		ATTACAGGTGTGAG CAC		
		TAATGTCCCACTC GTG		
		G		
GAM2080	LOC146656 3'	GCGCAGTGGCTCACACCTGTGA 78666	G	AA
	T	ATTACAGGTGTGAG CAC CGC		
		TAGTGTCCCACTC GTG GCG		
		G AC		
GAM2080	LOC146701 3'	GCACGGTGGCTCACACCTGTAA 84717	G	AAC
	T	ATTACAGGTGTGAG CAC GC		
		TAATGTCCCACTC GTG CG		
		G GCA		
GAM2080	LOC146713 3'	GCGCGGTGGCTCACGCCTGTAA 84734	G	AA
	T	ATTACAGGTGTGAG CAC CGC		
		TAATGTCCGCACTC GTG GCG		
		G GC		
GAM2080	LOC146756 3'	GCGCAGTGGCTCACGCCTGTAA 84805	G	AA
	T	ATTACAGGTGTGAG CAC CGC		
		TAATGTCCGCACTC GTG GCG		
		G AC		
GAM2080	LOC146756 3'	GCGCGGTGGCTCACGCCTGTAA 84806	G	AA
	T	ATTACAGGTGTGAG CAC CGC		
		TAATGTCCGCACTC GTG GCG		
		G GC		
GAM2080	LOC146923 3'	GCGCGGTGGCTCACACCTGTAA 78801	G	AA
	T	ATTACAGGTGTGAG CAC CGC		
		TAATGTCCCACTC GTG GCG		
		G GC		
GAM2080	LOC146975 5'	GCACGGTGGCTCACACCTATAA 78828	C	G AAC
	T	ATTA AGGTGTGAG CAC GC		

	TAAT TCCACACTC GTG CG	
	A G GCA	
GAM2080 LOC147669 3'	GCATGGTGACCCACACCTGTAA 85184	A _ AAC
T	ATTACAGGTGTG GG CAC GC	
	TAATGTCCACAC CC GTG CG	
	_ A GTA	
GAM2080 LOC147700 3'	GCGGTGGCTCACGCCTGTAAT 59884	G AA
	ATTACAGGTGTGAG CAC CGC	
	TAATGTCCGCACTC GTG GCG	
	G _	
GAM2080 LOC147837 3'	GTGGCTCACGCCTGTAAT 79208	G
	ATTACAGGTGTGAG CAC	
	TAATGTCCGCACTC GTG	
	G	
GAM2080 LOC147990 3'	GCATGGTGACACACACCTGTAA 85224	AGG AAC
T	ATTACAGGTGTG CAC GC	
	TAATGTCCACAC GTG CG	
	ACA GTA	
GAM2080 LOC148147 3'	GCGCGGTGGCTCACGCCTGTAA 79400	G AA
T	ATTACAGGTGTGAG CAC CGC	
	TAATGTCCGCACTC GTG GCG	
	G GC	
GAM2080 LOC148166 3'	GTGGCTCACACCTGTAAT 79421	G
	ATTACAGGTGTGAG CAC	
	TAATGTCCCACTC GTG	
	G	
GAM2080 LOC148198 3'	GCGCGGTGGCTCACGCCTGTAA 71225	G AA
T	ATTACAGGTGTGAG CAC CGC	
	TAATGTCCGCACTC GTG GCG	
	G GC	
GAM2080 LOC148397 3'	GCGCAGTGGCTCACGCCTGTAA 79571	G AA
T	ATTACAGGTGTGAG CAC CGC	
	TAATGTCCGCACTC GTG GCG	
	G AC	
GAM2080 LOC148734 3'	GCGCGGTGGCTCACGCCTGTAA 79712	G AA
T	ATTACAGGTGTGAG CAC CGC	
	TAATGTCCGCACTC GTG GCG	
	G GC	
GAM2080 LOC148749 3'	GCATGGTGGCTCACGCCTGTAA 79715	G AAC
T	ATTACAGGTGTGAG CAC GC	

	TAATGTCCGCACTC GTG CG		
	G GTA		
GAM2080 LOC148809 5'	GTGGCTCACGCCTGTAAT 79761	G	
	ATTACAGGTGTGAG CAC		
	TAATGTCCGCACTC GTG		
	G		
GAM2080 LOC148918 5'	GCGCAGTGGCTCACGCCTGTAA 79830	G	AA
T	ATTACAGGTGTGAG CAC CGC		
	TAATGTCCGCACTC GTG GCG		
	G AC		
GAM2080 LOC148936 3'	GTGGCTCACACCTGTAAT 85458	G	
	ATTACAGGTGTGAG CAC		
	TAATGTCCCACTC GTG		
	G		
GAM2080 LOC148938 3'	GTGGCTCACACCTGTAAT 85440	G	
	ATTACAGGTGTGAG CAC		
	TAATGTCCCACTC GTG		
	G		
GAM2080 LOC149073 3'	GCGGTGGCTCACGCCTATAAT 85485	C	G AA
	ATTA AGGTGTGAG CAC CGC		
	TAAT TCCGCACTC GTG GCG		
	A G _		
GAM2080 LOC149113 3'	GCGCAGTGGCTCACGCCTGTAA 79913	G	AA
T	ATTACAGGTGTGAG CAC CGC		
	TAATGTCCGCACTC GTG GCG		
	G AC		
GAM2080 LOC149113 5'	GCGGTGGCTCACTCCTGTAAT 79914	T	G AA
	ATTACAGG GTGAG CAC CGC		
	TAATGTCC CACTC GTG GCG		
	T G _		
GAM2080 LOC149113 3'	GTTGCTCACGCCTGTAAT 79917	GCA	
	ATTACAGGTGTGAG CAAC		
	TAATGTCCGCACTC GTTG		
	—		
GAM2080 LOC149175 3'	GCGTGGTGGCTCACTCCTGTAA 79953	T	G A
T	ATTACAGG GTGAG CAC ACGC		
	TAATGTCC CACTC GTG TGCG		
	T G G		
GAM2080 LOC149271 3'	GCATGGTGGCTCACGCCTGTAA 80006	G	AAC
T	ATTACAGGTGTGAG CAC GC		

	TAATGTCCGCACTC GTG CG	
	G GTA	
GAM2080 LOC149579 5'	GCGCAGTGGCTCACGCCTGTAA 71693	G AA
T	ATTACAGGTGTGAG CAC CGC	
	TAATGTCCGCACTC GTG GCG	
	G AC	
GAM2080 LOC149705 3'	GCGGTGGCTCACACCTGTAAT 85782	G AA
	ATTACAGGTGTGAG CAC CGC	
	TAATGTCCCACTC GTG GCG	
	G _	
GAM2080 LOC150245 3'	GCATGGTGGCTCACACCGGTAA 86113	A G AAC
T	ATTAC GGTGTGAG CAC GC	
	TAATG CCACACTC GTG CG	
	G G GTA	
GAM2080 LOC150343 3'	GCATGGTGGCTCACGCCTGTAA 80492	G AAC
T	ATTACAGGTGTGAG CAC GC	
	TAATGTCCGCACTC GTG CG	
	G GTA	
GAM2080 LOC150481 3'	GCGTGGTGGTTCACACCTGTAA 80706	G A
T	ATTACAGGTGTGAG CAC ACGC	
	TAATGTCCCACTT GTG TGCG	
	G G	
GAM2080 LOC150622 3'	GCGTGGTGGCTCACGCCTGTAA 80765	G A
T	ATTACAGGTGTGAG CAC ACGC	
	TAATGTCCGCACTC GTG TGCG	
	G G	
GAM2080 LOC151196 3'	GCGGTGGCTCACGCCTGTAAT 86453	G AA
	ATTACAGGTGTGAG CAC CGC	
	TAATGTCCGCACTC GTG GCG	
	G _	
GAM2080 LOC151248 3'	GCATGGTGGCTCACGCCTGTAA 80995	G AAC
T	ATTACAGGTGTGAG CAC GC	
	TAATGTCCGCACTC GTG CG	
	G GTA	
GAM2080 LOC151429 3'	GTGGCTCACACCTGTAAT 86547	G
	ATTACAGGTGTGAG CAC	
	TAATGTCCCACTC GTG	
	G	
GAM2080 LOC151556 3'	GCATGGTGGCTCACGCCTGTAA 81079	G AAC
T	ATTACAGGTGTGAG CAC GC	

		TAATGTCCGCACTC GTG CG	
		G GTA	
GAM2080	LOC151602 3'	GCGTGGTGGCTCACGCCTGTAA 81113	G A
	T	ATTACAGGTGTGAG CAC ACGC	
		TAATGTCCGCACTC GTG TGCG	
		G G	
GAM2080	LOC151614 3'	GCACGGTGGCTCACACCTGTAA 81122	G AAC
	T	ATTACAGGTGTGAG CAC GC	
		TAATGTCCCACTC GTG CG	
		G GCA	
GAM2080	LOC151632 3'	GCGTGGTGGCTCACACCTGTGA 86646	G A
	T	ATTACAGGTGTGAG CAC ACGC	
		TAGTGTCCCACTC GTG TGCG	
		G G	
GAM2080	LOC151904 3'	GCGTGGTGGCTCACGCCTGTAA 81206	G A
	T	ATTACAGGTGTGAG CAC ACGC	
		TAATGTCCGCACTC GTG TGCG	
		G G	
GAM2080	LOC152263 3'	GTGGCTCACACCTGTAAT 86859	G
		ATTACAGGTGTGAG CAC	
		TAATGTCCCACTC GTG	
		G	
GAM2080	LOC152271 3'	GCGTGTTGGCTCACACCTATGA 81359	C G CA
	T	ATTA AGGTGTGAG CA ACGC	
		TAGT TCCCACTC GT TGCG	
		A G TG	
GAM2080	LOC152317 3'	GCGTGGTGGCTCACACCTGTAA 86832	G A
		TTACAGGTGTGAG CAC ACGC	
		AATGTCCCACTC GTG TGCG	
		G G	
GAM2080	LOC152426 3'	GCGCGGTAGCTCACGCCTGTAA 86898	GC AA
	T	ATTACAGGTGTGAG AC CGC	
		TAATGTCCGCACTC TG GCG	
		GA GC	
GAM2080	LOC152445 3'	GCGGTGGCTCACACCTGTAAT 86951	G AA
		ATTACAGGTGTGAG CAC CGC	
		TAATGTCCCACTC GTG GCG	
		G _	
GAM2080	LOC152453 3'	GCACGGTGGCTCACGCCTGTAA 81475	G AAC
	T	ATTACAGGTGTGAG CAC GC	

		TAATGTCCGCACTC GTG CG		
		G GCA		
GAM2080	LOC152627 5'	GCATGGTGGCTCATACCTGTAA 81511		G AAC
	T	ATTACAGGTGTGAG CAC GC		
		TAATGTCCATACTC GTG CG		
		G GTA		
GAM2080	LOC152860 3'	GCGCGGTGGCTCACACCTATAA 81580	C	G AA
	T	ATTA AGGTGTGAG CAC CGC		
		TAAT TCCACACTC GTG GCG		
		A G GC		
GAM2080	LOC152897 3'	GCGGTGGCTCATACCTATAAT 81608	C	G AA
		ATTA AGGTGTGAG CAC CGC		
		TAAT TCCATACTC GTG GCG		
		A G _		
GAM2080	LOC153260 3'	GCGGTGGCTCACACCTGTAAT 81673		G AA
		ATTACAGGTGTGAG CAC CGC		
		TAATGTCCCACTC GTG GCG		
		G _		
GAM2080	LOC153579 3'	GCGGCTCACACCTGTAAT 81771		_____
		ATTACAGGTGTGAG GC		
		TAATGTCCCACTC CG		
		GG_		
GAM2080	LOC153642 3'	GTGGCTCACACCTGTAAT 81789		G
		ATTACAGGTGTGAG CAC		
		TAATGTCCCACTC GTG		
		G		
GAM2080	LOC154092 3'	GCGGTGGCCACATCTGTAAT 87370		A A A
		ATTACAGGTGTG GGC CA CGC		
		TAATGTCTACAC CCG GT GCG		
		_ _ G		
GAM2080	LOC154403 5'	GCGGTGGCTCACTCCTGTAAT 81978	T	G AA
		ATTACAGG GTGAG CAC CGC		
		TAATGTCC CACTC GTG GCG		
		T G _		
GAM2080	LOC154403 3'	GTTGCTCACGCCTGTAAT 81981		GCA
		ATTACAGGTGTGAG CAAC		
		TAATGTCCGCACTC GTTG		

GAM2080	LOC154791 3'	GCACGGTGGCTCACGCCTGTAA 82053		G AAC
	T	ATTACAGGTGTGAG CAC GC		

	TAATGTCCGCACTC GTG CG	
	G GCA	
GAM2080 LOC154992 3'	GTTGCTCACGCCTGTAAT 82140	GCA
	ATTACAGGTGTGAG CAAC	
	TAATGTCCGCACTC GTTG	
	—	
GAM2080 LOC155072 3'	GCATGGTGGCTCACGCCTGTAA 87668	G AAC
T	ATTACAGGTGTGAG CAC GC	
	TAATGTCCGCACTC GTG CG	
	G GTA	
GAM2080 LOC155072 3'	GTGGCTCACACCTGTAAT 87671	G
	ATTACAGGTGTGAG CAC	
	TAATGTCCCACTC GTG	
	G	
GAM2080 LOC155376 3'	GTGGCTCACACTTGTAAT 82249	G
	ATTACAGGTGTGAG CAC	
	TAATGTTCACTC GTG	
	G	
GAM2080 LOC155376 3'	TGGCAGGCACCTGTAAT 82252	GAG A
	ATTACAGGTGT GC CA	
	TAATGTCCACG CG GT	
	GA_ _	
GAM2080 LOC155438 3'	GTGGCTCACACCTGTAAT 87686	G
	ATTACAGGTGTGAG CAC	
	TAATGTCCCACTC GTG	
	G	
GAM2080 LOC157278 3'	GCGACTCACACCTGTAAT 87707	—
	ATTACAGGTGTGAG GC	
	TAATGTCCCACTC CG	
	AG_ _	
GAM2080 LOC157292 5'	TGATGGCACACACCTGTAAT 87703	AG A A
	ATTACAGGTGTG GC CA CG	
	TAATGTCCACAC CG GT GT	
	A_ _ A	
GAM2080 LOC157464 5'	CGCGGTGGCTCACGCCTGTAAT 87745	G AA
	ATTACAGGTGTGAG CAC CG	
	TAATGTCCGCACTC GTG GC	
	G GC	
GAM2080 LOC157562 5'	GTGACTCATCTGTAAT 87775	G
	ATTACAGGTGTGAG CAC	

	TAATGTCTACACTC GTG		
	A		
GAM2080 LOC157657 3'	GCATGGTAGCTCACGCCTGTAA 82435	GC	AAC
T	ATTACAGGTGTGAG AC GC		
	TAATGTCCGCACTC TG CG		
	GA GTA		
GAM2080 LOC157660 3'	GCGCGGTGGCTCACGCCTGTAA 87805	G	AA
T	ATTACAGGTGTGAG CAC CGC		
	TAATGTCCGCACTC GTG GCG		
	G GC		
GAM2080 LOC158235 3'	GCATGGTAACTCACGCCTGTAA 88006	GC	AAC
T	ATTACAGGTGTGAG AC GC		
	TAATGTCCGCACTC TG CG		
	AA GTA		
GAM2080 LOC158288 5'	GCGTGGTGGCTCACACCTGTCA 88024	T	G A
TT	AAT ACAGGTGTGAG CAC ACGC		
	TTA TGTCCACACTC GTG TGCG		
	C G G		
GAM2080 LOC158310 3'	GTGGCTCACACCTGTAAT 88089	G	
	ATTACAGGTGTGAG CAC		
	TAATGTCCACACTC GTG		
	G		
GAM2080 LOC158382 5'	GTGGCTCACACCTATAGT 88127	C	G
	ATTA AGGTGTGAG CAC		
	TGAT TCCACACTC GTG		
	A G		
GAM2080 LOC158819 3'	GCGCGGTGCTCACGCCTGTAAT 88280	G	AA
	ATTACAGGTGTGAG CAC CGC		
	TAATGTCCGCACTC GTG GCG		
	_ GC		
GAM2080 LOC158819 5'	GCGGTGGCTCACACCTGTAAT 88281	G	AA
	ATTACAGGTGTGAG CAC CGC		
	TAATGTCCACACTC GTG GCG		
	G _		
GAM2080 LOC158863 3'	GCATGGTGGCTCACACCTGTAA 88297	G	AAC
T	ATTACAGGTGTGAG CAC GC		
	TAATGTCCACACTC GTG CG		
	G GTA		
GAM2080 LOC158987 3'	GCGCAATGGCTCACACCTGT 88325	G	CAA
	ACAGGTGTGAG CA CGC		

		TGTCCCACTC GT GCG		
		G AAC		
GAM2080	LOC158987 3'	GCGGTGGCTCACGCCTGTAAT 88326		G AA
		ATTACAGGTGTGAG CAC CGC		
		TAATGTCCGCACTC GTG GCG		
		G _		
GAM2080	LOC159053 3'	GCGCAGTGGCTCACGCCTGTAA 88374		G AA
	T	ATTACAGGTGTGAG CAC CGC		
		TAATGTCCGCACTC GTG GCG		
		G AC		
GAM2080	LOC160646 3'	GCGGCTCACACCTGTAAT 83116		_____
		ATTACAGGTGTGAG GC		
		TAATGTCCCACTC CG		
		GG_____		
GAM2080	LOC167555 3'	GCGGCTCACACCCGTAAT 83564	A	_____
		ATTAC GGTGTGAG GC		
		TAATG CCACACTC CG		
		C GG_____		
GAM2080	LOC170395 3'	GTGGCTCACGCCTGTAAT 76875		G
		ATTACAGGTGTGAG CAC		
		TAATGTCCGCACTC GTG		
		G		
GAM2080	LOC196027 3'	GTGGCTCACACCTGTAAT 88941		G
		ATTACAGGTGTGAG CAC		
		TAATGTCCCACTC GTG		
		G		
GAM2080	LOC196047 5'	GTGGCTCACGCCTGTAAT 91163		G
		ATTACAGGTGTGAG CAC		
		TAATGTCCGCACTC GTG		
		G		
GAM2080	LOC196528 3'	GCACTGTGGCTTACACCTATAA 89106	C	G AC
	T	ATTA AGGTGTGAG CACA GC		
		TAAT TCCACATTC GTGT CG		
		A G CA		
GAM2080	LOC196540 3'	GCACGGTGGCTCACGCCTGTAA 91201		G AAC
	T	ATTACAGGTGTGAG CAC GC		
		TAATGTCCGCACTC GTG CG		
		G GCA		
GAM2080	LOC197196 3'	GCACGGTGGCTCACGCCTGTAA 91303		G AAC
	T	ATTACAGGTGTGAG CAC GC		

	TAATGTCCGCACTC GTG CG	
	G GCA	
GAM2080 LOC197201 3'	GCGGTGGCTCACGCCTGTAAT 89277	G AA
	ATTACAGGTGTGAG CAC CGC	
	TAATGTCCGCACTC GTG GCG	
	G _	
GAM2080 LOC197319 3'	GCGGTGGCTCACACCTGTAAT 89322	G AA
	ATTACAGGTGTGAG CAC CGC	
	TAATGTCCACACTC GTG GCG	
	G _	
GAM2080 LOC199733 3'	GCGCGGTGGCTCACTCCTGTAA 91441	T G AA
T	ATTACAGG GTGAG CAC CGC	
	TAATGTCC CACTC GTG GCG	
	T G GC	
GAM2080 LOC199786 3'	GCGTGGCAGTGCACACCTGTAA 89756	AG_ A A
T	ATTACAGGTGTG GC CA CGC	
	TAATGTCCACAC CG GT GCG	
	GTGA _ _	
GAM2080 LOC200014 3'	GTGGCTCACGCCTGTAAT 89945	G
	ATTACAGGTGTGAG CAC	
	TAATGTCCGCACTC GTG	
	G	
GAM2080 LOC200731 3'	GCGGCTCACACCTGTAAT 91697	_____
	ATTACAGGTGTGAG GC	
	TAATGTCCACACTC CG	
	GG_	
GAM2080 LOC200904 3'	GCATGGTGGCTCACACCTGTGA 91781	G AAC
T	ATTACAGGTGTGAG CAC GC	
	TAGTGTCCACACTC GTG CG	
	G GTA	
GAM2080 LOC201252 3'	CCAACGCGCGGCTCACGCCTGT 89549	_____ ACAAC
AAT	ATTACAGGTGTGAG GC G	
	TAATGTCCGCACTC CG C	
	GGCG_ CAACA	
GAM2080 LOC201685 3'	GCACGGTGGCTCACACCTGTAA 91841	G AAC
T	ATTACAGGTGTGAG CAC GC	
	TAATGTCCACACTC GTG CG	
	G GCA	
GAM2080 LOC201868 5'	GCGTTGTGAGACATCCCTATAA 90527	C TG AGG
TT	AATTA AGG TG CACAACGC	

	TTAAT TCC AC GTGTTGCG	
	A CT AGA	
GAM2080 LOC201868 5'	GTGGCTCACTCCTGTAAT 90531	T G
	ATTACAGG GTGAG CAC	
	TAATGTCC CACTC GTG	
	T G	
GAM2080 LOC201868 3'	GTTGCTCACGCCTGTAAT 90532	GCA
	ATTACAGGTGTGAG CAAC	
	TAATGTCCGCACTC GTTG	
	—	
GAM2080 LOC201868 3'	CGCAGTGGCTCACGCCTGTAAT 90523	G AA
	ATTACAGGTGTGAG CAC CG	
	TAATGTCCGCACTC GTG GC	
	G AC	
GAM2080 LOC201895 3'	GTGGCTCACACCTGTAAT 90547	G
	ATTACAGGTGTGAG CAC	
	TAATGTCCACACTC GTG	
	G	
GAM2080 LOC201911 3'	GCGCGGTGGCTCACGCCTGTAA 91867	G AA
T	ATTACAGGTGTGAG CAC CGC	
	TAATGTCCGCACTC GTG GCG	
	G GC	
GAM2080 LOC202020 3'	GCACGGTGGCTCACGCCTGTAA 90601	G AAC
T	ATTACAGGTGTGAG CAC GC	
	TAATGTCCGCACTC GTG CG	
	G GCA	
GAM2080 LOC202781 3'	GCGCGGTGGCTCACGCCTGTAA 91973	G AA
T	ATTACAGGTGTGAG CAC CGC	
	TAATGTCCGCACTC GTG GCG	
	G GC	
GAM2080 LOC202868 3'	GCATGGTGGCTCACGCCTGTAA 92005	G AAC
T	ATTACAGGTGTGAG CAC GC	
	TAATGTCCGCACTC GTG CG	
	G GTA	
GAM2080 LOC202868 3'	GTGGCTCACACCTGTAAT 92008	G
	ATTACAGGTGTGAG CAC	
	TAATGTCCACACTC GTG	
	G	
GAM2080 LOC203083 3'	GCGTGGTGGCTCACACCTGTGA 92091	G A
T	ATTACAGGTGTGAG CAC ACGC	

		TAGTGTCCCACTC GTG TGCG	
		G G	
GAM2080	LOC203246 3'	GCGCGGTGGCTCACGCCTGTAA 90835	G AA
	T	ATTACAGGTGTGAG CAC CGC	
		TAATGTCCGCACTC GTG GCG	
		G GC	
GAM2080	LOC203378 3'	GCGCGGTGGCTCACACCTGTAA 92291	G AA
	T	ATTACAGGTGTGAG CAC CGC	
		TAATGTCCCACTC GTG GCG	
		G GC	
GAM2080	LOC203378 3'	GTGGCTTACACCTGTAAT 92299	G
		ATTACAGGTGTGAG CAC	
		TAATGTCCACATTC GTG	
		G	
GAM2080	LOC203397 3'	GTGACTCACACCTGTAAT 90902	G
		ATTACAGGTGTGAG CAC	
		TAATGTCCCACTC GTG	
		A	
GAM2080	LOC219376 3'	GCATGGTGGCTACCCCTGTAA 95517	T G AAC
	TT	AATTACAGG GTGAG CAC GC	
		TTAATGTCC CACTC GTG CG	
		C G GTA	
GAM2080	LOC219406 3'	GCAGTGGCCACGCCTGTAA 95205	A A AC
		ATTACAGGTGTG GGC CA GC	
		TAATGTCCGCAC CCG GT CG	
		- - GA	
GAM2080	LOC219406 3'	TGTTGGCGCACACCTGCAAT 95210	A AG A
		ATT CAGGTGTG GC CAACG	
		TAA GTCCACAC CG GTTGT	
		C G_ _	
GAM2080	LOC219540 3'	GCATGGTGGTACACACCTGTAA 95244	AGG AAC
	T	ATTACAGGTGTG CAC GC	
		TAATGTCCACAC GTG CG	
		ATG GTA	
GAM2080	LOC219627 3'	GCGCGGTGGCTCACGCCTGTAA 93808	G AA
	T	ATTACAGGTGTGAG CAC CGC	
		TAATGTCCGCACTC GTG GCG	
		G GC	
GAM2080	LOC219673 3'	GCGCGGTGGCTCACGCCTGTAA 94626	G AA
	T	ATTACAGGTGTGAG CAC CGC	

	TAATGTCCGCACTC GTG GCG	
	G GC	
GAM2080 LOC219722 5'	GCACGGTGGCTCACACCTGTAA 94681	G AAC
T	ATTACAGGTGTGAG CAC GC	
	TAATGTCCCACTC GTG CG	
	G GCA	
GAM2080 LOC219722 5'	GCATTGTGGTGAGTACCTGTAA 94682	GAGG C
	TTACAGGTGT CACAA GC	
	AATGTCCATG GTGTT CG	
	AGTG A	
GAM2080 LOC219919 3'	GCGTGGTGGCTCACACCTGTGA 94927	G A
T	ATTACAGGTGTGAG CAC ACGC	
	TAGTGTCCCACTC GTG TGCG	
	G G	
GAM2080 LOC220575 3'	CCAACGCGCAGCTCACACTTGT 76812	_____ ACAAC
AAT	ATTACAGGTGTGAG GC G	
	TAATGTTCACTC CG C	
	GACG__ CAACA	
GAM2080 LOC220662 3'	GCATGGTGGCCACGCCTGTAA 92822	A _ AAC
T	ATTACAGGTGTG GGC AC GC	
	TAATGTCCGCAC CCG TG CG	
	_ G GTA	
GAM2080 LOC220662 3'	GCGGTGGCTCACGCCTGTAAT 92825	G AA
	ATTACAGGTGTGAG CAC CGC	
	TAATGTCCGCACTC GTG GCG	
	G _	
GAM2080 LOC220662 3'	GTGGCTCACACCTGTAAT 92830	G
	ATTACAGGTGTGAG CAC	
	TAATGTCCCACTC GTG	
	G	
GAM2080 LOC221042 3'	GCGCAGTGGCTCACGCCTGTAA 94805	G AA
T	ATTACAGGTGTGAG CAC CGC	
	TAATGTCCGCACTC GTG GCG	
	G AC	
GAM2080 LOC221271 3'	GCGCGGTGGCTCACACCTGTAA 93520	G AA
T	ATTACAGGTGTGAG CAC CGC	
	TAATGTCCCACTC GTG GCG	
	G GC	
GAM2080 LOC221271 3'	TGATGGCTCACACCTGTAAT 93533	G _
	ATTACAGGTGTGAG CA CA	

	TAATGTCCCACTC GT GT	
	G A	
GAM2080 LOC221474 3'	GTAAC TCACGCCTGTAAT 94000	GC
	ATTACAGGTGTGAG AC	
	TAATGTCCGCACTC TG	
	AA	
GAM2080 LOC221477 3'	GCATGGTGGCTCACACCTGTAA 93773	G AAC
TT	AATTACAGGTGTGAG CAC GC	
	TTAATGTCCCACTC GTG CG	
	G GTA	
GAM2080 LOC221489 3'	GCACGGTGGCTCACACCTGTAA 95289	G AAC
T	ATTACAGGTGTGAG CAC GC	
	TAATGTCCCACTC GTG CG	
	G GCA	
GAM2080 LOC221543 3'	GCACGGTAGCTCACACCTGTAA 95380	GC AAC
T	ATTACAGGTGTGAG AC GC	
	TAATGTCCCACTC TG CG	
	GA GCA	
GAM2080 LOC221543 5'	GCGCCCTGGCTCACACCTGTAA 95381	G CAA
T	ATTACAGGTGTGAG CA CGC	
	TAATGTCCCACTC GT GCG	
	G CCC	
GAM2080 LOC221795 3'	GCGTGGTGGCTCACACCTGTGA 94075	G A
T	ATTACAGGTGTGAG CAC ACGC	
	TAGTGTCCCACTC GTG TGCG	
	G G	
GAM2080 LOC221954 5'	GCGCAGTGGCTCACACCTGTAA 95648	G AA
T	ATTACAGGTGTGAG CAC CGC	
	TAATGTCCCACTC GTG GCG	
	G AC	
GAM2080 LOC222066 3'	GCGTGGTGGCTCACACCTGTAA 94322	G A
T	ATTACAGGTGTGAG CAC ACGC	
	TAATGTCCCACTC GTG TGCG	
	G G	
GAM2080 LOC222066 3'	GTGGCTCACACCTGTGAT 94324	G
	ATTACAGGTGTGAG CAC	
	TAGTGTCCCACTC GTG	
	G	
GAM2080 LOC222182 3'	GTGGCTCACGCCTGTAAT 95860	G
	ATTACAGGTGTGAG CAC	

	TAATGTCCGCACTC GTG		
	G		
GAM2080 LOC222865 3'	GCGCGGTGGCTCACGCCTGTAA 94446	G	AA
T	ATTACAGGTGTGAG CAC CGC		
	TAATGTCCGCACTC GTG GCG		
	G GC		
GAM2080 LOC253532 3'	GTGGCTCACACTTGTAAT 97738	G	
	ATTACAGGTGTGAG CAC		
	TAATGTTCACTC GTG		
	G		
GAM2080 LOC253532 3'	TGGCAGGCACCTGTAAT 97742	GAG	A
	ATTACAGGTGT GC CA		
	TAATGTCCACG CG GT		
	GA_ _		
GAM2080 LOC253778 5'	CGTGGTGCCTCACGCCTGCAAT 96525	A	A
	ATT CAGGTGTGAGGCAC ACG		
	TAA GTCCGCACTCCGTG TGC		
	C G		
GAM2080 LOC254176 3'	GCGTGGTGGCTCACACCTGTGA 99172	G	A
T	ATTACAGGTGTGAG CAC ACGC		
	TAGTGTCCCACTC GTG TGCG		
	G G		
GAM2080 LOC254387 3'	GCGTGGTGACTCACACCTGTAA 96581	G	A
T	ATTACAGGTGTGAG CAC ACGC		
	TAATGTCCCACTC GTG TGCG		
	A G		
GAM2080 LOC254531 5'	GCACGGTGGCTCACACCTGTAA 96669	G	AAC
T	ATTACAGGTGTGAG CAC GC		
	TAATGTCCCACTC GTG CG		
	G GCA		
GAM2080 LOC254875 3'	GTGGCTCACACTTGTAAT 97783	G	
	ATTACAGGTGTGAG CAC		
	TAATGTTCACTC GTG		
	G		
GAM2080 LOC254875 3'	TGGCAGGCACCTGTAAT 97786	GAG	A
	ATTACAGGTGT GC CA		
	TAATGTCCACG CG GT		
	GA_ _		
GAM2080 LOC255042 3'	GTGGCTCACGCCTGTAA 97055	G	
	ATTACAGGTGTGAG CAC		

	TAATGTCCGCACTC GTG		
	G		
GAM2080 LOC255177 3'	GCGCAGTGGCTCACACCTGTAA 98395	G	AA
T	ATTACAGGTGTGAG CAC CGC		
	TAATGTCCCACTC GTG GCG		
	G AC		
GAM2080 LOC255231 3'	GTGGTTCACACCTGTAAT 97122	G	
	ATTACAGGTGTGAG CAC		
	TAATGTCCCACTT GTG		
	G		
GAM2080 LOC255326 3'	GTGGCTCACGCCTGTAAT 98122	G	
	ATTACAGGTGTGAG CAC		
	TAATGTCCGCACTC GTG		
	G		
GAM2080 LOC255461 3'	GCGACTCACACCTGTAAT 99139	_____	
	ATTACAGGTGTGAG GC		
	TAATGTCCCACTC CG		
	AG_____		
GAM2080 LOC255516 3'	GCGACTCACACCTGTAAT 99153	_____	
	ATTACAGGTGTGAG GC		
	TAATGTCCCACTC CG		
	AG_____		
GAM2080 LOC255624 3'	GCGGTGGCTCACACCTGTAAT 96164	G	AA
	ATTACAGGTGTGAG CAC CGC		
	TAATGTCCCACTC GTG GCG		
	G _		
GAM2080 LOC255937 3'	CGCTGTGGCTCACACCTGTAAT 97679	G	A
	ATTACAGGTGTGAG CACA CG		
	TAATGTCCCACTC GTGT GC		
	G C		
GAM2080 LOC256073 3'	GTGGCTTACACCTGTAAT 98489	G	
	ATTACAGGTGTGAG CAC		
	TAATGTCCACATTC GTG		
	G		
GAM2080 LOC256277 3'	GCGCAGTGGCTCACGCCTGTAA 96351	G	AA
T	ATTACAGGTGTGAG CAC CGC		
	TAATGTCCGCACTC GTG GCG		
	G AC		
GAM2080 LOC256515 3'	GCGTGGTGGCTCACACCTGTGA 98213	G	A
T	ATTACAGGTGTGAG CAC ACGC		

		TAGTGTCCCACTC GTG TGCG		
		G G		
GAM2080	LOC256520 3'	GCGCGGTGACTCACGCCTATAA 97669	C	G AA
	T	ATTA AGGTGTGAG CAC CGC		
		TAAT TCCGCACTC GTG GCG		
		A A GC		
GAM2080	LOC257480 3'	GCATGGTGGCTCACGCCTGTAA 78433		G AAC
	T	ATTACAGGTGTGAG CAC GC		
		TAATGTCCGCACTC GTG CG		
		G GTA		
GAM2080	LOC257596 3'	GCACGGTAGCTCACACCTGTAA 99783		GC AAC
	T	ATTACAGGTGTGAG AC GC		
		TAATGTCCCACTC TG CG		
		GA GCA		
GAM2080	LOC257596 5'	GCGCCCTGGCTCACACCTGTAA 99784		G CAA
	T	ATTACAGGTGTGAG CA CGC		
		TAATGTCCCACTC GT GCG		
		G CCC		
GAM2080	LOC51279 3'	GCGCAGTGGCTCACGCCTGTAA 33760		G AA
	T	ATTACAGGTGTGAG CAC CGC		
		TAATGTCCGCACTC GTG GCG		
		G AC		
GAM2080	LOC51333 3'	GTGACTCACGCCTGTAAT 34054	G	
		ATTACAGGTGTGAG CAC		
		TAATGTCCGCACTC GTG		
		A		
GAM2080	LOC51336 3'	GCATGGTGGCTCACACCTGTAA 34072		G AAC
	TT	AATTACAGGTGTGAG CAC GC		
		TTAATGTCCCACTC GTG CG		
		G GTA		
GAM2080	LOC55974 3'	GCGCGGTGGCTCACGCCTGTAA 38747		G AA
	T	ATTACAGGTGTGAG CAC CGC		
		TAATGTCCGCACTC GTG GCG		
		G GC		
GAM2080	LOC57118 3'	GTGGCTCACGCCTGTAAT 40225	G	
		ATTACAGGTGTGAG CAC		
		TAATGTCCGCACTC GTG		
		G		
GAM2080	LOC64167 3'	GCGCGGTGGCTCACGCCTGTAA 42540		G AA
	T	ATTACAGGTGTGAG CAC CGC		

		TAATGTCCGCACTC GTG GCG		
		G GC		
GAM2080	LOC89890 3'	GCGCGGTGGCTCACGCCTGTAA 61207	G	AA
	T	ATTACAGGTGTGAG CAC CGC		
		TAATGTCCGCACTC GTG GCG		
		G GC		
GAM2080	LOC90072 3'	GTGGCTCACACCTGCAAT 61961 A	G	
		ATT CAGGTGTGAG CAC		
		TAA GTCCACACTC GTG		
		C G		
GAM2080	LOC90092 3'	GCAGCTCACACCTGTAAT 62063	_____	
		ATTACAGGTGTGAG GC		
		TAATGTCCACACTC CG		
		GA_____		
GAM2080	LOC90092 3'	GTGGCTCACACCTGTAAT 62074	G	
		ATTACAGGTGTGAG CAC		
		TAATGTCCACACTC GTG		
		G		
GAM2080	LOC90321 3'	GCGCAGTGGCTCACACCTGTAA 62936	G	AA
	T	ATTACAGGTGTGAG CAC CGC		
		TAATGTCCACACTC GTG GCG		
		G AC		
GAM2080	LOC90509 3'	GCACGGTGGCTCACGCCTGTAA 63793	G	AAC
	T	ATTACAGGTGTGAG CAC GC		
		TAATGTCCGCACTC GTG CG		
		G GCA		
GAM2080	LOC90591 3'	GTGGCTCACGCCTGTAA 64185	G	
		ATTACAGGTGTGAG CAC		
		TAATGTCCGCACTC GTG		
		G		
GAM2080	LOC90624 3'	GCGCTGTGGCTCACACCTGTAA 64370	G	A
	T	ATTACAGGTGTGAG CACA CGC		
		TAATGTCCACACTC GTGT GCG		
		G C		
GAM2080	LOC90639 3'	CCAACGCGCGGCTCACGCCTGC 64407	A	_____ ACAAC
	AAT	ATT CAGGTGTGAG GC G		
		TAA GTCCGCACTC CG C		
		C GGCG_____ CAACA		
GAM2080	LOC90777 3'	GCACGGTGGCTCACGCCTATAA 64666	C	G AAC
	T	ATTA AGGTGTGAG CAC GC		

		TAAT TCCGCACTC GTG CG		
		A G GCA		
GAM2080	LOC90785 3'	CCAACGCACAGGCTCACACCTG 64712	_____	ACAAC
	TGA	TTACAGGTGTGAG GC G		
		AGTGTCCCACTC CG C		
		GGACA__ CAACA		
GAM2080	LOC91035 3'	GTGGCTCACGCCTATAAT 65305 C G		
		ATTA AGGTGTGAG CAC		
		TAAT TCCGCACTC GTG		
		A G		
GAM2080	LOC91574 3'	GTGCCTCACATCTGTAAT 67116		
		ATTACAGGTGTGAGGCAC		
		TAATGTCTACACTCCGTG		
GAM2080	LOC91750 3'	GCATGGTGGCTCACGCCTGTAA 67655	G	AAC
	T	ATTACAGGTGTGAG CAC GC		
		TAATGTCCGCACTC GTG CG		
		G GTA		
GAM2080	LOC91862 3'	CCAACGCGCGGCTCACACCTGT 54572	_____	ACAAC
	AA	TTACAGGTGTGAG GC G		
		AATGTCCCACTC CG C		
		GGCG__ CAACA		
GAM2080	LOC92078 3'	CGAGGTGGCTCACACCTATAAT 68599 C G AA		
		ATTA AGGTGTGAG CAC CG		
		TAAT TCCCACTC GTG GC		
		A G GA		
GAM2080	LOC92223 3'	GCATGGTGGCTCACACCTGTAA 69051	G	AAC
	T	ATTACAGGTGTGAG CAC GC		
		TAATGTCCCACTC GTG CG		
		G GTA		
GAM2080	LOC92228 3'	GTGGCTCACGCCTGTAA 69080 G		
		ATTACAGGTGTGAG CAC		
		TAATGTCCGCACTC GTG		
		G		
GAM2080	LOC92267 3'	GCGCAGTGGCTCACACCTGTAA 69171	G	AA
	T	ATTACAGGTGTGAG CAC CGC		
		TAATGTCCCACTC GTG GCG		
		G AC		
GAM2080	LOC92270 5'	GCATGGTGGCTCACGCCTGTAA 69186	G	AAC
	T	ATTACAGGTGTGAG CAC GC		

		TAATGTCCGCACTC GTG CG	
		G GTA	
GAM2080	LOC92299 3'	GCGCAGTGGCTCACACCTGTAA 69369	G AA
	T	ATTACAGGTGTGAG CAC CGC	
		TAATGTCCCACTC GTG GCG	
		G AC	
GAM2080	LOC92299 3'	GCGCGGTGGCTCACGCCTGTAA 69370	G AA
	T	ATTACAGGTGTGAG CAC CGC	
		TAATGTCCGCACTC GTG GCG	
		G GC	
GAM2080	LOC92482 3'	GTGGCTCACGCCTGTAAT 70024	G
		ATTACAGGTGTGAG CAC	
		TAATGTCCGCACTC GTG	
		G	
GAM2080	LOC92573 5'	GCGGTGGCTCACACCTGTAAT 70376	G AA
		ATTACAGGTGTGAG CAC CGC	
		TAATGTCCCACTC GTG GCG	
		G _	
GAM2080	LOC92771 3'	GCGGCTCACACCTGTAAT 54213	_____
		ATTACAGGTGTGAG GC	
		TAATGTCCCACTC CG	
		GG_	
GAM2080	LOC93132 5'	GCACGGTGGCTCACACCTGTAA 71992	G AAC
	T	ATTACAGGTGTGAG CAC GC	
		TAATGTCCCACTC GTG CG	
		G GCA	
GAM2080	LOC93613 3'	GCATGGTGATGCACACCTGTAA 73076	AGG AAC
	T	ATTACAGGTGTG CAC GC	
		TAATGTCCACAC GTG CG	
		GTA GTA	
GAM2081	KLK4 3'	CCATGAAATTGACCCCA 63531	TGC
		TGGG CAATTCGTGG	
		ACCC GTTAAAGTACC	
		CCA	
GAM2081	POU2AF1 5'	CCACACCACCTTCACACCCA 21733	CCAATTC
		TGGGTG GTGGTGTGG	
		ACCCAC CACCACACC	
		ACTTC_	
GAM2081	SMAC 5'	TCACACACAACCTGGCACCCA 58028	ATTCG _
		TGGGTGCCA TG GTGTGG	

ACCCACGGT AC CACACT
 CA___ A
 GAM2081 ZRF1 5' CCACACCACGAAAGATCCA 95945 GCCAA
 TGGGT TTTCGTGGTGTGG
 |||| |||||
 ACCTA AAAGCACACACC
 G___
 GAM2081 FLJ23467 5' TCCAAGGCAAGACTGGCACCCA 45015 ATT GTG G_
 TGGGTGCCA TC GT TGA
 ||||| || || |||
 ACCCACGGT AG CG ACCT
 C__ AA_ GA
 GAM2081 MGC4093 3' CCACACCCCGACACCCA 48331 CCAAT T
 TGGGTG TTCG GGTGTGG
 |||| ||| |||||
 ACCCAC AGGC CCACACC
 _____ C
 GAM2081 PRO2325 3' CCACACCAGCCACCGGCCCA 98036 T AATTTCG
 TGGG GCC TGGTGTGG
 ||| ||| |||||
 ACCC CGG ACCACACC
 _ CCACCG_
 GAM2081 LOC147671 3' CCACACACACAGGCACCCA 79114 AATTTC _
 TGGGTGCC GTG GTGTGG
 ||||| ||| |||||
 ACCCACGG CAC CACACC
 A_____ A
 GAM2081 LOC201115 5' CCACACCATCAACACCC 89477 CCAAT C
 GGGTG TT GTGGTGTGG
 |||| || |||||
 CCCAC AA TACCACACC
 _____ C
 GAM2082 LGR6 3' AGCTGTGGACCAGAGACCT 85354 T AGTTA
 AG GTCTCTGGT GCAGCT
 || ||||| |||||
 TC CAGAGACCA TGTCGA
 _ GG_
 GAM2082 ATP6V1EL2 5' AAGTGGA ACTCCAGAGACACT 55558 T AGCA
 AGTGTCTCTGG AGTT GCTT
 ||||| ||| |||
 TCACAGAGACC TCAA TGAA
 _ GG_
 GAM2082 BCL2L12 3' AAGCTGCTACAAGATGACAC 57639 _ GGTAGT
 GTGTC TCT TAGCAGCTT
 |||| ||| |||||
 CACAG AGA ATCGTCGAA
 T AC_
 GAM2082 C8orf14 3' AGCTGCTAATAAAGACAT 55080 CTGGTA
 GTGTCT GTTAGCAGCT
 |||| |||||

TACAGA TAATCGTCGA
 AA____
 GAM2082 DKFZP434J193 5' AACCACCAAGGGGAGACATT 71552 ____ A
 AGTGTCTCT GGT GTT
 ||||| ||||
 TTACAGAGG CCA CAA
 GGAA C
 GAM2082 HSPC159 3' AAGCTGTTGGGACAAAGACAC 27193 CTG AG
 GTGTCT GT TTAGCAGCTT
 |||| || |||||
 CACAGA CA GGTTGTCGAA
 AA_ G_
 GAM2082 KIAA1143 3' CTGAGTACCAGAGCCACT 69239 T G
 AGTG CTCTGGTA TTAG
 ||| ||||| |||
 TCAC GAGACCAT AGTC
 C G
 GAM2082 MGC2452 5' AAGCCACTTCCTCAGAGAGAC 51962 G GT TT CA
 GT TCTCTG AG AG GCTT
 || |||| || || |||
 CA AGAGAC TC TC CGAA
 G _ CT AC
 GAM2082 NUBP1 3' AAGCCACTTTCTCAGAGACACT 11757 GT TT CA
 AGTGTCTCTG AG AG GCTT
 ||||| || || |||
 TCACAGAGAC TC TC CGAA
 _ TT AC
 GAM2082 RNF8 3' AAGCTGCTGTTGTACAGAAAGA 15550 _ GTAGT
 C GTC TCTG TAGCAGCTT
 || ||| |||||
 CAG AGAC GTCGTCGAA
 AA ATGTT
 GAM2082 LOC146445 3' AGCTGCCACCAGAGCCAC 84678 T AGTTA
 GTG CTCTGGT GCAGCT
 || |||| |||||
 CAC GAGACCA CGTCGA
 C C_
 GAM2082 LOC158709 3' AAGCTGCTATAACAGAACAC 82863 C GTAGT
 GTGT TCTG TAGCAGCTT
 ||| ||| |||||
 CACA AGAC ATCGTCGAA
 _ AAT_
 GAM2082 LOC203113 3' AAGCAAACTACCAAAGAC 90792 C AGCA
 GTCT TGGTAGTT GCTT
 ||| ||||| |||
 CAGA ACCATCAA CGAA
 A AA_
 GAM2082 LOC51313 3' CTGCAAACCAGAGACACT 33996 AGTTA
 AGTGTCTCTGGT GCAG
 ||||| |||

			TCACAGAGACCA	CGTC		
			AA__			
GAM2083	BSN	3'	CCAGCATCATGAGCAAG	14379	A	CTTCA AA
			CTTGCTCAT GT	GC GG		
			GAACGAGTA TA	CG CC		
			C ____ AC			
GAM2083	CLCA2	3'	CCTTACACTTTGGCTATGAACA	22563	C	TTCAGC_
	A		TTG TCATAGTC	AAGG		
			AAC AGTATCGG	TTCC		
			A TTTCA			
GAM2083	FADD	3'	TCCTCACTATGACACTGAGCAA	15126	TA	TTC CA
	G		CTTGCTCA GTC	AG AGGA		
			GAACGAGT CAG	TC TCCT		
			CA TA_ AC			
GAM2083	HLCS	5'	TCCATTGAAGACTTGAACAAG	6421	C T	CAA
			CTTG TCA AGTCTTCAG	GGA		
			GAAC AGT TCAGAAGTT	CCT		
			A _ A_			
GAM2083	MEST	3'	CTGAAAGACCTATGAGCAA	70459	_ _	
			TTGCTCATAG TCTT	CAG		
			AACGAGTATC AGAA	GTC		
			C A			
GAM2083	PLP2	5'	TCCTCGAAACCACGAGCAAG	12176	ATA C	AGCA
			CTTGCTC GT TTC	AGGA		
			GAACGAG CA AAG	TCCT		
			CAC _ C_			
GAM2083	PLXNA2	3'	TCCCTAAAGTTACTATGAGAAG	48003	G _	C CAA
			CTT CTCATAGT CTT AG	GGA		
			GAA GAGTATCA GAA TC	CCT		
			_ TT A _			
GAM2083	AP1GBP1	3'	CCTCAGACCAGTGAGCAA	24345	A_	TCAGCA
			TTGCTCAT GTCT	AGG		
			AACGAGTG CAGA	TCC		
			AC C_			
GAM2083	AP1GBP1	3'	CCTCAGACCAGTGAGCAA	24346	A_	TCAGCA
			TTGCTCAT GTCT	AGG		
			AACGAGTG CAGA	TCC		
			AC C_			
GAM2083	DDX34	3'	TCCCTGCTGGAGACCAACAAG	28679	CTCATA	A
			CTTG GTCTTCAGCA	GGA		

GAAC CAGAGGTCGT CCT
 AAC__ C
 GAM2083 DKFZP586G1122 3' CCGCAAAACTGTGAGCAA 61938 CTTCA AA
 TTGCTCATAGT GC GG
 ||||| || ||
 AACGAGTGTCA CG CC
 AAA__ __
 GAM2083 FAM10A6 3' CCTTGCTGAAGGAAAAGCAA 72782 CATAG
 TTGCT TCTTCAGCAAGG
 |||| |||||
 AACGA GGAAGTCGTTCC
 AAA__
 GAM2083 KIAA0475 5' CCTTAATACATGAGCAAG 30115 A C CAGC
 CTTGCTCAT GT TT AAGG
 ||||| || || ||
 GAACGAGTA CA AA TTCC
 _ T ____
 GAM2083 KIAA1655 5' CCTCACTGTGGATGAGCAA 67179 TAG T CA
 TTGCTCA TCT CAG AGG
 ||||| || || ||
 AACGAGT AGG GTC TCC
 ____ T AC
 GAM2083 MGC3077 3' TCCTTGTTTTTAGACTAT 44128 TC_
 ATAGTCT AGCAAGGA
 ||||| |||||
 TATCAGA TTGTTCCCT
 TTT
 GAM2083 RAB40C 3' CCTTGTTTGGGATTATGAACAA 41278 C TC
 TTG TCATAGTCT AGCAAGG
 || ||||| |||||
 AAC AGTATTAGG TTGTTCC
 A GT
 GAM2083 ST13 3' CCTTGCTGAAGGAAAAGCAA 15431 CATAG
 TTGCT TCTTCAGCAAGG
 |||| |||||
 AACGA GGAAGTCGTTCC
 AAA__
 GAM2083 LOC118491 5' TCCTGTTGGAGAACTATGAGCA 74358 _ A
 AG CTTGCTCATAGT CTTGAGCA GGA
 ||||| ||||| ||
 GAACGAGTATCA GAGGTTGT CCT
 A _
 GAM2083 LOC125228 3' CCTTTGGAACTATGGGCAA 74863 C GC
 TTGCTCATAGT TTCA AAGG
 ||||| || ||
 AACGGGTATCA AGGT TTCC
 A _
 GAM2083 LOC126751 3' CCCTGCTGAGATTGAGCCAG 75072 T TA T A
 CT GCTCA GTCT CAGCA GG
 || |||| || || || ||

		GA CGAGT TAGA GTCGT CC	
		C _ _ C	
GAM2083	LOC149052 3'	CCTTGCTGAAGGAAAAGCAA 79872	CATAG
		TTGCT TCTTCAGCAAGG	
		AACGA GGAAGTCGTTCC	
		AAA_	
GAM2083	LOC158886 3'	CCTTGCTGAAGGAAAAGCAA 83722	CATAG
		TTGCT TCTTCAGCAAGG	
		AACGA GGAAGTCGTTCC	
		AAA_	
GAM2083	LOC200197 3'	CCCTGCCGACATGAGCAA 90016	A TTCA A
		TTGCTCAT GTC GCA GG	
		AACGAGTA CAG CGT CC	
		_ C _ C	
GAM2083	LOC219731 5'	CCAGGTTAAACTATGAGGAAG 94699	G C C AA
		CTT CTCATAGT TT AGC GG	
		GAA GAGTATCA AA TTG CC	
		G A _ GA	
GAM2083	LOC221178 3'	CCCTGCTGATGATGAGCAAG 95168	AGTCT A
		CTTGCTCAT TCAGCA GG	
		GAACGAGTA AGTCGT CC	
		GT _ C	
GAM2083	LOC222407 5'	CCTACACTGAAAACAATGAGCA 95973	A C CA_
	A	TTGCTCAT GT TTCAG AGG	
		AACGAGTA CA AAGTC TCC	
		A A ACA	
GAM2083	LOC245718 3'	CCTTGCTGAAGGAAAAGCAA 92415	CATAG
		TTGCT TCTTCAGCAAGG	
		AACGA GGAAGTCGTTCC	
		AAA_	
GAM2083	LOC256228 5'	CCTTGCTGAAGCAGGACAGCAA 97969	CATAGT
	G	CTTGCT CTTCAGCAAGG	
		GAACGA GAAGTCGTTCC	
		CAGGAC	
GAM2084	BRCA1 3'	GTTTGCCAGAAAACACCA 24573	AA GC
		TGG TTTTCTGG CGAAT	
		ACC AAAAGACC GTTTG	
		AC _	
GAM2084	EYA4 3'	TATTTGGAATAAAAATTCCA 15886	C GG
		TGGAATTTT TG CCGAATA	

			ACCTTAAAA AT GGTTTAT		
			— AA		
GAM2084	MECP2	3'	ATTTGGCAGAAAATTACA 18385	G	GG
			TG AATTTTCT GCCGAAT		
			AC TTAAAAGA CGGTTTA		
			A —		
GAM2084	CG012	3'	TGGCTACCCAGAAAATTTCA 84171		—
			TGGAATTTTCTGG GCCG		
			ACTTTAAAAGACC CGGT		
			CAT		
GAM2084	HBXAP	3'	ATTTTTCCTAGAAAACCTCCA 33880	A	CC
			TGGA TTTTCTGGG GAAT		
			ACCT AAAAGATCC TTTA		
			C TT		
GAM2084	KIAA0997	3'	TCAACCCAAAAAGTTCCA 30889	C	CC
			TGGAATTTT TGGG GA		
			ACCTTGAAA ACCC CT		
			A AA		
GAM2084	KIAA1014	3'	GTATTCTCCATAAAATTCCA 65961	C	CC
			TGGAATTTT TGGG GAATAC		
			ACCTTAAAA ACCT CTTATG		
			T —		
GAM2084	MAGEH1	3'	GTATTCGTTTTTAAAATTCC 26771	CT	C
			GGAATTTT GGGC GAATAC		
			CCTTAAAA TTTG CTTATG		
			T_ —		
GAM2084	PSK	5'	TATTCGGGGTTCAGACCCCA 32882	AATTT	—
			TGG TCTGGGCC GAATA		
			ACC AGACTTGG CTTAT		
			CC_ GG		
GAM2084	SDF1	3'	TATTCCTAGAACTTCCA 92520	T	CC
			TGGAA TTTCTGGG GAATA		
			ACCTT AAAGATCC CTTAT		
			C —		
GAM2084	TAO1	5'	TATTCGGGGTTCAGACCCCA 17720	AATTT	—
			TGG TCTGGGCC GAATA		
			ACC AGACTTGG CTTAT		
			CC_ GG		
GAM2084	VMP	3'	GTACCCGGCCACCAGAAAACCC 55765	AA	— AA
	C		GG TTTTCTGG GCCG TAC		

		CC AAAAGACC CGGC ATG	
		CC AC CC	
GAM2084	LOC126295 3'	GTATAATGCTCCAGAAAATTC 74975	_ CGA
		GAATTTTCTGG GC ATAC	
		CTTAAAAGACC CG TATG	
		T TAA	
GAM2084	LOC146184 5'	ATTCAACCAGAAAATTTCA 84596	GCC
		TGGAATTTTCTGG GAAT	
		ACTTTAAAAGACC CTTA	
		AA_	
GAM2084	LOC150407 3'	GTATTCCAAGAAAATTTCA 80643	GGGCC
		TGGAATTTTCT GAATAC	
		ACTTTAAAAGA CTTATG	
		AC__	
GAM2084	LOC91496 5'	TTTGGCAGAAAATGCCA 66813	A GG
		TGG ATTTTCT GCCGAA	
		ACC TAAAAGA CGGTTT	
		G _	
GAM2085	ADCY2 3'	TACTTTGATTACAGTGCCTGT 65652	ATAG C_
		ACAGGTAC GTAA CAAAGTA	
		TGTCCGTG CATT GTTTCAT	
		A__ TA	
GAM2085	CSTA 5'	ACTTTGGTTCCAGCATCCTGT 19055	TACATA T
		ACAGG GG AACCAAAGT	
		TGTCC CC TTGGTTTCA	
		TACGA_ _	
GAM2085	DDEF2 3'	TACTTTGGTTGCAGCACAAGT 15289	GTACATAG
	T	ACAG GTAACCAAAGTA	
		TGTC CGTTGGTTTCAT	
		AACACGA_	
GAM2085	DFFA 3'	TTTGA CTACCTATGTACT 16599	AC
		GGTACATAGGTA CAAA	
		TCATGTATCCAT GTTT	
		CA	
GAM2085	DMD 5'	TACTCTGGTGACACAACCTGT 15717	ACATAG A A
		ACAGGT GT ACCA AGTA	
		TGTCCA CA TGGT TCAT	
		ACA__ G C	
GAM2085	DMD 5'	TACTCTGGTGACACAACCTGT 15727	ACATAG A A
		ACAGGT GT ACCA AGTA	

		TGTCCA CA TGGT TCAT		
		ACA__ G C		
GAM2085 DMD	5'	TACTCTGGTGACACAACCTGT 15703	ACATAG A A	
		ACAGGT GT ACCA AGTA		
		TGTCCA CA TGGT TCAT		
		ACA__ G C		
GAM2085 NPY1R	3'	TACTTTGATTACCTGTTCTCC 8063	TAC C	
		GG ATAGGTAA CAAAGTA		
		CC TGTCCATT GTTTCAT		
		TCT A		
GAM2085 POLQ	3'	ACTTTGTTCCACATCTGT 22734	ACATA T	
		ACAGGT GG AACCAAAGT		
		TGTCTA CC TTGGTTTCA		
		CA__ _		
GAM2085 SBF1	5'	GCTTCACCTATGTGCC 66070	AACCA	
		GGTACATAGGT AAGT		
		CCGTGTATCCA TTCG		
		C__		
GAM2085 USP14	3'	TACTGCACACCTATTACCT 18939	C AACCAA	
		AGGTA ATAGGT AGTA		
		TCCAT TATCCA TCAT		
		_ CACG__		
GAM2085 BZW2	3'	ACTTTGGTAGTTGTGTATCTG 26732	G A	
		CAGGTACATAG TA CCAAAGT		
		GTCTATGTGTT AT GGTTTCA		
		G _		
GAM2085 CDC14A	3'	ACTTTACACATGTGCCT 14781	AG CCAA	
		AGGTACAT GTAA AGT		
		TCCGTGTA CATT TCA		
		CA ____		
GAM2085 FLJ13187	3'	TACTTTGGCTTTTTCATATACC 45166	C AG T _	
T		AGGTA AT G AA CCAAAGTA		
		TCCAT TA T TT GGTTTCAT		
		A CT T C		
GAM2085 FLJ21870	3'	CTTTGGTCACATCTGT 43744	ACATAG A	
		ACAGGT GT ACCAAAG		
		TGTCTA CA TGGTTTC		
		_____ C		
GAM2085 FREQ	3'	ACTTTGGTCCTCGGTTCC 27367	T AT TA	
		GG AC AGG ACCAAAGT		

		CC TG TCC TGGTTTCA		
		T GC _		
GAM2085	HEF1	3' ACTTTGGTGCTACTACC	22155	CATA A
		GGTA GGTA CCAAAGT		
		CCAT TCGT GGTTC		
		CA_ _		
GAM2085	KIAA0981	3' ACTTTGGTTTTTGATACCTGT	62082	_ TAGGT
		ACAGGTA CA AACCAAAGT		
		TGTCCAT GT TTGGTTTCA		
		A TT_		
GAM2085	KIAA1240	3' TACTTTGGCCATAGCCTACTG	67291	GTACA AA_
		CAG TAGGT CCAAAGTA		
		GTC ATCCG GGTTTCAT		
		_ ATACC		
GAM2085	KIAA1649	3' ACCCTGGTTTTGTGTAGCC	67513	_ GT AA
		GGT ACATAG AACCA GT		
		CCG TGTGTT TTGGT CA		
		A _ CC		
GAM2085	KIAA1900	3' ACCTTGGTTACTCTGACCT	73633	A TA A
		AGGT CA GGTAACCAA GT		
		TCCA GT TCATTGGTT CA		
		_ C_ C		
GAM2085	MBD2	3' TACTTTACAAACCATTACCTGT	32336	C A AACC
		ACAGGTA AT GGT AAAGTA		
		TGTCCAT TA CCA TTTCAT		
		_ _ AACA		
GAM2085	MGC23980	3' ACTTTAGTCCTGTATCTGT	59396	TA TA C
		ACAGGTACA GG AC AAAGT		
		TGTCTATGT CC TG TTTCA		
		_ _ A		
GAM2085	MGC4840	3' TACCTTAGTGGATTACCTGT	72027	_ _
		ACAGGTA CAT AGGTA		
		TGTCCAT GTG TCCAT		
		TTAG AT		
GAM2085	TIP-1	3' TACTTTGGTTACCGTGGAAC	28233	A_ A
		GGT CAT GGTAACCAAAGTA		
		CCA GTG CCATTGGTTTCAT		
		AAG _		
GAM2085	LOC129011	3' ACTTTGGTTTTGTACT	75364	TAGGT
		GGTACA AACCAAAGT		

		TCATGT TTGGTTTCA		
		TT__		
GAM2085	LOC149134	5' ACTTTAGTGTCTATGTAC 85513	TA	C
		GTACATAGG AC AAAGT		
		CATGTATCC TG TTTCA		
		TG A		
GAM2085	LOC153856	3' ACTCTGTACATGTATCTGT 81872	AG	AC A
		ACAGGTACAT GTA CA AGT		
		TGTCTATGTA CAT GT TCA		
		__ __ C		
GAM2085	LOC200081	3' ACTTCAGCTACCTCTTAATGCC 89969	CAT__	ACCA
		TGT ACAGGTA AGGTA AAGT		
		TGTCCGT TCCAT TTCA		
		AATTC CGAC		
GAM2086	LOC93206	5' ATATTTCCGGATAACATATC 72189	C	__
		GGT TG ATCCGGAAATAT		
		CTA AC TAGGCCTTTATA		
		T AA		
GAM2087	A2M	5' CATCTGGTCTCCTCCAGCTCCT 5230	A	CT G
		T AAGGAGCT GAGGA TT AGATG		
		TTCCTCGA CTCCT GG TCTAC		
		C CT _		
GAM2087	ALPPL2	3' CATCCCGGAGTTCCTGCTCC 69425	T A	_ A
		GGAGC AG GGA CTTTG GATG		
		CCTCG TC CCT GAGGC CTAC		
		_ C T C		
GAM2087	BIN3	3' CATCCTGGGGAGCCCTCTGGCC 38574	A	A__ GA
		CCT AGG GCTAGAGG CTTT GATG		
		TCC CGGTCTCC GGGG CTAC		
		C CGA TC		
GAM2087	BSN	3' CATCTCAAAGCCATCCCCCT 14377	AGCTA	_ A
		AGG GA GG CTTTGAGATG		
		TCC CT CC GAAACTCTAC		
		CC__ A _		
GAM2087	CA14	3' CAAAGTCCTCTACCCCCT 25058	AGC	
		AGG TAGAGGACTTTG		
		TCC ATCTCCTGAAAC		
		CCC		
GAM2087	CD44	5' CAGGGATCCTCCAGCTCCTT 7026	A	_
		AAGGAGCT GAGGA CTTTG		

			TTCCTCGA CTCCT GGGAC		
			C A		
GAM2087	COL1A1	3'	ATCCCAACCTGGCTCC 5390	AG	ACT A
			GGAGCT AGG TTG GAT		
			CCTCGG TCC AAC CTA		
			— — C		
GAM2087	EIF4EBP2	3'	CATCTTTTGTCTCCCCTAGTCC 15854	AG	A CTTT_
			C GG CTAG GGA GAGATG		
			CC GATC CCT TTCTAC		
			CT C CTGTT		
GAM2087	GAB2	3'	ATCCTCCCTCTGGCCCCTT 25456	A	ACTTT _
			AAGG GCTAGAGG GAG AT		
			TTCC CGGTCTCC CTC TA		
			C — C		
GAM2087	GAB2	3'	ATCCTCCCTCTGGCCCCTT 55403	A	ACTTT _
			AAGG GCTAGAGG GAG AT		
			TTCC CGGTCTCC CTC TA		
			C — C		
GAM2087	GGT1	5'	CAGAGCCCTCTAGCTGCTT 26419	G	A
			AAG AGCTAGAGG CTTTG		
			TTC TCGATCTCC GAGAC		
			G C		
GAM2087	GGT2	5'	CAGAGCCCTCTAGCTGCTT 74085	G	A
			AAG AGCTAGAGG CTTTG		
			TTC TCGATCTCC GAGAC		
			G C		
GAM2087	GJA5	3'	CATCTGTCACCCTGCAGCTCCT 19162	AG	ACTTTG
	T		AAGGAGCT AGG AGATG		
			TTCCTCGA TCC TCTAC		
			CG CACTG_		
GAM2087	IGF1	3'	CATCTCAAAGAGCAGTAGCTCT 7062	GAGGA	
			GGAGCTA CTTTGAGATG		
			TCTCGAT GAAACTCTAC		
			GACGA		
GAM2087	KRT1	3'	CATCCTATTCCCCCAGCTCTT 21504	AGA	CTT A
			AAGGAGCT GGA TG GATG		
			TTTCTCGA CCT AT CTAC		
			CCC T_ C		
GAM2087	NRXN2	5'	CAGAGAGACCCCTAGCTCCT 57828	A A_	
			AGGAGCTAG GG CTTTG		

TCCTCGATC CC GAGAC
 C AGA
 GAM2087 PML 3' CATTTTCTGTCCTCTAAGTCCT 53808 GC TTT
 AGGA TAGAGGAC GAGATG
 |||| ||||| |||||
 TCCT ATCTCCTG TTTTAC
 GA TC_
 GAM2087 PML 3' CATTTTCTGTCCTCTAAGTCCT 53814 GC TTT
 AGGA TAGAGGAC GAGATG
 |||| ||||| |||||
 TCCT ATCTCCTG TTTTAC
 GA TC_
 GAM2087 SIAT7D 3' ATCTCAGGCTCCACTCC 27704 CTAGA C
 GGAG GGA TTTGAGAT
 |||| || |||||
 CCTC CCT GGA CTCTA
 A C
 GAM2087 C8orf14 5' CATCCAATGTCCCCTAACTCTT 55082 C A T A
 AGGAG TAG GGAC TTG GATG
 |||| || |||| || ||||
 TTCTC ATC CCTG AAC CTAC
 A C T _
 GAM2087 C9orf7 3' CTGGAGTCCTCTGCTCCTT 34581 T G
 AAGGAGC AGAGGACTTT AG
 ||||| ||||| || ||
 TTCCTCG TCTCCTGAGG TC
 - -
 GAM2087 DDM36 3' TCACCTCCCAGCTCCTT 40929 A_ ACTT
 AAGGAGCT GAGG TGA
 ||||| |||| |||
 TTCCTCGA CTCC ACT
 CC _
 GAM2087 DKFZP434J037 3' CATCTCAAGGGGCCAGCCTCC 48941 _ AGA A_
 T AGGAG CT GG CTTTGAGATG
 |||| || || |||||
 TCCTC GA CC GGA ACTCTAC
 C C_ GG
 GAM2087 KCND1 5' CATCTCAGTCTCTCTAAACCCT 18338 AGC _ TT
 AGG TAGAG GACT GAGATG
 || |||| |||| |||||
 TCC ATCTC CTGA CTCTAC
 CAA T _
 GAM2087 KIAA1163 3' TGAGGTCATCCCTAGCTCCTT 79656 AG_
 AAGGAGCTAG GACTTTG
 ||||| |||||
 TTCCTCGATC CTGGAGT
 CCTA
 GAM2087 KIAA1305 3' CATCCCAAAGCCTACAGTCCT 47623 G AG A A
 AGGA CT AGG CTTTG GATG
 |||| || || |||| ||||

		TCCT GA TCC GAAAC CTAC	
		_ CA _ C	
GAM2087 KIAA1904	3'	CTCCCTTGTCCTCCAGTTCCTT 73867	AGA TTT_
		AAGGAGCT GGAC GAG	
		TTCCTTGA CCTG CTC	
		CC_ TTCC	
GAM2087 MGC26655	5'	CTCCCTCCAGGCTCCTT 57124	A_ ACTTT
		AAGGAGCT GAGG GAG	
		TTCCTCGG CTCC CTC	
		AC _____	
GAM2087 NEIL1	5'	CATCTCAAGTGGGTCTACCTCC 45151	C GGAC
T		AGGAG TAGA TTTGAGATG	
		TCCTC ATCT GAACTCTAC	
		C GGGT	
GAM2087 RAB11B	3'	CGGTATCCTCTGGCCCCT 74335	A CT
		AGG GCTAGAGGA TTG	
		TCC CGGTCTCCT GGC	
		C AT	
GAM2087 TUBB5	3'	CATCTCCGACCCTGGCTCC 21411	A AC T
		GGAGCTAG GG TT GAGATG	
		CCTCGGTC CC AG CTCTAC	
		_ _ C	
GAM2087 LOC122664	3'	CATCTCAGCCTGCTAGCCCC 74614	A _ ACT
		GG GCTAG AGG TTGAGATG	
		CC CGATC TCC GACTCTAC	
		C G _	
GAM2087 LOC145547	3'	CATCCCAAAGCCTACAGTCCT 77780	G AG A A
		AGGA CT AGG CTTTG GATG	
		TCCT GA TCC GAAAC CTAC	
		_ CA _ C	
GAM2087 LOC148918	5'	CACTGTCTCTCCAGCTCCTT 79819	A _ TT
		AAGGAGCT GAG GAC TG	
		TTCCTCGA CTC CTG AC	
		C T TC	
GAM2087 LOC149271	3'	CATCTCAGAGTCTCCAATTCC 80001	CTA G
		GGAG GAG ACTTTGAGATG	
		CCTT CTC TGAGACTCTAC	
		AAC _	
GAM2087 LOC200032	5'	CATCTGTCAACCCTGCAGCTCCT 85473	AG ACTTTG
T		AAGGAGCT AGG AGATG	

		TTCCTCGA TCC TCTAC		
		CG CACTG_		
GAM2087	LOC222031 3'	CATCCCAAAGTCATCAGTTCCT 95673	A G	A
	T	AAGGAGCT GA GACTTTG GATG		
		TTCCTTGA CT CTGAAAC CTAC		
		_ A C		
GAM2087	LOC222182 3'	TAGGGTCCCCCAGTCCTT 95861	G AGA	
		AAGGA CT GGACTTTG		
		TTCCT GA CCTGGGAT		
		_ CCC		
GAM2088	CENTD2 5'	CTGGCCGGAGCTGTGGGA 31541	CAGA A A	
		TTCCACAGC TTTG CCA G		
		AGGGTGTCTG AGGC GGT C		
		_____ C C		
GAM2088	E2F3 3'	GCCTGACGGATGGGCTGTAGAA 10468	C AG AC A	
		TTC ACAGCC ATTTG CA GC		
		AAG TGTCGG TAGGC GT CG		
		A G_ A_ C		
GAM2088	HEM1 5'	GCCTGTGAGTATCTGTCTGTGG 19239	C TTGAC A	
	AA	TTCCACAG CAGAT CA GC		
		AAGGTGTC GTCTA GT CG		
		T TGAGT C		
GAM2088	MGAT5 5'	GCCTGGTCAAGGGCTCTG 11569	C AGA A	
		CA AGCC TTTGACCA GC		
		GT TCGG GAACTGGT CG		
		C _____ C		
GAM2088	PCDH11X 3'	CTGTAATCTGGCAATGGAA 28013	CA TGACCA	
		TTCCA GCCAGATT AG		
		AAGGT CGGTCTAA TC		
		AA TG_____		
GAM2088	PCDH11Y 3'	CTGTAATCTGGCAATGGAA 53161	CA TGACCA	
		TTCCA GCCAGATT AG		
		AAGGT CGGTCTAA TC		
		AA TG_____		
GAM2088	PIK3R3 3'	GCTTGACCCTGAGCCTGTGGAA 61707	__ ATTTGAC	
		TTCCACAG C CAG CAAGC		
		AAGGTGTC G GTC GTTCG		
		C A CCA_____		
GAM2088	PRKCABP 5'	GCCTGGCCGGGACCCGGCTGTG 25748	AGA_ A A	
	GGA	TTCCACAGCC TTTG CCA GC		

		AGGGTGTCCG	GGGC GGT CG	
		CCCA C C		
GAM2088 T	3'	GCTTACAGATGAACCCA	ACTGT 13507	CCAG____ ACC
		GGAG	TTCCACAG	ATTG AAGC
		GAGGTGTC	TAGAC	TTCG
		AACCCAAG	A__	
GAM2088 VIPR1	3'	CTTATCTCTCTGTGCTGTGGAA	17312	_ TTT CC
		TTCCACAGC	CAGA	GA AAG
		AAGGTGTCG	GTCT	CT TTC
		T	CT_ A_	
GAM2088 XRCC3	3'	TTACATCTGGCTGGAA	19523	CA T
		TTCCA	GCCAGAT	TGA
		AAGGT	CGGTCTA	ATT
		_	C	
GAM2088 YWHAG	3'	GCTCGGCAGGTGGCTGTGGGA	25944	GA A A
		TTCCACAGCCA	TTTG	CC AGC
		AGGGTGTCCGT	GGAC	GG TCG
		_	_ C	
GAM2088 ZNF266	5'	TTTGATGATCTGGCTGTGGA	89693	TGAC
		TCCACAGCCAGATT	CAAG	
		AGGTGTCGGTCTAG	GTTT	
		TA__		
GAM2088 ARHU	3'	GCCTGGCTTACCTATCTGTGGA	41361	CC ATT _ A
A		TTCCACAG	AG	TGA CCA GC
		AAGGTGTC	TC	ATT GGT CG
		TA C__	C C	
GAM2088 C20orf28	3'	GCCTGGTCGAGGGCCCTGGAA	31845	CA AGA A
		TTCCA	GCC	TTTGACCA GC
		AAGGT	CGG	GAGCTGGT CG
		CC	_	C
GAM2088 CNNM4	5'	GCTTGGTCAACGTGAGCCGCGG	39868	ACA _ GAT
GA		TTCC	GC CA	TTGACCAAGC
		AGGG	CG GT	AACTGGTTCG
		CGC	A GC_	
GAM2088 DKFZp761N1114	3'	CTGAGAATCTGGCTGGAA	79783	CA GACCA
		TTCCA	GCCAGATTT	AG
		AAGGT	CGGTCTAAG	TC
		_	AG__	
GAM2088 FLJ10204	3'	CTTGGTCTCAAGATGTGGAA	36357	GCCA TTT
		TTCCACA	GA	GACCAAG

		AAGGTGT CT CTGGTTC			
		AGAA ____			
GAM2088	FLJ11539	3' TTAAATCTGCTGCAGAA 45710	CA	C	
		TTC CAGC AGATTTGA			
		AAG GTCG TCTAAATT			
		AC _			
GAM2088	FLJ12056	3' TCATCTTCTGGCTGTGGAA 46824		TT_	
		TTCCACAGCCAGA TGA			
		AAGGTGTCGGTCT ACT			
		TCT			
GAM2088	FLJ13149	5' GCCTGGTCAAATCTGTGAGGA 41831	A GC	A	
		TCC CA CAGATTTGACCA GC			
		AGG GT GTCTAAACTGGT CG			
		A _ C			
GAM2088	FLJ20084	3' GCTTGGCCAATGACTGTGGAG 34997	C GAT	A	
		TTCCACAG CA TTG CCAAGC			
		GAGGTGTC GT AAC GGTTCG			
		A _ C			
GAM2088	FLJ20392	5' GCCTGGCCAAATCTGAAATAGG 35576	ACAGC	A A	
	A	TCC CAGATTTG CCA GC			
		AGG GTCTAAAC GGT CG			
		ATAAA C C			
GAM2088	FLJ21940	3' TCAGAACTCTTAGCTGTGGAA 43387	C_ _		
		TTCCACAGC AGA TTTGA			
		AAGGTGTCG TCT AGACT			
		AT CA			
GAM2088	KIAA0237	3' CTGGTCTGGCTGGGAA 29221	A	GATTT	A
		TTCC CAGCCA GACCA G			
		AAGG GTCGGT CTGGT C			
		_ _ _ C			
GAM2088	KIAA0596	3' CTTGAGCCAGCTGTGGGA 63488		CAGATT AC_	
		TTCCACAGC TG CAAG			
		AGGGTGTCTG AC GTTC			
		_ _ _ CGA			
GAM2088	KIAA0773	3' CTTGGTGTGGCTGTGGAG 28723		GATTTG	
		TTCCACAGCCA ACCAAG			
		GAGGTGTCGGT TGGTTC			
		G _ _ _			
GAM2088	KIAA0789	5' GCTTGGTCTTCAGCTGGGGAA 64433	A	CA TTT	
		TTCC CAGC GA GACCAAGC			

		AAGG GTCG CT CTGGTTCG	
		G A_ T__	
GAM2088	L3MBTL	3' CTTACCTCACTGTGGAA 70084	CCA TT CCA
		TTCCACAG GA TGA AG	
		AAGGTGTC CT ACT TC	
		A__ CC ____	
GAM2088	NUDEL	3' CTTGGTCACTGGATGCAGAA 48697	CA G ATT
		TTC CA CCAG TGACCAAG	
		AAG GT GGTC ACTGGTTC	
		AC A ____	
GAM2088	SAST	5' GCTCCCTTCATCTGGCTATGG 63662	C TT CCA_
		CCA AGCCAGA TGA AGC	
		GGT TCGGTCT ACT TCG	
		A ____ TCCC	
GAM2088	SLC26A8	5' CTCAGTCAGTATCTGTGGAA 54769	CCAGAT CA
		TTCCACAG TTGAC AG	
		AAGGTGTC GACTG TC	
		TAT__ AC	
GAM2088	SNURF	3' CTTGGTATCCATGACTGTGGAG 20261	C GATTTG
		TTCCACAG CA ACCAAG	
		GAGGTGTC GT TGGTTC	
		A ACCTA_	
GAM2088	TMG3	3' GCCTGGCCTGGGGGCTGTGGGA 44222	AGATTGGA A
		TTCCACAGCC CCA GC	
		AGGGTGTCCG GGT CG	
		GGGTCC__ C	
GAM2088	LOC158956	3' CTTGGTTACTGTGCTGTG 67213	_ ATT
		CACAGC CAG TGACCAAG	
		GTGTCTG GTC ATTGGTTC	
		T ____	
GAM2088	LOC159199	5' GCTTGGTCCAGAGGCCAGGAA 83063	ACA AGA _
		TTCC GCC TTTG ACCAAGC	
		AAGG CGG AGAC TGGTTCG	
		AC_ ____ C	
GAM2088	LOC83693	3' TCAAATCTGCTATGGAA 49607	C C
		TTCCA AGC AGATTGGA	
		AAGGT TCG TCTAAACT	
		A _	
GAM2089	ALOX12B	5' CAGCTGGGCTCCGCTGGG 8535	AG A _
		CCCAGTGGA G TCTA CTG	

GGGTCGCCT C GGGT GAC
 _ _ C
 GAM2089 KIF3C 3' CGGAAGTCCCTCCACTGG 11205 A T A
 CCAGTGGA GGA CT CTG
 ||||| ||| || |||
 GGTCACCT CCT GA GGC
 C _ A
 GAM2089 KRT6B 3' ATCAATACCTGTTCCACTG 19898 _ ATC C
 CAGTGGA AGG TA TGAT
 ||||| ||| || |||
 GTCACCT TCC AT ACTA
 TG _ A
 GAM2089 PDE7A 3' ATCTTGACCTTCCACTAAGTT 66133 CC ATC T_
 AAC AGTGGAAGG TAC GAT
 ||| ||||| ||| |||
 TTG TCACCTTCC ATG CTA
 AA _ TT
 GAM2089 PKP2 3' CAGTAGATACCGGCCACAGG 17107 A AA _
 CC GTGG GG ATCTACTG
 || ||| || |||||
 GG CACC CC TAGATGAC
 A GG A
 GAM2089 RALBP1 3' CAGCAAAGGCCTTCTCACTGGG 23272 _ A A_
 TT AACCCAGTG GAAGG TCT CTG
 ||||| |||| ||| |||
 TTGGGTCAC CTTCC GGA GAC
 T _ AAC
 GAM2089 SCN8A 3' TAGTCCCTTGCACTGGGT 27217 G AT
 ACCCAGTG AAGG CTA
 ||||| |||| |||
 TGGGTCAC TTCC GAT
 G CT
 GAM2089 SLC22A2 5' CAGGAGCCGCCTGCCACTGGG 60278 A AT_ A
 CCCAGTGGA AGG CT CTG
 ||||| ||| || |||
 GGGTCACC TCC GA GAC
 G GCC G
 GAM2089 DKFZP727G051 3' CAGCTGTCCCTCCACTGG 70002 A CTA
 CCAGTGGA GGAT CTG
 ||||| |||| |||
 GGTCACCT CCTG GAC
 C TC_
 GAM2089 DSCR1L1 3' ATCAAGTAATTCCTTCACTAGG 20624 C G TC _
 TT AACCCAGTG AAGGA TACT GAT
 ||| |||| |||| ||| |||
 TTGG TCAC TTCCT ATGA CTA
 A _ TA A
 GAM2089 FLJ11320 3' CAGCAGATCCCCAGGGG 37827 AG AA A
 CCC TGG GGATCT CTG
 ||| ||| ||||| |||

		GGG ACC CCTAGA GAC		
		G_ _ C		
GAM2089	KIAA0286	3' CAGTTTTTTTTCCACCGTGTT 68856	CCA	TCT
		AAC GTGGAAGGA ACTG		
		TTG CACCTTTTT TGAC		
		TGC TT_		
GAM2089	MGC13105	3' ATCTTGGCTCCTTCCATAGG 71968	A	T CT
		CC GTGGAAGGA CTA GAT		
		GG TACCTTCCT GGT CTA		
		A C T_		
GAM2089	MRPS18C	3' ATCAGTTCTGAGTTCCACTGG 32680		GGATCT
		CCAGTGGAA ACTGAT		
		GGTCACCTT TGA CTA		
		GAGTCT		
GAM2089	LOC144811	3' ATCAATAGATCCTGTTACT 84107	A	C
		AGTGG AGGATCTA TGAT		
		TCATT TCCTAGAT ACTA		
		G A		
GAM2089	LOC200276	3' ATCAGTAGATAAAAACTGTGTT 90104	C	GGAAGG
		AAC CAGT ATCTACTGAT		
		TTG GTCA TAGATGACTA		
		T AAAA_		
GAM2089	LOC203078	5' CAGCGACGCTTCTACTGGG 90788		GA TA
		CCCAGTGGAAG TC CTG		
		GGGTCATCTTC AG GAC		
		GC C_		
GAM2089	LOC254057	5' CAGCAGCTGGCCGCTGGG 98778	AA	AT A
		CCCAGTGG GG CT CTG		
		GGGTCGCC TC GA GAC		
		GG _ C		
GAM2090	ABP1	5' GCAGAGCGAACTGGGAGCAGAG 63799	CCGC	C
		CTCTGTTCTT CGCTC GC		
		GAGACGAGGG GCGAG CG		
		TCAA A		
GAM2090	AHCY	3' GGCAACTGAGAAAGAACAGAG 7304		_____
		CTCTGTTCTT C C GCC		
		GAGACAAGAA G G CGG		
		A A TCAA		
GAM2090	BSN	3' GGCAGAGGCAAGAGCAGAG 14387	CC	G _
		CTCTGTTCTT GCC CT CC		

		GAGACGAGAA CGG GA GG	
		___ A C	
GAM2090 CSE1L	5'	GCGGAGCGGCGGCAGGAGC 62513	—
		GTTCTT CCGCCGCTCCGC	
		CGAGGA GGCGGCGAGGCG	
		C	
GAM2090 EHD4	3'	AGTGGCAAAAAATAGAG 58362	C CC
		CTCTGTT TT GCCGCT	
		GAGATAA AA CGGTGA	
		A AA	
GAM2090 EIF2C1	3'	AGCCCAGCTGAAGAACAGA 25181	C C__
		TCTGTTCTTC GC GCT	
		AGACAAGAAG CG CGA	
		T ACC	
GAM2090 KCNK4	3'	GCGAGCAGCAGAGCAGG 33986	TCC C C
		TCTGTTCT GC GCTC GC	
		GGACGAGA CG CGAG CG	
		___ A A	
GAM2090 MYO1D	3'	GCGGAACAGCCCATCCAGCAGA 72249	CTTCC_ CGC
GT		ACTCTGTT GC TCCGC	
		TGAGACGA CG AGGCG	
		CCTACC ACA	
GAM2090 NUP62	3'	GGCAAAGCAGCACAGTGTGAAT 25650	TTCC___ C CC
AGA		TCTGTTC GC GCT GCC	
		AGATAAG CG CGA CGG	
		TGTGACA A AA	
GAM2090 RABIF	3'	GGCATGTGCAGAAAAACAGAGT 12728	C C C TCC
		ACTCTGTT TTC GC GC GCC	
		TGAGACAA AAG CG TG CGG	
		A A _ TA_	
GAM2090 RAX	3'	GCAGGGGAGGCGGAAAAATAGA 26466	C G _
GT		ACTCTGTT TTCCGCC CTCC GC	
		TGAGATAA AAGGCGG GGGG CG	
		A A A	
GAM2090 RBM10	3'	GGCAGGGAAGGACAGAGT 20247	—
		ACTCTGTTCTTCC GCC	
		TGAGACAGGAAGG CGG	
		GA	
GAM2090 RGS16	3'	GGCAGGGCCCAGGAGAACAAAG 12869	C T GCC C
T		ACT TGTTCT CC GCTC GCC	

			TGA ACAAGA GG CGGG CGG		
			A _ ACC A		
GAM2090	ROM1	3'	GGAACAGCAAAGAACAGAGT 6165	CC	CGC
			ACTCTGTTCTT GC TCC		
			TGAGACAAGAA CG AGG		
			A_ ACA		
GAM2090	SLC21A2	3'	GCAAAGCAAGTGATGAAGCAGA 20084	_ TTC	C_ CC
	GT		ACTCTGTT C CGC GCT GC		
			TGAGACGA G GTG CGA CG		
			A TA_ AA AA		
GAM2090	SMARCA5	5'	AGCCCCGCGGAAGAGCAGA 14588	C__	
			TCTGTTCTTCCGC GCT		
			AGACGAGAAGGCG CGA		
			CCC		
GAM2090	SYNGR1	3'	GGCAGAGCGGCAAGGACAGGG 17507	CC	C
			CTCTGTTCTT GCCGCTC GCC		
			GGGACAGGAA CGGCGAG CGG		
			_ A		
GAM2090	TRAM	5'	AGCAGCTGGGAAGAGCAGA 27451	_ C	
			TCTGTTCTTCC GC GCT		
			AGACGAGAAGG CG CGA		
			GT A		
GAM2090	VAT1	3'	AGCAGGGAAGTACAGAGT 22088	T	GCC
			ACTCTGT CTTCC GCT		
			TGAGACA GAAGG CGA		
			T GA_		
GAM2090	CBX1	3'	AGCAATGGAAAAGAACAGA 23308	_ CC	
			TCTGTTCT TCCG GCT		
			AGACAAGA AGGT CGA		
			AA AA		
GAM2090	CDC14A	5'	GGCGGAGCAGCAGCTGCAGCAG 14785	_ TCTTCC	C
			CT CTGT GC GCTCCGCC		
			GA GACG CG CGAGGCGG		
			C TCGA_ A		
GAM2090	CDC14A	5'	GGCGGAGCAGCAGCTGCAGCAG 14786	_ TCTTCC	C
			CT CTGT GC GCTCCGCC		
			GA GACG CG CGAGGCGG		
			C TCGA_ A		
GAM2090	DKFZp547I224	5'	GATGGGGAAAAAACAGAG 39956	C_ G	C
			CTCTGTT TTCC CCG TC		

		GAGACAA AAGG GGT AG	
		AA _ _	
GAM2090 ECE2	3'	GCAGGGAAAAGGAAGAACAGAG 28732	GCCG C
	T	ACTCTGTTCTTCC CTC GC	
		TGAGACAAGAAGG GGG CG	
		AAAA A	
GAM2090 FLJ10648	3'	CGAAGCAAACCAAGAACAGAG 36890	CCGCC C
		CTCTGTTCTT GCT CG	
		GAGACAAGAA CGA GC	
		CCAAA A	
GAM2090 GRIN3A	3'	GCGGAGCAAGTGCCAAGCAGA 56783	CTTC C_
		TCTGTT CGC GCTCCGC	
		AGACGA GTG CGAGGCG	
		ACC_ AA	
GAM2090 INE1	3'	GCAGGTGTTAGACGAAAGAACA 14757	C CC_ T _
	GA	TCTGTTCTT CG GC CC GC	
		AGACAAGAA GC TG GG CG	
		A AGAT T A	
GAM2090 KIAA0410	3'	GCAGAGCTTAAGAATAGA 29426	CCGCC C
		TCTGTTCTT GCTC GC	
		AGATAAGAA CGAG CG	
		TT_ A	
GAM2090 KIAA0964	5'	GCGGAACGGCAGAGCGGG 30448	TCC C
		TCTGTTCT GCCG TCCGC	
		GGGCGAGA CGGC AGGCG	
		_ A	
GAM2090 KIAA1218	5'	AGCAGCACAAAAGAAACAGAGT 95958	_ CC_ C
		ACTCTGTT CTT GC GCT	
		TGAGACAA GAA CG CGA	
		A AACA A	
GAM2090 KIAA1322	3'	GGCAGCCGAGAAGAACAGA 73112	_ CC _
		TCTGTTCTTC CG GCT CC	
		AGACAAGAAG GC CGA GG	
		A _ C	
GAM2090 KIAA1391	3'	AGTGGAGAAAAACAGAGT 67851	C CG
		ACTCTGTT TTC CCGCT	
		TGAGACAA AAG GGTGA	
		A A_	
GAM2090 MGC13251	3'	AGCAGCCATAGAAAGGACAGA 52134	_ C_ C
		TCTGTTCTT C GC GCT	

			AGACAGGAA G CG CGA		
			A ATAC A		
GAM2090 MYH7B	3'	GGCGGAGCAGCAGGCCAACA	71058	CTT _ C	
		TGTT CC GC GCTCCGCC			
		ACAA GG CG CGAGGCGG			
		CC_ A A			
GAM2090 NCOA2	3'	GGCAAGGAGAAGAGCAAAGT	22572	C CG GCT	
		ACT TGTTCTTC CC CC			
		TGA ACGAGAAG GG GG			
		A A_ AAC			
GAM2090 PTRF	3'	GGCAGTGGGGAAGACAGAG	64242	T G _	
		CTCTGT CTTCC CCGCT CC			
		GAGACA GAAGG GGTGA GG			
		_ _ C			
GAM2090 RHOBTB2	3'	AGCAGGAGGAAAAGCAGAGT	61593	C G _	
		ACTCTGTT TTCC CC GCT			
		TGAGACGA AAGG GG CGA			
		A A A			
GAM2090 TAGAP	3'	AGACTGCAAGGAACAGAGT	55099	CC CG_	
		ACTCTGTTCTT GC CT			
		TGAGACAAGGA CG GA			
		A_ TCA			
GAM2090 VELI1	3'	AGTGTAAGAAGAATAAAGT	17417	C CGC	
		ACT TGTTCTTC CGCT			
		TGA ATAAGAAG GTGA			
		A AAT			
GAM2090 LOC145783	5'	GCGGAGCGACGGAGACACAG	77949	TC C	
		CTGT TTCCG CGCTCCGC			
		GACA GAGGC GCGAGGCG			
		CA A			
GAM2090 LOC150157	3'	AGCAAATGGAAGAAGAACAGA	86020	_ CC_	
		TCTGTTCT TCCG GCT			
		AGACAAGA AGGT CGA			
		AA AAA			
GAM2090 LOC151516	5'	GGCGGAGCTTCCAGAACAAAG	81068	C TCCGCC	
		CT TGTTCT GCTCCGCC			
		GA ACAAGA CGAGGCGG			
		A CCTT_			
GAM2090 LOC153769	3'	GGCGGAGCAGCATGAGAAAGA	81807	G CC C	
		TCT TTCTT GC GCTCCGCC			

	AGA AAGAG CG CGAGGCGG	
	— TA A	
GAM2090 LOC161734 3'	GATGGGGAAAAACAGAG 88467	C_ G C
	CTCTGTT TTCC CCG TC	
	GAGACAA AAGG GGT AG	
	AA — —	
GAM2090 LOC167026 5'	GGCGGAGCGGCGGGCGGA 88620	TCTT
	TCTGT CCGCCGCTCCGCC	
	AGGCG GGCGGCGAGGCGG	
	—	
GAM2090 LOC196890 3'	AGCAAATGAAAAGAACAGA 91222	— CC_
	TCTGTTCT TCCG GCT	
	AGACAAGA AGGT CGA	
	AA AAA	
GAM2090 LOC200731 5'	AGCACTGAAGAACAGAGT 91688	CGCC
	ACTCTGTTCTTC GCT	
	TGAGACAAGAAG CGA	
	TCA_	
GAM2090 LOC221504 5'	CGGAGCGGCGGGGCAGGAG 94020	GTTC
	CTCT TTCCGCCGCTCCG	
	GAGG GGGGCGGCGAGGC	
	AC_	
GAM2090 LOC221663 5'	GCAAGCCCAGAACAGAGT 95463	TCCGCC CC
	ACTCTGTTCT GCT GC	
	TGAGACAAGA CGA CG	
	CC_ AA	
GAM2090 LOC256310 3'	GGCAGAGCAGCGGGAGCAGGAG 98102	GTT C C
	CTCT CTTCCGC GCTC GCC	
	GAGG GAGGGCG CGAG CGG	
	AC_ A A	
GAM2090 LOC51762 3'	GGCCTAGCAAAAGAACAGA 33708	CCGCC CC
	TCTGTTCTT GCT GCC	
	AGACAAGAA CGA CGG	
	AA_ TC	
GAM2090 LOC91266 5'	GGCTGAGGAAAAACAGAGT 66024	— C
	ACTCTGT TCTTC GCC	
	TGAGACA AGGAG CGG	
	AAA T	
GAM2091 BBS4 3'	ATTTGCCCAAAGGGAATCCAGA 53447	G_ G_ A
ACA	TGTTCTGGA CT TTGG CAAAT	

			ACAAGACCT GG AACG GTTTA	
			AA GA C	
GAM2091	CENTD2	3'	CCAACAACTCCAGAACA 58270	C_
			TGTTCTGGAG TGTTGG	
			ACAAGACCTC ACAACC	
			AA	
GAM2091	CENTD2	3'	CCAACAACTCCAGAACA 31539	C_
			TGTTCTGGAG TGTTGG	
			ACAAGACCTC ACAACC	
			AA	
GAM2091	HAMP	3'	TCCTGCTGCCCCAGAACA 41289	A T T
			TGTTCTGG GC GT GGA	
			ACAAGACC CG CG CCT	
			C T T	
GAM2091	ITGA11	3'	TCTGCCGGCCCCCAGGACA 25213	A_ TT
			TGTTCTGG GCTG GGA	
			ACAGGACC CGGC TCT	
			CC CG	
GAM2091	KITLG	3'	ATTTGCATGGCTCCAGAA 15671	TGGA
			TTCTGGAGCTGT CAAAT	
			AAGACCTCGGTA GTTTA	
			C_	
GAM2091	KITLG	3'	ATTTGCATGGCTCCAGAA 8023	TGGA
			TTCTGGAGCTGT CAAAT	
			AAGACCTCGGTA GTTTA	
			C_	
GAM2091	MAPK4	5'	CCTGGGCGAGCTCCAGATCA 12300	T _
			TG TCTGGAGCTGTT GG	
			AC AGACCTCGACGG CC	
			T GT	
GAM2091	MGAT2	3'	ATTTGTCCAAACAGGACA 11557	GAGCTG
			TGTTCTG TTGGACAAAT	
			ACAGGAC AACCTGTTTA	
			A_	
GAM2091	PSPHL	5'	TTGTCATACAGCTCCAAACA 94499	C TG
			TGTT TGGAGCTGT GACAA	
			ACAA ACCTCGACA CTGTT	
			_ TA	
GAM2091	TTC3	3'	TATTTGTCCAACACTGTCAGA 13885	_ C
	ATA		TGTTCTGG AG TGTTGGACAAATA	

		ATAAGACT TC ACAACCTGTTTAT	
		G A	
GAM2091	FLJ14213	3' TGATAACAGCTCCAGAA 46218	GA
		TTCTGGAGCTGTTG CA	
		AAGACCTCGACAAT GT	
		A_	
GAM2091	H2BFQ	3' TTTAAGAGAACTCCAGGACA 60079	_ G
		TGTTCTGGAG CT TTGGA	
		ACAGGACCTC GA AATTT	
		AA G	
GAM2091	LRG	3' TCCATCCATGCTTCCTAGAACA 54825	_ _ _ T_
		TGTTCT GGA GC TG TGGA	
		ACAAGA CCT CG AC ACCT	
		T T T CT	
GAM2091	NMT2	3' ATTTGTCCATGTAACAGAACA 17852	GA TGT
		TGTTCTG GC TGGACAAAT	
		ACAAGAC TG ACCTGTTTA	
		AA T_	
GAM2091	NYD-SP21	3' TATTTGTCCAATCTAGATTCAG 51863	G _
	AACA	TGTTCTGGA CT GTTGGACAAATA	
		ACAAGACTT GA TAACCTGTTTAT	
		A TC	
GAM2091	PSPH	3' TTGTCGTACAGCTCCAAACA 17143	C TG
		TGTT TGGAGCTGT GACAA	
		ACAA ACCTCGACA CTGTT	
		_ TG	
GAM2091	LOC122258	3' CCACCAGCCTCCGGAACA 59820	_ T
		TGTTCTGGAG CTG TGG	
		ACAAGGCCTC GAC ACC	
		C C	
GAM2091	LOC151826	3' ATTTGTCCAACCTAGCACA 81176	T AGCT
		TGT CTGG GTTGGACAAAT	
		ACA GATC CAACCTGTTTA	
		C _	
GAM2091	LOC169611	3' TCCAGTGGCAGCTCCAGAA 83663	_
		TTCTGGAGCTGT TGGA	
		AAGACCTCGACG ACCT	
		GTG	
GAM2091	LOC196746	3' TCAGAGCAGCTCCAAGACA 88903	TC G_
		TGT TGGAGCTGTT GA	

		ACA ACCTCGACGA CT	
		GA GA	
GAM2091	LOC204119 5'	TGCCACAACCTCAGAACAA 92343	G C T A
		TGTTCTG AG TGT GG CA	
		ACAAGAC TC ACA CC GT	
		_ A _ _	
GAM2091	LOC253142 5'	TTGCTAGGATGCCCCAGAATA 99230	A TG_ A
		TGTTCTGG GC TTGG CAA	
		ATAAGACC CG GATC GTT	
		C TAG _	
GAM2092	ITPR2 3'	AAAACAACCAAGTGCCAAG 11076	GGCC C
		CTTGGA CACT GT GTTTT	
		GAACCGTGA CA CAAAA	
		AC_ A	
GAM2092	MSF 3'	AAATGAGTGGCCAGCGCCAGG 89462	A _
		CTTGGC CTGGCCG TCGTTT	
		GGACCG GACCGGT AGTAAA	
		C G	
GAM2092	SEMG1 3'	AAAGGATGGACCAATATCAAG 13012	CAC _ G
		CTTGG TGG CCGTC TTT	
		GAACCT ACC GG TAG AAA	
		ATA A G	
GAM2092	TCF1 3'	AGCCTCGCAACCCGTGCCAAG 6781	T C_ TC
		CTTGGCAC GG CG GTT	
		GAACCGTG CC GC CGA	
		C AAC TC	
GAM2092	TCFL4 3'	AAAACAAGGTAGCCAGTGC 64205	CG _
		GCACTGGC TC GTTTT	
		CGTGACCG GG CAAAA	
		AT AA	
GAM2092	B3GALT1 5'	AAAACAACTAGTGCCAAG 40941	CCGTC
		CTTGGA CACTGG GTTTT	
		GAACCGTGATC CAAAA	
		AAA_	
GAM2092	C20orf42 3'	AAACACCTGCCAGTGTCAAG 35060	C_ C
		CTTGGA CACTGGC GT GTTT	
		GAACGTGACCG CA CAAA	
		TC _	
GAM2092	FLJ23548 3'	AAAACGTGCTGCTCAGTGCCA 45044	_ CGT_ _
	AG	CTTGGA CACTG GC C GTTTT	

			GAACCGTGAC CG G CAAAA	
			T TCCT T	
GAM2092	GRIN3A	3'	AAGCGGAGCAAGTGCCAAG 56775	G CG
			CTTGCGCACT GC TCGTTT	
			GAACCGTGA CG GGCGAA	
			A A_	
GAM2092	KIAA0546	3'	AAAAC TAGTTTCCAAGTGCCAA 71834	_ CCGTC_
	G		CTTGCGCACT GG GTTTT	
			GAACCGTGA CC CAAAA	
			A TTTGAT	
GAM2092	KIAA1143	3'	AAAGCGACCACTGCCAAG 69223	C CCG
			CTTGCGCA TGG TCGTTTT	
			GAACCGT ACC AGCGAAA	
			C _	
GAM2092	MGC3222	3'	AAAACACAGCCAGCCCAAG 44542	CA C C
			CTTGG CTGGC GT GTTTT	
			GAACC GACCG CA CAAAA	
			C_ A _	
GAM2092	RENT2	3'	AAAGTGATACCAGCCCAAG 32064	CA CC
			CTTGG CTGG GTCGTTTT	
			GAACC GACC TAGTGAAA	
			C_ A_	
GAM2092	SLC2A11	3'	AAAGGGGTGGCCAGAGCCAA 48691	A GT G
			TTGGC CTGGCC C TTTT	
			AACCG GACCGG G GAAA	
			A TG G	
GAM2092	WBSCR23	5'	AAAACGACAACCAATGCTGA 47402	TG C CC
			T GCA TGG GTCGTTTT	
			A CGT ACC CAGCAAAA	
			GT A AA	
GAM2092	LOC200014	5'	AGGCTGCGGCCAGTGCCAAG 89919	C
			CTTGCGCACTGGCCGT GTTT	
			GAACCGTGACCGGCG CGGA	
			T	
GAM2093	CD209	3'	ACAGTTCCTTCTCTCCATCCTT 41261	_ TC C
			AGGGATGGA AAG AC GT	
			TTCCTACCT TTC TG CA	
			CTC CT A	
GAM2093	CUL4B	3'	ACAGTGTTCCTAACTCATCCCT 14565	AA_ T_ C
			AGGGATGG AG CAC GT	

		TCCCTACT TC GTG CA	
		CAA TT A	
GAM2093 LMO1	5'	ACGAGATTCCCCCATCTCT 11343	AA_ AC
		AGGGATGG AGTC CGT	
		TCTCTACC TTAG GCA	
		CCC A_	
GAM2093 NAV2	3'	ACGGTATGTTTCCATCCT 60788	GTC
		GGGATGGAAA ACCGT	
		TCCTACCTTT TGGCA	
		GTA	
GAM2093 PIK3CG	3'	ACAGTGAGACTCCATCTCT 12116	AAG C
		AGGGATGGA TCAC GT	
		TCTCTACCT AGTG CA	
		CAG A	
GAM2093 RAB36	3'	TGCTGCCTCTCCATCCCT 18184	A T C
		AGGGATGGA AG CA CG	
		TCCCTACCT TC GT GT	
		C C C	
GAM2093 SULT2A1	3'	ACGGTGAAACCCCATCTCT 72221	AAAG
		AGGGATGG TCACCGT	
		TCTCTACC AGTGGCA	
		CCAA	
GAM2093 TP53	5'	ACGGTGACACGCTTCCCT 6790	T AAA
		AGGGA GG GTCACCGT	
		TCCCT TC CAGTGGCA	
		_ GCA	
GAM2093 TYRO3	3'	ACGGTGACCTTTAGTGCC 21934	G G A
		GG AT GAA GTCACCGT	
		CC TG TTT CAGTGGCA	
		G A C	
GAM2093 XRCC2	3'	ACGGTGAAACCCCATCTCT 19485	AAAG
		AGGGATGG TCACCGT	
		TCTCTACC AGTGGCA	
		CCAA	
GAM2093 ZNF255	5'	ACGGTATTTGGTTTCCATTCC 20495	GT ____
T		AGGGATGGAAA C ACCGT	
		TCCTTACCTTT G TGGCA	
		TG TTTA	
GAM2093 ANGPTL4	3'	ACGGTGACTCTTGGCTCT 32759	AT_ AA
		AGGG GGA GTCACCGT	

		TCTC TCT CAGTGGCA	
		GGT _	
GAM2093	APG3	5' ACGGCTGCACTTTCCATCCC 42826	--
		GGGATGGAAAGT CA CCGT	
		CCCTACCTTTCA GT GGCA	
		C C	
GAM2093	C20orf106	3' ACGGTGAAACCCCATCTCT 55889	AAAG
		AGGGATGG TCACCGT	
		TCTCTACC AGTGGCA	
		CCAA	
GAM2093	C6orf5	3' ACGGTGAAACTCCATCTCT 31961	AAG
		AGGGATGGA TCACCGT	
		TCTCTACCT AGTGGCA	
		CAA	
GAM2093	DEGS	3' ACGGTGAAACCCCATCTCT 14798	AAAG
		AGGGATGG TCACCGT	
		TCTCTACC AGTGGCA	
		CCAA	
GAM2093	DKFZP434D193	3' ACAGTGACTTATTATCCTT 90292	A C
		AGGGATGG AAGTCAC GT	
		TTCCTATT TTCAGTG CA	
		A A	
GAM2093	FHX	3' ACGAATGATCTTCCCATCCCT 37917	A _ C_
		AGGGATGG AAG TCA CGT	
		TCCCTACC TTC AGT GCA	
		C T AA	
GAM2093	FLJ14225	3' ACGGTGAAACCCCATCTCT 46380	AAAG
		AGGGATGG TCACCGT	
		TCTCTACC AGTGGCA	
		CCAA	
GAM2093	FLJ20296	5' ACGCGTTTCTCTCCATTCCT 35361	A TC _
		AGGGATGGA AG AC CGT	
		TCCTTACCT TC TG GCA	
		C TT C	
GAM2093	FLJ20783	3' ACGGTGAAACCCCATCTCT 36092	AAAG
		AGGGATGG TCACCGT	
		TCTCTACC AGTGGCA	
		CCAA	
GAM2093	HES2	3' ACGGTGAAACCCCATCTCT 39366	AAAG
		AGGGATGG TCACCGT	

	TCTCTACC AGTGGCA	
	CCAA	
GAM2093 KIAA0252	3' ACGGTGAAACCCCATCTCT 63447	AAAG
	AGGGATGG TCACCGT	
	TCTCTACC AGTGGCA	
	CCAA	
GAM2093 KIAA0746	3' ACAGTGCGTGCTTCATCCCT 69984	AA__T C
	AGGGATGGA G CAC GT	
	TCCCTACTT C GTG CA	
	CGTG_ A	
GAM2093 KIAA1328	3' ACGGTGAAACCCCATCTCT 62314	AAAG
	AGGGATGG TCACCGT	
	TCTCTACC AGTGGCA	
	CCAA	
GAM2093 KIAA1486	3' ACGGTGAGACCCCATCTCT 67965	AAAG
	AGGGATGG TCACCGT	
	TCTCTACC AGTGGCA	
	CCAG	
GAM2093 KIAA1948	3' ACGGTGAAACCCCATCTCT 83288	AAAG
	AGGGATGG TCACCGT	
	TCTCTACC AGTGGCA	
	CCAA	
GAM2093 MGC16142	3' ACGGTTGGCTGTTCCATCCT 52257	_ _
	GGGATGGAA AGTCA CCGT	
	TCCTACCTT TCGGT GGCA	
	G T	
GAM2093 MGC17330	3' ACAGTGCTCCTTGTCATCCCT 54629	_ T__ C
	AGGGATGGA AAG CAC GT	
	TCCCTACCT TTC GTG CA	
	G CTC A	
GAM2093 MGC2865	3' ACGGCATTGGCTCCATCCC 51455	AA ____
	GGGATGGA GTCA CCGT	
	CCCTACCT CGGT GGCA	
	_ TAC	
GAM2093 MGC29891	3' ACGGTGAAACTCCATCTCT 58844	AAG
	AGGGATGGA TCACCGT	
	TCTCTACCT AGTGGCA	
	CAA	
GAM2093 MGC4663	3' ACGGTGAAACCCCATCTCT 44779	AAAG
	AGGGATGG TCACCGT	

			TCTCTACC	AGTGGCA	
			CCAA		
GAM2093	PRO2949	3'	ACGGTGAAACCCCATCTCT	38217	AAAG
			AGGGATGG	TCACCGT	
			TCTCTACC	AGTGGCA	
			CCAA		
GAM2093	RoXaN	3'	ACGGTGAAACCCCATCTCT	47270	AAAG
			AGGGATGG	TCACCGT	
			TCTCTACC	AGTGGCA	
			CCAA		
GAM2093	Rpo1-2	3'	ACGGTGACAAGTCTCCTT	50865	T AAA
			AGGGA GG	GTCACCGT	
			TTCCT CT	CAGTGGCA	
			_ GAA		
GAM2093	Rpo1-2	3'	ACGGTGACAAGTCTCCTT	39208	T AAA
			AGGGA GG	GTCACCGT	
			TTCCT CT	CAGTGGCA	
			_ GAA		
GAM2093	SRPK2	3'	ACGGTGACTCTCATTCTT	13409	AA
			AGGGATGG	AGTCACCGT	
			TTCTTACT	TCAGTGGCA	
			C_		
GAM2093	T1A-2	3'	ACGGTGACCTCTCCGCTT	22388	A AA_
			GGG TGGA	GTCACCGT	
			TTC GCCT	CAGTGGCA	
			_ CTC		
GAM2093	ZNF287	5'	GGTCTCTTATCCATCCCT	40671	_ TC
			AGGGATGGA AAG	ACC	
			TCCCTACCT TTC	TGG	
			A TC		
GAM2093	LOC126282	3'	ACGGTGAAACCCCATCTCT	74937	AAAG
			AGGGATGG	TCACCGT	
			TCTCTACC	AGTGGCA	
			CCAA		
GAM2093	LOC131583	5'	ACGGGGGGGCTTTCCATCTC	76379	A_
			GGGATGGAAAGTC	CCGT	
			CTCTACCTTTCGG	GGCA	
			GG		
GAM2093	LOC132321	3'	ACAGTGAAATTTCCATCC	75570	G_ C
			GGATGGAAA	TCAC GT	

	CCTACCTTT AGTG CA	
	AA A	
GAM2093 LOC133121 3'	ACTGTTCCCTTCCATCCCT 75589	A TC C
	AGGGATGGAA G AC GT	
	TCCCTACCTT C TG CA	
	_ CT T	
GAM2093 LOC145482 3'	ACGGTGAAACCCCATCTCT 77737	AAAG
	AGGGATGG TCACCGT	
	TCTCTACC AGTGGCA	
	CCAA	
GAM2093 LOC146923 3'	ACGGTGAAACCCCATCTCT 78792	AAAG
	AGGGATGG TCACCGT	
	TCTCTACC AGTGGCA	
	CCAA	
GAM2093 LOC147057 3'	ACGAGTGCCCTCCATCCC 84972	AA T _
	GGGATGGA G CAC CGT	
	CCCTACCT C GTG GCA	
	CC _ A	
GAM2093 LOC149267 5'	ACAGTGGCTTCCTTCCATCCT 57474	___ C
	GGGATGGAA AGTCAC GT	
	TCCTACCTT TCGGTG CA	
	CCT A	
GAM2093 LOC168283 5'	ACGGTGGTGCACCATCCT 83574	AAA
	GGGATGG GTCACCGT	
	TCCTACC TGGTGGCA	
	ACG	
GAM2093 LOC202038 3'	ACGGTGAAACCCCATCTCT 90616	AAAG
	AGGGATGG TCACCGT	
	TCTCTACC AGTGGCA	
	CCAA	
GAM2093 LOC202781 3'	ACGGTGAAACCCCGTCCCT 91966	AAAG
	AGGGATGG TCACCGT	
	TCCCTGCC AGTGGCA	
	CCAA	
GAM2093 LOC203427 5'	ACGGGGCTTCCCGTCCCT 90918	A A
	AGGGATGG AAGTC CCGT	
	TCCCTGCC TTCGG GGCA	
	C _	
GAM2093 LOC221271 3'	ACGGTGAAACCCCATCTCT 93488	AAAG
	AGGGATGG TCACCGT	

		TCTCTACC	AGTGGCA		
		CCAA			
GAM2093	LOC222057	3'	ACGGTGACCTCTTTTCGGCC	94343	A A__
			GG TGGAA GTCACCGT		
			CC GCTTT CAGTGGCA		
			G CTC		
GAM2093	LOC257211	3'	ACGGTGAAAACCCATCTCT	97611	AAAG
			AGGGATGG TCACCGT		
			TCTCTACC AGTGGCA		
			CAAA		
GAM2093	LOC57109	3'	ACGGTGA CTGCGGTTATTCCT	40201	AA__
			AGGGATGG AGTCACCGT		
			TCCTTATT TCAGTGGCA		
			GGCG		
GAM2093	LOC92299	3'	ACGGTGAAACCCCATCTCT	69357	AAAG
			AGGGATGG TCACCGT		
			TCTCTACC AGTGGCA		
			CCAA		
GAM2094	GPD1	3'	TCATGCCACCACATTTG	60398	C C
			TAAATG GGTGGCAT GA		
			GTTTAC CCACCGTA CT		
			A _		
GAM2094	IL5RA	5'	TCGCATGGCCACCGCATTT	6906	AT__
			AAATGCGGTGGC CGA		
			TTTACGCCACCG GCT		
			GTAC		
GAM2094	MYO1C	3'	TGCCGATGCCAAATATTTG	61873	CGG A
			TAAATG TGGCATCG CA		
			GTTTAT ACCGTAGC GT		
			AA_ C		
GAM2094	C6orf37	3'	TGTCACACTGCATTTA	68097	GCATC
			TAAATGCGGTG GACA		
			ATTTACGTCAC CTGT		
			A__		
GAM2094	DNAJC6	3'	TTGCAGAACCACCGCATT	29498	CA GA
			AATGCGGTGG TC CAA		
			TTACGCCACC AG GTT		
			A_ AC		
GAM2094	FLJ11210	3'	GTCGATGTGCATGCTTTTA	60319	T GTG
			TAAA GCG GCATCGAC		

	ATTT CGT TGTAGCTG	
	T ACG	
GAM2094 FLJ12476 3'	TCGATCTTCTGCATTTA 43270	T C
	TAAATGCGG GG ATCGA	
	ATTTACGTC TC TAGCT	
	T _	
GAM2094 KIAA1034 3'	TCGATGGCATCCGCATTTG 63134	_ G
	TAAATGCGG TG CATCGA	
	GTTTACGCC AC GTAGCT	
	T G	
GAM2094 KIAA1987 3'	TCATGTAAGTGCATTTA 89391	G C
	TAAATGCGGT GCAT GA	
	ATTTACGTCA TGTA CT	
	A _	
GAM2094 MGC16063 3'	TGTCCTGGCCACTGCATT 54929	ATC
	AATGCGGTGGC GACA	
	TTACGTCACCG CTGT	
	GTC	
GAM2094 LOC147949 3'	TGTCAGATGTCCACATTGCA 79279	_ _ _
	TGCG GTGG CATC GACA	
	ACGT CACC GTAG CTGT	
	TA T A	
GAM2094 LOC150577 3'	GTCCTCACCGCATTTG 86258	CATC
	TAAATGCGGTGG GAC	
	GTTTACGCCACT CTG	
	C _	
GAM2094 LOC158219 3'	TGTGTGTCACCACATTT 82694	C CG
	AAATG GGTGGCAT ACA	
	TTTAC CCACTGTG TGT	
	A _	
GAM2094 LOC202020 3'	TGTCTCACACATTTA 90605	C CATC
	TAAATG GGTGG GACA	
	ATTTAC CCACT CTGT	
	A _	
GAM2094 LOC90826 5'	TGTCGATGCAGGTTTATTTG 64788	CGGTG
	TAAATG GCATCGACA	
	GTTTAT CGTAGCTGT	
	TTGGA	
GAM2094 LOC93587 3'	TTGTCTTTACCTGCATTTA 73042	_ CATC
	TAAATGC GGTGG GACAA	

		ATTTACG CCATT CTGTT			
		T T__			
GAM2095	ATSV	3' CAGGACAGGACGGGGTCAGCC 16307	AA_ AA G_		
		GG GCC CCTG CTGTCCTG			
		CC TGG GGGC GACAGGAC			
		GAC _ AG			
GAM2095	BLAME	3' CAGCACAGCTGGCCTCCA 39651	A ACCTG C		
		TGGA GCCA GCTGT CTG			
		ACCT CGGT CGACA GAC			
		C _ C			
GAM2095	BRF1	3' CAGCATCAGACGGGCTTCCA 9502	AAC _		
		TGGAAGCC CTG GCTG			
		ACCTTCGG GAC CGAC			
		GCA TA			
GAM2095	DRD2	3' CAGACTGCAGGTTGGACCCCA 7674	AAG GT C		
		TGG CCAACCTG C GTC TG			
		ACC GGTGGAC G CAG AC			
		CCA _ T _			
GAM2095	DTR	3' CAGAAGAGGTTGGGCTTCCA 10454	_ GG_		
		TGGAAGCC AACCT CTG			
		ACCTTCGG TTGGA GAC			
		G GAA			
GAM2095	F2RL3	3' CATGTTGGCCAGGCTGGTCTCC 15504	AG A TCC		
	A	TGGA CCA CCTGGCTG TG			
		ACCT GGT GGACCGGT AC			
		CT C TGT			
GAM2095	FCMD	3' CAGGACAACCAGGTAGTCACCC 23028	AA_ CA C		
	A	TGG GC ACCTGG TGTCCTG			
		ACC TG TGGACC ACAGGAC			
		CAC A_ A			
GAM2095	GABRA5	3' CAAGACAGCCATACTTCCA 60823	CCAACC C		
		TGGAAG TGGCTGTC TG			
		ACCTTC ACCGACAG AC			
		AT__ A			
GAM2095	IMPG1	3' TCATAAGCCAGGTTTGCTTCCA 9599	C GTCC		
		TGGAAGC AACCTGGCT TGA			
		ACCTTCG TTGGACCGA ACT			
		T AT__			
GAM2095	LIMK1	3' TCAGGGCAGAGGCCAAGTTCCA 11340	GCCAA GG		
		TGGAA CCT CTGTCCTGA			

		ACCTT GGA GACGGGACT	
		GAACC _	
GAM2095 LIMK1	3'	TCAGGGCAGAGGCCAAGTTCCA 34141	GCCAA GG
		TGGAA CCT CTGTCCTGA	
		ACCTT GGA GACGGGACT	
		GAACC _	
GAM2095 MRPL49	3'	AGGATAGTGCTGGCTTCCA 70160	ACCTG
		TGGAAGCCA GCTGTCCT	
		ACCTTCGGT TGATAGGA	
		CG_	
GAM2095 NHP2L1	3'	CAGGACAGAGATCTGGTTCCA 18448	G ACCTGG
		TGGAA CCA CTGTCCTG	
		ACCTT GGT GACAGGAC	
		_ CTAGA_	
GAM2095 PAX5	3'	TCAGAACAGCCAGGTAGAGCCC 34135	AA CA_ C
		GG GC ACCTGGCTGT CTGA	
		CC CG TGGACCGACA GACT	
		_ AGA A	
GAM2095 PIN4	3'	CAGGACAGGTGGTATTAGCTCC 21710	A CA_ T G
A		TGGAA GC ACC G CTGTCCTG	
		ACCT CG TGG T GACAGGAC	
		_ ATTA _ G	
GAM2095 PTPRA	5'	CAGGAATTGGGCAGCTTCCA 12601	CAA TG CTG
		TGGAAGC CC G TCCTG	
		ACCTTCG GG T AGGAC	
		AC_ GT A_	
GAM2095 SCRT1	3'	CAGCCAGGTCGGCTCTCA 49370	GA A
		TG AGCC ACCTGGCTG	
		AC TCGG TGGACCGAC	
		TC C	
GAM2095 TNFRSF6B	5'	TCAGGAAAGCGGTCGGCTCACA 33599	GA A TG G
		TG AGCC ACC GCT TCCTGA	
		AC TCGG TGG CGA AGGACT	
		AC C _ A	
GAM2095 WHSC1	3'	CACCCAGAGTGGCTTCCA 30579	AC C
		TGGAAGCCA CTGG TG	
		ACCTTCGGT GACC AC	
		GA C	
GAM2095 WHSC1	3'	CACCCAGAGTGGCTTCCA 56666	AC C
		TGGAAGCCA CTGG TG	

		ACCTTCGGT GACC AC	
		GA C	
GAM2095 WHSC1	3'	CACCCAGAGTGGCTTCCA 56677	AC C
		TGGAAGCCA CTGG TG	
		ACCTTCGGT GACC AC	
		GA C	
GAM2095 ARHGEF3	3'	CAGGACAGAAAGCGGCTGCCA 39458	A AAC GG
		TGG AGCC CT CTGTCCTG	
		ACC TCGG GA GACAGGAC	
		G C__ A_	
GAM2095 C1QR1	3'	ACAGCTTGGCTTCCA 24862	ACCT
		TGGAAGCCA GGCTGT	
		ACCTTCGGT TCGACA	
GAM2095 CFLAR	5'	GCACCAAGTCCGCTTCCA 15273	CA C C
		TGGAAGC AC TGG TGT	
		ACCTTCG TG ACC ACG	
		CC A _	
GAM2095 CNNM4	3'	ACAGCCAGATGGCCCCCA 39861	AA AC
		TGG GCCA CTGGCTGT	
		ACC CGGT GACCGACA	
		CC A_	
GAM2095 CST8	5'	TGGTCAGGTCAGCTCCCA 19715	A CA
		TGG AGC ACCTGGCTG	
		ACC TCG TGGACTGGT	
		C AC	
GAM2095 FLJ14642	3'	CAGGAAGTAGCTAGGTTCCA 52574	AGCCA _
		TGGA ACCTGGCTG TCCTG	
		ACCT TGGATCGAT AGGAC	
		GA	
GAM2095 FLJ20051	3'	CAAGACTATATTGGCTTC 39361	CC GCT C
		GAAGCCAA TG GTC TG	
		CTTCGGTT AT CAG AC	
		_ AT_ A	
GAM2095 FLJ21458	3'	CGGCCAAGGTGGCTTCCA 46279	A _
		TGGAAGCCA CCT GGCTG	
		ACCTTCGGT GGA CCGGC	
		_ A	
GAM2095 FLJ22729	5'	CAGAACAGCAGGCTTCCA 45508	AACCTG C
		TGGAAGCC GCTGT CTG	

ACCTTCGG CGACA GAC
 A_____ A
 GAM2095 FLJ22969 3' TCAGGACAACAGTTCCAATTCC 69218 GCCAAC GC
 A TGGAA CTG TGCCTGA
 ||||| ||| |||||
 ACCTT GAC ACAGGACT
 AACCTT A_
 GAM2095 FLJ31762 3' CAGGACAGTGAAGTCCA 58759 CCAACCTG
 TGGAAG GCTGTCCTG
 ||||| |||||
 ACCTTC TGACAGGAC
 AAG_____
 GAM2095 GRIN3A 3' CAGGACAGCCAAGTGAAGC 56777 CA_ C
 GC AC TGGCTGTCCTG
 || |||||
 CG TG ACCGACAGGAC
 AAG A
 GAM2095 HTF9C 5' CAGGACGAGGTGGCCAGGCGGC 42992 AA AA _____
 CCCCCA TGG GCC CCTGGCT GTCCTG
 ||| ||| ||||| |||||
 ACC CGG GGACCGG CAGGAC
 CC C_ TGGAG
 GAM2095 KIAA0082 3' CAGTGCCAGGCTGGTTTCCA 93781 A TGTC
 TGGAAGCCA CCTGGC CTG
 ||||| ||||| |||
 ACCTTTGGT GGACCG GAC
 C T____
 GAM2095 KIAA0202 3' AGAATAGCCAGCTCCA 65008 A CAACC C
 TGGA GC TGGCTGT CT
 |||| || ||||| ||
 ACCT CG ACCGATA GA
 _ _____ A
 GAM2095 KIAA0205 3' CATGTTGGCCAGGCTGGCCTC 30204 A A TCC
 GA GCCA CCTGGCTG TG
 || ||||| ||||| ||
 CT CGGT GGACCGGT AC
 C C TGT
 GAM2095 KIAA0284 3' CAGACCTGGCCAGGCCAGCCTC 63802 A CAA _ C
 C GGA GC CCTGGCT GTC TG
 ||| || ||||| ||| ||
 CCT CG GGACCGG CAG AC
 C ACC TC _
 GAM2095 KIAA0427 3' CATCGTGGCCAGGCAGCCTCCA 29374 A CAA TG CC
 TGGA GC CCTGGC T TG
 |||| || ||||| | ||
 ACCT CG GGACCG G AC
 C AC_ GT CT
 GAM2095 KIAA0447 3' CATGCCCAAGTCGGTTTCCA 72107 A CT_ _
 TGGAAGCC AC GGC TG
 ||||| || ||| ||

ACCTTTGG TG CCG AC
 C AAC T
 GAM2095 KIAA1867 3' CAGAATTGGCCACTTCCA 96480 CCAACC TC_
 TGGAAG TGGCTG CTG
 ||||| ||||| ||
 ACCTTC ACCGGT GAC
 _____ TAA
 GAM2095 KIAA1939 3' CAGGACAACAAATGGCTTCCA 46184 ACC GC
 TGGAAGCCA TG TGTCCTG
 ||||| || |||||
 ACCTTCGGT AC ACAGGAC
 AA_ A_
 GAM2095 MANBAL 3' TCAGAAGCCGGTCAGCTCACA 42220 GA CA GTC
 TG AGC ACCTGGCT CTGA
 || || ||||| ||||
 AC TCG TGGGCCGA GACT
 AC AC A_
 GAM2095 moblak 3' CAGGAGGCTGGATGGCTTCCA 56387 A T G
 TGGAAGCCA CC GGCT TCCTG
 ||||| || || |||||
 ACCTTCGGT GG TCGG AGGAC
 A _ _
 GAM2095 NXPH3 3' CAGAATGGCCAGCTGCCA 66339 A CAACC C
 TGG AGC TGGCTGT CTG
 || || ||||| ||||
 ACC TCG ACCGGTA GAC
 G _____ A
 GAM2095 RNP24 3' TCAGGATAAACCATACTTCCA 23328 CCAACC C_
 TGGAAG TGG TGTCCTGA
 ||||| || |||||
 ACCTTC ACC ATAGGACT
 AT_____ AA
 GAM2095 SCYA19 3' AGGAAGGACCAGGCTTCCA 21855 AACC _ G
 TGGAAGCC TGG CT TCCT
 ||||| || || |||||
 ACCTTCGG ACC GG AGGA
 _____ A A
 GAM2095 SERF1B 3' CATGTTGGCCAGGCTGGTCTCC 43691 AG A TCC
 A
 TGGA CCA CCTGGCTG TG
 |||| || ||||| ||
 ACCT GGT GGACCGGT AC
 CT C TGT
 GAM2095 LOC123316 5' CAGGCTGCGGAGGGCGGCTCCC 76122 A AA G_ T T
 A
 TGG AGCC CCT GC G CCTG
 || |||| || || |||||
 ACC TCGG GGA CG C GGAC
 C CG GG T_
 GAM2095 LOC132660 5' CAGACCCAGGCACGGCTTCCA 75575 AA_ CT C
 TGGAAGCC CCTGG GTC TG
 ||||| |||| || ||

	ACCTTCGG GGACC CAG AC	
	CAC _ _	
GAM2095 LOC137362 3'	AGAACGGTCAGATTA	75778 CC C C
	CTTC TT GACTGGCA GA	
	AA A A	
GAM2095 LOC146562 3'	TCAAAGGCAAGACAGGCTTCCA	58254 AAC G GTCC
	TGGAAGCC CT GCT TGA	
	ACCTTCGG GA CGG ACT	
	ACA A AA _	
GAM2095 LOC146599 5'	CAGTACAAAGCTGGCTTCCA	78610 ACCTG _ C
	TGGAAGCCA GCT GT CTG	
	ACCTTCGGT CGA CA GAC	
	AA T	
GAM2095 LOC147649 3'	CAGGTAGGTTGGCTCCA	79056 A G
	TGGA GCCAACCTG CTG	
	ACCT CGGTTGGAT GAC	
	G	
GAM2095 LOC152762 3'	TCAGGGCACCCAGGCTGGACCC	81537 AAG A C
CA	TGG CCA CCTGG TGTCTGA	
	ACC GGT GGACC ACGGACT	
	CCA C C	
GAM2095 LOC152765 5'	CAGAACAGCAGGGAAATTCCA	81542 GCCAA G C
	TGGAA CCTG CTGT CTG	
	ACCTT GGAC GACA GAC	
	AAAG _ _ A	
GAM2095 LOC158376 5'	CAGGACAGAGGCTGCAGCACCC	88135 AA _ A GG
A	TGG GC CA CCT CTGTCCTG	
	ACC CG GT GGA GACAGGAC	
	CA AC C _	
GAM2095 LOC160942 5'	CAGGATGCAGCCAGCTTTCA	88445 CAACC _
	TGGAAGC TGGCTGT CCTG	
	ACTTTCG ACCGACG GGAC	
	TA	
GAM2095 LOC197342 3'	CAGGAGACCTCAGGACGGCCCC	89353 AA AA CTG_
CA	TGG GCC CCTGG TCCTG	
	ACC CGG GGA CT AGGAC	
	CC CA CCAG	
GAM2095 LOC200488 5'	CAGGACAGCCGCCAGCCTCC	91649 A CAACC
	GGA GC TGGCTGTCCTG	

	CCT CG	GCCGACAGGAC	
	C ACC__		
GAM2095 LOC201910 3'	TCAGAATGGCAGTTGGCCACCC	90552	AA_ CTG C
A	TGG GCCAAC GCTGT CTGA		
	ACC CGGTTG CGGTA GACT		
	CAC A__ A		
GAM2095 LOC203025 3'	AGAACGGTCAGATTAAC TTC	90739	CC C C
	GAAG AA CTGGCTGT CT		
	CTTC TT GACTGGCA GA		
	AA A A		
GAM2095 LOC206426 3'	CAGGACAGACTAGCTGCCA	91097	A CAACC _
	TGG AGC TGG CTGTCCTG		
	ACC TCG ATC GACAGGAC		
	G ____ A		
GAM2095 LOC220020 3'	TCAGGACGTGGATGGCCTGCTT	95054	CAA TGGC_
CCA	TGGAAGC CC TGTCCTGA		
	ACCTTCG GG GCAGGACT		
	TCC TAGGT		
GAM2095 LOC221510 3'	CAGGACAGACCTTCAACTTCCA	92703	CCAACCT _
	TGGAAG GG CTGTCCTG		
	ACCTTC CC GACAGGAC		
	AACTT__ A		
GAM2095 LOC51086 3'	ACGGCAAGCTGGCTTCCA	32564	AC G
	TGGAAGCCA CT GCTGT		
	ACCTTCGGT GA CGGCA		
	C_ A		
GAM2095 LOC84548 3'	TCAGAATAGTGGCTAGCTTC	71768	CAA TG C
	GAAGC CC GCTGT CTGA		
	CTTCG GG TGATA GACT		
	ATC __ A		
GAM2095 LOC90494 5'	AGGATAATGGCTTCCA	63731	ACCTGGC
	TGGAAGCCA TGTCCT		
	ACCTTCGGT ATAGGA		
	A_____		
GAM2095 LOC90906 5'	TCAGGACACTCAGACCAGTTTC	64956	CAAC GC
CA	TGGAAGC CTG TGTCCTGA		
	ACCTTTG GAC ACAGGACT		
	ACCA TC		
GAM2095 LOC91759 3'	CAGGATGGATCCAGCCTCCA	67689	A CAACC _
	TGGA GC TGG CTGTCCTG		

ACCT CG ACC GGTAGGAC
 C _____ TA
 GAM2095 LOC93082 3' ACAGCCAGCCGGCTCCCA 57254 A AAC
 TGG AGCC CTGGCTGT
 ||| ||| |||||
 ACC TCGG GACCGACA
 C CC_

GAM2096 ATP7A 3' ACTTTCATTAGCTTCAAAG 5312 ACT TCC
 CTTTGAAG CTG GAAAGT
 ||||| ||| |||||
 GAAACTTC GAT CTTTCA
 _____ TA_

GAM2096 D8S2298E 3' TTGGAAGAAGCTTCAAAG 20240 AC G
 CTTTGAAG TCT TCCGA
 ||||| ||| |||||
 GAAACTTC AGA AGGTT
 GA _

GAM2096 OSR1 3' AACTTCAGCCATCAGATCCTTC 18834 AC TCCGA_
 AAAG CTTTGAAG TCTG AAGTT
 ||||| ||| |||||
 GAAACTTC AGAC TTCAA
 CT TACCGAC

GAM2096 WHSC1 3' TCGGAAGAGTCTTCAAA 30584 G
 TTTGAAGACTCT TCCGA
 ||||| |||||
 AAACTTCTGAGA AGGCT

GAM2096 WHSC1 3' TCGGAAGAGTCTTCAAA 56671 G
 TTTGAAGACTCT TCCGA
 ||||| |||||
 AAACTTCTGAGA AGGCT

GAM2096 WHSC1 3' TCGGAAGAGTCTTCAAA 56682 G
 TTTGAAGACTCT TCCGA
 ||||| |||||
 AAACTTCTGAGA AGGCT

GAM2096 ZNF26 3' AACGCAGGGAACAGAGTCTTAA 73335 A _ GAAA
 AG CTTTGA GACTCTGT CC GTT
 ||||| ||||| || |||
 GAAATT CTGAGACA GG CAA
 _ A GACG

GAM2096 FLJ25415 3' AACTTCATGGGACTCTTCAAAG 59170 CTCT GA_
 CTTTGAAGA GTCC AAGTT
 ||||| ||| |||||
 GAAACTTCT CAGG TTCAA
 _____ GTAC

GAM2096 MGC32104 3' AATGTGTGGAAGTCTTCAAA 59059 CTG AAA
 TTTGAAGACT TCCG GTT
 ||||| ||| |||

AAACTTCTGA AGGT TAA
AA_ GTG
GAM2096 OS4 3' TGGAACAGAGTCCCCAGA 20398 AA _
TTTG GACTCTGT CCG
|||| ||||||| |||
AGAC CTGAGACA GGT
CC A
GAM2097 DLEC1 3' ACAATGGTCTCAGCCTAGGC 24712 A ACCCA
GC TTAG AGACCATTGT
|| ||| |||||||
CG GATC TCTGGTAACA
_ CGAC_
GAM2097 DLEC1 3' ACAATGGTCTCAGCCTAGGC 96275 A ACCCA
GC TTAG AGACCATTGT
|| ||| |||||||
CG GATC TCTGGTAACA
_ CGAC_
GAM2097 KIAA1323 5' ACAATAATGGATTTAATGCTC 63719 C AGACC
GAGCATTAGA CCA ATTGT
||||||| ||| |||||
CTCGTAATTT GGT TAACA
A AA____
GAM2097 LOC115297 3' ACAAAAGTTTAAGTCTAATG 73259 CCA CA
CATTAGAC AGAC TTGT
||||||| ||| |||||
GTAATCTG TTTG AACA
AA_ AA
GAM2097 LOC147276 3' ACAACAGATTGTGGTCTAATCT 78946 C _ GACCA
C GAG ATTAGACC CAA TTGT
||| ||||||| ||| |||||
CTC TAATCTGG GTT AACA
_ T AGAC_
GAM2098 SCAMP1 3' GCTAAATAAATATTCTCC 54500 T C
GGA AATATT ATTTAGC
||| ||||||| |||||||
CCT TTATAA TAAATCG
C A
GAM2098 SCAMP1 3' GCTAAATAAATATTCTCC 54501 T C
GGA AATATT ATTTAGC
||| ||||||| |||||||
CCT TTATAA TAAATCG
C A
GAM2098 NX-17 3' TGAATATCAGCCCCTAATA 40706 ATA_
TATTAGGG ATATTCA
||||||| |||||||
ATAATCCC TATAAGT
CGAC
GAM2098 LOC161589 3' GCTAAATGAATATTATCCCTAA 83159
TA TATTAGGGATAATATTCATTTAGC
|||||||||||||||||||

ATAATCCCTATTATAAGTAAATCG

GAM2099 DLEC1 3' CATCTGGCCCTCCCTTG 24716 A A C
CAAGG AGGGC GG GTG
||||| ||||| || |||
GTTCC TCCCG TC TAC
C G _

GAM2099 DLEC1 3' CATCTGGCCCTCCCTTG 24728 A A C
CAAGG AGGGC GG GTG
||||| ||||| || |||
GTTCC TCCCG TC TAC
C G _

GAM2099 PIP5K1A 3' TATCCCACCCTGCCTTGATA 14520 A CA C
TATCAAGG AGGG GG GTG
||||||| |||| || |||
ATAGTTCC TCCC CC TAT
G A_ C

GAM2099 SOX11 3' ACCCACCCTTGGTA 13308 AA CA C
TATCAAGG GGG GG GT
||||||| ||| || ||
ATGGTTCC CCC CC CA
CC A_ _

GAM2099 CHL1 3' TGTTACCTTTCCTCAATA 22768 CA CA
TAT AGGAAGGG GGCG
||| ||||| |||||
ATA TCCTTTCC TTGT
AC A_

GAM2099 EPB41L1 3' CATTCTGCCCTTCCCTGA 71104 A C
TCA GGAAGGGCAGG GTG
||| ||||| ||||| |||
AGT CCTTCCCGTCT TAC
C _

GAM2099 FLJ00060 3' CATACCCCTGCCCTCCTCTGA 61741 _ A CGTG
TCA AGGA GGGCAGG ATG
||| ||||| ||||| |||
AGT TCCT CCCGTCC TAC
C _ CCCA

GAM2099 FLJ10898 5' CACCACAGCCCTTTCTCAATA 60126 CA AGGC
TAT AGGAAGGGC GTG
||| ||||| ||||| |||
ATA TCTTTCCCG CAC
AC ACAC

GAM2099 FLJ22557 3' ATCATCCCATCCTTAATA 45581 C A CAGGC
TAT AAGGA GGG GTGAT
||| ||||| ||| |||||
ATA TTCCT CCC TACTA
A A _

GAM2099 KIAA0574 3' CATCCCCTGCCCTCCCCTGA 69808 A A CGT
TCA GG AGGGCAGG GATG
||| || ||||| |||||

	AGT CC TCCCGTCC CTAC	
	C C C__	
GAM2099 KIAA0632	3' CACCTCAGAAACCCTTCCTTGA 32071	CA__ C
	TCAAGGAAGGG GG GTG	
	AGTTCCTTCCC CT CAC	
	AAAGA C	
GAM2099 KIAA1045	3' CATCACATGTCCTTCC 71599	GGC
	GGAAGGGCA GTGATG	
	CCTTCCTGT CACTAC	
	A__	
GAM2099 KIAA1354	5' CAGTGA CTGCCTTCCCTTGATA 61572	A G _
	TATCAAGG AGGGCAG CG TG	
	ATAGTTCC TTCCGTC GT AC	
	C A G	
GAM2099 MGC20460	5' CACCGCCTCCTACCCTTCTT 54901	C__ _
	AGGAAGGG AGGCG TG	
	TTCTTCCC TCCGC AC	
	ATCC C	
GAM2099 LOC158476	3' CACGCCCGCCCCCCCCATTGA 88186	_ AA_ A
	TCAA GG GGGC GGCGTG	
	AGTT CC CCGC CCGCAC	
	A CCC C	
GAM2099 LOC90459	3' CACACCCGCCTAATTTTTTG 63550	A_ A C
	CAAGGA GGGC GG GTG	
	GTTTTT TCCG CC CAC	
	AA C A	
GAM2100 D10S170	3' CATGAGTCGATAAATGTTGTC 19548	AA_ TC
	GACAACATT CGG CTCATG	
	CTGTTGTAA GCT GAGTAC	
	ATA _	
GAM2100 FLJ10232	3' GCACAAGGCAGATGTTGTC 36381	AACG T CA
	GACAACATT G CCT TGC	
	CTGTTGTAG C GGA ACG	
	A__ _ AC	
GAM2100 FLJ10748	3' CATGAGGAATGATCTTGTC 37096	C ACGG
	GACAA ATTA TCCTCATG	
	CTGTT TAGT AGGAGTAC	
	C A__	
GAM2100 KIAA1233	3' CATGAGAGTTAATGTTTC 63755	C GGTC
	A AACATTAAC CTCATG	

			C TTGTAATTG GAGTAC		
			T A__		
GAM2100	MRPS9	3'	GCATGAGGGCAGTACTGT 80746	T ACG	
			ACA TA GTCCTCATGC		
			TGT AT CGGGAGTACG		
			C GA_		
GAM2100	LOC220573	3'	AGCACAATCTACTAATGTTGTT 70203	AC TCCTCA	
			GACAACATTA GG TGCT		
			TTGTTGTAAT TC ACGA		
			CA TAAC__		
GAM2100	LOC54557	3'	CATGGGAACCAATGTTATC 73187	C AAC C	
			GA AACATT GGT CTCATG		
			CT TTGTAA CCA GGGTAC		
			A __ A		
GAM2101	ABCB4	5'	CATCCAGATAGGAATGTC 6531	CAC	
			GATGTTCC CTGGATG		
			CTGTAAGG GACCTAC		
			ATA		
GAM2101	ABCB4	5'	CATCCAGATAGGAATGTC 38756	CAC	
			GATGTTCC CTGGATG		
			CTGTAAGG GACCTAC		
			ATA		
GAM2101	ATRN	3'	GGACACAGGAAGGGGAACATC 58449	A__ GATG	
			GATGTTCCC CCTG CC		
			CTACAAGGG GGAC GG		
			GAA ACA_		
GAM2101	ATRN	3'	GGACACAGGAAGGGGAACATC 24859	A__ GATG	
			GATGTTCCC CCTG CC		
			CTACAAGGG GGAC GG		
			GAA ACA_		
GAM2101	BRCA1	3'	GGCATCTCAGGAACATC 24570	CACCT	
			GATGTTCC GGATGCC		
			CTACAAGG TCTACGG		
			AC__		
GAM2101	BRCA2	5'	GCATTGGAGGAATATCGTA 5344	CA TG	
			TACGATGTTCC CC GATGC		
			ATGCTATAAGG GG TTACG		
			A_ __		
GAM2101	CYP1A1	3'	GGACACAGTTCCTGGGAACATC 6691	C__ GATG	
			GATGTTCCCA CTG CC		

		CTACAAGGGT GAC GG	
		CCTT ACA_	
GAM2101 FUT6	5'	GGGCATCCAGACGGGATCCAGT 5643	GATGT AC
G		TAC TCCC CTGGATGCCC	
		GTG AGGG GACCTACGGG	
		ACCT_ CA	
GAM2101 HTR4	3'	GGGCAGGGCTAGCAACATCGTA 7886	CCCA_ GGA
		TACGATGTT CCT TGCCC	
		ATGCTACAA GGG ACGGG	
		CGATC ____	
GAM2101 NEBL	3'	CATCCTGTGAAACATCGT 22140	CC CT
		ACGATGTT CAC GGATG	
		TGCTACAA GTG CCTAC	
		A_ T_	
GAM2101 PUNC	5'	GGGCATCCAGGTGCTGGGCA 91231	C_
		TGTTT CACCTGGATGCCC	
		ACGGG GTGGACCTACGGG	
		TC	
GAM2101 SPOCK	3'	GGCCTACAAAGAACATCGTA 63474	CCACC GAT
		TACGATGTTT TG GCC	
		ATGCTACAAG AC CGG	
		AA__ ATC	
GAM2101 SWAP70	3'	CATTCGTATGAAAACATTGTA 71865	CC CC
		TACGATGTT CA TGGATG	
		ATGTTACAA GT GCTTAC	
		AA AT	
GAM2101 AFAP	3'	GGACATCCAGGCAGGTCG 41609	TGTT CA _
		CGA CC CCTGGATG CC	
		GCT GG GGACCTAC GG	
		____ AC A	
GAM2101 C20orf111	5'	GGCAACAGGAACATCG 33629	CACC GA
		CGATGTTCC TG TGCC	
		GCTACAAGG AC ACGG	
		____ A_	
GAM2101 CNNM4	3'	GGGCATCCAAATGGGTAGGCA 39872	_ CC
		TGTT CCCA TGGATGCCC	
		ACGG GGGT ACCTACGGG	
		AT AA	
GAM2101 CYB5-M	3'	GGCCAAGGTGGGAACATCG 48335	GGAT
		CGATGTTCCACCT GCC	

GCTACAAGGGTGA CGG
 AC__
 GAM2101 FLJ14153 3' CATCCAGGTGAACTTC 43011 T CC
 GA GTTC ACCTGGATG
 || ||| |||||
 CT CAAG TGGACCTAC
 T __
 GAM2101 FLJ22419 5' GGCGCGGCAAGGACATCG 45531 CCAC GA
 CGATGTTC CTG TGCC
 ||||| ||| |||
 GCTACAGG GGC GCGG
 AAC_ __
 GAM2101 GR6 3' GGCAGGTTTTAGGAACATC 24746 C__ GGAT
 GATGTTCC ACCT GCC
 ||||| ||| |||
 CTACAAGG TGGA CGG
 ATTT ____
 GAM2101 PPP4R2 5' CATCAGGAAGGAACATC 39558 CA G
 GATGTTCC CCTG ATG
 ||||| ||| |||
 CTACAAGG GGAC TAC
 AA _
 GAM2101 PREI3 3' GGCAGTAAGGGTGAAAACATTG 66927 CC GGA_
 TA TACGATGTT CACCT TGCC
 ||||| ||| |||
 ATGTTACAA GTGGG ACGG
 AA AATG
 GAM2101 LOC115110 3' GGGCATCCAGGCAGGTCCA 72182 TT CA
 TG CC CCTGGATGCCC
 || || |||||
 AC GG GGACCTACGGG
 CT AC
 GAM2101 LOC126392 5' CACCCAGGTGGGCCGTC 76204 TT A
 GATG CCCACCTGG TG
 ||| ||||| ||
 CTGC GGGTGGACC AC
 C_ C
 GAM2101 LOC129526 5' GCGCTACGGGAACATC 75386 ACC A
 GATGTTCCC TGG TGC
 ||||| ||| |||
 CTACAAGGG ATC GCG
 C_ _
 GAM2101 LOC144583 3' GGACATCCAGGTGCCCTCCATC 77418 TTCC_ _
 GATG CACCTGGATG CC
 ||| ||||| ||
 CTAC GTGGACCTAC GG
 CTCCC A
 GAM2101 LOC145384 3' GGACACAGGAAGGGGAACATC 77714 A__ GATG
 GATGTTCCC CCTG CC
 ||||| ||| ||

		CTACAAGGG GGAC GG		
		GAA ACA_		
GAM2101	LOC147080 3'	GGCATCCAAGTAGCATT 85042	CCC C	
		GATGTT AC TGGATGCC		
		TTACGA TG ACCTACGG		
		___ A		
GAM2101	LOC149401 3'	GGGCACAGTGGGGGAACATC 80116	A GA_	
		GATGTTCCC CCTG TGCCC		
		CTACAAGGG GGGT ACGGG		
		_ GAC		
GAM2101	LOC151040 3'	GGACACAGGAAGGGGAACATC 80906	A__ GATG	
		GATGTTCCC CCTG CC		
		CTACAAGGG GGAC GG		
		GAA ACA_		
GAM2101	LOC200854 5'	CATCAGGAAGGAACATC 88811	CA G	
		GATGTTCC CCTG ATG		
		CTACAAGG GGAC TAC		
		AA _		
GAM2101	LOC201304 3'	GGACAGAACCTGGGAACATGTA 89606	G CCTGGA _	
		TAC ATGTTCCCA TG CC		
		ATG TACAAGGGT AC GG		
		_ CCAAG_ A		
GAM2101	LOC202915 3'	GGCACCCAGGTGGGCCCCG 92019	TT A	
		TG CCCACCTGG TGCC		
		GC GGGTGGACC ACGG		
		CC C		
GAM2101	LOC204970 3'	GGGCACCCAGGTGGAGCA 90966	C A	
		TGTTCC ACCTGG TGCCC		
		ACGAGG TGGACC ACGGG		
		_ C		
GAM2101	LOC219623 5'	GTGCCCAGGCTGAAGGAACATC 93090	__ _ T__ ATGC	
		GATGTTCC CA CC GG C		
		CTACAAGG GT GG CC G		
		AA C A__ CGTA		
GAM2101	LOC222252 3'	GGACACAGGAAGGGGAACATC 95966	A__ GATG	
		GATGTTCCC CCTG CC		
		CTACAAGGG GGAC GG		
		GAA ACA_		
GAM2101	LOC91923 3'	GGACACAGGAAGGGGAACATC 68173	A__ GATG	
		GATGTTCCC CCTG CC		

		CTACAAGGG GGAC GG	
		GAA ACA_	
GAM2101	LOC92568	3' GGACACAGGAAGGGGAACATC 70330	A__ GATG
		GATGTTCCC CCTG CC	
		CTACAAGGG GGAC GG	
		GAA ACA_	
GAM2101	LOC92876	3' GGACACAGGAAGGGGAACATC 71350	A__ GATG
		GATGTTCCC CCTG CC	
		CTACAAGGG GGAC GG	
		GAA ACA_	
GAM2102	EPB72	3' GAGACATCTCTAGTTTTGC 15875	_A CCAA
		GCAAG C GG AGATGTCTC	
		CGTTT G TC TCTACAGAG	
		T A ____	
GAM2102	HDAC7A	3' AGAACAGCCTGCCTGCT 33921	A CAAAGA _
		AGCA GCAGGC TGT CT	
		TCGT CGTCCG ACA GA	
		C ____ A	
GAM2102	IL2RA	3' GAGACATCCGTTGTGCTTGC 6452	_ A_
		GCAGGC CAA GATGTCTC	
		CGTTCG GTT CTACAGAG	
		T GC	
GAM2102	SCA7	3' AGTGGTCTGAACTGCTTGCTA 6190	GCCAA GT
		TAGCAAGCAG AGAT CT	
		ATCGTTCGTC TCTG GA	
		AAG__ GT	
GAM2102	TRPV2	5' GAGACCAGAACCTGCTTGCTG 32771	CCAAAGAT
		TAGCAAGCAGG GTCTC	
		GTCGTTCTGCC CAGAG	
		AAGAC__	
GAM2102	C15orf15	3' AGACATCTTTCCTGCATTGC 33302	_ CC
		GCAA GCAGG AAAGATGTCT	
		CGTT CGTCC TTTCTACAGA	
		A _	
GAM2102	C20orf111	3' AGACATCTCTTTCTGCTCACTG 33627	CA CCAA
		TAG AGCAGG AGATGTCT	
		GTC TCGTCT TCTACAGA	
		AC TTC_	
GAM2102	C21orf61	3' GAGCACACCTAGCCTGCTTGCT 90103	CAA A _
		AGCAAGCAGGC AG TGT CTC	

TCGTTTCGTCCG TC ACA GAG
A__ C C
GAM2102 C6orf37 3' ACATCTTTGATCTGGTTGT 68089 G GC
GCAA CAG CAAAGATGT
||||| ||| |||||
TGTT GTC GTTTCTACA
G TA
GAM2102 CAMKK2 3' GGGTCGTCTGGCCTGCTTGCTG 22625 AA T
TAGCAAGCAGGCCA GATG CTC
||||||| ||| |||
GTCGTTTCGTCCGGT CTGC GGG
__ T
GAM2102 DKFZP434N1817 5' ACATCTTTTTATTCTTGC 68718 C GCC
GCAAG AG AAAGATGT
||||| || |||||
CGTTC TT TTTCTACA
_ ATT
GAM2102 EDR2 3' GAGCCTCCTGGCCTGCCTGC 61111 A AA TT
GCA GCAGGCCA GA G CTC
||| ||||| || |||
CGT CGTCCGGT CT C GAG
C C_ C_
GAM2102 FLJ22814 3' AGTCACTCTGACCTGCTTGCTG 46714 C A A T
TAGCAAGCAGG CA AG TG CT
||||||| || || ||
GTCGTTTCGTCC GT TC AC GA
A C _ T
GAM2102 GALNT12 5' GAGACATCCCCGGATATCCTGC 45317 ____ AAA
T AGCAGG CC GATGTCTC
||||| || |||||
TCGTCC GG CTACAGAG
TATA CCC
GAM2102 HCA4 3' AGACATCTTTATATGTTCTA 57736 CA GGCC
TAG AGCA AAAGATGTCT
||| ||| |||||
ATC TTGT TTTCTACAGA
_ ATA_
GAM2102 KIAA0317 3' GAGACACCCTCTTTGGCCCTCA 29743 CA CA ____
CTA TAG AG GGCCAAAGA TGTCTC
||| || ||||| |||||
ATC TC CCGGTTTCT ACAGAG
AC _ CCC
GAM2102 KIAA1877 3' AGACATCTCCTATAGCTTGCTA 66738 ____ CCAA
TAGCAAGC AGG AGATGTCT
||||| || |||||
ATCGTTTCG TCC TCTACAGA
ATA ____
GAM2102 NPEPL1 3' GAGACATCTTCTGTAACTGCT 45423 GC__ _
AGCAG CA AAGATGTCTC
||||| || |||||

		TCGTC GT TTCTACAGAG		
		AAAT C		
GAM2102	LOC145815 3'	ACACCTGTCTGCTTTCTA	84516	C CAA A
		TAG AAGCAGGC AG TGT		
		ATC TTCGTCTG TC ACA		
		T _ C		
GAM2102	LOC150951 5'	GATGCTTTTGGCCTGGTT	86344	G AT
		AA CAGGCCAAAG GTC		
		TT GTCCGGTTTT TAG		
		G CG		
GAM2102	LOC220431 5'	GAGACATCCTTGTCTTTGC	95996	GC C A
		GCAA AGGC AA GATGTCTC		
		CGTT TCTG TT CTACAGAG		
		_ _ C		
GAM2102	LOC254532 5'	AGGCCTGGCCTGCCTGC	98445	A AAGAT
		GCA GCAGGCCA GTCT		
		CGT CGTCCGGT CGGA		
		C C_		
GAM2102	LOC256273 3'	GAGGTTTTAGCCTGTTTGCTA	98141	CA G
		TAGCAAGCAGGC AAGAT TC		
		ATCGTTTGTCCG TTTTG AG		
		A_ G		
GAM2102	LOC257364 3'	AGACAGGGGCCTGCTTGC	96640	AAAGA
		GCAAGCAGGCC TGTCT		
		CGTTCGTCCGG ACAGA		
		GG_		
GAM2103	ALDH2 3'	TCAAATGTGTTATCCTCTCTCT	60436	AA T_
	GAAA	TTTCA GGAGAGGAT TATTGA		
		AAAGT TCTCTCCTA GTAAACT		
		C_ TTGT		
GAM2103	FKBP1A 3'	TAAACCCTCTGCCTTTGAAA	7686	_ A
		TTTCAAAGG AGAGG TTTA		
		AAAGTTTCC TCTCC AAAT		
		G C		
GAM2103	GNA15 3'	CAGTTTCCCTCCTTTGAAA	60587	A TTTAT
		TTTCAAAGGAG GGA TTG		
		AAAGTTTCCTC CCT GAC		
		_ TT_		
GAM2103	HNRPH1 3'	TCAAATAAATCCTCCTTTT	19812	A
		AAAGG GAGGATTTATTTGA		

TTTTC CTCCTAAATAAACT

GAM2103 NTS 3' TCAAATAAATCTAAATCTTC 21637 —
GGAGA GGATTTATTTGA
||||| |||||||||
CTTCT TCTAAATAAACT
AAA

GAM2103 TCF8 3' GAATTCTCTCCCCTGAAA 48431 AA
TTTCA GGAGAGGATTT
||||| |||||||||
AAAGT CCTCTCTTAAG
CC

GAM2103 UBE2G2 3' TCAAACAGGCTTCTCTTCTGAA 65494 A A A
A TTTCA AGGAGAGG TTT TTTGA
||||| ||||||| ||| |||||
AAAGT TTCTCTTC GGA AAAC
C _ C

GAM2103 COL12A1 3' TCAAATAATTCCCCTCCT 16471 A T
AGGAG GGA TTATTTGA
||||| ||| |||||||
TCCTC CCT AATAAACT
C T

GAM2103 COL12A1 3' TCAAATAATTCCCCTCCT 55535 A T
AGGAG GGA TTATTTGA
||||| ||| |||||||
TCCTC CCT AATAAACT
C T

GAM2103 EIF4B 3' CAAATAAATCTGATCTTT 76497 GA
AAGGA GGATTTATTTG
||||| |||||||||
TTTCT TCTAAATAAAC
AG

GAM2103 FLJ13955 3' AAGTCCTCCTTTGAAA 45747 GA
TTTCAAAGGA GGATTT
||||||| |||||
AAAGTTTCCT CCTGAA

GAM2103 FLJ14596 3' CAGGGCCCCCTCTCCCCTGAA 52513 AA ATTAA
TTCA GGAGAGG TTTG
||| ||||| |||
AAGT CCTCTCC GGAC
CC CCG__

GAM2103 KIAA0594 3' CAAACAAATTATCTTCTTTTAA 65507 C G A
A TTT AAAGGAGA GATTT TTTG
||| ||||| ||||| |||
AAA TTTCTTCT TTAAA AAAC
T A C

GAM2103 RHOBTB3 3' TCAAACACCTTTCTCTCTGAAA 30431 A _ ATTAA
TTTCA AG GAGAGG TTTGA
||||| || ||||| |||||

			AAAGT TC CTTTCC	AAACT		
			C T	AC__		
GAM2103	STK38L	3'	CAAACACATTCTCCTTTGAA	69686		GATTTA
			TTCAAAGGAGAG	TTTG		
			AAGTTTCCTCTT	AAAC		
			ACAC__			
GAM2103	LOC118611	3'	AAATCCATCTCCTTTTAAA	75992	C	_
			TTT AAAGGAGA	GGATTT		
			AAA TTTCTCT	CCTAAA		
			T	A		
GAM2103	LOC144866	5'	CAGTTATCCTCTCCTCTGAA	84135	A	TTAT
			TTCA AGGAGAGGAT	TTG		
			AAGT TCCTCTCCTA	GAC		
			C	TT__		
GAM2103	LOC145748	3'	CAAATACATAAATCTCTTTT	84470		GG_ T
			AAAGGAGA	AT TATTTG		
			TTTTCTCT	TA ATAAAC		
			AAA	C		
GAM2103	LOC51000	5'	CAGATCTCCTCTCCTCCAGAA	32539	AA_	TTT
			TTC AGGAGAGGA	ATTTG		
			AAG TCCTCTCCT	TAGAC		
			ACC	C__		
GAM2103	LOC54505	5'	AAATCCTTCCTTTGAAA	68445		G
			TTTCAAAGGA	AGGATTT		
			AAAGTTTCCT	TCCTAAA		
			-			
GAM2104	GNAS	3'	CAACGACTGCCGTGACATCATT	33914		
	CA		TGAATGATGTCACGGCAGTCGTTG			
			ACTTACTACAGTGCCGTCAGCAAC			
GAM2104	HIC2	3'	CAACGACTGATCTCTCCATTCA	65860		ATGTCACGG
			TGAATG	CAGTCGTTG		
			ACTTAC	GTCAGCAAC		
			CTCTCTA__			
GAM2104	MGC13114	3'	CTGCCGTGGCACCCTTCA	51392	A	A
			TGA TG	TGTCACGGCAG		
			ACT AC	ACGGTGCCGTC		
			C	C		
GAM2104	MGC19556	5'	CTGCCGTGACACCCTTCA	54339		TGA
			TGAA	TGTCACGGCAG		

ACTT ACAGTGCCGTC
 CCC
 GAM2104 NY-BR-1 5' CAACGACTCCTACATCGTCCA 54849 A CAC C
 TG ATGATGT GG AGTCGTTG
 || ||||| || |||||
 AC TGCTACA CC TCAGCAAC
 C T__ _
 GAM2105 GNAS 3' AGTTAATCACCCACCATAGGGC 6710
 AT ATGCCCTATGGTGGGTGATTA
 |||||
 TACGGGATACCACTAATTGA
 GAM2105 GNAS 3' AGTTAATCACCCACCATAGGGC 33913
 AT ATGCCCTATGGTGGGTGATTA
 |||||
 TACGGGATACCACTAATTGA
 GAM2105 GNAS 3' AGTTAATCACCCACCATAGGGC 55382
 AT ATGCCCTATGGTGGGTGATTA
 |||||
 TACGGGATACCACTAATTGA
 GAM2105 GNAS 3' AGTTAATCACCCACCATAGGGC 55386
 AT ATGCCCTATGGTGGGTGATTA
 |||||
 TACGGGATACCACTAATTGA
 GAM2105 MSH3 3' TTATCCACCAAGAACAT 11695 CC A
 ATG CT TGGTGGGTGA
 ||| || |||||
 TAC GA ACCACCTATT
 AA _
 GAM2105 PCDH12 5' AATCAAGACCATGGGCA 33884 T GGG
 TGCCC ATGGT TGATT
 |||| |||| ||||
 ACGGG TACCA ACTAA
 _ GA_
 GAM2105 DKFZP434C1715 3' AGTTAAAGGGTCCACCATAGGC 87349 C TGA_
 AT ATGCC TATGGTGGG TTA
 |||| ||||| ||||
 TACGG ATACCACCT AATTGA
 _ GGA
 GAM2105 FLJ10829 3' AGTCAGAAGTCACCATAGAGC 37255 C G_
 GC CTATGGTGG TGATT
 || ||||| ||||
 CG GATACCACT ACTGA
 A GAAG
 GAM2105 FLJ22843 3' ATTACCCACCAAAGACAT 48014 CC A
 ATG CT TGGTGGGTGAT
 ||| || |||||

			TAC GA ACCACCCATTA		
			A_ A		
GAM2105 NMU	3'	TAATTTTCCACAGAGCA	22909	C ATG	T
		TGC CT GTGGG GATTA			
		ACG GA CACCT TTAAT			
		A ____ T			
GAM2105 ZER6	3'	TGGAAGCCCATCATAAGGCAT	64119	C	GA
		ATGCC TATGGTGGGT TTA			
		TACGG ATACTACCCG GGT			
		A AA			
GAM2105 LOC158535	5'	AATCACTCCCACAAAGCAT	88592	CCTA	T
		ATGC TGG GGGTGATT			
		TACG ACC CTCATAA			
		AAAC _			
GAM2105 LOC164395	5'	TAATCATTCAGCAAGGGCAT	83403	A G	
		ATGCCCT TG TGGGTGATTA			
		TACGGGA AC ACTTACTAAT			
		_ G			
GAM2105 LOC253752	5'	AATGCACCCATTGGACAT	96364	C TAT	_
		ATG CC GGTGGGTG ATT			
		TAC GG TTACCCAC TAA			
		A ____ G			
GAM2106 CHRNA2	3'	TGGAGATGAGCCCAAAGTGC	7432	GTAG AC	C
		GCA TG GC CATCTCCA			
		CGT AC CG GTAGAGGT			
		GAA_ C_ A			
GAM2106 GNAS	3'	TGGAGATGGGCGTCACTACTGC	33919		
TA		TAGCAGTAGTGACGCCCATCTCCA			
		ATCGTCATCACTGCGGGTAGAGGT			
GAM2106 MYCL2	3'	GAGATGGGGTTTCACCAC	19376	A C	_
		GT GTGA GCCC ATCTC			
		CA CACT TGGG TAGAG			
		C T G			
GAM2106 PLAG1	3'	GAAATGACACAGAACTATTGCT	12148	GACGCC_	C
A		TAGCAGTAGT CAT TC			
		ATCGTTATCA GTA AG			
		AGACACA A			
GAM2106 CCR1	3'	GAAATGGGGGAAGTACTGCTG	8926	GACG	C
		TAGCAGTAGT CCCAT TC			

GTCGTCATCA GGGTA AG
 AGG_ A
 GAM2106 FLJ12960 3' GAGATGGGGTTTCACCGT 45297 A AGT G
 GC GT GAC CCCATCTC
 || || ||| |||||
 TG CA TTG GGGTAGAG
 C CT_ _
 GAM2106 GG2-1 3' GAGATGGAGCACTGCTG 27576 ACGC C
 CAGTAGTG CCATCT C
 ||||| |||||
 GTCGTCAC GGTAGA G
 GA_ A
 GAM2106 KIAA1297 3' AGATGGGCGGCAGCTGCT 72625 A GA
 AGCAGT GT CGCCCATCT
 ||||| || |||||
 TCGTCG CG GCGGGTAGA
 A _
 GAM2106 KIAA1449 3' GAGACAGGGTTCCTCACTGCT 40839 _ T C A_
 A TAGCAGT AG GA GCCC TCTC
 ||||| || || ||| |||
 ATCGTCA TC CT TGGG AGAG
 C C _ AC
 GAM2106 KIAA1643 3' TGGAGATGACACACCTACTGCT 65158 _ ACGCC
 AGCAGTAG TG CATCTCCA
 ||||| || |||||
 TCGTCATC AC GTAGAGGT
 C ACA_
 GAM2106 KIAA1755 3' GAGATGGGGCCTCACTAC 62016 C _
 GTAGTGA GCCC ATCTC
 ||||| ||| |||||
 CATCACT CGGG TAGAG
 C G
 GAM2106 KIAA1978 3' GAGATGGGCTTTCTCTGC 74892 T T C
 GCAG AG GA GCCCATCTC
 ||| || || |||||
 CGTC TC TT CGGGTAGAG
 _ T _
 GAM2106 MGC5149 3' GAGATGGGGTTTCACCAC 72757 A C _
 GT GTGA GCCC ATCTC
 || ||| ||| |||||
 CA CACT TGGG TAGAG
 C T G
 GAM2106 PRO1580 5' AGATAGTTACTACTGCTA 38124 GCCC
 TAGCAGTAGTGAC ATCT
 ||||| ||| |||
 ATCGTCATCATTG TAGA
 A_
 GAM2106 RPIA 3' GAAATGCTTGCCAGTACTGC 58591 G A CC C
 GCAGTA TG CG CAT TC
 ||||| || || ||| ||

		CGTCAT AC GT GTA AG		
		G C TC A		
GAM2106	TGIF2	3' GGAGACAAGCATGGTGCTGCTG 41753	G GAC CCA	
		TAGCAGTA T GC TCTCC		
		GTCGTCGT G CG AGAGG		
		G TA_ AAC		
GAM2106	LOC126327	3' TGGAGACAGAAAGCCACTGCTG 74986	AC CCA__	
		CAGTAGTG GC TCTCCA		
		GTCGTCAC CG AGAGGT		
		__ AAAGAC		
GAM2106	LOC126731	3' ATGAGTGTGAGCACTACTACTG 59835	C __ C	
		TAG AGTAGT GACGC CAT		
		GTC TCATCA CTGTG GTA		
		A CGA A		
GAM2106	LOC149117	3' TGGAAATAAGTTGTGTTACTAC 85509	CC__ C	
		GTAGTGACGC AT TCCA		
		CATCATTGTG TA AGGT		
		TTGAA A		
GAM2106	LOC149483	3' TGGAGATGAGCATCTGAACATG 80189	_ AGT C C	
	C	GCA GT GA GC CATCTCCA		
		CGT CA CT CG GTAGAGGT		
		A AGT A A		
GAM2106	LOC149832	5' GAGATGGGATTGTCAGCCAC 85863	A_ __	
		GT G TGACG CCCATCTC		
		CA C ACTGT GGGTAGAG		
		C G TA		
GAM2106	LOC89985	3' TGGAGATGGGCACCACTGC 61675	AC	
		GTAGTG GCCCATCTCCA		
		CGTCAC CGGGTAGAGGT		
		CA		
GAM2107	CARD15	3' GACTCATCCATCCAGGCCA 42470	TCAAG CA	
		TGGT GGATGGA AGTC		
		ACCG CCTACCT TCAG		
		GA__ AC		
GAM2107	TBX6	3' GGCCCCATCCCCACACCAA 55815	TCAA ACAA	
		TTGGT GGGATGG GTC		
		AACCA CCCTACC CGG		
		CACC C__		
GAM2107	USP2	5' GACTCGTCCATCCTCCAA 16110	TTCAA A	
		TTGG GGGATGGAC AGTC		

		AACC TCCTACCTG TCAG	
		_____ C	
GAM2108	TERF1	3' CCCAAATCCTGTTCCAATGA 34391	C TA C
		TCATTGGA ACG GATT GGG	
		AGTAACCT TGT CTAA CCC	
		_____ C_ A	
GAM2108	FLJ10159	3' CCATGTCACGCCATCCAATGAC 36334	CA_ A TC
		GTCATTGGA CGT GAT GG	
		CAGTAACCT GCA CTG CC	
		ACC _ TA	
GAM2108	FLJ14213	3' CCGATGCTCCCAATGACG 46216	ACAC GAT
		CGTCATTGG GTA TCGG	
		GCAGTAACC CGT AGCC	
		CT_ _	
GAM2108	MGC10715	3' ATTTACCAGACATCCAATGAC 44495	CAC_
		GTCATTGGA GTAGAT	
		CAGTAACCT CATTTA	
		ACAGAC	
GAM2108	MOST2	5' CCAGGACTGCCCAATGAC 40059	ACAC A _
		GTCATTGG GTAG TTC GG	
		CAGTAACC CGTC AGG CC	
		_____ _ A	
GAM2108	LOC150370	3' CCGGGTCTACGTGCCCATGAC 86123	T A
		GTCAT GG CACGTAGATTTCGG	
		CAGTA CC GTGCATCTGGGCC	
		C _	
GAM2108	LOC152620	3' CCCAAATCCTGTTCCAATGA 60707	C TA C
		TCATTGGA ACG GATT GGG	
		AGTAACCT TGT CTAA CCC	
		_____ C_ A	
GAM2108	LOC158668	3' CCCAAATCCTGTTCCAATGA 69896	C TA C
		TCATTGGA ACG GATT GGG	
		AGTAACCT TGT CTAA CCC	
		_____ C_ A	
GAM2109	ELF3	3' TGACCTTGACCTTGACCAA 16685	T GAT AAA
		TTGGT CAAGG GG GTCA	
		AACCA GTTCC TC CAGT	
		_____ AGT _	
GAM2109	JAK2	3' TGACCTTCATTCTGAGACCAA 18318	CAA AA
		TTGGTT GGGATGGA GTCA	

			AACCAG TCTTACTT CAGT		
			AG_ C_		
GAM2109	SLC10A2	5'	ACTCTCTGTCTTGACCAA 6590	CAA	A
			TTGGTT GGGATGGA AGT		
			AACCAG TTCTGTCT TCA		
			_____ C		
GAM2109	FLJ10803	3'	GTGACTTTTCAGTTAAAGCCAA 37205	CAAGG	G
			TTGGTT GAT GAAAGTCAC		
			AACCGA TTG CTTTCAGTG		
			AA_____ A		
GAM2109	KIAA1958	5'	GTGACTTTGAACCCCAAACC 82788	CAA	ATGG
			GGTT GGG AAAGTCAC		
			CCAA CCC TTTTCAGTG		
			A_____ CAAG		
GAM2109	MARCKS	3'	ACTTTCCACCCTGCCCA 11411	TTCA	A
			TGG AGGG TGGAAAGT		
			ACC TCCC ACCTTTCA		
			CG_____		
GAM2109	TUB	5'	GTGGGACCATCCCTTAAACC 13898	C	AAAG
			GGTT AAGGGATGG TCAC		
			CCAA TTCCCTACC GGTG		
			A AG_____		
GAM2109	LOC80298	3'	ACTTTTACCTTGAACCA 48062	GATG	
			TGGTTCAAGG GAAAGT		
			ACCAAGTTCC TTTTCA		
			A_____		
GAM2110	C18orf1	3'	CAGCCAAGTGAAGGACCT 60861	T	GTGCGT
			AGGT CCTTCACT GCTG		
			TCCA GGAAGTGA CGAC		
			_____ AC_____		
GAM2110	CNR1	3'	GGGGTTTACAGTGAAGAAAGCC 32720	C_	CG G
			GGTT CTTCACTGTG TCT		
			CCGA GAAGTGACAT GGG		
			AA TT G		
GAM2110	FACL2	3'	CAAAAACAATGAAGGAAACC 41208	_	C GCG
			GGTT CCTTCA TGT TG		
			CCAA GGAAGT ACA AC		
			A A AAA		
GAM2110	FADD	3'	AGCACAGAAGGAATCT 15122	ACTGTGC	
			AGGTTCCCTTC GTGCT		

		TCTAAGGAAG	CACGA	
		A_____		
GAM2110 HIS1	3'	CAGCTGAATGAGGAACC	22337	T CTGTG T
		GGTTCCT CA CG GCTG		
		CCAAGGA GT GT CGAC		
		_ AA _ _		
GAM2110 KMO	3'	TATCACAATGGAAGGAACCT	14847	AC_ C
		AGGTTCCCTT TGTG GTG		
		TCCAAGGAAG ACAC TAT		
		GTA _		
GAM2110 OGN	3'	TCAACAATGAGTAAAGGAACTT	26769	C GTGCG C
		AGGTTCCCTT ACT TG TGA		
		TTCAAGGAA TGA AC ACT		
		A GTA_ A		
GAM2110 OGN	3'	TCAACAATGTGTAAAGGAACTT	44591	CAC TG GC_
		AGGTTCCCTT TG CGT TGA		
		TTCAAGGAA AT GTA ACT		
		_ GT ACA		
GAM2110 OGN	3'	TCAACAATGTGTAAAGGAACTT	53401	CAC TG GC_
		AGGTTCCCTT TG CGT TGA		
		TTCAAGGAA AT GTA ACT		
		_ GT ACA		
GAM2110 DKFZP564M182	3'	TACTACAGTGAAGAAACCT	78641	C C
		AGGTT CTTCACTGTG GTG		
		TCCAA GAAGTGACAT CAT		
		A _		
GAM2110 FLJ12660	3'	TCAGCAATGTGGTGATGGAACC	47899	T TG GCG
T		AGGTTCC TCAC T TGCTGA		
		TCCAAGG AGTG G ACGACT		
		T GT TA_		
GAM2110 IMAGE3451454	5'	TCAGCACGGGTCGAAGGACCCT	54939	T _ GTG
		AGG TCCTTC ACT CGTGCTGA		
		TCC AGGAAG TGG GCACGACT		
		C C _		
GAM2110 KIAA0930	3'	CAACACGCACACCTCCAACCT	71065	CCTTCAC C
		AGGTT TGTGCGTG TG		
		TCCAA ACACGCAC AC		
		CCTCC_ A		
GAM2110 KIAA0930	3'	CAGCACACAGGCACCAAGGAAC	71066	CACT _
T		GGTTCCTT GTGC GTGCTG		

	TCAAGGAA CACG CACGAC	
	C___ GACA	
GAM2110 KIAA1247 3'	CAGCAGTTGGTATGAAGAACCT 62506	C CTGT_ G
	AGGTTC TTCA GC TGCTG	
	TCCAAG AAGT TG ACGAC	
	_ ATGGT _	
GAM2110 KIAA1737 3'	CAGCAAATGGAGGAACCT 67935	CTGTGCG
	AGGTTCCTTCA TGCTG	
	TCCAAGGAGGT ACGAC	
	AA_____	
GAM2110 MGC10955 3'	TTGGCCAAAATAAAGGAACCT 52034	CAC GCGT TG
	AGGTTCCTT TGT GC A	
	TCCAAGGAA ATA CG T	
	___ AAAC GT	
GAM2110 POLR3F 5'	CAACTCAGAATGAAGGAACC 60616	___ TGCG
	GGTTCCTTCA CTG TG	
	CCAAGGAAGT GAC AC	
	AA TCA_	
GAM2110 LOC127534 3'	CAACACACACAGTGTGTGCC 75965	TCCTT C C
	GGT CACTGTG GTG TG	
	CCG GTGACAC CAC AC	
	TGT___ A A	
GAM2110 LOC144600 3'	CAACACGCACACCTCCAACCT 84083	CCTTCAC C
	AGGTT TGTGCGTG TG	
	TCCAA ACACGCAC AC	
	CCTCC___ A	
GAM2110 LOC150282 3'	CAGCACACACAGTGGGTACTT 80538	T TT C
	AGGT CC CACTGTG GTGCTG	
	TTCA GG GTGACAC CACGAC	
	T ___ A	
GAM2110 LOC255231 3'	CAGCGGCTGAGCAGAGGAACC 97118	CA GT G
	GGTTCCTT CT GC TGCTG	
	CCAAGGAG GA CG GCGAC	
	AC GT _	
GAM2110 LOC91748 5'	CAGCACGCAGGTGCCAGAACC 67636	CTT G
	GGTTC CACT TGCGTGCTG	
	CCAAG GTGG ACGCACGAC	
	ACC _	
GAM2111 ADAT1 3'	CTCCAGCCTGGGTGATAGA 24915	CC TTTAT
	TC ATCACCC TTGGAG	

			AG TAGTGGG GACCTC		
			A_ TCC__		
GAM2111	ASH1	3'	CCAAAATGGAATCATGGGATA 38085	CAC_ TTTA	
			TATCCCAT CC TTTGG		
			ATAGGGTA GG AAACC		
			CTAA TA__		
GAM2111	KCNK3	3'	CTCCAGCCTGGGTGACAGGG 11174	A_ TTTAT	
			CCC TCACCC TTGGAG		
			GGG AGTGGG GACCTC		
			AC TCC__		
GAM2111	MS4A1	3'	CCAAGATTAAAAGGTGACAGG 5546	CA C _	
			CC TCACC TTTA TTTGG		
			GG AGTGG AAAT GAACC		
			AC A TA		
GAM2111	PART1	3'	CTCCATTCCAGGTGACATGGAT 33900	CA_ CTTTATT	
	A		TATCC TCACC TGGAG		
			ATAGG AGTGG ACCTC		
			TAC ACCTT__		
GAM2111	SNX5	3'	CTAAGAAAGGGTGTAGGA 27787	CAT A	
			TCC CACCCTTT TTTGG		
			AGG GTGGGAAA GAATC		
			AT_ _		
GAM2111	FADS1	3'	CTCCAGCCTGGGGTGATAGA 26378	CC TTAT	
			TC ATCACCCT TTGGAG		
			AG TAGTGGGG GACCTC		
			A_ TCC__		
GAM2111	FLJ10460	3'	CTCCAACCTGGGTGATGG 36615	TTTAT	
			CCATCACCC TTGGAG		
			GGTAGTGGG AACCTC		
			TCC__		
GAM2111	FLJ20220	3'	TCTTAAAAGCAATGGGATG 35277	CACC ATTT	
			TATCCCAT CTTT GGA		
			GTAGGGTA GAAA TCT		
			AC__ AT__		
GAM2111	FLJ20312	3'	CTCCAAATAAATCAAGATGAAG 35409	CC ACCC	
	TA		TAT CATC TTTATTTGGAG		
			ATG GTAG AAATAAACCTC		
			AA AACT		
GAM2111	FRAG1	3'	CTCCTTTGCAAAGGTATGGGAT 27944	CAC ATTT_	
	A		TATCCCAT CCTTT GGAG		

		ATAGGGTA GGAAA CCTC	
		T__ CGTTT	
GAM2111 KIAA1001	3'	CTCCAGCCTGGGTGATGG 31005	TTTAT
		CCATCACCC TTGGAG	
		GGTAGTGGG GACCTC	
		TCC__	
GAM2111 MESDC2	3'	CTCCAGCCTGGATGACGGGATG 72913	A C TTTAT
		TATCCC TCA CC TTGGAG	
		GTAGGG AGT GG GACCTC	
		C A TCC__	
GAM2111 MGC10612	3'	CCAGTGAGAAGGAAAATGGGAT 49521	CAC AT_
A		TATCCCAT CCTTT TTGG	
		ATAGGGTA GGAAG GACC	
		AAA AGT	
GAM2111 RNF8	3'	CCAAACAATGTACCAGTGATGG 15561	CCT____ A
G		CCCATCAC TT TTTGG	
		GGGTAGTG AA AAACC	
		ACCATGT C	
GAM2111 SEMA3C	3'	CTCCAAATAAAAATTAGATGG 22106	ACCC_
		CCATC TTTATTTGGAG	
		GGTAG AAATAAACCTC	
		ATTAA	
GAM2111 WBSCR23	3'	CTCCAGCCTGGGTGATAGA 47432	CC TTTAT
		TC ATCACCC TTGGAG	
		AG TAGTGGG GACCTC	
		A_ TCC__	
GAM2111 LOC124145	3'	GATAAAAAGTGATGGGGTA 74723	CC
		TATCCCATCAC TTTATT	
		ATGGGGTAGTG AAATAG	
		AA	
GAM2111 LOC147740	3'	CCAAATAAAGAGCACAGGATA 79153	CATCACC
		TATCC CTTTATTTGG	
		ATAGG GAAATAAACC	
		ACACGA_	
GAM2111 LOC159110	5'	CCAGGCGCGCGGCGATGGGATA 82987	A CTTTA
		TATCCCATC CC TTTGG	
		ATAGGGTAG GG GGACC	
		C CGCGC	
GAM2111 LOC159116	5'	CCAGGCGCGCGGCGATGGGATA 82970	A CTTTA
		TATCCCATC CC TTTGG	

		ATAGGGTAG GG GGACC		
		C CGCGC		
GAM2111	LOC255328	3' CTCCAGCCTGGGTGATAAGA 98339	CC	TTTAT
		TC ATCACCC TTGGAG		
		AG TAGTGGG GACCTC		
		AA TCC__		
GAM2111	LOC256980	3' CTCCACAAAGGTGAGGGGA 96928	A C	ATT
		TCCC TCACC TTT TGGAG		
		AGGG AGTGG AAA ACCTC		
		G _ C__		
GAM2111	LOC90573	3' CTCCAGGCTGGGTGACAGAT 63957	CCA	TTTA
		ATC TCACCC TTTGGAG		
		TAG AGTGGG GGACCTC		
		AC_ TC__		
GAM2112	ACADS	3' GTGGTGATTCATGCTGTGTG 5236	T _	AG
		TACACGG CGTGGA CG AT		
		GTGTGTC GTACTT GT TG		
		_ A GG		
GAM2112	ADCY3	3' TTTGTTCGTGGATGTGTG 15745	GT	
		TACACG CGTGGACGAG		
		GTGTGT GTGCTTGTTT		
		AG		
GAM2112	ADCY6	3' GAATATTTTGTACAATATTTTG 40953	CG CG	G
	TA	TACA GT TG ACGAGATGTTT		
		ATGT TA AC TGTTTTATAAG		
		TT TA A		
GAM2112	ANGPT1	3' GAGTATTTTGTCTTTTGTGT 58414	TCGT	
		ACACGG GGACGAGATGTTT		
		TGTGTT CCTGTTTTATGAG		
		TT__		
GAM2112	ARF3	3' GGATGGCAAGTCCATGGTGTGT 9776	G	GAGA
	G	TACACG TCGTGGAC TGTTC		
		GTGTGT GGTACCTG GTAGG		
		_ AACG		
GAM2112	ARHGEF7	3' GAATGCCTGCCCTGGTTGTGTG 15321	GT T A G	AT
		TACACG CG GG C AG GTTC		
		GTGTGT GT CC G TC TAAG		
		TG C __ CG		
GAM2112	BARHL1	3' GGATTAGTGAGTCTGTGGCCTG 39638	C	TG GAGAT_
	TG	TACA GGTCG GAC GTTC		

			GTGT CCGGT CTG TAGG	
			_ GT AGTGAT	
GAM2112	C21orf2	3'	GAGCGGTGATGCGTGACCGTGT 18205	GACGAGA
	G		TACACGGTCGTG TGTTT	
			GTGTGCCAGTGC GCGAG	
			GTAGTG_	
GAM2112	CABC1	5'	GGGCCCTGCAGTCCACGGCTGT 40041	GAGAT_
	G		CACGGTCGTGGAC GTTC	
			GTGTCGGCACCTG CGGG	
			ACGTCC	
GAM2112	CDKN1A	5'	GGATGCGTGTTTCGCGGGTGTGT 55270	G AGA
	G		TACACG TCGTGGACG TGTTT	
			GTGTGT GGCGCTTGT GTAGG	
			G GC_	
GAM2112	COIL	3'	GAATGTCTTGTGTTGTGAAAGTG 68459	GG TG
			CAC TCG GACGAGATGTTT	
			GTG AGT TTGTTCTGTAAG	
			AA GT	
GAM2112	COL18A1	3'	CTGGTTCTGTAATTGTGTG 56160	CG _G
			TACACGGT TGGA C AG	
			GTGTGTTA GTCT G TC	
			AT T G	
GAM2112	CYP7A1	3'	GAGTGTTTAAATGCCTGTGTA 7594	T GGACG TG
			TACACGG CGT AGA TTC	
			ATGTGTC GTA TTT GAG	
			C AA__ GT	
GAM2112	D12S2489E	3'	GGACGTTTCCTTTGCTATGATT 24762	C AC__
	TGTA		TACA GGTCGTGG GAGATGTTT	
			ATGT TTAGTATC CTTTGCAGG	
			_ GTTTT	
GAM2112	DDX6	3'	TCCACTTGTTTGCAGTGTGTG 16567	C TG A TTC
			TACACGGT G GACGAG TG	
			GTGTGTCA C TTGTTT AC	
			_ GT _ CTT	
GAM2112	DGAT2	5'	GACATCTCGTCACTCTGT 51774	TC G
			ACGG GTG ACGAGATGTT	
			TGTC CAC TGCTCTACAG	
			T_ _	
GAM2112	EPS15	3'	GAATATCTTATTTCTTTTATGA 10532	A C_____
	TTGGTG		TAC CGGTCGTGGA GAGATGTTT	

		GTG GTTAGTATTT TTCTATAAG	
		— TCTTTA	
GAM2112	FACL3	3' GAACAAAAGATTTGTTGCTGTG 16740	C TG CGAGA
	TA	TACACGGT G GA TGTTC	
		I	
		ATGTGTCG T TT ACAAG	
		T GT AGAAA	
GAM2112	FACL3	3' GAATATTTCTGTTGACTATATGT 16741	CG C G
	A	TACA GT GT GACGAGATGTTC	
		ATGT TA CA TTGCTTTATAAG	
		A_ T G	
GAM2112	FBXL2	5' GGGCGTCGCCGGCGCCGTGTG 25130	T GGA A_
		TACACGG CGT CG GATGTTC	
		GTGTGCC GCG GC CTGCGGG	
		— — CG	
GAM2112	GORASP1	3' GGATATCTTTTGGCCGTGTA 49957	TGGAC
		TACACGGTCG GAGATGTTC	
		ATGTGCCGGT TTCTATAGG	
		T_____	
GAM2112	HDAC4	3' GAGCATCTCCATCTGGTCGTG 21245	GT T AC
		CACG CG GG GAGATGTTC	
		GTGC GT CT CTCTACGAG	
		TG _ AC	
GAM2112	HRMT1L2	3' GGCACATCGTGACTGTGT 9518	GTGG GA
		ACACGGTC ACGA TGTT	
		TGTGTCAG TGCT ACGG	
		_____ AC	
GAM2112	IL11	3' ATTTCTGCCATGACTGTGTA 7178	AC
		TACACGGTCGTGG GAGAT	
		ATGTGTCAGTACC CTTTA	
		GT	
GAM2112	IPF1	3' TGGCGTTGTTTGTGGCTGTTG 5783	C TG GA C
		A ACGGTCG GAC GATGTT	
		I	
		G TGTCGGT TTG TTGCGG	
		T GT _ TT	
GAM2112	LASS2	5' GGGCGTGACGCGGCTGTG 68309	GA GAG
		CACGGTCGTG C ATGTTC	
		I	
		GTGTCGGCGC G TGCGGG	
		AG_____	
GAM2112	LGMN	3' CGCCCCACCGACTGTGTG 20033	_ A_
		TACACGGTCG TGG CG	

		GTGTGTCAGC ACC GC	
		C CC	
GAM2112 LOH11CR2A	5'	GAACATTTACGAGTTTGTGGCT 28272	A TG GA__
		GGTG TAC CGGTCG GAC GATGTTT	
		GTG GTCGGT TTG TTACAAG	
		_ GT AGCAT	
GAM2112 LY6E	3'	GGATGTGTGCCTGGCTGTGTA 11382	T A AG
		TACACGGTCG GG CG ATGTTT	
		ATGTGTCGGT CC GT TGTAGG	
		_ _ G_	
GAM2112 MADH7	3'	GAGTGTGAGTGTGCGGCTGTGT 20928	G GAG TG
		TACACGGTCGTG AC A TTC	
		GTGTGTCGGCGT TG T GAG	
		G AG_ GT	
GAM2112 MAN2A1	3'	GAACATGAATTCTGTGATTCTG 11435	CG TG CGAG
		TG TACA GTCG GA ATGTTT	
		GTGT TAGT CT TACAAG	
		CT GT TAAG	
GAM2112 MAP3K7IP2	3'	GGATATCTTGAGTTGATGGTTT 31355	C GT G _
		TGTG TACA G CGT GAC GAGATGTTT	
		GTGT T GTA TTG TTCTATAGG	
		T TG G AG	
GAM2112 MX2	3'	GACATTTAGTGACTGTTA 11724	C GTGG G
		A ACGGTC AC AGATGTT	
		A TGTCAG TG TTTACAG	
		T _ _ A	
GAM2112 NDRG3	3'	GAGCACGCGTGTCTGTGTTTGT 42767	T TG AGA_
		GTG TACACGG CG GACG TGTTC	
		GTGTGTT GT CTGT ACGAG	
		T GT GCGC	
GAM2112 NLGN2	3'	GAGCGTCACCGTGGCCGTG 89536	ACGA
		CACGGTCGTGG GATGTTT	
		GTGCCGGTGCC CTGCGAG	
		A_	
GAM2112 NR1I2	5'	GGACAGAGCTCTATGGCTGTG 42087	CGAGA
		CACGGTCGTGGA TGTTC	
		GTGTCGGTATCT ACAGG	
		CGAG_	
GAM2112 NTSR1	3'	GGGCGGGGTCTGTGGCTGTG 11863	TG GAGA
		CACGGTCG GAC TGTTC	

			GTGTCGGT CTG GCGGG	
			GT GG__	
GAM2112 OXCT	3'	GGACATCAATAATCATAATTGT 6488		CG ACGA_
	GTA	TACACGGT TGG GATGTTT		
		ATGTGTTA ACT CTACAGG		
		AT AATAA		
GAM2112 PACE4	3'	CTTTTCTGCGGCTGTGTA 11950		TG C
		TACACGGTCG GA GAG		
		ATGTGTCGGC CT TTC		
		GT T		
GAM2112 PACSIN1	3'	ACCTGTTTTGTACATGATTGTG 93876		G TTC
	TA	TACACGGTCGTG ACGAGATG		
		ATGTGTTAGTAC TGTTTTGT		
		A CCAC		
GAM2112 PAFAH1B1	3'	GGATATTTTGTGACATCGGTG 6476		A C G
		TAC CGGT GT GACGAGATGTTT		
		GTG GCTA CA TTGTTTATAGG		
		_ _ G		
GAM2112 PCDHB3	3'	GAACATTTTGTGTTATATATTG 38940		C_
		CGGT GTGGACGAGATGTTT		
		GTTA TATTTGTTTACAAG		
		TA		
GAM2112 PEX14	3'	AGTGTCTTGACTACCGTG 64400		C GGA TG
		CACGGT GT CGAGA TT		
		GTGCCA CA GTTCT GA		
		T _ GT		
GAM2112 PIK3R3	5'	GGGCATTTTGTGTTGTTCTGT 61709		T_ TG A
		ACGG CG G CGAGATGTTT		
		TGTC GT T GTTTTACGGG		
		TT GT_		
GAM2112 PIM1	3'	GGCATTGCTGACTGTGTA 92687		TGGACGA
		TACACGGTCG GATGTT		
		ATGTGTCAGT TTACGG		
		CG_____		
GAM2112 POLS	3'	GAGTGTTTTAACGGATCGTGT 23779		G GAC TG
		ACACGGTC TG GAGA TTC		
		TGTGCTAG GC TTTT GAG		
		_ AA_ GT		
GAM2112 PRV1	3'	AGCATTCAGGGCTGTGTG 73894		G GACGA
		TACACGGTC TG GATGTT		

		GTGTGTCGG AC TTACGA	
		G _____	
GAM2112	RAB36	3' GGACAGGAATTTCCGTGACTGT 18172	CGAGA_
	G	CACGGTCGTGGA TGTT	
		GTGTCAGTGCCT ACAGG	
		TTAAGG	
GAM2112	RAP1B	3' GAACAATGTTTATAGTCGTGTG 32234	TC AGA
		TACACGG GTGGACG TGTT	
		GTGTGCT TATTTGT ACAAG	
		GA A_	
GAM2112	REQ	3' GAGTGGCTCTCTGCGGCCCTGT 21841	C TG C A GT
	G	TACA GGTCG GA GAG T TC	
		GTGT CCGGC CT CTC G AG	
		C GT _ G TG	
GAM2112	REV3L	3' GAATATTTGTATAACTGTGTA 12823	CGTGG G
		TACACGGT AC AGATGTTC	
		ATGTGTCA TG TTTATAAG	
		ATA_ _	
GAM2112	RFX2	3' GAACGTTTCTTATGAATGTGTA 7157	G AC
		TACACG TCGTGG GAGATGTTC	
		ATGTGT AGTATT CTTTGCAAG	
		A _	
GAM2112	RHBDL	3' GGACGTCTCAGGGCTGCTGTG 15583	C GGAC
		CACGGT GT GAGATGTTC	
		GTGTCG CG CTCTGCAGG	
		T GGA_	
GAM2112	SGCG	3' AGTGTTGAGTTGCCGTGTG 5874	CGTG GA TG
		TACACGGT GAC GA TT	
		GTGTGCCG TTG TT GA	
		_ AG GT	
GAM2112	SHB	3' GCTGTGTCGTTTGTGTTGTGTG 13117	T TG G TTC
		TACACGG CG GACGA ATG	
		GTGTGTT GT TTGCT TGT	
		_ GT G CGG	
GAM2112	SLC12A7	3' GGGCGTCCCCTGCCATGGCCTG 22743	C ACGA_
	TG	TACA GGTCGTGG GATGTTC	
		GTGT CCGGTACC CTGCGGG	
		_ GTCCC	
GAM2112	SLC1A4	3' GAGCGTGCTGTTTGTGGCTGTT 13172	C TG AG
	G	A ACGGTCG GACG ATGTTC	

			G TGTCGGT TTGT TGCGAG		
			T GT CG		
GAM2112	SSX3	3'	GAACATGGGCATGGCTGTG 41015	GA	GAG
			CACGGTCGTG C ATGTTC		
			GTGTCGGTAC G TACAAG		
			GG _		
GAM2112	STX1A	3'	GGATGGGGCCGTGTCCGTGTG 17212	T	ACGAGA
			TACACGG CGTGG TGTC		
			GTGTGCC GTGCC GTAGG		
			T GGG _		
GAM2112	STXBP1	3'	GAACAGAGGGCTATGGCTGTG 13476	ACGAGA	
			CACGGTCGTGG TGTC		
			GTGTCGGTATC ACAAG		
			GGGAG _		
GAM2112	TCF8	3'	TCCTGTTCACTACTGTGTG 48433	C	A
			TACACGGT GTGGACG GA		
			GTGTGTCA CACTTGT CT		
			T C		
GAM2112	TEM6	3'	GAATGTTTTTCCCGATTGTG 43036	T	C
			CACGGTCG GGA GAGATGTTC		
			GTGTTAGC CCT TTTTGTAAAG		
			C _		
GAM2112	TFDP2	3'	TTTGTTCGCACTGTGTG 21891	C	TG
			TACACGGT G GACGAG		
			GTGTGTCA C TTGTTT		
			_GT		
GAM2112	TGM4	3'	GGACATTTCTCAAGGGCCATGT 13722	C	GTG C
	G		TACA GGTC GA GAGATGTTC		
			GTGT CCGG CT CTTTACAGG		
			A GAA _		
GAM2112	TIMP3	3'	ATCAATTTCAATTACCGTGTA 6281	C	CGA
			TACACGGT GTGGA GAT		
			ATGTGCCA TACTT CTA		
			T TAA		
GAM2112	TLL1	3'	GAATGTCTCCCTATGGCTGGTA 25877	A	AC
			TAC CGGTCGTGG GAGATGTTC		
			ATG GTCGGTATC CTCTGTAAG		
			_ C _		
GAM2112	TNFAIP2	3'	GGACATCTTTGGGAGGCCGTTA 21923	C	GTGGAC
			A ACGGTC GAGATGTTC		

		A TGCCGG TTCTACAGG	
		T AGGGT_	
GAM2112 TPMT	3'	GAGCTGGATTCATGGCTGT 6313	CGAGAT
		ACGGTCGTGGA GTTC	
		TGTCGGTACTT CGAG	
		AGGT_	
GAM2112 TRH	3'	GATGTCTTGAGCCCTGTG 24051	TCGT A_
		CACGG GG CGAGATGTT	
		GTGTC CC GTTCTGTAG	
		GA	
GAM2112 TRHDE	3'	GAATAGCCATTTTCATGGCTGT 26314	CGAGA_
GTG		TACACGGTCGTGGA TGTTC	
		GTGTGTCGGTACTT ATAAG	
		TTACCG	
GAM2112 UBE3A	5'	AATAGCTCGCGCCTGTA 6623	C TGGA A
		TACA GGTCTG CGAG TGTT	
		ATGT CCGGC GCTC ATAA	
		G	
GAM2112 ZNF146	3'	GGATATCTTGTCTTATTTTTTG 24076	CG TCGT
TA		TACA G GGACGAGATGTTC	
		ATGT T TCTGTTCTATAGG	
		TT TTAT	
GAM2112 ZNF239	5'	GGGCATTTGTGCAGATGGTTGT 20241	_G G G G
		ACA C GTC TG AC AGATGTTC	
		TGT G TAG AC TG TTTACGGG	
		T G _ G _	
GAM2112 54TM	5'	GGACGTGTCGCGCGGGCCGGGTG 96437	A GA G
		TAC CGGTCGTG CGA ATGTTC	
		GTG GCCGGCGC GCT TGCAGG	
		G _ G	
GAM2112 ACAS2L	3'	GGCATCTGAATGATCTGTA 68648	C GGACG
		TACA GGTCTG AGATGTT	
		ATGT CTAGTA TCTACGG	
		AG_	
GAM2112 ADAM7	3'	GGATATCCAAAATGGCCGTG 73827	GGACGA
		CACGGTCGT GATGTTC	
		GTGCCGGTA CTATAGG	
		AAAC_	
GAM2112 AFAP	3'	AATGTCTTTTTACTGTGTG 41600	CGTG C
		TACACGGT GA GAGATGTT	

GTGTGTCA TT TTCTGTAA
 _____ T
 GAM2112 BAG4 3' GGATATCTTGTACATTTTTGT 18047 TC _
 ACGG GTG GACGAGATGTTT
 |||| ||| |||||
 TGTT TAC CTGTTCTATAGG
 TT A
 GAM2112 BDG-29 3' GGCATCTCTGTGGCTGGTG 72805 A TG CGA
 TAC CGGTCG GA GATGTT
 ||| ||||| || |||||
 GTG GTCGGT CT CTACGG
 _ GT _
 GAM2112 BRD1 3' AATAAAGTTATGCTGTGTA 28142 T G GAGA
 TACACGG CGTG AC TGTT
 ||||| ||||| || |||||
 ATGTGTC GTAT TG ATAA
 _ _ AA _
 GAM2112 C13orf1 3' GAGCATTTTGTTCCTCAGGCT 40363 GT _ _
 GTGT ACACGGTC GG ACGAGATGTTT
 ||||| || |||||
 TGTGTCGG CC TGTTTTACGAG
 ACT GT
 GAM2112 CENTG1 3' GTTGTGTCTGTGACCGTG 29359 TG A
 CACGGTCG GACG GAT
 ||||| ||||| |||||
 GTGCCAGT CTGT TTG
 GT G
 GAM2112 cerk 3' GAGCGGGGCCGTGGCCGT 43166 ACGAGA
 ACGGTCGTGG TGTTT
 ||||| ||||| |||||
 TGCCGGTGCC GCGAG
 GGG _
 GAM2112 CG012 5' GAACATTTTGTTCATGTTTGTG 84158 C T G
 A ACGG CGTG ACGAGATGTTT
 | |||| ||||| |||||
 G TGTT GTAC TGTTTTACAAG
 T T _
 GAM2112 CKAP4 3' GAGCGTGCATACTGCGTTTGTG 23346 T TG ACGAG
 TA TACACGG CG G ATGTTT
 ||||| || | |||||
 ATGTGTT GC C TGCGAG
 T GT ATACG
 GAM2112 CLLD8 3' GGGTATCTTGTTCACTGCTGTG 50007 C TT
 CACGGT GTGGACGAGATG C
 ||||| ||||| ||||| |
 GTGTCG CACTTGTTCTAT G
 T GG
 GAM2112 COASTER 3' GGATATTTTCATCATGACTGTGA 32081 C AC
 A ACGGTCGTGG GAGATGTTT
 | ||||| ||||| |||||

A TGTCAGTACT CTTTATAGG
 T A_
 GAM2112 CSMD1 5' GAGTATCTGCAGACATGACTGC 73514 A GACG_
 GTG TAC CGGTCGTG AGATGTTC
 ||| ||||| |||||
 GTG GTCAGTAC TCTATGAG
 C AGACG
 GAM2112 DKFZP434A0131 5' GAGCGTCTACCCCATTTGTGTA 39150 GTC ACG
 TACACG GTGG AGATGTTC
 ||||| ||| |||||
 ATGTGT TACC TCTGCGAG
 ____ CCA
 GAM2112 DKFZP761C169 3' GAATGTTTTGTTGGGCTGTGT 68419 GTG
 ACACGGTC GACGAGATGTTC
 ||||| |||||
 TGTGTCGG TTGTTTTGTAAG
 G_
 GAM2112 DKFZp761F2014 3' AGCAGCTGAGGCCGTGTG 39938 GTGGACG A
 TACACGGTC AG TGTT
 ||||| || |||
 GTGTGCCGG TC ACGA
 AG____ G
 GAM2112 DKFZp761J139 5' GCGTTTCGTGGTTGTGTG 51108 GT GTGG TT
 TACACG C ACGAGATG C
 ||||| | ||||| |
 GTGTGT G TGCTTTGC G
 TG____ C
 GAM2112 DKFZp762P2111 3' GGGCTCAGTGTTTCATGGGTGTG 87637 G AGAT
 TA TACACG TCGTGGACG GTTC
 ||||| ||||| |||
 ATGTGT GGTACTTGT CGGG
 G GACT
 GAM2112 DNAJC5 3' GGACATTCCGCGGCATGACCGC 62138 A GA_ AG
 GTG TAC CGGTCGTG CG ATGTTC
 ||| ||||| || |||||
 GTG GCCAGTAC GC TACAGG
 C GGC CT
 GAM2112 DNCLI1 3' GGAATAAATTTATGTCGTGTG 60225 T CGAGAT
 TACACGG CGTGGA GTTC
 ||||| ||||| |||
 GTGTGCT GTATTT CAGG
 _ AAAT_
 GAM2112 EAT2 3' AGTTCCAGTCCTGTGGCTGTGT 80047 GT_ GA TGTTTC
 G TACACGGTC GGAC GA
 ||||| ||| ||
 GTGTGTCGG CCTG CT
 TGT AC TGAG
 GAM2112 ERG-1 5' GGACAAGTCTGTGGCCGTGTG 42100 TG GAGA
 TACACGGTCG GAC TGTTTC
 ||||| ||| |||||

			GTGTGCCGGT CTG ACAGG		
			GT A__		
GAM2112	FAM3C	3'	GGGCATTAAATATATGTTGTGT 30302	T	GACGA
	A		TACACGG CGTG GATGTTC		
			ATGTGTT GTAT TTACGGG		
			_ ATAAA		
GAM2112	FLJ10038	3'	GGGCACAGTTCATCACTGTGTG 36215	C	GAGA
			TACACGGT GTGGAC TGTTC		
			GTGTGTCA TACTTG ACGGG		
			C AC__		
GAM2112	FLJ10342	3'	GAACATGCCCTTCACTGGTTGT 36515	GT_	CGAG
	GTA		TACACG C GTGGA ATGTTC		
			ATGTGT G CACTT TACAAG		
			TG T CCCG		
GAM2112	FLJ12618	3'	GAGCTTATGTTTCATGACTCTGT 46506	C	A T
	A		TACA GGTCGTGGACG GA GTTC		
			ATGT TCAGTACTTGT TT CGAG		
			C A _		
GAM2112	FLJ12750	3'	GGGCATCAAGGCAGTTGTGTG 45440	TC	GGACGA
			TACACGG GT GATGTTC		
			GTGTGTT CG CTACGGG		
			GA GAA__		
GAM2112	FLJ12903	3'	GGGTATCTCGGGGAGCTTTGT 43075	C	CGTGGA TT
	G		TACA GGT CGAGATG C		
			GTGT TCG GCTCTAT G		
			T AGGGG_ GG		
GAM2112	FLJ13614	3'	GAATATTTTGTCTTCTGTG 58199	TCGT	
			CACGG GGACGAGATGTTC		
			GTGTC CCTGTTTATAAG		
			TT__		
GAM2112	FLJ13693	3'	GGATACCACTCTGTCACTGTGT 46075	CGTG _	A__
	G		TACACGGT GAC GAG TGTTC		
			GTGTGTCA CTG CTC ATAGG		
			__ T ACC		
GAM2112	FLJ14050	3'	GAATGTGTGTTCCCGGCTGTGT 60955	T	AG
	G		TACACGGTCG GGACG ATGTTC		
			GTGTGTCGGC CTTGT TGTAAG		
			C G_		
GAM2112	FLJ14251	3'	GAATATTTTGTAGTTGTGTGTG 46484	GT	TGG
	TG		TACACG CG ACGAGATGTTC		

	GTGTGT GT TGT TTTATAAG	
	GT TGA	
GAM2112 FLJ14457 5'	GGGCGTGGCTGTGGCCGTGT 52411	TG ACGAG
	ACACGGTCG G ATG TTC	
	TGTGCCGGT C TGCGGG	
	GT GG__	
GAM2112 FLJ14904 3'	AGCATCTTGGCATTGTG 52760	TC GA
	CACGG GTG CGAGATGTT	
	GTGTT TAC GTTCTACGA	
	__ G_	
GAM2112 FLJ20051 3'	GAATATTTTAACTGTGTA 39362	C GGAC
	TACACGGT GT GAGATG TTC	
	ATGTGTCA CA TTTTATAAG	
	_ AT__	
GAM2112 FLJ20378 3'	GGGTCGTGGGTCTGTGGTGGTG 35558	G TG GA__ GTTC
TG	TACAC GTCG GAC GAT	
	GTGTG TGGT CTG CTG	
	G GT GGTG GG	
GAM2112 FLJ20419 5'	GGGCGGGGCCACGGGCCGTGTG 35607	_ ACGAGA
	TACACGGTC GTGG TG TTC	
	GTGTGCCGG CACC GCGGG	
	G CGG__	
GAM2112 FLJ21791 3'	GGACAAAAATCATGATTGTG 62129	ACGAGA
	CACGGTCGTGG TG TTC	
	GTGTTAGTACT ACAGG	
	AAAA__	
GAM2112 FLJ22174 3'	GAATATCTTAACTGTGATTCT 41959	CG TG AC_
GTG	TACA GTCG G GAGATG TTC	
	GTGT TAGT C TTCTATAAG	
	CT GT ACA	
GAM2112 FLJ22548 5'	GGACGCGCTCTCTGCGGCTCTG 42634	C TG C A_
TG	TACA GGTG GAG TG TTC	
	GTGT TCGGC CT CTC GCAGG	
	C GT _ GC	
GAM2112 FLJ22843 5'	ATCAGTTTTATACTGTGTA 48013	CGT GA
	TACACGGT GGAC GAT	
	ATGTGTCA TTTG CTA	
	TAT A_	
GAM2112 FLJ22843 5'	GGACATTCAAGATTTATGACTG 48015	CGA__
TG	CACGGTCGTGGA GATG TTC	

		GTGTCAGTATTT TTACAGG		
		AGAAC		
GAM2112	GTF2A1	5' CCCTCTTGTTTGTGTTGTGTG 32402	T TG	TGTTT
		TACACGG CG GACGAGA		
		GTGTGTT GT TTGTTCT		
		_ GT CCCC		
GAM2112	HSA6591	3' GAGCTGCTCTGGTGGCCGTGTG 73248	TGGAC	AT
		TACACGGTCG GAG GTTC		
		GTGTGCCGGT CTC CGAG		
		GGT_ GT		
GAM2112	HSPC152	3' TTTTCTTGTTATGACTGTGTA 96155	G	TGTTT
		TACACGGTCGTG ACGAGA		
		ATGTGTCAGTAT TGTTC		
		_ TTTTG		
GAM2112	HSPC195	3' GAATGTTGATGGCGCCGTGTA 81866	T	GGACGA
		TACACGG CGT GATGTTC		
		ATGTGCC GCG TTGTAAG		
		_ GTAG_		
GAM2112	HUMNPIIY20	3' GGACGTGCGCGTGCGGCCGGTG 84323	A	GA AG
		TAC CGGTTCGTG CG ATGTTC		
		GTG GCCGGCGT GC TGCAGG		
		_ GC G_		
GAM2112	JWA	3' GGATATTTTGTACATTTTGT 22160	TC	_
		ACGG GTG GACGAGATGTTC		
		TGTT TAC TTGTTTATAGG		
		TT A		
GAM2112	KIAA0125	3' GGGCGTGTGTCAGTGGCTGTGT 29573	TG	AG
	G	TACACGGTCG GACG ATGTTC		
		GTGTGTCCGT CTGT TGCGGG		
		GA G_		
GAM2112	KIAA0227	3' GAGCATCTCGAGGCAACTGTTA 61350	C	C GGA
		A ACGGT GT CGAGATGTTC		
		A TGTCA CG GCTCTACGAG		
		T A GA_		
GAM2112	KIAA0355	3' GGGCATCAGCAGGACATTGTGT 28709	_	G GACGA
	G	TACACG GTC TG GATGTTC		
		GTGTGT CAG AC CTACGGG		
		TA G GA_		
GAM2112	KIAA0711	3' GGGCAGCTGTTGTGATCTGTG 30151	_	TG A G A
		CACGG TCG G C AG TGTTT		

GTGTC AGT T G TC ACGGG
 T GT__ G
 GAM2112 KIAA0924 3' GAGCATTAAATTGTATCACTGTG 30364 CGTGG __
 TA TACACGGT ACGA GATGTTC
 ||||| ||| |||||
 ATGTGTCA TGTT TTACGAG
 CTA__ AA
 GAM2112 KIAA0964 3' CTGCTCTATGCTGTGTA 30447 T CG
 TACACGG CGTGGA AG
 ||||| ||||| ||
 ATGTGTC GTATCT TC
 _ CG
 GAM2112 KIAA0971 3' GAATATCAAGGATTGTGGTCGG 30671 A GT TG ACGA_
 TG TAC CG CG G GATGTTC
 ||| || || | |||||
 GTG GC GT T CTATAAG
 _ TG GT AGGAA
 GAM2112 KIAA1058 3' ATGACCAGCTCGTCTTCGGTCG 83136 GT T AT_ C
 TGTG TACACG CG GGACGAG GTT
 ||||| || ||||| |||
 GTGTGC GC TCTGCTC CAG
 TG T GAC TAG
 GAM2112 KIAA1061 3' AACATATGCTGCTGTGTA 71712 C GGACGAG
 TACACGGT GT ATGTT
 ||||| || |||||
 ATGTGTCG CG TACAA
 T TA____
 GAM2112 KIAA1109 3' AACAAATTATGATTGTGT 65252 ACGAGA
 ACACGGTCGTGG TGTT
 ||||| ||||| |||||
 TGTGTTAGTATT ACAA
 AA____
 GAM2112 KIAA1111 3' GAACATTATCCACGTGGCTGTG 97945 __ CGA
 CACGGT CGTGGA GATGTTC
 ||||| ||||| |||||
 GTGTGC GCACCT TTACAAG
 GT A_
 GAM2112 KIAA1277 3' GGGCGGCGTCATGAGCCGTGTG 65081 _ G AGAT
 TACACGG TCGTG ACG GTTC
 ||||| ||||| ||| |||||
 GTGTGCC AGTAC TGC CGGG
 G _ GG__
 GAM2112 KIAA1328 3' GGACATTTTGTGGTGTGGTG 62327 GGT TG
 CAC CG GACGAGATGTTC
 ||| || ||||| |||||
 GTG GT TTGTTTTACAGG
 GTT GG
 GAM2112 KIAA1486 3' GAATATCTTTCTTCCTTGTGAT 67975 A T__ C__
 TGGTG TAC CGGTCG GGA GAGATGTTC
 ||| ||||| ||| ||||| |||||

		GTG GTTAGT CCT TTCTATAAG		
		_ GTT TCT		
GAM2112 KIAA1607	3'	GGGCCGCTGTCTGTGCGCCGTG 64538	_ TG G AT	
	TG	TACACGGT CG GAC AG GTTC		
		GTGTGCCG GT CTG TC CGGG		
		C GT _ GC		
GAM2112 KIAA1728	3'	GAACATCATTATGGTTTTGTA 68952	C GT ACGA	
		TACA G CGTGG GATGTTC		
		ATGT T GTATT CTACAAG		
		T TG A__		
GAM2112 KIAA1817	3'	GAGTATATGCTTTTGGCTGTGT 68780	T_ ACGAG	
	A	TACACGGTCG GG ATGTTC		
		ATGTGTCCGT TC TATGAG		
		TT GTA__		
GAM2112 KIAA1838	5'	GGCGCGTCTGCGGCTGGTG 65370	A TG AGA	
		TAC CGGTCTG GACG TGTT		
		GTG GTCGGC CTGC GCGG		
		_ GT _		
GAM2112 KIAA1922	5'	AGTATTTCCTTGAGTGTTGACCG 73985	TGGA_ TGTTTC	
	TGTG	TACACGGTCG CGAGA		
		GTGTGCCAGT GTTCT		
		TGTGA TTATGAG		
GAM2112 KIAA1924	3'	CTCAGCCATGGCTGTGTG 74046	AC	
		TACACGGTCGTGG GAG		
		GTGTGTCGGTACC CTC		
		GA		
GAM2112 LAMB4	3'	GGATGTCAGTCATGTGACTGTG 82082	TG_ GA	
		CACGGTCG GAC GATGTTC		
		GTGTCAGT CTG CTGTAGG		
		GTA A_		
GAM2112 LAT1-3TM	5'	GATATCTTGGCTGCTGT 49145	C GGA	
		ACGGT GT CGAGATGTT		
		TGTCG CG GTTCTATAG		
		T _		
GAM2112 MAP-1	3'	AACATTTTCACGATTGTTA 42426	C CGA C	
		A ACGGTCGTGGA GATGTT		
		A TGTTAGCACTT TTACAA		
		T _ T		
GAM2112 MGC11279	3'	AGCACAGCTGGACTGTGTG 44504	G ACGAGA	
		TACACGGTC TGG TGTT		

		GTGTGTCAG GTC ACGA	
		_ GAC__	
GAM2112	MGC13053	3' GAATGTCTTCGAATATTGTGTG 52108	C GGAC
		TACACGGT GT GAGATGTTC	
		GTGTGTTA TA TTCTGTAAG	
		_ AGC_	
GAM2112	MGC15437	3' GAATGTTTCGTTCCCTCTGGGT 52846	A TCGT
	A	TAC CGG GGACGAGATGTTC	
		ATG GTC CTTGCTTTGTAAG	
		G TCC_	
GAM2112	MGC15523	5' GGACGTTGGGACCTGTGACCGT 57548	TG ACGA_
	G	CACGGTCG G GATGTTC	
		GTGCCAGT C TTGCAGG	
		GT CAGGG	
GAM2112	MGC16279	5' GGATATTTTGCAGAAGACTGTG 52984	GTGGA
		CACGGTC CGAGATGTTC	
		GTGTCAG GTTTTATAGG	
		AAGAC	
GAM2112	MGC16279	5' GGATATTTTGCAGAAGACTGTG 52985	GTGGA
		CACGGTC CGAGATGTTC	
		GTGTCAG GTTTTATAGG	
		AAGAC	
GAM2112	MGC23401	5' GGACGGAGGGCTAAGGTTGTGT 59335	GT G ACGAGA
	G	TACACG C TGG TGTTC	
		GTGTGT G ATC GCAGG	
		TG A GGGAG_	
GAM2112	MGC3123	3' GAACATTACCGACAACCTGTGTG 44344	C _ ACGA
		TACACGGT GT GG GATGTTC	
		GTGTGTCA CA CC TTACAAG	
		A G A__	
GAM2112	MGC4172	5' GGCATCGGCGCGGCCGTG 44456	GACGA
		CACGGTCGTG GATGTT	
		GTGCCGGCGC CTACGG	
		GG__	
GAM2112	MGC4604	3' AACAGCACGTCCCCGGCCGTGT 49793	T AGA C
	G	TACACGGTCG GGACG TGTT	
		GTGTGCCGGC CCTGC ACAA	
		C ACG A	
GAM2112	MO25	3' GAATATCTGGCTGGCCCTGTA 33287	C TGGA G
		TACA GGTCTG C AGATGTTC	

ATGT CCGGT G TCTATAAG
 C CG__
 GAM2112 MOST2 5' GGGCGTTGAGGATGTTGCTGTG 40070 CG GACGA
 TG TACACGGT TG GATGTTC
 ||||| || |||||
 GTGTGTCG GT TTGCGGG
 TT AGGAG
 GAM2112 MSTP028 3' GATATGTGTGACTGTG 50064 GTGG AG
 CACGGTC ACG ATGTT
 ||||| || |||||
 GTGTCAG TGT TATAG
 ____ G_
 GAM2112 N4BP3 3' GGATGGTGTGTTTATGGCCATG 66858 C AGA
 TA TACA GGTCGTGGACG TGTTTC
 ||| ||||| |||||
 ATGT CCGGTATTTGT GTAGG
 A GTG
 GAM2112 NKD2 3' AGCAGCTGCCGGCTGTGTG 53591 GT A G A
 TACACGGTC GG C AG TGTT
 ||||| || || |||||
 GTGTGTCGG CC G TC ACGA
 ____ G
 GAM2112 OSBPL2 3' AACCGCTCCGTGACTGGTA 58474 A _ AGAT
 TAC CGGTCGTGGA CG GTT
 ||| ||||| || |||
 ATG GTCAGTGCCT GC CAA
 _ C ____
 GAM2112 P15-2 3' TGCATTGTTTCATGATTGTTG 38626 C GA TC
 A ACGGTCGTGGAC GATGT
 | ||||| |||||
 G TGTTAGTACTTG TTACG
 T _ TG
 GAM2112 PASK 3' GAGCGTCTCAAAGGCATGTGTG 31413 _ GTGGAC
 TACACG GTC GAGATGTTC
 ||||| || |||||
 GTGTGT CGG CTCTGCGAG
 A AAA__
 GAM2112 PLAC3 5' GAGTGTGTGTTTGTGAGTGTGT 69874 G TG AG TG
 A TACACG TCG GACG A TTC
 ||||| || ||||| | |||
 ATGTGT AGT TTGT T GAG
 G GT G_ GT
 GAM2112 PP2447 3' GAGTGTCTCGGTTGGCCGTG 48099 TGGA TG
 CACGGTCG CGAGA TTC
 ||||| ||||| |||
 GTGCCGGT GCTCT GAG
 TG__ GT
 GAM2112 PRO0159 5' GGATGTTCTCTGTGGCTGTG 26948 TG C G
 CACGGTCG GA GA ATGTTC
 ||||| || || |||||

			GTGTCGGT CT CT TGTAGG		
			GT _ _		
GAM2112	PTD012	5'	GGGTGTTTTGCTACCGTGACCG 26739	A__	TT
	T		ACGGTCGTGG CGAGATG C		
			TGCCAGTGCC GTTTTGT G		
			ATC GG		
GAM2112	PTPN3	3'	GGATGTTTTGTTTGTCTGTG 12587	TC	TG
	TG		TACACGG G GACGAGATGTTC		
			GTGTGTC T TTGTTTTGTAGG		
			TT GT		
GAM2112	RALGPS1A	3'	GGGCACAATTGTTGATGACCGT 28336	G	GA_
	GTG		TACACGGTCGT GACGA TGTTT		
			GTGTGCCAGTA TTGTT ACGGG		
			G AAC		
GAM2112	RGS19	3'	GAACAGAACCTCCGCATCGTGT 20800	C	CGAGA
	A		TACACGGT GTGGA TGTTT		
			ATGTGCTA CGCCT ACAAG		
			_ CCAAG		
GAM2112	RNO2	5'	GAACATCTGGCAGCGGCCCTGT 53936	C	GGA G
	G		TACA GGTCGT C AGATGTTC		
			GTGT CCGGCG G TCTACAAG		
			C ACG _		
GAM2112	SEMA5A	3'	TTTGTCCATCACTGTGTA 15603	C	
			TACACGGT GTGGACGAG		
			ATGTGTCA TACCTGTTT		
			C		
GAM2112	SEPT3	3'	GAGCATCTTGTCTGTGTGTGTG 39403	GT	TG
	TG		TACACG CG GACGAGATGTTC		
			GTGTGT GT CTGTTCTACGAG		
			GT GT		
GAM2112	SNURF	3'	GAACAGCAATCATGACTGTTG 20262	C	ACGAGA
			A ACGGTCGTGG TGTTT		
			G TGTCAGTACT ACAAG		
			T AACG__		
GAM2112	SOX30	5'	GGGTATCGGTCGTTGTGATTGG 23801	A	TG A _ TT
	GTG		TAC CGGTGCG G CGA GATG C		
			GTG GTTAGT T GCT CTAT G		
			G GT_ GG GG		
GAM2112	SOX6	3'	AACAAGTCCACGGCGTGTG 53983	G	GAGA
			TACACG TCGTGAC TGTT		

GTGTGC GGCACCTG ACAA
 _ A _
 GAM2112 SP2 3' AACACTGTGTACTGTGTG 13327 _ TG ACGAGA
 TACACGGT CG G TGTT
 ||||| || | |||
 GTGTGTCA GT C ACAA
 T GT _
 GAM2112 SS18L1 3' GAATATCTTGAATGTTGTGTA 65954 T GGA
 TACACGG CGT CGAGATGTTC
 ||||| ||| |||||
 ATGTGTT GTA GTTCTATAAG
 _ A _
 GAM2112 SSBP2 3' AACTATTTTGTGCTGTGTA 60272 CGTGG _
 TACACGGT ACGAGAT GTT
 ||||| ||||| |||
 ATGTGTCTG TGTTTCA CAA
 _ T
 GAM2112 TEX27 3' GAACAGCGGTTTGTGGCTGTG 41948 TG GAGA
 CACGGTCG GAC TGTT
 ||||| ||| |||
 GTGTCTGGT TTG ACAAG
 GT GCG _
 GAM2112 TRAD 3' GAGCATTTTATAGATCTTGTA 23920 C GTGGAC
 TACA GGTC GAGATGTTC
 ||| ||| |||||
 ATGT CTAG TTTTACGAG
 T ATA _
 GAM2112 TRAF2 5' GGCGCGCTGCGACCGTTG 41237 C TG A AGA
 A ACGGTCG G CG TGTT
 | ||||| | || |||
 G TGCCAGC C GC GCGG
 T GT _ _
 GAM2112 TSGA13 5' GGGCATGAGTACACACTGTGTG 54707 C G GAG
 TACACGGT GTG AC ATGTTC
 ||||| ||| || |||||
 GTGTGTCA CAC TG TACGGG
 _ A AG _
 GAM2112 TU12B1-TY 3' GGGTGTTTTGTTCTCTGATGTG 33858 G T_ TT
 CACG TCG GGACGAGATG C
 ||| ||| ||||| |||
 GTGT AGT CTTGTTTTGT G
 _ CT GG
 GAM2112 VAV3 3' GAATGTTTTGTCTGTTGCCGTC 21478 C C TG
 A A ACGGT G GACGAGATGTTC
 | |||| | |||||
 A TGCCG T CTGTTTTGTAAG
 C T GT
 GAM2112 VDU1 3' GAATGTGTCACTACGATTGTTG 31124 C AC G
 A ACGGTCGTGG GA ATGTTC
 | ||||| || |||||

		G TGTTAGCATC CT TGTAAG		
		T A_ G		
GAM2112 VIT1	3'	GGGTGTTTTAGCATTACTGTGT 38604	C GAC	TT
A		TACACGGT GTG GAGATG C		
		ATGTGTCA TAC TTTTGT G		
		T GA_ GG		
GAM2112 ZFR	3'	GAATGTTTCTGCAGATCTTGTG 32755	C _TG	CGA
		TACA GGTC G GA GATGTTC		
		GTGT CTAG C CT TTGTAAG		
		T A GT _		
GAM2112 ZNF297B	5'	GGGTATCTTGTGTTGTTTAACT 26667	C__ TG	TT
GT		ACGGT G GACGAGATG C		
		TGTCA T TTGTTCTAT G		
		ATTT GT GG		
GAM2112 LOC115110	5'	AAGCCAAACGTCTACAGTCGTG 72170	TC	AGAT C
TG		TACACGG GTGGACG GTT		
		GTGTGCT CATCTGC CGA		
		GA AAAC AG		
GAM2112 LOC116071	3'	GAGCAGGGCCCATGACCGGGTG 57420	A	ACGAGA
		TAC CGGTCGTGG TGTTC		
		GTG GCCAGTACC ACGAG		
		G CGGG_		
GAM2112 LOC120534	3'	GAATGTTGTTCTTGCTGCTGTG 74469	C _	G GTTC
TA		TACACGGT GT GGACGA AT		
		ATGTGTCG CG CTTGTT TA		
		T TT G AG		
GAM2112 LOC123876	5'	GAGCATCCACCACTCATCACTG 74718	C__	ACGA
TGTG		TACACGGT GTGG GATGTTC		
		GTGTGTCA CACC CTACGAG		
		CTACT AC_		
GAM2112 LOC124930	5'	CTGGTCCAGGCCGTGTA 74825	G G	
		TACACGGTC TGGAC AG		
		ATGTGCCGG ACCTG TC		
		_ G		
GAM2112 LOC125704	3'	GGGCATGTGTATGTGATTGTGT 74881	TGG	AG
G		TACACGGTCG ACG ATGTTC		
		GTGTGTAGT TGT TACGGG		
		GTA G_		
GAM2112 LOC145082	5'	GAGTATCTTGTATGTGTGTGTG 84190	GT	GG
		TACACG CGT ACGAGATGTTC		

	GTGTGT GTA TGTTCTATGAG	
	GT _	
GAM2112 LOC145482 5'	GAGCGGCTCCC GCGACTGTG 77744	AC A
	CACGGTCGTGG GAG TGTT	
	GTGTCAGCGCC CTC GCGAG	
	_ G	
GAM2112 LOC146013 3'	GAATGTGTGGCAGGCTGTGTG 84583	G GA AG
	TACACGGTC TG CG ATGTT	
	GTGTGTCGG AC GT TGTAAG	
	_ G_ G_	
GAM2112 LOC146657 3'	GAGTGTCTGCTGTAGCTGTGTG 61078	CG A G TG
	TACACGGT TGG C AGA TTC	
	GTGTGTCG GTC G TCT GAG	
	AT _ _ GT	
GAM2112 LOC147077 3'	GAATGTCTATATAGTGTATTGT 78850	_ GGACG
	GTG TACACGGT CGT AGATGTT	
	GTGTGTTA GTG TCTGTAAG	
	T ATATA	
GAM2112 LOC147123 3'	GGACAGGCACCCATGGCTGTG 78855	ACGAGA
	CACGGTCGTGG TGTT	
	GTGTCGGTACC ACAGG	
	CACGG_	
GAM2112 LOC148188 3'	GCTGCCTTGGCTGCGACTGTGT 79457	TG A ATGTT
	G TACACGGTCG G CGAG	
	GTGTGTCAGC C GTTC	
	GT G CGTCGG	
GAM2112 LOC150139 3'	GGGCCTGTGTGTCCACGGCCGT 80412	AGAT_
	GT ACACGGTCGTGGACG GTTC	
	TGTGCCGGCACCTGT CGGG	
	GTGTC	
GAM2112 LOC150208 3'	GAGTCAGCCATGTCTGTGCTGT 86076	T TG AGA_ _
	GTG TACACGG CG GACG TG TTC	
	GTGTGTC GT CTGT AC GAG	
	_ GT ACCG T	
GAM2112 LOC150445 3'	GGATATTTTGGTACTGTG 80679	CGTGGA
	CACGGT CGAGATGTT	
	GTGTCA GTTTTATAGG	
	TG_	
GAM2112 LOC150606 3'	GGGCATCTACCTGACTGTTGTG 86270	_ T ACG
	TACA CGGTCG GG AGATGTT	

GTGT GTCAGT CC TCTACGGG
 T _ A_
 GAM2112 LOC152897 5' TCTTGTCTGTGACTGTGTG 81611 TG
 TACACGGTCG GACGAGA
 ||||| |||||
 GTGTGTCAGT CTGTTCT
 GT
 GAM2112 LOC152941 3' GAATATTTTGTTCATGC 81634 T
 G CGTGGACGAGATGTTC
 | |||||
 C G TACTTGTTTTATAAG
 —
 GAM2112 LOC153416 3' GAACAATGTTTATAGTCGTGTG 61158 TC AGA
 TACACGG GTGGACG TGTTCT
 ||||| ||||| |||||
 GTGTGCT TATTTGT ACAAG
 GA A_
 GAM2112 LOC157254 5' GAGCAGGACTCAGGCTGTGTG 82312 G ACGAGA
 TACACGGTC TGG TGTTCT
 ||||| || |||||
 GTGTGTCGG ACT ACGAG
 _ CAGG_
 GAM2112 LOC157506 3' GAATGTCTTGTTTAAATAGTG 82366 GGTCTG
 CAC TGGACGAGATGTTC
 || |||||
 GTG ATTTGTTCTGTAAG
 ATAA_
 GAM2112 LOC158308 3' GAACCGTGTCTGTGGTCGGGTG 88067 A GT TG AGAT
 TAC CG CG GACG GTTC
 ||| || |||||
 GTG GC GT CTGT CAAG
 G TG GT GC_
 GAM2112 LOC161829 3' GAATGTTTTGTCTGTCTCTTA 83189 C TC TG
 A GG G GACGAGATGTTC
 | || |||||
 A TC T CTGTTTTGTAAG
 T TC GT
 GAM2112 LOC161829 5' GGGCGTCGCCTCTGCGGCGTGT 83191 G TG CGA
 G TACACG TCG GA GATGTTC
 ||||| || |||||
 GTGTGC GGC CT CTGCGGG
 _ GT CCG
 GAM2112 LOC165693 5' GGACACTTCTGTGGCTGT 83491 TG CG A
 ACGGTCG GA AG TGTTCT
 ||||| || |||||
 TGTCGGT CT TC ACAGG
 GT _ _
 GAM2112 LOC196812 3' GAGCATTGTTCCTTTGGTTTA 91125 C GT T_
 A G CG GGACGAGATGTTC
 | | || |||||

	A T GT CCTGTTTTACGAG T TG TT	
GAM2112 LOC197414 3'	GAGCTCAACGTGATTGTGACTG 89457 TG TG TGTG TACACGGTCG G ACG GTTC GTGTGTCAGT T TGC CGAG GT AG AACT	TG __ AGAT
GAM2112 LOC199675 3'	GAGTGTCTCGGAGTTGCTCGTG 89640 TG TACACG CG CGAGA TTC GTGTGC GT GCTCT GAG TC TGAG GT	GT TGGA TG
GAM2112 LOC199990 3'	GACCGTAGTCGTCTGTGATCTG 89907 TG CACGG TCG GACGA ATG TC GTGTC AGT CTGCT TGC AG T GT GA C	_ TG G_ T
GAM2112 LOC200235 3'	GAAGTGGCTTTGTGGCTGGTA 91569 TAC CGGTCG GA GTTC ATG GTCGGT TT CAAG _ GT CGGT__	A TG CGAGAT
GAM2112 LOC200853 3'	GAGCATTACCCCTGTGGCCCTG 90329 TG TACA GGTCG G GATGTTC GTGT CCGGT C TTACGAG C GT CCAC	C TG ACGA
GAM2112 LOC200953 5'	AGCCGTGTGTGGCTGTGTG 91801 TACACGGTC G ACG GTT GTGTGTCGG T TGC CGA TG G ____	GT G AGAT
GAM2112 LOC202024 5'	GGATATTTTGCAGAAGACTGTG 90613 CACGGTC CGAGATGTTC GTGTCAG GTTTTATAGG AAGAC	GTGGA
GAM2112 LOC202108 5'	GACATCTCAGGCTGTG 90631 CACGGTC GAGATGTT GTGTCCG CTCTACAG A_____	GTGGAC
GAM2112 LOC203286 5'	GGATGTTTGGATGCGGCTGGTA 92147 TAC CGGTCGTG C AGATGTTC ATG GTCGGCGT G TTTGTAGG _ AG _	A GA G
GAM2112 LOC203317 5'	AGCCACTCCCGACTGTGTG 90873 TACACGGTCG GGA GTT 	T CGAGAT

	GTGTGTCAGC CCT CGA		
	__ CAC__		
GAM2112 LOC219653 3'	GATGTCATGTGGCCGTG 92918	GTGG	A
	CACGGTC ACG GATGTT		
	GTGCCGG TGT CTGTAG		
	__ A		
GAM2112 LOC220790 3'	GAACAATGTTTATAGTCGTGTG 92871	TC	AGA
	TACACGG GTGGACG TGTTT		
	GTGTGCT TATTTGT ACAAG		
	GA A__		
GAM2112 LOC221042 3'	GAATAGCCCTTTGTGCTGTGTG 94801	T TG	CGAGA
	TACACGG CG GA TGTTT		
	GTGTGTC GT TT ATAAG		
	_ GT CCCG_		
GAM2112 LOC221576 3'	GGGCATGCAAAGCCGGCTGTGT 95322	TGGACGAG	
G	TACACGGTCG ATGTTT		
	GTGTGTCGGC TACGGG		
	CGAAACG_		
GAM2112 LOC221838 5'	GGACATCTCAGGCTGACTGTG 94119	TGGAC	
	CACGGTCG GAGATGTTT		
	GTGTCAGT CTCTACAGG		
	CGGA_		
GAM2112 LOC221895 3'	GAATATTTTGTTATACTGTGTA 94105	CGTG	
	TACACGGT GACGAGATGTTT		
	ATGTGTCA TTGTTTATAAG		
	TA__		
GAM2112 LOC221914 5'	GAGCGGTCCCGCGGCCGAGTA 95565	A	AC GA
	TAC CGGTCGTGG GA TGTTT		
	ATG GCCGGCGCC CT GCGAG		
	A __ G_		
GAM2112 LOC221922 5'	GGCAGCTCACGGCCGTG 94252	GGAC	A
	CACGGTCGT GAG TGTT		
	GTGCCGGCA CTC ACGG		
	__ G		
GAM2112 LOC253298 3'	AATATTTTGAGACTGTG 99010	GTGGA	
	CACGGTC CGAGATGTT		
	GTGTCAG GTTTTATAA		
	A__		
GAM2112 LOC253650 3'	GGTATGCTTCATGACCTGTG 97873	C	CGAG TT
	TACA GGTTCGTGGA ATG C		

GTGT CCAGTACTT TAT G
 _ CG_ GG
 GAM2112 LOC254587 5' GGGCGTCTCAGCCGGTGTGTG 99526 GTCG AC
 TACACG TGG GAGATGTTT
 ||||| || |||||
 GTGTGT GCC CTCTGCGGG
 G_ GA
 GAM2112 LOC255042 3' GGATAGGGTCACAACTGTGTG 97049 C ACGAGA
 TACACGGT GTGG TGTTC
 ||||| || ||||
 GTGTGTCA CACT ATAGG
 A GGG_
 GAM2112 LOC256021 3' GGGTGTCTTATCAAGTTCCGGC 98278 T _ TT
 TGTGTG TACACGGTCG GGAC GAGATG C
 ||||| || |||| |
 GTGTGTCCGC CTTG TTCTGT G
 _ AACTA GG
 GAM2112 LOC257463 5' GGGTGTGTCCTTTATGAGCTGT 71623 _ C G TT
 GTA TACACGG TCGTGGA GA ATG C
 ||||| ||||| || || |
 ATGTGTC AGTATTT CT TGT G
 G C G GG
 GAM2112 LOC257515 3' GGGCATGCAAAGCCGGCTGTGT 99622 TGGACGAG
 G TACACGGTCG ATGTTC
 ||||| ||||
 GTGTGTCCGC TACGGG
 CGAAACG_
 GAM2112 LOC257571 3' AATATTTTGAGACTGTG 99800 GTGGA
 CACGGTC CGAGATGTT
 ||||| |||||
 GTGTCAG GTTTTATAA
 A_
 GAM2112 LOC257572 3' GGGCATGCAAAGCCGGCTGTGT 99742 TGGACGAG
 G TACACGGTCG ATGTTC
 ||||| ||||
 GTGTGTCCGC TACGGG
 CGAAACG_
 GAM2112 LOC51195 3' AATATTATGTTGCCGTGTG 33402 CGTG A
 TACACGGT GACG GATGTT
 ||||| || |||||
 GTGTGCCG TTGT TTATAA
 _ A
 GAM2112 LOC90246 3' CTTTCCATGGCTGGTG 62585 A C
 TAC CGGTCGTGGA GAG
 || ||||| ||
 GTG GTCGGTACCT TTC
 _ _
 GAM2113 CENPA 3' GTAGAGAGATAATAAAATCAA 10170 A TTAC
 TTGA TTTT TCTCTCTAC
 ||| ||| |||||

			AACT AAAA AGAGAGATG		
			A TAAT		
GAM2113	CLTC	3'	AGAAGAGAGAAATTCAA 17956	TTTA	_
			TTGAATTT CTCTCT CT		
			AACTTAAA GAGAGA GA		
			_____ A		
GAM2113	ICA1	5'	GTAGAGAGAGAGAAACTCA 18312	A TA	
			TGA TTTTT CTCTCTCTAC		
			ACT AAAGA GAGAGAGATG		
			C _____		
GAM2113	IRTA1	3'	AGAGAGAGGAATTTAA 49238	TTTA	
			TTGAATTT CTCTCTCT		
			AATTTAAG GAGAGAGA		

GAM2113	MS4A4A	3'	TAGAGAGATAATAAATTCAA 44006	T C	
			TTGAATTT TTA TCTCTCTA		
			AACTTAAA AAT AGAGAGAT		
			T _____		
GAM2113	TOX	3'	GTAGAGAGTGTGAAATTCAA 28964	TT T	
			TTGAATTTT AC CTCTCTAC		
			AACTTAAAG TG GAGAGATG		
			T_ T		
GAM2113	UMOD	5'	AGAGAGAAAAATTCAA 14009	TTAC	
			TTGAATTTT TCTCTCT		
			AACTTAAAA AGAGAGA		

GAM2113	USF2	3'	TAGAGAGAGAGGTATTTAA 14016	TT A	
			TTGAAT TTT CTCTCTCTA		
			AATTTA GGA GAGAGAGAT		
			T_ _		
GAM2113	FLJ10359	3'	AGAAAGAGTAAATGATACA 36553	A T C	
			TG ATT TTTACTCT TCT		
			AC TAG AAATGAGA AGA		
			A T A		
GAM2113	FTS	3'	TAGAGAGAGCAGGTTT 42758	TTTA	
			GAATTT CTCTCTCTA		
			CTTGGA GAGAGAGAT		
			C_____		
GAM2113	KIAA0239	3'	TAGAGAGAGTTTTGAATTC 31617	TTT	
			GAATTT ACTCTCTCTA		

CTTAAG TGAGAGAGAT
TTT

GAM2113 KIAA0861 3' GTAGAGAGAGTTCGTTC 90357 TTTT
GAAT ACTCTCTCTAC
|||| |||||||
CTTG TGAGAGAGATG
CT__

GAM2113 KIAA1387 5' AGAGAGAGTTCGGGTTACAA 71442 _ TTT
TTG AATTT ACTCTCTCT
||| |||| |||||||
AAC TTGGG TGAGAGAGA
A C__

GAM2113 KIAA1557 3' TAGAGAGAATTCTAAATTCAG 61787 TTTAC
TTGAATTT TCTCTCTA
||||| |||||||
GACTTAAA AGAGAGAT
TCTTA

GAM2113 KIAA1715 3' GTAGAGAGAGTATGTATTTAA 68690 TTTT
TTGAAT TACTCTCTCTAC
||||| |||||||
AATTTA ATGAGAGAGATG
TGT_

GAM2113 MRPS10 3' AGAAAGAGTGAAAATTC 36811 T C
GAATTTTT ACTCT TCT
||||| ||||| |||
CTTAAAAG TGAGA AGA
_ A

GAM2113 ORCTL3 3' AGAGAGAAGATTCAG 16189 TTTAC
TTGAATTT TCTCTCT
||||| |||||||
GACTTAGA AGAGAGA

GAM2113 PRO0245 5' TAGAGGGAAAAAATCAA 26956 A AC
TTGA TTTTTT TCTCTCTA
||| ||||| |||||||
AACT AAAAAA AGGGAGAT

GAM2113 PRO2015 3' AGAGGGTAAAAATTTAA 38153 T
TTGAATTTTT ACTCTCT
||||||| |||||||
AATTTAAAAA TGGGAGA

GAM2113 SAE1 3' TAGAGAAAAGTGTGAATTCAG 19729 TT C_
TTGAATTT TACT TCTCTA
||||||| ||| |||||||
GACTTAAG GTGA AGAGAT
T_ AA

GAM2113 LOC130733 3' GTAGAGAAAGAAGAACTGCAA 75482 AA_ A C
TTG TTTTTT CT TCTCTAC
||| ||||| || |||||||

AAC AAAGAA GA AGAGATG
GTC _ A
GAM2113 LOC144596 3' TAGAGAGAGAGGTATTTAA 77428 TT A
TTGAAT TTT CTCTCTCTA
||||| ||| |||||||
AATTTA GGA GAGAGAGAT
T_ _
GAM2113 LOC157464 3' GTAGAGAGAGGCAATTTAA 87749 TTTTA
TTGAATT CTCTCTCTAC
||||| |||||||
AATTTAA GAGAGAGATG
CG__
GAM2113 LOC203429 3' GTAGGGAAAAATAAAAATTCAA 90933 TACTC
TTGAATTTTT TCTCTAC
||||||| |||||||
AACTTAAAAA AGGGATG
TAAAA
GAM2113 LOC220936 3' TAGAAGGGGAAAAATTCAA 93045 TA C
TTGAATTTTT CTCT TCTA
||||||| ||| |||
AACTTAAAAG GGGA AGAT
_ _
GAM2113 LOC221876 5' TAGAGAGAAAAAGCCAA 95543 AA TTAC
TTG TTTT TCTCTCTA
||| ||| |||||||
AAC AAAA AGAGAGAT
CG ____
GAM2114 SCAMP1 3' GCTAAATAAATATTCTCC 54500 T C
GGA AATATT ATTTAGC
||| ||||| |||||||
CCT TTATAA TAAATCG
C A
GAM2114 SCAMP1 3' GCTAAATAAATATTCTCC 54501 T C
GGA AATATT ATTTAGC
||| ||||| |||||||
CCT TTATAA TAAATCG
C A
GAM2114 NX-17 3' TGAATATCAGCCCCTAATA 40706 ATA_
TATTAGGG ATATTCA
||||||| |||||||
ATAATCCC TATAAGT
CGAC
GAM2114 LOC161589 3' GCTAAATGAATATTATCCCTAA 83159
TA TATTAGGGATAATATTCATTTAGC
|||||||
ATAATCCCTATTATAAGTAAATCG
GAM2115 GPD1 3' TCATGCCACCACATTTG 60398 C C
TAAATG GGTGGCAT GA
||||| ||||||| ||

		GTTTAC CCACCGTA CT		
		A _		
GAM2115 IL5RA	5'	TCGCATGGCCACCGCATTT	6906	AT__
		AAATGCGGTGGC CGA		
		TTTACGCCACCG GCT		
		GTAC		
GAM2115 MYO1C	3'	TGCCGATGCCAAATATTTG	61873	CGG A
		TAAATG TGGCATCG CA		
		GTTTAT ACCGTAGC GT		
		AA_ C		
GAM2115 C6orf37	3'	TGTCACACTGCATTTA	68097	GCATC
		TAAATGCGGTG GACA		
		ATTTACGTAC CTGT		
		A__		
GAM2115 DNAJC6	3'	TTGCAGAACCACCGCATT	29498	CA GA
		AATGCGGTGG TC CAA		
		TTACGCCACC AG GTT		
		A_ AC		
GAM2115 FLJ11210	3'	GTCGATGTGCATGCTTTTA	60319	T GTG
		TAAA GCG GCATCGAC		
		ATTT CGT TGTAGCTG		
		T ACG		
GAM2115 FLJ12476	3'	TCGATCTTCTGCATTTA	43270	T C
		TAAATGCGG GG ATCGA		
		ATTTACGTC TC TAGCT		
		T _		
GAM2115 KIAA1034	3'	TCGATGGCATCCGCATTTG	63134	_ G
		TAAATGCGG TG CATCGA		
		GTTTACGCC AC GTAGCT		
		T G		
GAM2115 KIAA1987	3'	TCATGTAAGTGCATTTA	89391	G C
		TAAATGCGGT GCAT GA		
		ATTTACGTCA TGTA CT		
		A _		
GAM2115 MGC16063	3'	TGTCCTGGCCACTGCATT	54929	ATC
		AATGCGGTGGC GACA		
		TTACGTCACCG CTGT		
		GTC		
GAM2115 LOC147949	3'	TGTCAGATGTCCACATTGCA	79279	_ _ _
		TGCG GTGG CATC GACA		

		ACGT CACC GTAG CTGT		
		TA T A		
GAM2115	LOC150577 3'	GTCCTCACCGCATTTG 86258	CATC	
		TAAATGCGGTGG GAC		
		GTTTACGCCACT CTG		
		C__		
GAM2115	LOC158219 3'	TGTGTGTCACCACATTT 82694	C	CG
		AAATG GGTGGCAT ACA		
		TTTAC CCACTGTG TGT		
		A _		
GAM2115	LOC202020 3'	TGTCTCACACATTTA 90605	C	CATC
		TAAATG GGTGG GACA		
		ATTTAC CCACT CTGT		
		A _		
GAM2115	LOC90826 5'	TGTCGATGCAGGTTTATTTG 64788	CGGTG	
		TAAATG GCATCGACA		
		GTTTAT CGTAGCTGT		
		TTGGA		
GAM2115	LOC93587 3'	TTGTCTTTACCTGCATTTA 73042	_	CATC
		TAAATGC GGTGG GACAA		
		ATTTACG CCATT CTGTT		
		T T__		
GAM2116	S100A11 5'	TGAGGAGAGGCTCCAGACCCG 20055	A	AG
		CG GTTTGGGGC TCTCCTCA		
		GC CAGACCTCG AGAGGAGT		
		C G_		
GAM2116	ZNF274 3'	TGAGGAGACTGCCCAGCAC 33343	TTG	
		GT GGGCAGTCTCCTCA		
		CA CCCGTCAGAGGAGT		
		CGA		
GAM2116	ZNF274 3'	TGAGGAGACTGCCCAGCAC 56867	TTG	
		GT GGGCAGTCTCCTCA		
		CA CCCGTCAGAGGAGT		
		CGA		
GAM2116	CCR5 3'	AGGAGACCACCAACAGCCCTC 6959	T_ G_ CA	
		GAG TTG GG GTCTCCT		
		CTC GAC CC CAGAGGA		
		CC AA AC		
GAM2116	FLJ00024 3'	TGAAGGACCCCGAACCCG 64507	A	CA CC
		CG GTTTGGGG GTCT TCA		

		GC CAAGCCCC CAGG AGT			
		C _ A_			
GAM2116	KIAA0924	3' AGAAGACTACCTTGAGCTC	30348	TG C C	
		GAGTT GGG AGTCT CT			
		CTCGA TCC TCAGA GA			
		GT A A			
GAM2116	KIAA1247	3' TGAAGAAACTGCCTTCATTGTA	62510	GTTT C C	
		TACGA GGGGCAGT TC TCA			
		ATGTT TTCCGTCA AG AGT			
		AC_ A A			
GAM2116	MGC16153	3' GAAAAGACTGCCCAACTGTA	52269	G T CC	
		TAC AGTT GGGGCAGTCT TC			
		ATG TCAA CCCCCTCAGA AG			
		_ _ AA			
GAM2116	MGC2217	5' TGAAGAACTCATGCACCAAAC	44432	G _ C C	
	TCG	CGAGTTTGG GCA GT TC TCA			
		GCTCAAACC CGT CA AG AGT			
		A ACT A A			
GAM2116	NETO2	3' AGAAGACTGCTCTTGACT	36593	T C	
		AGTT GGGGCAGTCT CT			
		TCAG TCTCGTCAGA GA			
		T A			
GAM2116	TBC1D2	5' GAGGATGTGCCCCAAACT	37930	GTC	
		AGTTTGGGGCA TCCTC			
		TCAAACCCCGT AGGAG			
		GT_			
GAM2116	LOC130029	3' GAGGAATCCCAAAC	75415	CAGTC	
		GAGTTTGGGG TCCTC			
		CTCAAACCCT AGGAG			
		A_			
GAM2116	LOC201176	3' GAAGAAACTGCCTTCTGTA	89510	G TTT C C	
		TAC AG GGGGCAGT TC TC			
		ATG TC TTCCGTCA AG AG			
		_ _ A A			
GAM2117	IL13RA1	3' ACATTGGTAGCCAGCCAG	9564	AG G	
		CTGGCTGGCT GC GGTGT			
		GACCGACCGA TG TTACA			
		_ G			
GAM2117	SLC25A13	5' CGCCAGCCAGCCAGTCA	27288	T A	
		TGA CTGGCTGGCT GGCG			

ACT GACCGACCGA CCGC

GAM2117 SLC7A8 3' ACACCCGCACACAGCCAGC 25298 AG__
GCTGGCT GCGGGTGT
||||| |||||
CGACCGA CGCCCACA
CACA

GAM2117 KIAA0337 3' ACACCCACTGGCCAGCCAGGCC 29474 AT GC
A TG CTGGCTGGCTAG GGGTGT
|| ||||| |||||
AC GACCGACCGGTC CCCACA
CG A_

GAM2117 MGC16186 5' ACAGCTAGCCAGCCAGCCAG 51408 A _ G
CTGGCTGGCT GGC GG TGT
||||| ||| |||
GACCGACCGA CCG TC ACA
_ A G

GAM2117 LOC158226 3' ACACCCGCGCACCAGCCAGG 82695 CTAG
TCTGGCTGG GCGGGTGT
||||| |||||
GGACCGACC CGCCCACA
ACG_

GAM2117 LOC256537 5' CACCCGCTGCCAAACCA 96935 C_ TA
TGG TGGC GGC GGGTG
||| ||| |||||
ACC ACCG TCGCCAC
AA _

GAM2118 EPHA8 3' GCTCACCCCTACGTCCCC 40436 A A TA CA
GG GA CGTAGGG GT AGC
|| ||||| || |||
CC CT GCATCCC CA TCG
C _ _ C_

GAM2118 MAGEA8 5' GCTCCGGCCCCACACTCTCCTG 19319 AC A AGTCA
TAGGAGA GT GGGT AGC
||||| || ||| |||
GTCCTCT CA CCCG TCG
CA _ GCC_

GAM2118 PDE6H 3' CTTGACCACCTTTTCCTA 21691 ACGTA A
TAGGAGA GGGT GTCAAG
||||| ||| |||||
ATCCTTT TCCA CAGTTC
_ C

GAM2118 RBBP9 3' CTTAACTACCCTTCTCT 70689 ACGT C
GGAGA AGGGTAGT AAG
|||| ||||| |||
TCTCT TCCCATCA TTC
_ A

GAM2118 KIAA1163 3' GCCTGACTATTAAGCTTCCTA 79651 AAC AG A
TAGGAG GT GG TAGTCA GC
||||| || ||||| ||

ATCCTT CG TTATCAGT CG
 ____ AA C
 GAM2118 KIAA1598 3' GCTTGACTGTTTCCATGTTCTC 37638 A ____
 C GGAGAACGT GGG TAGTCAAGC
 ||||| ||| |||||
 CCTCTTGTA CCT GTCAGTTCG
 _ TT
 GAM2118 NPFF 5' CTGCTCTAGATTCCCCTA 14939 A CG
 TAGG GAA TAGGGTAG
 ||| ||| |||||
 ATCC CTT ATCTCGTC
 C AG
 GAM2118 LOC147057 3' GCCTGGCTCCACGTCCCCCTG 84985 AGA AG T A
 TAGG ACGT GG AGTCA GC
 ||| ||| || ||||| ||
 GTCC TGCA CC TCGGT CG
 CCC _ _ C
 GAM2118 LOC149351 3' GCTTCCTACATTCCCCTG 80086 A C T
 TAGG GAA GTAGGG AGT
 ||| ||| ||||| |||
 GTCC CTT CATCCT TCG
 C A _
 GAM2118 LOC51031 3' GCCTGACGATACGCTCTTCTA 32708 A GGGTA A
 TAGGAGA CGTA GTCA GC
 ||||| ||| ||| ||
 ATCTTCT GCAT CAGT CG
 C AG _ C
 GAM2118 LOC92305 3' GGCTACCCACTCCCCTA 57235 A AC A
 TAGG GA GT GGGTAGTC
 ||| || || |||||
 ATCC CT CA CCCATCGG
 C _ _
 GAM2119 ANPEP 3' GCTCCAGGGCCAGATGAGC 8565 _ AGGGG
 GCTCATTTG C GGAGC
 ||||| | ||||
 CGAGTAGAC G CCTCG
 C GGA _
 GAM2119 CLU 3' GCTCCCCCAAGATGAGC 10213 GCA
 GCTCATTT GGGGGGAGC
 ||||| |||||
 CGAGTAGA CCCCCCTCG
 A _
 GAM2119 F13A1 3' CTCAGCCTTGCAAATAGC 92710 C GG
 GCT ATTTGCAGGG GAG
 || ||||| |||
 CGA TAAACGTTCC CTC
 _ GA
 GAM2119 HRH2 3' GCTCCCTTTTAAAAGGAGC 42510 A GC
 GCTC TTT AGGGGGGAGC
 ||| ||| |||||

			CGAG AAA TTTCCCTCG		
			G A_		
GAM2119	IFNGR2	3'	CTTGACTTTGGCAAATGAGC 19848	_	GG
			GCTCATTTGC AGGG GAG		
			CGAGTAAACG TTTC TTC		
			G AG		
GAM2119	MAP4	3'	TGGTCCCACAAATGGGC 48801	CAGGG	G
			GCTCATTTG GGA CCA		
			CGGGTAAAC CCCT GGT		
			A_____		
GAM2119	MAP4	3'	TGGTCCCACAAATGGGC 11454	CAGGG	G
			GCTCATTTG GGA CCA		
			CGGGTAAAC CCCT GGT		
			A_____		
GAM2119	PAK4	3'	TCCAGCCCCTGCAGCAAATGA 20829	_____	_____
			TCATT TGCAGGGG GGA		
			AGTAA ACGTCCCC CCT		
			ACG GA		
GAM2119	PIM2	3'	CCCAATCCTACAAAGGAGC 60651	A C	_____
			GCTC TTTG AGGG GGG		
			CGAG AAAC TCCT CCC		
			G A AA		
GAM2119	PKHD1	5'	TTTGGCTGGGACACAAACGAGT 57721	A	CAGGGGGG
			GCTC TTTG AGCCAAA		
			TGAG AAAC TCGGTTT		
			C ACAGGG_		
GAM2119	PLAT	3'	CTCCTCAAAAGCAAATGAG 53395	AGG_	
			CTCATTTGC GGGGAG		
			GAGTAAACG CTCCTC		
			AAAA		
GAM2119	PLAT	3'	CTCCTCAAAAGCAAATGAG 8117	AGG_	
			CTCATTTGC GGGGAG		
			GAGTAAACG CTCCTC		
			AAAA		
GAM2119	RAI2	3'	TTTGACTTTTCACAAATGAGT 41717	CAGG GG	C
			GCTCATTTG G GAG CAAA		
			TGAGTAAAC C TTC GTTT		
			A__TT A		
GAM2119	TGFB3	3'	GGCTCCGGGCAAATGGC 13719	T	AGGGG
			GC CATTTGC GGAGCC		

			CG GTAAACG CCTCGG		
			— GG—		
GAM2119	BTN2A2	3'	TCCAGCCTACAGATGAGC 23771	C	GG
			GCTCATTTG AGG GGA		
			CGAGTAGAC TCC CCT		
			A GA		
GAM2119	C20orf72	5'	TTCGACCGTTGCAAATAG 54609	C	G G_
			CT ATTTGCAG GG GAG		
			GA TAAACGTT CC CTT		
			— G AG		
GAM2119	C6orf37	3'	CTAACTCTTGACAAATGAGT 68092	_	GG
			GCTCATTTG CAGGGG AG		
			TGAGTAAAC GTTCTC TC		
			A AA		
GAM2119	DOC2A	3'	GCTAGTCCCTGCAAATATGC 14563	TC	GG
			GC ATTTGCAGGGG AGC		
			CG TAAACGTCCCT TCG		
			TA GA		
GAM2119	FADS1	3'	GCTCCATAAGCAAGTGAGC 26382		AGGGG
			GCTCATTTGC GGAGC		
			CGAGTGAACG CCTCG		
			AATA_		
GAM2119	FLJ20413	3'	CTCAATCCCTGCAAATGA 35595		G_
			TCATTTGCAGGGG GAG		
			AGTAAACGTCCCT CTC		
			AA		
GAM2119	HTATIP2	3'	CTTATGACCGTGCAAATGAGC 22167		G GG_
			GCTCATTTGCA GG GAG		
			CGAGTAAACGT CC TTC		
			G AGTA		
GAM2119	KIAA1423	3'	CCCAACCCACTAAATGAGC 62392	CA	_
			GCTCATTTG GGG GGG		
			CGAGTAAAT CCC CCC		
			CA AA		
GAM2119	MFN1	3'	TTCAACTTGAAAATGAGC 35965	G	GG
			GCTCATTT CAGG GGA		
			CGAGTAAA GTTC CTT		
			A AA		
GAM2119	MGC15619	3'	GCCTTAATTGAAAATGAGC 51402	G	GG A
			GCTCATTT CAG GGG GC		

CGAGTAAA GTT TTC CG
A AA _

GAM2119 MGEA6 5' GCTCCCCCGCAGCCGGC 21013 CAT A
GCT TTGC GGGGGGAGC
||| ||| |||||
CGG GACG CCCCCCTCG
CC_ _

GAM2119 NFASC 3' GCTCCCCCCTGCAAGC 70859 CATT _
GCT TGCAGGGGGG AGC
||| ||||| |||
CGA ACGTCCCCC TCG
_ C

GAM2119 NMT1 3' GCTCCCCTTCTGAATCAGC 41147 C TG _
GCT ATT CAGG GGGGAGC
||| ||| ||| |||||
CGA TAA GTCT CCCCTCG
C _ T

GAM2119 P114-RHO-GEF 3' CTCAGCCCCCGGGAAATGAGC 31669 GCA _
GCTCATTT GGGGG GAG
||||| ||| |||
CGAGTAAA CCCCC CTC
GGG GA

GAM2119 TRPV5 5' CTCAGCTCTGCAAAGAGC 39522 A GG
GCTC TTTGCAGGG GAG
|||| ||||| |||
CGAG AAACGTCTC CTC
_ GA

GAM2119 LOC126961 3' GGCTCCCCCGCGCGTGA 75121 T A
TCAT TGC GGGGGGAGCC
|||| ||| |||||
AGTG GCG CCCCCCTCGG
C _

GAM2119 LOC143915 3' CTCCCCTCGGGCAACAAGC 83906 CAT A_
GCT TTGC GGGGGGAG
||| ||| |||||
CGA AACG CTCCCCTC
AC_ GG

GAM2119 LOC145623 5' TTGGCAGCTCCAGCAAATGAGC 84398 AG GA
GCTCATTTGC GGGG GCCAA
||||| ||| |||||
CGAGTAAACG CCTC CGGTT
A_ GA

GAM2119 LOC146268 3' CCCGGGAATCTGCAAATGAGC 78335 _
GCTCATTTGCAGG GGG
||||||| |||
CGAGTAAACGTCT CCC
AAGGG

GAM2119 LOC148479 3' GGCTTTCTCTGAAATGA 79615 G GG A
TCATTT CAGGG G GCC
||||| |||| | |||

				AGTAAAG	GTCTC	T	CGG		
				—	TT	—			
GAM2119	LOC148887	3'	GGCTCCCCCGCATGCGC	85405	T	TT	AG		
			GC CA TGC GGGGGAGCC						
			CG GT ACG CCCCCTCGG						
			C — —						
GAM2119	LOC196403	3'	GGCCCCCTCCAAATGGGC	91191		GCA	A		
			GCTCATTT GGGGGG GCC						
			CGGGTAAA CCTCCC CGG						
			— —						
GAM2119	LOC205100	5'	TGGTCCCTGCAATGAGC	92393	T		GGGA		
			GCTCATT GCAGGG GCCA						
			CGAGTAA CGTCCC TGGT						
			— —						
GAM2119	LOC207043	3'	GCTCCCCCGGGTATCAGC	91078		CATT	A_		
			GCT TGC GGGGGGAGC						
			CGA ATG CCCCCCTCG						
			CT_ GG						
GAM2119	LOC253786	5'	TTAACTTTTGCAAATGAGC	98836			GG		
			GCTCATTTGCAGGGG AG						
			CGAGTAAACGTTTTTC TT						
			AA						
GAM2119	LOC253974	3'	TTTGGCTCCCCCCTGCAAATGA	99286					
	GC		GCTCATTTGCAGGGGGGAGCCAAA						
			CGAGTAAACGTCCCCCCTCGGTTT						
GAM2119	LOC256905	3'	TCCATGTCCCTGCAAATGA	98663					
			TCATTTGCAGGGG GGA						
			AGTAAACGTCCCT CCT						
			GTA						
GAM2119	LOC257395	3'	GGCTCCCCCGCGCGTGA	97149	T	A			
			TCAT TGC GGGGGGAGCC						
			AGTG GCG CCCCCTCGG						
			C —						
GAM2119	LOC90233	3'	CCCAGGTCCTGCAAAGGAGC	57193		A			
			GCTC TTTGCAGGG GGG						
			CGAG AAACGTCCT CCC						
			G GGA						
GAM2120	ACT	5'	CCACAATCCAGGGGGCCAT	40420		CCG	AAC		
			ATGGCCCT GGA TGTGG						

TACCGGGGG CCT ACACC
 A__ A__
 GAM2120 ADAM11 3' GCCACAGCTCAACTCGGGGGC 41490 TC AAA__
 GCCCC CGGG CTGTGGC
 |||| ||| |||||
 CGGGG GCTC GACACCG
 __ AACTC
 GAM2120 ADAM11 3' GCCACAGCTCAACTCGGGGGC 11487 TC AAA__
 GCCCC CGGG CTGTGGC
 |||| ||| |||||
 CGGGG GCTC GACACCG
 __ AACTC
 GAM2120 CDC34 3' GCCGCACCCCGGAGGAGCCA 16390 C AAAC
 TGGC CCTCCGGG TGTGGC
 ||| ||||| |||||
 ACCG GGAGGCC ACGCCG
 A C__
 GAM2120 CRI1 3' GCCACAGTTATCAAAGGCTA 27537 CCTCCG A
 TGGCC GG AACTGTGGC
 |||| || |||||
 ATCGG CT TTGACACCG
 AAA__ A
 GAM2120 FLII 3' GCCACAGTCCCCAGTAGCC 10656 CC CC AA
 GGC CT GGG ACTGTGGC
 ||| || ||| |||||
 CCG GA CCC TGACACCG
 AT __ C_
 GAM2120 FZD10 3' GCCCACCCCCAGGAAGGCCA 24214 CC _ AAAC T
 TGGCC TCC GGG TG GGC
 |||| ||| ||| |||||
 ACCGG AGG CCC AC CCG
 A_ A CC__ _
 GAM2120 GNA11 5' CCACAGCCCCGGGGGCCG 76585 TC AAA
 TGGCCCC CGGG CTGTGG
 ||||| ||| |||||
 GCCGGGG GCCC GACACC
 __ C_
 GAM2120 IGHMBP2 3' GCCACAGAGGAGCGGAGGGGCC 10984 GGAAA
 GGCCCCTCCG CTGTGGC
 ||||| |||||
 CCGGGGAGGC GACACCG
 GAGGA
 GAM2120 MAGEA3 5' CCAGAGGCCCCCGGAGGAGC 19315 C AAA G
 GC CCTCCGGG CT TGG
 || ||||| |||||
 CG GGAGGCC GA ACC
 A CCG G
 GAM2120 PYGB 3' CCAGGGGTCCCGGAGGAACC 12687 CC AA G
 GG CCTCCGGGA CT TGG
 || ||||| |||||

		CC GGAGGCCCT GG ACC		
		AA G_ G		
GAM2120 PYGB	3'	CCATGTTTCCAGGAGGGGCCAT 12689	G	T
		ATGGCCCCTCC GGAAAC GTGG		
		TACCGGGGAGG CCTTTG TACC		
		A _		
GAM2120 SLC6A6	3'	GCCACAGTCCTTCCTGGGGC 13183	TCC	_
		GCCCC GGGAA ACTGTGGC		
		CGGGG TCCTT TGACACCG		
		_ CC		
GAM2120 UBTF	3'	CCATTCCTTCCCAGAGGGGCC 27252	C	ACT
		GGCCCCTC GGGAA GTGG		
		CCGGGGAG CCCTT TACC		
		A CCT		
GAM2120 CBCIP2	3'	GCCACACGGA CTGAGAGGGGCC 52658	C	AAAC
A		TGGCCCCTC GGG TGTGGC		
		ACCGGGGAG CTC ACACCG		
		A AGGC		
GAM2120 FEM-2	3'	GCCACAGTCCCATGAGGGCC 28316	C C_	AA
		GGCCC TC GGGA CTGTGGC		
		CCGGG AG CCCT GACACCG		
		_ TA _		
GAM2120 FLJ10199	3'	GCCACAGTTGAGAAGCGGAGGG 71755	GGA	_
GCCA		TGGCCCCTCCG AACTGTGGC		
		ACCGGGGAGGC TTGACACCG		
		GAAGAG		
GAM2120 FLJ11715	3'	ACAGTGTCCCCAGGAGGCCAT 44972	_ CC	A
		ATGGCC CCT GGGA ACTGT		
		TACCGG GGA CCCT TGACA		
		A C_ G		
GAM2120 FLJ12505	5'	CCCGGTCCCGGAGCAGCCA 45713	CC	AA T
		TGGC CTCCGGGA CTG GG		
		ACCG GAGGCCCT GGC CC		
		AC _ _		
GAM2120 KIAA0828	3'	GTTTCCCAGGAAGGCCAT 82119	CC	_
		ATGGCC TCC GGGAAAC		
		TACCGG AGG CCCTTTG		
		A_ A		
GAM2120 KIAA1190	3'	CCACAGTTCTGGGAGCC 71643	CCC G	A
		GGC TCC GGAA CTGTGG		

		CCG AGG TCTT GACACC	
		___ G _	
GAM2120 KIAA1297	5'	CCATGCCCAGAAGGCCA 72634	CC C AAAC
		TGGCC TC GGG TGTGG	
		ACCGG AG CCC GTACC	
		A_ A _	
GAM2120 PASK	5'	GCCACAGAGTTGGGGGGCCAT 31415	T GAAA
		ATGGCCCC CCGG CTGTGGC	
		TACCGGGG GGTT GACACCG	
		_ GA_	
GAM2120 PCDH17	3'	GCCACAGTTCCCTGCAGCCA 27836	CCCTC A
		TGGC CGGG AACTGTGGC	
		ACCG GTCC TTGACACCG	
		AC_ C	
GAM2120 RIL	3'	CCATGCTGCCCTGAAGGGGCCA 14885	C AAAC
		TGGCCCCT CGGG GTGG	
		ACCGGGGA GTCC TACC	
		A CGTCG	
GAM2120 SREC	3'	GCAGTGCTCCCGAGGGGCC 14905	A_
		GGCCCCTCCGGGA ACTGT	
		CCGGGGAGGCCCT TGACG	
		CG	
GAM2120 TRAF2	3'	GCCGGCTCACGGAGGGGCCA 41236	G AACTG
		TGGCCCCTCCG GA TGGC	
		ACCGGGGAGGC CT GCCG	
		A CG_	
GAM2120 LOC123242	5'	CCACAGCCCACCTGGAGGCCA 76111	CC AAA_
		TGGCC TCCGGG CTGTGG	
		ACCGG AGGTCC GACACC	
		_ ACCC	
GAM2120 LOC124460	5'	CCAAGAGCTCGAAGGGGCCAT 76559	C AAA G
		ATGGCCCCT CGGG CT TGG	
		TACCGGGGA GCTC GA ACC	
		A GA_ _	
GAM2120 LOC132166	3'	GCCAGCGCCCGAGGGGGCCA 75537	TC AAAC
		TGGCCCC CGGG TGGC	
		ACCGGGG GCCC ACCG	
		GA GCG_	
GAM2120 LOC146958	5'	GCCACAGTCTCAAGTGGACAT 84944	G C CC AA
		ATG CC CT GGGA CTGTGGC	

	TAC GG GA CTCT GACACCG	
	A T A_ _	
GAM2120 LOC149420 3'	GCCACAGTTTCCTAAGCGC 80155	CC CC
	GC CT GGGAACTGTGGC	
	CG GA TCCTTTGACACCG	
	C_ A_	
GAM2120 LOC152317 3'	GCCACAGTCTGGGAGAGCCA 86831	CC G AA
	TGGC CTCC GGA CTGTGGC	
	ACCG GAGG TCT GACACCG	
	A_ G _	
GAM2120 LOC157450 3'	CCACAGCTTCCCGGGTCAT 71531	CTCC A
	ATGGCCC GGGAA CTGTGG	
	TACTGGG CCCTT GACACC	
	_____ C	
GAM2120 LOC157807 5'	GCCACAGTTTCAGCAGACCAT 82513	CCC CCGG
	ATGG CT GAAACTGTGGC	
	TACC GA CTTTGACACCG	
	A_ CGA_	
GAM2120 LOC157923 5'	GCCACAGTCCAGAGAAGGCCA 82526	C_ C GAA
	TGGCC CTC GG ACTGTGGC	
	ACCGG GAG CC TGACACCG	
	AA A _	
GAM2120 LOC158510 5'	CCAGAGGCCCGGAGGAGC 82833	C AAA G
	GC CCTCCGGG CT TGG	
	CG GGAGGCCC GA ACC	
	A CCG G	
GAM2120 LOC196860 3'	CCACAGTTCCCGGAAAGTGCT 91214	CCC_ A
	GGC TCCGGG AACTGTGG	
	TCG AGGCCC TTGACACC	
	TGAA C	
GAM2120 LOC203235 5'	GCCAGGGCCCCCAGAGGGGCC 92099	C AAA G
	GGCCCCTC GGG CT TGGC	
	CCGGGGAG CCC GG ACCG	
	A CC_ G	
GAM2120 LOC220739 3'	GCCACAGTAGGAGGGGCCA 94521	GGGAA
	TGGCCCCTCC ACTGTGGC	
	ACCGGGGAGG TGACACCG	
	A_____	
GAM2120 LOC222166 5'	CCCGGCCCGGAGGAGCC 95733	C AAA T
	GGC CCTCCGGG CTG GG	

		CCG GGAGGCCC GGC CC		
		A C__ _		
GAM2120	LOC253001 5'	CCACAGCCCACCTGGAGGCCA 97990	CC	AAA_
		TGGCC TCCGGG CTGTGG		
		ACCGG AGGTCC GACACC		
		_ ACCC		
GAM2120	LOC254057 3'	GCCCCTATCCCAGAGGGGCC 98782	C	AACTGT
		GGCCCCTC GGGA GGC		
		CCGGGGAG CCCT CCG		
		A ATCC_		
GAM2120	LOC92558 3'	GCCACCTCCCAGAGGGGCC 70312	C	AACT
		GGCCCCTC GGGA GTGGC		
		CCGGGGAG CCCT CACCG		
		A C_		
GAM2120	LOC93626 5'	CCACAGCCCCGGGGGCCG 73128	TC	AAA
		TGGCCCC CGGG CTGTGG		
		GCCGGGG GCCC GACACC		
		_ C_		
GAM2121	CDH12 3'	CTTATCATTTAAAGTGGTGTA 15777	CCCAA	GA
		TACACCACT GAA ATAAG		
		ATGTGGTGA TTT TATTC		
		AA_ AC		
GAM2121	GOCAP1 3'	ATTGTTCTTGGGAGCAGTGTA 43007	CA	G
		TACAC CTCCCAAGAA AAT		
		ATGTG GAGGGTTCTT TTA		
		AC G		
GAM2121	DKFZp434N2435 5'	CTTATTACTGTGGGGTGGT 98090	T	AGAAG
		ACCAC CCCA AATAAG		
		TGGTG GGGT TTATTC		
		_ GTCA_		
GAM2121	DKFZP564I122 3'	CTTATTCTTCTCCCTCATGTGT 63877	CACTCCCA	
	A	TACAC AGAAGAATAAG		
		ATGTG TCTTCTTATTC		
		TACTCCC_		
GAM2121	FLJ21791 3'	CTTATTTGCAGAAAGTGGTGTA 62126	CCCAAGAA	
		TACACCACT GAATAAG		
		ATGTGGTGA TTTATTC		
		AGACG_		
GAM2121	HMP19 3'	CTTATTCTTTGTTAGGAAAATG 88860	CCAC	CAA_
	TA	TACA TCC GAAGAATAAG		

		ATGT AGG TTTCTTATTC	
		AAA_ ATTG	
GAM2121 KIAA1579	3'	TACTCTTAGTGGTGTA 37154	CCCAAG A
		TACACCACT AAGA TA	
		ATGTGGTGGA TTCT AT	
		_____ C	
GAM2121 KIAA1719	3'	TCTGTCTTGGGAGTGGTGTA 68742	_
		TACACCACTCCCAAGA AGA	
		ATGTGGTGAGGGTTCT TCT	
		G	
GAM2121 KIAA1853	3'	TTTTTCTTGGAAGCAGTG 69929	CA C
		CAC CT CCAAGAAGAA	
		GTG GA GGTTCTTTTT	
		AC A	
GAM2121 KIAA1877	3'	CTTATTCTTCTGCCATGAGT 66748	CCA__
		ACTC AGAAGAATAAG	
		TGAG TCTTCTTATTC	
		TACCG	
GAM2121 KIAA1906	3'	CTTATTCTTCTTGACTTTTGG 73571	CTCC_
		CCA CAAGAAGAATAAG	
		GGT GTTCTTCTTATTC	
		TTTCA	
GAM2121 OSBPL11	3'	CTTAATTTCCCAAGAGTGGTG 43206	CCAA AA
		CACCACTC GAAG TAAG	
		GTGGTGAG CTTT ATTC	
		AACC A_	
GAM2121 YME1L1	3'	TCATTCTTGATGTGGTGTA 58438	TCC _
		TACACCAC CAAGAA GA	
		ATGTGGTG GTTCTT CT	
		TA_ A	
GAM2121 YME1L1	3'	TCATTCTTGATGTGGTGTA 27323	TCC _
		TACACCAC CAAGAA GA	
		ATGTGGTG GTTCTT CT	
		TA_ A	
GAM2121 ZNF262	3'	CTTATTTTGTGTTGGGAGT 18723	A
		ACTCCCAAG AGAATAAG	
		TGAGGGTTT TTTTATTC	
		G	
GAM2121 LOC91960	3'	TGTGGCTTGGAACGTGGTGTA 68294	TC_ AAGA
		TACACCAC CCAAG ATA	

ATGTGGTG GGTTC TGT
 CAA GG__
 GAM2122 PRO1257 5' ATGCTCATAAATAAGCCTGGGA 38326 A A_ C
 AG TTTC TCG CTTAT TATGAGCAT
 |||| ||| |||| |||||
 GAAG GGT GAATA ATACTCGTA
 _ CC A
 GAM2122 LOC90495 3' CACTGATAAGTCAGTGAAA 63735 C TA
 TTTCAT GACTTATC TG
 ||||| ||||| ||
 AAAGTG CTGAATAG AC
 A TC
 GAM2123 MNT 3' GTCCTCACCTGTGGGAGCG 40087 _ _C
 CGCTCCCAC GGTG G AC
 ||||| ||||| ||
 GCGAGGGTG CCAC C TG
 T TC
 GAM2123 TRPC6 3' TTCATGTGCATTTACCAAGAGG 17292 G CCAC ____
 T AC CTC GGTG GCACATGAA
 || ||| ||| |||||
 TG GAG CCAT CGTGTA CTT
 _ AA__ TTA
 GAM2123 VEGF 3' CACGTGCCCATTTGTGGAGGC 14039 TC _ A
 GC CCACGGTGG CAC TG
 || ||||| ||| ||
 CG GGTGTTACC GTG AC
 GA C C
 GAM2123 VPS26 3' CATGTACCACCATGTGCTGGAG 18106 _ _ C
 C GCTCC CAC GGTGG ACATG
 |||| ||| |||| ||||
 CGAGG GTG CCACC TGTAC
 TC TA A
 GAM2123 C6orf33 3' TTCATGTGGACATTCAGGAAGC 56723 C AC G_
 GCT CC GGTG CACATGAA
 ||| || ||| |||||
 CGA GG TTAC GTGTA CTT
 A AC AG
 GAM2123 FLJ22690 5' GTTCATACACTGTGGAAGC 45576 C GCAC
 GCT CCACGGTG ATGAAC
 ||| ||||| ||||
 CGA GGTGTCAC TACTTG
 A A__
 GAM2123 KIAA0227 3' TTCACATGCCACTGAAGC 61356 CCCA CA
 GCT CGGTGGCA TGAA
 ||| ||||| |||
 CGA GTCACCGT ACTT
 A__ AC
 GAM2123 KLF12 3' GTTCATGTCTATGTGGGA 33281 G C
 TCCCACG TGG ACATGAAC
 ||||| ||| |||||

AGGGTGT ATC TGTACTTG

GAM2123 MGC20806 3' TCGACGCCACGTGGGAGC 59390 G ACA
GCTCCCACG TGGC TGA
||||||| ||| |||
CGAGGGTGC ACCG GCT

CA_
GAM2123 NEU4 5' GTGCCACCGTGGGAGTGT 55793
ACGCTCCCACGGTGGCAC
|||||||
TGTGAGGGTGCCACCGTG

GAM2123 NSE1 3' GTTCTTTCCACCGTGGGAAGC 59678 _ CACAT
GCT CCCACGGTGG GAAC
||| ||||| |||
CGA GGGTGCCACC CTTG
A TTT_

GAM2123 PRO1635 3' CATGTGTGTCTGGGAAGC 38342 _ C GT G
GCT CCCA G G CACATG
||| ||| | |||||
CGA GGGT C T GTGTAC
A _TG_

GAM2123 RAB10 5' GCTCGCCCGTGGGAGCGT 86353 _ _
ACGCTCCCACGG TG GC
||||||| |||
TGCGAGGGTGCC GC CG
C T

GAM2123 ZNF387 3' GTTCATGTACTGCTAAGGCGT 28683 CCCAC TG C
ACGCT GG G ACATGAAC
||||| || | |||||
TGCGG TC C TGTACTTG
AA_ GT A

GAM2123 LOC150094 3' GTCCACGTGGTGTGGGAGC 86006 _ C
GCTCCCACG GTGG AC
||||||| ||| |||
CGAGGGTGT CACC TG
GGTG _

GAM2123 LOC158696 5' TTCATGTGTATTGACAAATGCG 82862 TCCCA_ G
T ACGC CGGTG CACATGAA
||| ||||| |||||
TGCG GTTAT GTGTACTT
TAAACA _

GAM2123 LOC163231 5' TCATCACTGTGGGAACGT 83335 C GCAC
ACG TCCCACGGTG ATGA
||| ||||| |||
TGC AGGGTGTAC TACT
A _

GAM2123 LOC197416 5' GTTCATGTCTTGATGGGA 91323 CGGT C
TCCCA GG ACATGAAC
||||| || |||||

AGGGT TC TGTACTTG
 AGT_ _
 GAM2123 LOC200689 5' GTTCTTTCCACCGTGGAAGC 91674 _ CACAT
 GCT CCCACGGTGG GAAC
 ||| ||||| |||
 CGA GGGTGCCACC CTTG
 A TTT_ _
 GAM2123 LOC222134 5' CATGTGCCTGGGAAAAGT 95799 GC CGGT
 AC TCCCA GGCACATG
 || ||| |||||
 TG AGGGT CCGTGTAC
 AA _ _ _
 GAM2124 DYSF 3' CAGACCTCCTAGGCCTGATTG 14490 C CTGCG
 TAATCAGGCC AGG TTG
 ||||| ||| |||
 GTTAGTCCGG TCC GAC
 A TCCA_ _
 GAM2124 RAB3A 3' CAACTACCCGGGCCTGA 12697 A C C
 TCAGGCCC GG TG GTTG
 ||||| || || |||
 AGTCCGGG CC AT CAAC
 C _ _
 GAM2124 CENTA1 3' CAGGCCCTGGGCCTGAT 23443 CT G
 ATCAGGCCCAGG GC TTG
 ||||| || |||
 TAGTCCGGGTCC CG GAC
 _ _
 GAM2124 FLJ14566 3' TTCAGCGTCCCTGGGCC 52503 CT
 GGCCCAGG GCGTTGAA
 ||||| |||||
 CCGGGTCC TGCGACTT
 C_ _
 GAM2124 FLJ21839 5' TTCAACGTGTGGACCCGA 41839 A C GGC
 TC GG CCA TCGTTGAA
 || ||| |||||
 AG CC GGT GTGCAACTT
 C A _ _
 GAM2124 KIAA0140 3' CAACTCGTGGGCCTGAT 28506 GGC C
 ATCAGGCCCA TG GTTG
 ||||| || |||
 TAGTCCGGGT GC CAAC
 _ _ T
 GAM2124 KIAA0453 3' CAGCCCCTGGGCCTGGT 69604 CTGC
 ATCAGGCCCAGG GTTG
 ||||| ||| |||
 TGGTCCGGGTCC CGAC
 C_ _
 GAM2124 MGC13114 3' ACGCAAGCCCAGGCCTGA 51390 A_ _
 TCAGGCCC GGCT GCGT
 ||||| ||| |||

AGTCCGGG CCGA CGCA
 AC A
 GAM2124 LOC131377 3' TCAATGTGCTGTGCCTGA 76780 CCA T
 TCAGGC GGC GCGTTGA
 ||||| ||| |||||
 AGTCCG TCG TGTAAC
 TG_ _
 GAM2124 LOC146733 3' CACTGCCCTGGGCCTG 84783 CT T
 CAGGCCAGG GCG TG
 ||||| ||| ||
 GTCCGGGTCC CGT AC
 _ C
 GAM2125 ALDH3B1 3' AGGCCGAGGCAGGCGGATCACC 93151 G C A
 GG GATCCGCC GCCTC GCCT
 || ||||| |||| ||||
 CC CTAGGCGG CGGAG CGGA
 A A C
 GAM2125 BHMT2 3' AGGCCGAGGCGGGCGGATCACC 34727 G A
 GG GATCCGCCCCGCCTC GCCT
 || ||||| |||| ||||
 CC CTAGGCGGGCGGAG CGGA
 A C
 GAM2125 CHST5 3' AGAGGCTGAGGCGGGTGGATCA 25084 G
 CC GG GATCCGCCCGCCTCAGCCTCT
 || ||||| ||||| |||||
 CC CTAGGTGGGCGGAGTCGGAGA
 A
 GAM2125 IL18 3' AGGCTGAGGCGGGCAGATCACC 9588 G C
 GG GATC GCCCGCCTCAGCCT
 || ||| ||||| |||||
 CC CTAG CGGGCGGAGTCGGA
 A A
 GAM2125 MYO1D 3' AGAGGCTGGGAGCAAATGCCCC 72238 ATCCGCCC _
 GGGG GC CTCAGCCTCT
 ||| || ||||| |||||
 CCCC CG GGGTCGGAGA
 GTAAA_ A
 GAM2125 NT5C2 3' AGGCCGAGACAGGCGGATCACC 25253 G CGC A
 GG GATCCGCC CTC GCCT
 || ||||| ||| ||||
 CC CTAGGCGG GAG CGGA
 A ACA C
 GAM2125 PCDHB9 3' AGGCCAAGGCGGGCAGATCACC 39436 G C CA
 GG GATC GCCCGCCT GCCT
 || ||| ||||| ||||
 CC CTAG CGGGCGGA CGGA
 A A AC
 GAM2125 PLA2G2D 3' CTGAGGCAGGCAGATCACC 25714 G C C
 GG GATC GCC GCCTCAG
 || ||| ||| |||||

			CC CTAG CGG CGGAGTC		
			A A A		
GAM2125	PSMB9	3'	AGGCCAAGGCAGGCGGATCACC 12486	G	C CA
			GG GATCCGCC GCCT GCCT		
			CC CTAGGCGG CGGA CGGA		
			A A AC		
GAM2125	RBL1	3'	AGGCCAAGGCGGGCAGATCACC 12783	G	C CA
			GG GATC GCCCGCCT GCCT		
			CC CTAG CGGGCGGA CGGA		
			A A AC		
GAM2125	ROCK2	3'	AGGCCAAGACGGGCGGATCACC 66612	G	C CA
			GG GATCCGCCCG CT GCCT		
			CC CTAGGCGGGC GA CGGA		
			A A AC		
GAM2125	SRC	3'	AGAGGCTGCCGAGACAGACCCT 19449	A	CGCC_ CCT
			GGGG TC CG CAGCCTCT		
			TCCC AG GC GTCGGAGA		
			_ ACAGA C__		
GAM2125	TBX6	3'	AGGCTGAGGCGGGCAGATCACC 55808	G	C
			GG GATC GCCCGCCTCAGCCT		
			CC CTAG CGGGCGGAGTCGGA		
			A A		
GAM2125	TEM7	3'	AGGCTGAGGCAGGCGGATCACC 40244	G	C
			GG GATCCGCC GCCTCAGCCT		
			CC CTAGGCGG CGGAGTCGGA		
			A A		
GAM2125	TNFSF14	3'	AGGCCAAGGCAGGCGGATCACC 15076	G	C CA
			GG GATCCGCC GCCT GCCT		
			CC CTAGGCGG CGGA CGGA		
			A A AC		
GAM2125	ANGPTL4	5'	AGAAGCCGAGCTGAGCGGATCC 32760		C C A C
	TC		GGGGATCCGC CG CTC GC TCT		
			CTCCTAGGCG GT GAG CG AGA		
			A C C A		
GAM2125	APOF	3'	AGAGGCTGAGGCGGGATGATCA 9688	G	CG
	CC		GG GATC CCCGCCTCAGCCTCT		
			CC CTAG GGGCGGAGTCGGAGA		
			A TA		
GAM2125	C11orf9	3'	GAGACTTGGGTGGACCCC 26118	A	CCTC C
			GGGG TCCGCCCC AG CTC		

CCCC AGGTGGGT TC GAG
 — ——— A
 GAM2125 C20orf177 3' AGGCCGAGGCAGGCGGATCACC 62827 G C A
 GG GATCCGCC GCCTC GCCT
 || ||||| |||| ||||
 CC CTAGGCGG CGGAG CGGA
 A A C
 GAM2125 C6orf29 3' AGAGGCTGAGGCGGGCGGATCA 48263 G
 CC GG GATCCGCCCGCCTCAGCCTCT
 || |||||
 CC CTAGGCGGGCGGAGTCGGAGA
 A
 GAM2125 C6orf29 3' AGAGGCTGAGGCGGGCGGATCA 52453 G
 CC GG GATCCGCCCGCCTCAGCCTCT
 || |||||
 CC CTAGGCGGGCGGAGTCGGAGA
 A
 GAM2125 C8orf2 3' AGGCCAAGGCAGGCGGATCACC 24144 G C CA
 GG GATCCGCC GCCT GCCT
 || ||||| |||| ||||
 CC CTAGGCGG CGGA CGGA
 A A AC
 GAM2125 C9orf12 5' GCGAGGCGGGCGGCCCC 43104 AT A
 GGGG CCGCCCGCCTC GC
 |||| ||||| ||
 CCCC GGCGGGCGGAG CG
 — —
 GAM2125 CGRP-RCP 3' GGGCAAGGCAGGCGGATCACC 27894 G C CA
 GG GATCCGCC GCCT GCCT
 || ||||| |||| ||||
 CC CTAGGCGG CGGA CGGG
 A A A_
 GAM2125 DDX34 3' AGGCCTAGGCGGGCAGATCACC 28658 G C CA
 GG GATC GCCCGCCT GCCT
 || |||| ||||| ||||
 CC CTAG CGGGCGGA CGGA
 A A TC
 GAM2125 DKFZp761J139 5' AGGTCGAGGCGGGCAGATCTCC 51099 C A
 GGGGATC GCCCGCCTC GCCT
 ||||| ||||| ||||
 CCTCTAG CGGGCGGAG TGGA
 A C
 GAM2125 EPS8R3 3' AGAGGCTGAAGCAAACAGTGTC 58167 CCGCCC_ C
 CC GGGAT GC TCAGCCTCT
 |||| || |||||
 CCCTG CG AGTCGGAGA
 TGACAAA A
 GAM2125 EPS8R3 3' AGAGGCTGAAGCAAACAGTGTC 56530 CCGCCC_ C
 CC GGGAT GC TCAGCCTCT
 |||| || |||||

			CCCTG	CG AGTCGGAGA		
			TGACAAA	A		
GAM2125	FAM3A	3'	AGAGGCTGAGGCTCACACCCC	41730	ATCCGCCC	
			GGGG	GCCTCAGCCTCT		
			CCCC	CGGAGTCGGAGA		
			ACACT__			
GAM2125	FBXO27	3'	AGGCTGAGGCAGGCGGATCACC	75001	G	C
			GG GATCCGCC	GCCTCAGCCT		
			CC CTAGGCGG	CGGAGTCGGA		
			A	A		
GAM2125	FKBP14	3'	AGGCTGAGGCAGGCGGATCACC	36061	G	
			GG GATCCGCC	CGCCTCAGCCT		
			CC CTAGGCGG	CGGAGTCGGA		
			A			
GAM2125	FLJ10826	3'	AGGCCAAGGCAGGCGGATCACC	37242	G	C CA
			GG GATCCGCC	GCCT GCCT		
			CC CTAGGCGG	CGGA CGGA		
			A	A AC		
GAM2125	FLJ11151	3'	AGGCTGAGACGGGCAGATCACC	68469	G	C C
			GG GATC	GCCCG CTCAGCCT		
			CC CTAG	CGGGC GAGTCGGA		
			A	A A		
GAM2125	FLJ12056	3'	AGGCCGAGGCAGGCGGATCACC	46817	G	C A
			GG GATCCGCC	GCCTC GCCT		
			CC CTAGGCGG	CGGAG CGGA		
			A	A C		
GAM2125	FLJ12671	3'	AGGCCGAGGCAGGCGGATCACC	49102	G	A
			GG GATCCGCC	CGCCTC GCCT		
			CC CTAGGCGG	CGGAG CGGA		
			A	C		
GAM2125	FLJ14397	3'	AGGCTGAGGCAGGCGGATCACC	52315	G	C
			GG GATCCGCC	GCCTCAGCCT		
			CC CTAGGCGG	CGGAGTCGGA		
			A	A		
GAM2125	FLJ20464	3'	AGGCTGAGGCAGGCGGATCACC	35686	G	
			GG GATCCGCC	CGCCTCAGCCT		
			CC CTAGGCGG	CGGAGTCGGA		
			A			
GAM2125	FLJ20464	3'	AGGTCGAGGCAGGCGGATCACC	35687	G	C A
			GG GATCCGCC	GCCTC GCCT		

			CC CTAGGCGG CGGAG TGA		
			A A C		
GAM2125	FLJ20783	3'	AGAGACCGAGGCGGGCGGATC 36094	AGC	
			GATCCGCCCCGCCTC CTCT		
			CTAGGCGGGCGGAG GAGA		
			CCA		
GAM2125	FLJ22167	3'	AGAGGCTGAGGCGGGTGGATCA 44858	G	
		CC	GG GATCCGCCCCGCCTCAGCCTCT		
			CC CTAGGTGGGCGGAGTCGGAGA		
			A		
GAM2125	FLJ23042	3'	AGGCCGAGGCGGGCGGATCACC 47935	G	A
			GG GATCCGCCCCGCCTC GCCT		
			CC CTAGGCGGGCGGAG CGGA		
			A C		
GAM2125	FLJ32915	5'	AGGCCAAGGCGGGCAGATCACC 59424	G	C CA
			GG GATC GCCCGCCT GCCT		
			CC CTAG CGGGCGGA CGGA		
			A A AC		
GAM2125	IRF7	3'	GGGAGGTGGGCGGACCCC 15738	A	AG
			GGGG TCCGCCCCGCCTC CC		
			CCCC AGGCGGGTGGAG GG		
			— —		
GAM2125	JAM1	3'	AGAGGCTGAGGCAGGCGGATCA 34216	G	C
		CC	GG GATCCGCC GCCTCAGCCTCT		
			CC CTAGGCGG CGGAGTCGGAGA		
			A A		
GAM2125	JAM1	3'	AGAGGCTGAGGCAGGCGGATCA 58507	G	C
		CC	GG GATCCGCC GCCTCAGCCTCT		
			CC CTAGGCGG CGGAGTCGGAGA		
			A A		
GAM2125	JAM1	3'	AGAGGCTGAGGCAGGCGGATCA 58535	G	C
		CC	GG GATCCGCC GCCTCAGCCTCT		
			CC CTAGGCGG CGGAGTCGGAGA		
			A A		
GAM2125	JAM1	3'	AGAGGCTGAGGCAGGCGGATCA 58562	G	C
		CC	GG GATCCGCC GCCTCAGCCTCT		
			CC CTAGGCGG CGGAGTCGGAGA		
			A A		
GAM2125	KIAA0159	3'	AGAGGCTGAGGCAGGAGAATCG 30135	G	CCG C
		CC	GG GAT CC GCCTCAGCCTCT		

CC CTA GG CGGAGTCGGAGA
 G AGA A
 GAM2125 KIAA0475 3' AGGCTGAGGCAGGCAGATCACC 30108 G C C
 GG GATC GCC GCCTCAGCCT
 || ||| ||| |||||
 CC CTAG CGG CGGAGTCGGA
 A A A
 GAM2125 KIAA0694 3' AGGCCAAGACAGGCGGATCCC 72963 CGC CA
 GGGATCCGCC CT GCCT
 ||||| || |||
 CCCTAGGCGG GA CGGA
 ACA AC
 GAM2125 KIAA1086 3' AGAGGCCGAGGTGGGCAGATCG 71279 G C A
 CC GG GATC GCCCGCCTC GCCTCT
 || ||| ||||| |||||
 CC CTAG CGGGTGGAG CGGAGA
 G A C
 GAM2125 KIAA1277 3' AGAGGCCAAGGCAGGCAGGTGG 65067 G C CA____
 ATCACC GG GATCCGCC GCCT GCCTCT
 || ||||| ||| |||||
 CC CTAGGTGG CGGA CGGAGA
 A A CGGAAC
 GAM2125 KIAA1456 5' AGGCCGAGGCAGGCGGATCACC 67531 G C A
 GG GATCCGCC GCCTC GCCT
 || ||||| |||| |||||
 CC CTAGGCGG CGGAG CGGA
 A A C
 GAM2125 KIAA1656 3' AGAGGCTGAGGCTGACCC 66357 A CGCCC
 GGG TC GCCTCAGCCTCT
 ||| || |||||
 CCC AG CGGAGTCGGAGA
 _ T____
 GAM2125 KIAA1677 5' GAGGCTGGACAGGACCCC 67664 A GCCCGCC
 GGGG TCC TCAGCCTC
 |||| ||| |||||
 CCCC AGG GGTCCGAG
 _ ACA____
 GAM2125 KIAA1841 3' AGGCCGAGGCGGGCAGATCACC 80846 G C A
 GG GATC GCCCGCCTC GCCT
 || ||| ||||| |||||
 CC CTAG CGGGCGGAG CGGA
 A A C
 GAM2125 KIAA1872 3' AGGCCGAGGCAGGCGGATCACC 63593 G C A
 GG GATCCGCC GCCTC GCCT
 || ||||| |||| |||||
 CC CTAGGCGG CGGAG CGGA
 A A C
 GAM2125 KIAA1979 3' AGAGGCTGAGACAGGTGGGCC 89645 A CGC
 GG TCCGCC CTCAGCCTCT
 || ||||| |||||

			CC GGGTGG GAGTCGGAGA			
			— ACA			
GAM2125	MGC16385	3'	AGGCCGAGACGGGCGGATCACC 59533	G	C	A
			GG GATCCGCCCCG CTC GCCT			
			CC CTAGGCGGGC GAG CGGA			
			A A C			
GAM2125	MGC3169	3'	AGGCCGAGGCGGGCAGATCACC 44180	G	C	A
			GG GATC GCCCGCCTC GCCT			
			CC CTAG CGGGCGGAG CGGA			
			A A C			
GAM2125	MGC39350	3'	AGGCCAAGGCGGGCGGATCACC 59314	G		CA
			GG GATCCGCCCCGCCT GCCT			
			CC CTAGGCGGGCGGA CGGA			
			A AC			
GAM2125	MRPL48	5'	AGGCCGAGGCGGGCGGATCACC 32653	G		A
			GG GATCCGCCCCGCCTC GCCT			
			CC CTAGGCGGGCGGAG CGGA			
			A C			
GAM2125	My015	3'	AGGCCAAAGCAGGCGGATCACC 67226	G	C	CTCA
			GG GATCCGCC GC GCCT			
			CC CTAGGCGG CG CGGA			
			A A AAAC			
GAM2125	PRIC285	3'	GCCGAGGCGGGCAGATCACC 62117	G	C	A
			GG GATC GCCCGCCTC GC			
			CC CTAG CGGGCGGAG CG			
			A A C			
GAM2125	PRO0255	3'	AGAGGCCGAGGCGGGCAGATCA 26963	G	C	A
	CC		GG GATC GCCCGCCTC GCCTCT			
			CC CTAG CGGGCGGAG CGGAGA			
			A A C			
GAM2125	PRO2730	3'	AGGCCGAGGCGGGCGGATCACC 48177	G		A
			GG GATCCGCCCCGCCTC GCCT			
			CC CTAGGCGGGCGGAG CGGA			
			A C			
GAM2125	RAB4B	5'	AGGCTGAGGCAGGCGGATCACC 32899	G	C	
			GG GATCCGCC GCCTCAGCCT			
			CC CTAGGCGG CGGAGTCGGA			
			A A			
GAM2125	RGS12	3'	AGAACTGAGGCGAGGCTCCC 12867	TCC	—	CC
			GGGA GCC CGCCTCAG TCT			

			CCCT CGG GCGGAGTC AGA			
			— A AA			
GAM2125	RRP4	3'	AGGCCAAGGCGGGCAGATCACC 27352	G	C	CA
			GG GATC GCCCGCCT GCCT			
			CC CTAG CGGGCGGA CGGA			
			A A AC			
GAM2125	SGKL	3'	AGGCTGAGGCGGGCAGATCACC 26054	G	C	
			GG GATC GCCCGCCTCAGCCT			
			CC CTAG CGGGCGGAGTCGGA			
			A A			
GAM2125	SS18L1	3'	AGGCCGAAGCGGGCGGATCACC 65947	G		C A
			GG GATCCGCCCGC TC GCCT			
			CC CTAGGCGGGCG AG CGGA			
			A A C			
GAM2125	WSB1	3'	TGAGGCGGGCAAATCACC 56984	G	CC	
			GG GAT GCCCGCCTCA			
			CC CTA CGGGCGGAGT			
			A AA			
GAM2125	WSB1	3'	TGAGGCGGGCAAATCACC 56996	G	CC	
			GG GAT GCCCGCCTCA			
			CC CTA CGGGCGGAGT			
			A AA			
GAM2125	YME1L1	3'	AGAGGCCAAGGCGGGCAAATCA 58420	G	CC	CA
	CC		GG GAT GCCCGCCT GCCTCT			
			CC CTA CGGGCGGA CGGAGA			
			A AA AC			
GAM2125	YME1L1	3'	AGAGGCCAAGGCGGGCAAATCA 27315	G	CC	CA
	CC		GG GAT GCCCGCCT GCCTCT			
			CC CTA CGGGCGGA CGGAGA			
			A AA AC			
GAM2125	ZFP106	3'	AGGCTGAGGCAGGCAGATCACC 42714	G	C	C
			GG GATC GCC GCCTCAGCCT			
			CC CTAG CGG CGGAGTCGGA			
			A A A			
GAM2125	LOC118471	3'	AGAGGCCGAGGCAGGCGGATCA 74350	G		C A
	CC		GG GATCCGCC GCCTC GCCTCT			
			CC CTAGGCGG CGGAG CGGAGA			
			A A C			
GAM2125	LOC126282	3'	AGAGGCTGAGGCGGGCGGATC 74941			
			GATCCGCCCGCCTCAGCCTCT			

CTAGGCGGGCGGAGTCGGAGA

GAM2125 LOC127294 3' AGGCCAAGGCGGGCAGATCACC 75143 G C CA
 GG GATC GCCCGCCT GCCT
 || ||| ||||| |||
 CC CTAG CGGGCGGA CGGA
 A A AC

GAM2125 LOC137362 3' AGAGGCCGAGGCGGGTGGGTCA 75780 G A
 CC GG GATCCGCCCGCCTC GCCTCT
 || ||||| ||||| |||||
 CC CTGGGTGGGCGGAG CGGAGA
 A C

GAM2125 LOC143465 3' AGGCTGAAGCAGGCAGATCACC 83867 G C C C
 GG GATC GCC GC TCAGCCT
 || ||| || |||||
 CC CTAG CGG CG AGTCGGA
 A A A A

GAM2125 LOC143943 3' AGAGGCCAAGGCGGGCGGATC 83910 CA
 GATCCGCCCGCCT GCCTCT
 ||||| |||||
 CTAGGCGGGCGGA CGGAGA
 AC

GAM2125 LOC144563 3' AGGCCGAGGCAGGCGGATCACC 77390 G C A
 GG GATCCGCC GCCTC GCCT
 || ||||| |||| |||
 CC CTAGGCGG CGGAG CGGA
 A A C

GAM2125 LOC145216 3' AGGCTGAGGCGGGCGGATCACC 84216 G
 GG GATCCGCCCGCCTCAGCCT
 || ||||| ||||| |||||
 CC CTAGGCGGGCGGAGTCGGA
 A

GAM2125 LOC147180 5' AGGCCGAGGCGGGCGGATCACC 85093 G A
 GG GATCCGCCCGCCTC GCCT
 || ||||| ||||| |||
 CC CTAGGCGGGCGGAG CGGA
 A C

GAM2125 LOC147664 3' AGGCTGAGGCAGGCAGATCACC 79041 G C C
 GG GATC GCC GCCTCAGCCT
 || ||| || |||||
 CC CTAG CGG CGGAGTCGGA
 A A A

GAM2125 LOC147700 3' AGGCCGAGGCGAGCAGATCACC 59875 G C C A
 GG GATC GC CGCCTC GCCT
 || ||| || ||||| |||
 CC CTAG CG GCGGAG CGGA
 A A A C

GAM2125 LOC150622 3' AGGCCGAGGCAGGCGGATCACC 80754 G C A
 GG GATCCGCC GCCTC GCCT
 || ||||| |||| |||

		CC CTAGGCGG CGGAG CGGA			
		A A C			
GAM2125	LOC151068 3'	AGGCTGAGGCAGGCAGTTC	86404	CC	C
		GGAT GCC GCCTCAGCCT			
		CTTG CGG CGGAGTCGGA			
		A_ A			
GAM2125	LOC152283 3'	GCTGAGGCGAGCAGATCACC	86872	G	C C
		GG GATC GC CGCCTCAGC			
		CC CTAG CG GCGGAGTCG			
		A A A			
GAM2125	LOC152445 3'	AGGCCAAGGCAGGCGGATCACC	86932	G	C CA
		GG GATCCGCC GCCT GCCT			
		CC CTAGGCGG CGGA CGGA			
		A A AC			
GAM2125	LOC154791 3'	AGGCCAAGGCAGGCGGATCACC	82048	G	C CA
		GG GATCCGCC GCCT GCCT			
		CC CTAGGCGG CGGA CGGA			
		A A AC			
GAM2125	LOC159053 3'	AGGCCAAGGCGGGCAGATCACC	88361	G	C CA
		GG GATC GCCCGCCT GCCT			
		CC CTAG CGGGCGGA CGGA			
		A A AC			
GAM2125	LOC196047 5'	AGGTTAAGGCAGGCGGATCACC	91144	G	C C
		GG GATCCGCC GCCT AGCCT			
		CC CTAGGCGG CGGA TTGGA			
		A A A			
GAM2125	LOC199858 3'	AGGCTGAGGCGGGCGGATCACC	89791	G	
		GG GATCCGCCCGCCTCAGCCT			
		CC CTAGGCGGGCGGAGTCGGA			
		A			
GAM2125	LOC200940 3'	AGGCTGAGGCAGGCGGATCTCC	90385		C
		GGGGATCCGCC GCCTCAGCCT			
		CCTCTAGGCGG CGGAGTCGGA			
		A			
GAM2125	LOC201685 3'	AGGCCGAGGCAGGCGGATCACC	91836	G	C A
		GG GATCCGCC GCCTC GCCT			
		CC CTAGGCGG CGGAG CGGA			
		A A C			
GAM2125	LOC203025 3'	AGAGGCCGAGGCGGGTGGGTCA	90741	G	A
	CC	GG GATCCGCCCGCCTC GCCTCT			

CC CTGGGTGGGCGGAG CGGAGA
 A C
 GAM2125 LOC203378 3' AGGCTGAGGCAAGCGAATCCCC 92274 C CC
 GGGGAT CGC GCCTCAGCCT
 ||||| ||| |||||
 CCCCTA GCG CGGAGTCGGA
 A AA
 GAM2125 LOC219406 3' AGGCCGAGGCGGGCAGATCACC 95203 G C A
 GG GATC GCCCGCCTC GCCT
 || |||| ||||| ||||
 CC CTAG CGGGCGGAG CGGA
 A A C
 GAM2125 LOC219919 3' AGGCCGAGGCGGGCAGATCACC 94917 G C A
 GG GATCCGCC GCCTC GCCT
 || ||||| |||| ||||
 CC CTAGGCGG CGGAG CGGA
 A A C
 GAM2125 LOC221795 3' AGGCCGAGGCGGGCAGATCACC 94067 G C A
 GG GATCCGCC GCCTC GCCT
 || ||||| |||| ||||
 CC CTAGGCGG CGGAG CGGA
 A A C
 GAM2125 LOC256594 3' AGGCCGAGGCGGGCAGATCACC 98854 G C A
 GG GATCCGCC GCCTC GCCT
 || ||||| |||| ||||
 CC CTAGGCGG CGGAG CGGA
 A A C
 GAM2125 LOC51277 5' AGAGACCGAGGCGGGTGGCCCC 80838 AT AGC
 GGGG CCGCCCGCCTC CTCT
 |||| ||||| ||||
 CCCC GGTGGGCGGAG GAGA
 CCA
 GAM2125 LOC92465 5' AGGCTGAGGCGGGCAGATCACC 69939 G C
 GG GATCCGCC GCCTCAGCCT
 || ||||| |||||
 CC CTAGGCGG CGGAGTCGGA
 A A
 GAM2126 ADRB1 5' CCCCCCGCCCCCGGCCTCC 7300 CA CAGA
 GGAG GCC GGCGGGGGG
 |||| ||| |||||
 CCTC CGG CCGCCCCC
 CCC_ _
 GAM2126 AR 5' CCCCCACCCCTGCCTTCCCC 5273 CAGCC A C
 GGGGAG CAG GG GGGGGG
 |||| ||| |||
 CCCCTT GTC CC CCCCC
 CC_ _ A
 GAM2126 ATBF1 5' CCCCCCGCCCCGCCCCCCCC 23526 A A_ CCAGA
 GGGG GC GC GGCGGGGGG
 |||| ||| |||||

CCCC CG CG CCGCCCCC
 C CC CC___
 GAM2126 AXIN1 5' CCGCCCCGGGCGCGCCCC 61537 A A AGA
 GGGG GC GCCC GGCGG
 |||| |||| ||||
 CCCC CG CGGG CCGCC
 G C CC_
 GAM2126 BLK 3' CCCCCGTGCTGGGCACCCCC 9937 AGCA AG
 GGGG GCCCAG GCGGGGG
 |||| |||| ||||
 CCCC CGGGTC TGCCCCC
 CA__ G_
 GAM2126 BMP1 3' CCCCCGAGCTGCTCCCT 21521 CCAGAGG
 GGGGAGCAGC CGGGGG
 |||| ||||
 TCCCTCGTCG GCCCCC
 A_____
 GAM2126 CALM3 3' CCCCCACCCCCTGCTTCCC 19003 CCCAGA C
 GGGGAGCAG GG GGGGGG
 |||| || ||||
 CCCTTCGTC CC CCCCCC
 CC___ A
 GAM2126 CCND1 3' CCGGCCCCAGGTGCTCCCC 54958 G CAGA G
 GGGGAGCA CC GGC GG
 |||| || ||||
 CCCCTCGT GG CCG CC
 _ ACC_ G
 GAM2126 CCNDBP1 5' CCCCCACGGAGGGGACTGCTC 54471 _ AGAGGC
 TCC GGGGAGCAG CCC GGGGGG
 |||| || ||||
 CCTCTCGTC GGG CCCCCC
 A GAGGCA
 GAM2126 CDC25B 5' CCCCCACCCCTCGCCCGCTGC 41853 GA CCA_ C_
 CTCCC GGG GCAGC GAGG GGGGGG
 || |||| |||| ||||
 CCC CGTCG CTCC CCCCCC
 TC CCGG CCA
 GAM2126 CDC25B 5' CCCCCACCCCTCGCCCGCTGC 41857 GA CCA_ C_
 CTCCC GGG GCAGC GAGG GGGGGG
 || |||| |||| ||||
 CCC CGTCG CTCC CCCCCC
 TC CCGG CCA
 GAM2126 CEP2 5' CCCCCGCCCTCGCTCCCT 24196 AGCCC A
 GGGGAGC AG GGCGGGGG
 |||| || ||||
 TCCCTCG TC CCGCCCCC
 C___ C
 GAM2126 DIPA 3' CCGGCCCGGATTGCTCCCC 23392 GC AGA
 GGGGAGCA CC GGCGGG
 |||| || ||||

		CCCCTCGT GG CCGCCC	
		TA C__	
GAM2126 EPHX1	3'	CCCCCGCCTGCCACCTCCCC 5505	CA_ CCAG
		GGGGAG GC AGGCGGGGGG	
		CCCCTC CG TCCGCCCCC	
		CAC ____	
GAM2126 FLRT1	3'	CCCACCCGGGCTGCCCC 60364 A	AGA C
		GGG GCAGCCC GG GGG	
		CCC CGTCGGG CC CCC	
		_ C__ A	
GAM2126 GFAP	3'	CCCCACCACCCAGCTGCTCCC 10779	CCAGA C _
C		GGGGAGCAGC GG GG GGGG	
		CCCCTCGTCG CC CC CCCC	
		ACC__ A A	
GAM2126 HPS1	5'	GCCTCCGGGCTGTCCCC 5764 G	A
		GGGGA CAGCCC GAGGC	
		CCCCT GTCGGG CTCCG	
		_ C	
GAM2126 IMPDH1	3'	CTCCTCAGGCCGCTCCCC 7951	A CA C
		GGGGAGC GCC GAGG GG	
		CCCCTCG CGG CTCC TC	
		C A_ _	
GAM2126 ITGA3	3'	CCCCCGCCCCCGGCCACC 11033	_ AGCA CAGA
		GG GG GCC GGCGGGGG	
		CC CC CGG CCGCCCC	
		A ____ CCC_	
GAM2126 KCNMB1	3'	CCCCCAGGGCTGCTCCCC 15957	AGAGGC
		GGGGAGCAGCCC GGGGG	
		CCCCTCGTCGGG CCCCC	
		A ____	
GAM2126 LFG	3'	CCCAGAGTCCCTAAGTGCTCCC 77231	G CC A GG_
C		GGGGAGCA C AG GGC GGG	
		CCCCTCGT G TC CTG CCC	
		_ AA C AGA	
GAM2126 LMO2	5'	CCCCGCCCTAGGCCGCGCCC 19936	GA A C A
		GGG GC GCC AG GGCGGGG	
		CCC CG CGG TC CCGCCCC	
		GC C A C	
GAM2126 LNK	3'	CCCACGTCCAGACTGCTTCCC 19637	CCCAGA G
		GGGGAGCAG GGCG GGG	

		CCCTTCGTC	CTGC CCC	
		AGAC__	A	
GAM2126 LOX	5'	CTCCGCGCCGCTCCCC	11345	AGCCCAGA G
		GGGGAGC	GGCG GGGG	
		CCCCTCG	CCGC CCTC	
		_____	G	
GAM2126 MGMT	5'	CCCCCGCCCCCCCCCGCCGCC	11574	A A CCAGA_
C		GGG GC GC	GGCGGGGGG	
		CCC CG CG	CCGCCCCC	
		_ C CCCCC		
GAM2126 MMP19	5'	CCCTCTGCCTAGCACTGCTCCC	11626	CCCAG
C		GGGGAGCAG	AGGCGGGGGG	
		CCCCTCGTC	TCCGTCTCCC	
		ACGA_		
GAM2126 MPP2	3'	CCCCTACCCTAAATGCCCC	60517	A GCCC A CG
		GGGG GCA	AG GG GGGG	
		CCCC CGT	TC CC CCCC	
		_ AAA_ _ AT		
GAM2126 PAX2	5'	CCCCCGCCCCCGGGCGCCCC	15652	A A AGA
		GGG GC GCCC	GGCGGGGGG	
		CCC CG CGGG	CCGCCCCC	
		_ _ CCC		
GAM2126 PAX2	5'	CCCCCGCCCCCGGGCGCCCC	15666	A A AGA
		GGG GC GCCC	GGCGGGGGG	
		CCC CG CGGG	CCGCCCCC	
		_ _ CCC		
GAM2126 PGF	5'	CCCCGCCGGGCGCTCCCC	12065	A AGA
		GGGGAGC GCCC	GGCGGGG	
		CCCCTCG CGGG	CCGCCCC	
		C _____		
GAM2126 PLOD3	5'	CCCAGCCAAGCTGCTCCCC	8430	CCAGA G
		GGGGAGCAGC	GGC GGGG	
		CCCCTCGTCG	CCG CCCC	
		AA__	A	
GAM2126 RAPSN	3'	CCTGCCCAGGGCTGCTCCCC	51972	AGA
		GGGGAGCAGCCC	GGCGGG	
		CCCCTCGTCGGG	CCGTCC	
		AC_		
GAM2126 RFX1	3'	CCCCCGCCCCACCCGCCCC	12848	A AGCCCAGA
		GGGG GC	GGCGGGGGG	

			CCCC CG CCGCCCCC		
			_ CCCACC_		
GAM2126	SEPX1	3'	CCCTGTCTCTGGACTCTCCCC 33377	C C	
			GGGGAG AG CCAGAGGCGGGG		
			CCCCTC TC GGTCTCTGTCCC		
			_ A		
GAM2126	SLC6A8	5'	CCCCCGCCTGACCGCCGCCCC 20069	A A CCAG	
	C		GGGG GC GC AGGCGGGGGG		
			CCCC CG CG TCCGCCCCC		
			_ C CCAG		
GAM2126	SLC9A1	3'	CCCCTTGTCCCTGGGGCACTCC 70923	CAG A	
	CC		GGGGAG CCCAG GGCGGGGGG		
			CCCCTC GGGTC CTGTTCCCC		
			ACG C		
GAM2126	SMS	5'	CCCCCAGTCTCCCGCGGCTGC 17186	CA_ _	
	TCCCC		GGGGAGCAGCC GAGGC GGGGGG		
			CCCCTCGTCGG CTCTG CCCCC		
			CGCC A		
GAM2126	SOCS5	5'	CCCCGACTCCCGGGCGGCCCCC 26680	A A A_ G	
			GGGG GC GCCC GAG CGGGG		
			CCCC CG CGGG CTC GCCCC		
			_ C CC A		
GAM2126	SOLH	3'	CCCCCGCCCCCCTCCTTCCC 20093	C CCCAGA	
			GGGGAG AG GGCGGGGGG		
			CCCTTC TC CCGCCCCC		
			C CCC_		
GAM2126	SOX10	3'	CCCCCGCCAGCCCCTGCCCC 23670	A CCCAGA	
	C		GGGG GCAG GGCGGGGGG		
			CCCC CGTC CCGCCCCC		
			_ CCGAC		
GAM2126	SOX10	5'	CCCCCGCCCCTCCCTCCC 23671	CAGCCC A	
			GGGAG AG GGCGGGGG		
			CCCTC TC CCGCCCCC		
			CC_ C		
GAM2126	STAT6	3'	CCCCCGTATCAAGGCCTCTCC 13451	CA CA G	
	CC		GGGGAG GCC GA GCGGGGGG		
			CCCCTC CGG CT TGCCCCC		
			TC AA A		
GAM2126	SYNGR2	3'	CCGGTGGCCTCTGGGCTGCCTC 17491	GA GGG_	
	CC		GGG GCAGCCCAGAGGC GG		

			CCC CGTCGGGTCTCCG	CC	
			TC	GTGG	
GAM2126	TCF3	3'	CCCCCCTAAGCTGCTCTCC	71272	CCAG C
			GGGGAGCAGC	AGG GGGG	
			CCTCTCGTCG	TCC CCCC	
			AA__ _		
GAM2126	TLX1	5'	CCCCTGCTAGCTGCCCCC	19817	A CCAGA
			GGGG GCAGC	GGCGGGGG	
			CCCC CGTCG	TCGTCCCC	
			_ A__ _		
GAM2126	WNT5A	5'	CCCCCGCGCTGGCCACCCC	14118	AGCA C AG
			GGGG GCC AG	GCGGGGGG	
			CCCC CGG TC	CGCCCCCC	
			AC__ _ G_		
GAM2126	ZNF219	5'	CCCCGCCGCGCCGCCCCC	33553	A A CCAGA
			GGGG GC GC	GGCGGGG	
			CCCC CG CG	CCGCCCC	
			_ C CG__ _		
GAM2126	ALTE	5'	CCCCCGTGCAGCCGCCCCC	60999	A A CCAGAG
			GGGG GC GC	GCGGGGG	
			CCCC CG CG	TGCCCCC	
			_ C ACG__ _		
GAM2126	APR-3	5'	CCCTGGTGCCCTGGGCTGCCGC	32728	GA A _
	CC		GGG GCAGCCCAG	GGCG GGGG	
			CCC CGTCGGGTC	CCGT TCCC	
			GC _ GG		
GAM2126	APR-3	5'	CCCTGGTGCCCTGGGCTGCCGC	55482	GA A _
	CC		GGG GCAGCCCAG	GGCG GGGG	
			CCC CGTCGGGTC	CCGT TCCC	
			GC _ GG		
GAM2126	C1QTNF6	3'	GCCTCTGGGCCGCCCTC	49993	A A
			GGGG GC GCCAGAGGC		
			CTCC CG CGGGTCTCCG		
			_ C		
GAM2126	CBX6	3'	CCCCCAACCCCTGCCCTC	27410	A CCCAGA C
			GGGG GCAG	GG GGGGGG	
			CTCC CGTC	CC CCCCC	
			_ CCC__ _ A		
GAM2126	CCNI	5'	CCCCCGCCTCTCCCCGGCCCC	23365	A AGCCC
	C		GGGG GC	AGAGCGGGGGG	

			CCCC CG	TCTCCGCCCCCC			
			_ GCCCC				
GAM2126	CECR2	5'	CCCCCGCCCGGCGCCCGCC	49431	_ A A	CAGA	
			GG GG GC GCC	GGCGGGGGG			
			CC CC CG CGG	CCGCCCCCC			
			G _ _ C__				
GAM2126	DKFZP434H0820	3'	CCGTGCCCTAGACCTGCTCCCC	64582		CCC_ A	G
			GGGGAGCAG	AG GGCG GG			
			CCCCTCGTC	TC CCGT CC			
			CAGA _ G				
GAM2126	DKFZp434I1930	3'	CCCCCACCCTCCCTGTCCCC	51041	G	CCC A C	
			GGGGA CAG	AG GG GGGGGG			
			CCCCT GTC	TC CC CCCCC			
			_ CC_ _ A				
GAM2126	DKFZP434M154	3'	TGCCTCCAGGCTACTGCCC	72798	G C	CA	
			GGG AG AGCC	GAGGCG			
			CCC TC TCGG	CTCCGT			
			G A AC				
GAM2126	EPS15R	3'	CCTCCGCCTCCGGGCCACCCC	41412	AGCA	A	
			GGGG	GCCC GAGGCGGGGG			
			CCCC	CGGG CTCCGCCTCC			
			AC__ C				
GAM2126	FKBP8	3'	CCACCCCGCCTGCCGCCCCC	25160	A A	CCAG	_
			GGGG GC GC	AGGCGGGG GG			
			CCCC CG CG	TCCGCCCC CC			
			_ C ____	A			
GAM2126	FLJ10101	3'	CCTCGCCCTGGGCTGCCCC	45593	A	A	
			GGG GCAGCCCAG	GGCGGGG			
			CCC CGTCGGGTC	CCGCTCC			
			-	-			
GAM2126	FLJ10101	3'	CCTCGCCCTGGGCTGCCCC	45594	A	A	
			GGG GCAGCCCAG	GGCGGGG			
			CCC CGTCGGGTC	CCGCTCC			
			-	-			
GAM2126	FLJ10101	3'	CCTCGCCCTGGGCTGCCCC	45595	A	A	
			GGG GCAGCCCAG	GGCGGGG			
			CCC CGTCGGGTC	CCGCTCC			
			-	-			
GAM2126	FLJ10101	3'	CCTCGCCCTGGGCTGCCCC	45596	A	A	
			GGG GCAGCCCAG	GGCGGGG			

CCC CGTCGGGTC CCGCTCC

GAM2126 FLJ10101 3' CCTCGCCCTGGGCTGCCCC 45597 A A
GGG GCAGCCCAG GGCGGGG
||| ||||| |||||
CCC CGTCGGGTC CCGCTCC

GAM2126 FLJ10748 3' CCCAGCCCTGGGTCTGCTCCCC 37098 _ A G
GGGGAGCAG CCCAG GGC GGG
||||||| |||| ||| |||
CCCCTCGTC GGGTC CCG CCC

T _ A
GAM2126 FLJ12190 3' CCCCCGCCAGCTCCATCCCC 47565 GC_ CCAGA
GGGGA AGC GGCGGGGGG
|||| ||| |||||
CCCCT TCG CCGCCCCC
ACC A_

GAM2126 FLJ14525 3' CCCGTCTGAGCCGCACCCC 52480 A A C AG
GGGG GC GC CAG GCGGG
|||| || ||| ||||
CCCC CG CG GTC TGCC
A C A _

GAM2126 FLJ23590 3' CCCATTCTCTAGTACTGCTCCC 45365 CCC_ CG
C GGGGAGCAG AGAGG GGG
||||||| |||| |||
CCCCTCGTC TCTCT CCC
ATGA TA

GAM2126 FLJ31978 3' CCCCCACCCCTCGCACCCC 59008 A AGCCC A C
GGGG GC AG GG GGGGG
|||| || ||| |||||
CCCC CG TC CC CCCCC
A C_ C A

GAM2126 FLJ32818 3' CCCAACCTGAACTGCTCCTC 59072 CCCAG CG
GGGGAGCAG AGG GGG
||||||| ||| |||
CTCCTCGTC TCC CCC
AAG_ AA

GAM2126 FYCO1 3' GCCCCTGGGCTGCCCT 44772 A A
GGGG GCAGCCCAG GGC
|||| ||||| |||
TCCC CGTCGGGTC CCG

_ C
GAM2126 GAL3ST2 3' CCCCACAGACCTAAGCTGCTCC 53483 CCAG CG_
C GGGAGCAGC AGG GGGG
||||||| ||| |||
CCCTCGTCG TCC CCCC

AA_ AGACA
GAM2126 GDF10 5' CCCTGCTGCCCGGGCTCTCCCC 18297 C AGA_
GGGGAG AGCCC GGCGGGG
||||| |||| |||||

CCCCTC TCGGG TCGTCCC
 _ CCGG
 GAM2126 HUMZD58C02 3' CCCCCAGCAGGGCTGCTCCCC 80574 AGAG _
 GGGGAGCAGCCC GC GGGGG
 ||||| |||||
 CCCCTCGTCGGG CG CCCCC
 A__ A
 GAM2126 KDELRI 5' CCCCCGCCAGCCTGCCTCCC 23297 GA CCCAGA
 GGG GCAG GGCGGGGGG
 ||| ||| |||||
 CCC CGTC CCGCCCCC
 TC CGA__
 GAM2126 KIAA0444 3' TCCCCGGGTGCTCCCC 63005 G AGAGGC
 GGGGAGCA CCC GGGGGG
 ||||| || |||||
 CCCCTCGT GGG CCCCCT
 _ _
 GAM2126 KIAA0616 3' CCCCCGCCAGCCCGCCCC 47313 A A_ CCAGA
 GGGG GC GC GGCGGGGGG
 ||| || |||||
 CCCC CG CG CCGCCCCC
 _ CC A__
 GAM2126 KIAA0930 3' CCCCCGCCCATCGCCCCC 71068 A AGCCCAGA
 GGGG GC GGCGGGGGG
 ||| || |||||
 CCCC CG CCGCCCCC
 C CTAC__
 GAM2126 KIAA1184 3' CCCCCAGCCCAGCCCACTCCCC 42924 CA_ CCAGA _
 GGGGAG GC GGC GGGGG
 |||| || |||||
 CCCCTC CG CCG CCCCC
 ACC AC__ A
 GAM2126 KIAA1303 3' CCCCCGCCCGCGCTCCACC 66602 _ AGCCCAGA
 GG GGAGC GGCGGGGGG
 || |||| |||||
 CC CCTCG CCGCCCCC
 A CCC__
 GAM2126 KIAA1831 5' CCCCCACCCAGCCTGCTCCTC 64523 CCCAGA C
 GGGGAGCAG GG GGGGGG
 ||||| |||||
 CTCCTCGTC CC CCCCC
 CGAC__ A
 GAM2126 KIAA1854 3' CCCCCACCCCGACCCCTGCC 72202 A CCCAGA_ C
 TC GGGG GCAG GG GGGGGG
 ||| ||| |||||
 CTCC CGTC CC CCCCC
 _ CCCACCC A
 GAM2126 KIAA1857 3' CCCCCGCCCGGCCGCGCTCC 51691 A__ CAGA
 C GGGAGC GCC GGCGGGGGG
 |||| || |||||

CCCTCG CGG CCGCCCCC
 CGCC C____
 GAM2126 KIAA1878 3' CCCCCGCCCCCACTCACTGCC 93365 A CCCAGA____
 CC GGG GCAG GGCGGGGGG
 ||| ||| |||||
 CCC CGTC CCGCCCCC
 _ ACTCACC
 GAM2126 KIAA1910 5' CCCCCGCCCCTCCGCCCCC 73715 A AGCCC A
 GGGG GC AG GGCGGGGGG
 ||| || |||||
 CCCC CG TC CCGCCCCC
 C CC_____
 GAM2126 KIAA1938 3' CCCCCGCCCCTCTGCTTCCC 93820 CCC A
 GGGGAGCAG AG GGCGGGGGG
 ||||| |||||
 CCCTTCGTC TC CCGCCCCC
 _ C
 GAM2126 KLK6 5' CCCCATCGCGCCTGGGCCTGCT 12423 _ AG _
 CCCC GGGGAGCAG CCCAG GCGG GGGG
 ||||| ||| |||
 CCCCTCGTC GGGTC CGCT CCCC
 C CG A
 GAM2126 MESDC1 5' CCCGCCTGAGCTGCCTCCC 42898 GA C GA
 GGG GCAGC CA GGCGGG
 || ||| || |||
 CCC CGTCG GT CCGCCC
 TC A _
 GAM2126 MGC10500 5' TCCCCGTGGGCGCTCCCC 49728 A AGAG
 GGGGAGC GCCC GCGGGGG
 ||||| ||| |||||
 CCCCTCG CGGG TGCCCCCT
 C _
 GAM2126 MGC12921 5' CCTGTCCCTGAACCAGCCCCC 64512 A AGCC_ A
 GGGG GC CAG GGCGGG
 ||| || |||||
 CCCC CG GTC CTGTCC
 _ ACCAA C
 GAM2126 MGC13186 5' CCCCAACCTGGACTGCTCCCC 51296 C GA CG
 GGGGAGCAG CCA GG GGGG
 ||||| ||| || |||
 CCCCTCGTC GGT CC CCCC
 A _ AA
 GAM2126 MGC2668 3' CCCACCGCCAGCAGCTGCTCC 61190 CCAGA _
 TC GGGGAGCAGC GGCGG GGGG
 ||||| ||| |||
 CTCCTCGTCG CCGCC CCCC
 ACGA_ A
 GAM2126 NY-REN-25 3' CCCATCCAGGCTGCTCCCT 61262 CAGA CG
 GGGGAGCAGCC GG GGG
 ||||| || |||

		TCCCTCGTCGG	CC	CCC		
		A__	TA			
GAM2126	OSBP2	5'	CCCCGCCCCCGGCCTGCCCCC	48479	A	C AGA
			GGGG GCAG CC	GGCGGGG		
			CCCC CGTC GG	CCGCCCC		
			_	C CCC		
GAM2126	PALM	5'	CCCCCGCCAGGCCGCGTCCCC	11962	_	A CAGA
			GGGGA GC GCC	GGCGGGGG		
			CCCCT CG CGG	CCGCCCCC		
			G	C A__		
GAM2126	PDE2A	3'	CCCTGCCCAGGCCACCTCCC	12003	CA_	CAGA
			GGGAG GCC	GGCGGGG		
			CCCTC CGG	CCGTCCC		
			CAC	AC__		
GAM2126	PPP2R2A	3'	CTGGCCTCCTGGACTGCTCCCC	12236	C	_ G
			GGGGAGCAG CCAG	AGGC GG		
			CCCCTCGTC GGTC	TCCG TC		
			A	C G		
GAM2126	Rab11-FIP2	5'	CCGTGCCCCTGGGCTGCCCCC	30454	A	A G
			GGGG GCAGCCCAG	GGCG GG		
			CCCC CGTCGGGTC	CCGT CC		
			_	C G		
GAM2126	SIAT8C	5'	CCCCCGCCCGGGTCCCC	32445	AGCA	AGA
			GGGG GCCC	GGCGGGGG		
			CCCC TGGG	CCGCCCCC		
			__	C__		
GAM2126	TP53TG3	3'	CCCCACCCAGGCTGCTTCCC	31729	CAGA	C
			GGGGAGCAGCC	GG GGGG		
			CCCTTCGTCGG	CC CCCC		
			AC__	A		
GAM2126	UBXD1	5'	CCCCCGCCCCCGCGGCCCCCC	48228	A	A CCAGA
			GGGG GC GC	GGCGGGGGG		
			CCCC CG CG	CCGCCCCC		
			C	G CCC__		
GAM2126	WBSCR17	3'	CCCCCAGGACATGGCTGCTCCC	82215		CAGAGGC
	C		GGGGAGCAGCC	GGGGG		
			CCCCTCGTCGG	CCCCC		
			TACAGGA			
GAM2126	LOC113521	5'	CCCGTCTCCGAGCTGCTCCC	73403	CCA	
			GGGGAGCAGC	GAGGCGGG		

	CCCCTCGTCG CTCTGCCC	
	AGC	
GAM2126 LOC115110 5'	CCTGGCCCTGGGCTCCCC 72176	GCA A G
	GGGGA GCCCAG GGC GGG	
	CCCCT CGGGTC CCG TCC	
	___ _ G	
GAM2126 LOC126661 3'	CCCTGTTTCTGGGCTGCCCGCC 75053	_ A
	GG GG GCAGCCCAGAGGCGGGG	
	CC CC CGTCGGGTCTTTGTCCC	
	G _	
GAM2126 LOC144600 5'	CCCCCGCCCATCGCCCCC 84084	A AGCCCAGA
	GGGG GC GGCGGGGGG	
	CCCC CG CCGCCCCC	
	C CTAC___	
GAM2126 LOC146957 5'	CCCTTCCACACTGCTCCCC 78813	CCCAGA CG
	GGGGAGCAG GG GGGG	
	CCCCTCGTC CC TCCC	
	ACA___ TT	
GAM2126 LOC150111 5'	CCCCTGCCCGAGCTCCCC 85998	AGCCCAGA
	GGGGAGC GGCGGGGGG	
	CCCCTCG CCGTCCCCC	
	AGC___	
GAM2126 LOC150113 5'	CCTCCCCAAGCTGCTGCCC 88565	G CCAGA C
	GGG AGCAGC GG GGGG	
	CCC TCGTCG CC CCTCC	
	G AA___ _	
GAM2126 LOC150135 3'	CCCCTGATCCCCTGAGTGCTCC 80392	G C A _
CC	GGGGAGCA C CAG GG CGGGGG	
	CCCCTCGT G GTC CC GTCCCC	
	_ A C TA	
GAM2126 LOC151534 5'	CCCAGTCAGACTGCTCCCC 57480	CCCAGA G
	GGGGAGCAG GGC GGG	
	CCCCTCGTC CTG CCC	
	AGA___ A	
GAM2126 LOC152189 5'	CCCCGGCGGGCGCCCCC 81328	A A AGAG G
	GGGG GC GCCC GC GGGG	
	CCCC CG CGGG CG CCCC	
	_ _ ___ G	
GAM2126 LOC153572 3'	CCCCCGCCCGAGGCCGCGCCC 87231	A A CAGA
C	GGGG GC GCC GGCGGGGGG	

	CCCC CG CGG CCGCCCCC		
	G C AGC_		
GAM2126 LOC158056 5'	CCCACCTGGGTGCTCCCC 82585	G	GA C
	GGGGAGCA CCCA GG GGG		
	CCCCTCGT GGGT CC CCC		
	_ _ _ A		
GAM2126 LOC170409 3'	GCCCCTGGTCTGCCCCC 83744	A	C A
	GGGG GCAG CCAG GGC		
	CCCC CGTC GGTC CCG		
	_ T C		
GAM2126 LOC199990 3'	CTGGCTCCTAAGCTGCCCCC 89906	A	CC AG G
	GGGG GCAGC AG GC GG		
	CCCC CGTCG TC CG TC		
	_ AA CT G		
GAM2126 LOC221463 3'	CCCCCGCCCCACCGTCTCTC 93703	CA	CCAGA_
CC	GGGAG GC GGCGGGGGG		
	CCCTC TG CCGCCCCC		
	TC CCACCC		
GAM2126 LOC222493 5'	CCCCCTGCCGAGCCGCCGCC 96010	_ A	A CCAGA
	GG GG GC GC GGCGGGGGG		
	CC CC CG CG CCGTCCCCC		
	G _ C AG__		
GAM2126 LOC257104 5'	CCCTGTTCCAGGCCCTCCCC 99364	CA	CA G
	GGGGAG GCC GAG CGGGG		
	CCCCTC CGG CTT GTCCC		
	C_ AC _		
GAM2126 LOC51236 3'	CCCTGCCCAAGCTTCTCCCC 33621	C	CCAGA
	GGGGAG AGC GGCGGGG		
	CCCCTC TCG CCGTCCC		
	T AAC__		
GAM2126 LOC91035 5'	CCAAAGCCTCTGGGGTGCCCCC 65297	A	G GGG
	GGGG GCA CCCAGAGGC GG		
	CCCC CGT GGGTCTCCG CC		
	_ G AAA		
GAM2126 LOC91179 3'	CCCCCAGCAGGGCTGCTCCCC 65763	AGAG	_
	GGGGAGCAGCCC GC GGGGG		
	CCCCTCGTCGGG CG CCCCC		
	A__ A		
GAM2126 LOC92078 3'	CCCCGGCTGAGCTGACCCCC 68596	AG	C AGG
	GGGG CAGC CAG CGGGG		

CCCC GTCG GTC GCCCC
 CA A G__
 GAM2127 FLJ13352 3' CATGGCAGTGCCACTCAAGAAA 45050 C_ A A
 A TTTTC GAGTGGCA CTG CATG
 |||| ||||| || ||||
 AAAAG CTCACCGT GAC GTAC
 AA _ G
 GAM2127 MYO5C 3' CAGCTGTATTTGGAAAAG 38714 G A
 TTTTCCGAGTG CA CTG
 ||||| || ||||
 GAAAAGGTTTAT GT GAC
 _ C
 GAM2127 LOC146520 5' CACTTGCCACTCGGAAAA 78515 C
 TTTTCCGAGTGGCAA TG
 ||||| || ||||
 AAAAGGCTCACCGTT AC
 C
 GAM2128 SCAMP1 3' GCTAAATAAATATTCTCC 54500 T C
 GGA AATATT ATTTAGC
 || |||| |||||
 CCT TTATAA TAAATCG
 C A
 GAM2128 SCAMP1 3' GCTAAATAAATATTCTCC 54501 T C
 GGA AATATT ATTTAGC
 || |||| |||||
 CCT TTATAA TAAATCG
 C A
 GAM2128 NX-17 3' TGAATATCAGCCCCTAATA 40706 ATA_
 TATTAGGG ATATTCA
 ||||| |||||
 ATAATCCC TATAAGT
 CGAC
 GAM2128 LOC161589 3' GCTAAATGAATATTATCCCTAA 83159
 TA TATTAGGGATAATATTCATTTAGC
 |||||
 ATAATCCCTATTATAAGTAAATCG
 GAM2129 BCL7A 3' TGCAAATCCAAGAAGACCC 40994 ACGAA C
 GGGTCTTC GAT TGCA
 ||||| || ||||
 CCCAGAAG CTA ACGT
 AAC__ A
 GAM2129 CAPN10 3' TGCAGACTCATGAAAGACCCTG 43872 _ C A A
 A TCAGGGTCTT CA GA G TCTGCA
 ||||| || || |||||
 AGTCCCAGAA GT CT C AGACGT
 A A __
 GAM2129 MMP25 3' TGCAGATCCCACACTCACCCCTG 42700 CTTACAGAA
 A TCAGGGT GATCTGCA
 ||||| |||||

		AGTCCCA	CTAGACGT		
		CTCACACC_			
GAM2129	PCOLN3	3'	TGCAGGAACGTGGAGACCCTGA	12417	AAGA
			TCAGGGTCTTCACG	TCTGCA	
			AGTCCCAGAGGTGC	GGACGT	
			AA_		
GAM2129	SPOCK	3'	GGCTTCGTAAATAACCCTGA	63476	CTTC_ A
			TCAGGGT	ACGAAG TC	
			AGTCCCA	TGCTTC GG	
			ATAAA	_	
GAM2129	DKFZP586J0619	3'	GCAGATCTCCGAGGCCCTGA	82318	TCA A
			TCAGGGTCT	CG AGATCTGC	
			AGTCCCGGA	GC TCTAGACG	
			_ C		
GAM2129	ERO1-L(BETA)	5'	GCAGACCTCTGACCCTGG	39581	TTCACGA A
			TCAGGGTC	AG TCTGC	
			GGTCCAG	TC AGACG	
			TC_	C	
GAM2129	FLJ10483	3'	TGCAGATCCTCACGAAGG	36658	AC A
			TCTTC	GA GATCTGCA	
			GGAAG	CT CTAGACGT	
			CA	C	
GAM2129	FLJ20422	3'	TGCAGACCCTCCAGGGGCCCTG	35616	CAC AGA
	A		TCAGGGTCTT	GA TCTGCA	
			AGTCCCGGGG	CT AGACGT	
			AC_	CCC	
GAM2129	HARSL	3'	TGCAGAACTGTAGAAGACCCTG	25211	ACGA A
	A		TCAGGGTCTTC	AG TCTGCA	
			AGTCCCAGAAG	TC AGACGT	
			ATG_	A	
GAM2129	KIAA1524	3'	ATTAGTAAAGACCCTGA	73837	C GA
			TCAGGGTCTT	AC AGAT	
			AGTCCCAGAA	TG TTTA	
			A	A_	
GAM2129	KIAA1719	3'	CAGCTAGTGCAAAGGCCCTGA	68728	_ GA AT
			TCAGGGTCTT	CAC AG CTG	
			AGTCCCGGAA	GTG TC GAC	
			AC	A_ _	
GAM2129	MGC14425	3'	GCGGCCGTGCAAGACCCCGA	52949	A _ AAGAT
			TC GGGTCTTC	ACG CTGC	

AG CCCAGAAG TGC GGCG
 C C C____
 GAM2129 MGC4737 5' CAGCCACGTGAAGACCCTGG 49638 AAGAT
 TCAGGGTCTTCACG CTG
 ||||| |||
 GGTCCCAGAAGTGC GAC
 ACC____
 GAM2129 SDC3 3' TGCAGATCCCTCAGGCCCGA 28484 A TCAC A_
 TC GGTCT GA GATCTGCA
 || ||||| || |||||
 AG CCCGA CT CTAGACGT
 C ____ CC
 GAM2129 LOC145748 3' CAGAAGCGAAGACCTTGA 84471 ACGAAGA
 TCAGGGTCTTC TCTG
 ||||| |||
 AGTTCCAGAAG AGAC
 CGA____
 GAM2129 LOC147353 3' CAGATTGGGGGCGAAGGCCCTG 85135 ACGAA_
 A TCAGGGTCTTC GATCTG
 ||||| |||||
 AGTCCCGGAAG TTAGAC
 CGGGGG
 GAM2129 LOC254746 3' AGATCTTCGTGAAGACCCTGA 96848
 TCAGGGTCTTCACGAAGATCT
 |||||
 AGTCCCAGAAGTGCTTCTAGA

 GAM2130 ALOX5AP 5' CAGCTGGAGGCAGAGCA 9678 G CAT
 TGC TC CTTCCAGCTG
 ||| || |||||
 ACG AG GGAGGTCGAC
 _ AC_
 GAM2130 AP2S1 3' CAGCTGGGTCTGGGCCA 41484 C TCT
 TG GTCCA TCCAGCTG
 || ||||| |||||
 AC CGGGT GGGTCGAC
 _ CT_
 GAM2130 BPAG1 3' CAGCTGGGAGGTTAGACCA 9948 C C_
 TG GTC ATCTTCCAGCTG
 || ||| |||||
 AC CAG TGGAGGGTCGAC
 _ AT
 GAM2130 BRCA1 3' CAGCTGGAAGAGTCTGGGC 24545 ____
 GTCCA TCTTCCAGCTG
 ||||| |||||
 CGGGT AGAAGGTCGAC
 CTG
 GAM2130 CHST1 5' CAGCTGGGCCTGGAGACGC 14694 CA ____
 GCGTC TCT TCCAGCTG
 ||||| ||| |||||

			CGCAG AGG GGGTCGAC		
			___ TCC		
GAM2130	COG8	3'	CAGCACGAGATGGACCA 51483	C	CCA
			TG GTCCATCTT GCTG		
			AC CAGGTAGAG CGAC		
			___ CA_		
GAM2130	EPB49	3'	CAGCTGGAGGGAAGATGCA 10523		CA
			TGCGTC TCTTCCAGCTG		
			ACGTAG GGGAGGTCGAC		
			AA		
GAM2130	FOXO1A	5'	CAGCTGGAGCGCGGCGCA 10647		CATC
			TGCGTC TTCCAGCTG		
			ACGCGG GAGGTCGAC		
			CGC_		
GAM2130	GAD1	5'	CAGCTGGAGGTGACGC 7697		CAT
			GCGTC CTTCCAGCTG		
			CGCAG GGAGGTCGAC		
			T_		
GAM2130	HLCS	3'	CAGCTGGAGATGAAGGCA 6407	GTC	T
			TGC CATCT CCAGCTG		
			ACG GTAGA GGTCGAC		
			GAA _		
GAM2130	ID3	3'	CAGCTGGAGGTACAGACCA 79805	C	CAT_
			TG GTC CTTCCAGCTG		
			AC CAG GGAGGTCGAC		
			_ ACAT		
GAM2130	INPP5D	3'	GGCTGGAAGAAAACGCA 83706		CCA
			TGCGT TCTTCCAGCT		
			ACGCA AGAAGGTCGG		
			AAA		
GAM2130	KLRG1	3'	CAGCCTGGGAGATAGAGCA 20555	G C	_
			TGC TC ATCTTCCAG CTG		
			ACG AG TAGAGGGTC GAC		
			_ A C		
GAM2130	LASS2	3'	CAGCTGGGGGAGGAGCA 68307	G A	
			TGC TCC TCTTCCAGCTG		
			ACG AGG AGGGGGTCGAC		
			_ _		
GAM2130	LIMK1	3'	CAGCTGGAGCAGCTGGAC 34138	T	_
			GTCCA CT TCCAGCTG		

			CAGGT GA AGGTCGAC		
			C CG		
GAM2130	MBNL	3'	CAGCTGGAAAGATACGC	41067	CC _
			GCGT ATCTT CCAGCTG		
			CGCA TAGAA GGTCGAC		
			_ A		
GAM2130	MOCS1	3'	CAGCTGGAGCTGGACAGCA	93666	_ T T
			TGC GTCCA CT CCAGCTG		
			ACG CAGGT GA GGTCGAC		
			A C _		
GAM2130	MYCL2	3'	CAGCTGGGTGTGGACGC	19372	CT
			GCGTCCAT TCCAGCTG		
			CGCAGGTG GGGTCGAC		
			T _		
GAM2130	MYLK2	3'	CAGCTGAAGCCTGGACGCA	53581	T _ C
			TGCGTCCA CTTC AGCTG		
			ACGCAGGT GAAG TCGAC		
			CC _		
GAM2130	PDE5A	5'	CAGCTGGGGTGGAAAAGCA	8428	G _ TT
			TGC TCCATC CCAGCTG		
			ACG AGGTGG GGTCGAC		
			AAA _		
GAM2130	PDE5A	5'	CAGCTGGGGTGGAAAAGCA	54219	G _ TT
			TGC TCCATC CCAGCTG		
			ACG AGGTGG GGTCGAC		
			AAA _		
GAM2130	PLXNA1	3'	CAGCTGGAGAAAGAGGCA	72769	G CA T
			TGC TC TCT CCAGCTG		
			ACG AG AGA GGTCGAC		
			G AA _		
GAM2130	PPP5C	3'	CAGCTGGGGCTGGGGGCA	21808	G T T
			TGC TCCA CT CCAGCTG		
			ACG GGGT GG GGTCGAC		
			G C _		
GAM2130	SERPINE1	3'	CAGCCAGAGGGTAGGGCACA	7009	C _ CA
			TG GTCC ATCTTC GCTG		
			AC CGGG TGGGAG CGAC		
			A A AC		
GAM2130	SH3BP2	3'	CAGCCGAGGCTGGAGCA	13052	G T CA
			TGC TCCA CTTC GCTG		

ACG AGGT GGAG CGAC
 _ C C_
 GAM2130 SLC4A1 3' CAGCTGGGATTGTAACCA 6221 C C TC
 TG GT CA TTCCAGCTG
 || || || || || || || ||
 AC CA GT AGGGTCGAC
 _ A TT
 GAM2130 SLC4A2 3' CAGCCGAGGGACCGATGGACG 13178 _ A_
 CGTCCATC TTCC GCTG
 || || || || || || || ||
 GCAGGTAG AGGG CGAC
 CC AGC
 GAM2130 TBX1 3' CAGCTGGATGGTGGGAAGCA 21138 G T
 TGC TCCATC TCCAGCTG
 || || || || || || || ||
 ACG AGGTGG AGGTTCGAC
 A T
 GAM2130 TCF2 3' GGCTGGGATGGAGCA 22409 G TT
 TGC TCCATC CCAGCT
 || || || || || || || ||
 ACG AGGTAG GGTCGG
 _ _
 GAM2130 TCF8 3' CAGCCAGAAGCCTCTGGAAGGC 48427 G_ T__ CA
 A TGC TCCA CTTC GCTG
 || || || || || || || ||
 ACG AGGT GAAG CGAC
 GA CTCC AC
 GAM2130 VHL 3' CAGCCTGGGGGACAGAGCA 6837 G CA _
 TGC TC TCTTCCAG CTG
 || || || || || || || ||
 ACG AG AGGGGGTC GAC
 _ AC C
 GAM2130 ALTE 3' CAGCTGGAAGGGACACA 17579 C AT
 TG GTCC CTTCCAGCTG
 || || || || || || || ||
 AC CAGG GAAGGTCGAC
 A _
 GAM2130 APCL 3' CAGCTGGGGCGGGGACCCA 20813 C ATC
 TG GTCC TTCCAGCTG
 || || || || || || || ||
 AC CAGG GGGGTCGAC
 C GGC
 GAM2130 C19orf7 3' CAGCCCAGAGATGGGCGCA 61778 _ CA
 TGC GTCCATCT TC GCTG
 || || || || || || || ||
 ACGCGGGTAGA AG CGAC
 G CC
 GAM2130 C21orf25 3' CAGCTGGGCAGCAGCGCA 64285 CCAT _
 TGC GT CT TCCAGCTG
 || || || || || || || ||

ACGCG GA GGGTCGAC
 AC__ C
 GAM2130 C6orf35 5' CAGTTGGGGACGGACGCA 38045 A T
 TCGTCC TCT CCAGCTG
 ||||| ||| |||||
 ACGCAGG AGG GGTTGAC
 C _
 GAM2130 CST7 3' CAGCTGGAATGGCAGCA 14683 GT CT
 TGC CCAT TCCAGCTG
 ||| ||| |||||
 ACG GGTA AGGTCGAC
 AC _
 GAM2130 DGKZ 3' CAGCTGGGTGTGACTCA 14677 C _ CTT
 TG GTC CAT CCAGCTG
 || ||| ||| |||||
 AC CAG GTG GGTCGAC
 T T _
 GAM2130 DKFZP586I2223 3' CAGCTGGAGGCTACGCA 31875 CCAT
 TGCGT CTTCCAGCTG
 |||| |||||
 ACGCA GGAGGTCGAC
 TC_
 GAM2130 DKFZP586I2223 3' CAGCTGGAGGCTACGCA 55767 CCAT
 TGCGT CTTCCAGCTG
 |||| |||||
 ACGCA GGAGGTCGAC
 TC_
 GAM2130 DKFZP586I2223 3' CAGCTGGAGGCTACGCA 55769 CCAT
 TGCGT CTTCCAGCTG
 |||| |||||
 ACGCA GGAGGTCGAC
 TC_
 GAM2130 DKFZP586M1120 3' CAGCTGGAGGACGAGCA 49278 G CA
 TGC TC TCTTCCAGCTG
 ||| || |||||
 ACG AG AGGAGGTCGAC
 _ C_
 GAM2130 DLX1 5' CAGCTGGGCCTGGAGCA 81040 G TCT
 TGC TCCA TCCAGCTG
 ||| ||| |||||
 ACG AGGT GGGTCGAC
 _ CC_
 GAM2130 FLJ11218 3' CAGCCAAAAGGTGGAAGCA 37756 G CCA
 TGC TCCATCTT GCTG
 ||| ||||| |||
 ACG AGGTGGAA CGAC
 A AAC
 GAM2130 FLJ12649 3' CAGCCTGGGAGATGAATACA 45086 CG C _
 TG T CATCTTCCAG CTG
 || | ||||| |||

AC A GTAGAGGGTC GAC
 AT A C
 GAM2130 FLJ13117 3' CAGCCTGGGAGACAGAGCA 43805 G CA _
 TGC TC TCTTCCAG CTG
 ||| || ||||| |||
 ACG AG AGAGGGTC GAC
 _ AC C
 GAM2130 FLJ20069 3' CAGCCTGGGGGACAGAGCA 34947 G CA _
 TGC TC TCTTCCAG CTG
 ||| || ||||| |||
 ACG AG AGGGGGTC GAC
 _ AC C
 GAM2130 FLJ21125 3' CAGCTGGAAGGTTTGGATGCA 45224 _
 TGC GTCCA TCTTCCAGCTG
 ||||| |||||
 ACGTAGGT GGAAGGTCGAC
 TT
 GAM2130 FLJ21709 3' CAGCTGGAAGATGAAGGC 78478 _
 GTC CATCTTCCAGCTG
 ||| |||||
 CGG GTAGAAGGTCGAC
 AA
 GAM2130 FLJ22037 5' CAGCTGGAGGAGGAGCA 95532 G A
 TGC TCC TCTTCCAGCTG
 ||| ||| |||||
 ACG AGG AGGAGGTCGAC
 _ _
 GAM2130 FLJ23185 3' CAGCTGGAAAAGCTGGAC 47511 T _
 GTCCA CT TCCAGCTG
 |||| || |||||
 CAGGT GA AGGTCGAC
 C AA
 GAM2130 GBL 3' CAGCTGGAGGGACCCA 42570 C ATC
 TG GTCC TTCCAGCTG
 || ||| |||||
 AC CAGG GAGGTCGAC
 C _
 GAM2130 HS322B1A 3' CAGCTGAGAAGATGGAGCA 31733 G _
 TGC TCCATCTTC CAGCTG
 ||| ||||| |||||
 ACG AGGTAGAAG GTCGAC
 _ A
 GAM2130 ICAM4 3' CAGCCTGGGGGACAGAGCA 9537 G CA _
 TGC TC TCTTCCAG CTG
 ||| || ||||| |||
 ACG AG AGGGGGTC GAC
 _ AC C
 GAM2130 ICAM4 3' CAGCCTGGGGGACAGAGCA 42591 G CA _
 TGC TC TCTTCCAG CTG
 ||| || ||||| |||

ACG AG AGGGGGTC GAC
 _ AC C
 GAM2130 KIAA0397 3' CAGCTGCCTTGGGGGACACA 62343 C A TC__
 TG GTCC TCT CAGCTG
 || ||| ||| |||||
 AC CAGG GGG GTCGAC
 A _ TTCC
 GAM2130 KIAA0992 3' CAGCTGGAAGTGTGGAGCA 32716 G _
 TGC TCCAT CTTCCAGCTG
 ||| ||||| |||||
 ACG AGGTG GAAGGTCGAC
 _ T
 GAM2130 KIAA1260 5' CAGCTGTGGATGTGGATGCA 60668 C _
 TGC GTCCAT TTC CAGCTG
 ||||| ||| |||||
 ACGTAGGTG AGG GTCGAC
 T T
 GAM2130 KIAA1372 3' CAGCCGAGATGGGCACA 93318 C CCA
 TG GTCCATCTT GCTG
 || ||||| |||
 AC CGGGTAGAG CGAC
 A C__
 GAM2130 KIAA1649 3' CAGCCAGAAGTGGGGGCA 67514 G T CA
 TGC TCCA CTTC GCTG
 ||| ||| ||| |||
 ACG GGGT GAAG CGAC
 G _ AC
 GAM2130 KIAA1649 5' CAGCCAGAAGTGGGGGCA 51220 G T CA
 TGC TCCA CTTC GCTG
 ||| ||| ||| |||
 ACG GGGT GAAG CGAC
 G _ AC
 GAM2130 KIAA1727 3' CAGCGTCCAGATGGATGCA 64752 TCCA
 TGC GTCCATCT GCTG
 ||||| |||
 ACGTAGGTAGA CGAC
 CCTG
 GAM2130 KIAA1872 3' CAGCCTGGGAGACAGAGCA 63602 G CA _
 TGC TC TCTTCCAG CTG
 ||| || ||||| |||
 ACG AG AGAGGGTC GAC
 _ AC C
 GAM2130 KIAA1879 3' CAGCCTGGGAGACAGAGCA 73932 G CA _
 TGC TC TCTTCCAG CTG
 ||| || ||||| |||
 ACG AG AGAGGGTC GAC
 _ AC C
 GAM2130 KIAA1957 3' CAGCTGGGAGCGACACGCA 76213 CCAT
 TGC GT CTTCCAGCTG
 ||||| |||||

ACGCA GAGGGTCGAC
 CAGC
 GAM2130 MGC16279 5' CAGCTGGGACTGGGACGTA 52982 ATC
 TCGTCC TTCCAGCTG
 ||||| |||||
 ATGCAGG AGGGTCGAC
 GTC
 GAM2130 MGC21854 5' CAGCTGGAGAGGAAGCA 54602 G A T
 TGC TCC TCT CCAGCTG
 ||| ||| ||| |||||
 ACG AGG AGA GGTCGAC
 A _ _
 GAM2130 MGC2477 5' CAGCTGGGGGCAGGACCA 44293 C AT
 TG GTCC CTTCCAGCTG
 || ||| |||||
 AC CAGG GGGGGTCGAC
 _ AC
 GAM2130 MGC2865 5' CAGCTGGAAGAGCCGAACG 51457 _ CA_
 CGT C TCTTCCAGCTG
 ||| | |||||
 GCA G AGAAGGTCGAC
 A CCG
 GAM2130 MGC4796 3' CAGCCTGGCTGGACAGCA 62159 _ TCTT _
 TGC GTCCA CCAG CTG
 ||| |||| ||| |||
 ACG CAGGT GGTC GAC
 A C_ C
 GAM2130 My015 3' CAGCCTGGGAGACAGAGCA 67229 G CA _
 TGC TC TCTTCCAG CTG
 ||| || ||||| |||
 ACG AG AGAGGGTC GAC
 _ AC C
 GAM2130 OSBPL3 3' CAGCCTGAATGGACGTA 32077 CT CA
 TCGTCCAT TC GCTG
 ||||| || |||
 ATGCAGGTA AG CGAC
 _ TC
 GAM2130 PDCD7 3' CAGCCTGGGAGACAGAGCA 72599 G CA _
 TGC TC TCTTCCAG CTG
 ||| || ||||| |||
 ACG AG AGAGGGTC GAC
 _ AC C
 GAM2130 PPP1R1A 3' CAGCTGGAAGACTCGGCGC 23093 CA_
 GCGTC TCTTCCAGCTG
 |||| |||||
 CGCGG AGAAGGTCGAC
 CTC
 GAM2130 PRO0478 3' CAGCCTGGGGGACAGAGCA 27025 G CA _
 TGC TC TCTTCCAG CTG
 ||| || ||||| |||

		ACG AG AGGGGGTC GAC		
		_ AC C		
GAM2130 PSR	3'	CAGCTGGAAGAATCCATGC 65777	CCA_	
		GCGT TCTTCCAGCTG		
		CGTA AGAAGGTCGAC		
		CCTA		
GAM2130 RPIA	3'	CAGCCAAGGTGGACGTA 58588	CCA	
		TGCGTCCATCTT GCTG		
		ATGCAGGTGGAA CGAC		
		C_		
GAM2130 SAC2	3'	CAGCCTGGGGGACAGAGCA 30723	G CA _	
		TGC TC TCTTCCAG CTG		
		ACG AG AGGGGGTC GAC		
		_ AC C		
GAM2130 SCAMP-4	3'	CAGCCAGGATGGAGCA 55340	G CCA	
		TGC TCCATCTT GCTG		
		ACG AGGTAGGA CGAC		
		_ C_		
GAM2130 SSBP3	5'	CAGCTGGAAAGAGCGCG 36548	CCA _	
		TGCGT TCTT CCAGCTG		
		GCGCG AGAA GGTCGAC		
		_ A		
GAM2130 TSARG1	5'	GGCTTGAATGGATGCA 58191	CT C	
		TGCGTCCAT TC AGCT		
		ACGTAGGTA AG TCGG		
		_ T		
GAM2130 TUB	3'	CAGCTGGGAAGGCCGCA 13892	T ATC	
		TGCG CC TTCCAGCTG		
		ACGC GG AGGGTCGAC		
		C A_		
GAM2130 TUBB4	3'	CAGCTGGAGTGAGAGGCA 71147	G _ CT	
		TGC TC CAT TCCAGCTG		
		ACG AG GTG AGGTCGAC		
		G A _		
GAM2130 LOC127696	5'	CAGCTGGAGGAGACGC 75979	CA	
		GCGTC TCTTCCAGCTG		
		CGCAG AGGAGGTCGAC		
		_		
GAM2130 LOC144698	5'	CAGCTCCGCGGGGATGGACGCA 77431	C_	
		TGCGTCCATCTTC AGCTG		

ACGCAGGTAGGGG TCGAC
 CGCC
 GAM2130 LOC147229 5' CAGCTGGGAGATGAATGCA 78916 C
 TGCGT CATCTTCCAGCTG
 |||| |||||
 ACGTA GTAGAGGGTCGAC
 A
 GAM2130 LOC147632 3' CAGTAAATATGGACGCA 57470 C CCA
 TGCGTCCAT TT GCTG
 ||||| || |||
 ACGCAGGTA AA TGAC
 T A__
 GAM2130 LOC149134 5' CAGCTGGAAGAAGTCGTA 85517 TCCA
 TGCG TCTTCCAGCTG
 ||| |||||
 ATGC AGAAGGTCGAC
 TGA_
 GAM2130 LOC150933 3' CAGCTGGAAGATGCTGT 86335 TC
 GCG CATCTTCCAGCTG
 ||| |||||
 TGT GTAGAAGGTCGAC
 C_
 GAM2130 LOC152485 3' CAGCTGGAGCTGGAGACGCA 81489 __ T T
 TGCG TCCA CT CCAGCTG
 ||| ||| || |||||
 ACGC AGGT GA GGTCGAC
 AG C _
 GAM2130 LOC152790 5' CAGCTGGGGGAGAACCA 87059 C CCA
 TG GT TCTTCCAGCTG
 || || |||||
 AC CA AGGGGGTCGAC
 _ AG_
 GAM2130 LOC153688 3' CAGAGGAGATGGAGGCA 87300 G CAG
 TGC TCCATCTTC CTG
 ||| ||||| |||
 ACG AGGTAGAGG GAC
 G A_
 GAM2130 LOC157556 3' CAGCTGGAAGGGGTGTA 87780 T A
 TGCG CC TCTTCCAGCTG
 |||| || |||||
 ATGT GG GGAAGGTCGAC
 _ _
 GAM2130 LOC167040 5' CAGCTGGAGGGATAGACCA 88621 C C _
 TG GTC ATCT TCCAGCTG
 || ||| ||| |||||
 AC CAG TAGG AGGTCGAC
 _ A G
 GAM2130 LOC196074 5' CAGCTGAGGCTGGAAACA 88968 CG T C
 TG TCCA CTTC AGCTG
 || ||| ||| |||||

AC AGGT GGAG TCGAC
 AA C _
 GAM2130 LOC199796 5' CAGCTGGAAGAGGAGCG 74921 G A
 TGC TCC TCTTCCAGCTG
 ||| ||| |||||
 GCG AGG AGAAGGTCGAC

 - -
 GAM2130 LOC200862 5' CAGCTGGTCCTCAGATGGGCAC 91766 C T____
 A TG GTCCATCT CCAGCTG
 || ||||| |||||
 AC CGGGTAGA GGTCGAC
 A CTCCT
 GAM2130 LOC203235 5' CAGCTCCGAGGATGGACGTA 92098 C_
 TCGTCCATCTTC AGCTG
 ||||| |||||
 ATGCAGGTAGGAG TCGAC
 CC
 GAM2130 LOC219920 5' CAGCTGGGATGGGAAGGCA 94940 G_ ATC
 TGC TCC TTCCAGCTG
 ||| ||| |||||
 ACG AGG AGGGTCGAC
 GA GT_
 GAM2130 LOC222631 5' CAGCTGGAAGCATCAGGA 94407 _ _
 TCC AT CTTCCAGCTG
 ||| || |||||
 AGG TA GAAGGTCGAC
 AC C
 GAM2130 LOC254173 3' GGCTGGAAAAGGACGCA 98645 ATC
 TCGTCC TTCCAGCT
 ||||| |||||
 ACGCAGG AAGGTCGG
 AA_
 GAM2130 LOC256895 3' CAGCTGGAAGTGCTGC 98653 TC T
 GCG CA CTTCCAGCTG
 ||| || |||||
 CGT GT GAAGGTCGAC
 C_ _
 GAM2130 LOC91069 3' CAGCTGGACTGGGACGTA 65399 ATCT
 TCGTCC TCCAGCTG
 ||||| |||||
 ATGCAGG AGGTCGAC
 GTC_
 GAM2130 LOC91355 5' CAGCCAGAGCCTGGGCGCA 66303 TC CA
 TCGTCCA TTC GCTG
 ||||| ||| |||
 ACGCGGGT GAG CGAC
 CC AC
 GAM2131 EPB49 3' CTCCACTTCAGCTTGCC 10528 T GTCTG C
 GG CAAGCTGA AG GGAG
 || ||||| || |||

			CC GTTCGACT TC CCTC		
			— A		
GAM2131	FUT8	3'	CGACCAAACCTCAGTTCGACC 16812	A	C AG
			GGTC AGCTGAGT TG CG		
			CCAG TTGACTCA AC GC		
			C A CA		
GAM2131	LZTR1	3'	CCTCCACCCAGTGGGGCTTGGC 23168		GA T AGC
	C		GGTCAAGCT G CTG GGAGG		
			CCGGTTCGG T GAC CCTCC		
			GG _ CCA		
GAM2131	LZTS1	3'	CCTCCGCTTCTCATCCCAACC 41030	CAAGC	TCT
			GGT TGAG GAGCGGAGG		
			CCA ACTC TTCGCCTCC		
			ACCCT _		
GAM2131	NKX2H	5'	CTCCGTTCCCAGCCTGCC 27630	T A	AGTCT
			GG CA GCTG GAGCGGAG		
			CC GT CGAC CTTGCCTC		
			_ C C _		
GAM2131	PML	3'	CCTCCATGGCTTCCCAGCTTGA 53810		___ TGAGC
	C		GTCAAGCTG AGTC GGAGG		
			CAGTTCGAC TCGG CCTCC		
			CCT TA _		
GAM2131	PML	3'	CCTCCATGGCTTCCCAGCTTGA 53816		___ TGAGC
	C		GTCAAGCTG AGTC GGAGG		
			CAGTTCGAC TCGG CCTCC		
			CCT TA _		
GAM2131	FLJ14299	3'	CTCCACTACTGCTTGACC 47551	TG CTG C	
			GGTCAAGC AGT AG GGAG		
			CCAGTTCG TCA TC CCTC		
			_ _ A		
GAM2131	MIDORI	3'	CCTCCACCCAGCAGCAGACC 74211	AA AGT AGC	
			GGTC GCTG CTG GGAGG		
			CCAG CGAC GAC CCTCC		
			A _ _ CCA		
GAM2132	ATRX	3'	AAGGCAGTACACTCTGGC 6671	G	GGGCC _
			GC CAGAGTGT GC GCCTT		
			CG GTCTCACA TG CGGAA		
			_ _ A		
GAM2132	ATRX	3'	AAGGCAGTACACTCTGGC 57075	G	GGGCC _
			GC CAGAGTGT GC GCCTT		

			CG GTCTCACA	TG CGGAA	
			— — A		
GAM2132	CHI3L1	5'	AAGAGGCCACACCCTGC	8881	A G GCGC
			GCAG GTGTGG CC CTT		
			CGTC CACACC GG GAA		
			C — A —		
GAM2132	COG7	3'	GCTGAGCCCACACTCTGC	68254	— C
			GCAGAGTGTGGGC CG GC		
			CGTCTCACACCCG GT CG		
			A —		
GAM2132	HAS3	3'	AAGACGCAAGGTGTGCTCTGAG	19230	G TG GG — C
	C		GC CAGAG T GCC GCG CTT		
			CG GTCTC G TGG CGC GAA		
			A GT — AA A		
GAM2132	NHLH1	3'	GAAGAGACCCCCAACTCTGCGC	20019	G CCGCGC
			GCGCAGAGT TGGG CTTT		
			CGCGTCTCA ACCC GAAG		
			— CCAGA—		
GAM2132	PCDH7	5'	AAGGCACGGA CTCTGCG	51615	GTGGG C
			CGCAGAGT CCG GCCTT		
			GCGTCTCA GGC CGGAA		
			— A		
GAM2132	PCDH7	5'	AAGGCACGGA CTCTGCG	51618	GTGGG C
			CGCAGAGT CCG GCCTT		
			GCGTCTCA GGC CGGAA		
			— A		
GAM2132	PCDH7	5'	AAGGCACGGA CTCTGCG	11986	GTGGG C
			CGCAGAGT CCG GCCTT		
			GCGTCTCA GGC CGGAA		
			— A		
GAM2132	C6orf31	3'	GTCCGGCCCCACTCTGCGC	48384	T C
			GCGCAGAGTG GGGCCG GC		
			CGCGTCTCAC CCCGGC TG		
			— C		
GAM2132	FLJ12768	5'	GAAGGCGCAGCCCGGAGGCCGC	47964	AGAGTG C
	GC		GCGC TGGGC GCGCCTT		
			CGCG GCCCG CGCGGAAG		
			CCGGAG A		
GAM2132	FLJ20374	5'	AAGGCGCGGAGCACCCGGCGC	35546	AGA GGG
			GCGC GTGT CCGCGCCTT		

CGCG CACG GGCGCGGAA
 GCC A__
 GAM2132 FLJ22693 5' GAAGGCGCAGCCGCTCAGCTGC 43049 AGT_ G C
 G CGCAG GTGG C GCGCCTTC
 |||| ||| | |||||
 GCGTC CGCC G CGCGGAAG
 GACT _ A
 GAM2132 FLJ23233 5' GAAGGCACGGTGGCGACTCACG 45517 CA _ GG C
 C GCG GAGT GT GCCG GCCTTC
 || |||| || |||| |||||
 CGC CTCA CG TGGC CGGAAG
 A_ G G_ A
 GAM2132 KIAA1036 5' AAGGCGCCTTGCACTCTGGC 30481 G TG CC
 GC CAGAGTG GG GCGCCTT
 || ||||| || |||||
 CG GTCTCAC TC CGCGGAA
 _ GT _
 GAM2132 STAG1 5' AAGGCGCGGCCCGCTC 20764 T
 GAGTG GGGCCGCGCCTT
 |||| |||||
 CTCGC CCCGGCGCGGAA
 C
 GAM2132 VDAC3 3' AAGAGGACACACTCTGC 20180 GG GCGC
 GCAGAGTGTG CC CTT
 ||||| || |||
 CGTCTCACAC GG GAA
 A_ A__
 GAM2132 LOC115219 5' AAGGCGCGAGCGCCACCCACGC 73682 CAGAGT _ _
 GCG GTGG GC CGCGCCTT
 || |||| || |||||
 CGC CACC CG GCGCGGAA
 ACC__ G A
 GAM2132 LOC137492 5' AAGACGCGGTCCCCAGCGC 75790 AGAG T C
 GCGC TG GGGCCGCG CTT
 ||| || ||||| |||
 CGCG AC CCTGGCGC GAA
 _ C A
 GAM2133 ABCC1 3' CTGGGGCTTCCCTCCCA 39605 A ATCA
 TGGG AGGGAAGTT AG
 ||| ||||| ||
 ACCC TCCCTTCGG TC
 C GG__
 GAM2133 AP1M1 3' TCGTCTCAGAAGCCCCTTTCCC 51655 AA A A_
 A TGGGAAGGG GTT TC AGACGA
 ||||| ||| || |||||
 ACCCTTTCC CGA AG TCTGCT
 C_ _ AC
 GAM2133 AP2S1 3' TCGCCTGCTCGCTTCCCCTTCC 41486 _ TATCA A
 CA TGGGAAGGG AAGT AG CGA
 ||||| ||| || |||

		ACCCTTCCC TTCG TC GCT	
		C CTCG_ C	
GAM2133 CAD	5'	CGCCTCTGAGCTCCCTTCCC 16352	A TA _ A
		GGGAAGGGA GT TCA AG CG	
		CCCTTCCCT CG AGT TC GC	
		_ _ C C	
GAM2133 CIT	3'	CTTGACGACTTCCCCTCCCA 70303	A TA
		TGGGA GGGAAGT TCAAG	
		ACCCT CCCTTCA AGTTC	
		C GC	
GAM2133 CYP2C9	3'	TCATCTCACATTTTCCCTTCCC 7577	TTATCA C
		GGGAAGGGAAG AGA GA	
		CCCTTCCCTTT TCT CT	
		TACAC_ A	
GAM2133 FY	5'	CTCTTTTCTCCCTTCCC 10738	A TTATC C
		GGGAAGGGA G AAGA G	
		CCCTTCCCT C TTCT C	
		_ TT_ A	
GAM2133 KCNJ10	3'	TCGCCTCCCACTGTCCCCTTTC 11157	A_ TATCA A
CA		TGGGAAGGG AGT AG CGA	
		ACCTTTCCC TCA TC GCT	
		CTG CCC_ C	
GAM2133 LIMK1	3'	TCATCTCAGAGCCCCTTCCC 11341	AA ATCA C
		GGGAAGGG GTT AGA GA	
		CCCTTCCC CGA TCT CT	
		_ GAC_ A	
GAM2133 LIMK1	3'	TCATCTCAGAGCCCCTTCCC 11342	AA ATCA C
		GGGAAGGG GTT AGA GA	
		CCCTTCCC CGA TCT CT	
		_ GAC_ A	
GAM2133 PDE4A	3'	TCCTGGCCGCACCCCCCTTTCC 21688	AA_ TA A
A		TGGGAAGGG GT TCA GA	
		ACCTTTCCC CG GGT CT	
		CCCA CC C	
GAM2133 REQ	3'	TCATCTTCTGCCTCCCTTCCTA 21843	A TATC C
		TGGGAAGGGA GT AAGA GA	
		ATCCTTCCCT CG TTCT CT	
		C TC_ A	
GAM2133 TGFB3	5'	CGTCCCCCTGGCCTCTCTTCCC 13717	A TCAA
A		TGGGAAGGGA GTTA GACG	

ACCCTTCTCT CGGT CTGC
 C CCCC
 GAM2133 WHSC1L1 5' CGTCCCTCGGCCTCCCCTTCCC 35498 A TTATCAA
 A TGGGAAGGG AG GACG
 ||||| || |||
 ACCCTTCCC TC CTGC
 C CGGCTCC
 GAM2133 FLJ10074 5' TCGTCCCCGGTCCCTCCCCTCC 36285 A A TT AA_
 CCA TGGG AGGG AG ATC GACGA
 ||| ||| || ||| |||
 ACCC TCCC TC TGG CTGCT
 C C CC CCC
 GAM2133 FLJ20195 3' TCTTTATAACTTCCTCCCCA 35223 AA C
 TGGG GGGAAGTTAT AAGA
 ||| ||||| |||
 ACCC TCCTTCAATA TTCT
 C_ T
 GAM2133 FLJ23537 3' CGCCTTCCCAACACCTCCTTCC 88919 AA_ ATC A
 CA TGGGAAGGG GTT AAG CG
 ||||| || ||| |||
 ACCCTTCCT CAA TTC GC
 CCA CCC C
 GAM2133 FLJ30058 3' CTTAGGATTTCCCCCTCCA 59303 AA ATC
 TGGG GGGAAGTT AAG
 ||| ||||| |||
 ACCT CCCTTTAG TTC
 CC GA_
 GAM2133 GSK3A 3' CGTCTCCTCTTCCCTTCCC 96980 TTATCA
 GGGAAGGGAAG AGACG
 ||||| ||| |||
 CCCTTCCCTC TCTGC
 TCC__
 GAM2133 KIAA0427 5' TCGTCCCTCCCTTCCCCTTCCC 29390 _ TTATCAA
 GGGAAGGG AAG GACGA
 ||||| || ||| |||
 CCCTTCCC TTC CTGCT
 C CCTCC__
 GAM2133 KIAA1054 3' TCGCCTCTCAGGCTCCCCTTCC 68971 A ATCA A
 C GGGAAGGG AGTT AG CGA
 ||||| ||| || |||
 CCCTTCCC TCGG TC GCT
 C ACTC C
 GAM2133 KIAA1904 3' TCCTGACACACTCCTTCCC 73876 AA TA A
 GGGAAGGG GT TCA GA
 ||||| || ||| |||
 CCCTTCCT CA AGT CT
 CA C_ C
 GAM2133 TXN2 3' CTCTTGGTCCCTTCC 25932 AGTTA C
 GGAAGGGA TCAAGA G
 ||||| ||||| |

			CCTTCCCT	GGTTCT C		
			_____ A			
GAM2133	LOC157931	3'	TCTCTGTACCTCCCTCCCA	87946	A	A T CA
			TGGGA GGGG GT AT AGA			
			ACCCT CCCT CA TG TCT			
			_ C C TC			
GAM2133	LOC222070	5'	TCATCTCTCCTCCCCTCCCCA	95823	A	A TTATCA C
			TGGG AGGG AG AGA GA			
			ACCC TCCC TC TCT CT			
			C C CTC___ A			
GAM2133	LOC254191	3'	CGTCCTTTTTCCCTTGCCA	96413	G	TTATCAA
			TGG AAGGGAAG GACG			
			ACC TTCCCTTT CTGC			
			G TTC___			
GAM2134	DLEC1	3'	CATCTGGCCCTCCCTTG	24716	A	A C
			CAAGG AGGGC GG GTG			
			GTTCC TCCCG TC TAC			
			C G _			
GAM2134	PIP5K1A	3'	TATCCCACCCTGCCTTGATA	14520	A	CA C
			TATCAAGG AGGG GG GTG			
			ATAGTTCC TCCC CC TAT			
			G A_ C			
GAM2134	SOX11	3'	ACCCACCCCCCCTTG GTA	13308	AA	CA C
			TATCAAGG GGG GG GT			
			ATGGTTCC CCC CC CA			
			CC A_ _			
GAM2134	CHL1	3'	TGTTACCTTTCCTCAATA	22768	CA	CA
			TAT AGGAAGGG GGCG			
			ATA TCCTTTCC TTGT			
			AC A_			
GAM2134	EPB41L1	3'	CATTCTGCCCTTCCCTGA	71104	A	C
			TCA GGAAGGGCAGG GTG			
			AGT CCTTCCCGTCT TAC			
			C _			
GAM2134	FLJ00060	3'	CATACCCCCTGCCCTCCTCTGA	61741	_ A	CGTG
			TCA AGGA GGGCAGG ATG			
			AGT TCCT CCCGTCC TAC			
			C _ CCCA			
GAM2134	FLJ10898	5'	CACCACAGCCCTTTCTCAATA	60126	CA	AGGC
			TAT AGGAAGGGC GTG			

		ATA TCTTTCCCG CAC		
		AC ACAC		
GAM2134	FLJ22557	3' ATCATCCCATCCTTAATA	45581	C A CAGGC
		TAT AAGGA GGG GTGAT		
		ATA TTCCT CCC TACTA		
		A A _____		
GAM2134	KIAA0574	3' CATCCCCTGCCCTCCCCTGA	69808	A A CGT
		TCA GG AGGGCAGG GATG		
		AGT CC TCCCGTCC CTAC		
		C C C__		
GAM2134	KIAA0632	3' CACCTCAGAAACCCTTCCTTGA	32071	CA__ C
		TCAAGGAAGGG GG GTG		
		AGTTCCTTCCC CT CAC		
		AAAGA C		
GAM2134	KIAA1354	5' CAGTGA CTGCCTTCCCTTGATA	61572	A G _
		TATCAAGG AGGGCAG CG TG		
		ATAGTTCC TTCCGTC GT AC		
		C A G		
GAM2134	MGC20460	5' CACCGCCTCCTACCCTTCTT	54901	C__ _
		AGGAAGGG AGGCG TG		
		TTCTTCCC TCCGC AC		
		ATCC C		
GAM2134	LOC158476	3' CACGCCCGCCCCCCCCATTGA	88186	_ AA_ A
		TCAA GG GGGC GGC GTG		
		AGTT CC CCG CCGCAC		
		A CCC C		
GAM2134	LOC90459	3' CACACCCGCTAATTTTTTG	63550	A_ A C
		CAAGGA GGGC GG GTG		
		GTTTTT TCCG CC CAC		
		AA C A		
GAM2135	ADH5	3' GCTTCTGTGATATTATCTTTAA	7267	T TT_
		TTAGGGATAATAT CAT AGC		
		AATTTCTATTATA GTG TCG		
		_ TCT		
GAM2135	AES	3' GTTAGGTGGATACCTGCCCTGA	8525	ATAA
		TTAGGG TATTCATTTAGC		
		AGTCCC ATAGGTGGATTG		
		GTCC		
GAM2135	AGL	3' GCCATTTGGGGTTATCTCTAGT	7215	A TTTA
	A	TATTAGGGATAAT TTCA GC		

			ATGATCTCTATTG GGGT CG		
			— TTAC		
GAM2135	APAF1	3'	GTTGGATGAATAATATTAATG 25979 GG A		
			TA GATA TATTCATTTAGC		
			GT TTAT ATAAGTAGGTTG		
			AA A		
GAM2135	APM1	3'	GCTAAATGGACATCATGTTTTTC 17784 GG TA__ A		
			TGGTG TATTAG A AT TTCATTTAGC		
			GTGGTC T TA AGGTAAATCG		
			TT TGTAC C		
GAM2135	APXL	3'	CTAATGGTTGGCCCTGGTG 9713 A ATTCAT		
			TATTAGGG TAAT TTAG		
			GTGGTCCC GTTG AATC		
			G GT__		
GAM2135	ARF3	3'	GTTGGATGGGTCATCTGTCCTT 9781 — —		
	GGT		ATTAGGGATA AT ATTCATTTAGC		
			TGGTTCCTGT TA TGGGTAGGTTG		
			C C		
GAM2135	BACE	3'	GAAGATGGGTGTTGTTTTCAAT 58086 AG AGC		
	G		TATT GGATAATATTCATTT		
			GTAA TTTGTTGTGGGTAGA		
			CT AG		
GAM2135	BACE	3'	GCTAAGTGTGGAATTACCTGAT 58088 GATAATATT		
	A		TATTAGG CATTTAGC		
			ATAGTCC GTGAATCG		
			ATTAAGGT_		
GAM2135	BACH2	3'	GCTGGATGTTTCAGATTCCTAA 41786 AATATT		
			TTAGGGAT CATTTAGC		
			AATCCTTA GTAGGTCTG		
			GACTT_		
GAM2135	BAZ2A	3'	GCTAGGTGGATTTTCTCT 26512 TAAT		
			AGGGA ATTCATTTAGC		
			TCTCT TAGGTGGATCG		
			TT__		
GAM2135	BCL11A	3'	GCTAAATGTCTGTCTCTAA 43467 ATATT		
			TTAGGGATA CATTTAGC		
			AATCTCTGT GTAAATCG		
			CT__		
GAM2135	C11orf8	3'	GCTAGCACAAAATATTGTCGCT 9624 G CAT__		
	AATA		TATTAG GATAATATT TTAGC		

		ATAATC CTGTTATAA GATCG	
		G AACAC	
GAM2135 C4BPB	5'	GCTGGGTGAATTCAGCCTGG 7389	GATAAT
		TTAGG ATTCATTTAGC	
		GGTCC TAAGTGGGTCG	
		GACCT_	
GAM2135 CAMLG	3'	GCTGAGTTTGTATTACTGA 10002	GG TC
TA		TATTAG ATAATAT ATTTAGC	
		ATAGTC TATTATG TGAGTCG	
		AT TT	
GAM2135 CAT	3'	GCTTAATGTTTATTCCTGATA 10021	TATT T
		TATTAGGGATAA CATT AGC	
		ATAGTCCTTATT GTAA TCG	
		T__ T	
GAM2135 CDKN1A	3'	GTTGAATGAGAGGTTCTTAA 55271	AATA
		TTAGGGAT TTCATTTAGC	
		AATCCTTG GAGTAAGTTG	
		GA__	
GAM2135 CHC1L	3'	GTATGAAGTATTATCTTTGA 8857	_ TTAGC
		TTAGGGATAATATT CAT	
		AGTTTCTATTATGA GTA	
		A TG	
GAM2135 CLN5	3'	GCTAAGTGATCTTTCTCTGG 22431	TAATAT
		TTAGGGA TCATTTAGC	
		GGTCTCT AGTGAATCG	
		TTCT__	
GAM2135 CUL4B	3'	GTTGAGTGGACTTTTCTC 14566	T TA
		GGGA AA TTCATTTAGC	
		CTCT TT AGGTGAGTTG	
		T TC	
GAM2135 CXorf6	3'	GTTGATTTGGGGTTTGTCTTTG 19709	TA T_
ATG		TATTAGGGATAA TTCA TTAGC	
		GTAGTTTCTGTT GGGT AGTTG	
		TG TT	
GAM2135 DAAM2	3'	CTGAGCTGGTCCTTAATA 93902	AATATT _
		TATTAGGGAT CA TTTAG	
		ATAATTCCTG GT GAGTC	
		_____ C	
GAM2135 DAG1	3'	CTGGTGAGATTATTTCTGATG 16554	GG A TAGC
		TATTAG ATAAT TTCATT	

			GTAGTC TATTA GAGTGG	
			TT _ TCC	
GAM2135 DNTT	3'	GCTGAAATACTGTCTATCTCTA 73663	_ TTCA	
ATA		TATTAGGGATA ATA TTTAGC		
		ATAATCTCTAT TGT AAGTCG		
		C CATA		
GAM2135 EIF4G2	3'	GCTAGATTTTAAATATCCTTGA 9219	A TTC	
		TTAGGGATA TA ATTTAGC		
		AGTTCCTAT AT TAGATCG		
		A TT_		
GAM2135 EYA4	3'	GCTGAATGGAGTTAAACTTTAG 15885	ATAATA	
TG		TATTAGGG TTCATTTAGC		
		GTGATTTC AGGTAAGTCG		
		AAATTG		
GAM2135 EZH1	3'	GCTAAGTGAAGTGTGGTCCCTG 10552	A _	
G		TTAGGGAT ATATT CATTTAGC		
		GGTCCCTG TGTGA GTGAATCG		
		G A		
GAM2135 FBXL7	3'	GCTGGATGCTGTCGTCTCTG 25496	TA TT	
		TAGGGA ATA CATTTAGC		
		GTCTCT TGT GTAGGTCG		
		GC C_		
GAM2135 FLRT2	3'	TTGAATGGAATTATTTTTGATA 26007	A C	
		TATTAGGGATAAT TTCATTTAG		
		ATAGTTTTTATTA AGGTAAGTT		
		-		
GAM2135 FMR2	3'	GCTGTAGTGTGTCTTTGATA 10696	CATT	
		TATTAGGGATAATATT TAGC		
		ATAGTTTCTGTTGTGA GTCG		
		T__		
GAM2135 FZD3	3'	GCTAAATGAAGCATGATTAGTC 34258	GA A__	
TTAGTA		TATTAGG TAAT TTCATTTAGC		
		ATGATTTC ATTA AAGTAAATCG		
		TG GTACG		
GAM2135 FZD7	3'	GCTGGGTGGGGGCCTGTTTCTG 14504	GG ATA_	
		TAG ATA TTCATTTAGC		
		GTC TGT GGGTGGGTCG		
		TT CCGG		
GAM2135 GALNT3	3'	GCTAAATGTAAC TTATTCCAAG 16826	A TATT	
TG		TATT GGGATAA CATTTAGC		

			GTGA CCTTATT GTAAATCG		
			A CAAT		
GAM2135	GAN	3'	GTTAGTCTCCATTATTTCCTAG 42122	TATTCAT	
	TA		TATTAGGGATAA TTAGC		
			ATGATCCTTATT GATTG		
			TACCTCT		
GAM2135	GPLD1	3'	GCTGGAGGCCATTATCCTTCAT 93660	T AT A	
	A		TAT AGGGATAAT TC TTTAGC		
			ATA TTCCTATTA GG AGGTCG		
			C CC _		
GAM2135	GRINL1A	3'	GTTAGGTGAAAGTGTTTTTGA 70069	ATA	
			TTAGGGATA TTCATTTAGC		
			AGTTTTTGT AAGTGGATTG		
			GA_		
GAM2135	HSPG2	3'	TGGGAATTGTCTTTAGTG 19841	A	
			TATTAGGGATAAT TTCA		
			GTGATTTCTGTGA GGGT		
			A		
GAM2135	KCND2	3'	GCTGAGTGTTTCATGTTCCATGG 25383	_ ATATT	
	TG		TATTA GGGATA CATTTAGC		
			GTGGT CTTGT GTGAGTCG		
			A ACTT_		
GAM2135	KCNK2	3'	ATGAATGAGAATTGTTTCTGGT 27237	GG A GC	
	A		TATTAG ATAAT TTCATTTA		
			ATGGTC TGTGA GAGTAAGT		
			TT A AA		
GAM2135	LMCD1	3'	GTTGGGTGGTGGTAGATCCTTG 28150	AATAT_	
	A		TTAGGGAT TCATTTAGC		
			AGTTCCTA GGTGGGTTG		
			GATGGT		
GAM2135	NBS1	3'	GCTGGGTGGGTGTCTGTTTTGA 70026	ATA	
			TTAGGG ATATTCATTTAGC		
			AGTTTT TGTGGGTGGGTCG		
			GTC		
GAM2135	NDST2	3'	CTAGAAATGTCCTTAATA 14664	ATATTCA	
			TATTAGGGATA TTTAG		
			ATAATTCCTGT AGATC		
			AA_____		
GAM2135	NEB	3'	GCTAATGCTTATTATTTCTAAT 17008	GG TT T	
			ATTAG ATAATA CATT AGC		

		TAATC TATTAT GTAA TCG	
		TT TC _	
GAM2135 NEB	3'	GCTTCTGCAATATTATTTCTG 17009	GG _ TTT
		TAG ATAATATT CA AGC	
		GTC TATTATAA GT TCG	
		TT C CT_	
GAM2135 NRXN1	5'	GCTAAATGGATTTACCTAGTG 17825	GATAAT
		TATTAGG ATTCATTTAGC	
		GTGATCC TAGGTAAATCG	
		ATT__	
GAM2135 NSF	3'	GTAAATGAGCTTAATGTCTTT 63750	A _
G		TAGGGATA TA TTCATTTAGC	
		GTTTCTGT AT GAGTAAATTG	
		A TC	
GAM2135 NTSR1	3'	GCTGGATGAGACTGTCCT 11858	ATA
		GGGATA TTCATTTAGC	
		TCCTGT GAGTAGGTCG	
		CA_	
GAM2135 OGG1	3'	CTAGATGGGGCACCCCTGG 34156	ATAATA
		TTAGGG TTCATTTAG	
		GGTCCC GGGTAGATC	
		ACG__	
GAM2135 PCDH12	5'	GTAAAGTGAAGTGTCCCAGATG 33888	A TAT
		TATT GGGATAA TCATTTAGC	
		GTAG CCCTGTT AGTGAATTG	
		A C_	
GAM2135 PIN4	3'	GCTAAGTGAATGTCAACTGTAG 21711	G ATA
TA		TATTA GG ATATTCATTTAGC	
		ATGAT TC TGTAAGTGAATCG	
		G AAC	
GAM2135 PMX1	3'	GTAAAGATATTTGTTGTCTTT 23572	TTCA__
GA		TTAGGGATAATA TTTAGC	
		AGTTTCTGTTGT AAATTG	
		TTATAG	
GAM2135 PMX1	3'	GTAAAGATATTTGTTGTCTTT 23573	TTCA__
GA		TTAGGGATAATA TTTAGC	
		AGTTTCTGTTGT AAATTG	
		TTATAG	
GAM2135 PPARGC1	3'	ACCATGGTGTGTTCTTGATG 26075	T TTAGC
		TATTAGGGATAATAT CAT	

			GTAGTTCTTGTTGTG GTA		
			— CCAG		
GAM2135	PPID	3'	TCTATGAATATGATCCCTAATG 88830	A	TTAGC
			TATTAGGGAT ATATTCAT		
			GTAATCCCTA TATAAGTA		
			G TCTG		
GAM2135	PTPN7	5'	GCTGAGTGAGCCTCCCCTGG 55463	ATAATA	
			TTAGGG TTCATTTAGC		
			GGTCCC GAGTGAGTCG		
			CTCC—		
GAM2135	QDPR	3'	GTTATTCAGAATGTTGTTCTTA 6147	ATT—	
	ATA		TATTAGGGATAATATTC TAGC		
			ATAATCCTTGTTGTAAG ATTG		
			ACTT		
GAM2135	RBL2	3'	GCTAAACATCCAATATTTTCTT 20041	T CA—	
	TAATG		TATTAGGGA AATATT TTTAGC		
			GTAATTTCT TTATAA AAATCG		
			T CCTAC		
GAM2135	RBM8A	3'	GCTGAAATGATTTTCCTGGTA 18810	TAATAT	—
			TATTAGGGA TCATT TAGC		
			ATGGTCCTT AGTAA GTCG		
			TT— A		
GAM2135	RECK	3'	GTAAAAATGTGTTGTTCCAAAT 41199	A TCA	
	A		TATT GGGATAATAT TTTAGC		
			ATAA CCTTGTTGTG AAATTG		
			A TA—		
GAM2135	RGL	3'	GTAAAGTGACACTTTTGTCTCT 31429	T TAT—	
	CATA		TAT AGGGATAA TCATTTAGC		
			ATA TCTCTGTT AGTGAATTG		
			C TTCAC		
GAM2135	RHAG	3'	ATGAATATTATTCTTAAT 6153		
			ATTAGGGATAATATTCAT		
			TAATTCTTATTATAAGTA		
GAM2135	ROCK2	3'	GTTGGAACATAATATATCCTTGA 66624	A CA—	
	TG		TATTAGGGATA TATT TTTAGC		
			GTAGTTCCTAT ATAA AGGTTG		
			— TCA		
GAM2135	RP42	3'	AGATGAAGATTATCTTTAGTG 40564	A	
			TATTAGGGATAAT TTCATTT		

			GTGATTTCTATTA AAGTAGA		
			G		
GAM2135	SART2	3'	TGAATGAATATTTCCCTTGATG 26253	T	GC
			TATTAGGGA AATATTCATTTA		
			GTAGTTCCT TTATAAGTAAGT		
			— A		
GAM2135	SDPR	3'	GTAAAGCTGTATTTTTCTTAA 17401	T	TCA
	TA		TATTAGGGA AATAT TTTAGC		
			ATAATTCTT TTATG AAATTG		
			T TCG		
GAM2135	SEL1L	3'	GCTGAATGAATCCAATTTTTTA 18603	TAAT_	
	ATG		TATTAGGGA ATTCATTTAGC		
			GTAATTTTT TAAGTAAGTCG		
			TAACC		
GAM2135	SEL1L	3'	GCTGGATATTTTTGTTTCTGA 18604	GG	TATTC
			TTAG ATAA ATTTAGC		
			AGTC TGTT TAGGTCG		
			TT TTA__		
GAM2135	SERPINA3	3'	GCTGGATGCCTGGGTCTCTGG 61821	AATATT	
			TTAGGGAT CATTTAGC		
			GGTCTCTG GTAGGTCG		
			GGTCC_		
GAM2135	SERPINB5	3'	GTTGGGTGGATAAGCTATCCCT 12072	A__	
	G		TAGGGATA TATTCATTTAGC		
			GTCCCTAT ATAGGTGGGTTG		
			CGA		
GAM2135	SLC20A2	3'	GCTGGATGGAGTATTTCTCTGA 23118	T	_
			TTAGGGA AATATTC ATTTAGC		
			AGTCTCT TTATGAG TAGGTCG		
			— G		
GAM2135	SLC6A6	3'	GCTGAATGAGGAGGCCCTA 13184	ATAATA	
			TAGGG TTCATTTAGC		
			ATCCC GAGTAAGTCG		
			GGAG__		
GAM2135	SNX6	3'	GTTAGTGACAGTTATTCCTGA 41443	AT	T
			TTAGGGATAAT TCATT AGC		
			AGTCCTTATTG AGTGA TTG		
			AC _		
GAM2135	SOCS5	3'	GTAAATGGAAATTGTTTTAAA 26684	AG	A
	TG		TATT GGATAAT TTCATTTAGC		

			GTAA TTTGTTA AGGTAAATTG		
			AT A		
GAM2135 SOX12	3'	CTGGATGGATGTTTCTGA	23685	GG AAT	
		TTAG AT ATTCATTTAG			
		AGTC TG TAGGTAGGTC			
		TT ____			
GAM2135 SPAP1	5'	GTTGAGAAAATTATCTCTAA	57835	A AT	
		TTAGGGATAAT TTC TTAGC			
		AATCTCTATTA AAG AGTTG			
		A ____			
GAM2135 SPAP1	5'	GTTGAGAAAATTATCTCTAA	57836	A AT	
		TTAGGGATAAT TTC TTAGC			
		AATCTCTATTA AAG AGTTG			
		A ____			
GAM2135 SSPN	3'	GCTGAATCTCTTTATTTTCCCT	18684	T TTC__	
		GGTA TATTAGGGA AATA ATTTAGC			
		ATGGTCCCT TTAT TAAGTCG			
		T TTCTC			
GAM2135 STK31	3'	TGAGTTGTATCTTTAGTA	53079	AT	
		TATTAGGGATA ATTCA			
		ATGATTCTAT TGAGT			
		GT			
GAM2135 SURF5	3'	GCTAGGTGGGACTCATTCTAA	56915	AATA	
		ATTAGGGAT TTCATTTAGC			
		TAATCCTTA GGGTGGATCG			
		CTCA			
GAM2135 SURF5	3'	GCTAGGTGGGACTCATTCTAA	56916	AATA	
		ATTAGGGAT TTCATTTAGC			
		TAATCCTTA GGGTGGATCG			
		CTCA			
GAM2135 SYT1	3'	GCTAAAGATTTATTTCTAGT	20113	GG TAT A	
		ATTAG ATAA TC TTTAGC			
		TGATC TATT AG AAATCG			
		TT T__ _			
GAM2135 TSN	3'	GCTTTCTGATGTTGCCTTAATA	17302	A T TTT	
		TATTAGGG TAATAT CA AGC			
		ATAATTCC GTTGTA GT TCG			
		_ _ CTT			
GAM2135 UBL3	3'	GTAAATGAAGTTTCCTCATA	24025	T TAATA	
		TAT AGGGA TTCATTTAGC			

		ATA TCCTT AAGTAAATTG	
		C TG__	
GAM2135 VBP1	3'	GCTGGGTGATACAGATTCTGAT 14030	ATAATAT
A		TATTAGGG TCATTTAGC	
		ATAGTCTT AGTGGGTCG	
		AGACAT_	
GAM2135 WHSC1L1	3'	GCTGGATGGGTACAGCTTAA 35500	GATAA
		TTAGG TATTCATTTAGC	
		AATTC ATGGGTAGGTCG	
		GAC__	
GAM2135 XPR1	3'	GCTGGGTGGGTGGGAAATATGA 17622	GGGATAA
TG		TATTA TATTCATTTAGC	
		GTAGT GTGGGTGGGTCG	
		ATAAAGG	
GAM2135 ZNF255	5'	TGAATAGTATTCCATGGTG 20499	_ A
		TATTA GGGATA TATTCA	
		GTGGT CCTTAT ATAAGT	
		A G	
GAM2135 A4GALT	3'	GCTGGGTGGGGAGGCTCTTTAG 34301	TAATA
		TTAGGGA TTCATTTAGC	
		GATTCT GGGTGGGTCG	
		CGGAG	
GAM2135 AKAP8	3'	CTGAATCAGTTCTCTAATA 20734	TAAT C
		TATTAGGGA ATT ATTTAG	
		ATAATCTCT TGA TAAGTC	
		__ C	
GAM2135 AKAP8	3'	GCTGAAGTACATTGTCCTTAG 20736	ATTCA
		TTAGGGATAAT TTTAGC	
		GATTCCTGTTA AAGTCG	
		CATG_	
GAM2135 ALLC	5'	ATTTTGTGAATATTATCTTTTG 37978	T TTAGC
TA		TAT AGGGATAATATTCAT	
		ATG TTTCTATTATAAGTG	
		T TTTAG	
GAM2135 ARG99	3'	GCTAAGTGAGCTTTATCT 50012	TA
		GGATAA TTCATTTAGC	
		TCTATT GAGTGAATCG	
		TC	
GAM2135 C1orf9	3'	TGGGTATTGTTTGTAATG 33162	G
		TATTA GGATAATATTCA	

		GTAAT TTTGTTATGGGT	
		G	
GAM2135	C20orf126 3'	GCTGAATGAAGAACAGAATCTT 48734	ATAATA__
		GGTG TATTAGGG TTCATTTAGC	
		GTGGTTCT AAGTAAGTCG	
		AAGACAAG	
GAM2135	C20orf142 3'	GTTAGGCACTTTTTGTCCCTGG 75287	TATTCA
		TA TATTAGGGATAA TTTAGC	
		ATGGTCCCTGTT GGATTG	
		TTTCAC	
GAM2135	C6.1A 3'	GCTAGGTGACAAGTTCTTGG 44533	AATAT
		TTAGGGAT TCATTTAGC	
		GGTTCTTG AGTGGATCG	
		AAC__	
GAM2135	C8orf4 3'	TGAGTATTGTCTATTGGTA 39692	_
		TATTAG GGATAATATTCA	
		ATGGTT TCTGTTATGAGT	
		A	
GAM2135	CAMKK2 3'	CTAGATGTGGCTCCTAGTG 22619	ATAATATT
		TATTAGGG CATTTAG	
		GTGATCCT GTAGATC	
		CGGT_____	
GAM2135	CBX8 3'	GTTGGAAAGATTATCTCTAG 40610	ATTCA
		TTAGGGATAAT TTTAGC	
		GATCTCTATTA AGGTTG	
		GAA__	
GAM2135	CDC14A 3'	ATGGTTTTGTCTCTAATG 53965	TAT
		TATTAGGGATAA TCAT	
		GTAATCTCTGTT GGTA	
		TT_	
GAM2135	CLIC2 3'	ATGAGTTTATTTCTGATA 8914	GG T
		TATTAG ATAA ATTCAT	
		ATAGTC TATT TGAGTA	
		TT _	
GAM2135	CPR2 3'	GCTGAGTGAAAGGCACCCTGA 48834	ATAATA
		TTAGGG TTCATTTAGC	
		AGTCCC AAGTGAGTCG	
		ACGGA_	
GAM2135	DCTD 3'	GCTGAATAATGAGTTGTTCTA 10392	_ C
		G TTAGGGATAAT ATT ATTTAGC	

			GATCCTTGTTG TAA TAAGTCG	
			AG _	
GAM2135	DDM36	3'	GTTAGGGTCTTTACTCCCTAAT 40928	_ TATTCA
	G		TATTAGGGA TAA TTTAGC	
			GTAATCCCT ATT GGATTG	
			C TCTG__	
GAM2135	DJ667H12.2	3'	GCTAGATGAAATGGCTTAATG 39478	GATA A
			TATTAGG AT TTCATTTAGC	
			GTAATTC TA AAGTAGATCG	
			GG__ _	
GAM2135	DKFZP434A0225	3'	GCTAGGTGGAGTATGCTTGATA 95524	G ATA
			TATTAGG ATA TTCATTTAGC	
			ATAGTTC TAT AGGTGGATCG	
			G G__	
GAM2135	DKFZP434H0820	3'	GTTGGGTGGGCCCTCCCTGA 64585	TAATA
			TTAGGGA TTCATTTAGC	
			AGTCCCT GGGTGGGTTG	
			CCC__	
GAM2135	DKFZP564O0523	3'	GCTAAGTTTGTGTTTTTTT 50421	T TC__
	GTA		TATTAGGGA AATAT ATTTAGC	
			ATGATTTTT TTGTG TGAATCG	
			T TTT	
GAM2135	DKFZP761E2110	3'	GAGTATTTATTCCTAATA 48963	_
			TATTAGGGATAA TATTC	
			ATAATCCTTATT ATGAG	
			T	
GAM2135	DKFZP761F241	3'	GCTGAGTAATTGTTTCTAATG 49582	GG ATTC
			TATTAG ATAAT ATTTAGC	
			GTAATC TGTTA TGAGTCG	
			TT A__	
GAM2135	DKFZP761F241	3'	GCTGAGTAATTGTTTCTAATG 49583	GG ATTC
			TATTAG ATAAT ATTTAGC	
			GTAATC TGTTA TGAGTCG	
			TT A__	
GAM2135	DKFZp761G0313	3'	AAATGAAATTATCTTTGATA 66390	A
			TATTAGGGATAAT TTCATTT	
			ATAGTTTCTATTA AAGTAAA	
			-	
GAM2135	DKFZp761O132	5'	GCTGGATGGATGTTTGTTGA 51170	G TA
			TTAG GA ATATTCATTTAGC	

AGTT TT TGTAGGTAGGTCG
 G _
 GAM2135 EIF2S1 3' GCTGAATATTTTTTATTTCTAA 15847 GG TATTC
 TTAG ATAA ATTTAGC
 ||| ||| |||||
 AATC TATT TAAGTCG
 TT TTTA
 GAM2135 ENPP4 3' GTTAAGTGGCAGAATAGCCTTA 30718 ATAATAT_
 GTG TATTAGGG TCATTTAGC
 ||||| |||||
 GTGATTCC GGTGAATTG
 GATAAGAC
 GAM2135 ERAP140 3' GTTGAATGCAATTTTTATTTTT 75707 T_ _
 GGTA TATTAGGGATAA ATT CATTTAGC
 ||||| ||| |||||
 ATGGTTTTTATT TAA GTAAGTTG
 TT C
 GAM2135 FBX30 3' CTAGATGGGTACCAGGTG 53745 TA GATAA
 TAT GG TATTCATTTAG
 ||| || |||||
 GTG CC ATGGGTAGATC
 GA _
 GAM2135 FLJ10300 3' ATGAATATTTCTTTGGTA 36468 T
 TATTAGGGA AATATTCAT
 ||||| |||||
 ATGGTTTCT TTATAAGTA
 _
 GAM2135 FLJ10375 5' GTTGAATGAATGTCTGGCTC 36560 ATA_
 GGG ATATTCATTTAGC
 ||| |||||
 CTC TGTAAGTAAGTTG
 GGTC
 GAM2135 FLJ10656 3' GTTAGGTGGATAGTCCTGTAGT 36909 _ AA
 G TATTA GGGAT TATTCATTAGC
 ||||| ||||| |||||
 GTGAT TCCTG ATAGGTGGATTG
 G _
 GAM2135 FLJ10980 3' GTGATGTTTGTCTCTAGTG 65254 TAT
 TATTAGGGATAA TCAT
 ||||| |||
 GTGATCTCTGTT AGTG
 TGT
 GAM2135 FLJ11149 3' GCTAAATGCTATCTTTAG 37687 ATATT
 TTAGGGATA CATTTAGC
 ||||| |||||
 GATTTCTAT GTAAATCG
 C_
 GAM2135 FLJ12649 3' GCTGTCAGATTGTTTCTAATA 45094 GG ATTCATT
 TATTAG ATAAT TAGC
 ||||| ||| |||

			ATAATC TGTTA GTCG		
			TT GACT__		
GAM2135	FLJ12787	3'	TCTGGGATGGATATTAATTTTA 50698	A	AGC
			ATA TATTAGGG TAATATTCATTT		
			ATAATTTT ATTATAGGTAGG		
			A GTCTA		
GAM2135	FLJ12892	3'	GCTGAATGTTGTGTTATCACTA 68453	G	T_
			ATA TATTAG GATAATAT CATTTAGC		
			ATAATC CTATTGTG GTAAGTCG		
			A TT		
GAM2135	FLJ13194	3'	GTTGGAACATTGTTATCCTTG 47873		TTCA
			TAGGGATAATA TTTAGC		
			G TTCCTATTGT AGGTTG		
			TACA		
GAM2135	FLJ13657	3'	GTTAGATGAGTATTTAGCTGTG 46140	G	AT_
			TA GG AATATTCATTTAGC		
			GT TC TTATGAGTAGATTG		
			G GAT		
GAM2135	FLJ13769	3'	GCTGGGTGGCCTGGCCCTGGTA 47257		ATAATAT
			TATTAGGG TCATTTAGC		
			ATGGTCCC GGTGGGTCG		
			GGTCC__		
GAM2135	FLJ14600	3'	TTAGGTGCTGGTTCCTAG 52530		AATATT
			TTAGGGAT CATTTAG		
			GATCCTTG GTGGATT		
			GTC__		
GAM2135	FLJ14668	3'	GCTGTGATATATTTTCCTAGTG 52588	T	_ TT
			TATTAGGGA AATAT TCAT AGC		
			GTGATCCTT TTATA AGTG TCG		
			_ T _		
GAM2135	FLJ14735	3'	TTGAGTGGAATTCCTGGGTA 52670	TA	TAAT
			TAT GGGA ATTCATTTAG		
			ATG TCCT TAGGTGAGTT		
			GG _		
GAM2135	FLJ20127	3'	GCTAAATGAGATGTTTCTAAT 35080	GG	ATA
			ATTAG ATA TTCATTTAGC		
			TAATC TGT GAGTAAATCG		
			TT A_		
GAM2135	FLJ20436	3'	GCTAGGTGGGAGCTGTCTTTG 35626		ATA
			TAGGGATA TTCATTTAGC		

GTTTCTGT GGGTGGATCG
 CGA
 GAM2135 FLJ20986 5' GCTAGGTGGATGGATGTT 44837 A_
 GATA TATTCATTTAGC
 |||| |||||
 TTGT GTAGGTGGATCG
 AG
 GAM2135 FLJ21596 3' GCTGAGTGGATGGTTGCTGA 46117 G AA
 TTAG GAT TATTCATTTAGC
 |||| || |||||
 AGTC TTG GTAGGTGAGTCG
 G _
 GAM2135 FLJ21615 3' AACTTGAATTTATCTTTGATA 50806 T TTTAGC
 TATTAGGGATAA ATTCA
 ||||| ||||
 ATAGTTTCTATT TAAGT
 _ TCAAA
 GAM2135 FLJ22969 3' GCTGAGTGTGTTGTTTCTA 69210 GG TATT
 TAG ATAA CATTTAGC
 || ||| |||||
 ATC TGTT GTGAGTCG
 TT T__
 GAM2135 FLJ23024 3' GTTGAATGAGTGAGATGTTTAG 46847 G AA
 TTAGG AT TATTCATTTAGC
 |||| || |||||
 GATTT TA GTGAGTAAGTTG
 G GA
 GAM2135 FLJ23058 3' GCTGGGTTCCGCTTTGTCCCTG 45526 TATTC_
 GT ATTAGGGATAA ATTTAGC
 ||||| |||||
 TGGTCCCTGTT TGGGTCG
 TCGCCT
 GAM2135 FLJ23416 3' GTTAAATGCTCTGGGTTTTCTC 50934 T ATT__
 TGATA TATTAGGGA AAT CATTTAGC
 ||||| || |||||
 ATAGTCTCT TTG GTAAATTG
 T GGTCTC
 GAM2135 FLJ23560 3' GTTGAATAAAACAGTGTTATCT 45509 C____
 TTAAT ATTAGGGATAATATT ATTTAGC
 ||||| |||||
 TAATTTCTATTGTGA TAAGTTG
 CAAAA
 GAM2135 GENX-3414 3' GCTGAGTGAGGTGGCCTGAATG 15457 A ATAATA
 TATT GGG TTCATTTAGC
 |||| || |||||
 GTAA TCC GAGTGAGTCG
 G GGTG__
 GAM2135 GMPPB 5' GCTGCTCTGTACTGTCCCTGGT 26223 A TCATT
 G TATTAGGGATA TAT TAGC
 ||||| || ||||

		GTGGTCCCTGT ATG GTCG	
		C TCTC_	
GAM2135 HSJ1	3'	GCTGGGCTTTTGTGCCCTGGTA 23082	_ TATTCA
		TATTAGGG ATAA TTTAGC	
		ATGGTCCC TGTT GGGTCG	
		G TTC__	
GAM2135 HSPC228	3'	GTTAATAATTTATTTCCCTAAT 33649	T TTCAT
A		TATTAGGGA AATA TTAGC	
		ATAATCCCT TTAT AATTG	
		_ TTAAT	
GAM2135 IPLA2(GAMMA)	5'	GCTGAGTGGGTGGCGACCTAG 61341	GATAA
		TTAGG TATTCATTTAGC	
		GATCC GTGGGTGAGTCG	
		AGCG_	
GAM2135 ITGB8	3'	GCTAGATGAATAAATGATTCGT 11056	G AA__
G		TA GGAT TATTCATTTAGC	
		GT CTTA ATAAGTAGATCG	
		G GTAA	
GAM2135 KALI	3'	GTTGGATGGGCCCATCCTGATA 54696	ATAATA
		TATTAGGG TTCATTTAGC	
		ATAGTCCT GGGTAGGTTG	
		ACCC__	
GAM2135 KIAA0161	3'	GTTGAGTGGACGGACTTATTCC 29208	TA__
TG		TAGGGATAA TTCATTTAGC	
		GTCCTTATT AGGTGAGTTG	
		CAGGC	
GAM2135 KIAA0226	3'	CTGGGTCCTTCCCTGGTG 64258	TAATATTC
		TATTAGGGA ATTTAG	
		GTGGTCCCT TGGGTC	
		TCC__	
GAM2135 KIAA0321	3'	GCTGAAGTCAGTGTCTCTGGTG 63055	ATATTCA
		TATTAGGGATA TTTAGC	
		GTGGTCTCTGT AAGTCG	
		GA CTG__	
GAM2135 KIAA0416	3'	CTGAGTGA CTCTTTAATA 32091	TAATAT
		TATTAGGGA TCATTTAG	
		ATAATTTCT AGTGAGTC	
		C__	
GAM2135 KIAA0459	3'	GTTAGGTGGATGTGAACTTAA 61658	GATA
		TTAGG ATATTCATTTAGC	

		AATTC TGTAGGTGGATTG		
		AAG_		
GAM2135 KIAA0711	3'	GTTAGATGAGGCTATTGCCTTG 30153	A	__
		ATG TATTAGGG TAATA TTCATTTAGC		
		GTAGTTCC GTTAT GAGTAGATTG		
		_ CG		
GAM2135 KIAA0769	3'	GCTAGCCAAATTGTCCTTGA 29757	ATTCAT	
		TTAGGGATAAT TTAGC		
		AGTTCCTGTTA GATCG		
		AACC__		
GAM2135 KIAA0794	3'	GTTATAGGATATGGTTTCTAAT 81237	GG A	ATT
		G TATTAG AT ATATTC TAGC		
		GTAATC TG TATAGG ATTG		
		TT G AT_		
GAM2135 KIAA0820	3'	GTTGAATGAAGTCTGAAACTCT 69591	ATAATA__	
		AGTA TATTAGGG TTCATTTAGC		
		ATGATCTC AAGTAAGTTG		
		AAAGTCTG		
GAM2135 KIAA0841	3'	GCTTTCCCATGTAGTCCTTAGT 71897	A	TCATTT
		G TATTAGGGAT ATAT AGC		
		GTGATTCCTG TGTA TCG		
		A CCCTT_		
GAM2135 KIAA1116	3'	GTTGGGTGAATTTTGTTTT TAG 30304	T	
		TTAGGGATAA ATTCATTTAGC		
		GATTTTGT TAAAGTGGGTTG		
		T		
GAM2135 KIAA1165	3'	GCTAAAACAATATTATTTCCAG 67994	A GG	CA
		TA TATT G ATAATATT TTTAGC		
		ATGA C TATTATAA AAATCG		
		C TT CA		
GAM2135 KIAA1229	3'	GCTAAATGAATGTATATT 62755	_	
		GATA ATATTCATTTAGC		
		TTAT TGTAAGTAAATCG		
		A		
GAM2135 KIAA1350	3'	GCTAAATGGATAAACCTCATA 73087	T	GATAA
		TAT AGG TATTCATTTAGC		
		ATA TCC ATAGGTAAATCG		
		C AA__		
GAM2135 KIAA1372	3'	GTTGGGTGAAGTGCCCTGA 93321	ATAATA	
		TTAGGG TTCATTTAGC		

		AGTCCC AAGTGGGTTG	
		GTG__	
GAM2135 KIAA1486	3'	TGAATATTGATGTCCTTA 67981	___
		TAGGGATA ATATTCA	
		ATTCCTGT TATAAGT	
		AGT	
GAM2135 KIAA1546	3'	GCTAAGAAAATGGTGTCTTTAA 68499	A CA
	TA	TATTAGGGATA TATT TTTAGC	
		ATAATTCTGT GTAA GAATCG	
		G AA	
GAM2135 KIAA1554	3'	GTTAGAGGCAGTATCCTTAATA 96860	ATATTCA
		TATTAGGGATA TTTAGC	
		ATAATTCCTAT AGATTG	
		GACGG__	
GAM2135 KIAA1557	3'	GCTTTAATGTTATCTTTGA 61786	CATTT
		TTAGGGATAATATT AGC	
		AGTTTCTATTGTAA TCG	
		TT__	
GAM2135 KIAA1822	3'	GTTGAGTGGGCATCTTCCT 68196	TA A
		GGGA AT TTCATTTAGC	
		TCCT TA GGGTGAGTTG	
		TC C	
GAM2135 KIAA1867	3'	GCTGAGTGCGCTGTGCTTAGTG 96483	G ATATT
		TATTAGG ATA CATTTAGC	
		GTGATTC TGT GTGAGTCG	
		G CGC__	
GAM2135 KIAA1878	3'	GCTGAGTGAGAAGTCTTTTGTA 93369	T AATA
		TAT AGGGAT TTCATTTAGC	
		ATG TTTCTG GAGTGAGTCG	
		T AA__	
GAM2135 KIAA1957	3'	GCTGACTGGAGTATTATTTTC 76215	T AT_
	ATG	TAT AGGGATAATATTC TTAGC	
		GTA TTTTATTATGAG AGTCG	
		C GTC	
GAM2135 KREMEN	3'	GCTAGATGGATGTGTACCTGGT 50235	GATA
	G	TATTAGG ATATTCATTTAGC	
		GTGGTCC TGTAGGTAGATCG	
		ATG__	
GAM2135 LANO	3'	TAAATGATGTCTCTGATG 47975	ATAT
		TATTAGGGATA TCATTTA	

GTAGTCTCTGT AGTAAAT

GAM2135 LCHN 3' GCTGGGCTGCCCTGTTGTTTCCT 87473 TT_ _
GA TTAGGGATAATA CA TTTAGC
||||||| || |||||
AGTCCTTGTTGT GT GGGTCG
CCC C

GAM2135 LGP2 5' GTTAAGTGGGACTGCCCTGG 44380 ATAATA
TTAGGG TTCATTTAGC
||||| |||||
GGTCCC GGGTGAATTG
GTCA_

GAM2135 LRMP 5' GCTGGATGCCTTATCTCTGG 21586 TATT
TTAGGGATAA CATTTAGC
||||||| |||||
GGTCTCTATT GTAGGTCG
CC_

GAM2135 LY6G6C 3' GCTTCTGTGTTGTCCCCAGTG 48273 A TCATT
TATT GGGATAATAT AGC
||| ||||| |||
GTGA CCCTGTTGTG TCG
C TCT_

GAM2135 MARK2 5' GCTGAATGGAAGTCGCTGGTA 66222 G AATA
TATTAG GAT TTCATTTAGC
||||| ||| |||||
ATGGTC CTG AGGTAAGTCG
G A_

GAM2135 MGC10981 3' GCTGAGTGTCTCATGTCTTAAT 51986 ATAATATT
G TATTAGGG CATTTAGC
||||||| |||||
GTAATTCT GTGAGTCG
GTAATTCT_

GAM2135 MGC12217 5' GTTGAATGAATGTCTGGCTC 52288 ATA_
GGG ATATTCATTTAGC
||| |||||
CTC TGTAAGTAAGTTG
GGTC

GAM2135 MGC12921 5' CTGAGTTCCTGTCCCTGA 64514 ATATTC
TTAGGGATA ATTTAG
||||||| |||||
AGTCCCTGT TGAGTC
CCT_

GAM2135 MGC12945 5' GCTAAGTGGTCGGTTCCTGG 51267 AATAT
TTAGGGAT TCATTTAGC
||||||| |||||
GGTCCTTG GGTGAATCG
GCT_

GAM2135 MGC16142 5' GCTAAATGGGTCGTGTTTCT 52265 GG AT_
GA TTAG ATA ATTCATTTAGC
||| ||| |||||

			AGTC TGT TGGGTAAATCG		
			TT GTGC		
GAM2135	MGC4268	3'	GCTGAGTGTTCCTTTGTCCTT 49544	TATT__	
	GG		TTAGGGATAA CATTAGC		
			GGTTCCTGTT GTGAGTCG		
			TCCTTT		
GAM2135	MGC4643	3'	GTTGAAGGAATATTGTTTCTAA 52146	GG A	
			TTAG ATAATATTC TTTAGC		
			AATC TGTTATAAG AAGTTG		
			TT G		
GAM2135	NCKX3	3'	GTTGAATGTTTCTGTCTGTGGT 40727	G ATATT	
	G		TATTA GGATA CATTAGC		
			GTGGT TCTGT GTAAGTTG		
			G CTTT_		
GAM2135	NEK1	3'	ATGTATATTATTTCTAATA 97560	GG T	
			TATTAG ATAATAT CAT		
			ATAATC TATTATA GTA		
			TT T		
GAM2135	POLYDOM	3'	GCTAGCATTGTTGTTCTTGGT 44687	TTCAT	
			ATTAGGGATAATA TTAGC		
			TGGTTCTTGTTGT GATCG		
			TAC__		
GAM2135	PPM1A	3'	GCTGGGCCTGCTGCTGTTTCTA 41009	ATATTCA_	
	GTA		TATTAGGGATA TTTAGC		
			ATGATCCTTGT GGGTCG		
			CGTCGTCC		
GAM2135	PPP1R10	3'	GCTAAGTTCATTATTCCTCATG 12231	T ATTC	
			TAT AGGGATAAT ATTTAGC		
			GTA TCCTTATTA TGAATCG		
			C CT__		
GAM2135	PRO0159	5'	GCTGGGTGGGTATAGGCT 26947	ATA	
			GG ATATTCATTTAGC		
			TC TATGGGTGGGTCTG		
			GGA		
GAM2135	PRO1430	3'	TGAGTATTGTCTATTGGTA 38357	_	
			TATTAG GGATAATATTCA		
			ATGGTT TCTGTTATGAGT		
			A		
GAM2135	PSMD10	3'	GTGTTGTTGTCCCCAGTG 12533	A TT	
			TATT GGGATAATA CAT		

			GTGA CCCTGTTGT GTG	
			C T_	
GAM2135	RAB40A	5'	GTTGGGTGAATATTATTTATGA 56016	GG
			TTA GATAATATTCATTTAGC	
			AGT TTATTATAAGTGGGTTG	
			AT	
GAM2135	RBM11	3'	TGCATATTGTTTCCTAATG 59239	T
			TATTAGGGATAATAT CA	
			GTAATCCTTGTTATA GT	
			C	
GAM2135	SCDGF-B	3'	GTTAGATGAGTGACCTAA 53634	GATAA
			TTAGG TATTCATTTAGC	
			AATCC GTGAGTAGATTG	
			A_	
GAM2135	SEMA7A	3'	GCTGGGTGGCTGGTGTTCTGA 14610	A TT
			TTAGGGATA TA CATTTAGC	
			AGTCCTTGT GT GTGGGTCG	
			G CG	
GAM2135	SGK2	3'	GCTGGGTACGTGACTATCCCTA 33252	A_ TC
	ATA		TATTAGGGATA TAT ATTTAGC	
			ATAATCCCTAT GTG TGGGTCG	
			CA CA	
GAM2135	ShrmL	3'	GTTATTGGTGTTTGTTCTGAT 40851	TAT TT
	G		TATTAGGGATAA TCA TAGC	
			GTAGTCCTTGTT GGT ATTG	
			TGT T_	
GAM2135	SLC38A4	3'	GCTTTTTCATGTTATTCCTAA 36343	TCATTT
			TTAGGGATAATAT AGC	
			AATCCTTATTGTA TCG	
			CTTT_	
GAM2135	SPTLC2	3'	GCTAGTTCTCTTTTATTCTTGA 17997	TATTCAT
	TG		TATTAGGGATAA TTAGC	
			GTAGTTCTTATT GATCG	
			TTCTCTT	
GAM2135	ST13	3'	TGGATATGTGGTTCCTGATG 15434	A_
			TATTAGGGAT ATATTCA	
			GTAGTCCTTG TATAGGT	
			GTG	
GAM2135	STRIN	3'	GTTAAAATTGGGTATGTTCTTA 33232	A _
	ATA		TATTAGGGATA TATTCA TTTAGC	

		ATAATTCTTGT ATGGGT AAATTG	
		— TA	
GAM2135	SWAP2	3' GCTGCTGGTTTTATCTCTAGTG 23901	TAT TT
		TATTAGGGATAA TCA TAGC	
		GTGATCTCTATT GGT GTCG	
		TT_ C_	
GAM2135	TEB4	3' GCTAGGTGAGGAAATTATTTTT 61284	A__
	AAT	ATTAGGGATAAT TTCATTTAGC	
		TAATTTTATTA GAGTGGATCG	
		AAG	
GAM2135	TTC2	3' GTTGGATGCCCTGTGTCTCTG 13877	ATATT
		TAGGGATA CATTTAGC	
		GTCTCTGT GTAGGTTG	
		GTCCC	
GAM2135	UBE3B	5' GCTGGGTGATTTGTTCTG 77446	TAT
		TAGGGATAA TCATTTAGC	
		GTCCTTGTT AGTGGGTCG	
		T__	
GAM2135	VEST1	3' GTTAAGTGAATGGATCTAA 54764	GATAA
		TTAGG TATTCATTTAGC	
		AATCT GTAAGTGAATTG	
		AG__	
GAM2135	WBSCR20A	5' GCTGGATGGAGTGCCCTGG 50572	ATAATA
		TTAGGG TTCATTTAGC	
		GGTCCC AGGTAGGTCG	
		GTG__	
GAM2135	XYLT1	3' TGAACTATTCTCCTTAGTA 78416	T _
		TATTAGGGA AATA TTCA	
		ATGATTCCT TTAT AAGT	
		C C	
GAM2135	ZFP95	3' GCTGGATGGTATGTGTTTCTG 28120	GG ATAT
		TAG ATA TCATTTAGC	
		GTC TGT GGTAGGTCG	
		TT GTAT	
GAM2135	ZNF197	3' GTTAAGTGAAAGGATCTTTG 23759	AATA
		TAGGGAT TTCATTTAGC	
		GTTTCTA AAGTGAATTG	
		GGA_	
GAM2135	ZNF225	5' GCTGCAGTTTTGTCCCTGGTA 26273	T CATT
		TATTAGGGATAA ATT TAGC	

	ATGGTCCCTGTT TGA GTCG		
	T C__		
GAM2135 ZNF33A 3'	CTAACATTATCCTTGATG 92994	ATTCAT	
	TATTAGGGATAAT TTAG		
	GTAGTTCCTATTA AATC		
	C__		
GAM2135 LOC115219 5'	GCTGGGTGAGTGTGCACTTGGT 73697	GATA	
	ATTAGG ATATTCATTTAGC		
	TGGTTC TGTGAGTGGGTCG		
	ACG_		
GAM2135 LOC127703 3'	GCTGAGGCTATTGTCCCTGATG 75178	TTCA	
	TATTAGGGATAATA TTTAGC		
	GTAGTCCCTGTTAT GAGTCG		
	CG_		
GAM2135 LOC130502 3'	GTTGAATGGGTTTTTTTAAATG 75444	TAAT	
	TATTAGGGA ATTCATTTAGC		
	GTAATTTT TGGGTAAGTTG		
	TT_		
GAM2135 LOC137221 5'	GCTGGCTGAGTTTTATTCTGA 76475	GG T T	
TG	TATTAG ATAA ATTCA TTAGC		
	GTAGTC TATT TGAGT GGTCTG		
	TT T C		
GAM2135 LOC137221 5'	TGAGTTTTATTCTGATG 76476	GG T	
	TATTAG ATAA ATTCA		
	GTAGTC TATT TGAGT		
	TT T		
GAM2135 LOC143381 3'	GTTGAATGAAAAGCCTTGA 77062	ATAATA	
	TTAGGG TTCATTTAGC		
	AGTTCC AAGTAAGTTG		
	GAA_		
GAM2135 LOC144809 3'	TGACAGTGAATAATTTCTAATA 84105	GG AA TAGC	
	TATTAG AT TATTCATT		
	ATAATC TA ATAAGTGA		
	TT _ CAGTA		
GAM2135 LOC145231 3'	AATGGGTATTGTCCCTAG 84234		
	TTAGGGATAATATTCATT		
	GATCCCTGTTATGGGTAA		
GAM2135 LOC146455 3'	TATTTGATTTGTCTCTGATA 78466	TAT TT	
	TATTAGGGATAA TCA TA		

	ATAGTCTCTGTT AGT AT	
	T__ TT	
GAM2135 LOC146723 3'	GCTAAAGACCTTATCCTTG 78681	TAT A
	TAGGGATAA TC TTTAGC	
	G TTCCTATT AG AAATCG	
	CC_ _	
GAM2135 LOC146990 5'	GTTGTTTTTGTGTTGTTCTG 84956	TCATT
	TAGGGATAATAT TAGC	
	GTCCTTGTTGTG GTTG	
	TTTTT	
GAM2135 LOC149832 5'	GTGATTTTGTCTCTAGTG 85869	TAT
	TATTAGGGATAA TCAT	
	GTGATCTCTGTT AGTG	
	TT_	
GAM2135 LOC149844 3'	GTTGAATGGGCTGATCCT 80347	AATA
	GGGAT TTCATTTAGC	
	TCCTA GGGTAAGTTG	
	GTC_	
GAM2135 LOC149911 3'	GCTAAGTGAGTGAAGAGTC 85874	AA__
	GAT TATTCATTTAGC	
	CTG GTGAGTGAATCG	
	AGAA	
GAM2135 LOC150372 3'	GCTGAATGAATGGGCCTGG 80617	GATAA
	TTAGG TATTCATTTAGC	
	GGTCC GTAAGTAAGTCG	
	GG__	
GAM2135 LOC150933 3'	GTTGATTTTGTGTTCTGA 86339	TTCAT
	TTAGGGATAATA TTAGC	
	AGTCCTTGTTGT AGTTG	
	TTTT_	
GAM2135 LOC151516 3'	GCTAGAAATGCTTGTCTTTGA 81067	_ CA
	TTAGGGATAA TATT TTTAGC	
	AGTTTCTGTT GTAA AGATCG	
	C _	
GAM2135 LOC152185 3'	TCACTGAGTTTGTTCTTAATA 59203	T TTTAGC
	TATTAGGGATAA ATTCA	
	ATAATTCTTGTT TGAGT	
	_ CACTC	
GAM2135 LOC152245 5'	GTTGGGTGGGCACCCCCTGAT 86784	ATAATA
	ATTAGGG TTCATTTAGC	

		TAGTCCC GGGTGGGTTG CCAC__	
GAM2135	LOC152674 5'	GTTGAGTGGAAGATGTCTTAGT 87005 A TATTAGGG TTCATTTAGC ATGATTCT AGGTGAGTTG GTAGA_	ATAATA
GAM2135	LOC153205 3'	GCTAACAATGGTTATCTCTGA 87160 TTAGGGATAAT TTAGC AGTCTCTATTG AATCG GTAAC_	ATTCAT
GAM2135	LOC157798 5'	CTGGATGAAACCTTAGTA 87857 TATTAGGG TTCATTTAG ATGATTCC AAGTAGGTC A_____	ATAATA
GAM2135	LOC157858 5'	GTTAAATGAGGGGCTCTCTGA 87895 TTAGGGA TTCATTTAGC AGTCTCT GAGTAAATTG CGGG_	TAATA
GAM2135	LOC161589 3'	GCTAAATGAATATTATCCCTAA 83158 TA TATTAGGGATAATATTCATTTAGC ATAATCCCTATTATAAGTAAATCG G	
GAM2135	LOC164971 5'	GCTAATATATTATCCTTTGGTG 83349 TATTAG GGATAATAT TTAGC GTGGTT CCTATTATA AATCG T T____	_ TCAT
GAM2135	LOC170127 3'	GCTGAGTGCCTGCCCTTGATG 83460 TATTAGGG CATTTAGC GTAGTTCC GTGAGTCG CGTCC_	ATAATATT
GAM2135	LOC196394 3'	GTTGGATGAGTCATTATTTTGTG 89032 A TTAGGGATAAT ATTCATTTAGC AGTTTTTATTA TGAGTAGGTTG C	_
GAM2135	LOC199704 5'	GCTCCTATGAGTGTTAACCTTG 89697 ATG TATTAGGG TAATATTCAT AGC GTAGTTCC ATTGTGAGTA TCG A TCC	A TT_
GAM2135	LOC199953 3'	TTGGGTGAGGGTCCTGGT 89887 ATTAGGG TTCATTTAG 	ATAATA

	TGGTCCT GAGTGGGTT		
	GG_____		
GAM2135 LOC200399 3'	GTTGGGCTGATGTTGTTGTTGG 90241	G	CA
TG	TATTAG GATAATATT TTTAGC		
	GTGGTT TTGTTGTAG GGGTTG		
	G TC		
GAM2135 LOC200734 3'	GCTGGAAAAGAGTATTTTTCTA 90280	GG T	A__
ATA	TATTAG A AATATTC TTTAGC		
	ATAATC T TTATGAG AGGTCG		
	TT _ AAA		
GAM2135 LOC200830 3'	TGAATTGTAATTCCTGATG 91731	A _	
	TATTAGGGAT ATA TTCA		
	GTAGTCCTTA TGT AAGT		
	A T		
GAM2135 LOC200942 3'	GTTAGGGGAGCCTTTGTCTTTA 90379	TA_ A	
GTG	TATTAGGGATAA TTC TTTAGC		
	GTGATTTCTGTT GAG GGATTG		
	TCC G		
GAM2135 LOC202460 5'	GCTGAGAGATATTATTCTTAG 90673	CA	
	TTAGGGATAATATT TTTAGC		
	GATTCTTATTATAG GAGTCG		
	A_		
GAM2135 LOC203286 3'	GCTGGATGTCCAAGTCCCTG 92146	AATATT	
	TAGGGAT CATTTAGC		
	GTCCCTG GTAGGTCG		
	AACCT_		
GAM2135 LOC219902 5'	GCTAACATGTTATCTCTGA 93129	TCAT	
	TTAGGGATAATAT TTAGC		
	AGTCTCTATTGTA AATCG		
	C__		
GAM2135 LOC221496 3'	GCTGGATGAATAAACTATTT 93642	A__	
	GGATA TATTCATTTAGC		
	TTTAT ATAAGTAGGTCG		
	CAA		
GAM2135 LOC221687 3'	GTTGAATGTATATATTTCTAA 93871	GG A T	
	TTAG ATA TAT CATTTAGC		
	AATC TAT ATA GTAAGTTG		
	TT _ T		
GAM2135 LOC221895 3'	GTTAGATGAGTAAACCTCTA 94106	ATAA	
	TAGGG TATTCATTTAGC		

	ATCTC ATGAGTAGATTG CAA_	
GAM2135 LOC221931 3'	GCTGGGTGATGTTAGGTTTCTG 95631 G TTAG AT TCATTTAGC GGTC TG AGTGGGTCG TT GATTGT	GG AATAT_
GAM2135 LOC222662 3'	GCTAAATGGGTCCATCTCTAG 94414 TTAGGGAT ATTCATTTAGC GATCTCTA TGGGTAAATCG CC_	AAT
GAM2135 LOC253698 3'	GCTGAAAATGTCATTTCTAGTA 96546 TATTAG AT ATATT TTTAGC ATGATC TA TGTA AAGTCG TT C _	GG A CA
GAM2135 LOC255391 5'	GTTGGGTGGGTTTCTCTGG 99458 TTAGGGA ATTCATTTAGC GGTCTCT TGGGTGGGTTG T_	TAAT
GAM2135 LOC257481 3'	GCTGTTCGGATGGTGTCTTTGA 61763 TG TATTAGGGATA TATT TAGC GTAGTTTCTGT GTAG GTCG G CCTT	A CATT
GAM2135 LOC51316 3'	TAAATGAATGTTGTCCCTGA 60248 TTAGGGATAATATTCATTTA AGTCCCTGTTGTAAGTAAAT A	GC
GAM2135 LOC83468 3'	CTTTATGAATATTACCTTTGAT 49342 A TATTAGGG TAATATTCAT AG ATAGTTTC ATTATAAGTA TC C TT T	A TT C
GAM2135 LOC90190 3'	GCTAACTTTTGTGTTGACTCTG 62427 GTG TATTAGGG TAATAT TTAGC GTGGTCTC GTTGTG AATCG A TTTTC	A TCAT_
GAM2135 LOC90246 3'	GCTAAATGGATGTTGCTTGA 62587 TTAGG TAATATTCATTTAGC AGTTC GTTGTAGGTAAATCG _	GA
GAM2135 LOC91137 3'	TGGTATAGTATCCTTAATA 57860 TATTAGGGATA TAT TCA 	A _

		ATAATTCCTAT ATA GGT	
		G T	
GAM2135	LOC92140	3' GCTTATGAAGTTATTTTGTATA 68826	A TT
		TATTAGGGGATAAT TTCAT AGC	
		ATAGTTTTTATTG AAGTA TCG	
		- T-	
GAM2135	LOC92344	3' TTTGAGGGTATTATCTTCTGGT 69579	- ATTTAGC
	A	TATTAGG GATAATATTC	
		ATGGTCT CTATTATGGG	
		T AGTTTG	
GAM2135	LOC92379	3' GTTAAATGTTTGATTGTTTTTG 69677	ATT-
	G	TTAGGGGATAAT CATTTAGC	
		GGTTTTTGTTA GTAAATTG	
		GTTT	
GAM2135	LOC92421	3' GCTGAATGAGAATCTCCTGG 69726	- AATA
		TTAGG GAT TTCATTTAGC	
		GGTCC CTA GAGTAAGTCG	
		T A__	
GAM2136	ATP8A2	3' GTATTTTCCTATTCTCTTG 95157	TCCAC
		CAAGGGGATA AGAGTAC	
		GTTCTCTTAT TTTTATG	
		CC__	
GAM2136	AVPR1A	3' GTACTCTGGACTTTCTCTTGGA 7383	TA CA
		TCCAAGGGGA TCCA GAGTAC	
		AGGTTCTCTT AGGT CTCATG	
		TC _	
GAM2136	CALB2	3' TGCTCCTTTTCTCTTTGGG 9982	TATCCACA
		TCCAAGGGGA GAGTA	
		GGGTTTCTCT CTCGT	
		TTTC__	
GAM2136	CALM2	3' GTACTCGTACACTATTTTTTTG 9987	TCCACA
		CAAGGGGATA GAGTAC	
		GTTTTTTTAT CTCATG	
		CACATG	
GAM2136	CD4	3' GTACTCAATGTGTACTTTTGGG 7048	GATATC _
		TCCAAGGG CACA GAGTAC	
		GGGTTTTC GTGT CTCATG	
		AT__ AA	
GAM2136	CRSP8	3' TGTTTTGTGGGGCTTGGG 81860	GGGATA
		TCCAAG TCCACAGAGTA	

			GGGTTC	GGGTGTTTTGT		
			G_____			
GAM2136	CYP19	3'	GTACTTTAATTTTGT	TTTCTGT 49167	_ GG	TCCAC
	GGA		TCCA AG GATA	AGAGTAC		
			AGGT TC TTGT	TTTCATG		
			G TT	TTTAA		
GAM2136	DBT	3'	TGCTTTGGTATTTTCTT	GGG 10386	GG	CCA C
			TCCAAG GATAT	CAGAGTA		
			GGGTTC TTATG	GTTTCGT		
			TT	_____		
GAM2136	DLEU2	3'	GTATTCTGTATCTTTCTTTTG	21208		TATCC
			CAAGGGGA	ACAGAGTAC		
			GTTTTCTT	TGTCTTATG		
			TCTA_			
GAM2136	DNMT1	3'	TACTTTGTGCATTCTGGA	9104	AGG	ATC
			TCCA GGAT	CACAGAGTA		
			AGGT CTTA	GTGTTTCAT		
			_____	C_		
GAM2136	DTNA	5'	GTGCTCTTACTTATTCTGTTGG	9142	G	TCCAC
	A		TCCAA GGGATA	AGAGTAC		
			AGGTT TCTTAT	TCTCGTG		
			G	TCAT_		
GAM2136	EIF2C1	3'	GTGTTCTGTACCCCTTTGGG	25198		ATATCC
			TCCAAGGGG	ACAGAGTAC		
			GGGTTTCCC	TGTCTTGTG		
			AC_____			
GAM2136	EIF3S2	3'	GTGCTTTGTGAGCTTTTGA	97161	C	ATATC
			TC AAGGGG	CACAGAGTAC		
			AG TTTTTC	GTGTTTCGTG		
			T	GA_____		
GAM2136	FMR1	3'	GTATTTTGTGAGTTTGTTTCTT	10680	GG	TC__
	TG		CAAGG ATA	CACAGAGTAC		
			GTTTC TGT	GTGTTTATG		
			TT	TTGA		
GAM2136	GPR44	3'	GTGTTCTGTGGGATCCCTCTGG	17701	AG	A
	G		TCCA GGGAT	TCCACAGAGTAC		
			GGGT CCCTA	GGGTGTCTTGTG		
			CT	_____		
GAM2136	HNRPF	3'	CTGTGATTTCCTTTTGGG	18304	T	C
			TCCAAGGGGA	ATC ACAG		

GGGTTTTCCT TAG TGTC
T _

GAM2136 HOXB9 3' GTGTTTCGTGATTTCTTTGGG 43999 GG ATC AG
TCCAAGG AT CAC AGTAC
||||| || ||| |||||
GGGTTTC TA GTG TTGTG
TT _ CT

GAM2136 HRH1 3' GTATTTTGTGTTCTCTT 7826 TATC
AAGGGGA CACAGAGTAC
||||| |||||
TTCTCCT GTGTTTATG
T_

GAM2136 ITK 3' GTGTTGGTCAATGTTCCCTTGG 19885 _ _ GAGTAC
CCAAGGGGATAT CCA CA
||||||| |||
GGTCCCTTGTA GGT GT
ACT T G C

GAM2136 ITS1 3' GTACTAGATGGTGTCTCTTTG 13094 TAT CAG
CAAGGGGA CCA AGTAC
||||| ||| |||||
GTTTCTCT GGT TCATG
TGT AGA

GAM2136 KIF1B 3' GTACTTTGGCTTCCTTTTG 31269 TATCCA
CAAGGGGA CAGAGTAC
||||| |||||
GTTTTCCT GTTTCATG
TCG_

GAM2136 MJD 3' GTGCTCCAGTGTTTTCTTG 18424 GG CCACA
CAAG GATAT GAGTAC
||| ||||| |||||
GTTT TTGTG CTCGTG
TT AC_

GAM2136 MME 3' GTATTTGCAATATTCCTTTGGG 8032 CCACA
TCCAAGGGGATAT GAGTAC
||||||| |||||
GGGTTTCCTTATA TTTATG
ACG_

GAM2136 NEBL 3' TATCCATGCCTTTTGGA 22141 ATATC CA
TCCAAGGGG CA GAGTA
||||||| || |||||
AGGTTTCC GT CTTAT
_ AC

GAM2136 PKM2 3' GTACTCTGTCCAGTTCCTTTAG 12143 C ATCC
A TC AAGGGGAT ACAGAGTAC
|| ||||| |||||
AG TTTCTTG TGTCTCATG
A ACC_

GAM2136 PKP2 3' GTGCTTGTTTTATCCCCTTGG 17110 TCC G
CCAAGGGGATA ACA AGTAC
||||||| ||| |||||

GGTCCCCCTAT TGT TCGTG
TTT _
GAM2136 PMX1 5' GTATTTTACTGTGGATTATCTC 23571 _ _
TTTGGA TCCAAGGGGATA TCCACAG AGTAC
||||| ||||| ||||
AGGTTTCTCTAT AGGTGTC TTATG
T ATT
GAM2136 POU4F1 3' TACAAGATACTCTTTGGA 21767 A CACAGA
TCCAAGGGG TATC GTA
||||| ||| |||
AGGTTTCTC ATAG CAT
_ AA _
GAM2136 PRKY 3' GTGAGAGTGTCTCTTTGGG 12382 _ _
TCCAAGGGGATA TC CAC
||||| || |||
GGGTTCTCTTGT AG GTG
G A
GAM2136 PSMD9 3' GTTTTTGT TTTTGT TTTTCTGGA 12529 A GG TCC TAC
TCCA G GATA ACAGAG
||| | ||| |||||
AGGT C TTGT TGTTTT
_ TT TTT TGT
GAM2136 PTGS1 3' GTGGGGTGTCTCTTCTTGGG 55478 TA _
TCCAAGGGGA TCCAC
||||| |||||
GGGTTCTTCT GGGTG
TGTG
GAM2136 RELA 3' CCAACTTTGTGGATGTCTTCCT 42025 _ AC
TGGA TCCAAGGG GATATCCACAGAGT
||||| |||||
AGGTTTCCT CTGTAGGTGTTTCA
T ACCC
GAM2136 SCN3A 3' GTATCATATGGTATCTCTCTGG 23618 AG T CAGA
A TCCA GGGATA CCA GTAC
||| ||||| ||| |||||
AGGT CTCTAT GGT TATG
CT _ ATAC
GAM2136 SDHC 3' GTATTTTCAGATCTCCTTGA 69914 ATCCAC
TCCAAGGGGAT AGAGTAC
||||| |||||
AGGTTCTCTA TTTTATG
GAC _
GAM2136 SHC1 3' GTGTTCTGTGGGCTTGGCCTTG 13122 GGATA
CAAGG TCCACAGAGTAC
||||| |||||
GTTCC GGGTGTCTTGTG
GGTTC
GAM2136 SLC17A2 5' TGCTTTTCTTCTTTTGGG 20692 TATCCAC
TCCAAGGGGA AGAGTA
||||| |||||

GGGTTTTTCT TTTCGT
TCT____

GAM2136 SNL 3' CCCTTGTTGGTGTTCCTTTGGG 13288 T AGTAC
TCCAAGGGGATA CCACAG
||||||| |||||
GGGTTTTTTTGT GGTGTT
_ CCCA

GAM2136 SNX5 3' GTGTTGTATGTCTTTGGG 27788 G C_
TCCAAGGG ATAT CAC
||||| ||| |||
GGGTTTCT TATG GTG
G TT

GAM2136 TEM8 3' GTATGCAGAAGGATGTTCTTCT 50827 AG ACAGA_
GGG TCCA GGGATATCC GTAC
||| ||||| |||
GGGT TCTTGTAGG TATG
CT AAGACG

GAM2136 TTC3 5' GTGTTCTGATAGGAGTTATTC 13884 GG _ A_
CTTGGG TCCAAGG ATA TCC CAGAGTAC
||||| ||| ||| |||||
GGGTTCC TAT AGG GTCTTGTG
TT TG ATA

GAM2136 USH2A 3' GTGCTTTGTATTTGTCTTTTGG 24058 TCC
CAAGGGGATA ACAGAGTAC
||||||| |||||
GTTTTTCTGT TGTTTCGTG
TTA

GAM2136 USP1 3' GTACCCTAGTATATCTTTTTGG 14021 CC _ A
G TCCAAGGGGATAT AC AG GTAC
||||||| || |||
GGGTTTTTCTATA TG TC CATG
_ A C

GAM2136 WHSC1 3' TACTTTGCTCTCCTTGCGG 24686 _ TATCCA
TC CAAGGGGA CAGAGTA
|| ||||| |||||
GG GTTCCTCT GTTTCAT
C C____

GAM2136 WNT11 3' TGCTTTCCTTCACTTGGA 17326 GG TATCCA
TCCAAG GA CAGAGTA
||||| || |||||
AGGTTC CT GTTTCGT
A_ TCC____

GAM2136 ALS2CR2 3' GTATTTTGCTGTCCCTTGGA 38321 A TCCA
TCC AGGGGATA CAGAGTAC
||| ||||| |||||
AGG TTCCCTGT GTTTTATG
G C____

GAM2136 C21orf108 3' GTGTTCTGTGACAGCATTTGGG 90118 GGGATATC
TCCAAG CACAGAGTAC
||||| |||||

			GGGTTT	GTGTCTTGTG		
			ACGACA__			
GAM2136	C9orf14	3'	TTGTGGAGGTTTCCTTGGA	87962	GG A	
			TCCAAGG AT TCCACAG			
			AGGTTCC TG AGGTGTT			
			TT G			
GAM2136	CAMKK1	3'	TGTGGGTGTCCTGTTGGA	51155	G	
			TCCAA GGGATATCCACA			
			AGGTT TCCTGTGGGTGT			
			G			
GAM2136	CCNB3	3'	GTATTCTCACCCGGTCTTCTTT	54465	C	ATCCAC
	GA		TC AAGGGGAT AGAGTAC			
			AG TTCTTCTG TCTTATG			
			T GCCCAC			
GAM2136	COLEC12	3'	GTGCTCTGCAGTCCACTTTGGG	48617	_	ATCCA
			TCCAAGG GGAT CAGAGTAC			
			GGGTTTC CCTG GTCTCGTG			
			A AC__			
GAM2136	DIO2	3'	TGAGGGGTTTCTTTTGGA	26557	T A_	
			TCCAAGGGGA ATCC CA			
			AGGTTTCTT TGGG GT			
			_ GA			
GAM2136	DKFZp434A2417	3'	GTGCTTTGAAGATTTCTTTG	66683	GG	ATCCA
			CAAGG AT CAGAGTAC			
			GTTTC TA GTTTCGTG			
			TT GAA__			
GAM2136	DKFZP434C212	3'	GTACTATGAAATGTCCTTTTG	69496	CCA	G
			CAAGGGGATAT CA AGTAC			
			GTTTTCCTGTA GT TCATG			
			AA_ A			
GAM2136	DKFZP586M0622	5'	GTATTTTGCCAACCTTTCCTTG	32102	GG	TATCCA
	G		TCCAAGG A CAGAGTAC			
			GGGTTCC T GTTTTATG			
			TT CAACC_			
GAM2136	DKFZp761B1514	3'	GTACTTTTGGTGTGTTTTTGGA	51140	ATAT	C
			TCCAAGGGG CCA AGAGTAC			
			AGGTTTTTT GGT TTTCATG			
			GT__ T			
GAM2136	FLJ10520	5'	CTGTGGGCATCTCTTTGGG	36707	AT	
			TCCAAGGGGAT CCACAG			

		GGGTTTCTCTA GGTGTC	
		CG	
GAM2136 FLJ10701	3'	GTGCTCTCTAGTTAGTTTTTTT 36966	ATCCAC_
		GGG TCCAAGGGGAT AGAGTAC	
		GGGTTTTTTTG TCTCGTG	
		ATTGATC	
GAM2136 FLJ10853	3'	GTGCTCTGTTGATCATTG 37319	GG ATCC
		TCCAAG GAT ACAGAGTAC	
		GGGTTT CTA TGTCTCGTG	
		A_ GT__	
GAM2136 FLJ14054	3'	TATTTGTGGAATCTCTTTGGG 44971	A GTAC
		TCCAAGGGGAT TCCACAGA	
		GGGTTTCTCTA AGGTGTTT	
		A ATC	
GAM2136 FLJ14511	3'	GTATTTTAATTATATTTTCTCG 53533	A GG CCAC
		GG TCC AG GATAT AGAGTAC	
		GGG TC TTATA TTTTATG	
		C TT TTAA	
GAM2136 FLJ20457	3'	GTACTCACACTGTTCTCTTG 35674	TCCACA
		CAAGGGGATA GAGTAC	
		GTTCTCTTGT CTCATG	
		CACA__	
GAM2136 FLJ21276	3'	CATCTGGGAATTCCTTGGG 45258	GG A A GTAC
		TCCAAGG AT TCC CAGA	
		GGGTTCC TA AGG GTCT	
		TT _ _ ACT	
GAM2136 FLJ21841	3'	GTGCTCTGAAGACCTCTTGGG 45155	ATA CA
		TCCAAGGGG TC CAGAGTAC	
		GGGTTCTCC AG GTCTCGTG	
		__ AA	
GAM2136 FLJ22002	3'	GTGTTTTTTGTTTGT TTTTGTG 96361	TC C
		G CCAAGGGGATA CA AGAGTAC	
		GGTTTTTTTGT GT TTTTGTG	
		TT T	
GAM2136 FLJ22558	5'	TTTGTGCTGCTTTTGGG 43035	ATATC
		TCCAAGGGG CACAGA	
		AGGTTTTTC GTGTTT	
		GTC__	
GAM2136 FLJ22584	3'	GTGTTTGTATTCCTTTAGA 44841	C C__
		TC AAGGGGATAT CAC	

		AG TTTCTTATG GTG	
		A TTT	
GAM2136	FLJ23091	3' TGGGGGTGTATTCCTTGGG 46667	_ A
		TCCAAGGGG ATATCC CA	
		GGGTTCTT TGTGGG GT	
		A G	
GAM2136	GABARAPL1	3' TGCTCCCTTCTCTTTGGG 49427	TATCCACA
		TCCAAGGGGA GAGTA	
		GGGTTTCTCT CTCGT	
		TCC_____	
GAM2136	GABARAPL3	3' TGCTCCCTTCTCTTTGGG 51790	TATCCACA
		TCCAAGGGGA GAGTA	
		GGGTTTCTCT CTCGT	
		TCC_____	
GAM2136	GRID1	3' GTAGAGGAAGAATATTCCTTG 69024	_____ ACAGAGTAC
	GG	TCCAAGGGGATA TCC	
		GGGTTCCCTTAT AGG	
		AAGA AGATG	
GAM2136	GRID1	3' GTATAGCTTGGATGTCTTCTTG 69025	C A_
	GA	TCCAAGGGGATATCCA AG GTAC	
		AGGTTCTTCTGTAGGT TC TATG	
		_ GA	
GAM2136	HIC	3' ACGTGTTTAAAAATTCCTTTT 68041	_____ TC AGAGTAC
	GGG	TCCAAGGGGA TA CAC	
		GGGTTTTCCT AT GTG	
		TTAAAA TT CAT	
GAM2136	HRIHFB2436	3' GTATTTTGTTAATTTTTTTGG 27571	ATCC
		CCAAGGGGAT ACAGAGTAC	
		GGTTTTTTTA TGTTTTATG	
		AT__	
GAM2136	KIAA0016	3' GTGTTCTGGGTATTTATCTCCT 29310	T__ A
	TG	CAAGGGGATA CC CAGAGTAC	
		GTTCTCTAT GG GTCTTGTG	
		TTAT _	
GAM2136	KIAA0125	3' TGTTGGCTGTTCTCTTGGG 29581	T _
		TCCAAGGGGATA CCA CA	
		GGGTTCTCTTGT GGT GT	
		C T	
GAM2136	KIAA0212	3' TCTTGATATTTTTTTGGG 28630	CAC
		TCCAAGGGGATATC AGA	

GGGTTTTTTTATAG TCT
T__

GAM2136 KIAA0295 3' GTACTCTGGGACCTGTTTCCTG 68670 A GG _ A
GA TCCA GG ATA TCC CAGAGTAC
||||| || ||| ||| |||||
AGGT CC TGT AGG GTCTCATG
_ TT CC _

GAM2136 KIAA0429 3' GTATTCTGGGTAATGTTTTTTG 29245 ATAT_ A
GA TCCAAGGGG CC CAGAGTAC
||||||| || |||||
AGGTTTTTT GG GTCTTATG
GTAAT _

GAM2136 KIAA0534 3' GTACTTTTCACATTCTTTGGA 71934 ATATCCAC
TCCAAGGGG AGAGTAC
||||||| |||||
AGGTTTCTT TTTTCATG
ACACT__

GAM2136 KIAA0534 3' TCTGTGGGGTTTTTTTGA 71936 A
TCCAAGGGGAT TCCACAGA
||||||| |||||
AGGTTTTTTTG GGGTGTCT

GAM2136 KIAA0825 3' TATTTTGTGATTCTTGGG 61689 GATATC
TCCAAGGG CACAGAGTA
||||||| |||||
GGGTTCTT GTGTTTTAT
A__

GAM2136 KIAA0830 3' GTACTAATAACATGTTCCCTTGG 70269 G CCACAG
A TCCAAGGG ATAT AGTAC
||||||| ||| |||||
AGGTTCCCT TGTA TCATG
_ CAATAA

GAM2136 KIAA0971 3' GTGCTTTAGTTACTGTTTTCTT 30676 C GG TCC _
TGA TC AAG GATA AC AGAGTAC
|| ||| ||| || |||||
AG TTC TTGT TG TTTTCGTG
T TT CAT A

GAM2136 KIAA1029 3' TATTCTGGTCCCCTTGA 24433 ATCCA _
TCCAAGGGGAT CAGAG TA
||||||| ||||| ||
AGGTTCCCCTG GTCTT AT
_____ T

GAM2136 KIAA1908 5' GTGCTCTGGGCAGTGGTTCCTT 73797 A _ A
GGG TCCAAGGGG TAT CC CAGAGTAC
||||||| ||| || |||||
GGGTTCCCTT GTG GG GTCTCGTG
G AC _

GAM2136 KLK6 3' GCTTACTGTCGGTGTCCCCTTGA 12426 C _ AC
GG TCCAAGGGGATATC ACAG AGT
||||||| ||||| ||| |||

GGGTTCCCCTGTGG TGTC TCG
C AT
GAM2136 KRTAP4-7 3' GTATTCTGTGTTTCTCCTAGGG 53517 A TATC
TCC AGGGGA CACAGAGTAC
||| ||||| |||||
GGG TCCTCT GTGTCTTATG
A TT__
GAM2136 LOXL4 3' GTGTTTCTATTATCCTTGA 50861 _ TC__
TCCAAGGG GATA CAC
||||| ||| |||
AGGTCCT TTAT GTG
A CTTT
GAM2136 MEF-2 3' GTATTTTAAATTTTCTTGGG 65028 GG TATCCAC
TCCAAG GA AGAGTAC
||||| || |||||
GGGTC TT TTTTATG
TT TAAAT__
GAM2136 MGC11082 5' TTTGTCTTCTCCTTGA 52075 TATCC
TCCAAGGGGA ACAGA
||||||| |||||
AGGTCCTCT TGTTT
TTC__
GAM2136 MGC2488 3' GTATTCTGTGTTTCTCCTTTT 44091 ____ TATC
TTGG CCA AGGGGA CACAGAGTAC
||| ||||| |||||
GGT TCTCCT GTGTCTTATG
TTTT TTT_
GAM2136 MGC2827 3' GTACTCTGTGTCTTTTCTTTA 43980 C TATC
GA TC AAGGGGA CACAGAGTAC
|| ||||| |||||
AG TTTCTT GTGTCTCATG
A TTCT
GAM2136 MGC4638 3' GTACTCTGTAGGCTTCTGGGA 49743 A ATAT _
TCC AGGGG CC ACAGAGTAC
||| ||||| || |||||
AGG TCTTC GG TGTCTCATG
G ____ A
GAM2136 MGC5508 3' GTGTTCTGTGGCTGCTTTGTG 44271 AG A T
CA GGG TA CCACAGAGTAC
|| ||| || |||||
GT TTC GT GGTGTCTTGTG
GT _ C
GAM2136 NAP1L2 3' GTGTTCTGTATTTTCTTG 42013 GG TATCC
CAAG GA ACAGAGTAC
||||| || |||||
GTTC TT TGTCTTGTG
TT TA__
GAM2136 NDRG4 3' TGTGGTGTCTTCTGGA 40386 AG T
TCCA GGGATA CCACA
||||| ||||| |||||

		AGGT TCTTGT GGTGT	
		CT _	
GAM2136	NDRG4	3' TGTGGTGTCTCTCTGGA 43580	AG T
		TCCA GGGATA CCACA	
		AGGT TCTTGT GGTGT	
		CT _	
GAM2136	NYD-SP25	3' GTGCTTTGTTTATAATTTCTTT 54305	GG _ CC
	G	CAAGG AT AT ACAGAGTAC	
		GTTTC TA TA TGTTTCGTG	
		TT A TT	
GAM2136	OSBPL11	3' GTATTATGTGTTATCCCTTTGG 43207	TC G
	A	TCCAAGGGGATA CACA AGTAC	
		AGGTTTCCCTAT GTGT TTATG	
		T_ A	
GAM2136	P2RXL1	3' GTGCACCTGATTCTCCTTGGG 19563	TATCCA A_
		TCCAAGGGGA CAG GTAC	
		GGGTTCTCT GTC CGTG	
		TA___ CA	
GAM2136	PRO0902	5' GTGCTCTGGAACATCTCTTTGG 54970	ATCCA
	G	TCCAAGGGGAT CAGAGTAC	
		GGGTTTCTCTA GTCTCGTG	
		CAAG_	
GAM2136	PSIP2	3' GTGCTCTGTATGGTTTTTTTGG 53782	T C_
	G	CCAAGGGGA ATC ACAGAGTAC	
		GGTTTTTTT TGG TGTCTCGTG	
		_ TA	
GAM2136	PTPNS1	3' GTATTTTAAAAGAATGTTTTCT 55843	GG _ CAC_
	TGG	CCAAG GATAT C AGAGTAC	
		GGTTC TTGTA G TTTTATG	
		TT A AAAA	
GAM2136	RAI	5' TGTGGGTGTCTTCCTGGG 22859	A _
		TCCA GGGGATATCCA CA	
		GGGT CTTCTGTGGGT GT	
		C T	
GAM2136	RNP24	3' GTGCTTTTTTTTTTTTTTTTGG 23327	TATCCAC
	GA	TCCAAGGGGA AGAGTAC	
		AGGTTTTTTT TTTCGTG	
		TTTTTTT	
GAM2136	SLC5A6	3' GTGCTCTGTTTCCTTTTGG 41179	TATCC
		TCCAAGGGGA ACAGAGTAC	

		AGGTTTTCTT	TGTCTCGTG		
		T_____			
GAM2136	TRAP150	5'	CTGCGGGTGTCTTTTGGG	18872	A
			TCCAAGGGGATATCC	CAG	
			GGGTTTTCTTGTGGG	GTC	
			C		
GAM2136	UST	3'	TCTCTTGGCTCTTTGGG	20355	ATAT C TAC
			TCCAAGGGG	CCA AGAG	
			GGGTTTCTC	GGT TCTC	
			_____	TT	
GAM2136	XPO5	3'	TGCTCTGGGTTTCTGTGGA	92878	A GG TAT A
			TCCA GG A	CC CAGAGTA	
			AGGT TC T	GG GTCTCGT	
			G TT		
GAM2136	ZDHC5	3'	GTGCTCCTACTGGCCCCCTTGGGA	93188	ATAT CA__
			TCCAAGGGG	CCA GAGTAC	
			AGGTTCCCC	GGT CTCGTG	
			_____	CATC	
GAM2136	ZIM2	5'	GACTCTGTTCCTGTGGA	31721	AG TATCC AC
			TCCA GGGA	ACAGAGT	
			AGGT TCCT	TGTCTCA	
			G_	GT	
GAM2136	LOC129526	3'	GTATTCAACATGACTTTTGGGA	75388	A CCACA
			TCCAAGGGG TAT	GAGTAC	
			AGGTTTTTC GTA	CTTATG	
			A CAA		
GAM2136	LOC144266	5'	GTGTAGGCAGATGGTTCCTTTG	77269	AT_____ GAGTAC
			GG	TCCAAGGGGAT	CC ACA
			GGGTTTCCTTG	GG TGT	
			GTAGAC A	G C	
GAM2136	LOC144747	5'	GTATTCCTATGTGTTTCTTTGG	77472	GG CCACA
			CCAAGG ATAT	GAGTAC	
			GGTTTC TGTG	CTTATG	
			TT TATC		
GAM2136	LOC144871	3'	GTACTTTGTGGATATTTGCCC	84129	_____
			GGG GATATCCACAGAGTAC		
			CCC TTATAGGTGTTTCATG		
			GTT		
GAM2136	LOC146059	3'	GTGTTTGTATCTCTTGGGA	78088	_____ TC
			TCCAAGGG	GATA CAC	

	AGGTTCTC TTGT GTG	
	TAT TT	
GAM2136 LOC146780 5'	TACTCCTACCCCTTTGGG 84822	A TCCACA
	TCCAAGGGG TA GAGTA	
	GGGTTTCCC AT CTCAT	
	C C_____	
GAM2136 LOC146819 3'	GTATTCTTCATTATCCTTTTG 78742	TCCAC
	CAAGGGGATA AGAGTAC	
	GTTTTCCTAT TCTTATG	
	TACT_	
GAM2136 LOC146821 3'	GTATTCTTAATTATCCTTTTG 78731	TCCAC
	CAAGGGGATA AGAGTAC	
	GTTTTCCTAT TCTTATG	
	TAAT_	
GAM2136 LOC147381 5'	GTACTTTTGTTTTTGTTTTTG 85140	G TCC _
	GA TCCAAGGG ATA ACAGA GTAC	
	AGGTTTTT TGT TGTTT CATG	
	_ TTT T	
GAM2136 LOC148932 3'	GTATTATACGTGTCCTCCTGGG 79849	A CCACAG
	TCCA GGGGATAT AGTAC	
	GGGT CTCCTGTG TTATG	
	C CATA__	
GAM2136 LOC149460 5'	GTGTTTCATATTTTTTTGGA 85615	C__
	TCCAAGGGGATAT CAC	
	AGGTTTTTTTATA GTG	
	CTTT	
GAM2136 LOC149461 3'	GTGTTTCATATTTTTTTGGA 80204	C__
	TCCAAGGGGATAT CAC	
	AGGTTTTTTTATA GTG	
	CTTT	
GAM2136 LOC150481 3'	TGGGGGGTGTCTTTTTTGGG 80718	_ A_
	TCCAAGG GGATATCC CA	
	GGGTTTT CCTGTGGG GT	
	T GG	
GAM2136 LOC154877 5'	TGCTCTGTGCTGCTTGGG 87582	G ATATC
	TCCAAG GG CACAGAGTA	
	AGGTTC TC GTGTCTCGT	
	G _____	
GAM2136 LOC158191 3'	TGGGGGGTGTCTTTTTTGGG 82687	_ A_
	TCCAAGG GGATATCC CA	

		GGGTTTT CCTGTGGG GT	
		T GG	
GAM2136	LOC158314 3'	GTGCTCATCACTTGGCTTTTTG 88099	ATATCCACA
	GG	TCCAAGGGG GAGTAC	
		GGGTTTTTC CTCGTG	
		GGTTCACTA	
GAM2136	LOC158819 3'	GTATTTCAAGATTATCCCTTAG 88285	TCCACA
	G	CC AAGGGGATA GAGTAC	
		GG TTCCCTTAT TTTATG	
		A TAGAC_	
GAM2136	LOC165283 3'	GTACAGGTCGGATGTGTTTTTG 88547	G _ AGA
	GG	TCCAAGGG ATATCC AC GTAC	
		GGGTTTTT TGTAGG TG CATG	
		G C GA_	
GAM2136	LOC200982 3'	GTATTTCTCCATGTCCCTATGG 91813	A CCACA
	G	TCCA GGGGATAT GAGTAC	
		GGGT TCCCTGTA TTTATG	
		A CCTC_	
GAM2136	LOC202020 5'	TGCTTTTGTGTCTCTTTG 90604	CCAC
		CAAGGGGATAT AGAGTA	
		GTTTCTCTGTG TTTCGT	
		T__	
GAM2136	LOC219540 3'	GTACTTAAATTTATTTTCTAGG 95246	A GG TCCACA
	A	TCC AG GATA GAGTAC	
		AGG TC TTAT TTCATG	
		A TT TTA__	
GAM2136	LOC221272 3'	GTACTTGTCTATGTCTTTGGG 95249	G TC CAG
		TCCAAGGG ATA CA AGTAC	
		GGGTTTCT TAT GT TCATG	
		G CT _	
GAM2136	LOC221288 3'	GTGCTTTATCTCTTTTGGA 95262	_ TC_
		TCCAAGGG GATA CAC	
		AGGTTTTCT CTAT GTG	
		T TTC	
GAM2136	LOC222060 5'	GTGCTCTGACCCTCTCCTGGG 95757	A TATCCA
		TCCA GGGGA CAGAGTAC	
		GGGT CCTCT GTCTCGTG	
		_ CCA_	
GAM2136	LOC222224 3'	GTGCTGAATATTCTCTTTGGG 95876	TATCCACAG
		TCCAAGGGGA AGTAC	

GGGTTTCTCT TCGTG
TATAAG____

GAM2136 LOC253698 3' GTGCTCTGTGCAGCCCCTTTGA 96547 C ATATC
TC AAGGGG CACAGAGTAC
|| ||| |
AG TTCCCC GTGTCTCGTG
T GAC__

GAM2136 LOC255838 3' GTGTTTTGTGCATGGAGTGCTT 97703 ATA ____
TTTGGG TCCAAGGGG TCC ACAGAGTAC
||||| || |||||
GGGTTTTTC AGG TGTTTTGTG
GTG TACG

GAM2136 LOC256374 3' GTGCTCTCACTGCATTTCCTT 96273 T C C__
TGGG TCCAAGGGGA AT CA AGAGTAC
||||| || |||||
GGGTTTCCT TA GT TCTCGTG
T C CAC

GAM2136 LOC91035 5' GTGCTCTGCCCTCTACCCTTGG 65304 GATATCCA
G TCCAAGGG CAGAGTAC
||||| |||||
GGGTTCCC GTCTCGTG
ATCTCCC_

GAM2136 LOC93259 5' GTTCTCCAGTGGCTTCTTGGG 72292 ATAT A_ T
TCCAAGGGG CCAC GAG AC
||||| ||| |||
AGGTTCTT GGTG CTC TG
_____ AC T

GAM2137 SCAMP1 3' GCTAAATAAATATTCTCC 18013 T C
GGA AATATT ATTTAGC
|| ||||| |||||
CCT TTATAA TAAATCG
C A

GAM2137 SCAMP1 3' GCTAAATAAATATTCTCC 54501 T C
GGA AATATT ATTTAGC
|| ||||| |||||
CCT TTATAA TAAATCG
C A

GAM2137 NX-17 3' TGAATATCAGCCCCTAATA 40706 ATA_
TATTAGGG ATATTCA
||||| |||||
ATAATCCC TATAAGT
CGAC

GAM2137 LOC161589 3' GCTAAATGAATATTATCCCTAA 83159
TA TATTAGGGATAATATTCATTAGC
|||||
ATAATCCCTATTATAAGTAAATCG

GAM2138 ACVR1 5' TGCAGTGCTGTGACCAT 8475 T TG
ATG TC ACAGCACTGCA
||| || |||||

			TAC AG TGTCGTGACGT		
			C _		
GAM2138	ATP7A	3'	GCACTGTGTATAAAACATCTA 5325	CTG_ G C	
			TAGATGTT ACA CA TGC		
			ATCTACAA TGT GT ACG		
			AATA _ C		
GAM2138	ELMO1	3'	GGTCAAGCTGTCAGACATC 56157	T AC C	
			GATGT CTGACAGC TG ACC		
			CTACA GACTGTCTG AC TGG		
			_ A _		
GAM2138	PPP3CA	3'	GTACAGTGATAAAGCATCTA 8138	CTGACAG C	
			TAGATGTT CACTG AC		
			ATCTACGA GTGAC TG		
			AATA_ A		
GAM2138	RHD	3'	GTGCAGTGCCGCAATCT 32838	GTTC ACA	
			AGAT TG GCACTGCAC		
			TCTA AC CGTGACGTG		
			_ GC_		
GAM2138	RHD	3'	GTGCAGTGCCGCAATCT 33149	GTTC ACA	
			AGAT TG GCACTGCAC		
			TCTA AC CGTGACGTG		
			_ GC_		
GAM2138	SEPX1	3'	GGCGCAGTGGTTGAAACATC 33378	CT AG A	
			GATGTT GAC CACTGC CC		
			CTACAA TTG GTGACG GG		
			AG _ C		
GAM2138	SLC17A5	3'	GCATGCTTTTCAGAACACCTA 25834	A C C	
			TAG TGTTCTGA AGCA TGC		
			ATC ACAAGACT TCGT ACG		
			C T _		
GAM2138	BCDO	3'	GCTCGGCTGTCAGAACTC 34285	T ACT	
			GA GTTCTGACAGC GC		
			CT CAAGACTGTCTG CG		
			_ GCT		
GAM2138	C5orf5	3'	AGTGTATCCAAACATCTA 33941	CT CA	
			TAGATGTT GA GCACT		
			ATCTACAA CT TGTGA		
			AC A_		
GAM2138	CASPR3	3'	GGTGCAGTGCTGTACCTGGCT 54456	ATGTTC	
	G		TAG TGACAGCACTGCACC		

GTC ACTGTCGTGACGTGG
 GGTCC_
 GAM2138 DKFZP434L1717 3' GGTGCAGCAGTGGAAACATCT 50454 G AGCA
 AGATGTTCT AC CTGCACC
 ||||| || |||||
 TCTACAAGG TG GACGTGG
 _ AC_
 GAM2138 DORFIN 5' GCTAGGACTACAGAACATC 31873 AC CA _
 GATGTTCTG AG CT GC
 ||||| || ||
 CTACAAGAC TC GA CG
 A_ AG T
 GAM2138 FLJ12270 5' GCAGTGGAATATCTA 48339 TGACAG
 TAGATGTTT CACTGC
 ||||| |||||
 ATCTATAAG GTGACG

 GAM2138 FLJ13193 3' TGCAATTGATAGAACATTTA 50739 A CAC
 TAGATGTTCTG CAG TGCA
 ||||| || ||||
 ATTTACAAGAT GTT ACGT
 A A_
 GAM2138 FLJ20123 5' GGTGCAGTGCCGGTACACATC 35073 TCTG A_
 GATGT AC GCACTGCACC
 |||| || |||||
 CTACA TG CGTGACGTGG
 CA_ GC
 GAM2138 GCMA 5' CAGTGCTGTCTGCTTCT 14668 T TCT
 AGA GT GACAGCACTG
 ||| || |||||
 TCT CG CTGTCGTGAC
 T T_
 GAM2138 ING4 3' GGCACAGTGCTGTCTATCCCTTC 60430 TGTTT CA
 T AGA TGACAGCACTG CC
 ||| ||||| ||
 TCT ACTGTCGTGAC GG
 TCCCT AC
 GAM2138 KIAA1037 3' GGTGCAGTGCCGGCCAGCTA 31136 A TT ACA
 TAG TG CTG GCACTGCACC
 ||| || |||||
 ATC AC GGC CGTGACGTGG
 G CC _
 GAM2138 MAP-1 3' GTGTCATCAAAACATCTA 42450 C CA
 TAGATGTT TGA GCAC
 ||||| || ||||
 ATCTACAA ACT TGTG
 A AC
 GAM2138 NS1-BP 3' TGCAGTACTAACATTTA 72942 CTGAC C
 TAGATGTT AG ACTGCA
 ||||| || |||||

ATTTACAA TC TGACGT
 _____ A
 GAM2138 PPP1R13B 3' TGCAGCACTGTAGCCCATC 31661 TT A CA
 GATG CTG CAG CTGCA
 |||| ||| ||| ||||
 CTAC GAT GTC GACGT
 CC _ AC
 GAM2138 SCAND1 5' GCAGTGCTGAGCACACAGCTA 54393 A TC A_
 TAG TGT TG CAGCACTGC
 ||| ||| || |||||
 ATC ACA AC GTCGTGACG
 G C_ GA
 GAM2138 SCAND1 5' GCAGTGCTGAGCACACAGCTA 33797 A TC A_
 TAG TGT TG CAGCACTGC
 ||| ||| || |||||
 ATC ACA AC GTCGTGACG
 G C_ GA
 GAM2138 SLC2A12 3' TAGTGCCAGAACACT 59741 A ACA
 AG TGTTCTG GCACTG
 || ||||| |||||
 TC ACAAGAC CGTGAT

 GAM2138 TSGA2 3' GGTGCAGTGCTGTGTGTATCTA 55953 TTCTG
 TAGATG ACAGCACTGCACC
 ||||| |||||
 ATCTAT TGTCGTGACGTGG
 GTG_
 GAM2138 LOC120526 3' GTGCAGTGCCATGATCTC 74466 T C ACA
 GA GTT TG GCACTGCAC
 || ||| || |||||
 CT TAG AC CGTGACGTG
 C T _
 GAM2138 LOC149401 3' GGCACAGTGGGGGGAACATC 80115 GACAG CA
 GATGTTCT CACTG CC
 ||||| ||||| ||
 CTACAAGG GTGAC GG
 GGG_ AC
 GAM2138 LOC207043 5' GTACAGTGCTGACATCTG 91079 TCTGA C
 TAGATGT CAGCACTG AC
 ||||| ||||| ||
 GTCTACA GTCGTGAC TG
 _____ A
 GAM2139 HOXC11 3' ACACACCTCGGCGACAATGT 60810 TG ACA
 ACATTGTTGCT GAG TGT
 ||||| ||| |||
 TGTAACAGCGG CTC ACA
 _ CAC
 GAM2139 CHL1 3' ACATGTTTTAGAAACAAT 22763 GCTTG
 ATTGTT GAGACATGT
 ||||| |||||

			TAACAA	TTTTGTACA		
			AGA__			
GAM2139	DKFZp547M236	5'	ACATGTTTAAAACAACG	38660	C	GG
			TGTTG TT AGACATGT			
			GCAAC AA TTTGTACA			
			_ AA			
GAM2139	EDG1	3'	GATTCATTTC AAGCAACAA	60051		ACAT
			TTGTTGCTTGGAG GTC			
			AACAACGAACTTT TAG			
			ACT_			
GAM2139	FLJ10120	3'	TCCCCAACAACAATGTG	36310	C	A
			CACATTGTTG TTGG GA			
			GTGTAACAAC AACC CT			
			_ C			
GAM2139	NR6A1	3'	ACATGTCTCTCCAACAACGT	9440	A	CTT
			AC TTGTTG GGAGACATGT			
			TG AACAAC TCTCTGTACA			
			C C_			
GAM2139	NR6A1	3'	ACATGTCTCTCCAACAACGT	54014	A	CTT
			AC TTGTTG GGAGACATGT			
			TG AACAAC TCTCTGTACA			
			C C_			
GAM2139	NR6A1	3'	ACATGTCTCTCCAACAACGT	54020	A	CTT
			AC TTGTTG GGAGACATGT			
			TG AACAAC TCTCTGTACA			
			C C_			
GAM2139	LOC124538	3'	ACACACTCGCAACAATG	76150		TTG ACA
			CATTGTTGC GAG TGT			
			GTAACAACG CTC ACA			
			_ AC_			
GAM2140	FGF13	3'	ACCAAGAAAATGTAAAAGACC	54441		CAGG _
			GGTCTT GC TTCTTGGT			
			CCAGAA TG AAGAACCA			
			AA_ TAA			
GAM2140	INSRR	3'	ACCCGTGGCCCTGAAGACGGTG	68987	G	TCTT
			CACCG TCTTCAGGGCT GGT			
			GTGGC AGAAGTCCCGG CCA			
			_ TGC_			
GAM2140	LOXL3	3'	ACCAAGAAACCCATGTCAGC	51865	CTT _	C
			GT CA GGG TTCTTGGT			

		CG GT CCC AAGAACCA		
		ACT A A		
GAM2140	RAP1GA1	3' ACCTCTGCCCTGAAGACC	12767	TTCTT
		GGTCTTCAGGGC	GGT	
		CCAGAAGTCCCG	CCA	
		TCT__		
GAM2140	XRCC5	5' ACCAAAGCGCCTGAGGACCGG	41239	_ CT
		CCGGTCTTCAGG	GCTT TGGT	
		GGCCAGGAGTCC	CGAA ACCA	
		G _		
GAM2140	EDG1	5' CCACCCCTGAAGCCAGTG	60049	C T CTTCT
		CAC GG CTTCAGGG	TGG	
		GTG CC GAAGTCCC	ACC	
		A _ C__		
GAM2140	KIAA0323	3' CCAAGAAGGGAAACGGTG	63947	GTC AGGG
		CACCG TTC CTTCTTGG		
		GTGGC AGG	GAAGAACC	
		AA_ _		
GAM2140	MGC15875	5' ACCAGCGCCCGAAGGCCG	53011	A TTC
		CGGTCTTC GGGC	TTGGT	
		GCCGGAAG CCCG	GACCA	
		_ C_		
GAM2140	LOC199786	3' ACCAAGTTGCGGAGACCGGT	89730	AGG TT
		ACCGGTCTTC GC CTTGGT		
		TGGCCAGAGG	CG GAACCA	
		_ TT		
GAM2140	LOC200030	3' ACCAAGAAGAGGAAGAAGACC	80119	AGGG_
		GGTCTTC CTTCTTGGT		
		CCAGAAG	GAAGAACCA	
		AAGGA		
GAM2140	LOC200030	3' ACCAAGAAGAGGAAGAAGACC	80120	AGGG_
		GGTCTTC CTTCTTGGT		
		CCAGAAG	GAAGAACCA	
		AAGGA		
GAM2140	LOC200030	3' ACCAAGAAGTGGAAGAAGACC	80121	AGG_
		GGTCTTC GCTTCTTGGT		
		CCAGAAG	TGAAGAACCA	
		AAGG		
GAM2140	LOC200030	3' ACCAAGAAGTGGAAGAAGACC	80122	AGG_
		GGTCTTC GCTTCTTGGT		

			CCAGAAG TGAAGAACCA		
			AAGG		
GAM2140	LOC200030	3'	ACCAAGAAGTGGGAAGAAGACC 80123	AGG_	
			GGTCTTC GCTTCTTGGT		
			CCAGAAG TGAAGAACCA		
			AAGG		
GAM2140	LOC204285	3'	ACCAAGAAGCTTCCAAACGAC 91009	TTCA__	
			GTC GGGCTTCTTGGT		
			CAG TTCGAAGAACCA		
			CAAACC		
GAM2140	LOC51629	3'	ACCAAGAAGCCCTCAGCCTGGT 32604	T TC	
		G	CACCGG CT AGGGCTTCTTGGT		
			GTGGTC GA TCCCGAAGAACCA		
			C C_		
GAM2141	AKAP1	3'	ACTATGGGTTCTCTTCGCAA 14472	A CTT C	
			TTTGT GA GGAACCCA AGT		
			AAACG CT TCTTGGGT TCA		
			_ TC_ A		
GAM2141	AKAP1	3'	ACTATGGGTTCTCTTCGCAA 58373	A CTT C	
			TTTGT GA GGAACCCA AGT		
			AAACG CT TCTTGGGT TCA		
			_ TC_ A		
GAM2141	EGF	3'	ACTATAGGTTTTGGTTCCACAA 10488	A C TG CAC	
			TTGT GA T GAACC AGT		
			AACA CT G TTTGG TCA		
			C T GT ATA		
GAM2141	EZH1	3'	GACTGTGGGTTCCAAATTAC 10551	AC	
			GTAG TTGGAACCCACAGTC		
			CATT AACCTTGGGTGTCAG		
			A_		
GAM2141	STAC	3'	GACTGTGGAGTAATAGCCACAA 13427	AGA TGGA _	
		A	TTTGT CT AC CCACAGTC		
			AAACA GA TG GGTGTCAG		
			CC_ TAA_ A		
GAM2141	CCR1	3'	GACTGTGGGCTCCATTC 8927	CT A	
			GA TGGA CCCACAGTC		
			CT ACCT GGGTGTCAG		
			T_ C		
GAM2141	FLJ10483	3'	GACTGTGGAAGAGATTACAAA 36652	A GGAAC	
			TTTGTAG CTT CCACAGTC		

		AAACATT GAG	GGTGT CAG	
		A AA__		
GAM2141 KIAA1871	3'	ACTGTAAGAGTCTACAAA	61890	GGAACCC
		TTTGTAGACTT ACAGT		
		AAACATCTGAG TGTCA		
		AA_____		
GAM2141 LOC150821	3'	GGGTTCCACATCCACAAA	60944	A CT
		TTTGT GA TGGAACCC		
		AAACA CT ACCTTGGG		
		C AC		
GAM2141 LOC151057	3'	ACTGTGGGTACACCTATAAA	86379	ACT GA
		TTTGTAG TG ACCCACAGT		
		AAATATC AC TGGGTGTCA		
		C__ A_		
GAM2141 LOC157507	5'	ACTGTAAAAGTCTGCAAA	82377	GGAACCC
		TTTGTAGACTT ACAGT		
		AAACGTCTGAA TGTCA		
		AA_____		
GAM2141 LOC203339	5'	GGATTCCCAGTCTACAAA	92214	T C
		TTTGTAGACT GGAA CC		
		AAACATCTGA CCTT GG		
		C A		
GAM2141 LOC51030	3'	ACTGTAAATTAAACCAATCTAC	32695	C AACCC__
	AAA	TTTGTAGA TTGG ACAGT		
		AAACATCT AACC TGTCA		
		_ AAATTA AA		
GAM2141 LOC90906	3'	GACTGTGGATCCCAAACCTTTGC	64951	C_ AAC
	A	TGTAGA TTGG CCACAGTC		
		ACGTTT AACC GGTGTCAG		
		CA CTA		
GAM2142 DBCCR1	3'	CCGGGACTCCTTGCCATG	28240	A AAGC
		TATGGCAAG AGTCC TGG		
		GTACCGTTC TCAGG GCC		
		C _____		
GAM2142 OPHN1	5'	CTCCAGCTCTAACCTCGCC	11908	AA A CCA
		GGC GA GT AGCTGGAG		
		CCG CT CA TCGACCTC		
		_ C ATC		
GAM2142 PBX3	3'	CTAAATTGAACTTCTTGC	21668	C GC
		GCAAGAAGT CAA TGG		

CGTTCTTCA GTT ATC
A AA
GAM2142 RFXANK 5' CTCCAGTTTGCCTCCTGCTATA 14941 A A TC
TATGGCA GA G CAAGCTGGAG
||||| ||| |||||
ATATCGT CT C GTTTGACCTC
C _C_
GAM2142 FLJ20174 3' CAGCTTGGACTTCCTGCC 35190 A
GGCA GAAGTCCAAGCTG
||| |||||
CCGT CTTCAGGTTTCGAC
C
GAM2142 KIAA0495 5' CTCCAGCTCGGACGGACCCA 63263 CAAGAA A
TGG GTCC AGCTGGAG
||| ||| |||||
ACC CAGG TCGACCTC
CAGG_ C
GAM2142 KIAA0522 3' CCAGCCCAGACCTCTTCGGCT 72422 _ A CAA
GGC AAGA GTC GCTGG
||| ||| ||| |||||
TCG TTCT CAG CGACC
GC C ACC
GAM2142 KIAA0557 3' CTCCAGCTTCTTCATCCTGCCA 78554 A_ TCC
TGGCA GAAG AAGCTGGAG
||||| ||| |||||
ACCGT CTTT TTCGACCTC
CCTA _
GAM2142 STK29 5' CTCTGCGCTGGACTTCTGCCA 88963 A A _
TGGCA GAAGTCCA GC TGGAG
||||| ||||| || |||||
ACCGT CTTCAGGT CG GTCTC
_ _ C
GAM2142 LOC257101 5' CCAGCCTGGACTTCCAGCT 98693 AA A
GGC GAAGTCCA GCTGG
||| ||||| |||||
TCG CTTCAGGT CGACC
AC C
GAM2143 AMPD3 5' GGGCCTCAGTGCCAGCAG 6655 GA TTA
CTGC GGC TGAGGCC
||||| ||| |||||
GACG CCG ACTCCGGG
A_ TG_
GAM2143 BMP1 3' GGGCCTCACATTCCAGT 21534 C GCTTA
ACTG GAG TGAGGCC
||||| ||| |||||
TGAC CTT ACTCCGGG
_ AC_
GAM2143 FMR1 5' TGGGCCTCGAGCGCCCGCAG 10682 A TTA
CTGCG GGC TGAGGCCCA
||||| ||| |||||

GACGC CCG GCTCCGGGT
 _ CGA
 GAM2143 PABPN1 5' TGGGCCTCACCCGGCCAACAGC 17360 A CGA TA_
 TC GA CTG GGCT TGAGGCCCA
 || ||| ||| |||||
 CT GAC CCGG ACTCCGGGT
 C AA_ CCC
 GAM2143 PRKY 5' TGGGCCCCCGCCTTCCTCGCAG 12390 CTTA A_
 CTGCGAGG TG GGCCA
 ||||| || |||||
 GACGCTCC GC CCGGT
 TTCC CC
 GAM2143 SLC9A3R2 3' TGGGCCTCAGCCTGCCCGAGC 62103 A G A TTA_
 TC GA CT CG GGC TGAGGCCCA
 || ||| ||| |||||
 CT GA GC CCG ACTCCGGGT
 C _ C TCCG
 GAM2143 TR2 5' TGGGCCTCATCGAGCGCAG 72779 GAG _
 CTGC GCTT ATGAGGCCCA
 ||| ||| |||||
 GACG CGAG TACTCCGGGT
 _ C
 GAM2143 WNT11 3' TGAGCCCCAGCCCGCCCCTGCA 17325 A_ TTA_ A C
 GTTC GAACTGCG GGC TG GGC CA
 ||||| ||| || ||| ||
 CTTGACGT CCG AC CCG GT
 CC CCCG C A
 GAM2143 DKFZP761G1913 3' TGGGCCTCATTATCTCCCA 49700 C CTT
 TG GAGG ATGAGGCCCA
 || ||| |||||
 AC CTCT TACTCCGGGT
 C AT_
 GAM2143 FLJ12700 3' TGAACCAGTGACCTGCAGTTC 46661 G C GA CC
 GAACTGC AGG TTAT GG CA
 ||||| ||| ||| || ||
 CTTGACG TCC AGTG CC GT
 _ _ A_ AA
 GAM2143 FLJ20424 5' GGGCCTCGCTTCCCCCAG 35618 C_ TTAT
 CTG GAGGC GAGGCC
 || ||| |||||
 GAC CTTG CTCCGGG
 CCC _
 GAM2143 GT650 3' TGGGCCCCATCTCTCCACTGTC 54556 AC_ C CTT A
 GA TG GAGG ATG GGCCA
 || || ||| ||| |||||
 CT AC CTCT TAC CCGGT
 GTC _ C_ C
 GAM2143 KIAA0408 5' TCAAAGCCTTGCAGTTC 28801 A
 GAACTGCGAGGCTT TGA
 ||||| ||| |||

CTTGACGTTCCGAA ACT

GAM2143 MGC23445 5' GGGCTTGAGAGCCTCGC 58773 ATG
GCGAGGCTT AGGCC
||||||| |||||
CGCTCCGAG TTCGGG

AG_

GAM2143 PDE4DIP 3' TGGGCCTCATTCCTCCAAGTC 97178 AC C CTT
GA TG GAGG ATGAGGCCCA
|| ||||| |||||
CT AC CTCC TACTCCGGGT

GA _ T_

GAM2143 PLEKHA3 5' TGGGCCCGCGCCTCGCGG 39381 TTA A
CTGCGAGGC TG GGCCA
||||||| |||||
GGCGCTCCG GC CCGGT

C_ _

GAM2143 SDCCAG3 5' GCCCGGAGCCTCGCCATTC 22801 CT A A
GAA GCGAGGCTT TG GGC
||| ||||| |||||
CTT CGCTCCGAG GC CCG

AC _ _

GAM2143 TBL1Y 5' GGGCCTCACAGGCTGC 53863 GA A
GC GGCTT TGAGGCC
|| ||||| |||||
CG TCGGA ACTCCGGG

_ C

GAM2143 TBL1Y 5' GGGCCTCACAGGCTGC 56953 GA A
GC GGCTT TGAGGCC
|| ||||| |||||
CG TCGGA ACTCCGGG

_ C

GAM2143 TBL1Y 5' GGGCCTCACAGGCTGC 56956 GA A
GC GGCTT TGAGGCC
|| ||||| |||||
CG TCGGA ACTCCGGG

_ C

GAM2143 TREX1 5' GGCCTCAGGACCACAGGTTTC 54383 GCGA C A
GAACT GG TT TGAGGCC
||||| |||||
CTTGG CC AG ACTCCGG

ACA_ _ G

GAM2143 TREX1 5' GGCCTCAGGACCACAGGTTTC 54389 GCGA C A
GAACT GG TT TGAGGCC
||||| |||||
CTTGG CC AG ACTCCGG

ACA_ _ G

GAM2143 LOC126528 5' GGTCAGCCTCGCAATTC 75030 C TATGA C
GAA TGCGAGGCT GGC C
||| ||||| |||

CTT ACGCTCCGA CTG G
 A _____ A
 GAM2143 LOC153260 5' GGGCCCAGCCCTCGCAG 81674 CTTA A
 CTGCGAGG TG GGCCC
 ||||| |||||
 GACGCTCC AC CCGGG
 CG__ _
 GAM2143 LOC155382 3' TGAGCCCTCGGCCCTCGCAG 87678 CTTA _ C
 CTGCGAGG TGAGG C CA
 ||||| |||||
 GACGCTCC GCTCC G GT
 CG__ C A
 GAM2143 LOC158434 5' GGGCCTCCTGCTCCAGCTC 88162 A C G TTAT
 GA CTG GAG C GAGGCC
 || ||| | |||||
 CT GAC CTC G CTCCGGG
 C _ _ TC__
 GAM2143 LOC196872 5' GGCCGGCTCTGAGCCTCACAGC 89158 A C TGA__
 TC GA CTG GAGGCTTA GGCC
 || ||| ||||| |||||
 CT GAC CTCCGAGT CCGG
 C A CTCGG
 GAM2143 LOC257428 3' GGCCTCATCATTACAGTC 95933 A C GCTT
 GA CTG GAG ATGAGGCC
 || ||| ||| |||||
 CT GAC CTT TACTCCGG
 _ A AC__
 GAM2144 GCNT2 3' CCTTAACAGTCACCACTGTGC 9453 CC
 GCACGGTGGTGA CTGT GGG
 ||||| ||||| |||||
 CGTGTCACTGACA TCC
 AT
 GAM2144 MAPK7 3' CCTGAGCCACCACCGAGC 12309 A ACT TC
 GC CGGTGGTG G CGGG
 || ||||| | |||||
 CG GCCACCAC C GTCC
 A ____ GA
 GAM2144 MAPK7 3' CCTGAGCCACCACCGAGC 58160 A ACT TC
 GC CGGTGGTG G CGGG
 || ||||| | |||||
 CG GCCACCAC C GTCC
 A ____ GA
 GAM2144 MAPK7 3' CCTGAGCCACCACCGAGC 58162 A ACT TC
 GC CGGTGGTG G CGGG
 || ||||| | |||||
 CG GCCACCAC C GTCC
 A ____ GA
 GAM2144 MAPK7 3' CCTGAGCCACCACCGAGC 58164 A ACT TC
 GC CGGTGGTG G CGGG
 || ||||| | |||||

			CG GCCACCAC C GTCC		
			A ____ GA		
GAM2144	PYGB	3'	CCCTGACCACCACTGTGC 12690	ACT	C
			GCACGGTGGTG GTC GGG		
			CGTGTCAACCAC CAG CCC		
			____ T		
GAM2144	RORB	5'	CATCAAAACAGTCACCACC 23586	CCGG	
			GGTGGTGACTGT GATG		
			CCACCACTGACA CTAC		
			AAA_		
GAM2144	HMG17L1	5'	CATCCCACTGCCATCATCACCA 41048	C	CT CC_
			TGC GCA GGTGGTGA GT GGGATG		
			CGT CCACTACT CG CCCTAC		
			A AC TCA		
GAM2144	KIAA1856	3'	CCCAAGGCCTCCACCGTGC 94228	T CT	C_
			GCACGGTGG GA GTC GGG		
			CGTGCCACC CT CGG CCC		
			_ C_ AA		
GAM2144	KIAA1879	5'	CTGTCTGCAGTCACCACCGGC 73940	A	C_
			GC CGGTGGTGACTGT CGG		
			CG GCCACCACTGACG GTC		
			_ TCT		
GAM2144	SCYA22	3'	CCCTTGGTCACCTCCGTGC 92586	T	TCC
			GCACGG GGTGACTG GGG		
			CGTGCC CCACTGGT CCC		
			T T_		
GAM2144	LOC92609	3'	CATCCAGACGCCACACCTGC 73206	C	G AC C
			GCA GGTG TG TGTC GGGATG		
			CGT CCAC AC GCAG CCCTAC		
			_ _ C_ A		
GAM2145	GPD1	3'	TCATGCCACCACATTTG 60398	C	C
			TAAATG GGTGGCAT GA		
			GTTTAC CCACCGTA CT		
			A _		
GAM2145	IL5RA	5'	TCGCATGGCCACCGCATTT 6906	AT_	
			AAATGCGGTGGC CGA		
			TTTACGCCACCG GCT		
			GTAC		
GAM2145	MYO1C	3'	TGCCGATGCCAAATATTTG 61873	CGG	A
			TAAATG TGGCATCG CA		

			GTTTAT ACCGTAGC GT	
			AA_ C	
GAM2145	C6orf37	3'	TGTCACACTGCATTTA 68097	GCATC
			TAAATGCGGTG GACA	
			ATTTACGTCAC CTGT	
			A____	
GAM2145	DNAJC6	3'	TTGCAGAACCACCGCATT 29498	CA GA
			AATGCGGTGG TC CAA	
			TTACGCCACC AG GTT	
			A_ AC	
GAM2145	FLJ11210	3'	GTCGATGTGCATGCTTTTA 60319	T GTG
			TAAA GCG GCATCGAC	
			ATTT CGT TGTAGCTG	
			T ACG	
GAM2145	FLJ12476	3'	TCGATCTTCTGCATTTA 43270	T C
			TAAATGCGG GG ATCGA	
			ATTTACGTC TC TAGCT	
			T _	
GAM2145	KIAA1034	3'	TCGATGGCATCCGCATTTG 63134	_ G
			TAAATGCGG TG CATCGA	
			GTTTACGCC AC GTAGCT	
			T G	
GAM2145	KIAA1987	3'	TCATGTAAGTGCATTTA 89391	G C
			TAAATGCGGT GCAT GA	
			ATTTACGTCA TGTA CT	
			A _	
GAM2145	MGC16063	3'	TGTCCTGGCCACTGCATT 54929	ATC
			AATGCGGTGGC GACA	
			TTACGTCACCG CTGT	
			GTC	
GAM2145	LOC147949	3'	TGTCAGATGTCCACATTGCA 79279	_ _ _
			TGCG GTGG CATC GACA	
			ACGT CACC GTAG CTGT	
			TA T A	
GAM2145	LOC150577	3'	GTCCTCACCGCATTTG 86258	CATC
			TAAATGCGGTGG GAC	
			GTTTACGCCACT CTG	
			C____	
GAM2145	LOC158219	3'	TGTGTGTCACCACATTT 82694	C CG
			AAATG GGTGGCAT ACA	

TTTAC CCACTGTG TGT
 A ____
 GAM2145 LOC202020 3' TGTCTCACCACATTTA 90605 C CATC
 TAAATG GGTGG GACA
 ||||| ||||| ||||
 ATTTAC CCACT CTGT
 A ____
 GAM2145 LOC90826 5' TGTCGATGCAGGTTTATTTG 64788 CGGTG
 TAAATG GCATCGACA
 ||||| |||||
 GTTTAT CGTAGCTGT
 TTGGA
 GAM2145 LOC93587 3' TTGTCTTTACCTGCATTTA 73042 _ CATC
 TAAATGC GGTGG GACAA
 ||||| ||||| ||||
 ATTTACG CCATT CTGTT
 T T____
 GAM2146 DFNA5 3' TGGTGACCCAGCATCTGA 16601 C CA
 TCA ATGC GGTCACCA
 ||| ||| |||||
 AGT TACG CCAGTGGT
 C AC
 GAM2146 MYO1C 3' TGACCCCTCCCTGGCATGGGA 61871 A TCACCA
 TC CATGCCAGG GGTCA
 || ||||| ||||
 AG GTACGGTCC CCAGT
 G CTCC____
 GAM2146 NUFIP1 3' TGGAACACCTGGCATGTGA 25638 CA_
 TCACATGCCAGGT CCA
 ||||| ||||| |||
 AGTGTACGGTCCA GGT
 CAA
 GAM2146 STAU 3' TGACCTGGCGGTCCCTACGCA 34351 C_ _ A
 TGC AGG TC CCAGGTCA
 ||| ||| || |||||
 ACG TCC GG GGTCCAGT
 CA CT C
 GAM2146 STAU 3' TGACCTGGCGGTCCCTACGCA 34354 C_ _ A
 TGC AGG TC CCAGGTCA
 ||| ||| || |||||
 ACG TCC GG GGTCCAGT
 CA CT C
 GAM2146 STAU 3' TGACCTGGCGGTCCCTACGCA 17203 C_ _ A
 TGC AGG TC CCAGGTCA
 ||| ||| || |||||
 ACG TCC GG GGTCCAGT
 CA CT C
 GAM2146 STAU 3' TGACCTGGCGGTCCCTACGCA 34357 C_ _ A
 TGC AGG TC CCAGGTCA
 ||| ||| || |||||

ACG TCC GG GGTCCAGT
 CA CT C
 GAM2146 FLJ20300 5' TGACCTGGTCATTTTGGCTGT 35380 T TC_
 ACA GCCAGG ACCAGGTCA
 ||| ||||| |||||
 TGT CGGTTT TGGTCCAGT
 _ TAC
 GAM2146 HEMK 3' TGACCTGGCAGCCCATGT 32967 CCA CA
 ACATG GGT CCAGGTCA
 |||| | |||||
 TGTAC CCG GGTCCAGT
 _ AC
 GAM2146 KIAA0495 5' GACCTGGTGGTGAAGCACCTGA 63267 CA CAGG
 TCA TGC TCACCAGGTC
 || | |||||
 AGT ACG GGTGGTCCAG
 CC AAGT
 GAM2146 KIAA0514 3' ACCCAAGTAGTGCCTGGCACTG 28735 _ T CA____
 CA TGCCAGG CAC GGT
 || ||||| || |
 GT ACGGTCC GTG CCA
 C _ ATGAAC
 GAM2146 KIAA1940 3' ACCTGGCTTGGACATG 80774 _ TCA
 CATG CCAGG CCAGGT
 ||| |||| |
 GTAC GGTTT GGTCCA
 A _
 GAM2146 MGC29761 5' GACCTTGCTCCTGGTCACGTGA 58976 A _ TCACC
 TCAC TG CCAGG AGGTC
 ||| || |||| |
 AGTG AC GGTCC TCCAG
 C T TCGT_
 GAM2146 SLC26A9 3' TGACCCAGTGACCTGGAGTTGA 54722 CATG CA
 TCA CCAGGTCAC GGTCA
 || | ||||| |||||
 AGT GGTCCAGTG CCAGT
 TGA_ AC
 GAM2146 SLC26A9 3' TGACCCAGTGACCTGGAGTTGA 57010 CATG CA
 TCA CCAGGTCAC GGTCA
 || | ||||| |||||
 AGT GGTCCAGTG CCAGT
 TGA_ AC
 GAM2146 LOC139221 5' TGACCTGGGCAATCTGCATGTG 76330 C CA_
 A TCACATGC AGGT CCAGGTCA
 ||||| || | |||||
 AGTGTACG TCTA GGTCCAGT
 _ ACG
 GAM2146 LOC150577 3' ACCTGGTGATGCACGTG 86248 A CAG
 CAC TGC GTCACCAGGT
 || | |||||

		GTG ACG TAGTGGTCCA		
		C ____		
GAM2146	LOC151258 5'	TGACCTGGTAACATTTGG	81003	C__
		CCAGGT ACCAGGTCA		
		GGTTTA TGGTCCAGT		
		CAA		
GAM2146	LOC219653 3'	GGTGACCTGGCTATGTGA	92920	_
		TCACAT GCCAGGTCACC		
		AGTGTA CGGTCCAGTGG		
		T		
GAM2146	LOC51696 3'	ACCTGATTTGGGCAGTGA	33075	A _ CCA
		TCAC TGCC AGGTCA GGT		
		AGTG ACGG TTTAGT CCA		
		_ G ____		
GAM2146	LOC90768 5'	GAGCTGGACCTGGCTGTGA	64654	T CA G
		TCACA GCCAGGT CCAG TC		
		AGTGT CGGTCCA GGTC AG		
		_ _ G		
GAM2146	LOC91464 5'	ACCTGGTGATTGTGCAGGCA	66708	A____
		TGCC GGTCACCAGGT		
		ACGG TTAGTGGTCCA		
		ACGTG		
GAM2147	CDC25C 5'	GCAGAGCTGCAATCTAGTT	10134	TCAGG
		AACTA GCAGCTCTGC		
		TTGAT CGTCGAGACG		
		CTAA_		
GAM2147	CDC25C 5'	GCAGAGCTGCAATCTAGTT	43332	TCAGG
		AACTA GCAGCTCTGC		
		TTGAT CGTCGAGACG		
		CTAA_		
GAM2147	FBXW1B 3'	GCACTGTTGCCCTGACAGT	54444	A TC
		ACT TCAGGGCAGC TGC		
		TGA AGTCCCGTTG ACG		
		C TC		
GAM2147	FBXW1B 3'	GCACTGTTGCCCTGACAGT	54447	A TC
		ACT TCAGGGCAGC TGC		
		TGA AGTCCCGTTG ACG		
		C TC		
GAM2147	FBXW1B 3'	GCACTGTTGCCCTGACAGT	25474	A TC
		ACT TCAGGGCAGC TGC		

			TGA AGTCCCGTTG ACG		
			C TC		
GAM2147	FOXD2	3'	CAGAATCTCGCAGATAGTTG 16784	AGG _ C_	
			CAACTATC GC AG TCTG		
			GTTGATAG CG TC AGAC		
			A_ C TA		
GAM2147	GALNT2	3'	GCAAAGCGTGCCGAAGTT 16816	A AG _ C	
			AACT TC GGCA GCT TGC		
			TTGA AG CCGT CGA ACG		
			_ _ G A		
GAM2147	GORASP1	3'	GCAGTCTGACCCAAAGTTG 49955	ATCA _ CT	
			CAACT GGG CAG CTGC		
			GTTGA CCC GTC GACG		
			AA_ A T_		
GAM2147	HEM1	5'	GCAGAGCTACTTTTCTTGTTG 19238	TATC C	
			CAAC AGGG AGCTCTGC		
			GTTG TTTC TCGAGACG		
			TTCT A		
GAM2147	ITGAM	3'	CAGAGCTGCCTCTCGGTG 7146	_ _	
			TATC AG GGCAGCTCTG		
			GTGG TC CCGTCGAGAC		
			C T		
GAM2147	KERA	3'	GCAGATTGCTAAGTAGCTG 23846	A CAG C	
			CA CTAT GGCAG TCTGC		
			GT GATG TCGTT AGACG		
			C AA_ _		
GAM2147	MPO	3'	GCAGAGCTGGACCAAGTGG 6002	CA G_	
			CTAT GG CAGCTCTGC		
			GGTG CC GTCGAGACG		
			A_ AG		
GAM2147	NFE2	5'	GCAGGGTGACCCCTGATGTTG 21601	T CA_	
			CAAC ATCAGGG GCTCTGC		
			GTTG TAGTCCC TGGGACG		
			_ CAG		
GAM2147	PIK3R3	5'	GCAGAGCTTGAGGGCAGTTG 61706	AT AGGG _	
			CAACT C CA GCTCTGC		
			GTTGA G GT CGAGACG		
			CG GA_ T		
GAM2147	PLXNA1	3'	CAGGCTGCCCTGGCAGCTG 72770	A AT T	
			CA CT CAGGGCAGC CTG		

GT GA GTCCCGTCG GAC
 C CG _
 GAM2147 PRODH 3' GCAGAGCTGCTGGAGGT 33395 A AG
 ACT TC GGCAGCTCTGC
 ||| || |||||
 TGG AG TCGTCGAGACG
 _ G_
 GAM2147 SACM1L 3' CAGAATTGATCTGATGTT 26693 T GG C
 AAC ATCAG CAG TCTG
 ||| ||||| ||| |||||
 TTG TAGTC GTT AGAC
 _ TA A
 GAM2147 SGK 3' CAGCTCTGCGCATTCCCTGATAA 20062 C _____ GCTC
 TTG CAA TATCAGG GCA TG
 ||| ||||| ||| ||
 GTT ATAGTCC CGT AC
 A TTACG____ CTCG
 GAM2147 TAF1C 3' GCAGAGCTGCTGATGAGGT 20266 A G_
 ACT TCA GGCAGCTCTGC
 ||| ||| |||||
 TGG AGT TCGTCGAGACG
 _ AG
 GAM2147 ZNF26 5' GCAGAGCTGTCCAGATGGCTG 73339 A A
 CA CTATC GGGCAGCTCTGC
 || ||||| |||||
 GT GGTAG CCTGTCGAGACG
 C A
 GAM2147 ARHGEF9 3' GCAGAGTGTTTTGGTAG 31487 G
 CTATCAGGGCA CTCTGC
 ||||| |||||
 GATGGTTTTGT GAGACG
 _
 GAM2147 CA5A 5' GCAGAGCTGCATTTAGTT 69154 TCAGG
 AACTA GCAGCTCTGC
 |||| |||||
 TTGAT CGTCGAGACG
 TTA_
 GAM2147 CLSTN2 3' CAGAGCTGGTCCCTAGTT 42400 ATC _
 AACT AGGG CAGCTCTG
 |||| ||| |||||
 TTGA TCCC GTCGAGAC
 _ TG
 GAM2147 DCTN3 3' GCAGAGGAGTGATAGCTG 44570 A AGG AG
 CA CTATC GC CTCTGC
 || ||||| || |||||
 GT GATAG TG GAGACG
 C _ AG
 GAM2147 DKFZp547I014 5' GCAGAGTACTGATGGTCA 39944 A GGCA
 C ACTATCAG GCTCTGC
 | ||||| |||||

A TGGTAGTC TGAGACG
 C A____
 GAM2147 DKFZP564I1171 3' GCAAAGCTGCCTTCCAAGT 72046 ATC C
 ACT AGGGCAGCT TGC
 ||| ||||| |||
 TGA TTCCGTCGA ACG
 ACC A
 GAM2147 ENAH 3' GCAAAGCTTGTTGATAGT 37157 GG _ C
 ACTATCA GCA GCT TGC
 ||||| ||| ||| |||
 TGATAGT TGT CGA ACG
 _ T A
 GAM2147 FLJ13263 3' GCAGAGTGCCTTCCCTGATG 47814 CA____
 TATCAGGG GCTCTGC
 ||||| |||||
 GTAGTCCC TGAGACG
 TTCCG
 GAM2147 FLJ13615 3' GCAGAAAGATCCTGATGTT 47796 T CAGC
 AAC ATCAGGG TCTGC
 ||| ||||| |||||
 TTG TAGTCCT AGACG
 _ AGAA
 GAM2147 FLJ20509 3' CAAAGCTGCCTTGACTGT 35757 TA C
 AC TCAGGGCAGCT TG
 || ||||| ||||| ||
 TG AGTTCCGTCGA AC
 TC A
 GAM2147 FLJ21916 3' GCAGAGCTGTTTGGCAG 43897 AT G
 CT CAGG CAGCTCTGC
 || ||| ||||| |||||
 GA GTTT GTCGAGACG
 CG _
 GAM2147 FLJ32499 3' GCAGAACTGTTTGATAGTT 58778 G C
 AACTATCAGG CAG TCTGC
 ||||| ||| |||||
 TTGATAGTTT GTC AGACG
 _ A
 GAM2147 FOXP1 3' GCAGAAATGTGATGGTT 52045 AGG GC
 AACTATC GCA TCTGC
 ||||| ||| |||||
 TTGGTAG TGT AGACG
 _ AA
 GAM2147 GGA2 3' CAGCTCTGCACAGGCCTGGTAG 31160 A _____ GCTC
 TCA C ACTATCAGG GCA TG
 | ||||| ||| ||
 A TGATGGTCC CGT AC
 C GGACA____ CTCG
 GAM2147 GGA2 3' CAGCTCTGCACAGGCCTGGTAG 57654 A _____ GCTC
 TCA C ACTATCAGG GCA TG
 | ||||| ||| ||

A TGATGGTCC CGT AC
 C GGACA__ CTCG
 GAM2147 HSPC065 3' GCAAAGCTGCCGTGATTC 27154 T G C
 C ATCA GGCAGCT TGC
 | ||| ||||| |||
 C TAGT CCGTCGA ACG
 T G A
 GAM2147 IL-17RE 3' GCAGAGCCGCCTAGAGCTGT 58939 TA_ A A
 AC TC GGGC GCTCTGC
 || || ||| |||||
 TG AG TCCG CGAGACG
 TCG A C
 GAM2147 KIAA0174 3' GCAAAGTTTGTCTTGACAGTTG 79295 A _ C
 CAACT TCAGGGCAG CT TGC
 |||| ||||| || |||
 GTTGA AGTTCTGTT GA ACG
 C T A
 GAM2147 KIAA0321 3' CAGAGCTGCCTGTTG 63045 TATCA
 CAAC GGGCAGCTCTG
 ||| |||||
 GTTG TCCGTCGAGAC

 GAM2147 KIAA0889 3' CAGCTCTGCACAGACCTGATGG 31763 A _____ GCTC
 TCA C ACTATCAGG GCA TG
 | ||||| ||| ||
 A TGGTAGTCC CGT AC
 C AGACA__ CTCG
 GAM2147 KIAA1508 3' GCAGAGTTCTTCCATTAGTTG 62553 TCA C_
 CAACTA GGG AGCTCTGC
 |||| || |||||
 GTTGAT CCT TTGAGACG
 TA_ TC
 GAM2147 KIAA1649 3' GCAGAGCTGGAGCCAGTTG 67516 ATCA G_
 CAACT GG CAGCTCTGC
 |||| || |||||
 GTTGA CC GTCGAGACG
 _____ GAG
 GAM2147 KIAA1649 3' GCAGAGCTGGAGCCAGTTG 51241 ATCA G_
 CAACT GG CAGCTCTGC
 |||| || |||||
 GTTGA CC GTCGAGACG
 _____ GAG
 GAM2147 KIAA1655 3' GCAGAGCTTTGACGGTCA 67189 A TA GGC
 C AC TCAG AGCTCTGC
 | || ||| |||||
 A TG AGTT TCGAGACG
 C GC ____
 GAM2147 KIAA1858 3' GCAGAGCCGCTGCCCTGG 67722 ____
 TCAGGGCAGC TCTGC
 ||||| |||

GGTCCCGTCG AGACG
CCG
GAM2147 KIAA1922 5' CAGAGCTGGGTCTCAGATG 73989 A ____
TATC GGG CAGCTCTG
||||| ||| |||||
GTAG CTC GTCGAGAC
A TGG
GAM2147 MDS006 3' CAGAGATGCCCTGGCAGTCA 39982 A AT G
C ACT CAGGGCA CTCTG
| ||| ||||| |||||
A TGA GTCCCGT GAGAC
C CG A
GAM2147 MGC2541 3' GCAGAGCCACTGGAGCTG 55624 A A GGCA
CA CT TCAG GCTCTGC
|| || ||| |||||
GT GA GGTC CGAGACG
C _ AC_
GAM2147 MOST2 5' GCAAAGCTCTCAGGCGACGGTT 40064 TA A__ C C
G CAAC TC GGG AGCT TGC
|||| | ||| ||| |||
GTTG AG CTC TCGA ACG
GC CGGA _ A
GAM2147 NBR2 3' GCAGAGCTGGAGCTCGATCA 20619 T A ____
C ATC GGGC AGCTCTGC
| ||| ||| |||||
A TAG CTCG TCGAGACG
C _ AGG
GAM2147 PEG10 3' ACTCTGCACGACCTGATAGTTG 31197 _____ GCTC
CAACTATCAGG GCA T
||||||| ||| |
GTTGATAGTCC CGT A
AGCA__ CTCG
GAM2147 PHF7 5' GCAAAGCCACCCCTCAGATGTT 33646 T _ CA_ C
AAC ATC AGGG GCT TGC
||| ||| ||| ||| |||
TTG TAG TCCC CGA ACG
_ AC CAC A
GAM2147 PRO2955 5' GCATCTTGAACCCCTGATAGTT 38240 CAG C__
G CAACTATCAGGG CT TGC
||||||| || |||
GTTGATAGTCCC GG ACG
AA_ TTCT
GAM2147 PROZ 3' GCAGAGCCGCCGTTTGCTGG 15306 T _ A
CTA CAG GGC GCTCTGC
||| ||| ||| |||||
GGT GTT CCG CGAGACG
C TG C
GAM2147 RASSF2 3' GCAGAGCTGGGCAGTTG 29099 AT AGGG
CAACT C CAGCTCTGC
|||| | |||||

GTTGA G GTCGAGACG
 CG ____
 GAM2147 RHOBTB3 3' GCAAAGCTGTTTTGCAGCTG 30427 A AT C
 CA CT CAGGGCAGCT TGC
 || || ||||| ||
 GT GA GTTTTGTCGA ACG
 C C_ A
 GAM2147 Rpo1-2 3' CAGCTCTGCACAATCCTGATAG 39215 _____ GCTC
 TT AACTATCAGG GCA TG
 ||||| || ||
 TTGATAGTCC CGT AC
 TAACA__ CTCG
 GAM2147 TLE4 3' GCAGATTGCTCCCTGATGGT 68512 C _
 ACTATCAGGG AGC TCTGC
 ||||| || ||||
 TGGTAGTCCC TCG AGACG
 _ TT
 GAM2147 LOC122553 3' CAGAGTTGGATAATTG 74591 C AGGG
 CAA TATC CAGCTCTG
 || || |||||
 GTT ATAG GTTGAGAC
 A ____
 GAM2147 LOC135307 3' GCAGTGATGACCCTGATGGCTG 75739 A _ GCT
 CA CTATCAGGG CA CTGC
 || ||||| || ||||
 GT GGTAGTCCC GT GACG
 C A AGT
 GAM2147 LOC143162 3' CAAAGTGCTTTGATGGTTG 77002 G C
 CAACTATCAGGGCA CT TG
 ||||| || ||
 GTTGGTAGTTTCGT GA AC
 _ A
 GAM2147 LOC145622 3' GCTAAGCCCTGGTAGTCA 77818 A _
 C ACTATCAGGGC AGC
 | ||||| ||
 A TGATGGTCCCG TCG
 C AA
 GAM2147 LOC146909 3' GCAGAGCTGCCCTTGAGTCC 78774 A ATC
 C ACT AGGGCAGCTCTGC
 | || |||||
 C TGA TCCCGTCGAGACG
 C GT_
 GAM2147 LOC148529 5' CAGAACCTTGATGTTG 85320 T CAGC
 CAAC ATCAGGG TCTG
 || ||||| ||||
 GTTG TAGTTCC AGAC
 _ A__
 GAM2147 LOC150095 5' GCAGAACCGTAAGCTGAAGTTG 85994 A G__ AGC
 CAACT TCAG GC TCTGC
 |||| || || ||||

GTTGA AGTC TG AGACG
 _ GAA CCA
 GAM2147 LOC150174 3' GCAGAGCTGCCCTCGGG 80436 ATC
 CT AGGGCAGCTCTGC
 || |||||
 GG TCCCGTCGAGACG
 GC_
 GAM2147 LOC150213 3' GCAGAGCTGCCCTCGGG 75355 ATC
 CT AGGGCAGCTCTGC
 || |||||
 GG TCCCGTCGAGACG
 GC_
 GAM2147 LOC150236 5' GCAGAGCTGCCCTCGGG 80500 ATC
 CT AGGGCAGCTCTGC
 || |||||
 GG TCCCGTCGAGACG
 GC_
 GAM2147 LOC153474 3' GCAAAGCTGCCTTCCAAGT 81703 ATC C
 ACT AGGGCAGCT TGC
 ||| ||||| |||
 TGA TTCCGTCGA ACG
 ACC A
 GAM2147 LOC154141 5' CAGAGTTGAGTAGTTG 87385 CAGGG
 CAACTAT CAGCTCTG
 ||||| |||||
 GTTGATG GTTGAGAC
 A____
 GAM2147 LOC158427 3' CAGAGTTGAATAGTTG 58351 CAGGG
 CAACTAT CAGCTCTG
 ||||| |||||
 GTTGATA GTTGAGAC
 A____
 GAM2147 LOC165721 3' GCAGACATAGCCTGATGGTT 83493 GCAGC
 AACTATCAGG TCTGC
 ||||| |||||
 TTGGTAGTCC AGACG
 GATAC
 GAM2147 LOC196738 3' CAAAGTGCTTTGATGGTTG 88886 G C
 CAACTATCAGGGCA CT TG
 ||||| |||||
 GTTGGTAGTTTCGT GA AC
 _ A
 GAM2147 LOC197209 5' GCAGAGCTGCATTTAGTT 88657 TCAGG
 AACTA GCAGCTCTGC
 |||| |||||
 TTGAT CGTCGAGACG
 TTA_
 GAM2147 LOC219848 3' GCAGAGCTACTTGAATAG 93125 _ GC
 CTAT CAGG AGCTCTGC
 |||| |||||

GATA GTTC TCGAGACG
 A A_
 GAM2147 LOC220595 5' GCAGCCTAAACTCTGATAGCTG 92775 A CAGCT_
 CA CTATCAGGG CTGC
 || ||||| |||
 GT GATAGTCTC GACG
 C AAATCC
 GAM2147 LOC64102 3' GCATCTGGCCCCTGGTAG 42425 CA C_
 CTATCAGGG GCT TGC
 ||||| ||| |||
 GATGGTCCC CGG ACG
 _ TCT
 GAM2147 LOC96597 5' CAGAGCTGCCCGTGTCACT 67448 AT _
 ACT CA GGGCAGCTCTG
 ||| || |||||
 TGA GT CCCGTCGAGAC
 CT G
 GAM2148 HAL 5' GCCACTCCTGCATAAAGCTC 10903 TGAAAA
 GAGCTTTATGC GGTGGC
 ||||| |||||
 CTCGAAATACG TCACCG
 TCC_
 GAM2148 HMGN2 3' GGCCACCTTGGCACAAAAGC 19809 A C AA
 GCTTT TG TG AAGGTGGCC
 |||| || |||||
 CGAAA AC AC TTCCACCGG
 _ _ GG
 GAM2148 NMI 5' GGCCACCTCCTCAGGAAG 17436 ATG AA
 CTTT CTGA AAGTGGCC
 |||| ||| |||||
 GAAG GACT TCCACCGG
 _ CC
 GAM2148 PACE 3' GGCCACCTCTCCAAGGGCTT 11944 A CT AAA
 GAGCTTT TG GA GGTGGCC
 ||||| || |||||
 TTCGGGA AC CT CCACCGG
 _ CT _
 GAM2148 PYCR1 3' CCACCTTCCTCTAGAGCTC 70639 TGCT A_
 GAGCTTTA GA AAGGTGG
 ||||| || |||||
 CTCGAGAT CT TTCCACC
 _ CC
 GAM2148 SDC1 3' GGCCACCTCCCCAGCATTCCAG 12991 TT_ AAA
 C GCT ATGCTG AAGTGGCC
 ||| |||| |||||
 CGA TACGAC TCCACCGG
 CCT CCC
 GAM2148 FLJ11560 5' GCCCAGGCCCCAGCATAAAG 48008 AAAA _
 CTTTATGCTG GGT GGC
 ||||| ||| |||

		GAAATACGAC CCG CCG	
		____ GAC	
GAM2148	KIAA0446	5' CCACCTTTTGAAGAGCTC 69446	ATGCTG
		GAGCTTT AAAAGGTGG	
		CTCGAGA TTTTCCACC	
		AG____	
GAM2148	KIAA0971	3' GTTGTCTCAGCATAAAGT 30677	AAA TG
		GCTTTATGCTGA GG GC	
		TGAAATACGACT TT TG	
		C__ GT	
GAM2148	KIAA1393	3' GGCCACCTTGGCACAAAAGC 72574	A C AA
		GCTTT TG TG AAGGTGGCC	
		CGAAA AC AC TTCCACCGG	
		_ _ GG	
GAM2148	KIAA1656	3' GGCCACCTCCTCCTAGAAGCC 66377	A ATGCT AA
		G GCTTT GA AGGTGGCC	
		C CGAAG CT TCCACCGG	
		_ ATC__ CC	
GAM2148	KIAA1884	3' GCCACCTTCATCTACCAAGGCT 73728	ATGCT A_
	C	GAGCTTT GA AAGGTGGC	
		CTCGGAA CT TTCCACCG	
		CCAT_ AC	
GAM2148	PP3501	3' GGCCACCGTTGACAGCATAAAG 41683	AAAA_
		CTTTATGCTG GGTGGCC	
		GAAATACGAC CCACCGG	
		AGTTG	
GAM2148	SDCCAG3	3' GGTGTTCTCAGCATGAAGCTC 22803	AAA TG
		GAGCTTTATGCTGA GG GCC	
		CTCGAAGTACGACT CT TGG	
		____ TG	
GAM2148	SP140	3' GGCCACCTCCATGCAGAAGC 24327	A TGAAA
		GCTTT TGC AGGTGGCC	
		CGAAG ACG TCCACCGG	
		_ TACC_	
GAM2148	LOC148760	3' GGCCACCTTCTCCAACAAGCTC 85364	TA CT A
		GAGCTT TG GA AAGGTGGCC	
		CTCGAA AC CT TTCCACCGG	
		CA __ C	
GAM2148	LOC150170	5' ACCTGTTTCACATAAAGC 80414	C _
		GCTTTATG TGAAA AGGT	

		CGAAATAC ACTTT TCCA		
		— G		
GAM2148	LOC150175 5'	ACCTGTTTCACATAAAGC 80453	C	—
		GCTTTATG TGAAA AGGT		
		CGAAATAC ACTTT TCCA		
		— G		
GAM2148	LOC150215 5'	ACCTGTTTCACATAAAGC 80456	C	—
		GCTTTATG TGAAA AGGT		
		CGAAATAC ACTTT TCCA		
		— G		
GAM2148	LOC150218 5'	ACCTGTTTCACATAAAGC 80525	C	—
		GCTTTATG TGAAA AGGT		
		CGAAATAC ACTTT TCCA		
		— G		
GAM2148	LOC152065 3'	GGCCACCTTCTCCTTGGCAGGC 86737	TTA	___ A
	TC	GAGCT TGCT GA AAGGTGGCC		
		CTCGG ACGG CT TTCCACCGG		
		___ TTC C		
GAM2148	LOC152267 3'	GGCCACCTTGGCACAAAAGC 61036	A C	AA
		GCTTT TG TG AAGGTGGCC		
		CGAAA AC AC TTCCACCGG		
		— _ GG		
GAM2148	LOC158292 5'	CCTCTGGACCCAGCATAAGGCT 88046	AAAA_	T
	C	GAGCTTTATGCTG GG GG		
		CTCGGAATACGAC TC CC		
		CCAGG T		
GAM2148	LOC219997 3'	GCCACCTCTTCAGCCTC 93256	CTTTAT	A
		GAG GCTGAA AGGTGGC		
		CTC CGACTT TCCACCG		
		___ C		
GAM2148	LOC256269 3'	GGCCACCTTGGCACAAAAGC 96608	A C	AA
		GCTTT TG TG AAGGTGGCC		
		CGAAA AC AC TTCCACCGG		
		— _ GG		
GAM2148	LOC91963 5'	GGCCACCTCCTCTGAGAAGC 68321	ATGCT	AA
		GCTTT GA AGGTGGCC		
		CGAAG CT TCCACCGG		
		AGT_ CC		
GAM2149	CCND2 3'	TCCCAGCAAATCATCGGGCCA 10055	CCACA	_ A
		TGGCCTGATGAT GC GG GA		

ACCGGGCTACTA CG CC CT
 AA__ A C
 GAM2149 GCN5L2 5' CTCCGCTGCGGGGGAGGCC 60529 GATGA A
 GGCCT TCC CAGCGGAG
 |||| | |||||
 CCGGA GGG GTCGCCTC
 GG__ C
 GAM2149 GJA5 3' CTGACCAGATCATCAGCCA 19164 C CACAG
 TGGC TGATGATC CGG
 ||| ||||| |
 ACCG ACTACTAG GTC
 _ ACCA_
 GAM2149 HIVEP3 3' TCCCCGCTGTGGTTGGCAGCCA 44702 C ATGAT A
 TGGC TG CCACAGCGG GA
 ||| | ||||| |
 ACCG AC GGTGTCGCC CT
 _ GGTT_ C
 GAM2149 HOXD1 5' CCGCCGGTATATTAGGCCA 44696 AT ACA
 TGGCCTGATG CC GCGG
 ||||| | |||
 ACCGGATTAT GG CGCC
 AT C__
 GAM2149 SUFU 3' CCTTGTGACCCATCAGGCCA 32934 ATC C
 TGGCCTGATG CACAG GG
 ||||| ||| |
 ACCGGACTAC GTGTT CC
 CCA _
 GAM2149 DKFZP586J1624 3' CTCCGCCAGTCACCATCAGGC 32043 ATCCACA_
 CA TGGCCTGATG GCGGAG
 ||||| |||||
 ACCGGACTAC CGCCTC
 CACTGACC
 GAM2149 KIAA1671 3' CTTTGCTTATGAATCATCAGAC 66282 C C C_
 C GG CTGATGAT CA AGCGGAG
 || ||||| || |||||
 CC GACTACTA GT TCGTTTC
 A A AT
 GAM2149 LOC159110 5' TCTCCGCTGCCCCGGTCAACCA 82995 CCTGA CA_
 TGG TGATC CAGCGGAGA
 || |||| |||||
 ACC ACTGG GTCGCCTCT
 A__ CCCC
 GAM2149 LOC159116 5' TCTCCGCTGCCCCGGTCAACCA 82978 CCTGA CA_
 TGG TGATC CAGCGGAGA
 || |||| |||||
 ACC ACTGG GTCGCCTCT
 A__ CCCC
 GAM2149 LOC165476 5' CTCCGCTGCCTGCTCAGCCA 88550 C TGATCCA
 TGGC TGA CAGCGGAG
 ||| || |||||

		ACCG ACT	GTCGCCTC		
		_ CGTCC_			
GAM2149	LOC200032	5'	CTGACCAGATCATCAGCCA	85475	C CACAG
			TGGC TGATGATC CGG		
			ACCG ACTACTAG GTC		
			_ ACCA_		
GAM2149	LOC219654	5'	CTCCGCTGCGGAGGGGGGCC	92932	GATGA A
			GGCCT TCC CAGCGGAG		
			CCGGG AGG GTCGCCTC		
			GGG_ C		
GAM2149	LOC255862	3'	TCAAATGTAGACTATCAGGCCA	96115	A C GCG
			TGGCCTGATG TC ACA GA		
			ACCGGACTAT AG TGT CT		
			C A AAA		
GAM2150	CDH12	3'	CTTATCATTTAAAGTGGTGTA	15777	CCCAA GA
			TACACCACT GAA ATAAG		
			ATGTGGTGA TTT TATTC		
			AA_ AC		
GAM2150	GOCAP1	3'	ATTGTTCTTGGGAGCAGTGTA	43007	CA G
			TACAC CTCCCAAGAA AAT		
			ATGTG GAGGGTTCTT TTA		
			AC G		
GAM2150	DKFZp434N2435	5'	CTTATTACTGTGGGGTGGT	98090	T AGAAG
			ACCAC CCCA AATAAG		
			TGGTG GGGT TTATTC		
			_ GTCA_		
GAM2150	DKFZP564I122	3'	CTTATTCTTCTCCCTCATGTGT	63877	CACTCCCA
	A		TACAC AGAAGAATAAG		
			ATGTG TCTTCTTATTC		
			TACTCCC_		
GAM2150	FLJ21791	3'	CTTATTTGCAGAAGTGGTGTA	62126	CCCAAGAA
			TACACCACT GAATAAG		
			ATGTGGTGA TTTATTC		
			AGACG_		
GAM2150	HMP19	3'	CTTATTCTTTGTTAGGAAAATG	88860	CCAC CAA_
	TA		TACA TCC GAAGAATAAG		
			ATGT AGG TTTCTTATTC		
			AAA_ ATTG		
GAM2150	KIAA1719	3'	TCTGTCTTGGGAGTGGTGTA	68742	_
			TACACCACTCCCAAGA AGA		

		ATGTGGTGAGGGTTCT TCT		
		G		
GAM2150 KIAA1853	3'	TTTTTCTTGGAAGCAGTG 69929	CA C	
		CAC CT CCAAGAAGAA		
		GTG GA GGTTCTTTT		
		AC A		
GAM2150 KIAA1877	3'	CTTATTCTTCTGCCATGAGT 66748	CCA__	
		ACTC AGAAGAATAAG		
		TGAG TCTTCTTATTC		
		TACCG		
GAM2150 KIAA1906	3'	CTTATTCTTCTTGACTTTTGG 73571	CTCC_	
		CCA CAAGAAGAATAAG		
		GGT GTTCTTCTTATTC		
		TTTCA		
GAM2150 OSBPL11	3'	CTTAATTTCCCAAGAGTGGTG 43206	CCAA AA	
		CACCACTC GAAG TAAG		
		GTGGTGAG CTTT ATTC		
		AACC A_		
GAM2150 YME1L1	3'	TCATTCTTGATGTGGTGTA 58438	TCC _	
		TACACCAC CAAGAA GA		
		ATGTGGTG GTTCTT CT		
		TA_ A		
GAM2150 ZNF262	3'	CTTATTTTGTGTTGGGAGT 18723	A	
		ACTCCCAAG AGAATAAG		
		TGAGGGTTT TTTTATTC		
		G		
GAM2150 LOC91960	3'	TGTGGCTTGGAACGTGGTGTA 68294	TC_ AAGA	
		TACACCAC CCAAG ATA		
		ATGTGGTG GGTTT TGT		
		CAA GG_		
GAM2151 CDH12	3'	CTTATCATTTAAAGTGGTGTA 15777	CCCAA GA	
		TACACCACT GAA ATAAG		
		ATGTGGTGA TTT TATTC		
		AA_ AC		
GAM2151 GOCAP1	3'	ATTGTTCTTGGGAGCAGTGTA 43007	CA G	
		TACAC CTCCCAAGAA AAT		
		ATGTG GAGGGTTCTT TTA		
		AC G		
GAM2151 DKFZp434N2435	5'	CTTATTACTGTGGGGTGGT 98090	T AGAAG	
		ACCAC CCCA AATAAG		

			TGGTG GGGT TTATTC	
			_ GTCA_	
GAM2151	DKFZP564I122	3'	CTTATTCTTCTCCCTCATGTGT 63877	CACTCCCA
	A		TACAC AGAAGAATAAG	
			ATGTG TCTTCTTATTC	
			TACTCCC_	
GAM2151	FLJ21791	3'	CTTATTTGCAGAAAGTGGTGTA 62126	CCCAAGAA
			TACACCACT GAATAAG	
			ATGTGGTGA TTTATTC	
			AGACG__	
GAM2151	HMP19	3'	CTTATTCTTTGTAGGAAAATG 88860	CCAC CAA_
	TA		TACA TCC GAAGAATAAG	
			ATGT AGG TTTCTTATTC	
			AAA_ ATTG	
GAM2151	KIAA1719	3'	TCTGTCTTGGGAGTGGTGTA 68742	_
			TACACCACTCCCAAGA AGA	
			ATGTGGTGAGGGTTCT TCT	
			G	
GAM2151	KIAA1853	3'	TTTTTCTTGAAGCAGTG 69929	CA C
			CAC CT CCAAGAAGAA	
			GTG GA GGTTCTTTTT	
			AC A	
GAM2151	KIAA1877	3'	CTTATTCTTCTGCCATGAGT 66748	CCA__
			ACTC AGAAGAATAAG	
			TGAG TCTTCTTATTC	
			TACCG	
GAM2151	KIAA1906	3'	CTTATTCTTCTTGACTTTTGG 73571	CTCC_
			CCA CAAGAAGAATAAG	
			GGT GTTCTTCTTATTC	
			TTTCA	
GAM2151	OSBPL11	3'	CTTAATTTCCCAAGAGTGGTG 43206	CCAA AA
			CACCACTC GAAG TAAG	
			GTGGTGAG CTTT ATTC	
			AACC A_	
GAM2151	YME1L1	3'	TCATTCTTGATGTGGTGTA 58438	TCC _
			TACACCAC CAAGAA GA	
			ATGTGGTG GTTCTT CT	
			TA_ A	
GAM2151	ZNF262	3'	CTTATTTTGTGTTGGGAGT 18723	A
			ACTCCCAAG AGAATAAG	

TGAGGGTTT TTTTATTC

G

GAM2151 LOC91960 3' TGTGGCTTGGAAACGTGGTGTA 68294 TC_ AAGA

TACACCAC CCAAG ATA

||||||| ||||| |||

ATGTGGTG GGTTC TGT

CAA GG_

GAM2152 ANKH 3' ATGGCGAAACCCTGTCTCTACT 55063 C T ATGG T

AG AGAG CAGGG G CCAT

|| ||||| ||||| | ||||

TC TCTC GTCCC C GGTA

A T AAAG_

GAM2152 ATM 3' ATGGTGAAACCCTGTCTCTACT 57130 C T ATGGGT

AG AGAG CAGGG CCAT

|| ||||| ||||| ||||

TC TCTC GTCCC GGTA

A T AAAGT_

GAM2152 ATM 3' ATGGTGAAACCCTGTCTCTACT 5289 C T ATGGGT

AG AGAG CAGGG CCAT

|| ||||| ||||| ||||

TC TCTC GTCCC GGTA

A T AAAGT_

GAM2152 ATP1A2 3' ATGGTGAAACCCTGTCTCTACT 7357 C T ATGGGT

AG AGAG CAGGG CCAT

|| ||||| ||||| ||||

TC TCTC GTCCC GGTA

A T AAAGT_

GAM2152 C21orf5 3' ATGGTGAGACCCTGTCTCTACT 18883 C T ATGGGT

AG AGAG CAGGG CCAT

|| ||||| ||||| ||||

TC TCTC GTCCC GGTA

A T AGAGT_

GAM2152 CD68 3' ATGGTGAAACCCTGTCTCTACT 60501 C T ATGGGT

AG AGAG CAGGG CCAT

|| ||||| ||||| ||||

TC TCTC GTCCC GGTA

A T AAAGT_

GAM2152 CERD4 3' ATGAACCCATCTTTTGCCTGC 24875 A C C

GCAG GT AGGGATGGGT CAT

||||| || ||||| ||||| ||||

CGTC CG TTTCTACCCA GTA

_ T A

GAM2152 CPM 3' ATGGTGAAACCCTGTCTCTACT 60403 C T ATGGGT

AG AGAG CAGGG CCAT

|| ||||| ||||| ||||

TC TCTC GTCCC GGTA

A T AAAGT_

GAM2152 DFFA 3' ATGGTGAAACCCTGTCTCTACT 16587 C T ATGGGT

AG AGAG CAGGG CCAT

|| ||||| ||||| ||||

			TC TCTC GTCCC	GGTA		
			A T AAAGT_			
GAM2152	EDAR	5'	GACCCATCTTCTGCTG	42527	GTCAG	
			CAGCAGA	GGATGGGTC		
			GTCGTCT	TCTACCCAG		
GAM2152	FAT2	3'	GGGCTCCCTGATCTGC	9350	G TGG	
			GCAGA TCAGGGA	GTCC		
			CGTCT AGTCCCT	CGGG		
GAM2152	FGFR2	3'	ATGGTGAAACCCTGTCTCTACT	43650	C T ATGGGT	
			AG AGAG CAGGG	CCAT		
			TC TCTC GTCCC	GGTA		
			A T AAAGT_			
GAM2152	FGFR2	3'	ATGGTGAAACCCTGTCTCTACT	43663	C T ATGGGT	
			AG AGAG CAGGG	CCAT		
			TC TCTC GTCCC	GGTA		
			A T AAAGT_			
GAM2152	IRAK1	3'	TGAGACCCTGTCTCTGC	9620	T GGGAT _	
			GCAGAG CA	GGGTC CA		
			CGTCTC GT	CCCAG GT		
			T _	A		
GAM2152	LAMC2	3'	ATGGTGAAACCCTGTCTCTACT	38766	C T ATGGGT	
			AG AGAG CAGGG	CCAT		
			TC TCTC GTCCC	GGTA		
			A T AAAGT_			
GAM2152	MOCS1	3'	ATGGAGGCCCTGACCTCTGCTG	93665	_ ATGGG	
			CAGCAGAG TCAGGG	TCCAT		
			GTCGTCTC AGTCCC	AGGTA		
			C GG_			
GAM2152	MYO1B	3'	ATGGCAAACCCTGTCTCTACT	25240	C T ATGG T	
			AG AGAG CAGGG	G CCAT		
			TC TCTC GTCCC	C GGTA		
			A T AAAA_			
GAM2152	MYO1C	3'	ATGTGTTTTCCCTGACTCCAGC	61852	A_ T TC	
			GC GAGTCAGGGA	GGG CAT		
			CG CTCAGTCCCT	TTT GTA		
			AC _	GT		
GAM2152	NF1	3'	ATGAACCCATCCGGTTTGC	6046	G AG C	
			GCAGA TC	GGATGGGT CAT		

CGTTT GG CCTACCCA GTA

— — A

GAM2152 PA2G4 3' ATGGCGAAACCCTGTCTCTACT 71823 C T ATGG T
AG AGAG CAGGG G CCAT
|| ||| |||| | |||
TC TCTC GTCCC C GGTA
A T AAAG_

GAM2152 PAICS 3' ATGGTGAAACCCTGTCTCTACT 22254 C T ATGGGT
AG AGAG CAGGG CCAT
|| ||| |||| |||
TC TCTC GTCCC GGTA
A T AAAGT_

GAM2152 PFKFB4 3' TGGACCTGGTGA CTCT 17090 G GGA
AGAGTCA TGGGTCCA
||||| |||||
TCTCAGT GTCCAGGT
G_

GAM2152 POLK 3' ATGGTGAGACCCTGTCTCTACT 33097 C T ATGGGT
AG AGAG CAGGG CCAT
|| ||| |||| |||
TC TCTC GTCCC GGTA
A T AGAGT_

GAM2152 PSMD5 3' ATGGCAAAACCCTGTCTCTACT 18554 C T ATGG T
AG AGAG CAGGG G CCAT
|| ||| |||| | |||
TC TCTC GTCCC C GGTA
A T AAAA_

GAM2152 RECQL5 3' ATGGCAAGACCCTGTCTCTACT 16198 C T ATGG T
AG AGAG CAGGG G CCAT
|| ||| |||| | |||
TC TCTC GTCCC C GGTA
A T AGAA_

GAM2152 SCAP2 3' ATGGTGAAACCCTGTCTCTACT 15422 C T ATGGGT
AG AGAG CAGGG CCAT
|| ||| |||| |||
TC TCTC GTCCC GGTA
A T AAAGT_

GAM2152 SUDD 3' ATGGCGAAACCCTGTCTCTACT 15153 C T ATGG T
AG AGAG CAGGG G CCAT
|| ||| |||| | |||
TC TCTC GTCCC C GGTA
A T AAAG_

GAM2152 SUV39H2 3' ATGGTGAAACCCTGTCTCTACT 45453 C T ATGGGT
G CAG AGAG CAGGG CCAT
||| ||| |||| |||
GTC TCTC GTCCC GGTA
A T AAAGT_

GAM2152 TBX6 3' ATGGTGAAACCCTGTCTCTGCT 55809 T ATGGGT
AGCAGAG CAGGG CCAT
||||| |||| |||

TCGTCTC GTCCC GGTA
T AAAGT_
GAM2152 TMPRSS4 3' ACCCATCCCCAAGCCTACT 39586 C A CA_
AG AG GT GGGATGGGT
|| ||| |||||
TC TC CG CCCTACCCA
A _ AAC
GAM2152 USP14 3' ATGGTGAAACCCTGTCTCTACT 18928 C T ATGGGT
AG AGAG CAGGG CCAT
|| ||| ||||| |||
TC TCTC GTCCC GGTA
A T AAAGT_
GAM2152 WBSCR5 3' ATGGACCCATCGCTGCCTT 42109 T G
GAG CAG GATGGGTCCAT
||| ||| |||||
TTC GTC CTACCCAGGTA
C G
GAM2152 WBSCR5 3' ATGGACCCATCGCTGCCTT 27113 T G
GAG CAG GATGGGTCCAT
||| ||| |||||
TTC GTC CTACCCAGGTA
C G
GAM2152 WBSCR5 3' ATGGACCCATCGCTGCCTT 51628 T G
GAG CAG GATGGGTCCAT
||| ||| |||||
TTC GTC CTACCCAGGTA
C G
GAM2152 AF020591 3' ATGGTGAAACCCTGTCTCTACT 27904 C T ATGGGT
AG AGAG CAGGG CCAT
|| ||| ||||| |||
TC TCTC GTCCC GGTA
A T AAAGT_
GAM2152 BIA2 3' ATGGTGAAACCCTGTCTCTACT 71791 C T ATGGGT
AG AGAG CAGGG CCAT
|| ||| ||||| |||
TC TCTC GTCCC GGTA
A T AAAGT_
GAM2152 C11orf14 3' GACCTTTTTTGACACTGC 40598 A T
GCAG GTCAGGGA GGGTC
||| ||||| |||||
CGTC CAGTTTTT TCCAG
A _
GAM2152 C13orf1 3' ATGGTGAAACCCTGGCTCTACT 40354 C ATGGGT
AG AGAGTCAGGG CCAT
|| ||||| ||||| |||
TC TCTCGGTCCC GGTA
A AAAGT_
GAM2152 C20orf106 3' ATGGTGAAACCCTGTCTCTACT 55895 C T ATGGGT
AG AGAG CAGGG CCAT
|| ||| ||||| |||

		TC TCTC GTCCC	GGTA		
		A T AAAGT_			
GAM2152	C20orf177	3' ATGGAGAAACCCTGTCTCCACT	62829	CA T	ATGGG
		AG GAG CAGGG	TCCAT		
		TC CTC GTCCC	AGGTA		
		AC T AAAG_			
GAM2152	C22orf19	3' ATGGTGAAACCCTGTCTCTACT	14818	C T	ATGGGT
		AG AGAG CAGGG	CCAT		
		TC TCTC GTCCC	GGTA		
		A T AAAGT_			
GAM2152	C4S-2	3' ATGGTGAAACCCTGTCTCTACT	38446	C T	ATGGGT
		AG AGAG CAGGG	CCAT		
		TC TCTC GTCCC	GGTA		
		A T AAAGT_			
GAM2152	CBCIP2	3' ATGGTGAAACCCTGTCTCTACT	52651	C T	ATGGGT
		AG AGAG CAGGG	CCAT		
		TC TCTC GTCCC	GGTA		
		A T AAAGT_			
GAM2152	CLDN15	3' ATGGTGAAACCCTGTCTCTACT	57369	C T	ATGGGT
		AG AGAG CAGGG	CCAT		
		TC TCTC GTCCC	GGTA		
		A T AAAGT_			
GAM2152	DKFZP434F091	3' ATGGTGAAACCCTGTCTCTACT	31893	C T	ATGGGT
		AG AGAG CAGGG	CCAT		
		TC TCTC GTCCC	GGTA		
		A T AAAGT_			
GAM2152	DKFZp434G171	3' ATGGTGAAACCCTGTCTCTACT	80234	C T	ATGGGT
		AG AGAG CAGGG	CCAT		
		TC TCTC GTCCC	GGTA		
		A T AAAGT_			
GAM2152	DKFZP434K028	3' GCCAACCCCTGCTCTGCTG	94860	T	ATG_
		CAGCAGAG CAGGG	GGT		
		GTCGTCTC GTCCC	CCG		
		_ CCAA			
GAM2152	DKFZP564B1023	3' ATGGAGAAACCCTGTCTCTACT	49359	C T	ATGGG
		AG AGAG CAGGG	TCCAT		
		TC TCTC GTCCC	AGGTA		
		A T AAAG_			
GAM2152	ERGL	3' ATGGTGAAACCCTGTCTCTACT	96730	C T	ATGGGT
	G	CAG AGAG CAGGG	CCAT		

			GTC TCTC GTCCC	GGTA		
			A T AAAGT_			
GAM2152	FLJ10314	3'	ATGGAGAAACCCTGTCTCTACT	36484	C T	ATGGG
			AG AGAG CAGGG	TCCAT		
			TC TCTC GTCCC	AGGTA		
			A T AAAG_			
GAM2152	FLJ10607	3'	ATGGTGAAACCCTGTCTCTACT	77624	C T	ATGGGT
			AG AGAG CAGGG	CCAT		
			TC TCTC GTCCC	GGTA		
			A T AAAGT_			
GAM2152	FLJ10704	3'	ATGGTGAAACCCTGTCTCTACT	36974	C T	ATGGGT
			AG AGAG CAGGG	CCAT		
			TC TCTC GTCCC	GGTA		
			A T AAAGT_			
GAM2152	FLJ10803	3'	ATGGCAAACCCTGTCTCTACT	37196	C T	ATGG T
			AG AGAG CAGGG	G CCAT		
			TC TCTC GTCCC	C GGTA		
			A T AAAA_			
GAM2152	FLJ11370	3'	ATGGTGAAACCCTGTCTCTACT	46961	C T	ATGGGT
			AG AGAG CAGGG	CCAT		
			TC TCTC GTCCC	GGTA		
			A T AAAGT_			
GAM2152	FLJ13055	5'	CCATCCCTGCCCTGCTG	43014	A T	
			CAGCAG G CAGGGATGG			
			GTCGTC C GTCCCTACC			
			C_			
GAM2152	FLJ13162	3'	ATGGAGAAATCCCGTCTCTACT	47180	C TCA	GGG
			AG AGAG GGGAT	TCCAT		
			TC TCTC CCCTA	AGGTA		
			A TG_ AAG			
GAM2152	FLJ13456	3'	ATGGTGAAACCCTGTCTCTACT	66529	C T	ATGGGT
			AG AGAG CAGGG	CCAT		
			TC TCTC GTCCC	GGTA		
			A T AAAGT_			
GAM2152	FLJ13848	3'	TATCCCTGAGCTCTGCTG	45830	_	
			CAGCAGAG TCAGGGATG			
			GTCGTCTC AGTCCCTAT			
			G			
GAM2152	FLJ20004	3'	ATGGTGAAAGCCCTGTCTCTACT	96998	C T	ATGGGT
			AG AGAG CAGGG	CCAT		

			TC TCTC GTCCC	GGTA		
			A T GAAGT_			
GAM2152	FLJ20059	3'	ATGGAGAAACCCCGTCTCTGCT	34922	TCA	ATGGG
			AGCAGAG GGG	TCCAT		
			TCGTCTC CCC	AGGTA		
			TG_ CAAAG			
GAM2152	FLJ20340	3'	ATGGTGAAACCCTGTCTCTACT	35450	C T	ATGGGT
	G		CAG AGAG CAGGG	CCAT		
			GTC TCTC GTCCC	GGTA		
			A T AAAGT_			
GAM2152	FLJ21369	3'	ATGGTGAGACCCTGTCTCTGCT	46047	T	ATGGGT
			AGCAGAG CAGGG	CCAT		
			TCGTCTC GTCCC	GGTA		
			T AGAGT_			
GAM2152	FLJ21736	3'	GACCACTTGACTCTCTG	46782	C	GATG
			CAG AGAGTCAGG	GGTC		
			GTC TCTCAGTTC	CCAG		
			_ A_			
GAM2152	FLJ22009	3'	GTGAGACCCTGTCTCTACT	60920	C	_ _
			AGT AGGGAT GGGTC	CAT		
			TCA TCTCTG CCCAG	GTG		
			_ T A			
GAM2152	FLJ22814	3'	ATGGCGAAACCCTGTCTCTACT	46715	C T	ATGG T
			AG AGAG CAGGG	G CCAT		
			TC TCTC GTCCC	C GGTA		
			A T AAAG_			
GAM2152	FLJ22965	3'	ATGGTGAAACCCTGTCTCTACT	42292	C T	ATGGGT
	G		CAG AGAG CAGGG	CCAT		
			GTC TCTC GTCCC	GGTA		
			A T AAAGT_			
GAM2152	FLJ23022	3'	ATGGTGAAACCCTGTCTCTACT	47490	C T	ATGGGT
			AG AGAG CAGGG	CCAT		
			TC TCTC GTCCC	GGTA		
			A T AAAGT_			
GAM2152	FLJ23235	3'	ATGGTGAAACCCTGTCTCTACT	46876	C T	ATGGGT
			AG AGAG CAGGG	CCAT		
			TC TCTC GTCCC	GGTA		
			A T AAAGT_			
GAM2152	FLJ23537	3'	ATGGAGAAACCCTGTCTCTACT	46539	C T	ATGGG
			AG AGAG CAGGG	TCCAT		

			TC TCTC GTCCC	AGGTA		
			A T	AAAG_		
GAM2152	FLJ30681	3'	ATGGTGAAACCCTGTCTCTACT	93431	C T	ATGGGT
			AG AGAG CAGGG	CCAT		
			TC TCTC GTCCC	GGTA		
			A T	AAAGT_		
GAM2152	FLJ31168	3'	ATGGTGAAACCCTGTCTCTACT	59175	C T	ATGGGT
			AG AGAG CAGGG	CCAT		
			TC TCTC GTCCC	GGTA		
			A T	AAAGT_		
GAM2152	FLJ32783	3'	GACCTAATGGCTCTGC	59307		GGGA
			GCAGAGTCA	TGGGTC		
			CGTCTCGGT	ATCCAG		
			A__			
GAM2152	FLJ32786	3'	TGGAAAACCTGCTCTGCTG	58965	T	GATGGG
			CAGCAGAG CAGG	TCCA		
			GTCGTCTC GTCC	AGGT		
			_ AAA__			
GAM2152	G0S2	3'	GGAGCCTGACTCCGCTG	32307	A	GATGGG
			CAGC GAGTCAGG	TCC		
			GTCG CTCAGTCC	AGG		
			C G__			
GAM2152	HSA250303	3'	ATGGTAAAACCCTGTCTCTACT	38018	C T	ATGGGT
	G		CAG AGAG CAGGG	CCAT		
			GTC TCTC GTCCC	GGTA		
			A T	AAAAT_		
GAM2152	HSPC043	3'	ATGGTGAAACCCTGTCTCTACT	68347	C T	ATGGGT
			AG AGAG CAGGG	CCAT		
			TC TCTC GTCCC	GGTA		
			A T	AAAGT_		
GAM2152	KIAA0184	3'	ATGGTGAAACCCTGTCTCTACT	65804	C T	ATGGGT
			AG AGAG CAGGG	CCAT		
			TC TCTC GTCCC	GGTA		
			A T	AAAGT_		
GAM2152	KIAA0618	3'	ATGGAGAAATCCCGTCTCTACT	29844	C TCA	GGG
			AG AGAG GGGAT	TCCAT		
			TC TCTC CCCTA	AGGTA		
			A TG_	AAG		
GAM2152	KIAA0884	3'	ATGGTGAAACCCTGTCTCTACT	70749	C T	ATGGGT
			AG AGAG CAGGG	CCAT		

			TC TCTC GTCCC	GGTA		
			A T AAAGT_			
GAM2152	KIAA1029	3'	TGGACCCCTGGACTTGCT	24435	G A	ATG
			AGCA AGTC GGG	GGTCCA		
			TCGT TCAG TCC	CCAGGT		
			_ G _			
GAM2152	KIAA1164	3'	ATGGCAAAACCCTGTCTCTACT	70033	C T	ATGG T
			AG AGAG CAGGG	G CCAT		
			TC TCTC GTCCC	C GGTA		
			A T AAAA _			
GAM2152	KIAA1164	3'	ATGGTGAAACCCTGTCTCTACT	70034	C T	ATGGGT
			AG AGAG CAGGG	CCAT		
			TC TCTC GTCCC	GGTA		
			A T AAAGT_			
GAM2152	KIAA1486	3'	GTGAGACCCCATCTCTACT	67978	C	_ _
			AGT AGGGATGGG TC	CAT		
			TCA TCTCTACCC	AG GTG		
			_ C A			
GAM2152	KIAA1969	3'	ATGGTGAAACCCTGTCTCTACT	79473	C T	ATGGGT
			AG AGAG CAGGG	CCAT		
			TC TCTC GTCCC	GGTA		
			A T AAAGT_			
GAM2152	KLHL8	3'	ATGGTGAAACCCTGTCTCTACT	63506	C T	ATGGGT
			AG AGAG CAGGG	CCAT		
			TC TCTC GTCCC	GGTA		
			A T AAAGT_			
GAM2152	LIM	3'	ATGGTGAAACCCTGTCTCTACT	22316	C T	ATGGGT
			AG AGAG CAGGG	CCAT		
			TC TCTC GTCCC	GGTA		
			A T AAAGT_			
GAM2152	LRG	3'	ATGGTGAAACCCTGTCTCTACT	54814	C T	ATGGGT
			AG AGAG CAGGG	CCAT		
			TC TCTC GTCCC	GGTA		
			A T AAAGT_			
GAM2152	LRRFIP1	3'	ATGGTGAAACCCTGTCTCTACT	17608	C T	ATGGGT
			AG AGAG CAGGG	CCAT		
			TC TCTC GTCCC	GGTA		
			A T AAAGT_			
GAM2152	LSR68	3'	ATGGCGAAACCCTGTCTCTACT	38549	C T	ATGG T
			AG AGAG CAGGG	G CCAT		

			TC TCTC GTCCC C GGTA			
			A T AAAG_			
GAM2152	MESDC2	3'	ATGGTGAAGCCCTGTCTCTACT 72908	C T	ATGGGT	
			AG AGAG CAGGG CCAT			
			TC TCTC GTCCC GGTA			
			A T GAAGT_			
GAM2152	MGC11386	3'	ATGGTGAAACCCTGTCTCTACT 53056	C T	ATGGGT	
			AG AGAG CAGGG CCAT			
			TC TCTC GTCCC GGTA			
			A T AAAGT_			
GAM2152	MGC29762	3'	GTGAGACCCCATCTCTACT 59147	C	--	
			AGT AGGGATGGG TC CAT			
			TCA TCTCTACCC AG GTG			
			_ C A			
GAM2152	MGC35558	3'	GGTCCATATAACCCTGACTCTC 59417	C	G_____	GGTC
			CTG CAG AGAGTCAGG ATG C			
			GTC TCTCAGTCC TAC G			
			C CAATA___ CTGG			
GAM2152	MGC5384	3'	GGGTGAATCCCTGTCTCTACT 49093	C T	GGG	
			AG AGAG CAGGGAT TCC			
			TC TCTC GTCCCTA GGG			
			A T AGT			
GAM2152	MKRN4	3'	ATGGCGAAACCCTGTCTCTACT 48452	C T	ATGG T	
			AG AGAG CAGGG G CCAT			
			TC TCTC GTCCC C GGTA			
			A T AAAG_			
GAM2152	MOST2	5'	ATGGTAAAACCCTGTCTCTACT 40053	C T	ATGGGT	
			AG AGAG CAGGG CCAT			
			TC TCTC GTCCC GGTA			
			A T AAAAT_			
GAM2152	MRPS25	3'	GAATATCCCTGCTCTGCTG 42859	T	GG	
			CAGCAGAG CAGGGATG TC			
			GTCGTCTC GTCCCTAT AG			
			_ A_			
GAM2152	NTSR2	3'	ATCAACCCTGCTCTGCTG 25633	T	ATG	
			CAGCAGAG CAGGG GGT			
			GTCGTCTC GTCCC CTA			
			_ CAA			
GAM2152	NUDEL	3'	GCCCCACTCTGCTG 48699	CAG AT		
			CAGCAGAGT GG GGGT			

GTCGTCTCA CC CCCG

GAM2152 OSBPL10 3' GTGCACCCCCACACTCTGCT 35526 CAG AT C
AGCAGAGT GG GGGT CAT
||||||| || ||| |||
TCGTCTCA CC CCCA GTG
CA_ _ C

GAM2152 PRO0478 5' ATGGATTAACCCTGTCTCTACT 27019 C T ATG
AG AGAG CAGGG GGTCCAT
|| ||| |||| |||||
TC TCTC GTCCC TTAGGTA
A T AA_

GAM2152 PRO0618 3' ATGGTGAAACCCTGTCTCTACT 27046 C T ATGGGT
AG AGAG CAGGG CCAT
|| ||| |||| |||
TC TCTC GTCCC GGTA
A T AAAGT_

GAM2152 RNO2 3' ATGGTGAAACCCTGTCTCTACT 53923 C T ATGGGT
AG AGAG CAGGG CCAT
|| ||| |||| |||
TC TCTC GTCCC GGTA
A T AAAGT_

GAM2152 SIMRP7 3' ATGGACAAGAGTCTGACTCAGC 93965 A GATGG
GC GAGTCAGG GTCCAT
|| ||||| |||||
CG CTCAGTCT CAGGTA
A GAGAA

GAM2152 TRIM38 3' ATGGTGAAACCCTGTCTCTACT 22053 C T ATGGGT
AG AGAG CAGGG CCAT
|| ||| |||| |||
TC TCTC GTCCC GGTA
A T AAAGT_

GAM2152 ust3 3' ATGGTGAAACCCTGTCTCTACT 94851 C T ATGGGT
AG AGAG CAGGG CCAT
|| ||| |||| |||
TC TCTC GTCCC GGTA
A T AAAGT_

GAM2152 WBSCR21 3' ATGGTGAAACCCTGTCTCTACT 49295 C T ATGGGT
AG AGAG CAGGG CCAT
|| ||| |||| |||
TC TCTC GTCCC GGTA
A T AAAGT_

GAM2152 X123 5' ATGGACGCATCCCCGACCCTG 70478 A A G
CAG GTC GGGATG GTCCAT
||| ||| ||||| |||||
GTC CAG CCCTAC CAGGTA
C C G

GAM2152 LOC115273 3' ATGGTGAAACCCTGTCTCTACT 73746 C T ATGGGT
AG AGAG CAGGG CCAT
|| ||| |||| |||

		TC TCTC GTCCC	GGTA			
		A T AAAGT_				
GAM2152	LOC131965 3'	GTGAGACCCCATCTCTACT	75526	C	_ _	
		AGT AGGGATGGG TC CAT				
		TCA TCTCTACCC AG GTG				
		_ C A				
GAM2152	LOC138428 3'	ATGGTGAAACCCTGTCTCTACT	75854	C T	ATGGGT	
		AG AGAG CAGGG CCAT				
		TC TCTC GTCCC GGTA				
		A T AAAGT_				
GAM2152	LOC145387 3'	ATGGTGAAACCCTGTCTCTACT	84328	C T	ATGGGT	
		AG AGAG CAGGG CCAT				
		TC TCTC GTCCC GGTA				
		A T AAAGT_				
GAM2152	LOC147990 3'	GTGGAACCCTATCTCTACT	85232	C	_ _	
		AGT AGGGAT GGGT CCAT				
		TCA TCTCTA CCCA GGTG				
		_ T A				
GAM2152	LOC148254 3'	ATGGTGAAACCCTGTCTCTACT	79498	C T	ATGGGT	
		AG AGAG CAGGG CCAT				
		TC TCTC GTCCC GGTA				
		A T AAAGT_				
GAM2152	LOC148809 3'	GTGGAACCCCATCTCTACT	79760	C	_	
		AGT AGGGATGGG TCCAT				
		TCA TCTCTACCC AGGTG				
		_ CA				
GAM2152	LOC149271 3'	ATGGTGAAACCCTGTCTCTGCT	79996	T	ATGGGT	
		AGCAGAG CAGGG CCAT				
		TCGTCTC GTCCC GGTA				
		T AAAGT_				
GAM2152	LOC149319 3'	ATGGTGAAACCCTGTCTCTACT	80066	C T	ATGGGT	
		AG AGAG CAGGG CCAT				
		TC TCTC GTCCC GGTA				
		A T AAAGT_				
GAM2152	LOC150481 3'	ATGGTGAAACCCTGTCTCTACT	80694	C T	ATGGGT	
		AG AGAG CAGGG CCAT				
		TC TCTC GTCCC GGTA				
		A T AAAGT_				
GAM2152	LOC150622 3'	GTGAGACCCCGTCTCTACT	80767	C	_ _	
		AGT AGGGATGGG TC CAT				

		TCA TCTCTGCCC AG GTG			
		— C A			
GAM2152	LOC151720 3'	ATGGTGAAACCCTGTCTCTACT 81145	C	T	ATGGGT
	G	CAG AGAG CAGGG CCAT			
		GTC TCTC GTCCC GGTA			
		A T AAAGT_			
GAM2152	LOC152627 5'	ATGGTGAAACCCTGTCTCTACT 81503	C	T	ATGGGT
		AG AGAG CAGGG CCAT			
		TC TCTC GTCCC GGTA			
		A T AAAGT_			
GAM2152	LOC153642 3'	ATGGTGAAACCCTGTCTCTACT 81782	C	T	ATGGGT
		AG AGAG CAGGG CCAT			
		TC TCTC GTCCC GGTA			
		A T AAAGT_			
GAM2152	LOC155006 3'	ATGGTGAAACCCTGTCTCTACT 82162	C	T	ATGGGT
		AG AGAG CAGGG CCAT			
		TC TCTC GTCCC GGTA			
		A T AAAGT_			
GAM2152	LOC158187 3'	ATGGTGACACCCTGTCTCTACT 87986	C	T	A GGT
		AG AGAG CAGGG TG CCAT			
		TC TCTC GTCCC AC GGTA			
		A T _ AGT			
GAM2152	LOC158191 3'	ATGGTGAAACCCTGTCTCTACT 82665	C	T	ATGGGT
		AG AGAG CAGGG CCAT			
		TC TCTC GTCCC GGTA			
		A T AAAGT_			
GAM2152	LOC158677 5'	ATGGCGAAACCCTGTCTCTACT 88245	C	T	ATGG T
		AG AGAG CAGGG G CCAT			
		TC TCTC GTCCC C GGTA			
		A T AAAG_			
GAM2152	LOC196955 5'	ATGGACCCATTTCAGACCCCAGC 77860	AGA_	AG	
		GC GTC GGATGGGTCCAT			
		CG CAG CTTACCCAGGTA			
		ACCC A_			
GAM2152	LOC200803 3'	ATGGTGAAACCCTGTCTCTACT 90295	C	T	ATGGGT
		AG AGAG CAGGG CCAT			
		TC TCTC GTCCC GGTA			
		A T AAAGT_			
GAM2152	LOC201564 3'	ATGGAGAAACCCTGTCTCTACT 81271	C	T	ATGGG
		AG AGAG CAGGG TCCAT			

		TC TCTC GTCCC	AGGTA			
		A T	AAAG_			
GAM2152	LOC201895 3'	ATGGTGAAACCCTGTCTCTACT	90540	C	T	ATGGGT
		AG AGAG CAGGG	CCAT			
		TC TCTC GTCCC	GGTA			
		A T	AAAGT_			
GAM2152	LOC202868 3'	ATGGTGAAACCCTGTCTCTACT	91989	C	T	ATGGGT
		AG AGAG CAGGG	CCAT			
		TC TCTC GTCCC	GGTA			
		A T	AAAGT_			
GAM2152	LOC219627 3'	ATGGTGAAACCCTGTCTCTACT	93800	C	T	ATGGGT
		AG AGAG CAGGG	CCAT			
		TC TCTC GTCCC	GGTA			
		A T	AAAGT_			
GAM2152	LOC221641 3'	TGAGACCCCATCTCTACT	95349	C		--
		AGT AGGGATGGG TC CA				
		TCA TCTCTACCC	AG GT			
			C A			
GAM2152	LOC222256 3'	ATGGCAAACCCCTGTCTCTACT	95908	C	T	ATGG T
		AG AGAG CAGGG	G CCAT			
		TC TCTC GTCCC	C GGTA			
		A T	AAAA_			
GAM2152	LOC222484 5'	ATGGGCCCACTCTACT	95998	C	A	
		AGT AGGG TGGGTCCAT				
		TCA TCTC ACCCGGGTA				
			--			
GAM2152	LOC254531 5'	ATGGCAAACCCCATCTCTGCT	96662			TCA ATGG T
		AGCAGAG GGG	G CCAT			
		TCGTCTC CCC	C GGTA			
		TAC	AAAA_			
GAM2152	LOC255042 3'	ATGGTGAAACCCTGTCTCTACT	97033	C	T	ATGGGT
		AG AGAG CAGGG	CCAT			
		TC TCTC GTCCC	GGTA			
		A T	AAAGT_			
GAM2152	LOC255671 3'	ATGGTGAAACCCTGTCTCTACT	99063	C	T	ATGGGT
		AG AGAG CAGGG	CCAT			
		TC TCTC GTCCC	GGTA			
		A T	AAAGT_			
GAM2152	LOC51157 3'	ACCCCTGGCTCTGCTG	33013			ATG
		CAGCAGAGTCAGGG	GGT			

GTCGTCTCGGTCCC CCA

GAM2152 LOC64167 3' GTGAGACCCCGTCTCCGCT 42542 CA _ _
AGT GGGATGGG TC CAT
||| ||||| || |||
TCG CTCTGCCC AG GTG
C_ C A

GAM2152 LOC91750 3' ATGGTGAAACCCTGTCTCTACT 67647 C T ATGGGT
AG AGAG CAGGG CCAT
|| ||| |||| ||||
TC TCTC GTCCC GGTA
A T AAAGT_

GAM2152 LOC92080 3' ACAGTCCCCGACCCTCTG 68615 C A A GG
CAG AG GTC GGGAT GT
||| || ||| |||| ||
GTC TC CAG CCCTG CA
_ C C A_

GAM2152 LOC92228 3' GTGAGACCCCATCTCTGCT 69079 T _ _
AG CAGGGATGGG TC CAT
|| ||||| || |||
TC GTCTCTACCC AG GTG
_ C A

GAM2152 LOC92482 3' ATGGTGAAACCCTGTCTCTACT 70015 C T ATGGGT
G CAG AGAG CAGGG CCAT
||| ||| |||| ||||
GTC TCTC GTCCC GGTA
A T AAAGT_

GAM2152 LOC93132 5' ATGGTGAAACCCTGTCTCTACT 71979 C T ATGGGT
AG AGAG CAGGG CCAT
|| ||| |||| ||||
TC TCTC GTCCC GGTA
A T AAAGT_

GAM2153 EDNRA 3' CCAAGAAGAAATGCTTTC 64799 T GATT C
GAGA CATT TCTTC TGG
||| ||| |||| |||
CTTT GTAA AGAAG ACC
C _ _ A

GAM2153 PRPH 3' CCCGATAAGAAGCCAATGATC 21831 AT CC
GATCATTG TTCTT TGGG
||||| |||| ||||
CTAGTAAC AAGAA GCCC
CG TA

GAM2153 TMEM2 3' CCCAGAAAGCTTAATGAT 26336 TTT C
ATCATTGA CTT CTGGG
||||| || |||||
TAGTAATT GAA GACCC
C_ A

GAM2153 TNFSF4 3' CCTTATGAAAAATAATGATCTC 13912 A_ TTCCT
T AGAGATCATTG TTTC GG
||||||| ||| ||

TCTCTAGTAAT AAAG CC
 AA TATT_
 GAM2153 DCLRE1A 3' CCCAGGAAAAATATAAACTCT 69683 ATCATTG C
 AGAG ATTT TTCCTGGG
 |||| ||| |||||
 TCTC TAAA AAGGACCC
 AAAATA_ _
 GAM2153 DKFZp434F2322 3' CCCATCTGAATCAGTAATCCCT 70300 A C CTTCC
 AG GAT ATTGATTT TGGG
 || ||| ||||| |||
 TC CTA TGA CTAAG ACCC
 C A TCT_
 GAM2153 DKFZP566G1424 5' CCTGGAAGAAACCCATAATCCC 85941 A CAT A_ T
 T AG GAT TG TTTCTTCC GG
 || ||| || ||||| ||
 TC CTA AC AAAGAAGG CC
 C AT_ CC T
 GAM2153 FLJ14326 3' CCATGAGTCAATGACCTC 50764 A TTCT C
 GAG TCATTGAT TC TGG
 ||| ||||| || |||
 CTC AGTAACTG AG ACC
 C _ T
 GAM2153 FLJ20170 5' CCAGGAAACCAGATCTC 35164 AT ATTTC
 GAGATC TG TTCCTGG
 ||||| || |||||
 CTCTAG AC AAGGACC
 _ CA_
 GAM2153 FLJ20249 3' CCCAGAAAGGAAACTGATCTCT 80220 TTGA C
 AGAGATCA TTTCTT CTGGG
 ||||| ||||| |||||
 TCTCTAGT AAGGAA GACCC
 CA_ A
 GAM2153 KIAA0295 3' CCCAGGAAGCTTTCCAGTGATC 68661 ATTT_
 TC GAGATCATTG CTTCTGCG
 ||||| ||||| |||||
 CTCTAGTGAC GAAGGACCC
 CTTTC
 GAM2153 KIAA0825 3' CCCAGGAAGACACTGACCTGCT 61683 _ A T ATT
 AG AG TCA TG TCTTCCTGGG
 || ||| || ||||| |||||
 TC TC AGT AC AGAAGGACCC
 G C C _
 GAM2153 KIAA1190 3' CCCAAAAAAGTTGATCTCT 71644 TTG C CC
 AGAGATCA ATTT TT TGGG
 ||||| ||| || |||
 TCTCTAGT TGAA AA ACCC
 _ A A_
 GAM2153 MGC4638 3' CCAGAAAGCATGATTTT 49733 T ATTT C
 GAGATCAT G CTT CTGG
 ||||| | ||| |||

CTTTAGTA C GAA GACC
 _ _ _ _ A
 GAM2153 PLPL 3' CCAGGAAAAAGAGTCTC 39820 CATTGA C
 GAGAT TTT TTCCTGG
 |||| | |||||
 CTCTG AAA AAGGACC
 AG _ _

GAM2153 RIN3 5' CCCAGGAAAAAACGGATCTCT 46161 ATTGA C
 AGAGATC TTT TTCCTGGG
 |||| | |||||
 TCTCTAG AAA AAGGACCC
 GC _ A

GAM2153 SLC26A1 3' CCCAAACACTCAGAAATCAAGA 42126 ATCA TCC _
 ACCTCT AGAG TTGATTCT TGGG
 || | |||| | |||
 TCTC AACTAAAGA ACCC
 CAAG CTCACAA

GAM2153 LOC121838 5' CCAGGAAGGACAATCTCTC 76512 TC AT
 GAGA ATTG TTCTTCCTGG
 || | |||||
 CTCT TAAC AGGAAGGACC
 C _

GAM2153 LOC200138 5' CCCAGGAAAAAATCAATGATCT 91540 C
 C GAGATCATTGATTT TTCCTGGG
 ||||| |||||
 CTCTAGTAACTAAA AAGGACCC
 A

GAM2153 LOC220000 3' CCAGGAAGATCTGGCCTCT 93231 AT TT TT
 AGAG CA GA TCTTCCTGG
 || | || || |||||
 TCTC GT CT AGAAGGACC
 CG _ _

GAM2153 LOC221550 5' CCCAGGAAAAAGAATAGATC 93745 _ GA C
 GATC ATT TTT TTCCTGGG
 || | || |||||
 CTAG TAA AAA AAGGACCC
 A G _

GAM2153 LOC255721 3' CCAGGAAGATCTGGCCTCT 96487 AT TT TT
 AGAG CA GA TCTTCCTGG
 || | || || |||||
 TCTC GT CT AGAAGGACC
 CG _ _

GAM2153 LOC257495 5' CCCAGGAAAAAGAATAGATC 99572 _ GA C
 GATC ATT TTT TTCCTGGG
 || | || |||||
 CTAG TAA AAA AAGGACCC
 A G _

GAM2153 LOC257576 5' CCCAGGAAAAAGAATAGATC 99709 _ GA C
 GATC ATT TTT TTCCTGGG
 || | || |||||

		CTAG TAA AAA AAGGACCC	
		A G_ _	
GAM2154 DDX11	3'	GCCGGTGTCTGACTTCCGGC 16576	A_ A C
		GC GAA TCAG ACGCTGGC	
		CG CTT AGTC TGTGGCCG	
		GC C _	
GAM2154 DLG5	3'	AGCTGTGCTGATGCCTGCCA 83809	AA _
		TGGCAG ATCAGCAC GCT	
		ACCGTC TAGTCGTG CGA	
		CG T	
GAM2154 DUOX2	3'	CCACTGATGTGATTTCTACCA 26863	C G _ C
		TGG AGAAATCA CA CG TGG	
		ACC TCTTTAGT GT GT ACC	
		A _ A C	
GAM2154 GJA5	3'	GCCAGTGGAATTTCCCA 75168	CA CAGCA
		TGG GAAAT CGCTGGC	
		ACC CTTA GTGACCG	
		C_ AG__	
GAM2154 HIP12	3'	GGCCAGCGTGGGGCTCCCTGCC 66817	AAA_ AG
		GGCAG TC CACGCTGGCC	
		CCGTC GG GTGCGACCGG	
		CCTC G_	
GAM2154 MAP1B	3'	GCCAACCCAACTGACTTCTGCT 20963	A CACGC_
A		TGGCAGAA TCAG TGGC	
		ATCGTCTT AGTC ACCG	
		C AACCCA	
GAM2154 PVR	3'	GCTGCAGCCACTTTCTGCCA 22494	TCA AC T
		TGGCAGAAA GC GC GGC	
		ACCGTCTTT CG CG TCG	
		CAC A_ _	
GAM2154 STXBP1	3'	GGCCAGCGTCCTCCTCCA 13478	C AAATC C
		TGG AG AG ACGCTGGCC	
		ACC TC TC TGCGACCGG	
		_ C__ C	
GAM2154 TBL1X	3'	CGTCGCTAATAATTTCTGCCA 20131	C__ _
		TGGCAGAAAT AGC ACG	
		ACCGTCTTTA TCG TGC	
		ATAA C	
GAM2154 VIPR1	5'	GGCCAGCGCCACTCTGCCA 17314	AATCAGCA
		TGGCAGA CGCTGGCC	

		ACCGTCT	GCGACCGG		
		CACC_____			
GAM2154	AGS3	5'	GGCCAGCGTGGGCAGCCTGCC	73511	AAATCAG
			GGCAG CACGCTGGCC		
			CCGTC GTGCGACCGG		
			CGACGG_		
GAM2154	DKFZP564O1664	5'	GGCCAGCGCTTGGCCTTCCCGC	48668	A_ A_ CA
	C		GGC GAA TCAG CGCTGGCC		
			CCG CTT GGTT GCGACCGG		
			CC CC C_		
GAM2154	EZF-2	3'	GGCCAGCGCCATCTCCCGCC	37678	A_ A CAGCA
			GGC GA AT CGCTGGCC		
			CCG CT TA GCGACCGG		
			CC C CC_____		
GAM2154	FLJ10948	3'	CCAAGGTGCTGATCCTACCA	37454	C AA GC
			TGG AG ATCAGCAC TGG		
			ACC TC TAGTCGTG ACC		
			A C_ GA		
GAM2154	FLJ11370	3'	GCTGTGCGTGCTGACCCCTCCA	46965	C AAA _
			TGG AG TCAGCACGC TGGC		
			ACC TC AGTCGTGCG GTCG		
			_ CCC T		
GAM2154	FLJ20048	3'	GGCCCATGGCTGATTTTACCA	34900	CA A CT
			TGG GAAATCAGC CG GGCC		
			ACC TTTTAGTCG GT CCGG		
			A_ _ AC		
GAM2154	FLJ20309	3'	GCCAACGTTGGCCTTACTTCTG	35407	ATCA_ _ C
	CCA		TGGCAGAA GC ACG TGGC		
			ACCGTCTT CG TGC ACCG		
			CATTC GT A		
GAM2154	FOXN4	3'	GGCCCCCGTGCTGACTCACGCC	76090	AGAAA CT
	A		TGGC TCAGCACG GGCC		
			ACCG AGTCGTGC CCGG		
			CACTC CC		
GAM2154	IL22R	3'	CCAGAACAACCTGCACTTCTGC	41468	AT_ CACG_
	CA		TGGCAGAA CAG CTGG		
			ACCGTCTT GTC GACC		
			CAC CAACAA		
GAM2154	KIAA0586	3'	GCCAGCACAGTGTTTATGCCA	29238	GAAATC _
			TGGCA AGCAC GCTGGC		

	ACCGT TTGTG CGACCG	
	AT____ ACA	
GAM2154 KIAA1287 3'	GGCTCACTGCAACTTCTGCCA 78939	ATCA CGCT
	TGGCAGAA GCA GGCC	
	ACCGTCTT CGT TCGG	
	CAA_ CAC_	
GAM2154 KIAA1649 3'	CCAGATGTGACTCTGCCA 51224	AATCAG _
	TGGCAGA CACG CTGG	
	ACCGTCT GTGT GACC	
	CA____ A	
GAM2154 KIAA1941 3'	GGCTGTGACTACTTCTGCCA 75342	ATC _ GCT
	TGGCAGAA AG CAC GGCC	
	ACCGTCTT TC GTG TCGG	
	CA_ A ____	
GAM2154 MGC3123 3'	GGCCAGCGTCCTACCCTGCC 44346	AAATC C
	GGCAG AG ACGCTGGCC	
	CCGTC TC TGCGACCGG	
	CCA__ C	
GAM2154 PTPRT 3'	GGCCAGTGATGATTTCCCCCA 56505	CA GCA
	TGG GAAATCA CGCTGGCC	
	ACC CTTTAGT GTGACCGG	
	CC A__	
GAM2154 RES4-25 3'	GGCCAGTGTAATTTCTGTCA 65269	CAGC
	TGGCAGAAAT ACGCTGGCC	
	ACTGTCTTTA TGTGACCGG	
	A__	
GAM2154 LOC145761 5'	GGCTTCTTGCTAGCTTCTGCCA 84483	ATC CGCT
	TGGCAGAA AGCA GGCC	
	ACCGTCTT TCGT TCGG	
	CGA TCT_	
GAM2154 LOC152078 3'	GCCTGCTGTGATTTCTACCA 81288	C G C T
	TGG AGAAATCA CA GC GGC	
	ACC TCTTTAGT GT CG CCG	
	A _ _ T	
GAM2154 LOC197131 3'	CAGAGGATGATTTCTGCCA 89232	GCACG
	TGGCAGAAATCA CTG	
	ACCGTCTTTAGT GAC	
	AGGA_	
GAM2154 LOC200032 5'	GCCAGTGGAATTTCCCCA 85476	CA CAGCA
	TGG GAAAT CGCTGGC	

		ACC CTTTA GTGACCG	
		C_ AG__	
GAM2154	LOC204970 5'	GGCCAGCGCGCAGATCCCCCA 90965	CAGAA A A
		TGG ATC GC CGCTGGCC	
		ACC TAG CG GCGACCGG	
		CCCC_ A C	
GAM2154	LOC221490 5'	GCCACAATGTGATTTTGGCA 95305	G CGC
		TGGCAGAAATCA CA TGGC	
		ACCGTTTTTAGT GT ACCG	
		_ AAC	
GAM2154	LOC253263 3'	CAGTGACCAGTTTCTGCCA 98814	CAGCA
		TGGCAGAAAT CGCTG	
		ACCGTCTTTG GTGAC	
		ACCA_	
GAM2154	LOC253782 3'	AGCAACTGATTTTCAGCCA 97396	A CAC
		TGGC GAAATCAG GCT	
		ACCG CTTTAGTC CGA	
		A AA_	
GAM2154	LOC256364 5'	GGTCTCTGTGCTGACTTCCACC 96447	CA A CT
		GG GAA TCAGCACG GGCC	
		CC CTT AGTCGTGT CTGG	
		AC C CT	
GAM2154	LOC58525 3'	GGCCAGCGTGTGTTTTTCTGTC 79345	TCA
A		TGGCAGAAA GCACGCTGGCC	
		ACTGTCTTT TGTGCGACCGG	
		TTG	
GAM2154	LOC91812 5'	GCCAGACTGTACTGCCTTCTGC 67818	AT C _
CA		TGGCAGAA CAG ACG CTGGC	
		ACCGTCTT GTC TGT GACCG	
		CC A CA	
GAM2154	LOC91813 5'	GCCAGACTGTACTGCCTTCTGC 67843	AT C _
CA		TGGCAGAA CAG ACG CTGGC	
		ACCGTCTT GTC TGT GACCG	
		CC A CA	
GAM2155	ATP6V0C 3'	CCCCAGTAGTTGGTCTTGTA 88658	CTG _ A
		TACAAGATCA ACT CTG GG	
		ATGTTCTGGT TGA GAC CC	
		_ T C	
GAM2155	DLX4 3'	GTCCCCAGAACCCTTGGTCTTG 57114	CTGAC A
		CAAGATCA TCTG GGAC	

			GTTCTGGT AGAC CCTG TCCCA C	
GAM2155 DLX4	3'	GTCCCCAGAACCTTGGTCTTG 10421		CTGAC A
			CAAGATCA TCTG GGAC GTTCTGGT AGAC CCTG TCCCA C	
GAM2155 MNT	3'	TCCTCAGAGGCTGAGCCTGTA 40089		AGA CTGA
			TACA TCA CTCTGAGGA ATGT AGT GAGACTCCT CCG CG__	
GAM2155 SIAH2	3'	TCTCATCAGTGATCTT 18616		CTC
			AAGATCACTGA TGAGG TTCTAGTGACT ACTCT	
GAM2155 TCF2 G	3'	GTCCCCAGAACCTGCTGCAGAT 22411		AGAT _ AC A
			CA CA CTG TCTG GGAC GT GT GAC AGAC CCTG AGAC C CA C	
GAM2155 TCL1A	3'	CCTGGACCACTGGTCT 42017		AC G
			AGATCACTG TCT AGG TCTGGTGAC AGG TCC C_ _	
GAM2155 TOB1	3'	TTTTGAGTCAGTGTCTT 20437	T T	
			AAGA CACTGACTC GAG TTCT GTGACTGAG TTT _ T	
GAM2155 VNN1	3'	TCCTCAGAGCAATTCTCTGTA 17423	_ TCAC A	
			TACA AGA TG CTCTGAGGA ATGT TCT AC GAGACTCCT C TA_ _	
GAM2155 BMF	5'	CCTCAGAGTCAAACCTTTGTG 54280		ATCAC
			TACAAG TGA CTCTGAGG GTGTTT ACTGAGACTCC CAA_	
GAM2155 DDX33	3'	GTCCTCAGTGCGTGACCCTGT 39786		AGA T ACT
			ACA TCAC G CTGAGGAC TGT AGTG C GACTCCTG CCC _GT_	
GAM2155 FLJ20364	3'	CCTCAGAGCCATGTATTTG 35528		AT C A
			CAAG CA TG CTCTGAGG 	

GTTT GT AC GAGACTCC
 AT _ C
 GAM2155 HMGN4 3' TCCTTTCCCCAGTGATTTGTA 22034 A ACTCT
 TACA GATCACTG GAGGA
 |||| ||||| ||||
 ATGT TTAGTGAC TTCCT
 _ CCCT_
 GAM2155 KIAA0377 3' CCTCAGAGCCAGTCTCT 28501 TC A
 AGA ACTG CTCTGAGG
 || ||| |||||
 TCT TGAC GAGACTCC
 C_ C
 GAM2155 KIAA0449 3' TCCCCAGCACTCATGATCTTG 34639 C CT_ A
 CAAGATCA TGA CTG GGA
 ||||| || ||| |||
 GTTCTAGT ACT GAC CCT
 _ CAC C
 GAM2155 KIAA1061 3' GTCCTCAGAGTGCATTTCTG 71723 A TCAC _
 CA GA TG ACTCTGAGGAC
 || || |||||
 GT CT AC TGAGACTCCTG
 C TT_ G
 GAM2155 KIAA1535 3' GTCCTCAGCTCAAGAATCCTGT 80214 A CAC CT
 A
 TACA GAT TGA CTGAGGAC
 |||| || ||| |||||
 ATGT CTA ACT GACTCCTG
 C AGA C_
 GAM2155 LCHN 3' TCCTCAGAGTATGTCTTG 87478 CACTG
 CAAGAT ACTCTGAGGA
 |||| |||||
 GTTCTG TGAGACTCCT
 TA_
 GAM2155 MAGEH1 3' TCATAATCTATGATCTTGTA 26772 CT CTC
 TACAAGATCA GA TGA
 ||||| || |||
 ATGTTCTAGT CT ACT
 AT AAT
 GAM2155 LOC154789 5' TCCTCAGAGCTCTCCTGTG 82034 A TCACT _
 TACA GA GA CTCTGAGGA
 |||| || |||||
 GTGT CT CT GAGACTCCT
 C _ C
 GAM2155 LOC197201 3' TCCTCAGAAGGTATTTGTA 89289 ATC GAC
 TACAAG ACT TCTGAGGA
 |||| || |||||
 ATGTTT TGG AGACTCCT
 A_ A_
 GAM2155 LOC200178 3' CCTCAGATGCCTTGTA 89998 AT CTGAC
 TACAAG CA TCTGAGG
 |||| || |||||

		ATGTTC GT AGACTCC	
		C_ _____	
GAM2155	LOC255193 3'	CCTCAGAGTCAGGCCTGTA 97103	AGATCA
		TACA CTGACTCTGAGG	
		ATGT GACTGAGACTCC	
		CCG_	
GAM2155	LOC96597 5'	TCCCCAGAATTCTTGT 67468	TCACT C_ A
		ACAAGA GA TCTG GGA	
		TGTTCT CT AGAC CCT	
		_____ TA C	
GAM2156	IRS1 3'	CCATAGATGGTTCTCAATTGTA 19874	C TGAAC
		TACA ATTGAGAACC ATGG	
		ATGT TAACTCTTGG TACC	
		_____ TAGA_	
GAM2156	SERPINF1 3'	CCTGTAAGGTTTCAATG 12038	A GA T
		CATTGAGA CCT ACA GG	
		GTAAC TT GGA TGT CC	
		_____ A_ _	
GAM2156	HSA243396 3'	CCATGTTCAAGCAATGTCAATG 37844	GAAC_
		CATTGA CTGAACATGG	
		GTAAC T GACTTGTACC	
		GTAAC	
GAM2156	KIAA1387 3'	CAGGAATTTTCAATATGTA 71444	C _
		TACA ATTGAGAA CCTG	
		ATGT TAACTTTT GGAC	
		A AA	
GAM2156	MGC16063 3'	TTCAAATTCCAATGTGTA 54930	A CC
		TACACATTG GAA TGAA	
		ATGTGTAAC CTT ACTT	
		_____ AA	
GAM2156	SMCR8 3'	CCATGCTCAGGTTTGACTATGT 59253	TGA_ A
		ACAT GAACCTGA CATGG	
		TGTA TTTGGACT GTACC	
		TCAG C	
GAM2156	UPLC1 3'	CCATGCTAGGCCCAATGT 35227	AGAA AA
		ACATTG CCTG CATGG	
		TGTAAC GGAT GTACC	
		CCC_ C_	
GAM2156	ZNF334 3'	CCATAAGTCAACCCTCAATGT 36637	AACC AC_
		ACATTGAG TGA ATGG	

		TGTAAGCTC ACT TACC	
		CCA_ GAA	
GAM2156	LOC145082 3'	TATGGAATGCCCTTAATGTGTA 84196	AACCTGAA
		TACACATTGAG CATG	
		ATGTGTAATTC GTAT	
		CCGTAAG_	
GAM2156	LOC157723 3'	CCAAGTAAGGTTCTCAAATGT 82465	_ GA A
		ACATT GAGAACCT AC TGG	
		TGTAA CTCTTGGA TG ACC	
		A A_ A	
GAM2156	LOC219988 5'	CCATGTTCGGCCCCCAATG 93262	AGAAC
		CATTG CTGAACATGG	
		GTAAC GGCTTGTACC	
		CCCC_	
GAM2157	ASNS 5'	ACTCATCAAGTGACTTGCTGA 9808	_ GGAGTA C
		TCAGCAAG CA TGA GAGT	
		AGTCGTTT GT ACT CTCA	
		A GA___ A	
GAM2157	CCND2 3'	ACTCAAGAGACACCCCTTCCTG 10044	AGC A ATGAC__
	CTGA	TCAGCA AGG GT GAGT	
		AGTCGT TCC CA CTCA	
		CCT C CAGAGAA	
GAM2157	FRAP1 3'	ACTCATCATAAGTACTTGCTGA 18269	CAGGAG C
		TCAGCAAG TATGA GAGT	
		AGTCGTTT ATACT CTCA	
		ATGA__ A	
GAM2157	SMT3H1 3'	TCATCTCTTGCTTGCTTGA 60631	_ T
		TCA GCAAGCAGGAG ATGA	
		AGT CGTTCGTTCTC TACT	
		T _	
GAM2157	TPD52L2 3'	ACTCCAACCCTCCTGCTTGCTG 13828	TATGAC
		CAGCAAGCAGGAG GAGT	
		GTCGTTTCGTCCTC CTCA	
		CCAAC_	
GAM2157	DKFZp586l021 3'	ACTCGTCACACCCAAGCTGCTG 51080	A A_ A A
	G	TCAGCA GC GG GT TGACGAGT	
		GGTCGT CG CC CA ACTGCTCA	
		_ AA _ C	
GAM2157	EHM2 3'	TCACCTCCTGCTCGCTGA 39419	A TA
		TCAGC AGCAGGAG TGA	

AGTCG TCGTCCTC ACT
 C C_
 GAM2157 FLJ23017 3' ACTCACATAAGCCACCGCTTGC 43414 A__ AG AC
 TGA TCAGCAAGC GG TATG GAGT
 ||||| || ||| |||
 AGTCGTTTCG CC ATAC CTCA
 CCA GA A_
 GAM2157 FLJ32670 3' ACTCATCTTAGCATCTGCTTGC 58790 GA AT_ C
 T AGCAAGCAG GT GA GAGT
 ||||| || || |||
 TCGTTTCGTC CG CT CTCA
 TA ATT A
 GAM2157 GFR 3' CTCACCAACTGCTTGCTGA 25445 GA_ ATGAC
 TCAGCAAGCAG GT GAG
 ||||| || |||
 AGTCGTTTCGTC CA CTC
 AAC ____
 GAM2157 MGC4604 3' ACTCGCCACTGGCTGCTTGTT 49794 GAGTA A
 AGCAAGCAG TG CGAGT
 ||||| || |||
 TTGTTTCGTC AC GCTCA
 GGTC_ C
 GAM2157 LOC129607 3' ACTCGTCATGATGGGCTCGCTG 75396 A AGGAG
 CAGC AGC TATGACGAGT
 ||| ||| |||||
 GTCG TCG GTACTGCTCA
 C GGTA_
 GAM2157 LOC146780 5' ACTCATCAGTTTCTGCTTACTG 84815 C GTA C
 G TCAG AAGCAGGA TGA GAGT
 ||| ||||| || |||
 GGTC TTCGTCTT ACT CTCA
 A TG_ A
 GAM2157 LOC153886 3' ACTCACCAATCATCTCCTTCCT 60265 AGC T C____
 GCT AGCA AGGAG ATGA GAGT
 ||| ||||| ||| |||
 TCGT TCCTC TACT CTCA
 CCT _ AACCA
 GAM2157 LOC51008 3' ACCGTCATACTACCAGCTGA 32523 AAGCA _ A
 TCAGC GG AGTATGACG GT
 |||| || ||||| |||
 AGTCG CC TCATACTGC CA
 A__ A C
 GAM2158 CHD2 3' TACCAGCCCACAGTCCTT 8870 A CA
 AAG AT TGGGCTGGTA
 ||| || |||||
 TTC TG ACCCGACCAT
 C AC
 GAM2158 GPRK5 3' ACAGTGGAACCAGCCCAGACCC 19184 AA A AT__
 TT AAG TC TGGGCTGGT TTGT
 ||| || ||||| |||

TTC AG ACCCGACCA GACA
 CC _ AGGT
 GAM2158 AAK1 3' ATGCCCAGCCCAGATTCTT 30516 A _
 AAGAATC TGGGCTGG TAT
 ||||| ||||| |||
 TTCTTAG ACCCGACC GTA
 _ C
 GAM2158 C21orf25 3' CAAAACCAGCCCTGAT 64284 T A
 ATCA GGGCTGGT TTTG
 ||| ||||| |||
 TAGT CCCGACCA AAAC
 _ _
 GAM2158 FLJ10244 3' TACAAATACCTCATCTGTTCTT 36405 T T GCT
 AAGAA CA GG GGTATTTGTA
 |||| || |||||
 TTCTT GT CT CCATAAACAT
 _ _ ACT
 GAM2158 KIAA0855 3' CACTTGGCAGCCTCATGATCCT 31105 A _ G TT
 T AAG ATCATG GGCTG TA TG
 || ||||| |||| || ||
 TTC TAGTAC CCGAC GT AC
 C T G TC
 GAM2158 KIAA1116 3' TACAAATGTTGGCCCCAGATTC 30305 AT GG
 TT AAGAATC GGGCT TATTTGTA
 ||||| |||| |||||
 TTCTTAG CCCGG GTAAACAT
 AC TT
 GAM2158 MGC3040 3' TACAGTGCAAGCGCACGATTCT 67385 A G G T
 T AAGAATC TG GCT GTATT GTA
 ||||| || ||||| |||
 TTCTTAG AC CGA CGTGA CAT
 C G A _
 GAM2158 MGC8407 3' TACAATCTCAGCCCACAAGTC 44117 ATCA TAT
 GA TGGGCTGG TTGTA
 || ||||| ||||
 CT ACCCGACT AACAT
 GAAC CT_
 GAM2158 ZNF185 3' TACAGAGCCCATGCTCTT 24096 AT G_
 AAGA CATGGGCT GTA
 ||| ||||| |||
 TTCT GTACCCGA CAT
 C_ GA
 GAM2158 LOC158332 3' GCTGGGCCAGCCCAGGACTCT 82766 A A ATTT
 AGA TC TGGGCTGGT GT
 ||| || ||||| ||
 TCT AG ACCCGACCG CG
 C G GGT_
 GAM2158 LOC254043 3' TACCTTGTCAGCCCATTACCCT 96766 AATC GT TTT
 T AAG ATGGGCTG A GTA
 ||| ||||| | |||

TTC TACCCGAC T CAT
 CCAT TG TC_
 GAM2159 CDH1 3' TGTGTTTCTGACACAAGAT 16411 C CC
 ATC TG TCAGAAACATG
 ||| || |||||
 TAG AC AGTCTTTGTGT
 A AC
 GAM2159 HIP1 3' GTCCATGCTCCAGGGT 19262 CCTCA AA
 ATCCTG GA CATGGAC
 ||||| || |||||
 TGGGAC CT GTACCTG
 _____ C_
 GAM2159 PLA2G5 5' AGACCCCTAGAGCAGGAT 8112 _ C AAACAT A
 ATCCTGC CT AG GG CT
 ||||| || || ||
 TAGGACG GA TC CC GA
 A _ C_____ A
 GAM2159 SLC8A2 3' AGCCAATCCGGGCAGGA 66931 CA AACA A
 TCCTGCCT GA TGG CT
 ||||| || || ||
 AGGACGGG CT ACC GA
 C_ A_____ _
 GAM2159 FLJ12875 3' CCATGCCTCCAATGGCAGGAT 44915 TCA_ AA
 ATCCTGCC GA CATGG
 ||||| || ||||
 TAGGACGG CT GTACC
 TAAC CC
 GAM2159 FLJ22195 3' CAGGCCACCTCTGGGCAGGA 43107 T AACA A
 TCCTGCC CAGA TGG CTG
 ||||| ||| || |||
 AGGACGG GTCT ACC GAC
 _ CC_ G
 GAM2159 KIAA0326 5' CAGTCCGTCCTCCCGAGGCAGGG 64960 AGAAAC
 TCCTGCCTC ATGGACTG
 ||||| |||||
 GGGACGGAG TGCCTGAC
 CCCCC_
 GAM2159 KIAA0451 3' GTCTATTTCTGAGAAAG 29778 GC AC
 CT CTCAGAA ATGGAC
 || ||||| |||||
 GA GAGTCTT TATCTG
 AA _
 GAM2159 LANCL2 3' CAGCCCACACCTGCAGGCAGGA 38618 _ AAACA A
 T ATCCTGCCT CAG TGG CTG
 ||||| || || |||
 TAGGACGGA GTC ACC GAC
 C CAC_ C
 GAM2159 NKX2C 3' CAGGACTGTCTCTGAGGCAG 59907 A TGGA
 CTGCCTCAGA ACA CTG
 ||||| || || |||

		GACGGAGTCT TGT GAC		
		C CAG_		
GAM2159	SEMA4G 5'	CTATGTGCTTCTGAGGCAG 96326	___	
		CTGCCTCAGAA ACATGG		
		GACGGAGTCTT TGTATC		
		CG		
GAM2159	LOC125875 3'	AGCCTGCCTGGGGCAG 74885	AAA T A	
		CTGCCTCAG CA GG CT		
		GACGGGGTC GT CC GA		
		C_ _ _		
GAM2159	LOC149721 5'	CAGCCCTCACTCTGAGGCGAGA 80315	C AACAT A	
		TC TGCCTCAGA GG CTG		
		AG GCGGAGTCT CC GAC		
		A CACT_ C		
GAM2159	LOC149830 3'	CCATCTCTAAGGCAGGAT 85887	C AAC	
		ATCCTGCCT AGA ATGG		
		TAGGACGGA TCT TACC		
		A C_		
GAM2159	LOC152195 5'	CAGCCCATGTTTTTTGGGAAGG 86746	G C A	
	AT	ATCCT CCT AGAAACATGG CTG		
		TAGGA GGG TTTTGTACC GAC		
		A T C		
GAM2159	LOC153469 3'	GTGTGCTCCTAGGCAGGAT 81699	CA A_	
		ATCCTGCCT GA ACAT		
		TAGGACGGA CT TGTG		
		TC CG		
GAM2159	LOC157247 5'	CAGCCCTCAGCTCTGCAGCAGG 82289	CT AACAT A	
	AT	ATCCTGC CAGA GG CTG		
		TAGGACG GTCT CC GAC		
		AC CGACT C		
GAM2159	LOC196214 5'	CAGTCCACAATGTGGGAGGCAG 91173	AGAA _	
	GAT	ATCCTGCCTC ACA TGGACTG		
		TAGGACGGAG TGT ACCTGAC		
		GG_ AAC		
GAM2159	LOC255852 5'	CTTTGTCTCTGGGCAGGA 99430	T A T	
		TCCTGCC CAGA ACA GG		
		AGGACGG GTCT TGT TC		
		_ C T		
GAM2159	LOC51321 5'	CAGTTCCTGTTTCTGTAACAAG 34030	C CCT T	
	AT	ATC TG CAGAAACA GGA CTG		

			TAG AC GTCTTTGT CTTGAC		
			A AAT C		
GAM2159	LOC92370	3'	CTCTGTTTCTGAAGCAGGA 69665	C	T
			TCCTGC TCAGAAACA GG		
			AGGACG AGTCTTTGT TC		
			A C		
GAM2160	ADAMTS5	3'	ACACTGGTATACCTCCTACCAG 23858	A	GATT_
			CTGGTGGGA GTG GTGT		
			GACCATCCT CAT CACA		
			C ATGGT		
GAM2160	MUCDHL	3'	ACAGCACCTCCCACCA 49199	A	GA
			TGGTGGGA GTG TTGT		
			ACCACCCT CAC GACA		
			C _		
GAM2160	MUCDHL	3'	ACAGCACCTCCCACCA 88632	A	GA
			TGGTGGGA GTG TTGT		
			ACCACCCT CAC GACA		
			C _		
GAM2160	SERPINB9	3'	ACCATTCCACATTCCCACCAG 16005	_	T T
			CTGGTGGGAA GTGGA TG GT		
			GACCACCCTT CACCT AC CA		
			A T _		
GAM2160	FLJ22167	5'	TTCACTCCCCACCAGTGA 44881	A	
			TTACTGGTGGG AGTGGA		
			AGTGACCACCC TCACTT		
			C		
GAM2161	FLT1	3'	ACAGTTGGGACCCAAAACA 10657	C	GGAAGTG
			TGT TTGGG CAACTGT		
			ACA AACCC GTTGACA		
			A AGG_		
GAM2161	CRELD1	5'	CGGACACCTCCCCCAAGACA 31952	A	CAA
			TGTCTTGGGGGA GTG CTG		
			ACAGAACCCCCT CAC GGC		
			C A_		
GAM2161	CSEN	3'	CACAGCCACCTCCACCCCAAG 26456	AA_	CAA
	A		TCTTGGGGG GTG CTGTG		
			AGAACCCCC CAC GACAC		
			ACCTC C_		
GAM2161	KIAA0441	3'	CACAGTTGTTACCACAAGACA 29626	G	GAAGT
			TGTCTTG GG GCAACTGTG		

ACAGAAC CC TGTGACAC
 A AT____
 GAM2161 KIAA0841 3' CACCTCACCTCCCCAGGACA 71887 A CAACT
 TGTCTTGGGGGA GTG GTG
 ||||| ||| |||
 ACAGGACCCCT CAC CAC
 C TC____
 GAM2161 KIAA1393 3' CACAGTTACACCTCAATGTA 72570 TC GAAG C
 TG TTGGGG TG AACTGTG
 || |||| || |||||
 AT AACTCC AC TTGACAC
 GT ____ A
 GAM2161 MGC8974 5' ACAGTTGCAACCAAGGCA 54735 GGGAAG
 TGTCTTGG TGCAACTGT
 ||||| |||||
 ACGGAACC ACGTTGACA
 A_____
 GAM2161 SCOP 3' ACATCCTTCCCCCAGACA 93425 T TGCAAC
 TGTCT GGGGGAAG TGT
 |||| ||||| |||
 ACAGA CCCCCTTC ACA
 - CT____
 GAM2161 LOC149322 3' ACAGTTACAGTTCCAAGA 60286 GGG G C
 TCTT GGAA TG AACTGT
 ||| ||| || |||||
 AGAA CCTT AC TTGACA
 ____ G A
 GAM2161 LOC220635 3' ACAGTTACAGTTCCAAGA 92452 GGG G C
 TCTT GGAA TG AACTGT
 ||| ||| || |||||
 AGAA CCTT AC TTGACA
 ____ G A
 GAM2161 LOC255515 3' CACAAGTGCTCTCCCAAACA 97811 C AGT AC
 TGT TTGGGGGA GCA TGTG
 || ||||| || |||
 ACA AACCTCT CGT ACAC
 A ____ GA
 GAM2161 LOC86651 3' ACAGTTACAGTTCCAAGA 69309 GGG G C
 TCTT GGAA TG AACTGT
 ||| ||| || |||||
 AGAA CCTT AC TTGACA
 ____ G A
 GAM2162 PDGFRB 3' AGGCCCCCAGCAAGTCTCA 66578 A A AA
 TGA ACTTGCTG GG CT
 || ||||| || ||
 ACT TGAACGAC CC GA
 C C CG
 GAM2162 PPP1R12B 5' CATGAGCCCTCAGCAGTTCCA 50348 A T AA T
 TG AACT GCTGAGG CTC ATG
 || ||| ||||| || |||

			AC TTGA CGACTCC GAG TAC		
			C _ C _		
GAM2162	PPP1R12B	5'	CATGAGCCCTCAGCAGTTCCA	50371	A T AA T
			TG AACT GCTGAGG CTC ATG		
			AC TTGA CGACTCC GAG TAC		
			C _ C _		
GAM2162	PTPN13	3'	AGAGCAGCAAGTTCA	55638	A AGGAA
			TGAA CTTGCTG CTCT		
			ACTT GAACGAC GAGA		
			— ———		
GAM2162	PTPN13	3'	AGAGCAGCAAGTTCA	55639	A AGGAA
			TGAA CTTGCTG CTCT		
			ACTT GAACGAC GAGA		
			— ———		
GAM2162	PTPN13	3'	AGAGCAGCAAGTTCA	21833	A AGGAA
			TGAA CTTGCTG CTCT		
			ACTT GAACGAC GAGA		
			— ———		
GAM2162	FLJ22679	3'	AGAGAGCAAGTTGTCA	35174	_ GAGGAA
			TGA AACTTGCT CTCT		
			ACT TTGAACGA GAGA		
			G ———		
GAM2162	FLJ22679	3'	AGAGAGCAAGTTGTCA	50906	_ GAGGAA
			TGA AACTTGCT CTCT		
			ACT TTGAACGA GAGA		
			G ———		
GAM2162	FLJ23563	3'	CATAGAGTTCCTTTGGGATTTC	68212	_ CT
	A		TGAAA CTTG GAGGAACTCTATG		
			ACTTT GGGT TTCCTTGAGATAC		
			A —		
GAM2162	KIAA1033	3'	CATAGAGTCCTGTTTGAAGCTT	65130	A GCTG_ A
	CA		TGAA CTT AGGA CTCTATG		
			ACTT GAA TCCT GAGATAC		
			C GTTTG _		
GAM2162	KIAA1674	3'	CATAAAGTTCCTCTTATTTTCA	69332	CTTGCT C
			TGAAA GAGGAACT TATG		
			ACTTT CTCCTTGA ATAC		
			TATT_ A		
GAM2162	KIAA1808	3'	AGAGCTCCCTGTCTAGTTTC	87046	T_ TGA A
			GAAACT GC GGA CTCT		

		CTTTGA TG CCT GAGA		
		TC TC_ C		
GAM2162	LOC202934 3'	CATAGAGTCCCTACTGCAGCA 92031	_____	A
		TGCTG AGG ACTCTATG		
		ACGAC TCC TGAGATAC		
		GTCA C		
GAM2162	LOC255465 3'	CATAGAGTCCCTACTGCAGC 99106	_____	A
		GCTG AGG ACTCTATG		
		CGAC TCC TGAGATAC		
		GTCA C		
GAM2162	LOC51315 3'	CATAAAGTTTCTAAAGTTTCA 34010	GCTG	C
		TGAAACTT AGGAACT TATG		
		ACTTTGAA TCTTTGA ATAC		
		A_____ A		
GAM2163	CDO1 3'	ACATGATCCCCAGACCACAACA 10162		GA
		TGTTGTGGTCTGGGGA ATGT		
		ACAACACCAGACCCCT TACA		
		AG		
GAM2163	SMTN 3'	ACACCCTCCCCCCCACATACAC 23651	_	TCT AA
	A	TGTGT TGTGG GGGGAG TGT		
		ACACA ACACC CCCCTC ACA		
		T C_____ CC		
GAM2163	SMTN 3'	ACACCCTCCCCCCCACATACAC 23652	_	TCT AA
	A	TGTGT TGTGG GGGGAG TGT		
		ACACA ACACC CCCCTC ACA		
		T C_____ CC		
GAM2163	HB-1 5'	TCCTCTGCCACACCACA 41317	T	CT
		TGTG TGTGGT GGGGA		
		ACAC ACACCG CTCCT		
		C T_____		
GAM2164	AOX1 3'	ACAGAATAGGATAAAATATTTG 8571	C	AAA
	TA	TACAAG ATTTTG TATTCTGT		
		ATGTTT TAAAAT ATAAGACA		
		A AGG		
GAM2164	KLHL1 3'	ACAGAATATTTTCATCTGACAGT 40868	AAG TTT	
	A	TAC CA TGAAATATTCTGT		
		ATG GT ACTTTATAAGACA		
		ACA CT_____		
GAM2164	PODXL 3'	ACAGAATATTCTTTGCGTTGTA 19410	_	TTTT A
		TACAA GCA GAA TATTCTGT		

ATGTT CGT CTT ATAAGACA
 G TT__ _
 GAM2164 ROCK2 3' ACAAATATTTTATTTGCTTTA 66609 C TTT C
 A AAGCA TGAAATATT TGT
 ||||| ||||| |||
 A TTCGT ATTTTATAA ACA
 T TT_ A
 GAM2164 CDA02 3' ACAGAATATTCCTGTGC 68451 TTT A
 GCAT GAA TATTCTGT
 |||| ||| |||||
 CGTG CTT ATAAGACA
 TC_ _
 GAM2164 FLJ14050 3' AGTATTTCAAATAGTTGTA 60954 GC
 TACAA ATTTTGAAATATT
 ||||| |||||
 ATGTT TAAACTTTATGA
 GA
 GAM2164 FLJ20094 3' ACAGAATATTATCACTTG 35043 CATTT _
 CAAG TGA AATATTCTGT
 |||| ||| |||||
 GTTC ACT TTATAAGACA
 _ A
 GAM2164 FLJ20413 3' ACAGAATGGGAGAAAATGTCTG 35586 AG GAAA
 CA CATTTT TATTCTGT
 || ||||| |||||
 GT GTAAAA GTAAGACA
 CT GAGG
 GAM2164 KIAA1301 3' ACAGAATATTCATTTCTTGCTT 66943 TTT_ A
 AAGCA TGAA TATTCTGT
 |||| ||| |||||
 TTCGT ACTT ATAAGACA
 TCTTT _
 GAM2164 MGC32104 3' ACAGAATGGGAGAAAATGTTT 59060 GAAA
 AAGCATTTT TATTCTGT
 ||||| |||||
 TTTGTAAAA GTAAGACA
 GAGG
 GAM2164 STIP-1 3' ACAATGATTTCAAATACTTG 70236 C ATTC
 CAAG ATTTTGAAAT TGT
 |||| ||||| |||
 GTTC TAAACTTTA ACA
 A GTA_
 GAM2164 LOC121504 3' ACAGAATATCTCAAACGT 74535 T A
 CA TTTGA ATATTCTGT
 || ||||| |||||
 GT AAAC TATAAGACA
 C C
 GAM2164 LOC203276 3' ACAGAATATTTTCAAATTGT 92104 T _
 GCA TTTGAAA TATTCTGT
 ||| ||||| |||||

			TGT AAAC TTT ATAAGACA		
			T T		
GAM2164	LOC203305	3'	ACAGAATATTTTCAAATTGT	92157	T _
			GCA TTTGAAA TATTCTGT		
			TGT AAAC TTT ATAAGACA		
			T T		
GAM2165	ACE2	3'	TTGATCAACATCTCCCTGACA	41729	C CTGCA
			TGTCAGGGAG TG GGT CAG		
			ACAGTCCCTC AC CTAGTT		
			T AA _		
GAM2165	DTNA	3'	CCCAGCAGCTCCTGACA	53206	G CA
			TGTCAGG AGCTGCTG GG		
			ACAGTCC TCGACGAC CC		
			_ _		
GAM2165	DTNA	3'	CCCAGCAGCTCCTGACA	53274	G CA
			TGTCAGG AGCTGCTG GG		
			ACAGTCC TCGACGAC CC		
			_ _		
GAM2165	EZH1	3'	CCCAGCAACTCCTGACA	10550	G C CA
			TGTCAGG AG TGCTG GG		
			ACAGTCC TC ACGAC CC		
			_ A _		
GAM2165	HDAC7A	3'	CTGAGACGAAGCTCCCTGACA	31831	GCTG _
			TGTCAGGGAGCT CAG		
			ACAGTCCCTCGA GTC		
			AGCAGA		
GAM2165	HDAC7A	3'	CTGAGACGAAGCTCCCTGACA	33924	GCTG _
			TGTCAGGGAGCT CAG		
			ACAGTCCCTCGA GTC		
			AGCAGA		
GAM2165	MPP2	3'	CTGACCTGTGACCCCCTGCCA	60519	T AGCTGCT
			TG CAGGG GCAGGTCAG		
			AC GTCCC TGTCCAGTC		
			C CCAG _		
GAM2165	NKX2E	3'	CTCAACAGCTCCCTGAC	16521	C C
			GTCAGGGAGCTG TG AG		
			CAGTCCCTCGAC AC TC		
			A _		
GAM2165	RAI3	3'	CTCAGCAGCTCCCCAGCA	15620	CA C
			TGT GGGAGCTGCTG AG		

ACG CCCTCGACGAC TC
 AC _
 GAM2165 BAD 5' GACAGCCTCAGCTCCCTGCCA 16314 T CT AG
 TG CAGGGAGCTG GC GTC
 || ||||| || ||
 AC GTCCCTCGAC CG CAG
 C TC A_
 GAM2165 BNIP-S 5' GACAACCAGCTCCCCGACA 57088 A CTGCAG
 TGTC GGGAGCTG GTC
 ||| ||||| ||
 ACAG CCCTCGAC CAG
 C CAA_
 GAM2165 CENTA1 3' ACCTGCCCTCCCTGAC 23442 CTGCT
 GTCAGGGAG GCAGGT
 ||||| |||||
 CAGTCCCTC CGTCCA
 CC_
 GAM2165 KIAA0992 3' ACCCATCTCACCTGACA 32714 _ C CTGCA
 TGTCAGG GAG TG GGT
 ||||| ||| ||
 ACAGTCC CTC AC CCA
 A T _
 GAM2165 KIAA1854 3' CTGACCTGCAGCCCAAACCGAC 72207 A GAGCT
 GTC GG GCTGCAGGTCAG
 ||| || |||||
 CAG CC CGACGTCCAGTC
 _ AAACC
 GAM2165 KRTAP1-1 5' ACCTTCAGATCAACTCCTGACA 49045 G C _ C
 TGTCAGG AG TG CTG AGGT
 ||||| || || |||||
 ACAGTCC TC AC GAC TCCA
 _ A TA T
 GAM2165 MGC12760 3' CTGGAGCAACAGCTCCCCACA 52159 CA C AGG
 TGT GGGAGCTG TGC TCAG
 || ||||| || |||||
 ACA CCCTCGAC ACG GGTC
 C_ A A_
 GAM2165 MIC2L1 3' CCAATAGACAGCCCCTGACA 49599 A _ CA
 TGTCAGGG GCTG CTG GG
 ||||| ||| || ||
 ACAGTCCC CGAC GAT CC
 _ A AA
 GAM2165 PTK6 5' CCACAGCAGCTCCTGACA 21070 G CA
 TGTCAGG AGCTGCTG GG
 ||||| ||||| ||
 ACAGTCC TCGACGAC CC
 _ A_
 GAM2165 LOC166341 3' TGACCTACCACTCCCTGA 83519 C CTGC
 TCAGGGAG TG AGGTCA
 ||||| || |||||

		AGTCCCTC AC TCCAGT	
		_ CA_	
GAM2165	LOC199733 3'	CTGTGAGAACAGCTCCCTGGCA 91440	__ _
		TGTCAGGGAGCTG CT GCAG	
		ACGGTCCCTCGAC GA TGTC	
		AA G	
GAM2166	MASP1 3'	CAAGGTTCTGAGTCCTGTGGTA 58210	GA T
		TACCATAGGAC AG AACCTTG	
		ATGGTGTCTG TC TTGGAAC	
		AG _	
GAM2166	KNSL5 3'	CAAAGCTTTCCCTATGGT 17952	AC AACC
		ACCATAGG GAAGT TTG	
		TGGTATCC TTTCG AAC	
		C_ A_	
GAM2166	SH120 3'	CAAGACATGTCTATGGTA 33389	G AA AAC
		TACCATAG ACG GT CTG	
		ATGGTATC TGT CA GAAC	
		_ A_ _	
GAM2166	LOC149992 5'	GCAAAATTGCTGTCCTGTGGTA 80376	GA CC
		TACCATAGGAC AGTAA TTGC	
		ATGGTGTCTG TCGTT AACG	
		_ AA	
GAM2167	LOC155036 5'	TGGACACGGAGACCAGGA 87616	G A AT GC
		TC CT GTCTCCGT G CCG	
		AG GA CAGAGGCA C GGT	
		_ C _ A_	
GAM2168	CDH12 3'	CTTATCATTTAAAGTGGTGTA 15777	CCCAA GA
		TACACCACT GAA ATAAG	
		ATGTGGTGA TTT TATTC	
		AA_ AC	
GAM2168	GOCAP1 3'	ATTGTTCTTGGGAGCAGTGTA 43007	CA G
		TACAC CTCCCAAGAA AAT	
		ATGTG GAGGGTTCTT TTA	
		AC G	
GAM2168	DKFZP434N2435 5'	CTTATTACTGTGGGGTGGT 98090	T AGAAG
		ACCAC CCCA AATAAG	
		TGGTG GGGT TTATTC	
		_ GTCA_	
GAM2168	DKFZP564I122 3'	CTTATTCTTCTCCCTCATGTGT 63877	CACTCCCA
	A	TACAC AGAAGAATAAG	

		ATGTG	TCTTCTTATTC		
		TACTCCC_			
GAM2168	FLJ21791	3'	CTTATTTGCAGAAAGTGGTGTA	62126	CCCAAGAA
			TACACCACT	GAATAAG	
			ATGTGGTGA	TTTATTC	
			AGACG__		
GAM2168	HMP19	3'	CTTATTCTTTGTTAGGAAAATG	88860	CCAC CAA_
	TA		TACA TCC	GAAGAATAAG	
			ATGT AGG	TTTCTTATTC	
			AAA_	ATTG	
GAM2168	KIAA1719	3'	TCTGTCTTGGGAGTGGTGTA	68742	_
			TACACCACTCCCAAGA	AGA	
			ATGTGGTGAGGGTTCT	TCT	
			G		
GAM2168	KIAA1853	3'	TTTTTCTTGGAAGCAGTG	69929	CA C
			CAC CT	CCAAGAAGAA	
			GTG GA	GGTTCTTTTT	
			AC A		
GAM2168	KIAA1877	3'	CTTATTCTTCTGCCATGAGT	66748	CCA_
			ACTC	AGAAGAATAAG	
			TGAG	TCTTCTTATTC	
			TACCG		
GAM2168	KIAA1906	3'	CTTATTCTTCTTGACTTTTGG	73571	CTCC_
			CCA	CAAGAAGAATAAG	
			GGT	GTTCTTCTTATTC	
			TTTCA		
GAM2168	OSBPL11	3'	CTTAATTTCCCAAGAGTGGTG	43206	CCAA AA
			CACCACTC	GAAG TAAG	
			GTGGTGAG	CTTT ATTC	
			AACC	A_	
GAM2168	YME1L1	3'	TCATTCTTGATGTGGTGTA	58438	TCC _
			TACACCAC	CAAGAA GA	
			ATGTGGTG	GTTCTT CT	
			TA_	A	
GAM2168	ZNF262	3'	CTTATTTTGTGTTGGGAGT	18723	A
			ACTCCCAAG	AGAATAAG	
			TGAGGGTTT	TTTTATTC	
			G		
GAM2168	LOC91960	3'	TGTGGCTTGGAACGTGGTGTA	68294	TC_ AAGA
			TACACCAC	CCAAG ATA	

		ATGTGGTG GGTTC TGT		
		CAA GG__		
GAM2169	BSN	3' CCCAGCATCATGAGCAAG 14380	A	CTTCA AA
		CTTGCTCAT GT GC GG		
		GAACGAGTA TA CG CC		
		C ____ AC		
GAM2169	CLCA2	3' CCTTACACTTTGGCTATGAACA 22563	C	TTCAGC_
	A	TTG TCATAGTC AAGG		
		AAC AGTATCGG TTCC		
		A TTTACA		
GAM2169	CRY2	3' CCTTGCTCCGTGAGCAA 72661	AGTCTTC	
		TTGCTCAT AGCAAGG		
		AACGAGTG TCGTTCC		
		CC____		
GAM2169	FADD	3' TCCTCACTATGACACTGAGCAA 15126	TA	TTC CA
	G	CTTGCTCA GTC AG AGGA		
		GAACGAGT CAG TC TCCT		
		CA TA_ AC		
GAM2169	HLCS	5' TCCATTGAAGACTTGAACAAG 6421	C T	CAA
		CTTG TCA AGTCTTCAG GGA		
		GAAC AGT TCAGAAGTT CCT		
		A _ A__		
GAM2169	MEST	3' CTGAAAGACCTATGAGCAA 70459	_ _	
		TTGCTCATAG TCTT CAG		
		AACGAGTATC AGAA GTC		
		C A		
GAM2169	PCDH7	5' CCCCCTGCATGAGCAG 51616	A TCTT	AA
		TTGCTCAT G CAGC GG		
		GACGAGTA C GTCG CC		
		_ ____ CC		
GAM2169	PCDH7	5' CCCCCTGCATGAGCAG 51619	A TCTT	AA
		TTGCTCAT G CAGC GG		
		GACGAGTA C GTCG CC		
		_ ____ CC		
GAM2169	PCDH7	5' CCCCCTGCATGAGCAG 11987	A TCTT	AA
		TTGCTCAT G CAGC GG		
		GACGAGTA C GTCG CC		
		_ ____ CC		
GAM2169	PLP2	5' TCCTCGAAACACGAGCAAG 12176	ATA C	AGCA
		CTTGCTC GT TTC AGGA		

GAACGAG CA AAG TCCT
CAC _ C____

GAM2169 PLXNA2 3' TCCCTAAAGTTACTATGAGAAG 48003 G _ C CAA
CTT CTCATAGT CTT AG GGA
||| ||||| ||| || |||
GAA GAGTATCA GAA TC CCT
_ TT A _

GAM2169 AP1GBP1 3' CCTCAGACCAGTGAGCAA 24346 A_ TCAGCA
TTGCTCAT GTCT AGG
||||||| |||| |||
AACGAGTG CAGA TCC
AC C_____

GAM2169 AP1GBP1 3' CCTCAGACCAGTGAGCAA 55438 A_ TCAGCA
TTGCTCAT GTCT AGG
||||||| |||| |||
AACGAGTG CAGA TCC
AC C_____

GAM2169 AP1GBP1 3' CCTCAGACCAGTGAGCAA 55444 A_ TCAGCA
TTGCTCAT GTCT AGG
||||||| |||| |||
AACGAGTG CAGA TCC
AC C_____

GAM2169 CAP350 3' CCTACTGAAGACTGGGC 29703 TA CA
GCTCA GTCTTCAG AGG
||||| ||||| |||
CGGGT CAGAAGTC TCC
_ A_

GAM2169 DDX34 3' TCCCTGCTGGAGACCAACAAG 28679 CTCATA A
CTTG GTCTTCAGCA GGA
||||| ||||| ||||| |||
GAAC CAGAGGTCGT CCT
AAC_____ C

GAM2169 DKFZP586G1122 3' CCGCAAAACTGTGAGCAA 61938 CTTCA AA
TTGCTCATAGT GC GG
||||||| || |||
AACGAGTGTCA CG CC
AAA_ _

GAM2169 FAM10A6 3' CCTTGCTGAAGGAAAAGCAA 72782 CATAG
TTGCT TCTTCAGCAAGG
||||| ||||| ||||| |||
AACGA GGAAGTCGTTCC
AAA_

GAM2169 FLJ10546 5' TGCAAAGACTATGAGCA 60184 CA
TGCTCATAGTCTT GCA
||||||| |||
ACGAGTATCAGAA CGT
A_

GAM2169 FLJ10726 3' CTTAACTATGAGCAGG 37042 CTTCAGC
CTTGCTCATAGT AAG
||||||| |||

			GGACGAGTATCA	TTC	
			A_____		
GAM2169	KIAA0475	5'	CCTTAATACATGAGCAAG	30115	A C CAGC
			CTTGCTCAT GT TT	AAGG	
			GAACGAGTA CA AA	TTCC	
			_ T _____		
GAM2169	KIAA1655	5'	CCTCACTGTGGATGAGCAA	67179	TAG T CA
			TTGCTCA TCT CAG	AGG	
			AACGAGT AGG GTC	TCC	
			_____ T AC		
GAM2169	MGC3077	3'	TCCTTGTTTTTAGACTAT	44128	TC_
			ATAGTCT AGCAAGGA		
			TATCAGA TTGTTCCCT		
			TTT		
GAM2169	RAB40C	3'	CCTTGTTTGGGATTATGAACAA	41278	C TC
			TTG TCATAGTCT	AGCAAGG	
			AAC AGTATTAGG	TTGTTCC	
			A GT		
GAM2169	SEN2	3'	CTGCTGAAGAGCAGG	76832	ATAGTC A
			CTTGCTC TTCAGCA	G	
			GGACGAG AAGTCGT	C	
			_____ C		
GAM2169	ST13	3'	CCTTGCTGAAGGAAAAGCAA	15431	CATAG
			TTGCT TCTTCAGCAAGG		
			AACGA GGAAGTCGTTCC		
			AAA_		
GAM2169	LOC118491	5'	TCCTGTTGGAGAACTATGAGCA	74358	_ A
			AG CTTGCTCATAGT	CTTCAGCA GGA	
			GAACGAGTATCA GAGGTTGT	CCT	
			A _		
GAM2169	LOC125228	3'	CCTTTGGAAACTATGGGCAA	74863	C GC
			TTGCTCATAGT TTCA	AAGG	
			AACGGGTATCA AGGT	TTCC	
			A _		
GAM2169	LOC126751	3'	CCCTGCTGAGATTGAGCCAG	75072	T TA T A
			CT GCTCA GTCT CAGCA	GG	
			GA CGAGT TAGA GTCGT	CC	
			C _ _ C		
GAM2169	LOC144840	3'	CCTACTGAAGACTGGAG	77526	A CA
			CTC TAGTCTTCAG	AGG	

		GAG GTCAGAAAGTC TCC	
		— A—	
GAM2169	LOC149052 3'	CCTTGCTGAAGGAAAAGCAA 79872	CATAG
		TTGCT TCTTCAGCAAGG	
		AACGA GGAAGTCGTTCC	
		AAA—	
GAM2169	LOC158886 3'	CCTTGCTGAAGGAAAAGCAA 83722	CATAG
		TTGCT TCTTCAGCAAGG	
		AACGA GGAAGTCGTTCC	
		AAA—	
GAM2169	LOC200197 3'	CCCTGCCGACATGAGCAA 90016	A TTCA A
		TTGCTCAT GTC GCA GG	
		AACGAGTA CAG CGT CC	
		— C— C	
GAM2169	LOC219731 5'	CCAGGTTAAACTATGAGGAAG 94699	G C C AA
		CTT CTCATAGT TT AGC GG	
		GAA GAGTATCA AA TTG CC	
		G A _ GA	
GAM2169	LOC221178 3'	CCCTGCTGATGATGAGCAAG 95168	AGTCT A
		CTTGCTCAT TCAGCA GG	
		GAACGAGTA AGTCGT CC	
		GT— C	
GAM2169	LOC222407 5'	CCTACACTGAAAACAATGAGCA 95973	A C CA_
	A	TTGCTCAT GT TTCAG AGG	
		AACGAGTA CA AAGTC TCC	
		A A ACA	
GAM2169	LOC245718 3'	CCTTGCTGAAGGAAAAGCAA 92415	CATAG
		TTGCT TCTTCAGCAAGG	
		AACGA GGAAGTCGTTCC	
		AAA—	
GAM2169	LOC256228 5'	CCTTGCTGAAGCAGGACAGCAA 97969	CATAGT
	G	CTTGCT CTTCAGCAAGG	
		GAACGA GAAGTCGTTCC	
		CAGGAC	
GAM2170	APM1 3'	AAGCCAACTCCATCTCT 17750	C A
		AG AGGT GAGTTGGCTT	
		TC TCTA CTCAACCGAA	
		— C	
GAM2170	CYP4A11 3'	AACTCCTGCCTGCCCTCCA 7584	AA _
		TGGA GCAGGTAG AGTT	

ACCT CGTCCGTC TCAA
 CC C
 GAM2170 EHD2 3' AAGCCAAGGCTTCTTCCCA 28207 A C AGAG
 TGG AAG AGGT TTGGCTT
 ||| ||| ||| ||| |||
 ACC TTC TTCG AACCGAA
 C _ G__
 GAM2170 GALE 3' AAAGCAGCAGCTGCCTGCTCTC 63858 A AGTTG
 CA TGGGA AGCAGGTAG GCTTT
 ||| ||| ||| ||| |||
 ACCT TCGTCCGTC CGAAA
 C GACGA
 GAM2170 LCP1 3' AAAGCCAACATGTGGCTCCTCC 11280 A_ AGGTAGA
 GGA AGC GTTGGCTTT
 ||| ||| ||| ||| |||
 CCT TCG CAACCGAAA
 CC GTGTA__
 GAM2170 NEDD4 3' CCACTTTCTACTTTCCA 70543 C TA T
 TGGAAAG AGG GAGT GG
 ||| ||| ||| ||| |||
 ACCTTTC TCT TTCA CC
 A _ _
 GAM2170 VIPR1 3' AGCCTACCTGCTCTCCA 17309 A A
 TGGGA AGCAGGTAG GTT
 ||| ||| ||| ||| |||
 ACCT TCGTCCATC CGA
 C _
 GAM2170 BTBD3 3' AAAGCCAAACTCTTCTCTCCA 31024 AA C T _
 TGGGA G AGG AGAGTT GGCTTT
 ||| ||| ||| ||| |||
 ACCT C TCT TCTCAA CCGAAA
 _ _ _ A
 GAM2170 FLJ20694 3' AAAGCCAAACTGACCATCTGCT 35966 AG__ _
 TTCCA TGGAAAGCAGGT AGTT GGCTTT
 ||| ||| ||| ||| |||
 ACCTTTCGTCTA TCAA CCGAAA
 CCAG A
 GAM2170 HSPC157 5' GTCCTACTACCTGCTTTCCA 27191 _ TT
 TGGAAAGCAGGTAG AG GGC
 ||| ||| ||| ||| |||
 ACCTTTCGTCCATC TC CTG
 A _
 GAM2170 KIAA1522 3' CCACCCTCCTGCCTTCCA 65604 A T A T
 TGGAA GCAGG AG GT GG
 ||| ||| ||| ||| |||
 ACCTT CGTCC TC CA CC
 C _ C _
 GAM2170 PP1628 5' AAGCCAGCCCCTCCTCCCA 48069 AA C TAGA
 TGG AG AGG GTTGGCTT
 ||| ||| ||| ||| |||

ACC TC TCC CGACCGAA
 C_ C C_
 GAM2170 TIX1 3' AGTTGGCTTTAAACCACCTGCT 62405 A T_____ TTGG
 TCCCA TGG AAGCAGG AGAG CT
 ||| ||||| ||| ||
 ACC TTCGTCC TTTC GA
 C ACCAAA_ GGT
 GAM2170 LOC118987 3' CCAACCCAAGGATCTGCTTC 74393 AGA_
 GAAAGCAGGT GTTGG
 ||||| ||||
 CTTTCGTCTA CAACC
 GGAACC
 GAM2170 LOC132617 3' AAAGCCAACCTCTACAATGCTCA 76405 A G_
 A AGCA GTAGAGTTGGCTTT
 | ||| ||||| |||||
 A TCGT CATCTCAACCGAAA
 C AA
 GAM2170 LOC152503 3' CCACTTTCCTGCTTTCCA 86976 T T
 TGGAAAGCAGG AGAGT GG
 ||||| |||| ||
 ACCTTTCGTCC TTTCA CC
 - -
 GAM2171 AQP6 5' ATCCTTTCAGTGGCCTC 54983 A CA
 GA GCCATTGAAA GAT
 || ||||| |||
 CT CGGTGACTTT CTA
 C C_
 GAM2171 ATP11B 3' GATCACCTGTTAATGGC 81126 AA A_
 GCCATTG ACAG TGATC
 ||||| ||| ||||
 CGGTAAT TGTC ACTAG
 CC
 GAM2171 TRPC5 3' ATCATCTGTTCTGGAACCTC 25924 AG_ TT A
 GA CCA GAA CAGATGAT
 || ||| ||| |||||
 CT GGT CTT GTCTACTA
 CAA _ _
 GAM2171 C1orf34 3' CATGTGTCTTCATGGCTTC 61301 T _ G
 GAAGCCAT GAA ACA ATG
 ||||| ||| ||| |||
 CTTTCGGTA CTT TGT TAC
 _ C G
 GAM2171 DKFZp761B1514 3' ATCATCTGTTTGAACCTC 51138 C TTGA
 GAAG CA AACAGATGAT
 ||| || |||||
 CTTTC GT TTGTCTACTA
 A _
 GAM2171 FLJ10346 5' GATCATCTGCCCTCCTCGGCCT 36525 A ATT AA_
 C GA GCC GA CAGATGATC
 || ||| || |||||

CT CGG CT GTCTACTAG
 C CTC CCC
 GAM2171 FLJ12960 3' GATCATCTGTCCCAGGT 45300 AT AA
 GCC TG ACAGATGATC
 ||| || |||||
 TGG AC TGTCTACTAG
 _ CC
 GAM2171 FLJ23563 3' CACCTGTAGGCCCTGGCTTTGT 68211 TTGAA_ A
 ACGAAGCCA ACAG TG
 ||||| ||| ||
 TGTTCGGT TGTC AC
 CCCGGA C
 GAM2171 MGC10911 5' TCCGTTTCAATGCCCGT 51182 AA C A
 ACG GC ATTGAAAC GA
 ||| || ||||| ||
 TGC CG TAACTTTG CT
 CC _ C
 GAM2171 LOC123095 5' TCTGTCTTTAATGGCTTC 76522 _
 GAAGCCATTGAA ACAGA
 ||||| ||||
 CTTCGGTAATTT TGTCT
 C
 GAM2171 LOC132617 5' CTGGGGCCCAATGGCTTCGT 76416 AAA_
 ACGAAGCCATTG CAG
 ||||| |||
 TGCTTCGGTAAC GTC
 CCGGG
 GAM2171 LOC135138 3' ATCATCTGTCTCTGTTGC 75710 C T A
 GC AT GA ACAGATGAT
 || || || |||||
 CG TG CT TGTCTACTA
 T T C
 GAM2171 LOC196860 5' TCTGTCTTTAATGGCTTC 91217 _
 GAAGCCATTGAA ACAGA
 ||||| ||||
 CTTCGGTAATTT TGTCT
 C
 GAM2171 LOC221477 3' GATCATCTGGAGGCCGGCTTTG 93772 ATTGAAA
 T ACGAAGCC CAGATGATC
 ||||| |||||
 TGTTCGG GTCTACTAG
 CCGGAG_
 GAM2171 LOC56270 3' CGTTAGCTTCAGTGGCTCCG 39505 A ACA
 CG AGCCATTGAA GATG
 || ||||| |||
 GC TCGGTGACTT TTGC
 C CGA
 GAM2172 ALPP 3' GAAGCACCCAGACCCG 69418 AAGAC T
 CGGGGTCTG TG CTTC
 ||||| || |||

		GCCCCAGAC AC GAAG	
		CC__ _	
GAM2172 ATF4	5'	ACAGCCCTCGGACCCCGAG 9809	AGA
		CTCGGGGTCTGA CTGT	
		GAGCCCCAGGCT GACA	
		CCC	
GAM2172 C14orf1	3'	GAAGACAACATAACCCCGAG 24168	CTGA AC
		CTCGGGGT AG TGTCTTC	
		GAGCCCCA TC ACAGAAG	
		AA__ A_	
GAM2172 HEM1	5'	GAAGACTTGTTCAGACCCC 19237	GACT
		GGGGTCTGAA GTCTTC	
		CCCCAGACTT CAGAAG	
		GTT_	
GAM2172 HTR4	3'	GAAGACAGCCATGCCTCCGA 7883	_ C AAGA
		TCGG GGT TG CTGTCTTC	
		AGCC CCG AC GACAGAAG	
		T T C__	
GAM2172 MYEOV	5'	GAAAGTTCATCTCAGACCCT 57848	A__ G
		GGGGTCTGA GACT TC	
		TCCCAGACT TTGA AG	
		CTAC A	
GAM2172 PRX	3'	GGAAGGGTCCCCCAGCCCGAG 40898	T AA_ GT
		CTCGGGG CTG GACT CTTCC	
		GAGCCCC GAC CTGG GAAGG	
		_ CCC _	
GAM2172 PTMA	3'	ACAATCTTATTCCGAG 12556	CTG C
		CTCGGGGT AAGA TGT	
		GAGCCTTA TTCT ACA	
		_ A	
GAM2172 TIMP3	5'	GAAAACAGTCTTCTATC 6286	CT C
		GGT GAAGACTGT TTC	
		CTA CTTCTGACA AAG	
		T_ A	
GAM2172 TNFRSF14	3'	GAGGGCCCTTCAGACCCC 15113	ACT
		GGGGTCTGAAG GTCTTC	
		CCCCAGACTTC CGGGAG	
		C__	
GAM2172 VDR	3'	GAAGAATTTTCAGACCCC 6344	CTG
		GGGGTCTGAAGA TCTTC	

CCCCAGACTTTT AGAAG
 A__
 GAM2172 C20orf177 5' AAGACAGTCCATCAAACCCGAG 62822 GTC A_
 CTCGGG TGA GACTGTCTT
 ||||| || |||||
 GAGCCC ACT CTGACAGAA
 AA_ AC
 GAM2172 DKFZp434O0320 3' GGAATTCTCTCCAGGCCCGA 84699 A CT_
 TCGGGGTCTG AGA GTCT
 ||||| || |||
 AGCCCCGGAC TCT CAGG
 C CTT
 GAM2172 FLJ20507 3' GGCCCAACCTTCAAACCCTGAG 60849 C ACT_
 CTCGGGGT TGAAG GTC
 ||||| |||| |||
 GAGTCCCA ACTTC CGG
 A CAACC
 GAM2172 FLJ20507 3' GGCCCAACCTTCAAACCCTGAG 35745 C ACT_
 CTCGGGGT TGAAG GTC
 ||||| |||| |||
 GAGTCCCA ACTTC CGG
 A CAACC
 GAM2172 FLJ21562 5' GGAATAGCTCTCCAGACCCC 47794 A _ CT
 GGGGTCTG AGA CTGT TCC
 ||||| || ||| |||
 CCCCAGAC TCT GATA AGG
 C C _
 GAM2172 FLJ22938 3' AGAAGTCCCAGACCCCG 45479 AA G
 CGGGGTCTG GACT TCT
 ||||| |||| |||
 GCCCCAGAC CTGA AGA
 C_ _
 GAM2172 FLNC 3' AGATACCCTCCTGACCCCGAG 9388 TGA AC
 CTCGGGGTCT AG TGTCT
 ||||| || ||||
 GAGCCCCAG TC ATAGA
 TCC CC
 GAM2172 KIAA1819 3' GGAAGACAATTTACAAACTCC 70253 C A C
 GGGGT TG AGA TGTCTTCC
 |||| || || |||||
 CCTCA AC TTT ACAGAAGG
 A A A
 GAM2172 NXP-2 3' GAAGACAGTCTTTCTC 71659 TCT
 GGG GAAGACTGTCTTC
 || |||||
 CTC TTTCTGACAGAAG
 _
 GAM2172 PRO2389 5' GGGATCTCAGCCCGAG 64481 T A CTG
 CTCGGGG CTGA GA TCTT
 ||||| |||| || |||

GAGCCCC GACT CT AGGG

GAM2172	SMARCF1	3'	GGACCTATCTCCATACCCCGAG	38042	C A CT_
			CTCGGGGT TG AGA GTCT		
			GAGCCCCA AC TCT CAGG		
			T C ATC		
GAM2172	TGFB1I1	3'	AAGCCGGGTCCTCCAGACCCCG	32495	AA_ _T
	AG		CTCGGGGTCTG GACT G CTT		
			GAGCCCCAGAC CTGG C GAA		
			CTC G C		
GAM2172	LOC143677	3'	GAAGAGCCAGCCAGACCCC	83897	AAGA _
			GGGGTCTG CTG TCTTC		
			CCCCAGAC GAC AGAAG		
			C_ CG		
GAM2172	LOC145694	5'	AGACGCCTGCCCCAGCCCCGA	84438	T AAGAC_
	G		CTCGGGG CTG TGTCT		
			GAGCCCC GAC GCAGA		
			_ CCCC GTCC		
GAM2172	LOC148936	5'	GAAGAGGTCCTCCAGACCCC	85453	AA_ G
			GGGGTCTG GACT TCTTC		
			CCCCAGAC CTGG AGAAG		
			CTC _		
GAM2172	LOC148938	5'	GAAGAGGTCCTCCAGACCCC	85436	AA_ G
			GGGGTCTG GACT TCTTC		
			CCCCAGAC CTGG AGAAG		
			CTC _		
GAM2172	LOC152273	3'	GAAAACAAGTTAGACTCC	81374	AGAC C
			GGGGTCTGA TGT TTC		
			CCTCAGATT ACA AAG		
			GA_ A		
GAM2172	LOC158288	3'	GAAGACAGTCCCCCAGGCTGAG	88021	GG AA_
			CTC GGTCTG GACTGTCTTC		
			GAG TCGGAC CTGACAGAAG		
			_ CCC		
GAM2172	LOC201910	3'	AGATTTGTCCATTCAAACCCC	90549	C _ T_
			GGGGT TGAA GAC GTCT		
			CCCCA ACTT CTG TAGA		
			A AC TT		
GAM2172	LOC220177	5'	GGATACTTCAAACCCC	95968	C AC
			GGGGT TGAAG TGTCT		

CCCC ACTTC ATAGG
 A _
 GAM2172 LOC255974 5' GGAAGCTGCTCCTCAGACCCC 99343 A CT_ T
 GGGGTCTGA GA G CTTCC
 ||||| || | ||||
 CCCCAGACT CT C GAAGG
 C CGT _
 GAM2172 LOC257485 5' GAAGAGTCAGACCTCGA 66210 AGACTG
 TCGGGGTCTGA TCTTC
 ||||| ||||
 AGCTCCAGACT AGAAG
 G _
 GAM2172 LOC64167 5' GAAAATATTGTTTCAGACCCC 42539 GAC C
 GGGGTCTGAA TGT TTC
 ||||| ||||
 CCCCAGACTT ATA AAG
 GTT A
 GAM2172 LOC90190 3' GGAAGACTTGATCCTCAGCCCC 62428 T A CT_
 GAG CTCGGGG CTGA GA GTCTTCC
 ||||| |||| |||||
 GAGCCCC GACT CT CAGAAGG
 _ C AGTT
 GAM2173 EPB41L2 3' TTAAAGCTGGCACCAGAGACC 9295 C A_ A
 GGTC CTG TCA TTTTAA
 |||| |||| |||||
 CCAG GAC GGT GAAATTT
 A CAC C
 GAM2173 GAB2 3' GTTTAGGACCTGGGACCA 25464 TGATCAA
 TGGTCCC TTTTAAAC
 ||||| |||||
 ACCAGGG AGGATTTG
 TCC_
 GAM2173 GAB2 3' GTTTAGGACCTGGGACCA 55408 TGATCAA
 TGGTCCC TTTTAAAC
 ||||| |||||
 ACCAGGG AGGATTTG
 TCC_
 GAM2173 BTN2A2 3' TGTTTAAAATCAGGATAACCA 23772 C_ CAAT
 TGGT CCTGAT TTTAAACA
 |||| |||| |||||
 ACCA GGACTA AAATTTGT
 ATA _
 GAM2173 FLJ21369 3' AAAGTGCCAGGGACCAT 46044 ATCA
 ATGGTCCCTG ATTTT
 ||||| ||||
 TACCAGGGAC TGAAA
 CG_
 GAM2173 HELO1 3' TGTTTAGAAAAAATCAAAGACC 41799 CC CAA
 AT ATGGTC TGAT TTTTAAACA
 ||||| |||| |||||

		TACCAG ACTA AAGATTTGT		
		AA AAA		
GAM2173 KIAA1918	5'	TGTTTAAAATCAATCAGTTTAA 73540	CC__	CA
		CC GGT CTGAT ATTTTAAACA		
		CCA GACTA TAAAATTTGT		
		ATTT AC		
GAM2173 LOC149707	5'	TGTTTAAAATGAAGTGACCA 80300	C	GATCA
		TGGTC CT ATTTTAAACA		
		ACCAG GA TAAAATTTGT		
		T AG__		
GAM2173 LOC151888	3'	TGTTTCTGACTCCAACAGGGAC 86704	ATCAA_	TT
		CAT ATGGTCCCTG TT AAACA		
		TACCAGGGAC AG TTTGT		
		AACCTC TC		
GAM2173 LOC200227	5'	TGTTTAAAATGAAGTGACCA 90045	C	GATCA
		TGGTC CT ATTTTAAACA		
		ACCAG GA TAAAATTTGT		
		T AG__		
GAM2173 LOC200583	3'	TTAAAATTGATCAGGGACCA 90254		
		TGGTCCCTGATCAATTTTAA		
		ACCAGGGACTAGTTAAAATT		
GAM2174 ADAM12	3'	GGCAGCATCCCCTTGAAC 14424	T	GAAA
		GTTCAAGGG ATG GTC		
		CAAGTTCCC TAC CGG		
		C GA__		
GAM2174 CASQ2	3'	GCTCCCTCCATACCTCGAAC 8782	AA	A__
		GTTC GGGTATGGA AGT		
		CAAG TCCATACCT TCG		
		C_ CCC		
GAM2174 CCND2	3'	GTGACTGACCCTTGAGC 10053	ATGGAA	
		GTTCAAGGGT AGTCAC		
		CGAGTTCCCA TCAGTG		
		G_____		
GAM2174 GRINL1A	3'	GGTGACTTTCATGTGCTTGAA 70064	G	G
		TTCAAG GTATG AAAGTCACC		
		AAGTTC TGTAC TTTCAGTGG		
		G _		
GAM2174 LRRC2	3'	GGCTACCATACTCCTGAAC 44754	A	AA
		GTTCA GGGTATGG AGTC		

		CAAGT CTCATACC TCGG		
		C A_		
GAM2174	NOTCH2	3' GGTGACTCTCTGCCCTTGGAC 44578	AT	A
		GTTCAAGGGT GGA AGTCACC		
		CAGGTTCCCG TCT TCAGTGG		
		___ C		
GAM2174	Nrap	3' TGACCTCCACCCTCCTTGGAC 58323	_ TA	AA
		GTTCAAGG G TGGA GTCA		
		CAGGTTCC C ACCT CAGT		
		T CC C_		
GAM2174	Nrap	3' TGACCTCCACCCTCCTTGGAC 43624	_ TA	AA
		GTTCAAGG G TGGA GTCA		
		CAGGTTCC C ACCT CAGT		
		T CC C_		
GAM2174	PITX2	3' GGCAACTCCGCCCTTGAA 6157	AT	AA_
		TTCAAGGGT GGA GTC		
		AAGTTCCCG CCT CGG		
		___ CAA		
GAM2174	RAB36	3' GGTAAC TCACTCTGCAGCCCTT 18174	AT_	A_ C
	GAAC	GTTCAAGGGT GGA AGT ACC		
		CAAGTTCCCG TCT TCA TGG		
		ACG CAC A		
GAM2174	SCD	3' ACTCTCTTTCTTCTGAGC 18588	TAT	A
		GTTCAAGGG GGA AGT		
		CGAGTTCCT TCT TCA		
		T_ C		
GAM2174	AAMP	3' TGA CTTTCCAGCCTCTTCAAC 8437	C	TA
		GTT AAGGG TGGAAAGTCA		
		CAA TTCTC ACCTTTCAGT		
		C CG		
GAM2174	CNNM4	3' GATGAGCCATACCCTGGAAC 39866	A	AAA
		GTTC AGGGTATGG GTC		
		CAAG TCCCATACC TAG		
		G GAG		
GAM2174	EPB41L1	3' TGA CTTCTCCTTTGAA 71118	TAT	AA
		TTCAAGGG GGA GTCA		
		AAGTTTCC TCT CAGT		

GAM2174	FER1L4	3' GTGACTCTCGCTGACCTTGGAC 48134	GTATG	A
		GTTCAAGG GA AGTCAC		

CAGGTTCC CT TCAGTG
 AGTCG C
 GAM2174 FLJ21324 3' GGTGACCTTCTGGATGCCTTTA 92858 C ___ A
 AC GTT AAGGGTAT GGAA GTCACC
 ||| ||||| ||| |||||
 CAA TTTCCGTA TCTT CAGTGG
 _ GG C
 GAM2174 KIAA1656 3' GGTGCTAACATACCCTCAGAC 66383 CA GAA T
 GTT AGGGTATG AG CACC
 ||| ||||| || ||||
 CAG TCCCATAC TC GTGG
 AC AA_ _
 GAM2174 SLC26A10 3' GATGAGGACCATGACCCTTGAA 56846 _ AAA_
 C GTTCAAGGGT ATGG GTC
 ||||| ||| |||
 CAAGTTCCCA TACC TAG
 G AGGAG
 GAM2174 LOC120939 5' GGTGACTTTACCCCTGCAAC 76767 CA ATG
 GTT AGGGT GAAAGTCACC
 ||| |||| |||||
 CAA TCCCA CTTTCAGTGG
 CG _
 GAM2174 LOC133584 3' TGACTGTGTGACCTTGAAC 75599 G GGAA
 GTTCAAGG TAT AGTCA
 ||||| || ||||
 CAAGTTCC GTG TCAGT
 A TG_
 GAM2174 LOC145761 5' GACTCCATCTTGAAC 84479 GGT AA
 GTTCAAG ATGGA GTC
 ||||| |||| |||
 CAAGTTC TACCT CAG
 _ _
 GAM2174 LOC146337 5' GGCAACTCTAGCCTTTGAAC 84644 A AA_
 GTTCAAGGGT TGGA GTC
 ||||| ||| |||
 CAAGTTTCCG ATCT CGG
 _ CAA
 GAM2174 LOC148930 3' ACTTCCTCTCTTTGAAC 79837 TAT A
 GTTCAAGGG GGAA GT
 ||||| |||| ||
 CAAGTTTCT CCTT CA
 CT_ _
 GAM2174 LOC152018 3' GACCTCCACCCCTTGAAC 86729 TA AA
 GTTCAAGGG TGGA GTC
 ||||| ||| |||
 CAAGTTCCC ACCT CAG
 CC C_
 GAM2174 LOC152982 3' TGACTTTCATGTGCTTGAA 81638 G G
 TTCAAG GTATG AAAGTCA
 ||||| |||| |||||

		AAGTTC TGTAC TTTCAGT		
		G _		
GAM2174	LOC155435 3'	GGTGA	TTTGGTAGCCCTTGAG 82271	ATGG
	C	GTTCAAGGGT	AAAGTCACC	
		CGAGTTCCCG	TTTCAGTGG	
		ATGG		
GAM2174	LOC253336 3'	GTAAC	TTTCTTCATCCCTTGAA 99182	TAT_ C
	T	GTTCAAGGG	GGAAAGT AC	
		TAAGTTCCC	TCTTTCA TG	
		TACT	A	
GAM2174	LOC80298 3'	GTAAC	TTTTACCTTGAAC 48066	GTATG C
		GTTCAAGG	GAAAGT AC	
		CAAGTTCC	TTTTCA TG	
		A	A	
GAM2175	BACE 3'	ACTTG	GTTGTGAACCAA 25027	ATGG
		TTGGTTCACGG	CAAGT	
		AACCAAGTGTT	GTTCA	
		G		
GAM2175	BACE 3'	ACTTG	GTTGTGAACCAA 58078	ATGG
		TTGGTTCACGG	CAAGT	
		AACCAAGTGTT	GTTCA	
		G		
GAM2175	DRIL1 3'	GTGAA	ACCCCTGAACCAA 19081	C AT CAAG
		TTGGTTCA	GG GG TCAC	
		AACCAAGT	CC CC AGTG	
		_ _	AA	
GAM2175	TMEFF1 3'	TGAC	CCAAGCATGAACCTAA 14893	CGGA CAA
		TTGGTTCA	TGG GTCA	
		AATCAAGT	ACC CAGT	
		ACGA		
GAM2175	KCND1 3'	GACCT	GCCATCCCCAG 18346	TTCAC A
		TTGG	GGATGGCA GTC	
		GACC	CCTACCGT CAG	
			C	
GAM2175	KIAA0373 5'	GATG	AGTAGAACCATGAACCAA 28690	C ATG_ AA
		TTGGTTCA	GG GC GTC	
		AACCAAGT	CC TG TAG	
		A	AAGA AG	
GAM2175	KIAA0495 3'	GACAG	AAGCTCCGTGAACCAA 63266	TG AA
		TTGGTTCACGGA	GC GTC	

AACCAAGTGCCT CG CAG
 ___ AAGA
 GAM2175 KIAA1918 3' TGA CT TGCCACCATATCCA 73539 TTCAC A
 TGG GG TGGCAAGTCA
 ||| || |||||
 ACC CC ACCGTT CAGT
 TATA_ _
 GAM2175 PASK 3' TGACAGCTTCCGTGAATCAA 31423 T AA
 TTGGTTCACGGA GGC GTCA
 ||||| ||| |||
 AACTAAGTGCCT TCG CAGT
 _ A_
 GAM2175 SMC4L1 3' TACTTGCCAACTAA 19722 CACGGA C
 TTGGTT TGGCAAGT A
 ||||| ||||| |
 AATCAA ACCGTTCA T
 A
 GAM2175 LOC199704 3' GGTGACTTACAATGAACCA 89698 CGGA GC
 TGGTTCA TG AAGTCACC
 ||||| || |||||
 ACCAAGT AC TTCAGTGG
 A_ A_
 GAM2175 LOC255743 5' TGA CT TGCACTGGGAACCAA 97605 A ATG
 TTGGTTC CGG GCAAGTCA
 ||||| ||| |||||
 AACCAAG GTC CGTTCAGT
 G A_
 GAM2176 MCM6 3' GAACTGTGGCACAGCACCTCGT 20975 A_ _
 G CACGAGGTGC CAC GTTC
 ||||| ||| |||
 GTGCTCCACG GTG CAAG
 ACACG T
 GAM2176 PRIM2A 3' GGACACACAGGTGTGCACCTC 8142 GTTC
 GAGGTGCACAC GTGTCC
 ||||| |||||
 CTCCACGTGTG CACAGG
 GACA
 GAM2176 DKFZP434L0718 3' GGTTACTACACGTGCACCTGT 50459 G AC TC T
 AC AGGTGCAC GT GTG CC
 || ||||| || |||
 TG TCCACGTG CA CAT GG
 _ CA T_ T
 GAM2176 MAPK11 3' ATGAGCGTGCACTCCCCGTG 12311 A TGCA
 CACG GG CACGTT CGT
 ||| || |||||
 GTGC CC GTGCGAGTA
 C TCAC
 GAM2176 NIR3 3' GGACACGGGCCGCACC 66830 ACAC
 GGTGC GTTCGTGTCC
 |||| |||||

	CCACG CGGGCACAGG	
	C_____	
GAM2176 SLC19A3 3'	GGACTATGGGTGCACACCACCA 48245	A CACA_ TT _
CG	CG GGTG CG CGT GTCC	
	GC CCAC GT GTA CAGG	
	A CACAC GG T	
GAM2176 LOC132793 5'	GACACGAACAATCCTGTG 76449	G TGCACAC
	CAC AGG GTTCGTGTC	
	GTG TCC CAAGCACAG	
	_ TAA_____	
GAM2176 LOC146485 5'	ACACATTTGGTGCACCTC 60491	A TTC
	GAGGTGCAC CG GTGT	
	CTCCACGTG GT CACA	
	_ TTA	
GAM2176 LOC257052 3'	GACACACGTGTGCACC 98010	TC
	GGTGCACACGT GTGTC	
	CCACGTGTGCA CACAG	

GAM2176 LOC257052 3'	GGCACACGTGTGCACC 98011	TC
	GGTGCACACGT GTGTC	
	CCACGTGTGCA CACGG	

GAM2176 LOC257101 5'	GGACCTGAACCTGTGCACC 98694	C T
	GGTGACA GTTCG GTCC	
	CCACGTGT CAAGT CAGG	
	C C	
GAM2176 LOC58525 3'	ACACAACACGCACCTCGTG 79338	ACAC C
	CACGAGGTGC GTT GTGT	
	GTGCTCCACG CAA CACA	
	CA_____	
GAM2177 BDKRB2 3'	GTAGATCAGTGGTCTCCA 7113	C GGCAA
	TGGAGATCAT GA TCTAC	
	ACCTCTGGTG CT AGATG	
	A _____	
GAM2177 GLP1R 3'	TGTAGATTACCTGCCACTTCCA 10801	ATCATCG C
	TGGAG AGG AATCTACA	
	ACCTT TCC TTAGATGT	
	CACCG_ A	
GAM2177 C8orf13 3'	TGCAAATGAATGATCTCTA 82484	_ AG_
	TGGAGATCAT CG GCA	

ATCTCTAGTA GT CGT
 A AAA
 GAM2177 KIAA1449 3' GTAGATTAAGCTGTCCCCA 40842 A CATCGA ____
 TGG GAT GGC AATCTAC
 ||| ||| ||| |||||
 ACC CTG TCG TTAGATG
 C _____ AA
 GAM2178 SCAMP1 3' GCTAAATAAATATTCTCC 18013 T C
 GGA AATATT ATTTAGC
 ||| ||||| |||||
 CCT TTATAA TAAATCG
 C A
 GAM2178 SCAMP1 3' GCTAAATAAATATTCTCC 54501 T C
 GGA AATATT ATTTAGC
 ||| ||||| |||||
 CCT TTATAA TAAATCG
 C A
 GAM2178 NX-17 3' TGAATATCAGCCCCTAATA 40706 ATA_
 TATTAGGG ATATTCA
 ||||| |||||
 ATAATCCC TATAAGT
 CGAC
 GAM2178 LOC161589 3' GCTAAATGAATATTATCCCTAA 83159
 TA TATTAGGGATAATATTCATTTAGC
 |||||
 ATAATCCCTATTATAAGTAAATCG
 GAM2179 CCND2 3' TCCCCAGCAAATCATCGGGCCA 10056 CCACA _ A
 TGGCCTGATGAT GC GG GA
 ||||| || ||
 ACCGGGCTACTA CG CC CT
 AA__ A C
 GAM2179 GCN5L2 5' CTCCGCTGCGGGGGAGGCC 60529 GATGA A
 GGCCT TCC CAGCGGAG
 |||| ||| |||||
 CCGGA GGG GTCGCCTC
 GG__ C
 GAM2179 GJA5 3' CTGACCAGATCATCAGCCA 19164 C CACAG
 TGGC TGATGATC CGG
 |||| ||||| |||
 ACCG ACTACTAG GTC
 _ ACCA_
 GAM2179 HIVEP3 3' TCCCCGCTGTGGTTGGCAGCCA 44702 C ATGAT A
 TGGC TG CCACAGCGG GA
 |||| || ||||| ||
 ACCG AC GGTGTCGCC CT
 _ GGTT_ C
 GAM2179 HOXD1 5' CCGCCGGTATATTAGGCCA 44696 AT ACA
 TGGCCTGATG CC GCGG
 ||||| || |||

		ACCGGATTAT GG CGCC		
		AT C__		
GAM2179	SUFU	3' CCTTGTGACCCATCAGGCCA 32934	ATC	C
		TGGCCTGATG CACAG GG		
		ACCGGACTAC GTGTT CC		
		CCA _		
GAM2179	ARHGEF15	3' CTGTGGACCACAGGCCA 30953	A	A
		TGGCCTG TG TCCACAG		
		ACCGGAC AC AGGTGTC		
		_ C		
GAM2179	DKFZP586J1624	3' CTCCGCCAGTCACCATCAGGC 32043	ATCCACA_	
	CA	TGGCCTGATG GCGGAG		
		ACCGGACTAC CGCCTC		
		CACTGACC		
GAM2179	KIAA1671	3' CTTTGCTTATGAATCATCAGAC 66282	C	C C_
	C	GG CTGATGAT CA AGCGGAG		
		CC GACTACTA GT TCGTTTC		
		A A AT		
GAM2179	MGC18079	3' CCGCGGACCTCAGGCCA 59033	TGA	ACA
		TGGCCTGA TCC GCGG		
		ACCGGACT AGG CGCC		
		CC_ _		
GAM2179	LOC115110	3' TGCAGACATCAGGCCA 72186	A	CACA
		TGGCCTGATG TC GCG		
		ACCGGACTAC AG CGT		
		_ A_		
GAM2179	LOC159110	5' TCTCCGCTGCCCCGGTCAACCA 82995	CCTGA	CA_
		TGG TGATC CAGCGGAGA		
		ACC ACTGG GTCGCCTCT		
		A_ CCCC		
GAM2179	LOC159116	5' TCTCCGCTGCCCCGGTCAACCA 82978	CCTGA	CA_
		TGG TGATC CAGCGGAGA		
		ACC ACTGG GTCGCCTCT		
		A_ CCCC		
GAM2179	LOC165476	5' CTCCGCTGCCTGCTCAGCCA 88550	C	TGATCCA
		TGGC TGA CAGCGGAG		
		ACCG ACT GTCGCCTC		
		_ CGTCC_		
GAM2179	LOC200032	5' CTGACCAGATCATCAGCCA 85475	C	CACAG
		TGGC TGATGATC CGG		

ACCG ACTACTAG GTC
 _ ACCA_
 GAM2179 LOC219654 5' CTCCGCTGCGGAGGGGGGCC 92932 GATGA A
 GGCCT TCC CAGCGGAG
 ||||| ||| |||||
 CCGGG AGG GTCGCCTC
 GGG_ C
 GAM2179 LOC255862 3' TCAAATGTAGACTATCAGGCCA 96115 A C GCG
 TGGCCTGATG TC ACA GA
 ||||| || ||| ||
 ACCGGACTAT AG TGT CT
 C A AAA
 GAM2180 FLT1 3' ACCCAGGGCAACAAGCCCGTTA 10658 CC CG GG
 TAACGGGT TG GT TGGGT
 ||||| || || |||||
 ATTGCCCG AC CG ACCCA
 A_ AA GG
 GAM2180 GPR81 5' ACCCACACACACAGGACCCG 51732 CG _
 CGGGTCCTG GTG GTGGGT
 ||||| ||| |||||
 GCCCAGGAC CAC CACCCA
 A_ A
 GAM2180 HOXB9 3' ACCCCTAATGCAAATACCC 43996 CC_ G T
 GGGT TGCG TGG GGGT
 ||| ||| ||| |||
 CCCA ACGT ATC CCCA
 TAA A _
 GAM2180 ITGB2 3' ACCCACCATGTCTGCCCC 5798 TCCT _
 GGG GCGG TGGTGGGT
 ||| ||| |||||
 CCC CGTC ACCACCCA
 _ TGT
 GAM2180 ZNFN2A1 5' ACCCACCACCGTGAACCC 61387 CC
 GGGT TGC GGTGGTGGGT
 ||| |||||
 CCCA GTGCCACCACCCA
 A_
 GAM2180 DKFZP434C131 3' ACTCAGCCCCACAGAACCC 69635 C C T _
 GGGT CTG GG GG TGGGT
 ||| ||| || |||
 CCCA GAC CC CC ACTCA
 A A _ G
 GAM2180 FLJ22757 3' ACCCACCAGCTCAAACACACC 46601 _ CC_ C _
 GG GT TG GG TGGTGGGT
 || || || || |||||
 CC CA AC TC ACCACCCA
 A CAA _ G
 GAM2180 GMEB2 3' ACCCACCAGCTCAGAACCTGT 25658 C C _
 ACGGGT CTG GG TGGTGGGT
 ||||| ||| || |||||

			TGTCCA GAC TC ACCACCCA		
			A _ G		
GAM2180	HIC2	3'	ACCCA	ACTCCCAA	AATCCGT 65856 CC C T
			ACGGGT	TG GG GGTGGGT	
			TGCCTA	AC CC TCACCCA	
			AA _ _		
GAM2180	KIAA0352	3'	ACTGATGCCACAGCACCCG	29823	C C G G
			CGGGT	CTG GGTG T GGT	
			GCCCA	GAC CCGT A TCA	
			C A _ G		
GAM2180	KIAA1023	3'	ACCCAAAGTGCAGGACCCG	34671	GTGG
			CGGGT	CCTGCG TGGGT	
			GCCCAGGACGT	ACCCA	
			GAA_		
GAM2180	PALM	3'	ACCCACACACAGACACCC	11960	C_ C GT
			GGGT	CTG GGTG GGGT	
			CCCA	GAC CCAC CCCA	
			CA A AC		
GAM2180	TEX27	3'	ACCCACCAGAGTGGAACCCG	41945	C TG GG
			CGGGT	C C TGGTGGGT	
			GCCCA	G G ACCACCCA	
			A GT AG		
GAM2180	LOC146429	5'	ACCCACCACACGCACA	ACT 84655	CC _
			GGT	TGC GGTGGTGGGT	
			TCA	ACG CCACCACCCA	
			AC CA		
GAM2180	LOC155179	3'	ACCCAAAGTGCAGGACCCG	82220	GTGG
			CGGGT	CCTGCG TGGGT	
			GCCCAGGACGT	ACCCA	
			GAA_		
GAM2180	LOC222962	3'	ACCCAGGACAGCAGACACCCG	94452	C_ G GG
			CGGGT	CTGC GT TGGGT	
			GCCCA	GACG CA ACCCA	
			CA A GG		
GAM2180	LOC93297	3'	ATTCACCACCACAAGACCTATT	72417	CG C C
	A		TAA	GGTC TG GGTGGTGGGT	
			ATT	CCAG AC CCACCACTTA	
			AT A A		
GAM2181	NCAM2	3'	AATACTTCAAATCATATCCTCA	16999	C_ TCG
			TGAGGATATG	TTGG GGTATT	

			ACTCCTATAC AACT TCATAA		
			TA ____		
GAM2181	MPZL1	3'	AATACCTAGAACATATCCTCA 15536	C	GGTC
			TGAGGATATG TT GGGTATT		
			ACTCCTATAC AG TCCATAA		
			A A____		
GAM2182	ASGR2	3'	AGTTTAAGAGTCCCTGAC 56038	A	CC
			GTCA GGA CT C AAGCT		
			CAGT CCTGAG TTTGA		
			C AA		
GAM2182	HDAC7A	3'	AGAACAGCCTGCCTGCTTTGAC 33922	ACTCC	A C
	A		TGTCAAGG CA GCTG TCT		
			ACAGTTTC GT CGAC AGA		
			GTCC_ C A		
GAM2182	TRHDE	3'	AGAGGTAAAATAGCCCTTGACA 26312	A	CCCA TG
			TGTCAAGG CT GC CTCT		
			ACAGTTCC GA TG GAGA		
			C TAAAA ____		
GAM2182	ZFP93	3'	AGAGCTTCAAAGAATCTTGACA 16173	AC	CCAAGCT
			TGTCAAGG TC GCTCT		
			ACAGTTCT AG CGAGA		
			A_ AA ACTT_		
GAM2182	CFDP1	3'	AGAGCAGCTTAATCCTGTTTAC 21986	CA_	CTCCC
	A		TGT AGGA AAGCTGCTCT		
			ACA TCCT TTCGACGAGA		
			TTTG AA____		
GAM2182	DKFZP434A0131	3'	AGAGCAGCCTGGGCAACCT 39148	ACT	A
			AGG CCA GCTGCTCT		
			TCC GGGT CGACGAGA		
			AAC C		
GAM2182	GLTP	3'	AGAGCAGCCCAGGGTCCT 33579	CCAA	
			AGGACTC GCTGCTCT		
			TCCTGGG CGACGAGA		
			ACC_		
GAM2182	KIAA0847	3'	GAGCAAGAGTTCTTAACA 78074	C	CCAAGC
			TGT AAGGACTC TGCTC		
			ACA TTCTTGAG ACGAG		
			A A____		
GAM2182	KIAA1237	3'	AGCAGCTTGTTGAGCCCCTGCA 81297	T A A	C_
			TG CA GG CTC CAAGCTGCT		

		AC GT CC GAG GTTCGACGA		
		_ C C TT		
GAM2182	KIAA1393	5' AGCTTGGACATCCCTGACA	72567	A CTC
		TGTCA GGA CCAAGCT		
		ACAGT CCT GGTTCGA		
		C ACA		
GAM2182	KIAA1887	3' AGCCTTGGGAGCCCCTGCCA	77276	T A A CT
		TG CA GG CTCCCAAG GCT		
		AC GT CC GAGGGTTC CGA		
		C C C _		
GAM2182	NYD-SP14	3' AGCAGCTTTTCACTTAACA	50071	C _ CTCCC
		TGT AAG GA AAGCTGCT		
		ACA TTC CT TTCGACGA		
		A A T _		
GAM2182	OAZ3	3' AGGGGCTGGAAGCCTTGACA	32974	A C A G
		TGTCAAGG CT CCA GCT CT		
		ACAGTTCC GA GGT CGG GA		
		_ A _ G		
GAM2182	LOC114926	3' AGTGGCTCAAAGGCCTTGACA	57387	A CCCA TG
		TGTCAAGG CT AGC CT		
		ACAGTTCC GA TCG GA		
		G AAAC GT		
GAM2182	LOC115219	3' AGAGCAGCCTGGACGGTCC	73687	C_ A
		GGACT CCA GCTGCTCT		
		CCTGG GGT CGACGAGA		
		CA C		
GAM2182	LOC145439	5' AGAGCAGCCCTGGCACCCGACA	77723	AA ACTC A_
		TGTC GG CCA GCTGCTCT		
		ACAG CC GGT CGACGAGA		
		C_ AC_ CC		
GAM2182	LOC151610	3' AGAGCAGCCTCATTCCTTCACA	81089	C CTCCCAA
		TGT AAGGA GCTGCTCT		
		ACA TTCCT CGACGAGA		
		C TACTC_		
GAM2182	LOC152018	3' AGGTTAGGAGACCCCTGACA	86726	A A_ C G
		TGTCA GG CTCC AA CT		
		ACAGT CC GAGG TT GA		
		C CA A G		
GAM2182	LOC158863	5' GGTGATGAGAATGCCTTGACA	88298	AC_ C A_
		TGTCAAGG TC CA GCT		

ACAGTTCC AG GT TGG
 GTA A AG
 GAM2182 LOC199796 5' GAGCAGCTCAAAGCCGAC 74923 AA A CCCA
 GTC GG CT AGCTGCTC
 ||| ||| |||||
 CAG CC GA TCGACGAG
 _ _ AAC_
 GAM2182 LOC254003 5' AGAGCAGCTCAGGACAAGGACA 98026 AAGGAC CA
 TGTC TCC AGCTGCTCT
 ||| ||| |||||
 ACAG AGG TCGACGAGA
 GAAC_ AC
 GAM2182 LOC256300 5' AGAGCAGCAGGACCCTTCACA 99445 C AC CAA
 TGT AAGG TCC GCTGCTCT
 ||| ||| ||| |||||
 ACA TTCC AGG CGACGAGA
 C C_ A_
 GAM2182 LOC92106 5' AGAGCAGCTTAGCCTCCTCGAC 57225 A CTCCC
 GTC AGGA AAGCTGCTCT
 ||| ||| |||||
 CAG TCCT TTCGACGAGA
 C CCGA_
 GAM2183 CD4 3' ACACAGCCAAGCCAGTCA 7041 GA A
 TGGCTGGCTT GGTG TGT
 ||||| ||| |||
 ACTGACCGAA CCGAC ACA
 _ _
 GAM2183 TERF1 3' ACACACCACCAGCCAGCTA 34385 TGA T A
 TGGCTGGCT GGT G TGT
 ||||| ||| |||
 ATCGACCGA CCA C ACA
 CCA _ _
 GAM2183 FLJ21945 3' ATATTAACCTCAAACCAGC 48091 C
 GCTGG TTGAGGTTGATGT
 |||| |||||
 CGACC AACTCCAATTATA
 A
 GAM2183 KIAA0256 3' CATACATCACAGAATCAACCA 65048 C GGT_
 TGG TTGA TGATGTATG
 ||| ||| |||||
 ACC AACT ACTACATAC
 _ AAGAC
 GAM2183 MGC2491 3' CATACATCAACCTCAAGCCAGC 44095
 CA TGGCTGGCTTGAGGTTGATGTATG
 |||||
 ACCGACCGAACTCCAACACTACATAC
 _ _
 GAM2183 LOC197358 3' ACACACCAGAGCCAGCTA 89405 GA T A
 TGGCTGGCTT GGT G TGT
 ||||| ||| |||

ATCGACCGAG CCA C ACA
 A_ _ _
 GAM2184 STATI2 5' GCCCCTTCCGGGCGCGCA 15270 A TAATAA
 TGC CGTCT GAAGGGGC
 ||| ||||| |||||
 ACG GCGGG CTTCCCCG
 C C_ _ _
 GAM2184 LOC127703 3' CCCCTTCTTTCACTGCA 75176 C CTTAAT
 TGCA GT AAGAAGGGG
 |||| || |||||
 ACGT CA TTCTTCCCC
 _ CT_ _ _
 GAM2185 A1BG 3' ATTTTTGTAGAGATGAGTCTC 56280 A CC T
 A TGA AC CATCTCTAC AAAAAT
 ||| || ||||| |||||
 ACT TG GTAGAGATG TTTTTA
 C A_ T
 GAM2185 A1BG 3' TTTTGTAGAGATGGGGTTTC 56303
 A TGAAACCCCATCTCTACTAAAAA
 ||||| ||||| ||||| |||||
 ACTTTGGGGTAGAGATGATTTTT

 GAM2185 ACADSB 3' AGTAGAGATGGGGTTTTA 9643
 TGAAACCCCATCTCTACT
 ||||| ||||| |||||
 ATTTTGGGGTAGAGATGA

 GAM2185 ADAMTS4 3' ATTTTTAGTAGAGACAGGGTTT 18752 CA
 CA TGAAACCC TCTCTACTAAAAAT
 ||||| ||||| ||||| |||||
 ACTTTGGG AGAGATGATTTTTA
 AC
 GAM2185 ADAMTS4 3' ATTTTTAGTAGAGACGGGGTTT 18753 A
 CA TGAAACCC TCTCTACTAAAAAT
 ||||| ||||| ||||| |||||
 ACTTTGGGG AGAGATGATTTTTA
 C
 GAM2185 ADCY6 5' ATTTTTAGTAGAGACGAGGTTT 31586 CCA
 CA TGAAACC TCTCTACTAAAAAT
 ||||| ||||| ||||| |||||
 ACTTTGG AGAGATGATTTTTA
 AGC
 GAM2185 AIM1 3' TTTTGTAGAGATGGGGTTTCA 93475 T
 TGAAACCCCATCTCTAC AAAA
 ||||| ||||| ||||| |||||
 ACTTTGGGGTAGAGATG TTTT

 GAM2185 ALDH1B1 3' ATTTTTAGTAGAGATGAGGTTT 7317 C
 CA TGAAACC CATCTCTACTAAAAAT
 ||||| ||||| ||||| |||||

		ACTTTGG GTAGAGATGATTTT		
		A		
GAM2185	APAF1	3' ATTTT	8581	A
	CA	TGAAACCCC TCTCTACTAAAAAT		
		ACTTTGGGG AGAGATGATTTT		
		C		
GAM2185	APAF1	3' ATTTT	25963	A
	CA	TGAAACCCC TCTCTACTAAAAAT		
		ACTTTGGGG AGAGATGATTTT		
		C		
GAM2185	APM1	3' ATTTT	17760	CA C
	CA	TGAAACCC TCT TACTAAAAAT		
		ACTTTGGG AGA ATGATTTT		
		AC A		
GAM2185	APM1	3' ATTTT	17761	C
	C	GAAACCCCAT TCTACTAAAAAT		
		CTTTGGGGTA AGATGATTTT		
		A		
GAM2185	APM1	3' ATTTT	17762	A T
	CA	TGAAACCCC TCTCTAC AAAAAT		
		ACTTTGGGG AGAGATG TTTT		
		C C		
GAM2185	APOL1	3' ATTTT	14729	C
	CA	TGAAACCCCATCTCTA TAAAAAT		
		ACTTTGGGGTAGAGAT ATTTT		
		A		
GAM2185	APPL	3' ATTTT	24943	A
	CA	TGAAACCCC TCTCTACTAAAAAT		
		ACTTTGGGG AGAGATGATTTT		
		C		
GAM2185	AQP6	3' ATTTT	9724	
	CA	TGAAACCCCATCTCTACTAAAAAT		
		ACTTTGGGGTAGAGATGATTTT		
GAM2185	AQP6	3' ATTTT	54984	
	CA	TGAAACCCCATCTCTACTAAAAAT		
		ACTTTGGGGTAGAGATGATTTT		
GAM2185	ARCN1	3' TTTT	9761	A
		TGAAACCCC TCTCTACTAAAA		

			ACTTTGGGG AGAGATGATTTT		
			C		
GAM2185	ATP6V1A1	3'	ATTTTGTAGTAGAAACGGGGTTT 9865	ATC	
	CA		TGAAACCCC TCTACTAAAAAT		
			ACTTTGGGG AGATGATTTTTA		
			CAA		
GAM2185	ATP7A	3'	ATTTTTCAGTAGAGACGGGGTT 5316	A	—
	TC		GAAACCCC TCTCTACT AAAAAT		
			CTTTGGGG AGAGATGA TTTTTA		
			C C		
GAM2185	ATP8B2	3'	ATTTTGTAGTAGAGATGTTTCA 65830	CCC	
			TGAAAC ATCTCTACTAAAAAT		
			ACTTTG TAGAGATGATTTTTA		
			—		
GAM2185	AXL	3'	ATTTTGTAGTAGAGACAGGGTTT 9901	CA	
	CA		TGAAACCC TCTCTACTAAAAAT		
			ACTTTGGG AGAGATGATTTTTA		
			AC		
GAM2185	AXL	3'	ATTTTGTAGTAGAGACAGGGTTT 41877	CA	
	CA		TGAAACCC TCTCTACTAAAAAT		
			ACTTTGGG AGAGATGATTTTTA		
			AC		
GAM2185	B4GALT5	3'	ATTTTGTAGTAGAGACAGGGTTT 17682	A_	
	TC		GAAACCCC TCTCTACTAAAAAT		
			CTTTGGGG AGAGATGATTTTTA		
			AC		
GAM2185	BRIP1	3'	ATTTTGTAGTAGAGATGGGGTTT 50207		
	CA		TGAAACCCCATCTCTACTAAAAAT		
			ACTTTGGGGTAGAGATGATTTTTA		
			—		
GAM2185	C7	3'	ATTTTGTAGTAGAGATGGGTTTC 6981	C	
	A		TGAAACCC ATCTCTACTAAAAAT		
			ACTTTGGG TAGAGATGATTTTTA		
			—		
GAM2185	CASP10	3'	TTTTTGTGGAGATGGGGTTTC 53231	T	
	A		TGAAACCCCATCTCTAC AAAAA		
			ACTTTGGGGTAGAGGTG TTTT		
			T		
GAM2185	CASP10	3'	TTTTTGTGGAGATGGGGTTTC 53269	T	
	A		TGAAACCCCATCTCTAC AAAAA		

			ACTTTGGGGTAGAGGTG TTTT	
			T	
GAM2185	CASP2	3'	ATTTT TAGTAGAGACAGGGTTT 53286	CA
	CA		TGAAACCC TCTCTACTAAAAAT	
			ACTTTGGG AGAGATGATTTT	
			AC	
GAM2185	CASP2	3'	ATTTT TAGTAGAGACAGGGTTT 53302	CA
	CA		TGAAACCC TCTCTACTAAAAAT	
			ACTTTGGG AGAGATGATTTT	
			AC	
GAM2185	CASP2	3'	ATTTT TAGTAGAGACAGGGTTT 53323	CA
	CA		TGAAACCC TCTCTACTAAAAAT	
			ACTTTGGG AGAGATGATTTT	
			AC	
GAM2185	CASP2	3'	ATTTT TAGTAGAGACAGGGTTT 8705	CA
	CA		TGAAACCC TCTCTACTAAAAAT	
			ACTTTGGG AGAGATGATTTT	
			AC	
GAM2185	CASP8	3'	ATTTT TAGTAGAGACAGGGTTT 8746	CA
	CA		TGAAACCC TCTCTACTAAAAAT	
			ACTTTGGG AGAGATGATTTT	
			AC	
GAM2185	CASP8	3'	ATTTT TAGTAGAGACAGGGTTT 54070	CA
	CA		TGAAACCC TCTCTACTAAAAAT	
			ACTTTGGG AGAGATGATTTT	
			AC	
GAM2185	CASP8	3'	ATTTT TAGTAGAGACAGGGTTT 54095	CA
	CA		TGAAACCC TCTCTACTAAAAAT	
			ACTTTGGG AGAGATGATTTT	
			AC	
GAM2185	CASP8	3'	ATTTT TAGTAGAGACAGGGTTT 54111	CA
	CA		TGAAACCC TCTCTACTAAAAAT	
			ACTTTGGG AGAGATGATTTT	
			AC	
GAM2185	CBFA2T2	3'	ATTTT TAGTGGAGACGGGGTTT 18701	A
	C		GAAACCCC TCTCTACTAAAAAT	
			CTTTGGGG AGAGGTGATTTT	
			C	
GAM2185	CCNF	3'	ATTTT CGGTAGAGACGGGATTT 10067	C A TA
	CA		TGAAA CCC TCTCTAC AAAAT	

		ACTTT GGG AGAGATG TTTTA		
		A C GC		
GAM2185	CDC6	3'	ATTTT TAGTAGAGACAGGGTTT 8817	CA
	TA		TGAAACCC TCTCTACTAAAAAT	
			ATTTTGGG AGAGATGATTTT	
			AC	
GAM2185	CDH17	3'	ATTTT AATAGAGACGGGGTTT 15781	A C
	C		GAAACCC TCTCTA TAAAAAT	
			CTTTGGGG AGAGAT ATTTT	
			C A	
GAM2185	CLECSF11	5'	ATTTT TAGTAGAGATGGGGTTT 56147	
	CA		TGAAACCCCATCTCTACTAAAAAT	
			ACTTTGGGGTAGAGATGATTTT	
GAM2185	CLECSF12	3'	TTTTT TAGTAGAGACAGGGTTT 77223	CA
			GAAACCC TCTCTACTAAAAA	
			CTTTGGG AGAGATGATTTT	
			AC	
GAM2185	CNGA1	5'	ATTTT TAGTAGAGATGGGATTT 60235	C
	CA		TGAAA CCCATCTCTACTAAAAAT	
			ACTTT GGGTAGAGATGATTTT	
			A	
GAM2185	CNN2	3'	ATTTT TAGTAGAGATGGGGTTT 16457	
	C		GAAACCCCATCTCTACTAAAAAT	
			CTTTGGGGTAGAGATGATTTT	
GAM2185	COX15	3'	ATTTT TAGTAGAGAAGGGGTTT 55278	A
	CA		TGAAACCC TCTCTACTAAAAAT	
			ACTTTGGGG AGAGATGATTTT	
			A	
GAM2185	CR1	3'	ATTTT TAGTAGAGACGGGGTTT 6939	A
	CA		TGAAACCC TCTCTACTAAAAAT	
			ACTTTGGGG AGAGATGATTTT	
			C	
GAM2185	CXCL16	3'	ATTTT TAGTAGAGACGGGGTTT 42161	A
	CA		TGAAACCC TCTCTACTAAAAAT	
			ACTTTGGGG AGAGATGATTTT	
			C	
GAM2185	CYP1A2	3'	ATTTT TAGTAGAGACGAGGTTT 7503	CCA
	CA		TGAAACC TCTCTACTAAAAAT	

			ACTTTGG AGAGATGATTTT	
			AGC	
GAM2185	CYP1A2	3'	ATTTTGGTAGAGACGGGTTTC 7504	CA
	A		TGAAACCC TCTCTACTAAAAAT	
			ACTTTGGG AGAGATGGTTTTTA	
			C_	
GAM2185	CYP1A2	3'	TTTAGTGGAGATGGGGTTTCA 7533	
			TGAAACCCCATCTCTACTAAAA	
			ACTTTGGGGTAGAGGTGATTTT	
GAM2185	CYP2B6	3'	ATTTTAGTAGAGATGGGGTTT 7552	
	CA		TGAAACCCCATCTCTACTAAAAAT	
			ACTTTGGGGTAGAGATGATTTT	
GAM2185	CYP51	3'	ATTTTAGTAGAGACGGGGTT 7611	A_
	TCA		TGAAACCC TCTCTACTAAAAAT	
			ACTTTGGG AGAGATGATTTT	
			GC	
GAM2185	CYP8B1	3'	ATTTTAGTAGAGACGGCGTTT 16530	C A
	CA		TGAAAC CC TCTCTACTAAAAAT	
			ACTTTG GG AGAGATGATTTT	
			C C	
GAM2185	DFFB	3'	ATTTTAGTAGAGACGGGGTTT 88760	A
	CA		TGAAACCC TCTCTACTAAAAAT	
			ACTTTGGG AGAGATGATTTT	
			C	
GAM2185	DFFB	3'	TTAGTAGAAACGGGGTTTCA 88792	ATC
			TGAAACCC TCTACTAA	
			ACTTTGGG AGATGATT	
			CAA	
GAM2185	DHFR	3'	ATTTTAGTAGAGATGGGGTTT 7643	
	CA		TGAAACCCCATCTCTACTAAAAAT	
			ACTTTGGGGTAGAGATGATTTT	
GAM2185	DISC1	3'	ATTTTAGTAGAGACAGGGCTT 38501	A CA
	CA		TGAA CCC TCTCTACTAAAAAT	
			ACTT GGG AGAGATGATTTT	
			C AC	
GAM2185	DSC3	3'	ATTTTAATAGAGACGGGGTTT 44614	A C
	CA		TGAAACCC TCTCTA TAAAAAT	

			ACTTTGGGG AGAGAT ATTTTTA		
			C A		
GAM2185	DSC3	3'	ATTTTAAATAGACGGGGTTT 10434	A	C
	CA		TGAAACCCC TCTCTA TAAAAAT		
			ACTTTGGGG AGAGAT ATTTTTA		
			C A		
GAM2185	DSCR3	3'	ATTTTATAGTAGACGGGGCTT 21307	A	A
	CA		TGAA CCCC TCTCTACTAAAAAT		
			ACTT GGGG AGAGATGATTTTTA		
			C C		
GAM2185	EHD2	3'	AGTAGAGACGGGGTTTCA 28214	A	
			TGAAACCCC TCTCTACT		
			ACTTTGGGG AGAGATGA		
			C		
GAM2185	EIF2S3	3'	TTAGTAGAGACGGGGTTTCA 9216	A	
			TGAAACCCC TCTCTACTAA		
			ACTTTGGGG AGAGATGATT		
			C		
GAM2185	EPB72	3'	TTTTTAGTAGAGACGGGGTTTC 15883	A	
	A		TGAAACCCC TCTCTACTAAAAA		
			ACTTTGGGG AGAGATGATTTTT		
			C		
GAM2185	F2RL2	3'	ATTTTATAGTAGAGACGGGGTTT 15893	A	
	CA		TGAAACCCC TCTCTACTAAAAAT		
			ACTTTGGGG AGAGATGATTTTTA		
			C		
GAM2185	F3	3'	TTTTTAGTAGAGATGGGGTTTC 67687		
	A		TGAAACCCCATCTCTACTAAAAA		
			ACTTTGGGGTAGAGATGATTTTT		
GAM2185	FANCF	3'	ATTTTATAGTAGAGACGGGGTTT 42974	A	
	CA		TGAAACCCC TCTCTACTAAAAAT		
			ACTTTGGGG AGAGATGATTTTTA		
			C		
GAM2185	FCAR	3'	ATTTTATAGTAGAGATGGGGTTT 10583		
	CA		TGAAACCCCATCTCTACTAAAAAT		
			ACTTTGGGGTAGAGATGATTTTTA		
GAM2185	FCAR	3'	ATTTTATAGTAGAGATGGGGTTT 56561		
	CA		TGAAACCCCATCTCTACTAAAAAT		

ACTTTGGGGTAGAGATGATTTTTA

GAM2185 FCAR 3' ATTTTATAGTAGAGATGGGGTTT 56590
CA TGAAACCCCATCTCTACTAAAAAT
|||||
ACTTTGGGGTAGAGATGATTTTTA

GAM2185 FCAR 3' ATTTTATAGTAGAGATGGGGTTT 56602
CA TGAAACCCCATCTCTACTAAAAAT
|||||
ACTTTGGGGTAGAGATGATTTTTA

GAM2185 FCAR 3' ATTTTATAGTAGAGATGGGGTTT 56614
CA TGAAACCCCATCTCTACTAAAAAT
|||||
ACTTTGGGGTAGAGATGATTTTTA

GAM2185 FCGR2A 3' TTTTATAGTAGAGACAGGGTTTC 80035 CA
GAAACCC TCTCTACTAAAAA
|||||
CTTTGGG AGAGATGATTTT
AC

GAM2185 FGF5 3' ATTTTATAGTAGAGACGGGGTTT 16758 A
CA TGAAACCC TCTCTACTAAAAAT
|||||
ACTTTGGG AGAGATGATTTT
C

GAM2185 FGF5 3' ATTTTATAGTAGAGACGGGGTTT 53651 A
CA TGAAACCC TCTCTACTAAAAAT
|||||
ACTTTGGG AGAGATGATTTT
C

GAM2185 FUT1 3' ATTTTATAGTAGAGACAGGGTTT 5584 CA
CA TGAAACCC TCTCTACTAAAAAT
|||||
ACTTTGGG AGAGATGATTTT
AC

GAM2185 FUT1 3' ATTTTATAGTAGAGACGGGGTTT 5585 A
CA TGAAACCC TCTCTACTAAAAAT
|||||
ACTTTGGG AGAGATGATTTT
C

GAM2185 G6PC 3' TTTTAGAAGAGATGGGATTTC 5669 C A
TGAAA CCCATCTCT CTA
|||||
ACTTT GGGTAGAGA GATTTT
A A

GAM2185 GHR 3' TTTTAGCAGAGACGGGGTTTC 5708 A A
TGAAACCC TCTCT CTA
|||||

		ACTTTGGGG AGAGA GATTTT	
		C C	
GAM2185	GM2A	3' ATTTTATAGTAGAGATGGGGTTT 68376	
	CA	TGAAACCCCATCTCTACTAAAAAT	
		ACTTTGGGGTAGAGATGATTTT	
GAM2185	GNE	3' ATTTTATAGTGGACAGGGTTTCA 19662	CATC
		TGAAACCC TCTACTAAAAAT	
		ACTTTGGG AGGTGATTTT	
		AC_	
GAM2185	GPR81	3' ATTTTATAGTACAGACGGGGTTT 51737	A C
	CA	TGAAACCC TCT TACTAAAAAT	
		ACTTTGGGG AGA ATGATTTT	
		C C	
GAM2185	GPR81	3' ATTTTATAGTAGAGACAGGGTTT 51738	CA
	T	GAAACCC TCTCTACTAAAAAT	
		TTTGGG AGAGATGATTTT	
		AC	
GAM2185	GRM7	5' ATTTTATAGTAGAGATTGGGGTTT 7782	C
	CA	TGAAACCC ATCTCTACTAAAAAT	
		ACTTTGGG TAGAGATGATTTT	
		T	
GAM2185	HCS	3' ATTTTATAGTGGAGATGGTGTTT 38969	C
	CA	TGAAAC CCATCTCTACTAAAAAT	
		ACTTTG GGTAGAGGTGATTTT	
		T	
GAM2185	HCS	3' TTTTATAGTAGAGACAGGGTTTC 38998	CA
		GAAACCC TCTCTACTAAAAA	
		CTTGGG AGAGATGATTTT	
		AC	
GAM2185	HLCS	5' ATTTTATAGTAGAGGCGGGGGTT 6406	A_
	TCA	TGAAACCC TCTCTACTAAAAAT	
		ACTTTGGGG GGAGATGATTTT	
		GC	
GAM2185	HTR1D	3' ATTTTAAATAAAGACGGGGTTT 7839	A C C
	CA	TGAAACCC TCT TA TAAAAAT	
		ACTTTGGGG AGA AT ATTTT	
		C A A	
GAM2185	HTR1E	5' ATTTTATAGTGGAGACGGGATTT 7859	C A
	CA	TGAAA CCC TCTCTACTAAAAAT	

		ACTTT GGG AGAGGTGATTTT		
		A C		
GAM2185 HUNK	3'	TTTGTAGAAATGGGGTTTC 28198	C	T
		GAAACCCCAT TCTAC AAAA		
		CTTTGGGGTA AGATG TTTT		
		A _		
GAM2185 HYAL4	5'	ATTTTGTAGAGATGGGGTTT 25365		
CA		TGAAACCCCATCTCTACTAAAAAT		
		ACTTTGGGGTAGAGATGATTTT		
GAM2185 IFNAR2	3'	ATTTTGTAGTGAGACAGGATT 7897	C	CA
TA		TGAAA CC TCTCTACTAAAAAT		
		ATTTT GG AGAGGTGATTTT		
		A AC		
GAM2185 IGF1	3'	ATTTTAAATAGAGACGGGGTTT 7061	A	C
TA		TGAAACCCC TCTCTA TAAAAAT		
		ATTTTGGGG AGAGAT ATTTT		
		C A		
GAM2185 IL11	3'	ATTTTGTAGTAGAGACAGGGTTT 7179	CA	
CA		TGAAACCC TCTCTACTAAAAAT		
		ACTTTGGG AGAGATGATTTT		
		AC		
GAM2185 INMT	3'	ATTTTGTAGTAGATATGGGGTTT 23209	C	
CA		TGAAACCCCAT TCTACTAAAAAT		
		ACTTTGGGGTA AGATGATTTT		
		T		
GAM2185 JAK3	3'	ATTTTAAATAGAGATGAGGTTT 5827	C	C
CA		TGAAACC CATCTCTA TAAAAAT		
		ACTTTGG GTAGAGAT ATTTT		
		A A		
GAM2185 LLGL1	3'	ATTTTGTAGTAGAGATGGGGTTT 67415		
CA		TGAAACCCCATCTCTACTAAAAAT		
		ACTTTGGGGTAGAGATGATTTT		
GAM2185 LNK	3'	ATTTTGTAGTAGAGACAGGGTTT 19633	CA	
CA		TGAAACCC TCTCTACTAAAAAT		
		ACTTTGGG AGAGATGATTTT		
		AC		
GAM2185 LTB4R	5'	ATTTTGTAGTAGAGACGGGGTTT 7460	A	
CA		TGAAACCCC TCTCTACTAAAAAT		

			ACTTTGGGG AGAGATGATTTTTA	
			C	
GAM2185	LYZ	3'	ATTTTATAGTAGAGACAGGGTTT 5892	CA
	CA		TGAAACCC TCTCTACTAAAAAT	
			ACTTTGGG AGAGATGATTTTTA	
			AC	
GAM2185	MAK	3'	TTAGTAGAGACAGGGTTTCA 20955	CA
			TGAAACCC TCTCTACTAA	
			ACTTTGGG AGAGATGATT	
			AC	
GAM2185	MDM2	3'	TTTAGTAGAGACAGGGTTTCA 23466	CA
			TGAAACCC TCTCTACTAAAA	
			ACTTTGGG AGAGATGATTTT	
			AC	
GAM2185	MDM2	3'	TTTAGTAGAGACAGGGTTTCA 23479	CA
			TGAAACCC TCTCTACTAAAA	
			ACTTTGGG AGAGATGATTTT	
			AC	
GAM2185	MDM2	3'	TTTAGTAGAGACAGGGTTTCA 23492	CA
			TGAAACCC TCTCTACTAAAA	
			ACTTTGGG AGAGATGATTTT	
			AC	
GAM2185	MDM2	3'	TTTAGTAGAGACAGGGTTTCA 23506	CA
			TGAAACCC TCTCTACTAAAA	
			ACTTTGGG AGAGATGATTTT	
			AC	
GAM2185	MDM2	3'	TTTAGTAGAGACAGGGTTTCA 11504	CA
			TGAAACCC TCTCTACTAAAA	
			ACTTTGGG AGAGATGATTTT	
			AC	
GAM2185	MEF2A	5'	ATTTTATAGTAGAGATGGAGTTT 19992	C
	CA		TGAAAC CCATCTCTACTAAAAAT	
			ACTTTG GGTAGAGATGATTTTTA	
			A	
GAM2185	MEFV	3'	ATTTTATAGTAGACATGAGGTTT 5928	C C
	CA		TGAAACC CAT TCTACTAAAAAT	
			ACTTTGG GTA AGATGATTTTTA	
			A C	
GAM2185	MEFV	3'	ATTTTATAGTAGACGGGGGTT 5929	A_
	TCA		TGAAACCCC TCTCTACTAAAAAT	

			ACTTTGGGG AGAGATGATTTT	
			GC	
GAM2185	MHC2TA	3'	TTTTTAGCGGAGACGGAGTCCC 5999	AA C A TA
	A		TG AC CC TCTC CTA	
			AC TG GG AGAG GATTTT	
			CC A C GC	
GAM2185	MICB	3'	ATTTTTGTAGAGACGGGTTT 21019	A T
	C		GAAACCCC TCTCTAC AAAA	
			CTTTGGGG AGAGATG TTTT	
			C T	
GAM2185	MLANA	3'	TTTAGTAGAGACGGGTTTC 19774	A
			GAAACCCC TCTCTACTAAA	
			CTTTGGGG AGAGATGATTTT	
			C	
GAM2185	MPL	3'	ATTTTAGTAGAGACAGGTTT 19341	CA
	T		GAAACCC TCTCTACTAAAA	
			TTTTGGG AGAGATGATTTT	
			AC	
GAM2185	MRPL49	3'	ATTTTAGTAGAGATGGGTTT 70162	
	CA		TGAAACCCCATCTCTACTAAAA	
			ACTTTGGGGTAGAGATGATTTT	
GAM2185	MTR	3'	AGTAGAGACAGGATTTCA 6013	C CA
			TGAAA CC TCTCTACT	
			ACTTT GG AGAGATGA	
			A AC	
GAM2185	MYCL2	3'	ATTTTAGTAGAGATGGGTTT 19371	
	CA		TGAAACCCCATCTCTACTAAAA	
			ACTTTGGGGTAGAGATGATTTT	
GAM2185	NDRG3	3'	ATTTTAGTAGAGATGGAGTTT 50118	C
	CA		TGAAAC CCATCTCTACTAAAA	
			ACTTTG GGTAGAGATGATTTT	
			A	
GAM2185	NQO1	3'	ATTTTAGTAGAGACGGCGTTT 8043	C A
	CA		TGAAAC CC TCTCTACTAAAA	
			ACTTTG GG AGAGATGATTTT	
			C C	
GAM2185	PCDHA9	3'	ATTTTAGTAGAGATGGGTTT 26612	
	CA		TGAAACCCCATCTCTACTAAAA	

ACTTTGGGGTAGAGATGATTTTTA

GAM2185	PCDHA9	3'	ATTTT	AGTAGAGATGGGGTTT	26613	
	CA			TGAAACCCCATCTCTACTAAAAAT		
				ACTTTGGGGTAGAGATGATTTTTA		
GAM2185	PCDHB11	3'	TTTAG	TAGAGACGGGGTTTCA	38932	A
				TGAAACCCC TCTCTACTAAA		
				ACTTTGGGG AGAGATGATT		
				C		
GAM2185	PCDHB9	3'	ATTTTC	CAGTAGAGACGGGGTTTC	39438	CA A
	A			TGAAACCC TCTCTACT AAAAT		
				ACTTTGGG AGAGATGA TTTTA		
				C_ C		
GAM2185	PDE6B	3'	ATTTTC	CAGTACAGATGGGGTTT	6071	C A
	CA			TGAAACCCCATCT TACT AAAAT		
				ACTTTGGGGTAGA ATGA TTTTA		
				C C		
GAM2185	PER2	3'	ATTTT	TAGTAGAGACAGGGTTT	43344	CA
	CA			TGAAACCC TCTCTACTAAAAAT		
				ACTTTGGG AGAGATGATTTTTA		
				AC		
GAM2185	PIGR	3'	ATTTT	TAGTAGAGACAGGGTTT	72990	CA
	CA			TGAAACCC TCTCTACTAAAAAT		
				ACTTTGGG AGAGATGATTTTTA		
				AC		
GAM2185	PIK3C2B	3'	ATTTT	TAGTAGAGACGGGGTTT	12091	A
	CA			TGAAACCCC TCTCTACTAAAAAT		
				ACTTTGGGG AGAGATGATTTTTA		
				C		
GAM2185	PIK3CD	3'	TTT	TAGTAGAGACGGGGTTTC	18505	A_
	A			TGAAACCCC TCTCTACTAAAA		
				ACTTTGGGG AGAGATGATTTT		
				GC		
GAM2185	PMCHL1	3'	ATTTT	TAGTAGAGGCAAGGTTT	49912	CCA
	CA			TGAAACC TCTCTACTAAAAAT		
				ACTTTGG GGAGATGATTTTTA		
				AAC		
GAM2185	POU2AF1	3'	ATTTT	TAGTAGAGACGGGGTTT	21732	A
	CA			TGAAACCCC TCTCTACTAAAAAT		

		ACTTTGGGG AGAGATGATTTTTA	
		C	
GAM2185 PPEF2	3'	ATTTT TAGTAGACACAGGGTTT 21771	CATC
	C	GAAACCC TCTACTAAAAAT	
		CTTTGGG AGATGATTTTTA	
		ACAC	
GAM2185 PPID	3'	ATTTT TAGTAGAGATGGGGTTT 88821	
	CA	TGAAACCCCATCTCTACTAAAAAT	
		ACTTTGGGGTAGAGATGATTTTTA	
GAM2185 PPT2	3'	ATTTT TAGTAGAGACGGGGTTT 57799	A
	TA	TGAAACCC TCTCTACTAAAAAT	
		ATTTTGGGG AGAGATGATTTTTA	
		C	
GAM2185 PPT2	3'	ATTTT TAGTAGAGACGGGGTTT 18947	A
	TA	TGAAACCC TCTCTACTAAAAAT	
		ATTTTGGGG AGAGATGATTTTTA	
		C	
GAM2185 PRKR	3'	TTTTTAATAAAGACAGGGTTTC 12354	CA C C
	A	TGAAACCC TCT TA TAAAAA	
		ACTTTGGG AGA AT ATTTT	
		AC A A	
GAM2185 PRKWNK3	3'	ATTTT TAGTAGAGGATGGGGTT 62226	—
	TCA	TGAAACCCCATC TCTACTAAAAAT	
		ACTTTGGGGTAG AGATGATTTTTA	
		G	
GAM2185 PTGES	3'	ATTTT TAGTAGAGACGGGGTTCA 18057	AC A
		TGAA CCC TCTCTACTAAAAAT	
		ACTT GGG AGAGATGATTTTTA	
		— C	
GAM2185 PTGIS	3'	ATTTT TAGTAGAGACGGGGTTT 8195	A
	C	GAAACCC TCTCTACTAAAAAT	
		CTTTGGGG AGAGATGATTTTTA	
		C	
GAM2185 PTGIS	3'	ATTTT TAGTAGAGATGGGATTT 8196	C
	CA	TGAAA CCCATCTCTACTAAAAAT	
		ACTTT GGGTAGAGATGATTTTTA	
		A	
GAM2185 RAB36	3'	ATTTT TAGTAGAGAGAGGTTTC 18155	CCA
	A	TGAAACC TCTCTACTAAAAAT	

		ACTTTGG AGAGATGATTTT	
		AG_	
GAM2185	RAB36	3' ATTTTATAGTAGAGATGGGGTTT 18156	
	C	GAAACCCCATCTCTACTAAAAAT	
		CTTTGGGGTAGAGATGATTTT	
GAM2185	RABL2A	3' ATTTTATAGTAGAGACGGGGTTT 26406	A
	CA	TGAAACCC TCTCTACTAAAAAT	
		ACTTTGGGG AGAGATGATTTT	
		C	
GAM2185	RABL2B	3' ATTTTATAGTAGAGACGGGGTTT 23974	A
	CA	TGAAACCC TCTCTACTAAAAAT	
		ACTTTGGGG AGAGATGATTTT	
		C	
GAM2185	RBBP9	3' ATTTTATAGTAGAGACAGGGTTT 70684	CA
	CA	TGAAACCC TCTCTACTAAAAAT	
		ACTTTGGG AGAGATGATTTT	
		AC	
GAM2185	RGS9	5' TTTTAGTAAAGACGGGGTTT 15175	A C
		GAAACCC TCT TACTAAAA	
		TTTTGGGG AGA ATGATTTT	
		C A	
GAM2185	RHD	3' ATTTTACTTGACAGGGTTTCA 32816	CA TCTAC
		TGAAACCC TC TAAAAAT	
		ACTTTGGG AG ATTTT	
		AC TTC_	
GAM2185	RHD	3' ATTTTATAGTAAAGATGGGGTTT 32817	C
	CA	TGAAACCCCATCT TACTAAAAAT	
		ACTTTGGGGTAGA ATGATTTT	
		A	
GAM2185	RHD	3' ATTTTACTTGACAGGGTTTCA 33136	CA TCTAC
		TGAAACCC TC TAAAAAT	
		ACTTTGGG AG ATTTT	
		AC TTC_	
GAM2185	RHD	3' ATTTTATAGTAAAGATGGGGTTT 33137	C
	CA	TGAAACCCCATCT TACTAAAAAT	
		ACTTTGGGGTAGA ATGATTTT	
		A	
GAM2185	RPH3AL	3' ATTTTAGAAGAGATGGGGTTT 23730	A
	C	GAAACCCCATCTCT CTAAAAAT	

			CTTTGGGGTAGAGA GATTTT		
			A		
GAM2185	RPP30	3'	TTTAGCAGAGACGGGGTTTCA 2212	A	A
			TGAAACCCC TCTCT CTA		
			ACTTTGGGG AGAGA GATTT		
			C C		
GAM2185	SAS	3'	ATTTTATAGTAGAGACAGGGTTT 21096	CA	
	CA		TGAAACCC TCTCTACTAAAAAT		
			ACTTTGGG AGAGATGATTTT		
			AC		
GAM2185	SCML2	3'	TTTTGTAGAGATGGGGTTTC 21436	T	
			GAAACCCCATCTCTAC AAA		
			CTTTGGGGTAGAGATG TTT		
			—		
GAM2185	SEDL	3'	ATTTTATAGTAGAGACAGGGTTT 28078	CA	
	CA		TGAAACCC TCTCTACTAAAAAT		
			ACTTTGGG AGAGATGATTTT		
			AC		
GAM2185	SEDL	3'	ATTTTATAGTAGAGACAGGGTTT 28079	CA	
	CA		TGAAACCC TCTCTACTAAAAAT		
			ACTTTGGG AGAGATGATTTT		
			AC		
GAM2185	SEDL	3'	TTTTATAGTAGAGACGGGGTTTC 28118	A	
			GAAACCC TCTCTACTAAAA		
			CTTTGGGG AGAGATGATTTT		
			C		
GAM2185	SEPN1	3'	ATTTTATAGTAGAGATGGGGTTT 66961		
	CA		TGAAACCCCATCTCTACTAAAAAT		
			ACTTTGGGGTAGAGATGATTTT		
GAM2185	SERPINB9	3'	ATTTTATAGTAGAGACGGGGTTT 16009	A	
	CA		TGAAACCC TCTCTACTAAAAAT		
			ACTTTGGGG AGAGATGATTTT		
			C		
GAM2185	SERPINB9	3'	ATTTTTCAGTAGAGACGGGGTT 16010	A	—
	TC		GAAACCC TCTCTACT AAAAT		
			CTTTGGGG AGAGATGA TTTT		
			C C		
GAM2185	SH3BP2	3'	ATTTTATAGTAGAGACGGGATTT 13050	C	A
	TA		TGAAA CCC TCTCTACTAAAAAT		

			ATTTT GGG AGAGATGATTTT		
			A C		
GAM2185	SH3BP2	3'	ATTTT TAGT GGAACCGGGTTT 13051	ATC	
	CA		TGAAACCCC TCTACTAAAAAT		
			ACTTTGGGG AGGTGATTTT		
			CCA		
GAM2185	SH3GL3	5'	AGTAGAGATGGGTTTCA 13104	C	
			TGAAACCC ATCTCTACT		
			ACTTTGGG TAGAGATGA		
			—		
GAM2185	SHOX	3'	ATTTATAGTAGAGACGGCGTTT 6564	C A	A
	CA		TGAAAC CC TCTCTACTA AAAT		
			ACTTTG GG AGAGATGAT TTTA		
			C C A		
GAM2185	SHOX	3'	ATTTTCAGTAGAGATGGGGTTT 23516		A
			AAACCCCATCTCTACT AAAAT		
			TTTGGGGTAGAGATGA TTTTA		
			C		
GAM2185	SIL	3'	ATTTT TAGTAGAGACTGGTTTC 13153	CCA	
			GAAACC TCTCTACTAAAAAT		
			CTTTGG AGAGATGATTTT		
			TC_		
GAM2185	SLA2	3'	ATTTT TAGTAGACATGGGGTTT 50881		C
	CA		TGAAACCCCAT TCTACTAAAAAT		
			ACTTTGGGGTA AGATGATTTT		
			C		
GAM2185	SLC14A2	5'	ATTTT TAGTAGAGACGGGGTTT 24110		A
	CA		TGAAACCCC TCTCTACTAAAAAT		
			ACTTTGGGG AGAGATGATTTT		
			C		
GAM2185	SLC15A1	3'	ATTTT TAGTAGAGATGGGGTTT 18636		
	CA		TGAAACCCCATCTCTACTAAAAAT		
			ACTTTGGGGTAGAGATGATTTT		
GAM2185	SLC17A5	3'	TTTTGTAGAGATGGGGTCTC 25837	A	T
			GA ACCCATCTCTAC AAAA		
			CT TGGGGTAGAGATG TTTT		
			C		
			—		
GAM2185	SMAC	5'	AGTAGAGATGGGGTTTCA 58015		
			TGAAACCCCATCTCTACT		

ACTTTGGGGTAGAGATGA

GAM2185	SNAP23	3'	ATTTT	TAGTAGAGACAGGGTTT	56335	CA
	CA			TGAAACCC TCTCTACTAAAAAT		
				ACTTTGGG AGAGATGATTTT		
				AC		
GAM2185	SNAP23	3'	ATTTT	TAGTAGAGACAGGGTTT	15136	CA
	CA			TGAAACCC TCTCTACTAAAAAT		
				ACTTTGGG AGAGATGATTTT		
				AC		
GAM2185	SNX15	3'	ATTTT	CAGTAGGGACGGGGTTA	74115	A A A
	CA			TG AACCCC TCTCTACT AAAAT		
				AC TTGGGG AGGGATGA TTTTA		
				A C C		
GAM2185	SPN	3'	ATTTT	TGGTAGAGATGGGGTTT	13370	
	CA			TGAAACCCCATCTCTACTAAAAAT		
				ACTTTGGGGTAGAGATGGTTTTTA		
GAM2185	TAPBP	3'	ATTTT	TAGTAGAGACGGGGTTT	13552	A
	CA			TGAAACCC TCTCTACTAAAAAT		
				ACTTTGGGG AGAGATGATTTT		
				C		
GAM2185	TAPBP	3'	TTTT	TAGTAGAGACGGGGTTTC	13594	A
	A			TGAAACCC TCTCTACTAAAA		
				ACTTTGGGG AGAGATGATTTT		
				C		
GAM2185	TAPBP	3'	TTTT	TAGTAGAGACGGGGTTTC	13595	A
	A			TGAAACCC TCTCTACTAAAA		
				ACTTTGGGG AGAGATGATTTT		
				C		
GAM2185	TAT	3'	ATTTT	TAGTAGAGACAGGGTTT	6250	CA
	CA			TGAAACCC TCTCTACTAAAAAT		
				ACTTTGGG AGAGATGATTTT		
				AC		
GAM2185	TBXA2R	3'	ATTTT	TAGTAGAGACGGGGTTT	8345	A
	CA			TGAAACCC TCTCTACTAAAAAT		
				ACTTTGGGG AGAGATGATTTT		
				C		
GAM2185	TDGF1	3'	TTTT	TAGTAGAGATGGGGTTTC	13665	—
	A			TGAAACCC ATCTCTACTAAAA		

		ACTTTGGGG TAGAGATGATTTT	
		G	
GAM2185	TERF1	3' ATTTT TAGAGACGGGGTTT 34389	AT
	CA	TGAAACCCC CTCTACTAAAAAT	
		ACTTTGGGG GAGATGATTTT	
		CG	
GAM2185	TERF2	3' ATTTT TAGAGACGGGGTTT 20145	A
	CA	TGAAACCCC TCTCTACTAAAAAT	
		ACTTTGGGG AGAGATGATTTT	
		C	
GAM2185	TES	3' ATTTT TAGAGACAGGTTT 72460	C CA
	CA	TGAAA CC TCTCTACTAAAAAT	
		ACTTT GG AGAGATGATTTT	
		T AC	
GAM2185	TIM3	3' ATTTT TAGAGACAGGTTT 52352	CA
	CA	TGAAACCC TCTCTACTAAAAAT	
		ACTTTGGG AGAGATGATTTT	
		AC	
GAM2185	TPRSS3	3' ATTTT TAGAGACAGGTTT 51512	CA
	CA	TGAAACCC TCTCTACTAAAAAT	
		ACTTTGGG AGAGATGATTTT	
		AC	
GAM2185	TPRSS3	3' ATTTT TAGAGACAGGTTT 51540	CA
	CA	TGAAACCC TCTCTACTAAAAAT	
		ACTTTGGG AGAGATGATTTT	
		AC	
GAM2185	TPRSS3	3' ATTTT TAGAGACAGGTTT 44015	CA
	CA	TGAAACCC TCTCTACTAAAAAT	
		ACTTTGGG AGAGATGATTTT	
		AC	
GAM2185	TNFRSF10B	3' ATTTT TAGAGACGGGGTTT 15218	A
	CA	TGAAACCCC TCTCTACTAAAAAT	
		ACTTTGGGG AGAGATGATTTT	
		C	
GAM2185	TP53	3' TTTTGTAGAGATGGGGTCTCA 6809	A T
		TGA ACCCATCTCTAC AAAA	
		ACT TGGGGTAGAGATG TTTT	
		C	
GAM2185	TPMT	3' TTTT TAGTGAGACGGGGTTTC 6322	A
	A	TGAAACCCC TCTCTACTAAAAA	

		ACTTTGGGG AGAGGTGATTTT			
		C			
GAM2185	TRAF5	3'	ATTTTATAGTAGAGACGGAGTTT 17268	C	A
	T		GAAAC CC TCTCTACTAAAAAT		
			TTTTG GG AGAGATGATTTT		
			A C		
GAM2185	TRIM9	5'	AGTAGAGACGGGGTTTCA 31444	A	
			TGAAACCCC TCTCTACT		
			ACTTTGGGG AGAGATGA		
			C		
GAM2185	TRPM6	3'	ATTTTATAGTAGAGATGGGGTTT 35027		
	CA		TGAAACCCCATCTCTACTAAAAAT		
			ACTTTGGGGTAGAGATGATTTT		
GAM2185	TRPV1	3'	ATTTTAAATAGAGACGGGGTTT 38689	A	C
	CA		TGAAACCCC TCTCTA TAAAAAT		
			ACTTTGGGG AGAGAT ATTTT		
			C A		
GAM2185	TRPV1	3'	ATTTTAAATAGAGACGGGGTTT 55660	A	C
	CA		TGAAACCCC TCTCTA TAAAAAT		
			ACTTTGGGG AGAGAT ATTTT		
			C A		
GAM2185	TRPV1	3'	ATTTTAAATAGAGACGGGGTTT 55705	A	C
	CA		TGAAACCCC TCTCTA TAAAAAT		
			ACTTTGGGG AGAGAT ATTTT		
			C A		
GAM2185	TRPV1	3'	ATTTTAAATAGAGACGGGGTTT 55736	A	C
	CA		TGAAACCCC TCTCTA TAAAAAT		
			ACTTTGGGG AGAGAT ATTTT		
			C A		
GAM2185	TUFT1	3'	ATTTTATAGTAGAGATGGGGTTT 39670		
	CA		TGAAACCCCATCTCTACTAAAAAT		
			ACTTTGGGGTAGAGATGATTTT		
GAM2185	UGDH	3'	ATTTTATAGTAGAGACAGGGTTT 13992	CA	
	CA		TGAAACCC TCTCTACTAAAAAT		
			ACTTTGGG AGAGATGATTTT		
			AC		
GAM2185	VENTX2	3'	ATTTTATAGTAGAAATGGGGTTT 27857	C	
	CA		TGAAACCCCAT TCTACTAAAAAT		

		ACTTTGGGGTA AGATGATTTTTA			
		A			
GAM2185	VHL	3'	TTTTAGTAGAGACAGTGTTC 6886	CCCA	
			GAAAC TCTCTACTAAAA		
			CTTTG AGAGATGATTTT		
			TGAC		
GAM2185	VHL	3'	TTTTTAGTGGAGACGGGGTTC 6887	A	
	A		TGAAACCCC TCTCTACTAAAAA		
			ACTTTGGGG AGAGGTGATTTTT		
			C		
GAM2185	VIPR2	3'	ATTTTATAGTAGAGACAGGGTTT 14059	CA	
	CA		TGAAACCC TCTCTACTAAAAAT		
			ACTTTGGG AGAGATGATTTTTTA		
			AC		
GAM2185	WHSC1	3'	ATTTTATAGTAGAGACAGGGTTT 56691	CA	
	C		GAAACCC TCTCTACTAAAAAT		
			CTTTGGG AGAGATGATTTTTTA		
			AC		
GAM2185	XRCC2	3'	ATTTTAAATAGAGACGGGGTTC 19493	A C	
	CA		TGAAACCCC TCTCTA TAAAAAT		
			ACTTTGGGG AGAGAT ATTTTTTA		
			C A		
GAM2185	YES1	3'	ATTTTATAGTAGAGACGCAGTTT 19530	CCCA	
	CA		TGAAAC TCTCTACTAAAAAT		
			ACTTTG AGAGATGATTTTTTA		
			ACGC		
GAM2185	ZNF133	5'	ATTTTATAGTAGAGACGGAGTTT 14292	C A	
	CA		TGAAAC CC TCTCTACTAAAAAT		
			ACTTTG GG AGAGATGATTTTTTA		
			A C		
GAM2185	ZNF157	3'	ATTTTATAGTAAAGACGGGTTC 14328	CA C	
	A		TGAAACCC TCT TACTAAAAAT		
			ACTTTGGG AGA ATGATTTTTTA		
			C_ A		
GAM2185	ZNF264	3'	ATTTTATAGTAGAGACGGGGTTC 14198	A	
	CA		TGAAACCCC TCTCTACTAAAAAT		
			ACTTTGGGG AGAGATGATTTTTTA		
			C		
GAM2185	ZNF264	3'	ATTTTATAGTAGAGACGGGGTTC 14199	A	
	CA		TGAAACCCC TCTCTACTAAAAAT		

			ACTTTGGGG AGAGATGATTTTTA	
			C	
GAM2185	ZNF74	5'	ATTTTATAGTAGAGACGGGGTTT 14257	A
	T		GAAACCCC TCTCTACTAAAAAT	
			TTTGGGG AGAGATGATTTTTA	
			C	
GAM2185	AAK1	3'	ATTTTATAGTAGAGATGGGGTTT 30517	
	C		GAAACCCCATCTCTACTAAAAAT	
			CTTTGGGGTAGAGATGATTTTTA	
GAM2185	AP3S2	3'	TTTAGTAGAGACAGGGTTTCA 20661	CA
			TGAAACCC TCTCTACTAAA	
			ACTTTGGG AGAGATGATTT	
			AC	
GAM2185	ARHF	3'	ATTTTATAGTAGAGACAGGGTTT 39262	CA
	CA		TGAAACCC TCTCTACTAAAAAT	
			ACTTTGGG AGAGATGATTTTTA	
			AC	
GAM2185	ARHGAP11A	3'	ATTTTATAGTAGAGACGGTTTCA 29443	CCA
			TGAAACC TCTCTACTAAAAAT	
			ACTTTGG AGAGATGATTTTTA	
			C__	
GAM2185	ARHGAP5	5'	ATTTTATAGTAGAGATGGGGTTT 77596	
	C		GAAACCCCATCTCTACTAAAAAT	
			CTTTGGGGTAGAGATGATTTTTA	
GAM2185	ASB16	3'	ATTTTGGTGGAGACGGGGTCT 55973	A A
	C		GA ACCCC TCTCTACTAAAAAT	
			CT TGGGG AGAGGTGGTTTTTA	
			C C	
GAM2185	ASE-1	3'	ATTTTATAGTAGAGACAGGGGT 24971	A_
	TCA		TGAAACCCC TCTCTACTAAAAAT	
			ACTTTGGGG AGAGATGATTTTTA	
			AC	
GAM2185	ASE-1	3'	TTTTATAGTAGAGATGGGGTTTC 25001	
	A		TGAAACCCCATCTCTACTAAAAA	
			ACTTTGGGGTAGAGATGATTTT	
GAM2185	ATP1B4	3'	ATTTTGGCGGAGACAGGGTTT 24836	CA TA
	CA		TGAAACCC TCTC CTA AAAAT	

			ACTTTGGG AGAG GGTTTTTA		
			AC GC		
GAM2185	BA108L7.2	3'	ATTTTTCAGCAGAGATGGGGGTT 49066	_	A
		TCA	TGAAACCCC ATCTCT CTAAAAAT		
			ACTTTGGGG TAGAGA GATTTTTTA		
			G C		
GAM2185	BM-002	3'	ATTTTTCAGCAGAGACAGGG 34006	CA	A
			CCC TCTCT CTAAAAAT		
			GGG AGAGA GATTTTTTA		
			AC C		
GAM2185	BNIP-S	3'	ATTTTTCAGTAGAGACGGGGTTT 57087		A
		CA	TGAAACCCC TCTCTACTAAAAAT		
			ACTTTGGGG AGAGATGATTTTTTA		
			C		
GAM2185	BTN3A1	3'	TTTTCAGTACAGATGAGGGTTCA 23897	A _	C
			TGAA CCC CATCT TACTAAAA		
			ACTT GGG GTAGA ATGATTTT		
			_ A C		
GAM2185	C11orf17	3'	ATTTTTCAGTAGAGACGGGGTTT 40576		A
			AAACCCC TCTCTACTAAAAAT		
			TTTGGGG AGAGATGATTTTTTA		
			C		
GAM2185	C13orf1	3'	ATTTTTCAGTAGAGATGGGGTTT 40355		
		CA	TGAAACCCCATCTCTACTAAAAAT		
			ACTTTGGGGTAGAGATGATTTTTTA		
GAM2185	C1orf24	3'	ATTTTTCAGTGGAGATGGGTTTT 54783		C
		CA	TGAAA CCCATCTCTACTAAAAAT		
			ACTTT GGGTAGAGGTGGTTTTTA		
			T		
GAM2185	C1QTNF6	3'	ATTTTTCAGTAGAGATGGGGTTT 49989		
		CA	TGAAACCCCATCTCTACTAAAAAT		
			ACTTTGGGGTAGAGATGATTTTTTA		
GAM2185	C20orf142	3'	ATTTTTCAGTAGAGATGGGGTTT 75272		
		C	GAAACCCCATCTCTACTAAAAAT		
			CTTTGGGGTAGAGATGATTTTTTA		
GAM2185	C21orf25	3'	TTTTCAGTAAATGGAGTCTCA 64308	A C	C
			TGA AC CCAT TCTACTAA		

			ACT TG GGTA AGATGATTT	
			C A A	
GAM2185	C6orf5	3'	ATTTT TAGTAGAGACAGGGTTT 31974	CA
	CA		TGAAACCC TCTCTACTAAAAAT	
			ACTTTGGG AGAGATGATTTT	
			AC	
GAM2185	C9orf9	3'	ATTTT TAGTAGAGACAGCGTTT 39010	CCCA
	CA		TGAAAC TCTCTACTAAAAAT	
			ACTTTG AGAGATGATTTT	
			CGAC	
GAM2185	C9orf9	3'	TTTTT TAGTAGAGACGGGGCTTC 39041	A A
	A		TGAA CCCC TCTCTACTAAAAA	
			ACTT GGGG AGAGATGATTTT	
			C C	
GAM2185	CARD6	3'	ATTTT TAGTAGAGGCAGGGTTT 51838	CA
	C		GAAACCC TCTCTACTAAAAAT	
			CTTTGGG GGAGATGATTTT	
			AC	
GAM2185	CCRN4L	3'	ATTTT TAGTAGAGACGGGGTTT 25067	A
	CA		TGAAACCCC TCTCTACTAAAAAT	
			ACTTTGGGG AGAGATGATTTT	
			C	
GAM2185	CDC14B	3'	ATTTT TAGTAGAGACAGGGTTT 54001	CA
	CA		TGAAACCC TCTCTACTAAAAAT	
			ACTTTGGG AGAGATGATTTT	
			AC	
GAM2185	CEACAM8	3'	ATTTT TAGTAGAGACGGGGTTT 10177	A
	CA		TGAAACCCC TCTCTACTAAAAAT	
			ACTTTGGGG AGAGATGATTTT	
			C	
GAM2185	CENPH	3'	TTT TAGTAGAGACGGGGTTTCA 43574	A
			TGAAACCCC TCTCTACTAAAA	
			ACTTTGGGG AGAGATGATTTT	
			C	
GAM2185	CHRA1	3'	TTTTT TAGTAGAGACGGGGTTCA 34340	A A
			TGAA CCCC TCTCTACTAAAAA	
			ACTT GGGG AGAGATGATTTT	
			_ C	
GAM2185	CHSY1	3'	ATTTT TAGTAGAGACGGGGTTT 30564	A
	CA		TGAAACCCC TCTCTACTAAAAAT	

			ACTTTGGGG AGAGATGATTTTTA	
			C	
GAM2185	CIP29	3'	ATTTTtagtagagacggggTTT 51371	A
	CA		TGAAACCCC TCTCTACTAAAAAT	
			ACTTTGGGG AGAGATGATTTTTA	
			C	
GAM2185	COLEC12	3'	ATTTTtagtagagaggggTTTC 48606	A
	A		TGAAACCCC TCTCTACTAAAAAT	
			ACTTTGGGG AGAGATGATTTTTA	
			—	
GAM2185	CPSF2	3'	ATTTTtagtagagacggggTTT 62263	A
	C		GAAACCCC TCTCTACTAAAAAT	
			CTTTGGGG AGAGATGATTTTTA	
			C	
GAM2185	CPSF2	3'	ATTTTGGtagagacagggTTT 62264	CA
	CA		TGAAACCC TCTCTACTAAAAAT	
			ACTTTGGG AGAGATGGTTTTTA	
			AC	
GAM2185	DBR1	3'	ATTTTtagtaatgacagggTTT 33061	CA TC
	CA		TGAAACCC TC TACTAAAAAT	
			ACTTTGGG AG ATGATTTTTA	
			AC TA	
GAM2185	DKFZp434A2417	3'	ATTTTtagtagagacggggTTT 66674	A
	C		GAAACCCC TCTCTACTAAAAAT	
			CTTTGGGG AGAGATGATTTTTA	
			C	
GAM2185	DKFZP434B044	3'	ATTTTtagtagagatggggTTT 49711	
	CA		TGAAACCCCATCTCTACTAAAAAT	
			ACTTTGGGGTAGAGATGATTTTTA	
GAM2185	DKFZP434C212	3'	ATTTTtagtagaaacggggTTT 69482	ATC
	CA		TGAAACCCC TCTACTAAAAAT	
			ACTTTGGGG AGATGATTTTTA	
			CAA	
GAM2185	DKFZP434D146	3'	ATTTTtagtagagacagggTTT 32132	CA
	CA		TGAAACCC TCTCTACTAAAAAT	
			ACTTTGGG AGAGATGATTTTTA	
			AC	
GAM2185	DKFZP434F0318	3'	ATTTTtagtagagacagggTTT 48745	CA
	C		GAAACCC TCTCTACTAAAAAT	

	CTTTGGG AGAGATGATTTT		
	AC		
GAM2185 DKFZp434F1719 3'	TTTTTAGTAGAGATGGGATTTC 51021	C	
	GAAA CCCATCTCTACTAAAA		
	CTTT GGGTAGAGATGATTTT		
	A		
GAM2185 DKFZp434J037 3'	ATTTTATAGTAGAGACAGGGTTT 48940	CA	
C	GAAACCC TCTCTACTAAAAAT		
	CTTTGGG AGAGATGATTTT		
	AC		
GAM2185 DKFZp547H025 3'	ATTTTATAGTAGAGATGAGGGTTT 39771	C	
CA	TGAAACC CATCTCTACTAAAAAT		
	ACTTTGG GTAGAGATGATTTT		
	A		
GAM2185 DKFZp564G092 5'	ATTTTATAGTAGAGACAGGATT 32154	C CA	
CA	TGAAA CC TCTCTACTAAAAAT		
	ACTTT GG AGAGATGATTTT		
	A AC		
GAM2185 DKFZp564O0423 3'	TTTTCATAGAGATGGGGTCTCA 93362	A	CT
	TGA ACCCCATCTCTA AAAA		
	ACT TGGGGTAGAGAT TTTT		
	C AC		
GAM2185 DKFZp564O0523 3'	AGTAGAGATGGGGTTTCA 50417	C	
	TGAAA CCCATCTCTACT		
	ACTTT GGGTAGAGATGA		
	T		
GAM2185 DKFZp761J139 5'	ATTTTATAGTAGAGATGGGGTTT 51102		
	AAACCCCATCTCTACTAAAAAT		
	TTTGGGGTAGAGATGATTTT		
GAM2185 DKFZp761N1114 3'	ATTTTATAGTAGAGACGGGATT 79775	C A	
CA	TGAAA CCC TCTCTACTAAAAAT		
	ACTTT GGG AGAGATGATTTT		
	A C		
GAM2185 DKFZp761O0113 5'	ATTTTGGTGGAGACGGGGTTT 37889	A	
C	GAAACCC TCTCTACTAAAAAT		
	CTTTGGGG AGAGGTGGTTT		
	C		
GAM2185 DKFZp762P2111 3'	ATTTTATAGTAGAGACAGGGTT 87625	CA	
CA	TGAAACCC TCTCTACTAAAAAT		

			ACTTTGGG AGAGATGATTTT	
			AC	
GAM2185	DSCR6	3'	ATTTTGTAGTAGAGACTCGGTTT 39058	CCA
	CA		TGAAACC TCTCTACTAAAAAT	
			ACTTTGG AGAGATGATTTT	
			CTC	
GAM2185	EREG	3'	ATTTTGTAGTAGAGGCGGGTTT 9302	AT
	CA		TGAAACCCC CTCTACTAAAAAT	
			ACTTTGGGG GAGATGATTTT	
			CG	
GAM2185	EVI5	3'	ATTTTGTAGTAGAGATGGGGTTT 20198	
	C		GAAACCCCATCTCTACTAAAAAT	
			CTTTGGGGTAGAGATGATTTT	
GAM2185	EVI5	3'	ATTTTGTAGTAGAGATGGGGTTT 20199	
	CA		TGAAACCCCATCTCTACTAAAAAT	
			ACTTTGGGGTAGAGATGATTTT	
GAM2185	FBP17	3'	ATTTTGTAGTAGAGACAGGGTTT 73147	CA
	CA		TGAAACCC TCTCTACTAAAAAT	
			ACTTTGGG AGAGATGATTTT	
			AC	
GAM2185	FER1L4	3'	ATTTTGTAGTAGAGACAGGGTTT 48113	CA
	CA		TGAAACCC TCTCTACTAAAAAT	
			ACTTTGGG AGAGATGATTTT	
			AC	
GAM2185	FKBP9	3'	ATTTTGGTAGAGACGGGGTTT 95713	A
	CA		TGAAACCCC TCTCTACTAAAAAT	
			ACTTTGGGG AGAGATGGTTTT	
			C	
GAM2185	FLJ00060	5'	ATTTTGTAGTAGAGATGGAATTT 61737	CC
	CA		TGAAA CCATCTCTACTAAAAAT	
			ACTTT GGTAGAGATGATTTT	
			AA	
GAM2185	FLJ10232	3'	ATTTTGTAGTAGAGGTGGGGTTT 36373	
	CA		TGAAACCCCATCTCTACTAAAAAT	
			ACTTTGGGGTGGAGATGATTTT	
GAM2185	FLJ10298	3'	ATTTTGTAGTAGAGACGGGGTTT 36454	A
	CA		TGAAACCCC TCTCTACTAAAAAT	

ACTTTGGGG AGAGATGATTTTTA
 C
 GAM2185 FLJ10346 5' ATTTTATAGTAGAGGCAGGGTTT 36521 CA
 CA TGAAACCC TCTCTACTAAAAAT
 ||||| |||||
 ACTTTGGG GGAGATGATTTTTA
 AC
 GAM2185 FLJ10352 3' TTTGGTGGAGATGAAATTTCA 50475 CCC
 TGAA CATCTCTACTAAA
 ||| |||||
 ACTTT GTAGAGGTGGTTT
 AAA
 GAM2185 FLJ10535 3' ATTTTATAGTAGAGATGGGGTTT 36739
 CA TGAAACCCCATCTCTACTAAAAAT
 |||||
 ACTTTGGGGTAGAGATGATTTTTA

 GAM2185 FLJ10560 3' ATTTTATAGTAGAGACGGGGTTT 36792 A
 CA TGAAACCC TCTCTACTAAAAAT
 ||||| |||||
 ACTTTGGGG AGAGATGATTTTTA
 C
 GAM2185 FLJ10713 3' ATTTTATAGTAGAGATGGGGTTT 36999
 CA TGAAACCCCATCTCTACTAAAAAT
 |||||
 ACTTTGGGGTAGAGATGATTTTTA

 GAM2185 FLJ10846 3' TTTTCAGTAGAGACAGGGTCTC 37295 A CA A
 A TGA ACCC TCTCTACT AAAA
 ||| ||| ||||| |||
 ACT TGGG AGAGATGA TTTT
 C AC C
 GAM2185 FLJ10901 3' ATTTTATAGTAGAGATGGGGTTT 37354
 CA TGAAACCCCATCTCTACTAAAAAT
 |||||
 ACTTTGGGGTAGAGATGATTTTTA

 GAM2185 FLJ10956 3' ATTTTATAGTGGAGACGGGGTTT 37462 A
 CA TGAAACCC TCTCTACTAAAAAT
 ||||| |||||
 ACTTTGGGG AGAGGTGATTTTTA
 C
 GAM2185 FLJ11800 3' TTTTATAGTAGAAATGAGGTCTC 47044 A C C
 GA ACC CAT TCTACTAAAAA
 || ||| |||||
 CT TGG GTA AGATGATTTT
 C A A
 GAM2185 FLJ12363 3' ATTTTATAGTGGGGATGGGGTTT 50629
 CA TGAAACCCCATCTCTACTAAAAAT
 |||||

ACTTTGGGGTAGGGGTGATTTTTA

GAM2185 FLJ12488 5' TTAGTAGACATGAGTTCA 49160 ACCC C
TGAA CAT TCTACTAA
|||| ||| |||||
ACTT GTA AGATGATT
GA__ C

GAM2185 FLJ12581 3' ATTTTATAGTAGACAGGGTTT 46330 CA
CA TGAAACCC TCTCTACTAAAAAT
||||| |||||
ACTTTGGG AGAGATGATTTT
AC

GAM2185 FLJ12649 3' TTTTAGTAGAGATAGGGTTT 45099 C
TGAAACCC ATCTCTACTAAAA
||||| |||||
ATTTTGGG TAGAGATGATTT
A

GAM2185 FLJ12668 3' ATTTTATAGTAGAGATGAGGTTT 47155 C
CA TGAAACC CATCTCTACTAAAAAT
||||| |||||
ACTTTGG GTAGAGATGATTTT
A

GAM2185 FLJ12687 3' ATTTTGTAGTAGACAGGGTTT 46746 CA
CA TGAAACCC TCTCTACTAAAAAT
||||| |||||
ACTTTGGG AGAGATGGTTT
AC

GAM2185 FLJ12687 3' TTTTTTTTTGGGATGGGGTCTC 46760 A TACT
A TGA ACCCCATCTC AAAAA
||| ||||| |||||
ACT TGGGGTAGGG TTTT
C TTTT

GAM2185 FLJ12787 3' TTTTAGTAGAGACGGGGTTTCA 50700 A
TGAAACCCC TCTCTACTAAAA
||||| |||||
ACTTTGGGG AGAGATGATTT
C

GAM2185 FLJ12876 3' ATTTTATAGTAGAGACGGGGTTT 43086 A
CA TGAAACCCC TCTCTACTAAAAAT
||||| |||||
ACTTTGGGG AGAGATGATTTT
C

GAM2185 FLJ12903 3' TTTTATAGTAGAGACAGGATTC 43081 C CA
GAAA CC TCTCTACTAAAA
||| || |||||
CTTT GG AGAGATGATTTT
A AC

GAM2185 FLJ12960 3' ATTTTATAGTAGAGATGGGGTTT 45291
CA TGAAACCCCATCTCTACTAAAAAT
|||||

ACTTTGGGGTAGAGATGATTTTTA

GAM2185 FLJ12973 3' ATTTTATAGTAGAGATGGGGTTT 46640
CA TGAAACCCCATCTCTACTAAAAAT
|||||
ACTTTGGGGTAGAGATGATTTTTA

GAM2185 FLJ12975 3' ATTTTATAGTAGAGACAGGGTTC 70185 A CA
CA TG AACCC TCTCTACTAAAAAT
|| ||| |||||
AC TTGGG AGAGATGATTTTTA
C AC

GAM2185 FLJ12975 3' ATTTTGGTAAAGACGGGGTTT 70186 A C
C GAAACCC TCT TACTAAAAAT
||||| ||| |||||
CTTTGGGG AGA ATGGTTTTTA
C A

GAM2185 FLJ13072 5' ATTTTATAGTAGAGACAGGGTTC 91387 CA
CA TGAAACCC TCTCTACTAAAAAT
||||| |||||
ACTTTGGG AGAGATGATTTTTA
AC

GAM2185 FLJ13114 3' ATTTTATAGTAGAGATGGAGTTT 44896 C
CA TGAAAC CCATCTCTACTAAAAAT
||||| |||||
ACTTTG GGTAGAGATGATTTTTA
A

GAM2185 FLJ13188 3' ATTTTATAGTAGAGACAGAGTTT 42188 CCCA
T GAAAC TCTCTACTAAAAAT
|||| |||||
TTTTG AGAGATGATTTTTA
AGAC

GAM2185 FLJ13197 3' ATTTTATAGTAGAGACAAGAGTT 45175 CCCA_
TC GAAAC TCTCTACTAAAAAT
|||| |||||
CTTTG AGAGATGATTTTTA
AGAAC

GAM2185 FLJ13952 3' ATTTTAAATAGAGACGGGTTTC 46005 CA C
A TGAAACCC TCTCTA TAAAAAT
||||| ||||| |||||
ACTTTGGG AGAGAT ATTTTTA
C_ A

GAM2185 FLJ14442 3' ATTTTAGCAGAGATGGGGTTT 52376 A
TA TGAAACCCCATCTCT CTAAAAAT
||||| |||||
ATTTGGGGTAGAGA GATTTTTA
C

GAM2185 FLJ14950 3' ATTTTATAGTAGAGACAGGGTTC 52782 CA
CA TGAAACCC TCTCTACTAAAAAT
||||| |||||

		ACTTTGGG AGAGATGATTTT		
		AC		
GAM2185	FLJ14957	3' TTTAGTAGAGACGGGGTTTCA	52830	A
		TGAAACCCC TCTCTACTAA		
		ACTTTGGG AGAGATGATT		
		C		
GAM2185	FLJ20034	3' TTTTAGTAGAGATGGGGTCTC	34859	A
		GA ACCCATCTCTACTAAAA		
		CT TGGGGTAGAGATGATTTT		
		C		
GAM2185	FLJ20045	3' ATTTTAGTAGAAATGGGGATT	34874	A C
	CA	TGAA CCCCAT TCTACTAAAA		
		ACTT GGGGTA AGATGATTTT		
		A A		
GAM2185	FLJ20079	3' ATTTTAGTAGAGACAGGGTTT	34967	CA
	C	GAAACCC TCTCTACTAAAA		
		CTTTGGG AGAGATGATTTT		
		AC		
GAM2185	FLJ20136	3' ATTTTAGTAGAGATGAGTTTC	35092	CC
	A	TGAAAC CATCTCTACTAAAA		
		ACTTTG GTAGAGATGATTTT		
		A_		
GAM2185	FLJ20344	3' ATTTTAGTAGAGACAGGGTTT	35477	CA
	CA	TGAAACCC TCTCTACTAAAA		
		ACTTTGGG AGAGATGATTTT		
		AC		
GAM2185	FLJ20507	3' ATTTTAGTAGAGACAGGGTTT	35732	CA
	CA	TGAAACCC TCTCTACTAAAA		
		ACTTTGGG AGAGATGATTTT		
		AC		
GAM2185	FLJ20507	3' ATTTTAGTAGAGACAGGGTTT	60840	CA
	CA	TGAAACCC TCTCTACTAAAA		
		ACTTTGGG AGAGATGATTTT		
		AC		
GAM2185	FLJ20700	3' ATTTTAGTAGAGACGGGTTTC	35997	CA
	A	TGAAACCC TCTCTACTAAAA		
		ACTTTGGG AGAGATGATTTT		
		C_		
GAM2185	FLJ20813	3' ATTTTAGTAGAGATGGGCTTT	36127	C
	CA	TGAA CCCATCTCTACTAAAA		

			ACTTT GGGTAGAGATGATTTT		
			C		
GAM2185	FLJ21302	3'	ATTTT TAGTAGAGACAGGGTTT 43505	CA	
		CA	TGAAACCC TCTCTACTAAAAAT		
			ACTTTGGG AGAGATGATTTT		
			AC		
GAM2185	FLJ21324	5'	ATTTT TAGTAGAGATGGGGTTT 92845		
		CA	TGAAACCCCATCTCTACTAAAAAT		
			ACTTTGGGGTAGAGATGATTTT		
GAM2185	FLJ21603	3'	ATTTT TAGTAGAGATGGGGTTT 45768		
		CA	TGAAACCCCATCTCTACTAAAAAT		
			ACTTTGGGGTAGAGATGATTTT		
GAM2185	FLJ22002	3'	ATTTT AATAGAGATGAGGTTT 46193	C	C
		C	GAAACC CATCTCTA TAAAAAT		
			CTTTGG GTAGAGAT ATTTT		
			A A		
GAM2185	FLJ22167	5'	ATTTT TAGTAGAGATGGGGTCT 44861	A	
		CA	TGA ACCCATCTCTACTAAAAAT		
			ACT TGGGGTAGAGATGATTTT		
			C		
GAM2185	FLJ22329	3'	ATTTT TAGTAGAGACGGGGTTT 45394	A	
		CA	TGAAACCC TCTCTACTAAAAAT		
			ACTTTGGG AGAGATGATTTT		
			C		
GAM2185	FLJ22529	3'	ATTTT TAGTAGAGACAGGGTTT 45940	CA	
		CA	TGAAACCC TCTCTACTAAAAAT		
			ACTTTGGG AGAGATGATTTT		
			AC		
GAM2185	FLJ22529	3'	TTTAGTAGAGACAGGGTTTCA 45959	CA	
			TGAAACCC TCTCTACTAAA		
			ACTTTGGG AGAGATGATT		
			AC		
GAM2185	FLJ22684	3'	ATTTT ACTAGAGACAGGGTTT 47466	CA	C
		CA	TGAAACCC TCTCTA TAAAAAT		
			ACTTTGGG AGAGAT ATTTT		
			AC C		
GAM2185	FLJ22794	3'	ATTTT TAGTAGAGACAGGGTTT 93239	CA	
		CA	TGAAACCC TCTCTACTAAAAAT		

		ACTTTGGG AGAGATGATTTT		
		AC		
GAM2185	FLJ22800	3' ATTTT	AGATGGGG	45991
			CCCCATCTCTACTAAAAAT	
			GGGGTAGAGATGATTTT	
GAM2185	FLJ22969	3' ATTTT	TGTAGACAGGGTTT	69198
		CA	TGAAACCC TCTCTAC AAAAAT	T
			ACTTTGGG AGAGATG TTTT	
			AC T	
GAM2185	FLJ23024	3' ATTTT	AGACGGGGTTT	46838
		CA	TGAAACCC TCTCTACTAAAAAT	A
			ACTTTGGGG AGAGATGATTTT	
			C	
GAM2185	FLJ23392	3' ATTTT	AGACAGGGTTT	45881
		CA	TGAAACCC TCTCTACTAAAAAT	CA
			ACTTTGGG AGAGATGATTTT	
			AC	
GAM2185	FLJ23392	3' ATTTT	AGACAGGGTTT	45882
		CA	TGAAACCC TCTCTACTAAAAAT	CA
			ACTTTGGG AGAGATGATTTT	
			AC	
GAM2185	FLJ23392	3' TTTT	AGACGGGGTTTC	45915
		A	TGAAACCC TCTCTACTAAAA	A
			ACTTTGGGG AGAGATGATTTT	
			C	
GAM2185	FLJ23519	3' TTTT	AGATGGGGTTTCA	50969
			TGAAACCCCATCTCTACTAAAA	
			ACTTTGGGGTAGAGATGATTTT	
GAM2185	FLJ23556	3' ATTTT	AGCAGACGGGGTTT	46429
		CA	TGAAACCC TCTCT CTAAAAAT	A A
			ACTTTGGGG AGAGA GATTTT	
			C C	
GAM2185	FLJ23556	3' ATTTT	AGACCGGGCTT	46430
		CA	TGAA CCC TCTCTACTAAAAAT	A CA
			ACTT GGG AGAGATGATTTT	
			C CC	
GAM2185	FLJ23563	3' ATTTT	AGACAGGGTT	68210
			AACCC TCTCTACTAAAAAT	CA

			TTGGG AGAGATGATTTT		
			AC		
GAM2185	FLJ25416	5'	TTTAGTGGAGATGGGGTTTCA	59462	
			TGAAACCCCATCTCTACTAAA		
			ACTTTGGGGTAGAGGTGATT		
GAM2185	FLJ30532	3'	ATTTTATAGTAGAGACAGGATT	59216	C CA
			CA		
			TGAA CC TCTCTACTAAAAAT		
			ACTTT GG AGAGATGATTTT		
			A AC		
GAM2185	FLJ31101	3'	ATTTTATAGTAAAGACGGGG	36157	A C
			CCCC TCT TACTAAAAAT		
			GGGG AGA ATGATTTT		
			C A		
GAM2185	FLJ31153	3'	ATTTTATAGTAGAGATGGGGTT	58744	
			CA		
			TGAAACCCCATCTCTACTAAAAAT		
			ACTTTGGGGTAGAGATGATTTT		
GAM2185	FLJ32865	3'	ATTTTATAGTAGAGACGGGGTT	58801	A
			C		
			GAAACCC TCTCTACTAAAAAT		
			CTTTGGGG AGAGATGATTTT		
			C		
GAM2185	FLJ32894	3'	AGTAGAGATGGGATTTC	58991	C
			TGAA CCCATCTCTACT		
			ACTTT GGGTAGAGATGA		
			A		
GAM2185	GGA2	3'	ATTTTATAGTAGAGACAGGATT	57652	C CA
			CA		
			TGAA CC TCTCTACTAAAAAT		
			ACTTT GG AGAGATGATTTT		
			A AC		
GAM2185	GGA2	3'	ATTTTATAGTAGAGACAGGATT	31158	C CA
			CA		
			TGAA CC TCTCTACTAAAAAT		
			ACTTT GG AGAGATGATTTT		
			A AC		
GAM2185	GMPPB	5'	ATTTTATAGTAGAGACAGGGTT	97437	CA
			CA		
			TGAAACCC TCTCTACTAAAAAT		
			ACTTTGGG AGAGATGATTTT		
			AC		
GAM2185	GNG4	3'	ATTTTATAGTAAAGACGGGGTT	16842	A C
			CA		
			TGAAACCC TCT TACTAAAAAT		

			ACTTTGGGG AGA ATGATTTT	
			C A	
GAM2185	GOLGA3	3'	ATTTTAGTAGCAATGGGGTTT 20883	CT
	CA		TGAAACCCCAT CTACTAAAAAT	
			ACTTTGGGGTA GATGATTTT	
			AC	
GAM2185	GREB1	3'	TTTTTAGTAGAGACGGGGTTTC 28584	A
	A		TGAAACCCC TCTCTACTAAAAA	
			ACTTTGGGG AGAGATGATTTT	
			C	
GAM2185	GREB1	3'	TTTTTAGTAGAGATGGGGTTTC 28585	
			GAAACCCCATCTCTACTAAAAA	
			CTTTGGGGTAGAGATGATTTT	
GAM2185	GRWD	3'	ATTTTAGTAGAGACGGGGTTT 49775	A
	CA		TGAAACCCC TCTCTACTAAAAAT	
			ACTTTGGGG AGAGATGATTTT	
			C	
GAM2185	GTF2E1	3'	ATTTTAGTAGAGGCAGGGTTT 19792	CA
	CA		TGAAACCC TCTCTACTAAAAAT	
			ACTTTGGG GGAGATGATTTT	
			AC	
GAM2185	GTPBG3	3'	ATTTTAGTAGAGACAAGGTTT 51890	CCA
	CA		TGAAACC TCTCTACTAAAAAT	
			ACTTTGG AGAGATGATTTT	
			AAC	
GAM2185	H2AV	3'	ATTTTAGTAGACGTGGGGTTT 57627	C
	CA		TGAAACCCCAT TCTACTAAAAAT	
			ACTTTGGGGTG AGATGATTTT	
			C	
GAM2185	HCA4	3'	TTTAGTAGAGACGGGGTTT 78048	A
			GAAACCCC TCTCTACTAAAA	
			TTTGGGG AGAGATGATTT	
			C	
GAM2185	HRH4	3'	ATTTTAGTAGAGATGAGGTTT 41528	C
	T		GAAACC CATCTCTACTAAAAAT	
			TTTGG GTAGAGATGATTTT	
			A	
GAM2185	HRH4	3'	TTTCTGTAGAGATGAAGTCTCA 41555	A CC TA
			TGA AC CATCTCTAC AAA	

			ACT TG GTAGAGATG TTT		
			C AA TC		
GAM2185	HSMPP8	3'	ATTTT TAGTAGAGATGGGGTTT 95126		
			AAACCCCATCTCTACTAAAAAT		
			TTTGGGGTAGAGATGATTTT		
GAM2185	HSNOV1	3'	ATTTT TAGTAGACATGGGGTTT 34429	C	
	CA		TGAAACCCCAT TCTACTAAAAAT		
			ACTTTGGGGTA AGATGATTTT		
			C		
GAM2185	HSPC065	3'	ATTTT TAGTAGAGATGGGGTTT 27143		
	CA		TGAAACCCCATCTCTACTAAAAAT		
			ACTTTGGGGTAGAGATGATTTT		
GAM2185	HSPC065	3'	ATTTT TAGTAGAGATGGGGTTT 27144		
	CA		TGAAACCCCATCTCTACTAAAAAT		
			ACTTTGGGGTAGAGATGATTTT		
GAM2185	HSPC232	3'	ATTTT TGTAGAGATGGGGTTC 33656	A	T
	A		TGAA CCCCATCTCTAC AAAAAT		
			ACTT GGGGTAGAGATG TTTT		
			T		
GAM2185	ICK	3'	ATTTT TAGTAGAGACGGGGTTT 30592	A	
	CA		TGAAACCC TCTCTACTAAAAAT		
			ACTTTGGGG AGAGATGATTTT		
			C		
GAM2185	JAM1	3'	TTTT TAGTAGAGACAGGGTTC 34251	CA	
	A		TGAAACCC TCTCTACTAAAA		
			ACTTTGGG AGAGATGATTTT		
			AC		
GAM2185	JAM1	3'	TTTT TAGTAGAGACAGGGTTC 58527	CA	
	A		TGAAACCC TCTCTACTAAAA		
			ACTTTGGG AGAGATGATTTT		
			AC		
GAM2185	JAM1	3'	TTTT TAGTAGAGACAGGGTTC 58554	CA	
	A		TGAAACCC TCTCTACTAAAA		
			ACTTTGGG AGAGATGATTTT		
			AC		
GAM2185	JAM1	3'	TTTT TAGTAGAGACAGGGTTC 58584	CA	
	A		TGAAACCC TCTCTACTAAAA		

		ACTTTGGG AGAGATGATTTT		
		AC		
GAM2185	JM11	3' TTAGTAGAGACAAGGTTTCA	54376	CCA
		TGAAACC TCTCTACTAA		
		ACTTTGG AGAGATGATT		
		AAC		
GAM2185	KIAA0022	3' ATTTTGGTAGAGACGGGGTTT	30276	A
	C	GAAACCCC TCTCTACTAAAAAT		
		CTTTGGGG AGAGATGGTTTTTA		
		C		
GAM2185	KIAA0063	3' ATTTTAGTAGAGATGGGGTTT	30252	
	C	GAAACCCCATCTCTACTAAAAAT		
		CTTTGGGGTAGAGATGATTTTTA		
GAM2185	KIAA0087	3' ATTTTAGTAGAGATGGGGTTT	29340	
	CA	TGAAACCCCATCTCTACTAAAAAT		
		ACTTTGGGGTAGAGATGATTTTTA		
GAM2185	KIAA0161	3' ATTTTCAGTAGAGACGGGGTTT	29192	A A
	CA	TGAAACCCC TCTCTACT AAAAT		
		ACTTTGGGG AGAGATGA TTTTA		
		C C		
GAM2185	KIAA0186	3' ATTTTAGTAGAGACAGAGTTT	41099	CCCA
	TA	TGAAAC TCTCTACTAAAAAT		
		ATTTTG AGAGATGATTTTTA		
		AGAC		
GAM2185	KIAA0186	3' ATTTTGTGGAGATGGGGTTT	41100	T
	CA	TGAAACCCCATCTCTAC AAAAAT		
		ACTTTGGGGTAGAGGTG TTTTTA		
		T		
GAM2185	KIAA0205	3' ATTTTAGTAGAGATGGGGTTT	30203	
	CA	TGAAACCCCATCTCTACTAAAAAT		
		ACTTTGGGGTAGAGATGATTTTTA		
GAM2185	KIAA0210	5' ATTTTAGTAGAGACGGGGTTT	29149	A
	CA	TGAAACCCC TCTCTACTAAAAAT		
		ACTTTGGGG AGAGATGATTTTTA		
		C		
GAM2185	KIAA0391	3' ATTTTAGTAGAGACGGGGTTT	28601	C A
	CA	TGAAA CCC TCTCTACTAAAAAT		

			ACTTT GGG AGAGATGATTTT			
			T C			
GAM2185	KIAA0426	3'	ATTTT	AGTAGACGGGGTTT	28920	A
	CA			TGAAACCCC TCTCTACTAAAAAT		
				ACTTTGGGG AGAGATGATTTT		
				C		
GAM2185	KIAA0459	3'	ATTTT	AGTAGACGGGGTTT	61646	A
	CA			TGAAACCCC TCTCTACTAAAAAT		
				ACTTTGGGG AGAGATGATTTT		
				C		
GAM2185	KIAA0469	3'	ATTTT	AGTAGACGGGATTT	29971	C A
	CA			TGAAA CCC TCTCTACTAAAAAT		
				ACTTT GGG AGAGATGATTTT		
				A C		
GAM2185	KIAA0472	5'	ATTTT	CAGTAGACGGGGTCT	72336	A A A
	C			GA ACCCC TCTCTACT AAAAT		
				CT TGGGG AGAGATGA TTTA		
				C C C		
GAM2185	KIAA0475	3'	ATTTT	AGTGGAGACAGGGTTT	30111	CA
	C			GAAACCC TCTCTACTAAAAAT		
				CTTTGGG AGAGGTGATTTT		
				AC		
GAM2185	KIAA0495	3'	ATTTT	AGTAGAGATGGGATTT	63260	C
	CA			TGAAA CCCATCTCTACTAAAAAT		
				ACTTT GGGTAGAGATGATTTT		
				A		
GAM2185	KIAA0513	3'	ATTTT	TGGTAGAGATGGGGTTT	29019	
	CA			TGAAACCCCATCTCTACTAAAAAT		
				ACTTTGGGGTAGAGATGGTTTTT		
GAM2185	KIAA0513	5'	TTTT	AGTAGAGACAGGGTTTC	29061	CA
				GAAACCC TCTCTACTAAAAA		
				CTTTGGG AGAGATGATTTT		
				AC		
GAM2185	KIAA0527	3'	ATTTT	AGTAGAGATGGAGTTT	97490	C
	CA			TGAAAC CCATCTCTACTAAAAAT		
				ACTTTG GGTAGAGATGATTTT		
				A		
GAM2185	KIAA0532	3'	ATTTT	TCTAGAGATGAGGTCT	71317	A C CT
	CA			TGA ACC CATCTCTA AAAAAT		

		ACT TGG GTAGAGAT TTTTTA	
		C A CT	
GAM2185 KIAA0544	3'	ATTTT TAGTAGAGAAGGGATTT 71458	C A
	CA	TGAAA CCC TCTCTACTAAAAAT	
		ACTTT GGG AGAGATGATTTTTA	
		A A	
GAM2185 KIAA0555	3'	ATTTT TAGTAGAGACAGGGTTT 29545	CA
	CA	TGAAACCC TCTCTACTAAAAAT	
		ACTTTGGG AGAGATGATTTTTA	
		AC	
GAM2185 KIAA0557	3'	ATTTT TAGTAGAGATGGGGTTT 78547	
	C	GAAACCCCATCTCTACTAAAAAT	
		CTTTGGGGTAGAGATGATTTTTA	
GAM2185 KIAA0561	3'	ATTTT TAGTACAGACGGGGTTT 66466	A C
	CA	TGAAACCC TCT TACTAAAAAT	
		ACTTTGGGG AGA ATGATTTTTA	
		C C	
GAM2185 KIAA0562	3'	ATTTT TAGTAGAGACGGGGTTT 28816	A
	CA	TGAAACCC TCTCTACTAAAAAT	
		ACTTTGGGG AGAGATGATTTTTA	
		C	
GAM2185 KIAA0563	5'	ATTTT TAGTAGAGCGGAGTTT 29869	C AT
	C	GAAAC CC CTCTACTAAAAAT	
		CTTTG GG GAGATGATTTTTA	
		A CG	
GAM2185 KIAA0594	3'	TTT TAGTAGAGATGGGGTTTCA 65523	
		TGAAACCCCATCTCTACTAAAA	
		ACTTTGGGGTAGAGATGATTTT	
GAM2185 KIAA0599	3'	ATTTT TAGTAGAGACGGGGTTT 77686	A
	C	GAAACCC TCTCTACTAAAAAT	
		CTTTGGGG AGAGATGATTTTTA	
		C	
GAM2185 KIAA0682	3'	ATTTT TCATAGAGACTGGGTTT 30016	CA CT
	CA	TGAAACCC TCTCTA AAAAAT	
		ACTTTGGG AGAGAT TTTTTA	
		TC AC	
GAM2185 KIAA0682	3'	ATTTT TGGTAGACGGGGTTTCA 30017	ATC
		TGAAACCC TCTACTAAAAAT	

			ACTTTGGGG AGATGGTTTTTA		
			C__		
GAM2185	KIAA0720	3'	ATTTTAAGTAGAGACGGCATT 62974	CC A	A
	CA		TGAAA CC TCTCTACT AAAAT		
			ACTTT GG AGAGATGA TTTTA		
			AC C A		
GAM2185	KIAA0737	3'	AGTAGAGATGGGGTCTCA 29801	A	
			TGA ACCCCATCTCTACT		
			ACT TGGGGTAGAGATGA		
			C		
GAM2185	KIAA0737	3'	ATTTTATAGTAGAGACAGGGTTT 29802	CA	
	CA		TGAAACCC TCTCTACTAAAAAT		
			ACTTTGGG AGAGATGATTTTTA		
			AC		
GAM2185	KIAA0798	3'	ATTTTGGTAGAGACGGGGTTT 28442	A	
	CA		TGAAACCCC TCTCTACTAAAAAT		
			ACTTTGGGG AGAGATGGTTTTTA		
			C		
GAM2185	KIAA0841	3'	TTTAGTAGGGACGGGGTTTCA 71909	A	
			TGAAACCCC TCTCTACTAAAA		
			ACTTTGGGG AGGGATGATTTT		
			C		
GAM2185	KIAA0861	3'	ATTTTATAGTAGAGACGGGGTTT 90342	A	
	C		GAAACCCC TCTCTACTAAAAAT		
			CTTTGGGG AGAGATGATTTTTA		
			C		
GAM2185	KIAA0889	3'	TTTTTGGTGGAGACGGGGTTTC 31793	A	
	A		TGAAACCCC TCTCTACTAAAA		
			ACTTTGGGG AGAGGTGGTTTTT		
			C		
GAM2185	KIAA0924	3'	ATTTTGGCAGAGATGGGGTTT 30355	A	
	CA		TGAAACCCCATCTCT CTAAAAAT		
			ACTTTGGGGTAGAGA GGTTTTTA		
			C		
GAM2185	KIAA0931	3'	TTTTTTTATAGAGACGGGGTTTC 68027	A	CT
	A		TGAAACCCC TCTCTA AAAAA		
			ACTTTGGGG AGAGAT TTTTT		
			C TT		
GAM2185	KIAA0961	3'	ATTTTATAGTGGAGATGGGGTTT 30392		
	CA		TGAAACCCCATCTCTACTAAAAAT		

ACTTTGGGGTAGAGGTGATTTT

GAM2185 KIAA1026 3' ATTTTGTAGAGATGAGATT 71732 CCC
CA TGAACATCTCTACTAAAAAT

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ACTTT GTAGAGATGATTTT
AGA

GAM2185 KIAA1028 3' ATTTTGTAGAGATGGGGTTT 93586
CA TGAAACCCCATCTCTACTAAAAAT

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ACTTTGGGGTAGAGATGATTTT

GAM2185 KIAA1040 3' ATTTTGTAGAGATGGGGTTT 72682
CA TGAAACCCCATCTCTACTAAAAAT

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ACTTTGGGGTAGAGATGATTTT

GAM2185 KIAA1041 3' TTTTAGTAGAGATGGGGTTTCA 30838
TGAAACCCCATCTCTACTAAAA

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ACTTTGGGGTAGAGATGATTT

GAM2185 KIAA1054 3' TTTTAGTAGAGGTGGGGTTTCA 68976
TGAAACCCCATCTCTACTAAAA

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ACTTTGGGGTGGAGATGATTT

GAM2185 KIAA1110 3' AGCAGAGATGGGGCTCA 62498 AA A
TGA CCCCATCTCTCT

||| ||||||| ||
ACT GGGGTAGAGA GA
C_ C

GAM2185 KIAA1115 5' ATTTTGGTAGAGACAGGGTTT 30687 CA
C GAAACCC TCTCTACTAAAAAT

||||| |||||||||
CTTTGGG AGAGATGGTTTTT
AC

GAM2185 KIAA1128 3' ATTTTGTAGAGATGAGATT 68997 CCC
CA TGAACATCTCTACTAAAAAT

||||| |||||||||
ACTTT GTAGAGATGATTTT
AGA

GAM2185 KIAA1143 3' ATTTTAAATAGAGACGGGGTTT 69229 A C
CA TGAAACCC TCTCTA TAAAAAT

||||| ||||| |||||
ACTTTGGGG AGAGAT ATTTT
C A

GAM2185 KIAA1161 5' TTTTAGTAGAGATGGGGTTT 82655
AAACCCCATCTCTACTAAAA

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TTTGGGGTAGAGATGATTTTT

GAM2185 KIAA1170 3' ATTTTATAGTAGAAACAGGGTTT 70410 CATC
CA TGAAACCC TCTACTAAAAAT

||||| |||||
ACTTTGGG AGATGATTTT
ACAA

GAM2185 KIAA1185 3' ATTTTATAGTAGACGGGGTTT 63284 A
CA TGAAACCCC TCTCTACTAAAAAT

||||| |||||
ACTTTGGGG AGAGATGATTTT
C

GAM2185 KIAA1193 3' ATTTTGTAGAGATGGGGTTT 68263 T
C GAAACCCCATCTCTAC AAAAAT

||||| |||||
CTTTGGGGTAGAGATG TTTT
T

GAM2185 KIAA1198 3' ATTTTATAGTAGACAGTGTTT 64004 CCCA
CA TGAAAC TCTCTACTAAAAAT

||||| |||||
ACTTTG AGAGATGATTTT
TGAC

GAM2185 KIAA1198 3' ATTTTATAGTAGACGGGGTTT 64005 A
CA TGAAACCCC TCTCTACTAAAAAT

||||| |||||
ACTTTGGGG AGAGATGATTTT
C

GAM2185 KIAA1198 3' ATTTTATAGTAGACGGGGTTT 64006 A
CA TGAAACCCC TCTCTACTAAAAAT

||||| |||||
ACTTTGGGG AGAGATGATTTT
C

GAM2185 KIAA1198 3' ATTTTATAGTAGAGATGGGGTTT 64007
CA TGAAACCCCATCTCTACTAAAAAT

||||| |||||
ACTTTGGGGTAGAGATGATTTT

GAM2185 KIAA1198 3' ATTTTATAGTGGAGACGGGGTTT 64008 A
CA TGAAACCCC TCTCTACTAAAAAT

||||| |||||
ACTTTGGGG AGAGGTGATTTT
C

GAM2185 KIAA1198 3' TTTTAGTAGAGATGGGGTTT 64076
GAAACCCCATCTCTACTAAAA

||||| |||||
CTTTGGGGTAGAGATGATTT

GAM2185 KIAA1200 3' ATTTTATAGTAGACGGGGTTT 63032 A
CA TGAAACCCC TCTCTACTAAAAAT

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ACTTTGGGG AGAGATGATTTTTA
 C
 GAM2185 KIAA1209 3' AGTAGAGGCGGGGTTTCA 61400 AT
 TGAAACCCC CTCTACT
 ||||| |||||
 ACTTTGGGG GAGATGA
 CG
 GAM2185 KIAA1210 3' ATTTTATAGTAGAGACGGGGTTT 98065 A
 CA TGAAACCCC TCTCTACTAAAAAT
 ||||| |||||
 ACTTTGGGG AGAGATGATTTTTA
 C
 GAM2185 KIAA1254 3' ATTTTATAGTAGAGATGGGGTTT 70556
 CA TGAAACCCCATCTCTACTAAAAAT
 ||||| |||||
 ACTTTGGGGTAGAGATGATTTTTA
 C
 GAM2185 KIAA1257 3' ATTTTGGTAGAGACGAGGTTT 63391 CCA
 C GAAACC TCTCTACTAAAAAT
 |||| |
 CTTTGG AGAGATGGTTTSTA
 AGC
 GAM2185 KIAA1257 3' ATTTTGTAGAGATGGGGTTT 63392 T
 CA TGAAACCCCATCTCTAC AAAAAT
 ||||| |||||
 ACTTTGGGGTAGAGATG TTTSTA
 T
 GAM2185 KIAA1287 3' ATTTTATAGTAAAGACGGGGGTT 78933 A_ C
 T AAACCCC TCT TACTAAAAAT
 ||||| || |||||
 TTTGGGG AGA ATGATTTTSTA
 GC A
 GAM2185 KIAA1320 5' ATTTTATAGTAGAGATGGGATTT 69833 C
 CA TGAAA CCCATCTCTACTAAAAAT
 |||| |
 ACTTT GGGTAGAGATGATTTTSTA
 A
 GAM2185 KIAA1328 3' AGCAGAGATGGGCTTTCA 62315 C A
 TGAAA CCCATCTCT CT
 |||| ||||| ||
 ACTTT GGGTAGAGA GA
 C C
 GAM2185 KIAA1373 3' ATTTTATAGTAGAGATGGGGTTT 71502
 TA TGAAACCCCATCTCTACTAAAAAT
 ||||| |||||
 ATTTTGGGGTAGAGATGATTTTSTA
 C
 GAM2185 KIAA1443 3' ATTTTATAGTAGAGACGGGGTTTC 64566 CA
 A TGAAACCC TCTCTACTAAAAAT
 ||||| |||||

		ACTTTGGG AGAGATGATTTT		
		C_		
GAM2185	KIAA1456	3' ATTTT	AGAGACGGGGTTT 67533	A A
	CA		TGAAACCCC TCTCT CTA	
			ACTTTGGG AGAGA GATTTT	
			C G	
GAM2185	KIAA1465	3' ATTTT	AGAGACGGGGTTT 61486	A
	CA		TGAAACCCC TCTCTACTA	
			ACTTTGGG AGAGATGATTTT	
			C	
GAM2185	KIAA1467	3' ATTTT	AGAGACGGGGTTT 72061	A
	CA		TGAAACCCC TCTCTACTA	
			ACTTTGGG AGAGATGATTTT	
			C	
GAM2185	KIAA1493	3' ATTTT	AGTAGAGATGGGGTTT 64835	
	CA		TGAAACCCCATCTCTACTA	
			ACTTTGGGTAGAGATGATTTT	
GAM2185	KIAA1497	5' ATTTT	AGTAGAGACAGGGTTT 68114	CA
	CA		TGAAACCC TCTCTACTA	
			ACTTTGG AGAGATGATTTT	
			AC	
GAM2185	KIAA1530	3' ATTTT	AGTAGAGACGGGATTT 68548	C A
	CA		TGAAA CCC TCTCTACTA	
			ACTTT GGG AGAGATGATTTT	
			A C	
GAM2185	KIAA1530	3' ATTTT	TGTAGAGATGAGGTCT 68549	A C T
	CA		TGA ACC CATCTCTAC A	
			ACT TGG GTAGAGATG TTTT	
			C A T	
GAM2185	KIAA1571	3' ATTTT	AGTAGAGTTGGGGTT 61612	AT_
	TCA		TGAAACCCC CTCTACTA	
			ACTTTGGG GAGATGATTTT	
			GTT	
GAM2185	KIAA1615	3' ATTTT	AGTAGAGACGGG 69269	A
			CCC TCTCTACTA	
			GGG AGAGATGATTTT	
			C	
GAM2185	KIAA1615	3' TTTT	AGTAGATATGGAGTTTCA 69294	C C
			TGAAAC CCAT TCTACTA	

		ACTTTG GGTA AGATGATTTT		
		A T		
GAM2185	KIAA1617	3' ATTTTGGTAGAGACAGGGTTT 93071	CA	
	CA	TGAAACCC TCTCTACTAAAAAT		
		ACTTTGGG AGAGATGGTTTTTA		
		AC		
GAM2185	KIAA1649	3' ATTTTGTAGAGATGAGGTTTC 51217	C	T
	A	TGAAACC CATCTCTAC AAAAAT		
		ACTTTGG GTAGAGATG TTTTTA		
		A _		
GAM2185	KIAA1655	3' ATTTTGTAGAGACAGGTTTC 67175	CCA	
	A	TGAAACC TCTCTACTAAAAAT		
		ACTTTGG AGAGATGATTTTTA		
		AC_		
GAM2185	KIAA1655	3' ATTTTGTAGAGACGAGGTGT 67176	A	CCA
	CA	TGA ACC TCTCTACTAAAAAT		
		ACT TGG AGAGATGATTTTTA		
		G AGC		
GAM2185	KIAA1668	3' ATTTTGTAGAGACGGGGTTT 67060	A	
	CA	TGAAACCCC TCTCTACTAAAAAT		
		ACTTTGGGG AGAGATGATTTTTA		
		C		
GAM2185	KIAA1674	3' TTTTGGTAAATATGGTTTCA 69353	CCATCTC	
		TGAAACC TACTAAAA		
		ACTTTGG ATGGTTT		
		TATAA_		
GAM2185	KIAA1712	3' ATTTTGTAGAGACAGGTTTC 68150	CA	T
	A	TGAAACCC TCTCTAC AAAAAT		
		ACTTTGGG AGAGATG TTTTTA		
		AC _		
GAM2185	KIAA1727	3' TTTTGTAGAGATGGGATCTCA 64768	AAC	T
		TGA CCCATCTCTAC AAAA		
		ACT GGGTAGAGATG TTTT		
		CTA _		
GAM2185	KIAA1737	3' ATTTTGTAGAAATGGGGTTT 67933	C	
	TA	TGAAACCCCAT TCTACTAAAAAT		
		ATTTTGGGGTA AGATGATTTTTA		
		A		
GAM2185	KIAA1784	3' TTTTAGTAGAAACGGGGTTTCA 65758	ATC	
		TGAAACCCC TCTACTAAAA		

		ACTTTGGGG AGATGATTTT		
		CAA		
GAM2185 KIAA1829	3'	ATTTTGTAGTAGAGACGGGGTTT 62633	A	
	CA	TGAAACCCC TCTCTACTAAAAAT		
		ACTTTGGGG AGAGATGATTTTTA		
		C		
GAM2185 KIAA1877	3'	ATTTTGTAGTAGAGACAGGGTTT 66741	CA	
	CA	TGAAACCC TCTCTACTAAAAAT		
		ACTTTGGG AGAGATGATTTTTA		
		AC		
GAM2185 KIAA1922	5'	ATTTTGGTGGAGATGGGGTTT 73988		
	C	GAAACCCCATCTCTACTAAAAAT		
		CTTTGGGGTAGAGGTGGTTTTTA		
GAM2185 KIAA1924	3'	ATTTTGTAGTAGAGATAGGCTTT 74041	C C	
	CA	TGAAA CC ATCTCTACTAAAAAT		
		ACTTT GG TAGAGATGATTTTTA		
		C A		
GAM2185 KIAA1924	3'	TTTTTGTAGAGATAGGGTTTCA 74066	C T	
		TGAAACCC ATCTCTAC AAAAA		
		ACTTTGGG TAGAGATG TTTT		
		A _		
GAM2185 KIAA1971	3'	TTTTTAGTAGAGACGAGGTTTC 74701	CCA	
	A	TGAAACC TCTCTACTAAAAA		
		ACTTTGG AGAGATGATTTT		
		AGC		
GAM2185 KIAA1975	5'	ATTTTGTAGTAGAGATGGGGTTT 74415		
	CA	TGAAACCCCATCTCTACTAAAAAT		
		ACTTTGGGGTAGAGATGATTTTTA		
GAM2185 KLK7	3'	ATTTTACTAGAGACAGGGTTT 18541	CA C	
	CA	TGAAACCC TCTCTA TAAAAAT		
		ACTTTGGG AGAGAT ATTTTTA		
		AC C		
GAM2185 KLK7	3'	ATTTTACTAGAGACAGGGTTT 58388	CA C	
	CA	TGAAACCC TCTCTA TAAAAAT		
		ACTTTGGG AGAGAT ATTTTTA		
		AC C		
GAM2185 LAMP3	3'	ATTTTATTATAGACGGGGTTT 60198	A C C	
	CA	TGAAACCCC TCT TA TAAAAAT		

			ACTTTGGGG AGA AT ATTTT		
			C T T		
GAM2185 LNIR	3'	TTTTTTT	AGAGATGGAGTCTC 48877	A C	CT
A			TGA AC CCATCTCTA AAAAA		
			ACT TG GGTAGAGAT TTTT		
			C A TT		
GAM2185 LY75	3'	ATTTT	AGTAGAGATGGGGTTT 11389		
CA			TGAAACCCCATCTCTACTAAAAAT		
			ACTTTGGGGTAGAGATGATTTT		
GAM2185 MAP-1	3'	AGTAGAGACGGGGTTTCA 42436		A	
			TGAAACCC TCTCTACT		
			ACTTTGGGG AGAGATGA		
			C		
GAM2185 MCLC	3'	TTTTTAGTAGAGATGGGGTTTC 31390			
A			TGAAACCCCATCTCTACTAAAA		
			ACTTTGGGGTAGAGATGATTTT		
GAM2185 MEF-2	3'	ATTTTAGTAGAGACTGGGGTTT 65018		CA	
CA			TGAAACCC TCTCTACTAAAAAT		
			ACTTTGGG AGAGATGATTTT		
			TC		
GAM2185 MGC10200	3'	TTTTTGAGAGATGGGGTTTCA 59654		A	
			TGAAACCCCATCTCT CTAAAAA		
			ACTTTGGGGTAGAGA GGTTTT		
GAM2185 MGC12466	3'	TTTTTATAGAGATGGGATCTC 79802	AAC	C	
			GA CCCATCTCTA TAAAA		
			CT GGTAGAGAT ATTTT		
			CTA		
GAM2185 MGC12518	3'	ATTTTAGTAGAGTGAGGGTTT 64774		_ T	
CA			TGAAACCC CA CTCTACTAAAAAT		
			ACTTTGGG GT GAGATGATTTT		
			A _		
GAM2185 MGC13204	3'	ATTTTAGTAGAGATGTGGTTT 49626		C	
C			GAAACC CATCTCTACTAAAAAT		
			CTTTGG GTAGAGATGATTTT		
			T		
GAM2185 MGC1842	3'	ATTTTAGTAGAGACCAGGCTT 66249	A CCA		
C			GAA CC TCTCTACTAAAAAT		

		CTT GG AGAGATGATTTT		
		C ACC		
GAM2185	MGC20235	3' TTTTGGTAGAGACAGAGTCTC	59566	A CCCA
	A	TGA AC TCTCTACTAAAA		
		ACT TG AGAGATGGTTTT		
		C AGAC		
GAM2185	MGC21675	3' ATTTTGTAGTAGAGATGGGGTTT	54587	
	CA	TGAAACCCCATCTCTACTAAAAAT		
		ACTTTGGGGTAGAGATGATTTT		
GAM2185	MGC2474	3' ATTTTGTAGTAGAGATGGGGTTT	43951	
	CA	TGAAACCCCATCTCTACTAAAAAT		
		ACTTTGGGGTAGAGATGATTTT		
GAM2185	MGC2474	3' TTTTGCAGAGATGGGGTT	43974	AC
		AACCCCATCTCT TAAAAA		
		TTGGGGTAGAGA GTTTT		
		C_		
GAM2185	MGC2477	5' ATTTTGTAGTAGAGAAAGAGTTT	44291	CCCA
	CA	TGAAAC TCTCTACTAAAAAT		
		ACTTTG AGAGATGATTTT		
		AGAA		
GAM2185	MGC2603	3' ATTTTGTAGTAGAGACGAGGTTT	44071	CCA
	CA	TGAAACC TCTCTACTAAAAAT		
		ACTTTGG AGAGATGATTTT		
		AGC		
GAM2185	MGC29898	3' ATTTGCTTGTAGAGATGGGATC	59583	AAC TAA_
	TCA	TGA CCCATCTCTAC AAAT		
		ACT GGGTAGAGATG TTTA		
		CTA TTCG		
GAM2185	MGC3113	3' TTTTGTAGAGACAGGGTTTC	44065	CA T
		GAAACCC TCTCTAC AAAA		
		CTTTGGG AGAGATG TTTT		
		AC _		
GAM2185	MGC4638	3' TTAGTAGAAACGAGGTTTCA	49745	CCATC
		TGAAACC TCTACTAA		
		ACTTTGG AGATGATT		
		AGCAA		
GAM2185	MGC4766	5' AGTAGAGACGGGGTTTCA	49555	A
		TGAAACCC TCTCTACT		

		ACTTTGGGG AGAGATGA			
		C			
GAM2185	MGC5149	3'	ATTTTTCAGCAGAGATGGGGTTT 72755	A	
	CA		TGAAACCCCATCTCT CTA AAAAT		
			ACTTTGGGGTAGAGA GATTTT		
		C			
GAM2185	MKRN4	3'	ATTTTTCAGTAAACGGGGTTT 48453	ATC	
	CA		TGAAACCC TCTACTAAAAAT		
			ACTTTGGGG AGATGATTTT		
		CAA			
GAM2185	MLZE	5'	ATTTTCAGTAGAGACAGGGTTT 49448	CA	A
	CA		TGAAACCC TCTCTACT AAAAT		
			ACTTTGGG AGAGATGA TTTT		
		AC C			
GAM2185	moblak	3'	TTTTCAGTAGAGACAAGATTTC 56417	CCCCA	
			TGAAA TCTCTACTAAAA		
			ACTTT AGAGATGATTT		
		AGAAC			
GAM2185	moblak	3'	TTTTCAGTAGAGACAGGGTTTC 56418	CA	
			TGAAACCC TCTCTACTAAAA		
			ACTTTGGG AGAGATGATTT		
		AC			
GAM2185	MOCS3	3'	ATTTTTCAGTACAGAGGGGGTTT 27927	A	C
	CA		TGAAACCC TCT TACTAAAAAT		
			ACTTTGGGG AGA ATGATTTT		
		G C			
GAM2185	MRPL20	3'	ATTTTTCAGTAGAGACCGGGTTC 36200	A	CA
	CG		TG AACCC TCTCTACTAAAAAT		
			GC TTGGG AGAGATGATTTT		
		C CC			
GAM2185	MRPL44	3'	ATTTTTCAGTAGAGATGGGGTTT 43592		
	CA		TGAAACCCCATCTCTACTAAAAAT		
			ACTTTGGGGTAGAGATGGTTT		
GAM2185	MRPS27	3'	ATTTTTCAGTAGAGATGGGGTTT 31323		
	CA		TGAAACCCCATCTCTACTAAAAAT		
			ACTTTGGGGTAGAGATGATTTT		
GAM2185	MtFMT	3'	ATTTTTCAGTAGAGATGGGGTTT 58331		
	CA		TGAAACCCCATCTCTACTAAAAAT		

ACTTTGGGGTAGAGATGATTTTTA

GAM2185 MYO5C	3'	ATTTT	AGTGGAGACAGGTTTC	38713	CCA
A			TGAAACC TCTCTACTAAAAAT		
			ACTTTGG AGAGGTGATTTTTA		
			AC_		
GAM2185 NDP52	3'	TTTTT	AGTAGAGACAGGGTTTC	20681	CA
A			TGAAACCC TCTCTACTAAAAA		
			ACTTTGGG AGAGATGATTTTT		
			AC		
GAM2185 NDUFC2	3'	TTTTT	AGTAGAGACGGGGTTTC	17040	A
A			TGAAACCCC TCTCTACTAAAAA		
			ACTTTGGGG AGAGATGATTTTT		
			C		
GAM2185 NINJ2	3'	ATTTT	AGTAGAGACGGGGTTT	33718	A
C			GAAACCCC TCTCTACTAAAAAT		
			CTTTGGGG AGAGATGATTTTTA		
			C		
GAM2185 Nup43	3'	TTTT	AGTGGAGATGGGGTTTCA	45361	
			TGAAACCCCATCTCTACTAAAA		
			ACTTTGGGGTAGAGGTGATTTT		
GAM2185 NXN	3'	ATTTT	AGTAGAGATGGGGTTT	42668	
CA			TGAAACCCCATCTCTACTAAAAAT		
			ACTTTGGGGTAGAGATGATTTTTA		
GAM2185 OCT11	3'	ATTTT	AGTAGAGATGGGGTTT	27584	
CA			TGAAACCCCATCTCTACTAAAAAT		
			ACTTTGGGGTAGAGATGATTTTTA		
GAM2185 OR51E2	3'	TTTTT	AGTAGAGACAGAGTTTC	48523	CCCA
A			TGAAAC TCTCTACTAAAAA		
			ACTTTG AGAGATGATTTTT		
			AGAC		
GAM2185 OSBPL2	3'	ATTTT	AGTAGACACGGGTTTT	58479	C ATC
CA			TGAAA CCC TCTACTAAAAAT		
			ACTTT GGG AGATGATTTTTA		
			T CAC		
GAM2185 OSBPL2	3'	ATTTT	AGTAGACACGGGTTTT	29896	C ATC
CA			TGAAA CCC TCTACTAAAAAT		

		ACTTT GGG AGATGATTTT	
		T CAC	
GAM2185 PELI1	5'	ATTTT TAGTAGAGACCAGGTTT 40627	CCA
		AAACC TCTCTACTAAAAAT	
		TTTGG AGAGATGATTTT	
		ACC	
GAM2185 PELI1	5'	ATTTT TAGTAGAGACGGGGTTT 40628	A
CA		TGAAACCCC TCTCTACTAAAAAT	
		ACTTTGGGG AGAGATGATTTT	
		C	
GAM2185 PELI1	5'	TTAGTGAGATGGGGTTTCA 40664	
		TGAAACCCCATCTCTACTAA	
		ACTTTGGGGTAGAGGTGATT	
GAM2185 PIP3-E	3'	ATTTT TAGTAGAGACGGGGTT 67346	A_
T		AAACCCC TCTCTACTAAAAAT	
		TTTGGGG AGAGATGATTTT	
		CC	
GAM2185 PRO0365	5'	ATTTT CAGTAGAGACGGGGTTT 26978	A A
CA		TGAAACCCC TCTCTACT AAAAT	
		ACTTTGGGG AGAGATGA TTTT	
		C C	
GAM2185 PRO1843	5'	ATTTT TAGTTTCAAGGTTTCA 38139	CCATCTCT
		TGAAACC ACTAAAAAT	
		ACTTTGG TGATTTT	
		AACTT__	
GAM2185 PRO1992	3'	ATTTT TAGTAGAGATGGGGTTT 26896	
TA		TGAAACCCCATCTCTACTAAAAAT	
		ATTTTGGGGTAGAGATGATTTT	
GAM2185 PRO2955	3'	ATTTT TAGTAGAGACAGGGTTT 38234	CA
TA		TGAAACCC TCTCTACTAAAAAT	
		ATTTTGGG AGAGATGATTTT	
		AC	
GAM2185 PSPH	3'	ATTTT TAGTAGAGACGGGGTTT 17130	A
		AAACCCC TCTCTACTAAAAAT	
		TTTGGGG AGAGATGATTTT	
		C	
GAM2185 PSTPIP2	3'	ATTTT TAGTAGAGACAGGGTTT 44650	CA
TA		TGAAACCC TCTCTACTAAAAAT	

			ATTTTGGG AGAGATGATTTT		
			AC		
GAM2185	PTPRR	5'	GGAGAGGTGGAATTTCA 12628	CC	A
			TGAAA CCATCTCT CT		
			ACTTT GGTGGAGA GG		
			AA _		
GAM2185	RAB21	3'	ATTTTGTAGTAGAGACGGGGTTT 31084		A
	CA		TGAAACCCC TCTCTACTAAAAAT		
			ACTTTGGGG AGAGATGATTTT		
			C		
GAM2185	RAB33B	3'	ATTTTGTAGTATAGATGGGGTTT 49320		C
	CA		TGAAACCCCATCT TACTAAAAAT		
			ACTTTGGGGTAGA ATGATTTT		
			T		
GAM2185	RAI	5'	ATTTTGTAGTAGAGACAGGGTT 22850	CA	
			AACCC TCTCTACTAAAAAT		
			TTGGG AGAGATGATTTT		
			AC		
GAM2185	RAP140	3'	ATTTTGTAGTAGAGACAGGGTTT 31509	CA	
	CA		TGAAACCC TCTCTACTAAAAAT		
			ACTTTGGG AGAGATGATTTT		
			AC		
GAM2185	RASSF2	3'	TTTGTAGTAGAGGTGGGGTTTCA 29117		
			TGAAACCCCATCTCTACTAAAA		
			ACTTTGGGGTGGAGATGATTTT		
GAM2185	RES4-25	3'	ATTTTGTAGTAGAGACGGGGTTT 65261	A	
	C		GAAACCCC TCTCTACTAAAAAT		
			CTTTGGGG AGAGATGATTTT		
			C		
GAM2185	RNF8	3'	TTTCTGTAGAGACAGGGTTTCA 15580	CA	TA
			TGAAACCC TCTCTAC AAA		
			ACTTTGGG AGAGATG TTT		
			AC TC		
GAM2185	RNO2	5'	TTTTGTAGTGGAGATGGGGTGTC 53945	A	
	A		TGA ACCCATCTCTACTAAAA		
			ACT TGGGGTAGAGGTGATTTT		
			G		
GAM2185	SC4MOL	3'	ATTTTGTAGAGATGGGGTTTC 23102		T
			GAAACCCCATCTCTAC AAAAT		

CTTTGGGGTAGAGATG TTTTTA

GAM2185 SCAMP-4 3' ATTTTACAGATGGGGTTT 55339 C
CA TGAAACCCCATCT TACTAAAAAT
||||||| |||||
ACTTTGGGGTAGA ATGATTTTTC
C

GAM2185 SCYA16 3' ATTTTGGTAGAGACGGGATTC 17167 A CA
GAA CCC TCTCTACTAAAAAT
||| ||| |||||
CTT GGG AGAGATGGTTTTTA
A C_

GAM2185 SCYA22 3' ATTTTAGTAGAGACAGGTTTC 92580 CCA
A TGAAACC TCTCTACTAAAAAT
||||| |||||
ACTTTGG AGAGATGATTTTTC
AC_

GAM2185 SCYA22 3' ATTTTAGTAGAGACGAGGCTT 92581 A CCA
CA TGAA CC TCTCTACTAAAAAT
||| ||| |||||
ACTT GG AGAGATGATTTTTC
C AGC

GAM2185 SCYA28 3' TTTTGTACAGACGGGGTTTC 39547 A C C
A TGAAACCCC TCT TA TAAAAA
||||| ||| |||
ACTTTGGGG AGA AT GTTTTTC
C C T

GAM2185 SERF1B 3' TTAGTAGAGATGGGGTTTCA 43710
TGAAACCCCATCTCTACTAA
|||||||
ACTTTGGGGTAGAGATGATT

GAM2185 SFXN2 3' TTTTAGTGGAGACGGGGTTTCA 74388 A
TGAAACCCC TCTCTACTAAAA
||||| |||||
ACTTTGGGG AGAGGTGATTTTTC
C

GAM2185 SIRPB1 3' ATTTTACAGATGGGGTTT 21357
C GAAACCCCATCTCTACTAAAAAT
|||||||
CTTTGGGGTAGAGATGATTTTTC

GAM2185 SLC12A8 3' ATTTTACTGGAGACAGGGTTT 45233 CA C
CA TGAAACCC TCTCTA TAAAAAT
||||| ||| |||||
ACTTTGGG AGAGGT ATTTTTC
AC C

GAM2185 SLC16A4 3' ATTTTAGTAGAGGCGGGTTT 17447 AT
CA TGAAACCCC CTCTACTAAAAAT
||||| |||||

			ACTTTGGGG GAGATGATTTT	
			CG	
GAM2185	SLC19A3	3'	ATTTTGTAGTGGAGATGGGGTTT 48237	
	CA		TGAAACCCCATCTCTACTAAAAAT	
			ACTTTGGGGTAGAGGTGATTTT	
GAM2185	SLC2A10	3'	ATTTTGTAGCAGAGATGGGGTTT 48544	A
	CA		TGAAACCCCATCTCT CTAAAAAT	
			ACTTTGGGGTAGAGA GATTTT	
			C	
GAM2185	SLC6A14	3'	ATTTTGTAGTAGAGGCGAAGTTT 24304	CCCA
	C		GAAAC TCTCTACTAAAAAT	
			CTTTG GGAGATGATTTT	
			AAGC	
GAM2185	SREC	3'	TTTAATAGAGACAGGGTTTCA 14912	CA C
			TGAAACCC TCTCTA TAAA	
			ACTTTGGG AGAGAT ATTT	
			AC A	
GAM2185	SS-56	3'	ATTTTGTAGTAGAGACGGAGTTT 60345	C A
	CA		TGAAAC CC TCTCTACTAAAAAT	
			ACTTTG GG AGAGATGATTTT	
			A C	
GAM2185	STAF65(gamma)	3'	ATTTTGTAGTAGAGATGAGGTTT 30063	C
	CA		TGAAACC CATCTCTACTAAAAAT	
			ACTTTGG GTAGAGATGATTTT	
			A	
GAM2185	STARD7	3'	AGTAGAGATGGAGTTTCA 58368	C
			TGAAAC CCATCTCTACT	
			ACTTTG GGTAGAGATGA	
			A	
GAM2185	STARD7	3'	AGTAGAGATGGAGTTTCA 39735	C
			TGAAAC CCATCTCTACT	
			ACTTTG GGTAGAGATGA	
			A	
GAM2185	SULT1C2	3'	TTAGTAGAGACGAGGTTTCA 22724	CCA
			TGAAACC TCTCTACTAA	
			ACTTTGG AGAGATGATT	
			AGC	
GAM2185	SUN1	3'	ATTTTGTAGTAGAGACAGGGTTT 47909	CA
	CA		TGAAACCC TCTCTACTAAAAAT	

			ACTTTGGG AGAGATGATTTT	
			AC	
GAM2185	SYT13	3'	TTTGTAGAGATGGGGTTTCA 95113	
			TGAAACCCCATCTCTACTAAA	
			ACTTTGGGGTAGAGATGATTTT	
GAM2185	TADA3L	3'	ATTTTGTAGAGACGGGGTTT 56805	A
	CA		TGAAACCC TCTCTACTAAAAAT	
			ACTTTGGGG AGAGATGATTTT	
			C	
GAM2185	TBCC	3'	ATTTTGTAGAGACGGGGTTT 13601	A
	C		GAAACCC TCTCTACTAAAAAT	
			CTTTGGGG AGAGATGATTTT	
			C	
GAM2185	TCL6	3'	ATTTTGTAGAGACAGGGTTT 27754	CA
	CA		TGAAACCC TCTCTACTAAAAAT	
			ACTTTGGG AGAGATGATTTT	
			AC	
GAM2185	TCL6	5'	ATTTTGTAGAGACGAGGTTT 27755	CCA
	CA		TGAAACC TCTCTACTAAAAAT	
			ACTTTGG AGAGATGATTTT	
			AGC	
GAM2185	TCL6	3'	ATTTTGTAGAGACAGGGTTT 25902	CA
	CA		TGAAACCC TCTCTACTAAAAAT	
			ACTTTGGG AGAGATGATTTT	
			AC	
GAM2185	TCL6	5'	ATTTTGTAGAGACGAGGTTT 25903	CCA
	CA		TGAAACC TCTCTACTAAAAAT	
			ACTTTGG AGAGATGATTTT	
			AGC	
GAM2185	TCL6	5'	ATTTTGTAGAGACGAGGTTT 40463	CCA
	CA		TGAAACC TCTCTACTAAAAAT	
			ACTTTGG AGAGATGATTTT	
			AGC	
GAM2185	TCL6	5'	ATTTTGTAGAGACGAGGTTT 40507	CCA
	CA		TGAAACC TCTCTACTAAAAAT	
			ACTTTGG AGAGATGATTTT	
			AGC	
GAM2185	TERA	3'	TTTGTAGAGACGGGGTTTCA 41428	A
			TGAAACCC TCTCTACTAAA	

			ACTTTGGGG AGAGATGATTTT		
			C		
GAM2185	TGIF2	3'	TTTTAGTAGAGACGGGGTTTCA 41762	A	
			TGAAACCCC TCTCTACTAAAA		
			ACTTTGGGG AGAGATGATTTT		
			C		
GAM2185	THEA	3'	ATTTTtagTGGAGATGGGGTTT 66874		
	CA		TGAAACCCCATCTCTACTAAAAAT		
			ACTTTGGGGTAGAGGTGATTTTTA		
GAM2185	TRIM16	3'	ATTTTtagTAGAGATGGGGTTT 22366		
	CA		TGAAACCCCATCTCTACTAAAAAT		
			ACTTTGGGGTAGAGATGATTTTTA		
GAM2185	TRIM5	3'	ATTTTCAGTAGAGACGGGGTTT 53465	A	A
	C		GAAACCCC TCTCTACT AAAAT		
			CTTTGGGG AGAGATGA TTTTA		
			C C		
GAM2185	TRIM5	3'	ATTTTCAGTAGAGACGGGGTTT 53538	A	A
	C		GAAACCCC TCTCTACT AAAAT		
			CTTTGGGG AGAGATGA TTTTA		
			C C		
GAM2185	TRIM6	3'	ATTTTtATAGAGATAGGGTTTC 55174	C	C
	A		TGAAACCC ATCTCTA TAAAAAT		
			ACTTTGGG TAGAGAT ATTTTTA		
			A _		
GAM2185	TU12B1-TY	3'	ATTTCTAGTAGAGATGGGGTTT 33830		A
	C		GAAACCCCATCTCTACTA AAAT		
			CTTTGGGGTAGAGATGAT TTTA		
			C		
GAM2185	TU12B1-TY	3'	ATTTTtagTAGAGACGGGGTTT 33831	A	
	CA		TGAAACCCC TCTCTACTAAAAAT		
			ACTTTGGGG AGAGATGATTTTTA		
			C		
GAM2185	TU12B1-TY	3'	TTTtAATAGAGATGGGGTTTCA 33870		C
			TGAAACCCCATCTCTA TAAAA		
			ACTTTGGGGTAGAGAT ATTTT		
			A		
GAM2185	TUCAN	3'	ATTTTtagTAGAGACAGAGTTT 30966	CCCA	
	T		GAAAC TCTCTACTAAAAAT		

		TTTTG AGAGATGATTTTA	
		AGAC	
GAM2185 TUCAN	3'	ATTTTATAGTAGAGACAGGGTTT 30967	CA
CA		TGAAACCC TCTCTACTAAAAAT	
		ACTTTGGG AGAGATGATTTTA	
		AC	
GAM2185 TUSP	3'	ATTTTAAATAGAGATGGGGTTT 40016	C
T		GAAACCCCATCTCTA TAAAAAT	
		TTTTGGGGTAGAGAT ATTTTA	
		A	
GAM2185 TXI1	5'	GGTAGGACGGGGTCTCA 37972	A A T
		TGA ACCCC TC CTACT	
		ACT TGGGG AG GATGG	
		C C _	
GAM2185 UBF-fl	3'	ATTTCTATTAGCAATGGGGTTT 52619	CT C A
CA		TGAAACCCCAT CTA TA AAAT	
		ACTTTGGGGTA GAT AT TTTA	
		AC T C	
GAM2185 VDU1	3'	TTTTAGTAGAGATGGGGTTTCA 31133	
		TGAAACCCCATCTCTACTAAAA	
		ACTTTGGGGTAGAGATGATTTT	
GAM2185 VPS33A	3'	ATTTTATAGTAGCCATGGTGTTT 43610	C CT
CA		TGAAAC CCAT CTACTAAAAAT	
		ACTTTG GGTA GATGATTTTTA	
		T CC	
GAM2185 WBSCR23	3'	ATTTTATAGTAGAGACGGGGTTT 47416	A
CA		TGAAACCC TCTCTACTAAAAAT	
		ACTTTGGGG AGAGATGATTTTA	
		C	
GAM2185 ZNF221	3'	ATTTTATAGTAAAAACGGGGTTT 26266	ATCTC
CA		TGAAACCC TACTAAAAAT	
		ACTTTGGGG ATGATTTTTA	
		CAAAA	
GAM2185 ZNF228	3'	TTTAATGAGAGGGGTTTCA 60601	A TAC
		TGAAACCC TCTC TAAA	
		ACTTTGGGG AGAG ATTT	
		_ TA_	
GAM2185 ZNF338	3'	TTTAATAGAGGCGGGTTTCA 42264	AT C
		TGAAACCC CTCTA TAAA	

		ACTTTGGGG GAGAT ATTT	
		CG A	
GAM2185	ZTL1 3'	ATTTTATAGTAGAGACGGGGCTT 44138	A A
	CA	TGAA CCCC TCTCTACTAAAAAT	
		ACTT GGGG AGAGATGATTTTTA	
		C C	
GAM2185	LOC112687 3'	ATTTTATAGTAGAGATGGGGTTT 73220	
		AAACCCCATCTCTACTAAAAAT	
		TTTGGGGTAGAGATGATTTTTA	
GAM2185	LOC112817 3'	ATTTTATAGCAGAGATGGGGTTT 57317	A
	CA	TGAAACCCCATCTCT CTAAAAAT	
		ACTTTGGGGTAGAGA GATTTTTA	
		C	
GAM2185	LOC115219 5'	ATTTTGGTAGAGACGGGGTTT 73689	A
	CA	TGAAACCCC TCTCTACTAAAAAT	
		ACTTTGGGG AGAGATGGTTTTTA	
		C	
GAM2185	LOC115648 3'	TTTTAGTGGAGACGGGGTTTC 60035	A
	A	TGAAACCCC TCTCTACTAAAAA	
		ACTTTGGGG AGAGGTGATTTTT	
		C	
GAM2185	LOC119392 3'	ATTTTATAGTAGAGACTGGGTTT 59811	CA
	CA	TGAAACCC TCTCTACTAAAAAT	
		ACTTTGGG AGAGATGATTTTTA	
		TC	
GAM2185	LOC120114 3'	ATTTTATAGTAGAGATGGGGTTT 76041	
	CA	TGAAACCCCATCTCTACTAAAAAT	
		ACTTTGGGGTAGAGATGATTTTTA	
GAM2185	LOC120224 5'	TTTAGTAGAGACAGGGTTTCA 57899	CA
		TGAAACCC TCTCTACTAAA	
		ACTTTGGG AGAGATGATTT	
		AC	
GAM2185	LOC120939 3'	ATTTTATAGTGGAGAGGGGGTTT 76756	A
	CA	TGAAACCCC TCTCTACTAAAAAT	
		ACTTTGGGG AGAGGTGATTTTTA	
		G	
GAM2185	LOC124216 3'	ATTTTATAGTAGAGATGGTTTCA 74734	CC
		TGAAACC ATCTCTACTAAAAAT	

ACTTTGG TAGAGATGATTTT

GAM2185 LOC126661 3' ATTTT TAGTAGAGATGGGGTTT 75051
CA TGAAACCCCATCTCTACTAAAAAT
|||||
ACTTTGGGGTAGAGATGATTTT

GAM2185 LOC126669 3' ATTTT TAGTAGAGATGGGGTTT 75925
C GAAACCCCATCTCTACTAAAAAT
|||||
CTTTGGGGTAGAGATGATTTT

GAM2185 LOC128077 3' ATTTT TAGTAGAGACAGGGTTT 75205 CA
CA TGAAACCC TCTCTACTAAAAAT
|||||
ACTTTGGG AGAGATGATTTT
AC

GAM2185 LOC128077 3' ATTTT TAGTAGAGACGGGGTTT 75206 A
CA TGAAACCC TCTCTACTAAAAAT
|||||
ACTTTGGG AGAGATGATTTT
C

GAM2185 LOC128989 3' TTTT TAGTAGAGACGGGGTTT 75328 A
A TGAAACCC TCTCTACTAAAA
|||||
ACTTTGGG AGAGATGATTTT
C

GAM2185 LOC129880 3' TTTT GGTGGAGACGGGGTTT 75410 A
GAAACCC TCTCTACTAAAA
|||||
CTTTGGG AGAGGTGGTTTT
C

GAM2185 LOC130813 3' ATTTT TAGTAGAGATGGGGTTT 76266
C GAAACCCCATCTCTACTAAAAAT
|||||
CTTTGGGGTAGAGATGATTTT

GAM2185 LOC130813 3' TTTT ATGTAGAGATAGGGTCTC 76284 A C _
A TGA ACCC ATCTCTAC TAAAA
|||
ACT TGGG TAGAGATG ATTTT
C A T

GAM2185 LOC132241 5' ATTTT TAGTAGAGAGTGGGGTTT 75554 CA
CA TGAAACCC TCTCTACTAAAAAT
|||||
ACTTTGGG AGAGATGATTTT
TG

GAM2185 LOC132625 3' ATTTT TAGTAGAGATGGGGTTT 76435
CA TGAAACCCCATCTCTACTAAAAAT
|||||

ACTTTGGGGTAGAGATGATTTTTA

GAM2185 LOC133686 3' ATTTTATAGTAGATATGGGGATT 75612 A C
CA TGAA CCCCAT TCTACTAAAAAT

||||| ||||| |||||
ACTT GGGGTA AGATGATTTTTA
A T

GAM2185 LOC135154 3' ATTTTATAGTAAAGACAAGGTTT 75722 CCA C
CA TGAAACC TCT TACTAAAAAT

||||| ||| |||||
ACTTTGG AGA ATGATTTTTA
AAC A

GAM2185 LOC135293 3' ATTTTATAGTAGAGACGGCATT 76678 CC A
CA TGAAA CC TCTCTACTAAAAAT

||||| || |||||
ACTTT GG AGAGATGATTTTTA
AC C

GAM2185 LOC135818 3' TTTTATAGTAGAGATGGGGTTTC 75757
GAAACCCCATCTCTACTAAAAA

||||| |||||
CTTTGGGGTAGAGATGATTTT

GAM2185 LOC143187 3' TTTTGTAGAGATGGAGTTTCA 59769 C T
TGAAAC CCATCTCTAC AAAA

||||| ||||| |||||
ACTTTG GGTAGAGATG TTTT
A _

GAM2185 LOC143916 3' TTTTATAGTAGAGATGGGGTTTCA 77153
TGAAACCCCATCTCTACTAAAA

||||| |||||
ACTTTGGGGTAGAGATGATTTT

GAM2185 LOC144317 5' ATTTTATAGTAGAGACTGGGGTT 77289 _
TC GAAACCCCA TCTCTACTAAAAAT

||||| |||||
CTTTGGGGT AGAGATGATTTTTA
C

GAM2185 LOC144524 5' ATTTTATAGTAGAAACCGGGTTT 84049 CATC
CA TGAAACCC TCTACTAAAAAT

||||| |||||
ACTTTGGG AGATGATTTTTA
CCAA

GAM2185 LOC144667 3' TTTTGTAGAGATGGGGTCTC 84094 A T
GA ACCCATCTCTAC AAAA

|| ||||| |||||
CT TGGGGTAGAGATG TTTT
C _

GAM2185 LOC144742 5' ATTTTATAGTAGAGACAGGTTT 77454 C CA
CA TGAAA CC TCTCTACTAAAAAT

||||| || |||||

		ACTTT GG AGAGATGATTTT	
		T AC	
GAM2185	LOC144871 3'	ATTTT TAGTAGAAATGGGGTTT 84120	C
	CA	TGAAACCCCAT TCTACTAAAAAT	
		ACTTTGGGGTA AGATGATTTT	
		A	
GAM2185	LOC145009 3'	ATTTT TAGTAGACAGGGTTT 60969	CA
	CA	TGAAACCC TCTCTACTAAAAAT	
		ACTTTGGG AGAGATGATTTT	
		AC	
GAM2185	LOC145268 5'	ATTTT TAGTAGACAGAGTTT 77572	CCCA
	CA	TGAAAC TCTCTACTAAAAAT	
		ACTTTG AGAGATGATTTT	
		AGAC	
GAM2185	LOC145622 3'	ATTTT TAGTAGAGAGGGGGTTT 77804	A
	CA	TGAAACCCCATCTCTACTAAAAAT	
		ACTTTGGGG AGAGATGATTTT	
		G	
GAM2185	LOC146050 3'	ATTTT TAGTAGAGATGGGGTTT 78103	
	C	GAAACCCCATCTCTACTAAAAAT	
		CTTTGGGGTAGAGATGATTTT	
GAM2185	LOC146050 3'	ATTTT TAGTAGAGATGGGGTTT 78104	
	CA	TGAAACCCCATCTCTACTAAAAAT	
		ACTTTGGGGTAGAGATGATTTT	
GAM2185	LOC146229 3'	ATTTT TAATAGACGGGGTTT 78261	A C
	CA	TGAAACCCCATCTCTA TAAAAAT	
		ACTTTGGGG AGAGAT ATTTT	
		C A	
GAM2185	LOC146229 3'	ATTTT TAGTAGACGGGGTTT 78262	A
	TA	TGAAACCCCATCTCTACTAAAAAT	
		ATTTTGGGG AGAGATGATTTT	
		C	
GAM2185	LOC146229 3'	ATTTT TAGTAGTGACGGGGTTT 78263	A T
	CA	TGAAACCCCATCTCTACTAAAAAT	
		ACTTTGGGG AG GATGATTTT	
		C T	
GAM2185	LOC146346 5'	ATTTT TAGTAGACAGGATTT 78387	C CA
	CA	TGAA CC TCTCTACTAAAAAT	

		ACTTT GG AGAGATGATTTT		
		A AC		
GAM2185	LOC146346 5'	ATTTT TAGTAGAGACGGGGTTT 78388	A	
	CA	TGAAACCCC TCTCTACTAAAAAT		
		ACTTTGGGG AGAGATGATTTT		
		C		
GAM2185	LOC146429 5'	ATTTT TAGTAAAGACAGGGTTT 84661	CA	C
	CA	TGAAACCC TCT TACTAAAAAT		
		ACTTTGGG AGA ATGATTTT		
		AC A		
GAM2185	LOC146603 5'	ATTTT CAGTAGAGACGGGGTTT 78590	A	A
	CA	TGAAACCCC TCTCTACT AAAAT		
		ACTTTGGGG AGAGATGA TTTT		
		C C		
GAM2185	LOC146784 5'	TTTTT TAGTAGAGATGGGGTTTC 78722		
	A	TGAAACCCCATCTCTACTAAAA		
		ACTTTGGGGTAGAGATGATTTT		
GAM2185	LOC146839 3'	TTTTT TAGTAGAGACGGGGTTTC 84858	A	
	A	TGAAACCCC TCTCTACTAAAA		
		ACTTTGGGG AGAGATGATTTT		
		C		
GAM2185	LOC146894 3'	TTTTT AGTAGAGATGGGGTTTCA 59870		
		TGAAACCCCATCTCTACTAAAA		
		ACTTTGGGGTAGAGATGATTTT		
GAM2185	LOC146901 3'	ATTTT TAACAGAGACGGGGTTT 84891	A	AC
	CA	TGAAACCCC TCTCT TAAAAAT		
		ACTTTGGGG AGAGA ATTTT		
		C CA		
GAM2185	LOC146909 3'	ATTTT TAGTAGAGATGGGGTTT 78761		
	CA	TGAAACCCCATCTCTACTAAAAAT		
		ACTTTGGGGTAGAGATGATTTT		
GAM2185	LOC146952 5'	ATTTT TAGTAGAGACAGGGTTT 84923	CA	
	CA	TGAAACCC TCTCTACTAAAAAT		
		ACTTTGGG AGAGATGATTTT		
		AC		
GAM2185	LOC147054 3'	ATTTT TAGTAGGGATGGGGTTT 85002		
	C	GAAACCCCATCTCTACTAAAAAT		

CTTTGGGGTAGGGATGATTTTTA

GAM2185 LOC147071 5' ATTTTATAGTAGAGACGGAGTTT 73352 C A
CA TGAAAC CC TCTCTACTAAAAAT

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ACTTTG GG AGAGATGATTTTTA
A C

GAM2185 LOC147080 5' ATTTTCAGTAGAGACAAGGTTT 85027 CCA A
CA TGAAACC TCTCTACT AAAAT

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ACTTTGG AGAGATGA TTTTA
AAC C

GAM2185 LOC147166 3' ATTTTATAGTAGAGATGGGGTTT 78883
CA TGAAACCCCATCTCTACTAAAAAT

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ACTTTGGGGTAGAGATGATTTTTA

GAM2185 LOC147276 3' ATTTTATAGTAGAGACGGGGCTT 78952 A A
C GAA CCCC TCTCTACTAAAAAT

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CTT GGGG AGAGATGATTTTTA
C C

GAM2185 LOC147429 3' ATTTTATAGTAGAGATGGGGTTT 78993
CA TGAAACCCCATCTCTACTAAAAAT

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ACTTTGGGGTAGAGATGATTTTTA

GAM2185 LOC147694 3' ATTTTATAGTAGAGACGGGGTTT 79090 A
CA TGAAACCCC TCTCTACTAAAAAT

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ACTTTGGGG AGAGATGATTTTTA
C

GAM2185 LOC147817 3' ATTTTATAGTAGAGACAGGGCTT 79168 A CA
CA TGAA CCC TCTCTACTAAAAAT

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ACTT GGG AGAGATGATTTTTA
C AC

GAM2185 LOC147817 3' ATTTTATAGTAGAGACGGAGTTT 79169 C A
CA TGAAAC CC TCTCTACTAAAAAT

||||| || |||||||||
ACTTTG GG AGAGATGATTTTTA
A C

GAM2185 LOC147841 3' TTTGGTAGAGATGGAGTTTCA 79234 C
TGAAAC CCATCTCTACTAAA

||||| |||||||||
ACTTTG GGTAGAGATGGTTT
A

GAM2185 LOC147990 3' ATTTTACTAGAGACGGGGTTT 85212 A C
CA TGAAACCCC TCTCTA TAAAAAT

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		ACTTTGGGG AGAGAT ATTTTTA		
		C C		
GAM2185	LOC148137 3'	ATTTTGTAGAGACGGTGTTT 59089	C A	
	CA	TGAAAC CC TCTCTACTAAAAAT		
		ACTTTG GG AGAGATGATTTTTA		
		T C		
GAM2185	LOC148147 3'	ATTTTGTAGAGATGAGGTTTC 79391	C T	
	A	TGAAACC CATCTCTAC AAAAAT		
		ACTTTGG GTAGAGATG TTTTTA		
		A _		
GAM2185	LOC148189 5'	ATTTTGTAGAGACGGGGTTT 79446	A	
	CA	TGAAACCCC TCTCTACTAAAAAT		
		ACTTTGGGG AGAGATGATTTTTA		
		C		
GAM2185	LOC148195 3'	ATTTTCAGTAGAGACAGGTTTC 85270	CCA A	
	A	TGAAACC TCTCTACT AAAAT		
		ACTTTGG AGAGATGA TTTTA		
		AC_ C		
GAM2185	LOC148195 5'	TTTTTAGTGACGGGGTCTCA 85301	A A TCT	
		TGA ACCCC TC ACTAAAAA		
		ACT TGGGG AG TGATTTT		
		C C _		
GAM2185	LOC148709 3'	ATTTTGTAGAGACAGGGTTT 79688	CA	
	C	GAAACCC TCTCTACTAAAAAT		
		CTTTGGG AGAGATGATTTTTA		
		AC		
GAM2185	LOC148887 5'	ATTTTGTAGAGACAGGGTTT 85392	CA	
	CA	TGAAACCC TCTCTACTAAAAAT		
		ACTTTGGG AGAGATGATTTTTA		
		AC		
GAM2185	LOC149171 5'	ATTTTGTAGAGATGGGGTTT 79963		
	C	GAAACCCCATCTCTACTAAAAAT		
		CTTTGGGGTAGAGATGATTTTTA		
GAM2185	LOC149421 3'	ATTTTGTAGAGACGGGGTTT 80140	A	
	CA	TGAAACCCC TCTCTACTAAAAAT		
		ACTTTGGGG AGAGATGATTTTTA		
		C		
GAM2185	LOC149478 3'	ATTTTGTAGAGACGGGGTT 80164	A_	
	TCA	TGAAACCCC TCTCTACTAAAAAT		

		ACTTTGGGG AGAGATGATTTT	
		GC	
GAM2185	LOC149506 3'	ATTTT	A CA_
	CA	TGAA CCC TCTCTACTAAAAAT	
		ACTT GGG AGAGATGATTTT	
		_ AGC	
GAM2185	LOC149577 3'	ATTTT	C CA
	C	GAAA CC TCTCTACTAAAAAT	
		CTTT GG AGAGATGATTTT	
		C AC	
GAM2185	LOC149577 3'	TTTAGTAGAGATGGGGTTT 85685	
		GAAACCCCATCTCTACTAAA	
		TTTTGGGGTAGAGATGATT	
GAM2185	LOC149692 3'	ATTTT	CA
	CA	TGAAACCC TCTCTACTAAAAAT	
		ACTTTGGG AGAGATGATTTT	
		AC	
GAM2185	LOC149692 3'	TTTAGTAGAGACGAGTTTCA 85749	CCCCA
		TGAAA TCTCTACTAAAA	
		ACTTT AGAGATGATTT	
		TGAGC	
GAM2185	LOC149703 5'	ATTTT	A
	T	GAAACCC TCTCTACTAAAAAT	
		TTTTGGGG AGAGATGATTTT	
		C	
GAM2185	LOC149711 3'	ATTTT	
	TA	TGAAACCCCATCTCTACTAAAAAT	
		ATTTTGGGGTAGAGATGATTTT	
GAM2185	LOC149821 5'	ATTTT	C A C
	CA	TGAAAC CC TCT TACTAAAAAT	
		ACTTTG GG AGA ATGATTTT	
		A C C	
GAM2185	LOC150166 5'	TTTTGTAGAAATGGGGTTTCA 86048	C T
		TGAAACCCCAT TCTAC AAAA	
		ACTTTGGGGTA AGATG TTTT	
		A _	
GAM2185	LOC150282 5'	ATTTT	C
	CA	TGAAAC CCATCTCTACTAAAAAT	

		ACTTTG GGTAGAGATGATTTTTA	
		C	
GAM2185	LOC150397 3'	ATTTTATAGTAGAGACGCAGTTT 80654	CCCA
	CA	TGAAAC TCTCTACTAAAAAT	
		ACTTTG AGAGATGATTTTTA	
		ACGC	
GAM2185	LOC150630 5'	ATTTTATAGTAGAGAGGGGGTTT 86291	A
	CA	TGAAACCCC TCTCTACTAAAAAT	
		ACTTTGGGG AGAGATGATTTTTA	
		G	
GAM2185	LOC150960 3'	AGTAGAGATGGGGTCTCA 80866	A
		TGA ACCCCATCTCTACT	
		ACT TGGGGTAGAGATGA	
		C	
GAM2185	LOC151050 5'	ATTTTATAGTAGAGACAGAGTTT 80916	CCCA
	CA	TGAAAC TCTCTACTAAAAAT	
		ACTTTG AGAGATGATTTTTA	
		AGAC	
GAM2185	LOC151057 3'	TTAGTAGAGACGGGGTTTCA 86401	A
		TGAAACCCC TCTCTACTAA	
		ACTTTGGGG AGAGATGATT	
		C	
GAM2185	LOC151201 3'	ATTTTATAGTAGAGACGGGGTTT 86467	A
	CA	TGAAACCCC TCTCTACTAAAAAT	
		ACTTTGGGG AGAGATGATTTTTA	
		C	
GAM2185	LOC151475 5'	ATTTTATAGTAGAGACGAGGTTT 86584	CCA
	CA	TGAAACC TCTCTACTAAAAAT	
		ACTTTGG AGAGATGATTTTTA	
		AGC	
GAM2185	LOC151701 3'	ATTTTATAGTAGAGACGGGGTTT 86667	A
	CA	TGAAACCCC TCTCTACTAAAAAT	
		ACTTTGGGG AGAGATGATTTTTA	
		C	
GAM2185	LOC151826 3'	TTTTATAGTAGAGACAGGGTTTC 81191	CA
	A	TGAAACCC TCTCTACTAAAAA	
		ACTTTGGG AGAGATGATTTT	
		AC	
GAM2185	LOC151979 5'	TTTTATAGTAGAGACGGGGTTTC 81258	A
	A	TGAAACCCC TCTCTACTAAAAA	

		ACTTTGGGG AGAGATGATTTT	
		C	
GAM2185	LOC152137 3'	ATTTTGTAGTAAAGAGCGGGTTT 81308	CA C
	CA	TGAAACCC TCT TACTAAAAAT	
		ACTTTGGG AGA ATGATTTT	
		CG A	
GAM2185	LOC152220 3'	ATTTTGTAGTAGAGACAGAGTCT 86760	A CCCA
	CA	TGA AC TCTCTACTAAAAAT	
		ACT TG AGAGATGATTTT	
		C AGAC	
GAM2185	LOC152300 3'	TTTTTAGTAGAGACAGGGTTTC 81392	CA
	A	TGAAACCC TCTCTACTAAAA	
		ACTTTGGG AGAGATGATTTT	
		AC	
GAM2185	LOC152343 3'	ATTTTGTAGTAGAGAGGGGGTGT 81420	A A
	CA	TGA ACCCC TCTCTACTAAAAAT	
		ACT TGGGG AGAGATGATTTT	
		G G	
GAM2185	LOC152445 3'	ATTTTGAATAGAGACAGGGTTT 86935	CA C
	CA	TGAAACCC TCTCTA TAAAAAT	
		ACTTTGGG AGAGAT ATTTT	
		AC A	
GAM2185	LOC152620 3'	ATTTTGTAGTAGAGGCGGGGTTA 60705	A AT
	CA	TG AACCC CTCTACTAAAAAT	
		AC TTGGGG GAGATGATTTT	
		A CG	
GAM2185	LOC152719 5'	ATTTTGTAGTTGAGACGGGGTTT 87016	A T
	CA	TGAAACCC TCTC ACTAAAAAT	
		ACTTTGGGG AGAG TGATTTT	
		C T	
GAM2185	LOC152794 5'	ATTTTGTGGAGATGGGGTTT 81555	T
	CA	TGAAACCCCATCTCTAC AAAAAT	
		ACTTTGGGGTAGAGGTG TTTT	
		T	
GAM2185	LOC152851 3'	TTTTTAGTAGAGACAGGATTTC 81601	C CA
	A	TGAAA CC TCTCTACTAAAA	
		ACTTT GG AGAGATGATTTT	
		A AC	
GAM2185	LOC153077 3'	ATTTTGTAGTAGAGATGGGGCTT 87112	A
	CA	TGAA CCCCATCTCTACTAAAAAT	

	ACTT GGGGTAGAGATGATTTTTA	
	C	
GAM2185 LOC153606 5'	TTT TAGTAGAGATAGGGTTTCA 87262	C
	TGAAACCC ATCTCTACTAAAA	
	ACTTTGGG TAGAGATGATTTT	
	A	
GAM2185 LOC153688 3'	ATTTT TAGTAGAGACAGGGTTT 87295	CA
CA	TGAAACCC TCTCTACTAAAAAT	
	ACTTTGGG AGAGATGATTTTTA	
	AC	
GAM2185 LOC153688 3'	ATTTT TGGATAGAGACAGGATT 87296	C CA _
TC	GAAA CC TCTCTA CTA AAAAT	
	CTTT GG AGAGAT GGTTTTTA	
	A AC A	
GAM2185 LOC153811 3'	ATTTT TAGTAGAAACGAGGTTT 81824	CCATC
CA	TGAAACC TCTACTAAAAAT	
	ACTTTGG AGATGATTTTTA	
	AGCAA	
GAM2185 LOC153883 5'	AGTAGAAATGGGGTTTTA 81886	C
	TGAAACCCCAT TCTACT	
	ATTTTGGGGTA AGATGA	
	A	
GAM2185 LOC154282 5'	TTTTT TAGTAGAGATGGTGTTTC 87416	C
A	TGAAAC CCATCTCTACTAAAAA	
	ACTTTG GGTAGAGATGATTTT	
	T	
GAM2185 LOC154877 5'	ATTTT TAGTAGAGATGGGGTTT 87528	
T	GAAACCCCATCTCTACTAAAAAT	
	TTTTGGGGTAGAGATGATTTTTA	
GAM2185 LOC154877 3'	ATTTT TAGTAGAGTCGGGGTTT 87529	AT
CA	TGAAACCC CTCTACTAAAAAT	
	ACTTTGGGG GAGATGATTTTTA	
	CT	
GAM2185 LOC154877 3'	TTTTT GGTGGAGACAGGGTCTC 87587	A CA
A	TGA ACCC TCTCTACTAAAAA	
	ACT TGGG AGAGGTGGTTTTT	
	C AC	
GAM2185 LOC154930 3'	TTTTT TAGTAGAGACAGGATTTT 82098	C CA
A	TGAAA CC TCTCTACTAAAAA	

		ATTTT GG AGAGATGATTTT		
		A AC		
GAM2185	LOC157247 5'	ATTTTGGTAGAGACGGGGTTT 82286	A	
	CA	TGAAACCCC TCTCTACTAAAAAT		
		ACTTTGGGG AGAGATGGTTTTTA		
		C		
GAM2185	LOC157506 3'	ATTTTGTAGTAGAGACGGGGTTT 82363	A	
	CA	TGAAACCCC TCTCTACTAAAAAT		
		ACTTTGGGG AGAGATGATTTTTA		
		C		
GAM2185	LOC157623 3'	ATTTTGCAGAGATGGAGTTTC 82411	C	AC
	A	TGAAAC CCATCTCT TAAAAAT		
		ACTTTG GGTAGAGA GTTTTTA		
		A C_		
GAM2185	LOC157798 5'	ATTTTGTAGTAGAGACGGGGTTT 87854	A	
	CA	TGAAACCCC TCTCTACTAAAAAT		
		ACTTTGGGG AGAGATGATTTTTA		
		C		
GAM2185	LOC157858 5'	ATTTTACTAGAGACAGGGTTT 87883	CA	C
	CA	TGAAACCC TCTCTA TAAAAAT		
		ACTTTGGG AGAGAT ATTTTTA		
		AC C		
GAM2185	LOC158014 5'	ATTTTGTAGTAGAGACGGAGTTT 82554	C	A
	CA	TGAAAC CC TCTCTACTAAAAAT		
		ACTTTG GG AGAGATGATTTTTA		
		A C		
GAM2185	LOC158014 5'	ATTTTTTTTTTGAGATGGGGTCT 82555	A	TACT
	C	GA ACCCCATCTC AAAAAAT		
		CT TGGGGTAGAG TTTTTA		
		C TTTT		
GAM2185	LOC158310 5'	ATTTTAAATAGAGACAGGGTTT 88076	CA	C
	CA	TGAAACCC TCTCTA TAAAAAT		
		ACTTTGGG AGAGAT ATTTTTA		
		AC A		
GAM2185	LOC158402 5'	ATTTTGTAGTAGAGAGGGGGGTT 88142	A_	
	TCA	TGAAACCCC TCTCTACTAAAAAT		
		ACTTTGGGG AGAGATGATTTTTA		
		GG		
GAM2185	LOC158476 3'	ATTTTGTAGAGACAGGGTTTC 88185	CA	T
	A	TGAAACCC TCTCTAC AAAAAAT		

		ACTTTGGG AGAGATG TTTT		
		AC _		
GAM2185	LOC158476 3'	TTTGGTAGAGACAGGGTTTCA	88211	CA
		TGAAACCC TCTCTACTAAA		
		ACTTTGGG AGAGATGGTTT		
		AC		
GAM2185	LOC158549 5'	ATTTTGTAGAGATAGGGGTT	88216	_
	TCA	TGAAACCCC ATCTCTACTAAAAAT		
		ACTTTGGG TAGAGATGATTTT		
		A		
GAM2185	LOC158668 3'	ATTTTGTAGAGGTGGGGTTT	69894	
	CA	TGAAACCCCATCTCTACTAAAAAT		
		ACTTTGGG GTGAGATGATTTT		
GAM2185	LOC158865 5'	ATTTTGTAGAGATGGGG	88305	
		CCCCATCTCTACTAAAAAT		
		GGGGTAGAGATGATTTT		
GAM2185	LOC160646 3'	ATTTTGTAGAGATGGGGCTT	83107	A
	CA	TGAA CCCCATCTCTACTAAAAAT		
		ACTT GGGGTAGAGATGATTTT		
		C		
GAM2185	LOC161829 3'	ATTTTGTAGAGATGGGGTTT	83184	
	CA	TGAAACCCCATCTCTACTAAAAAT		
		ACTTTGGG GTAGAGATGATTTT		
GAM2185	LOC162427 3'	ATTTTGTAGAGAAATGGGGTTT	83224	C
	CA	TGAAACCCCAT TCTACTAAAAAT		
		ACTTTGGG GTAGATGATTTT		
		A		
GAM2185	LOC169286 5'	TTTATGGAACAGATGGGGCTCG	83615	AA CTA A
		TGA CCCCATCT CTA AAA		
		GCT GGGGTAGA GGT TTT		
		C_ CAA A		
GAM2185	LOC169611 3'	ATTTTGTAGAGACAGGATTT	83636	C CA
	CA	TGAAA CC TCTCTACTAAAAAT		
		ACTTT GG AGAGATGATTTT		
		A AC		
GAM2185	LOC169611 3'	ATTTTGTAGAGACAGGGGTT	83637	A_
	TCA	TGAAACCCC TCTCTACTAAAAAT		

	ACTTTGGGG AGAGATGATTTT	
	AC	
GAM2185 LOC170082 5'	ATTTTGTAGAGATGGGGTTT 83440	
CA	TGAAACCCCATCTCTACTAAAAAT	
	ACTTTGGGGTAGAGATGATTTT	
GAM2185 LOC196047 5'	TTAGTAGAGCCAGGGTTTCA 91169	CAT
	TGAAACCC CTCTACTAA	
	ACTTTGGG GAGATGATT	
	ACC	
GAM2185 LOC196264 3'	TTTTTAGTAGAGACGGGGTTTC 88997	A
A	TGAAACCC TCTCTACTAAAA	
	ACTTTGGGG AGAGATGATTTT	
	C	
GAM2185 LOC196411 3'	ATTTTGTAGAGATGGGGTTT 89041	
CA	TGAAACCCCATCTCTACTAAAAAT	
	ACTTTGGGGTAGAGATGATTTT	
GAM2185 LOC196529 3'	ATTTTGTGTGAGACAGGGTTT 89124	CA T
CA	TGAAACCC TCTC ACTAAAAAT	
	ACTTTGGG AGAG TGATTTT	
	AC T	
GAM2185 LOC196529 3'	TTTGTAGTAGAGATGGTGTTTC 89147	C
	GAAAC CCATCTCTACTAAAA	
	CTTTG GGTAGAGATGATTTT	
	T	
GAM2185 LOC197358 3'	ATTTTGTAGTAGAGATGGGGTTT 89422	
CA	TGAAACCCCATCTCTACTAAAAAT	
	ACTTTGGGGTAGAGATGATTTT	
GAM2185 LOC197358 3'	TTTGTAGTAGAGACGGGGTTTCA 89453	A
	TGAAACCC TCTCTACTAAAA	
	ACTTTGGGG AGAGATGATTTT	
	C	
GAM2185 LOC199699 3'	ATTTTGTAAAGACAGGGTTT 89667	CA C
CA	TGAAACCC TCT TACTAAAAAT	
	ACTTTGGG AGA ATGATTTT	
	AC A	
GAM2185 LOC199699 3'	ATTTTGTAGTAGAGACAGAGTTT 89668	CCCA
CA	TGAAAC TCTCTACTAAAAAT	

	ACTTTG AGAGATGATTTTTA	
	AGAC	
GAM2185 LOC199725 5'	ATTTT TAGTAGAGACGGGATTT 91410	C A
CA	TGAAA CCC TCTCTACTAAAAAT	
	ACTTT GGG AGAGATGATTTTTA	
	A C	
GAM2185 LOC199786 3'	TTT TAGTAGAGACGGTGGTTTC 89773	_ A
	GAAACC CC TCTCTACTAAAA	
	CTTTGG GG AGAGATGATTTT	
	T C	
GAM2185 LOC199786 3'	TTTTT TAGTAGAGATGGGGTTTC 89775	
A	TGAAACCCCATCTCTACTAAAAA	
	ACTTTGGGGTAGAGATGATTTT	
GAM2185 LOC199906 3'	ATTTT TAGTAAAGACAGGGTTT 89846	CA C
CA	TGAAACCC TCT TACTAAAAAT	
	ACTTTGGG AGA ATGATTTTTA	
	AC A	
GAM2185 LOC200014 3'	ATTTT TAGTAGAGACGGTGTTT 89920	C A
CA	TGAAAC CC TCTCTACTAAAAAT	
	ACTTTG GG AGAGATGATTTTTA	
	T C	
GAM2185 LOC200169 5'	ATTTT TAGTAGAGACGGAGTTT 91552	C A
CA	TGAAAC CC TCTCTACTAAAAAT	
	ACTTTG GG AGAGATGATTTTTA	
	A C	
GAM2185 LOC200301 5'	ATTTT TAGTAGAGACGGGGTTT 90134	A
CA	TGAAACCC TCTCTACTAAAAAT	
	ACTTTGGGG AGAGATGATTTTTA	
	C	
GAM2185 LOC200310 3'	ATTTT TAGTAGAGACGGGGTTT 66321	A
CA	TGAAACCC TCTCTACTAAAAAT	
	ACTTTGGGG AGAGATGATTTTTA	
	C	
GAM2185 LOC200314 3'	TAGTAGAGATGGGGTTTCA 91602	
	TGAAACCCCATCTCTACTA	
	ACTTTGGGGTAGAGATGAT	
GAM2185 LOC200316 5'	ATTTT TAGTAGAGACGGGGTTT 90172	A
C	GAAACCC TCTCTACTAAAAAT	

		CTTTGGGG AGAGATGATTTT	
		C	
GAM2185	LOC200316 3'	ATTTT	CA T
	CA	TGAAACCC TC CTA	
		ACTTTGGG AG GATGATTTT	
		TC T	
GAM2185	LOC200339 3'	ATTTT	C
	T	GAAA CCCATCTCTACTAAAAAT	
		TTTT GGGTAGAGATGATTTT	
		A	
GAM2185	LOC200407 3'	ATTTT	CA
	T	GAAACCC TCTCTACTAAAAAT	
		TTTTGGG AGAGATGATTTT	
		AC	
GAM2185	LOC200845 5'	ATTTT	
	CA	TGAAACCCCATCTCTACTAAAAAT	
		ACTTTGGGGTAGAGATGATTTT	
GAM2185	LOC200860 3'	ATTTT	A
	C	GAAACCC TCTCTACTAAAAAT	
		CTTTGGGG AGAGATGATTTT	
		C	
GAM2185	LOC201164 3'	ATTTT	CA
	CA	TGAAACCC TCTCTACTAAAAAT	
		ACTTTGGG AGAGATGATTTT	
		AC	
GAM2185	LOC201173 5'	ATTTT	C A
	CA	TGAAAC CC TCTCTACTAAAAAT	
		ACTTTG GG AGAGATGATTTT	
		A C	
GAM2185	LOC201220 5'	ATTTT	C
	CA	TGAAAC CCATCTCTACTAAAAAT	
		ACTTTG GGTAGAGATGATTTT	
		A	
GAM2185	LOC201294 3'	ATTTT	A
	CA	TGAAACCC TCTCTACTAAAAAT	
		ACTTTGGGG AGAGATGATTTT	
		C	
GAM2185	LOC201411 3'	ATTTT	CA
	CA	TGAAACCC TCTCTACTAAAAAT	

		ACTTTGGG AGAGATGATTTT		
		AC		
GAM2185	LOC201626 3'	ATTTT	AGTAGAAATGGGGTTT 90427	C
	C		GAAACCCCAT TCTACTAAAAAT	
			CTTTGGGGTA AGATGATTTT	
		A		
GAM2185	LOC201627 3'	ATTTT	AGTAGAGATGGGGTTT 90449	
	C		GAAACCCCATCTCTACTAAAAAT	
			CTTTGGGGTAGAGATGATTTT	
GAM2185	LOC201696 3'	ATTTT	AGTAGAGACGAGGTTT 63812	CCA
	C		GAAACC TCTCTACTAAAAAT	
			CTTTGG AGAGATGATTTT	
		AGC		
GAM2185	LOC202460 5'	ATTTT	AGTAGAGATGGGGTTT 90668	
	CA		TGAAACCCCATCTCTACTAAAAAT	
			ACTTTGGGGTAGAGATGATTTT	
GAM2185	LOC202908 5'	ATTTT	TGTAGAGATGAGGTTT 90712	C T
	CA		TGAAACC CATCTCTAC AAAAAT	
			ACTTTGG GTAGAGATG TTTT	
		A T		
GAM2185	LOC202934 3'	ATTTT	AGTAGAGACAGGGTTT 92027	CA
	CA		TGAAACCC TCTCTACTAAAAAT	
			ACTTTGGG AGAGATGATTTT	
		AC		
GAM2185	LOC203197 3'	TTTT	AGTAGAGATGGGGTTTC 90823	
			GAAACCCCATCTCTACTAAAA	
			CTTTGGGGTAGAGATGATTTT	
GAM2185	LOC203339 3'	ATTTT	AGTAGAGATGGGGTTT 92207	
	CA		TGAAACCCCATCTCTACTAAAAAT	
			ACTTTGGGGTAGAGATGATTTT	
GAM2185	LOC203350 3'	ATTTT	ATTAGAGACGGGGTTT 92229	A C
	CA		TGAAACCC TCTCTA TAAAAAT	
			ACTTTGGGG AGAGAT ATTTT	
		C T		
GAM2185	LOC203378 3'	ATTTT	AGTAGAGATGGGATTT 92278	C
	TA		TGAAA CCCATCTCTACTAAAAAT	

		ATTTT GGGTAGAGATGATTTTTA		
		A		
GAM2185	LOC204804 3'	ATTTT TAGTAGAGATGAGGTTT 91035	C	
	CA	TGAAACC CATCTCTACTAAAAAT		
		ACTTTGG GTAGAGATGATTTTTA		
		A		
GAM2185	LOC219445 5'	AGTAGGGACGGGTTTCA 93198	A	
		TGAAACCCC TCTCTACT		
		ACTTTGGGG AGGGATGA		
		C		
GAM2185	LOC219445 5'	TTTTT TAGTAGAGACGGTGTTTC 93220	C A	
	A	TGAAAC CC TCTCTACTAAAAA		
		ACTTTG GG AGAGATGATTTTTT		
		T C		
GAM2185	LOC219673 5'	ATTTTGTAGAAAAGGGTTTC 94611	ATC T	
	A	TGAAACCCC TCTAC AAAAAT		
		ACTTTGGGG AGATG TTTTTA		
		AAA _		
GAM2185	LOC219673 5'	TTTTTGTAGAGATGAGGTCTCA 94638	A C T	
		TGA ACC CATCTCTAC AAAAA		
		ACT TGG GTAGAGATG TTTTT		
		C A _		
GAM2185	LOC219735 3'	ATTTT TAGTAGAGACGGGTTT 94724	A	
	CA	TGAAACCCC TCTCTACTAAAAAT		
		ACTTTGGGG AGAGATGATTTTTA		
		C		
GAM2185	LOC219894 3'	ATTTT TAGTAGAGATGGGGTTT 94899		
	CA	TGAAACCCCATCTCTACTAAAAAT		
		ACTTTGGGGTAGAGATGATTTTTA		
GAM2185	LOC220064 3'	ATTTT TAGTAGAGATGGGGTTT 95061		
	T	GAAACCCCATCTCTACTAAAAAT		
		TTTTGGGGTAGAGATGATTTTTA		
GAM2185	LOC220074 3'	ATTTT TAGTAGAGACGGGTTT 59964	A	
	CA	TGAAACCCC TCTCTACTAAAAAT		
		ACTTTGGGG AGAGATGATTTTTA		
		C		
GAM2185	LOC220074 3'	ATTTT TAGTAGAGATGGGGTTT 59965		
	C	GAAACCCCATCTCTACTAAAAAT		

CTTTGGGGTAGAGATGATTTTTA

GAM2185 LOC220074 3' TTTTAGTAGAGACAAGGTTTC 60002 CCA
GAAACC TCTCTACTAAAA
||||| |||||||||
CTTTGG AGAGATGATTTT
AAC

GAM2185 LOC220575 3' TTTTATAGTAAATGAGGTCTC 76818 A C C
GA ACC CAT TCTACTAAAAA
|| ||| ||| |||||||||
CT TGG GTA AGATGATTTTT
C A A

GAM2185 LOC221060 3' ATTTTATAGTACAGACGGTGTTT 94829 C A C
CA TGAAAC CC TCT TACTAAAAAT
||||| || ||| |||||||||
ACTTTG GG AGA ATGATTTTTTA
T C C

GAM2185 LOC221271 3' AGTAGAGAGGGGGTTTCA 93495 A
TGAAACCCC TCTCTACT
||||||| |||||||
ACTTTGGGG AGAGATGA
G

GAM2185 LOC221296 3' ATTTTATAGTAGAGACGGGGTTT 93605 A
CA TGAAACCCC TCTCTACTAAAAAT
||||||| |||||||||
ACTTTGGGG AGAGATGATTTTTTA
C

GAM2185 LOC221964 3' ATTTTATAGTAGAGACAGGGTTT 95600 CA
T GAAACCC TCTCTACTAAAAAT
||||||| |||||||||
TTTTGGG AGAGATGATTTTTTA
AC

GAM2185 LOC222031 3' ATTTTATAGTAGAGACGAGGTTT 95670 CCA
CA TGAAACC TCTCTACTAAAAAT
||||||| |||||||||
ACTTTGG AGAGATGATTTTTTA
AGC

GAM2185 LOC222068 3' ATTTTATAGTAGAGATGGGGTTT 94270
TA TGAAACCCCATCTCTACTAAAAAT
||||||| |||||||||
ATTTTGGGGTAGAGATGATTTTTTA

GAM2185 LOC222070 5' ATTTTATAGTGGAGACGGTGTTT 95809 C A
CA TGAAAC CC TCTCTACTAAAAAT
||||||| || ||| |||||||||
ACTTTG GG AGAGGTGATTTTTTA
T C

GAM2185 LOC222224 5' ATTTTGTAGAGACAGGGTTT 95870 CA T
CA TGAAACCC TCTCTAC AAAAAT
||||||| ||||||| |||||

		ACTTTGGG AGAGATG TTTTTA	
		AC T	
GAM2185	LOC245771 5'	ATTTTATAGTAGAGATGGGGTTT 94468	
	CA	TGAAACCCCATCTCTACTAAAAAT	
		ACTTTGGGGTAGAGATGATTTTTA	
GAM2185	LOC253664 3'	ATTTTCAGTAGAGATGGGGTTT 96459	A
	C	GAAACCCCATCTCTACT AAAAT	
		CTTTGGGGTAGAGATGA TTTTA	
		C	
GAM2185	LOC253666 3'	AGTAGAGACGGGGTTTCA 96760	A
		TGAAACCCC TCTCTACT	
		ACTTTGGGG AGAGATGA	
		C	
GAM2185	LOC253805 3'	ATTTTATAGTGGAGATAGGGTTT 98168	C
	CA	TGAAACCC ATCTCTACTAAAAAT	
		ACTTTGGG TAGAGGTGATTTTTA	
		A	
GAM2185	LOC253842 5'	ATTTTATAGTAGAAACATTGTTT 99234	CCCATC
	CA	TGAAAC TCTACTAAAAAT	
		ACTTTG AGATGATTTTTA	
		TTACAA	
GAM2185	LOC253981 3'	ATTTTATAGGAGAGACGGGGTTT 97530	A A
	CA	TGAAACCCC TCTCT CTAAAAAT	
		ACTTTGGGG AGAGA GATTTTTA	
		C G	
GAM2185	LOC253981 3'	ATTTTATAGTAGAGACGGGGTAT 97531	A A
	CA	TGA ACCCC TCTCTACTAAAAAT	
		ACT TGGGG AGAGATGATTTTTA	
		A C	
GAM2185	LOC254018 5'	TTTTTAGTAGAGATGGGGTTTC 98745	
		GAAACCCCATCTCTACTAAAAA	
		CTTTGGGGTAGAGATGATTTT	
GAM2185	LOC254100 3'	ATTTTTGTAGAGATGGGGTTT 98147	T
	C	GAAACCCCATCTCTAC AAAAAT	
		CTTTGGGGTAGAGATG TTTTTA	
		T	
GAM2185	LOC254268 3'	ATTTTTGGTAGAGATGGGGTTT 97139	
	CA	TGAAACCCCATCTCTACTAAAAAT	

ACTTTGGGGTAGAGATGGTTTTTA

GAM2185	LOC254295	5'	ATTTT	AGTAGAGACGGGGTTT	97888	A	
	CA			TGAAACCCC TCTCTACTAAAAAT			
				ACTTTGGGG AGAGATGATTTTTTA			
				C			
GAM2185	LOC254655	3'	ATTTT	AGTAGAGACGGGGTTT	97215	A	
	CA			TGAAACCCC TCTCTACTAAAAAT			
				ACTTTGGGG AGAGATGATTTTTTA			
				C			
GAM2185	LOC254672	3'	ATTTT	AGTAGAGGCAAGGTTT	96290	CCA	
	CA			TGAAACC TCTCTACTAAAAAT			
				ACTTTGG GGAGATGATTTTTTA			
				AAC			
GAM2185	LOC255308	3'	TTAGT	AGAGACGGGGTTTC	96181	A	
				GAAACCCC TCTCTACTAA			
				CTTTGGGG AGAGATGATT			
				C			
GAM2185	LOC255465	3'	ATTTT	AGTAGAGACGGGGTTTC	99103	CA	
	A			TGAAACCC TCTCTACTAAAAAT			
				ACTTTGGG AGAGATGATTTTTTA			
				C_			
GAM2185	LOC255497	3'	ATTTT	AGTAGAGACGGGGTTT	98984	A	
	CA			TGAAACCCC TCTCTACTAAAAAT			
				ACTTTGGGG AGAGATGATTTTTTA			
				C			
GAM2185	LOC255927	5'	ATTTG	TAGTAGAGACGGGGTTT	97710	A	A
	CA			TGAAACCCC TCTCTACTA AAAT			
				ACTTTGGGG AGAGATGAT TTTA			
				C G			
GAM2185	LOC256221	3'	TTTTT	AGTAGAGACGGGGTTTC	96923	A	
	A			TGAAACCCC TCTCTACTAAAAA			
				ACTTTGGGG AGAGATGATTTTTT			
				C			
GAM2185	LOC256267	3'	ATTTT	AGTAGAGATGGG	98605		
				CCCATCTCTACTAAAAAT			
				GGGTAGAGATGATTTTTTA			
GAM2185	LOC256306	3'	ATTTT	AGTAGAGACGGGGTTT	98505	A	
	CA			TGAAACCCC TCTCTACTAAAAAT			

	ACTTTGGGG AGAGATGATTTT	
	C	
GAM2185 LOC257465 3'	TTT TAGTAGAGATGGTGTTC	82505 C
	TGAAAC CCATCTCTACTAAA	
	ACTTTG GGTAGAGATGATTT	
	T	
GAM2185 LOC257486 3'	ATTTT TAGTAGAGACGGGGTTT	69766 A
CA	TGAAACCCC TCTCTACTAAAAAT	
	ACTTTGGGG AGAGATGATTTT	
	C	
GAM2185 LOC51008 5'	ATTTCTAGTAGAGATGGGGTTT	32529 A
C	GAAACCCCATCTCTACTA AAAT	
	CTTTGGGGTAGAGATGAT TTTA	
	C	
GAM2185 LOC51159 5'	TTT TAGTAGAGACGGGATTTCA	33035 C A
	TGAAA CCC TCTCTACTAAA	
	ACTTT GGG AGAGATGATTT	
	A C	
GAM2185 LOC51193 5'	ATTTTCAGTCGAGACGGGGTTT	33360 A T A
C	GAAACCCC TCTC ACT AAAAT	
	CTTTGGGG AGAG TGA TTTA	
	C C C	
GAM2185 LOC51200 3'	TTT TAGTAGAGACAGGGTTTC	33443 CA
	GAAACCC TCTCTACTAAAA	
	CTTTGGG AGAGATGATTTT	
	AC	
GAM2185 LOC51219 5'	ATTTT TAGTGAGACGGGGTTT	33539 A
C	GAAACCCC TCTCTACTAAAAAT	
	CTTTGGGG AGAGGTGATTTT	
	C	
GAM2185 LOC51696 3'	ATTTT TAGTAGAGACAGCGTTT	33078 CCA
CA	TGAAAC TCTCTACTAAAAAT	
	ACTTTG AGAGATGATTTT	
	CGAC	
GAM2185 LOC56181 5'	ATTTT TAGTAGAGACAGGGCTT	97270 A CA
CA	TGAA CCC TCTCTACTAAAAAT	
	ACTT GGG AGAGATGATTTT	
	C AC	
GAM2185 LOC57107 3'	ATTTT TAGTAGAGATGGGGTTT	40181
CA	TGAAACCCCATCTCTACTAAAAAT	

ACTTTGGGGTAGAGATGATTTTTA

GAM2185 LOC57146 3' TTTT TAGTACAGATGGGGTTC 40301 C
A TGAACCCCATCT TACTAAAA

||||| |||||
ACTTTGGGGTAGA ATGATTTT
C

GAM2185 LOC81034 3' ATTTT GAGTAGAAATGGGGTTT 48585 C A
CA TGAAACCCCAT TCTACT AAAAT

||||| ||||| |||||
ACTTTGGGGTA AGATGA TTTTA
A G

GAM2185 LOC89919 3' ATTTT TATTAGAGACGGGGTTT 61371 A C
CA TGAAACCCC TCTCTA TAAAAAT

||||| ||||| |||||
ACTTTGGGG AGAGAT ATTTT
C T

GAM2185 LOC89932 3' ATTTT TAGTAGAGACGGGGTTT 61448 A
C GAAACCCC TCTCTACTAAAAAT

||||| |||||||
CTTTGGGG AGAGATGATTTT
C

GAM2185 LOC89932 3' ATTTT TAGTTGAGATGGGGTTT 61449 T
CA TGAAACCCCATCTC ACTAAAAAT

||||| |||||
ACTTTGGGGTAGAG TGATTTT
T

GAM2185 LOC90288 3' ATTTT TAGTAGAGACGGGGTTT 62774 A
CA TGAAACCCC TCTCTACTAAAAAT

||||| |||||||
ACTTTGGGG AGAGATGATTTT
C

GAM2185 LOC90288 3' ATTTT TAGTAGAGATGGGGTTT 62775
CA TGAAACCCCATCTCTACTAAAAAT

||||| |||||||
ACTTTGGGGTAGAGATGATTTT

GAM2185 LOC90333 3' TTTT TAGTAGAGACTGGGGTTC 62970 CA
A TGAACCC TCTCTACTAAAA

||||| |||||||
ACTTTGGG AGAGATGATTTT
TC

GAM2185 LOC90459 3' ATTTT TGGTAGAGGCGGGGTTT 63548 AT
CA TGAAACCCC CTCTACTAAAAAT

||||| |||||||
ACTTTGGGG GAGATGGTTT
CG

GAM2185 LOC90485 3' ATTTT TAGTAGAGGCAGGGTTT 63689 CA
CA TGAAACCC TCTCTACTAAAAAT

||||| |||||||

		ACTTTGGG GGAGATGATTTT	
		AC	
GAM2185	LOC90485 3'	TTTTAGTAGAGGCGGGTTTCA 63717	AT
		TGAAACCCC CTCTACTAAA	
		ACTTTGGG GAGATGATTT	
		CG	
GAM2185	LOC90591 3'	ATTTTAGTAGAGACGGGGCTT 64149	A A
	CA	TGAA CCCC TCTCTACTAAAAAT	
		ACTT GGGG AGAGATGATTTT	
		C C	
GAM2185	LOC90591 3'	ATTTTAGTAGAGATGAGGTCT 64150	A C
	CA	TGA ACC CATCTCTACTAAAAAT	
		ACT TGG GTAGAGATGATTTT	
		C A	
GAM2185	LOC90591 3'	TTTTAGTAGAGACGGAGTTTC 64199	C A
	A	TGAAAC CC TCTCTACTAAAA	
		ACTTTG GG AGAGATGATTTT	
		A C	
GAM2185	LOC90784 5'	ATTTTAGTAGAGATGGGGTTT 64691	
	CA	TGAAACCCCATCTCTACTAAAAAT	
		ACTTTGGGGTAGAGATGATTTT	
GAM2185	LOC91115 3'	ATTTTAGTAGAGATGGGGTTT 65550	
	CA	TGAAACCCCATCTCTACTAAAAAT	
		ACTTTGGGGTAGAGATGATTTT	
GAM2185	LOC91115 3'	ATTTTAGTAGAGATGGGGTTT 65551	
	CA	TGAAACCCCATCTCTACTAAAAAT	
		ACTTTGGGGTAGAGATGATTTT	
GAM2185	LOC91250 5'	ATTTTAGTAGAGATGGGGTTT 65908	
	CA	TGAAACCCCATCTCTACTAAAAAT	
		ACTTTGGGGTAGAGATGATTTT	
GAM2185	LOC91291 5'	TTTTAGTAGAGACAAGGTTTCA 66096	CCA
		TGAAACC TCTCTACTAAA	
		ACTTTGG AGAGATGATTT	
		AAC	
GAM2185	LOC91308 3'	ATTTTAGTAGAGACGGGGTTT 66162	A
		AAACCCC TCTCTACTAAAAAT	

		TTTGGGG AGAGATGATTTT		
		C		
GAM2185	LOC91373 3'	ATTTT TAGTAGAGATGGGGTTT 66408		
		AAACCCCATCTCTACTAAAAAT		
		TTTGGGGTAGAGATGATTTT		
GAM2185	LOC91893 3'	ATTTT TAGTAGAGACGAGGTTT 68068	CCA	
	CA	TGAAACC TCTCTACTAAAAAT		
		ACTTTGG AGAGATGATTTT		
		AGC		
GAM2185	LOC91963 3'	ATTTT TGTAGAGGTGAGGTCT 68312	A C T	
	CA	TGA ACC CATCTCTAC AAAAAT		
		ACT TGG GTGGAGATG TTTT		
		C A T		
GAM2185	LOC92148 5'	TTTTT AGGAGAGACGGGGTTTC 68891	A A	
	A	TGAAACCCC TCTCT CTAAAAA		
		ACTTTGGGG AGAGA GATTTT		
		C G		
GAM2185	LOC92267 3'	ATTTT TAGTAGAGATGGGGTTT 69164		
	CA	TGAAACCCCATCTCTACTAAAAAT		
		ACTTTGGGGTAGAGATGATTTT		
GAM2185	LOC92303 3'	ATTTT CAGTAGAGATGGGTTTC 69386	C A	
	A	TGAAACCC ATCTCTACT AAAAT		
		ACTTTGGG TAGAGATGA TTTT		
		- C		
GAM2185	LOC92466 3'	ATTTT TAGTAGAGATGGG 69961		
		CCCATCTCTACTAAAAAT		
		GGGTAGAGATGATTTT		
GAM2185	LOC92661 5'	ATTTT TAGTAGAGGCGGGGTTT 70619	AT	
	CA	TGAAACCCC CTCTACTAAAAAT		
		ACTTTGGGG GAGATGATTTT		
		CG		
GAM2185	LOC92689 3'	ATTTT TAGTAGAGACAGGGTTT 70771	CA	
	CA	TGAAACCC TCTCTACTAAAAAT		
		ACTTTGGG AGAGATGATTTT		
		AC		
GAM2185	LOC92697 5'	ATTTT TAGTACAGATAGGGTTT 70804	C C	
	C	GAAACCC ATCT TACTAAAAAT		

	CTTTGGG TAGA ATGATTTT	
	A C	
GAM2185 LOC92697 5'	TTTTTGGTGGAGACGGGGTTTC 70820	A
	GAAACCCC TCTCTACTAAAA	
	CTTTGGGG AGAGGTGGTTTT	
	C	
GAM2185 LOC92841 3'	AGTAGAGACGGGGTTTCA 71247	A
	TGAAACCCC TCTCTACT	
	ACTTTGGGG AGAGATGA	
	C	
GAM2185 LOC92841 3'	TTTTAGTAGAGACAGGGTTTCA 71267	CA
	TGAAACCC TCTCTACTAAAA	
	ACTTTGGG AGAGATGATTTT	
	AC	
GAM2185 LOC93129 3'	TTTTTTGTAGAGACGGGGTTTC 71960	A T
	GAAACCCC TCTCTAC AAAAA	
	CTTTGGGG AGAGATG TTTT	
	C T	
GAM2185 LOC93349 3'	ATTTTGTAGAGACGGGGTTT 57264	A
CA	TGAAACCCC TCTCTACTAAAAAT	
	ACTTTGGGG AGAGATGATTTT	
	C	
GAM2186 PTPRG 3'	AGCAAACCCTGATGTGAC 12611	CATGCAA
	GTCACATTG GTTTGCT	
	CAGTGTAGT CAAACGA	
	CC_____	
GAM2186 KIAA0222 3'	CAAACGATGCAATGTAAC 28392	C GCAA
	GT ACATTGCAT GTTTG	
	CA TGTAACGTA CAAAC	
	A G_____	
GAM2186 MGC15482 3'	CAGCAAACCCCGTGTTAATG 52853	_ CAA
	CATTG CATG GTTTGCTG	
	GTAAT GTGC CAAACGAC	
	T CC_	
GAM2186 SMAP-5 3'	CAGCAAACCTGCTGCAGCGCAA 48656	A_ _
	TTGC TGCA AGTTTGCTG	
	AACG ACGT TCAAACGAC	
	CG CG	
GAM2186 LOC146512 3'	CAGCAAACCCTCAGAGGCAAAT 78497	_ ATGCAA_
GTGAC	GTCACATT GC GTTTGCTG	

CAGTGTAACG CAAACGAC
 A GAGACTCC
 GAM2186 LOC157292 3' CAGCAAACCTTCTAAAAAGCAA 87696 A__ C
 TTGC TG AAGTTTGCTG
 ||| || |||||
 AACG AT TTCAAACGAC
 AAAA C
 GAM2187 DDX6 3' ACACACAAGCTTGTCA 16563 CCA
 TGGCAAGC TGTGTGT
 ||||| |||||
 ACTGTTTCG ACACACA
 A__
 GAM2187 GATA1 5' CTGGGATCACACTGAGCTTGCC 10766 C T __ G
 A TGGCAAGC CA GTGTG TC AG
 ||||| || |||| || ||
 ACCGTTTCG GT CACAC GG TC
 A _ TA G
 GAM2187 INPP5A 3' ACACACATGGCCTCGCCA 19861 A C
 TGGC AG CCATGTGTGT
 ||| || |||||
 ACCG TC GGTACACACA
 C C
 GAM2187 KIAA0442 3' GACACACACAGGTCGCCA 32095 AA CA
 TGGC GCC TGTGTGTC
 ||| || |||||
 ACCG TGG ACACACAG
 C_ AC
 GAM2187 PATE 3' CTCACACACTTGAGCTTGCCA 57152 C T C
 TGGCAAGC CA GTGTGT GAG
 ||||| || ||||| ||
 ACCGTTTCG GT CACACA CTC
 A T _
 GAM2187 BC022889 3' CTCCTGTGCACATGAACCTTCCC 84626 C CC TG C_
 A TGG AAG CATGTG T GAG
 ||| || ||||| | |||
 ACC TTC GTACAC G CTC
 C AA GT TC
 GAM2187 C22orf2 3' CTCTCCACACACAAGCTCGC 96088 A CCA C
 GC AGC TGTGTGT GAGAG
 || ||| ||||| |||||
 CG TCG ACACACA CTCTC
 C A__ C
 GAM2187 EPB41L1 3' CTCCCATCACAAGCTTGGCA 71107 G CCA _ TC
 TG CAAGC TGTG TG GAG
 || |||| ||| || |||
 AC GTTCG ACAC AC CTC
 G A__ T C_
 GAM2187 FLJ10898 5' CTCTCAATACACATGAGCTTAG 60131 _ C C
 C GC AAGC CATGTGTGT GAGAG
 || |||| ||||| |||||

CG TTCG GTACACATA CTCTC
A A A
GAM2187 FLJ12587 3' TGGCACACACCTGCCA 42786 A CCCA
TGGCA G TGTGTGTCG
||||| | |||||
ACCGT C ACACACGGT
_C__

GAM2187 FLJ22529 3' CTGTGGTGCACACAGGCCTGCC 45942 A CA TG _
A
TGGCA GCC TGTG TCG AG
||||| ||| ||| ||| ||
ACCGT CGG ACAC GGT TC
C AC GT G

GAM2187 H105E3 3' CTCTCGACACGTTGCTCAGCCA 32489 A_ CCATG
TGGC AGC TGTGTCGAGAG
||| ||| |||||
ACCG TCG GCACAGCTCTC
AC TT__

GAM2187 KIAA0494 3' CTCAAAGGCCCAGGCGCTGCCA 29401 A_ CATG T GA_
TGGCA GCC TG GTC GAG
||||| ||| ||| ||| |||
ACCGT CGG AC CGG CTC
CG ____ C AAA

GAM2187 PRRG1 3' CTCTATCACATGCTTGCCA 8149 CCAT TCG
TGGCAAGC GTGTG AGAG
||||| ||| ||| |||
ACCGTTCG TACAC TCTC
____ TA_

GAM2187 LOC93349 3' TGACACACAGGCCTGGCA 57277 G A CA
TG CA GCC TGTGTGTCG
|| ||| |||||
AC GT CGG ACACACAGT
G C _

GAM2188 ATP10C 3' TCTCTCCACATTCCAAACAGA 44670 CGCAA A
TTTG AATGTGGA AGA
||| ||||| |||
AGAC TTACACCT TCT
AAACC C

GAM2188 CHN1 3' CTTTCTTTCCAGCAAAAGCAAA 10196 GCAAAA _
TTTGC TG TGGAAAGAAAG
||||| || |||||
AAACG AC ACCTTTCTTTC
AAA__ G

GAM2188 DCN 5' CTTTCCACACCTGCAAA 10387 CAAAA
TTTGCG TGTGGAAAG
||||| |||||
AAACGT ACACCTTTC
CC__

GAM2188 DNMT1 5' CTCCCCATCGGTTTCCGCGCGA 9103 A_ _ AA
A
TTTGCGC AAAT GTGG AG
||||| ||| ||| ||

		AAGCGCG TTTG TACC TC		
		CC GC CC		
GAM2188 EVA1	3'	CTTGAGTGTATTTTGTGCAAA 59234	TGGA_	
		TTTGCGCAAAATG AAG		
		AAACGTGTTTTAT TTC		
		GTGAG		
GAM2188 FABP3	3'	TTCCTCTGCATTTTGTACAAA 71926	CG TG AA	
		TTTG CAAAATG GA GAA		
		AAAC GTTTTAC CT CTT		
		AT GT C_		
GAM2188 FANCC	5'	CTTCCTTTCCGCCACTGCCCAA 71040	C AAAT A	
A		TTTG GCA GTGGAAAG AAG		
		AAAC CGT CGCCTTTC TTC		
		C CAC_ C		
GAM2188 MAP3K11	5'	TCCCTCCACCCCCTGCGCAAA 11600	AAAT AA	
		TTTGCGCA GTGGA GA		
		AAACGCGT CACCT CT		
		CCCC CC		
GAM2188 CFP1	3'	CTTTCCTTTTCTTTTTTTACGC 59407	C TGT _	
A		TGCG AAAA GGAAAG AAAG		
		ACGC TTTT CTTTTC TTTC		
		A TTT C		
GAM2188 FLJ10261	3'	CTTTCCTTGTTTTTGCACAAA 36418	C TGT__	
		TTTG GCAAAA GGAAAG		
		AAAC CGTTTT CCTTTC		
		A TGTTT		
GAM2188 FLJ20274	5'	CTTTCCTCTCAGTTTGCAGCA 63324	A T__	
		TGCGCAAA TG GGAAAG		
		ACGCGTTT AC CCTTTC		
		G TCT		
GAM2188 FLJ23311	3'	CTTAAACATTTTGCACAAA 45498	C GGA	
		TTTG GCAAAATGT AAG		
		AAAC CGTTTTACA TTC		
		A AA_		
GAM2188 KIAA0889	3'	TCTCTGTTGCATTTGCACAAG 31789	C A TG AA_	
		TTTG GCAAA TG G AGA		
		GAAC CGTTT AC T TCT		
		A _ GT GTC		
GAM2188 KIAA1805	3'	TTCCCCATTTTGCATAA 80773	T	
		TTTGCGCAAAATG GGAA		

AAATGCGTTTTAC CCTT
 C
 GAM2188 PLA2G3 3' TCCATGCCTTTGCGCAAA 32311 A_
 TTTGCGCAAA TGTGGA
 ||||| |||||
 AAACGCGTTT GTACCT
 CC
 GAM2188 LOC124446 5' CTTTCTTTTCTCTTTGCGTAAA 74775 ATGT
 TTTGCGCAAA GGAAAGAAAG
 ||||| |||||
 AAATGCGTTT CTTTCTTTC
 CT_
 GAM2188 LOC151103 3' CTTTCCTTGTTTACGTAAA 86411 C ATGT
 TTTGCG AAA GGAAAG
 ||||| |||||
 AAATGC TTT CCTTTC
 A GTT_
 GAM2188 LOC151647 3' CTTTCTTTCTGCTTTTACAAA 81142 CGC T TG
 TTTG AAAA G GAAAGAAAG
 ||| ||| |||||
 AAAC TTTT C CTTTCTTTC
 A__ _GT
 GAM2188 LOC199787 3' GCTTTCCTCCAAGTCTTCATT 89777 C ____ AA ____
 TTGCACGAA TTTG GCAAAATG TGGG GAAAG C
 ||| ||||| ||| ||||| |
 AAGC CGTTTTAC ACCT CTTTC G
 A TTCTGA CC ____
 GAM2188 LOC51312 5' TCTTTTTACTCTGCTCAAA 38328 C AAAT
 TTTG GCA GTGGAAAGA
 ||||| |||||
 AAAC CGT CATTTTTCT
 T CT_
 GAM2188 LOC90072 3' TCTCTGTTGCATTTGCACAAG 61967 C A TG AA_
 TTTG GCAAA TG G AGA
 ||||| ||||| ||| |||
 GAAC CGTTT AC T TCT
 A _ GT GTC
 GAM2189 FER1L4 3' TGTGGAGGAGGCCGAG 48140 CTTGGGG
 CTTGGCC CCTCCACA
 ||||| |||||
 GAGCCGG GGAGGTGT
 A_____
 GAM2189 FLJ20085 3' ACCGTGCCCCGCCCAAGAGC 35000 C CTC A
 GC CTTGGGGC CAC GT
 || ||||| ||| ||
 CG GAACCCCG GTG CA
 A CCC C
 GAM2189 JM5 3' ACTGTGTGCCCCAAGGGCCAGG 23957 CTC
 CTTGGCCCTTGGGGC CACAGT
 ||||| |||||

			GGACCGGGAACCCCG	GTGTCA			
			T__				
GAM2189	KIAA0781	3'	ACCGTGGAGGCAGGGGGCAAG	68054	G	GGG	A
			CTTG CCCTT GCCTCCAC GT				
			GAAC GGGGA CGGAGGTG CA				
			G ____ C				
GAM2189	MGC19556	5'	TGGAACCCCAAGGCCAAG	54345	C	CC	
			CTTGGCC TTGGGG TCCA				
			GAACCGG AACCCC AGGT				
			_ A_				
GAM2189	MGC20235	3'	CTACAGAGGCTTTGCCAA	59551	CCTT	CAC	
			TTGGC GGGGCCTC AG				
			AACCG TTTCGGAG TC				
			____ ACA				
GAM2189	LOC144893	3'	CTGACCCCAAGGCCCAAG	84110	C	CCTCCA	
			CTTGG CCTTGGGG CAG				
			GAACC GGAACCCC GTC				
			C A_____				
GAM2189	LOC147157	5'	CTGAAGCCCCAAGACCAAG	85081	CC	CTCCA	
			CTTGG CTTGGGGC CAG				
			GAACC GAACCCCG GTC				
			A_ AA_____				
GAM2189	LOC152464	3'	ACTGTGTGCCCCAAGGGCCAGG	60646		CTC	
			CTTGGCCCTTGGGGC CACAGT				
			GGACCGGGAACCCCG GTGTCA				
			T__				
GAM2189	LOC158969	5'	ACTGTGAATGCTTCAAGAGCCA	82932	C	CTC	
			TGGC CTTGGGGC CACAGT				
			ACCG GAACTTCG GTGTCA				
			A TAA				
GAM2189	LOC166042	5'	GGAGGCCCCGAAGGCCAAG	83505	C		
			CTTGGCC TTGGGGCCTCC				
			GAACCGG AGCCCCGGAGG				
			A				
GAM2189	LOC221294	3'	ACTGTAAAAGACTTTAAGGAAC	93456	GC	C CC_	
	AAG		CTTG CCTTGGGG CT ACAGT				
			GAAC GGAATTTTCA TGTCA				
			AA A AAA				
GAM2189	LOC256310	5'	AGGACCCCAAGGGTCAAG	98096	_		
			CTTGGCCCTTGGGG CCT				

			GA	ACTGGGAACCCC	GGA		
				A			
GAM2189	LOC257128	5'	ACTGTGGAGGAATGGGG	ACCAG	97807	_	TGGGG
			G	CTTGG CCCT CCTCCACAGT			
				GGACC GGGG GGAGGTGTCA			
				A TAA__			
GAM2190	GPD1	3'	TCATGCCACCACATTTG	60398		C	C
				TAAATG GGTGGCAT GA			
				GTTTAC CCACCGTA CT			
				A _			
GAM2190	IL5RA	5'	TCGCATGGCCACCGCATTT	6906		AT__	
				AAATGCGGTGGC CGA			
				TTTACGCCACCG GCT			
				GTAC			
GAM2190	MYO1C	3'	TGCCGATGCCAAATATTTG	61873		CGG	A
				TAAATG TGGCATCG CA			
				GTTTAT ACCGTAGC GT			
				AA_ C			
GAM2190	C6orf37	3'	TGTCACACTGCATTTA	68097		GCATC	
				TAAATGCGGTG GACA			
				ATTTACGTAC CTGT			
				A__			
GAM2190	DNAJC6	3'	TTGCAGAACCACCGCATT	29498		CA GA	
				AATGCGGTGG TC CAA			
				TTACGCCACC AG GTT			
				A_ AC			
GAM2190	FLJ11210	3'	GTCGATGTGCATGCTTTTA	60319		T GTG	
				TAAA GCG GCATCGAC			
				ATTT CGT TGTAGCTG			
				T ACG			
GAM2190	FLJ12476	3'	TCGATCTTCTGCATTTA	43270		T C	
				TAAATGCGG GG ATCGA			
				ATTTACGTC TC TAGCT			
				T _			
GAM2190	KIAA1034	3'	TCGATGGCATCCGCATTTG	63134		_ G	
				TAAATGCGG TG CATCGA			
				GTTTACGCC AC GTAGCT			
				T G			
GAM2190	KIAA1987	3'	TCATGTAAGTGCATTTA	89391		G C	
				TAAATGCGGT GCAT GA			

	ATTACGTCA TGTA CT		
	A _		
GAM2190 MGC16063 3'	TGTCCTGGCCACTGCATT 54929	ATC	
	AATGCGGTGGC GACA		
	TTACGTCACCG CTGT		
	GTC		
GAM2190 LOC147949 3'	TGTCAGATGTCCACATTGCA 79279	— _ _	
	TGCG GTGG CATC GACA		
	ACGT CACC GTAG CTGT		
	TA T A		
GAM2190 LOC150577 3'	GTCCTCACCGCATTTG 86258	CATC	
	TAAATGCGGTGG GAC		
	GTTTACGCCACT CTG		
	C_		
GAM2190 LOC158219 3'	TGTGTGTCACCACATTT 82694	C CG	
	AAATG GGTGGCAT ACA		
	TTTAC CCACTGTG TGT		
	A _		
GAM2190 LOC202020 3'	TGTCTCACCATTTA 90605	C CATC	
	TAAATG GGTGG GACA		
	ATTAC CCACT CTGT		
	A _		
GAM2190 LOC90826 5'	TGTCGATGCAGGTTTATTTG 64788	CGGTG	
	TAAATG GCATCGACA		
	GTTTAT CGTAGCTGT		
	TTGGA		
GAM2190 LOC93587 3'	TTGTCTTTACCTGCATTTA 73042	_ CATC	
	TAAATGC GGTGG GACAA		
	ATTACG CCATT CTGTT		
	T T_		
GAM2191 MSR1 3'	TTGACCTAGAGTCTTGAACC 11707	GA_ AA	
	GGTTCAAGG TGG GTCAA		
	CCAAGTTCT ATC CAGTT		
	GAG _		
GAM2191 FLJ10157 5'	GCAGCCCCCTGAACCAA 36331	A AT AA	
	TTGGTTCA GGG GG GT		
	AACCAAGT CCC CC CG		
	_ _ GA		
GAM2191 GLCCI1 5'	GCTTCATCTCCCAAACCAA 94171	CAA TG_	
	TTGGTT GGGA GAAGT		

AACCAA CCCT CTTCG
 A__ CTA
 GAM2191 MGC22014 3' ACTTCAACATACCCTGGACCAA 65106 A _ _
 TTGGTTCA GGG ATG GAAGT
 ||||| ||| ||| |||||
 AACCAGGT CCC TAC CTTC A
 _ A AA
 GAM2191 RNF38 3' GTTGACTTCCACCAGAAC 43262 AAG A
 GTTC GG TGGAAGTCAAC
 ||| || |||||
 CAAG CC ACCTTCAGTTG
 A__ _
 GAM2191 TUB 5' TGGGACCATCCCTTAAACC 13901 C AAG
 GGTT AAGGGATGG TCA
 ||| ||||| |||
 CCAA TTCCCTACC GGT
 A AG_
 GAM2191 LOC202347 3' GTTGACCCTCTTCTGAACCAA 91948 AG T AA
 TTGGTTCA GGA GG GTCAAC
 ||||| ||| ||| |||||
 AACCAAGT TCT CC CAGTTG
 CT _ _
 GAM2192 APXL 3' ATTCATCCAGGCATGGGCTGC 9711 CA A
 GC TCTGTGCCTGGAT AAT
 || ||||| |||
 CG GGGTACGGACCTA TTA
 TC C
 GAM2192 HS3ST4 3' ATCTGGTTGACCAGATGGC 73855 T__ T
 GCCATCTG GCC GGAT
 ||||| ||| |||
 CGGTAGAC TGG TCTA
 CAGT _
 GAM2192 MLLT2 3' ATTTATACCTGACCAGATGGCT 21028 TGCCT _
 A TAGCCATCTG GG ATAAAT
 ||||| || |||||
 ATCGGTAGAC CC TATTTA
 CAGT_ A
 GAM2192 PPARGC1 3' TATTTATCAGTTGCAGATAGC 26084 C GC G
 GC ATCTGT CTG ATAAATA
 || ||||| ||| |||||
 CG TAGACG GAC TATTAT
 A TT _
 GAM2192 DKFZP434I092 3' TATTTAGAGAGGCACAGATG 68413 GGA
 CATCTGTGCCT TAAATA
 ||||| ||| |||
 GTAGACACGGA ATTTAT
 GAG
 GAM2192 FLJ21603 3' TATTTATCCAGAAGTCTGGCTG 45778 T_ GTGC
 TAGCCA CT CTGGATAAATA
 ||||| || |||||

GTCGGT GA GACCTATTTAT
 CT A___
 GAM2192 KIAA0247 3' TATTCAGCTGCATAGATG 29077 ___
 CATCTGTGC CTGGATA
 ||||| |||||
 GTAGATACG GACTTAT
 TC
 GAM2192 KIAA0924 3' TATTTATCCAGACTCAGTATAG 30374 C _ TGC
 CT AGC AT CTG CTGGATAAATA
 ||| || ||| |||||
 TCG TA GAC GACCTATTTAT
 A T TCA
 GAM2192 KIAA1077 3' TATCCAATCAAGATGGCTA 73292 G CC
 TAGCCATCT TG TGGATA
 ||||| || |||||
 ATCGGTAGA AC ACCTAT
 _ TA
 GAM2192 KIAA1318 3' TAAACAGGCATAGATAGCTA 67878 C GA
 TAGC ATCTGTGCCTG TA
 ||| ||||| ||| ||
 ATCG TAGATACGGAC AT
 A AA
 GAM2192 KIAA1396 3' TCCGGCACAGATACTA 63676 CC T
 TAG ATCTGTGCC GGA
 ||| ||||| |||
 ATC TAGACACGG CCT
 A_ _
 GAM2192 KIAA1958 3' TCTGGCACAGAAGCTA 82793 CA T
 TAGC TCTGTGCC GGA
 ||| ||||| |||
 ATCG AGACACGG TCT
 A_ _
 GAM2192 MGC4730 3' TATTTAGCCTCACAGATGACT 64915 C CCT A
 AG CATCTGTG GG TAAATA
 || ||||| || |||||
 TC GTAGACAC CC ATTTAT
 A T_ G
 GAM2192 ZDHC7 3' TATTTATAGTCACAGATGGC 35322 C GG
 GCCATCTGTG CT ATAAATA
 ||||| || |||||
 CGGTAGACAC GA TATTTAT
 T _
 GAM2192 LOC150368 3' TTTGTTTAAACACAGATAGC 80520 C CC
 GC ATCTGTG TGGATAAA
 || ||||| |||||
 CG TAGACAC ATTTGTTT
 A AA
 GAM2192 LOC203292 5' ATCCTAGGCACAGATGCTA 92153 C _
 TAGC ATCTGTGCCT GGAT
 ||| ||||| ||| |||

			ATCG TAGACACGGA CCTA		
			— T		
GAM2192	LOC255811	5'	GTTTAACAAAGATGGCTA 96309	G CC	
			TAGCCATCT TG TGGAT		
			ATCGGTAGA AC ATTTG		
			A A_		
GAM2192	LOC90499	5'	ATCCTAGGCACAGATGCTA 63739	C _	
			TAGC ATCTGTGCCT GGAT		
			ATCG TAGACACGGA CCTA		
			— T		
GAM2193	GPD1	3'	TCATGCCACCACATTTG 60398	C C	
			TAAATG GGTGGCAT GA		
			GTTTAC CCACCGTA CT		
			A _		
GAM2193	IL5RA	5'	TCGCATGGCCACCGCATTT 6906	AT__	
			AAATGCGGTGGC CGA		
			TTTACGCCACCG GCT		
			GTAC		
GAM2193	MYO1C	3'	TGCCGATGCCAAATATTTG 61873	CGG A	
			TAAATG TGGCATCG CA		
			GTTTAT ACCGTAGC GT		
			AA_ C		
GAM2193	C6orf37	3'	TGTCACACTGCATTTA 68097	GCATC	
			TAAATGCGGTG GACA		
			ATTTACGTAC CTGT		
			A_____		
GAM2193	DNAJC6	3'	TTGCAGAACCACCGCATT 29498	CA GA	
			AATGCGGTGG TC CAA		
			TTACGCCACC AG GTT		
			A_ AC		
GAM2193	FLJ11210	3'	GTCGATGTGCATGCTTTTA 60319	T GTG	
			TAAA GCG GCATCGAC		
			ATTT CGT TG TAGCTG		
			T ACG		
GAM2193	FLJ12476	3'	TCGATCTTCTGCATTTA 43270	T C	
			TAAATGCGG GG ATCGA		
			ATTTACGTC TC TAGCT		
			T _		
GAM2193	KIAA1034	3'	TCGATGGCATCCGCATTTG 63134	_ G	
			TAAATGCGG TG CATCGA		

		GTTTACGCC AC GTAGCT		
		T G		
GAM2193	KIAA1987	3' TCATGTAAGTGCATTTA 89391	G C	
		TAAATGCGGT GCAT GA		
		ATTTACGTCA TGTA CT		
		A _		
GAM2193	MGC16063	3' TGTCCTGGCCACTGCATT 54929	ATC	
		AATGCGGTGGC GACA		
		TTACGTCACCG CTGT		
		GTC		
GAM2193	LOC147949	3' TGTCAGATGTCCACATTGCA 79279	_ _ _	
		TGCG GTGG CATC GACA		
		ACGT CACC GTAG CTGT		
		TA T A		
GAM2193	LOC150577	3' GTCCTCACCGCATTTG 86258	CATC	
		TAAATGCGGTGG GAC		
		GTTTACGCCACT CTG		
		C_		
GAM2193	LOC158219	3' TGTGTGTCACCACATTT 82694	C CG	
		AAATG GGTGGCAT ACA		
		TTTAC CCACTGTG TGT		
		A _		
GAM2193	LOC202020	3' TGTCTCACACATTTA 90605	C CATC	
		TAAATG GGTGG GACA		
		ATTTAC CCACT CTGT		
		A _		
GAM2193	LOC90826	5' TGTCGATGCAGTTTATTTG 64788	CGGTG	
		TAAATG GCATCGACA		
		GTTTAT CGTAGCTGT		
		TTGGA		
GAM2193	LOC93587	3' TTGTCTTTACCTGCATTTA 73042	_ CATC	
		TAAATGC GGTGG GACAA		
		ATTTACG CCATT CTGTT		
		T T_		
GAM2194	FHL1	3' ACAGTGACTAGTTGAATCCCTT 9360	GGA_ C	
	G	CAAGGGAT AGTCAC GT		
		GTTCCCTA TCAGTG CA		
		AGTTGA A		
GAM2194	LTB	3' ACGGTGACTCCAGTGCTGGA 24806	AGGGA A	
		TTCA TGGA GTCACCGT		

			AGGT ACCT CAGTGGCA		
			CGTG_ _		
GAM2194	MNDA	5'	ACAGTGACTCCAGGATTTCTGA 11662	A GG_ _	A C
	A		TTCA G A TGGA GTCAC GT		
			AAGT C T ACCT CAGTG CA		
			_ TT AGG _ A		
GAM2194	PIK3CG	3'	ACAGTGAGACTCCATCTCTT 12117	AG_ C	
			AAGGGATGGA TCAC GT		
			TTCTCTACCT AGTG CA		
			CAG A		
GAM2194	CGRP-RCP	3'	ACGGTGACTCATGCTT 27881	G GA	
			AGG ATG AGTCACCGT		
			TTC TAC TCAGTGGCA		
			G _		
GAM2194	CLIPR-59	3'	GGAATTCCTCCATCCCTGGAA 32017	A A CA	
			TTC AGGGATGG AGT CC		
			AAG TCCCTACC TTA GG		
			G C A_		
GAM2194	DDX34	3'	GTCTCTCTACCCCTTGAA 28675	A A TC	
			TTCAAGGG TGG AG AC		
			AAGTTCCC ATC TC TG		
			C C TC		
GAM2194	FLJ22477	3'	ACGGTGACTGTGGCCTTGAA 45664	GATGGA	
			TTCAAGG AGTCACCGT		
			AAGTTCC TCAGTGGCA		
			GGTG_		
GAM2194	KIAA1204	3'	GCGAGACCCCATCTCTT 69740	AA AC	
			AAGGGATGG GTC CGT		
			TTCTCTACC CAG GCG		
			C_ A_		
GAM2194	MGC3020	3'	ACGGTGACTAAAAGCCCCTGAA 44121	A ATGGA	
			TTCA GGG AGTCACCGT		
			AAGT CCC TCAGTGGCA		
			C GAAAA		
GAM2194	MRVI1	3'	ACAGTGACTTGATGTTCTTGGA 56092	ATGG C	
			TTCAAGGG AAGTCAC GT		
			AGGTTCTT TTCAGTG CA		
			GTAG A		
GAM2194	MRVI1	3'	ACAGTGACTTGATGTTCTTGGA 21379	ATGG C	
			TTCAAGGG AAGTCAC GT		

		AGGTTCTT	TTCAGTG CA		
		GTAG	A		
GAM2194	SRPK2	3'	ACGGTGACTCTCATTCTTT	13410	GA
			AAGGGATG AGTCACCGT		
			TTTCTTAC TCAGTGGCA		
			TC		
GAM2194	LOC115761	3'	ACGGTGGGGGAATCCCTTGAG	93392	GGAAG
			TTCAAGGGAT TCACCGT		
			GAGTTCCCTA GGTGGCA		
			AGGG_		
GAM2194	LOC116113	3'	ACTGTGCCTCCATCCCCAGAA	93829	AA A T C
			TTC GGGATGGA G CAC GT		
			AAG CCCTACCT C GTG CA		
			AC C _ T		
GAM2194	LOC130535	3'	ACGGTGACTCACACTTG	76637	GGA GA
			CAAG TG AGTCACCGT		
			GTTC AC TCAGTGGCA		
			_ AC		
GAM2194	LOC143196	3'	TGTTTTCCATCCACTGAA	83806	AG T
			TTCA GGATGGAAG CA		
			AAGT CCTACCTTT GT		
			CA T		
GAM2194	LOC145138	3'	GCGGTGACCTCTCGAA	84211	A ATGGAA
			TTC AGGG GTCACCGT		
			AAG TCTC CAGTGGCG		
			C _ _ _ _		
GAM2194	LOC149013	5'	ACGGTGACCCATGCCTAGA	79857	A G AA
			TC AGG ATGG GTCACCGT		
			AG TCC TACC CAGTGGCA		
			A G _		
GAM2194	LOC149837	5'	GGCCTGGCTCCATCCTCTGAA	85900	AG A _
			TTCA GGATGGA GTCA CC		
			AAGT CCTACCT CGGT GG		
			CT _ CC		
GAM2194	LOC154386	3'	ACGGCTGTCTCCCCCTGAA	81985	A AT A T _
			TTCA GGG GGA G CA CCGT		
			AAGT CCC CCT C GT GGCA		
			_ _ _ T C		
GAM2194	LOC255743	3'	ACAGTGATACCCCTCCTTGAA	97600	AT AA C
			TTCAAGGG GG GTCAC GT		

			AAGTTCCT CC TAGTG CA		
			__ CA A		
GAM2194	LOC92080	3'	ACGGTGGCCACCCCTGAG 68616	A	AT AA
			TTCA GGG GG GTCACCGT		
			GAGT CCC CC CGGTGGCA		
			_ _ AC		
GAM2195	GPD1	3'	TCATGCCACCACATTTG 60398	C	C
			TAAATG GGTGGCAT GA		
			GTTTAC CCACCGTA CT		
			A _		
GAM2195	IL5RA	5'	TCGCATGGCCACCGCATTT 6906	AT__	
			AAATGCGGTGGC CGA		
			TTTACGCCACCG GCT		
			GTAC		
GAM2195	MYO1C	3'	TGCCGATGCCAATATTTG 61873	CGG	A
			TAAATG TGGCATCG CA		
			GTTTAT ACCGTAGC GT		
			AA_ C		
GAM2195	C6orf37	3'	TGTCACACTGCATTTA 68097	GCATC	
			TAAATGCGGTG GACA		
			ATTTACGTAC CTGT		
			A__		
GAM2195	DNAJC6	3'	TTGCAGAACCACCGCATT 29498	CA GA	
			AATGCGGTGG TC CAA		
			TTACGCCACC AG GTT		
			A_ AC		
GAM2195	FLJ11210	3'	GTCGATGTGCATGCTTTTA 60319	T	GTG
			TAAA GCG GCATCGAC		
			ATTT CGT TGTAGCTG		
			T ACG		
GAM2195	FLJ12476	3'	TCGATCTTCTGCATTTA 43270	T	C
			TAAATGCGG GG ATCGA		
			ATTTACGTC TC TAGCT		
			T _		
GAM2195	KIAA1034	3'	TCGATGGCATCCGCATTTG 63134	_	G
			TAAATGCGG TG CATCGA		
			GTTTACGCC AC GTAGCT		
			T G		
GAM2195	KIAA1987	3'	TCATGTAAGTGCATTTA 89391	G	C
			TAAATGCGGT GCAT GA		

ATTTACGTCA TGTA CT
 A _
 GAM2195 MGC16063 3' TGTCCTGGCCACTGCATT 54929 ATC
 AATGCGGTGGC GACA
 ||||| |||
 TTACGTCACCG CTGT
 GTC
 GAM2195 LOC147949 3' TGTCAGATGTCCACATTGCA 79279 _ _ _
 TGCG GTGG CATC GACA
 ||| ||| ||| |||
 ACGT CACC GTAG CTGT
 TA T A
 GAM2195 LOC150577 3' GTCCTCACCGCATTTG 86258 CATC
 TAAATGCGGTGG GAC
 ||||| |||
 GTTTACGCCACT CTG
 C_
 GAM2195 LOC158219 3' TGTGTGTCACCACATTT 82694 C CG
 AAATG GGTGGCAT ACA
 |||| ||||| |||
 TTTAC CCACTGTG TGT
 A _
 GAM2195 LOC202020 3' TGTCTCACCATTTA 90605 C CATC
 TAAATG GGTGG GACA
 |||| |||| |||
 ATTTAC CCACT CTGT
 A _
 GAM2195 LOC90826 5' TGTCGATGCAGGTTTATTTG 64788 CGGTG
 TAAATG GCATCGACA
 |||| |||||
 GTTTAT CGTAGCTGT
 TTGGA
 GAM2195 LOC93587 3' TTGTCTTTACCTGCATTTA 73042 _ CATC
 TAAATGC GGTGG GACAA
 ||||| |||| |||
 ATTTACG CCATT CTGTT
 T T_
 GAM2196 EIF3S6 3' GTGACTTACATTTTGGAAACAA 9604 G G GC
 TTG TTCCAGG ATG AAGTCAC
 || ||||| || |||||
 AAC AAGGTTT TAC TTCAGTG
 A _ A_
 GAM2196 DREV1 3' GACTTCATGGAACCAA 32618 GG TGGCA
 TTGGTTCCA GA AGTC
 ||||| || |||
 AACCAAGGT CT TCAG
 A_ _
 GAM2196 FLJ10948 3' TGA CTGGCGTGATGCCTGGAAC 37456 G G A_
 CAA TTGGTTCCAGG AT GC AGTCA
 ||||| || ||| |||

			AACCAAGGTCC TA TG TCAGT		
			G G CGG		
GAM2196	IGSF2	3'	GTGACCTAGTCACCTGGAACCA 16196	GA	AA_
		G	TTGGTTCCAGG TGGC GTCAC		
			GACCAAGGTCC ACTG CAGTG		
			___ ATC		
GAM2196	KCND1	3'	GACCTGCCATCCCCAGGCC 18348	CCA	A
			GGTT GGGATGGCA GTC		
			CCGG CCCTACCGT CAG		
			AC_ C		
GAM2196	KIAA0420	3'	GCACATCTCTGGAACCAA 64090	_	
			TTGGTTCCAGGGATG GC		
			AACCAAGGTCTCTAC CG		
			A		
GAM2196	KIAA1069	3'	ACTCCCATCTCTAAAACCAA 68523	CC	CA
			TTGGTT AGGGATGG AGT		
			AACCAA TCTCTACC TCA		
			AA C_		
GAM2196	KIAA1271	3'	ACCTGCACCCTGGAACCAG 70124	ATG	A
			TTGGTTCCAGGG GCA GT		
			GACCAAGGTCCC CGT CA		
			A_ C		
GAM2196	KIAA1399	3'	TGGCACCCCCGGAGCCAA 70794	A	A G
			TTGGTTCC GGG TG CA		
			AACCGAGG CCC AC GT		
			C C G		
GAM2196	MGC11242	3'	TGACTACTCCCTGGACCAA 44484	T	TGGCA
			TTGGT CCAGGGA AGTCA		
			AACCA GGTCCCT TCAGT		
			_ CA_		
GAM2196	LOC255743	5'	TGACTTGCACTGGGAACCAA 97606	AGGGATG	
			TTGGTTCC GCAAGTCA		
			AACCAAGG CGTTCAGT		
			GTCA_		
GAM2196	LOC257354	3'	GCACATCTCTGGAACCAA 96792	_	
			TTGGTTCCAGGGATG GC		
			AACCAAGGTCTCTAC CG		
			A		
GAM2196	LOC88523	5'	TGACTTGGGAGCTGGAATCAA 53575	GGATGG	
			TTGGTTCCAG CAAGTCA		

			AACTAAGGTC	GTTCAGT		
			GAGG__			
GAM2197	ABCC5	3'	TGCAGAGCGCCGTGAGTTCTCA	20298	CA AT TC	
			TGAGAACTC GG TG CTGCA			
			ACTCTTGAG CC GC GACGT			
			TG __ GA			
GAM2197	AIM1	3'	GCAATCTTGGAATCCTCA	93467	AAC	
			TGAG TCCAGGATTGT			
			ACTC AGGTTCTAACG			
			CTA			
GAM2197	AIPL1	3'	GCAGGACACTTAGAGCTCTC	60534	A C AT	
			GAGA CTC AGG TGCCTGC			
			CTCT GAG TTC ACAGGACG			
			C A __			
GAM2197	BSG	3'	GCAAGATTCCAAGTTCTCA	9956	CCA TT C	
			TGAGAACT GGA GTC TGC			
			ACTCTTGA CCT TAG ACG			
			A__ __ A			
GAM2197	C7	3'	ACAGTCCCAGAGTTTTCA	6975	CA	
			TGAGAACTC GGATTGT			
			ACTTTTGAG CCTGACA			
			AC			
GAM2197	CCND1	5'	TGCAAAGTCCTGGAGCCTC	54962	AA	GTCC
			GAG CTCCAGGATT TGCA			
			CTC GAGGTCCTGA ACGT			
			C_ A__			
GAM2197	EPHA8	3'	CAGGACCTGGAGTTATCA	40430	G	ATTG
			TGA AACTCCAGG TCCTG			
			ACT TTGAGGTCC AGGAC			
			A			
GAM2197	HUNK	3'	CAGAATGGCCTGGAGTCTTCA	28179	GA	A TG C
			TGA ACTCCAGG T T CTG			
			ACT TGAGGTCC G A GAC			
			TC _GT A			
GAM2197	IGFBP3	3'	GCATGCTCCTGGAGCTCA	7000	AA	TT CC
			TGAG CTCCAGGA GT TGC			
			ACTC GAGGTCCT CG ACG			
			_ _ T_			
GAM2197	JAG1	3'	CAAACTCATCTGGAGTTCTCA	5810	ATT CC	
			TGAGAACTCCAGG GT TG			

ACTCTTGAGGTCT CA AC
 ACT AA
 GAM2197 RRP22 3' GCAGCCTGCTCCTGGAGCTTC 22393 _ TTGTC
 GAA CTCCAGGA CTGC
 ||| ||||| |||
 CTT GAGGTCCT GACG
 C CGTCC
 GAM2197 DKFZP434O125 3' CAGGTTCTGGAATTCTCA 65584 C TTGT
 TGAGAA TCCAGGA CCTG
 ||||| ||||| |||
 ACTCTT AGGTCTT GGAC
 A ____
 GAM2197 DKFZP434P0721 3' AGGAAGCCCAGAGTTCTCA 64454 CA ATTG
 TGAGAACTC GG TCCT
 ||||| || |||
 ACTCTTGAG CC AGGA
 AC GA____
 GAM2197 FLJ20457 3' GCAGGACTTGAGTTCTCA 35672 CAGGATT
 TGAGAACTC GTCCTGC
 ||||| |||||
 ACTCTTGAG CAGGACG
 TT____
 GAM2197 FLJ20485 3' TGCAGTGCAATCCTGCAATTCT 39295 CTC TC
 CA TGAGAA CAGGATTG CTGCA
 ||||| ||||| |||||
 ACTCTT GTCCTAAC GACGT
 AAC GT
 GAM2197 FLJ21820 3' CAGGACAACCAGCAAGTTCT 41917 CCA_ A
 AGAACT GG TTGTCCTG
 ||||| || |||||
 TCTTGA CC AACAGGAC
 ACGA _
 GAM2197 HRIHFB2122 3' TGCAGGACAGGGGAGCCTC 57619 AA AGGAT
 GAG CTCC TGTCTGCA
 ||| ||| |||||
 CTC GAGG ACAGGACGT
 C_ GG____
 GAM2197 KIAA0563 5' CAGAAAATTTGGAGTCCTC 29872 A G GTC
 GAG ACTCCAG ATT CTG
 ||| ||||| ||| |||
 CTC TGAGGTT TAA GAC
 C _ AA_
 GAM2197 KIAA0596 3' TGCAGGACAGTAAGCCCTCA 63497 AA CCAGG
 TGAG CT ATTGTCCTGCA
 |||| || |||||
 ACTC GA TGACAGGACGT
 CC A____
 GAM2197 KIAA1706 3' GCAGGACAAGAATTCTC 94366 C CAGGA
 GAGAA TC TTGTCCTGC
 ||||| || |||||

			CTCTT AG AACAGGACG			
			A _			
GAM2197	MGC23284	3'	GGAATTCTGGAATTCCCA	59359	A C	TG
			TG GAA TCCAGGAT TCC			
			AC CTT AGGTCTTA AGG			
			C A _			
GAM2197	NCK1	5'	GCAGTGGCGTCCTGGAGCCCTC	21588	AA	T _
			GAG CTCCAGGAT GTC CTGC			
			CTC GAGGTCCTG CGG GACG			
			CC _ T			
GAM2197	NFASC	3'	GCAGACCTGCAGTTCTCA	70858	C A	
			TGAGAACT CAGG TTGT			
			ACTCTTGA GTCC GACG			
			C A			
GAM2197	NUBP2	3'	GCAGGACTTCTGCAGTCCTCA	64890	A C	TT
			TGAG ACT CAGGA GTCCTGC			
			ACTC TGA GTCTT CAGGACG			
			C C _			
GAM2197	SPIB	3'	CAGACTCCCTGGGATCCTCA	13353	AAC	ATT C
			TGAG TCCAGG GTC TG			
			ACTC GGGTCC CAG AC			
			CTA CT_ _			
GAM2197	TIP47 CA	3'	TGCAGCTGTGCTCTGGAGTCCT	20610	A	ATTGTC
			TGAG ACTCCAGG CTGCA			
			ACTC TGAGGTCT GACGT			
			C CGTGTC			
GAM2197	TRIM5	3'	GGCATCCTGGGCTCTCA	53472	A T	T
			TGAGA C CCAGGAT GTC			
			ACTCT G GGTCCCTA CGG			
			C _ _			
GAM2197	WDR7	3'	GCAATCCTGTAGTTCCCA	31610	A C	
			TG GAACT CAGGATTGT			
			AC CTTGA GTCCTAACG			
			C T			
GAM2197	ZFPL1	3'	TGCAGGCCAGGCCTGGAGT	60390	A T	
			ACTCCAGG TTG CCTGCA			
			TGAGGTCC GAC GGACGT			
			G C			
GAM2197	LOC143308 A	5'	TGCATCCAGCTCCCGGGTTCTC	83839	T A	_ TCC
			TGAGAAC CC GGA TTG TGCA			

ACTCTTG GG CCT GAC ACGT
 _ C C CT_
 GAM2197 LOC145844 3' GCAAAACAGGATGGGGAATTTC 77997 A_ GGA CC
 A TGAGA CTCCA TTGT TGC
 |||| |||| ||| |||
 ACTTT GGGGT GACA ACG
 AA AG_ AA
 GAM2197 LOC146733 3' TGCAGGACCGGCCAGAGTTC 84788 CA ATT
 GAACTC GG GTCCTGCA
 ||||| || |||||
 CTTGAG CC CAGGACGT
 AC GGC
 GAM2197 LOC146909 5' TGCAGGGCCTAGAGCCCTT 78787 AA C ATTG
 GAG CTC AGG TCCTGCA
 ||| ||| ||| |||||
 TTC GAG TCC GGGACGT
 CC A ____
 GAM2197 LOC157931 3' GCAGGGCTGGCATTCCCA 87942 A CT GGATT
 TG GAA CCA GTCCTGC
 || ||| ||| |||||
 AC CTT GGT CGGGACG
 C AC ____
 GAM2197 LOC201173 5' CAGAAAATTTGGAGTCCTC 88674 A G GTC
 GAG ACTCCAG ATT CTG
 ||| ||||| ||| |||
 CTC TGAGGTT TAA GAC
 C _ AA_
 GAM2197 LOC201220 5' CAGAAAATTTGGAGTCCTC 88709 A G GTC
 GAG ACTCCAG ATT CTG
 ||| ||||| ||| |||
 CTC TGAGGTT TAA GAC
 C _ AA_
 GAM2197 LOC220534 3' TGCAGGACACCTAGGAG 92417 _ AT
 CTCC AGG TGCCTGCA
 |||| ||| |||||
 GAGG TCC ACAGGACGT
 A _
 GAM2197 LOC220538 3' TGCAGGACACCTAGGAG 92430 _ AT
 CTCC AGG TGCCTGCA
 |||| ||| |||||
 GAGG TCC ACAGGACGT
 A _
 GAM2197 LOC93134 3' ACATCTTGAAGTTCTCA 72011 C T
 TGAGAACT CAGGAT GT
 ||||| ||||| |||
 ACTCTTGA GTTCTA CA
 A _
 GAM2198 KIAA1100 5' AGCTCTTAAAGGATCC 30437 AAAA C
 GGAT TCT TAAGAGCT
 |||| ||| |||||

CCTA GGA ATTCTCGA
 _____ A
 GAM2198 LOC152373 5' AGCTCTTCTTTGTTTCATCTGAT 81448 A ATCTCT
 A TATCGGAT AA AAGAGCT
 ||||| || |||||
 ATAGTCTA TT TTCTCGA
 C GTTTC_

GAM2199 N33 3' ATGAAGATAAACTGTTCTGAC 23152 A ACTTC
 GTCA GAA TTATCTTCAT
 ||| ||| |||||
 CAGT CTT AATAGAAGTA
 C GTCA_

GAM2199 RNF26 3' ATGAATAAAGTTCTCTTGACA 50132 _ CTTATC
 TGTCAAGA AACTT TTCAT
 ||||| ||||| |||||
 ACAGTTCT TTGAA AAGTA
 C AT_____

GAM2199 AOP2 3' TATGAAAATGGCACTAAAAGTT 18137 C_____ C ____
 TCTTGA TCAAGAACTT TTAT TTCAT A
 ||||| ||| ||||| |
 AGTTCTTTGAA GGTA AAGTA T
 AATCAC A ____

GAM2199 FLJ22643 3' AAGGTTAATAAATTTCTTGACA 45264 CTTCTT_
 TGTCAAGAAA ATCTT
 ||||| |||||
 ACAGTTCTTT TGGAA
 AAATAAT

GAM2199 KIAA1979 3' GTAAGAGTTTTTGACA 89653 AC
 TGTCAAGAA TTCTTAT
 ||||| |||||
 ACAGTTTTT GAGAATG

GAM2199 PRO0255 3' ATGAAAAGTTTAAAGTTTCTTG 26965 CTTATC_
 A TCAAGAACTT TTCAT
 ||||| |||||
 AGTTCTTTGAA AAGTA
 ATTTGAA

GAM2199 ZNF-U69274 3' ATGAAGATAAAAAGAAGTGACA 27741 AGAAA C
 TGTCA CTT TTATCTTCAT
 |||| ||| |||||
 ACAGT GAA AATAGAAGTA
 GAA__ A

GAM2199 LOC91181 3' ATGAAGATTTCTAGTCCTCGAC 65769 A AA TCTT
 A TGTC AG ACT ATCTTCAT
 ||| || ||| |||||
 ACAG TC TGA TAGAAGTA
 C C_ TCTT

GAM2200 RRBP1 3' TTACAAATAAACCAACCA 17160 C A
 TGG TGG TTATTTGTAA
 ||| ||| |||||

		ACC ACC AATAAACATT	
		A A	
GAM2200 KIAA1495	3'	CAGCATTACAAATTAAGTGACC 73564	CTGGATT
	A	TGG ATTTGTAATGCTG	
		ACC TAAACATTACGAC	
		AGTGAAT	
GAM2200 MGC1842	3'	AGCACCTCAGTCCAGCCA 66246	TATT TAA
		TGGCTGGAT TG TGCT	
		ACCGACCTG AC ACGA	
		____ TCC	
GAM2200 PPP2R3A	3'	CAGCAGGCCACAGTCCAGCCA 12240	ATT TAA
		TGGCTGGATT TG TGCTG	
		ACCGACCTGA AC ACGAC	
		C__ CGG	
GAM2200 LOC143310	3'	CATGGACAAATAATCCACCA 77039	C A_
		TGG TGGATTATTTGT ATG	
		ACC ACCTAATAAACA TAC	
		_ GG	
GAM2200 LOC151719	3'	TAGTGACAAAAATCCAGCCA 81161	A AA
		TGGCTGGATT TTTGT TGCTG	
		ACCGACCTAA AAACA GTGAT	
		_ _	
GAM2200 LOC196477	3'	ACAATCCATAATCCAGTCA 89062	____
		TGGCTGGATTAT TTGT	
		ACTGACCTAATA AACA	
		CCT	
GAM2200 LOC222066	3'	CAGCACCAGTGCAGTCCAGCCA 94313	TTATTT AA
		TGGCTGGA GT TGCTG	
		ACCGACCT CA ACGAC	
		CACGT_ CC	
GAM2201 ATF7	3'	TCCCAGCCCCGAGCCTCATA 23404	_ TAGA CC
		TATGAGGC CC GCT GGGA	
		ATACTCCG GG CGA CCCT	
		A CCC_ _	
GAM2201 CREBBP	5'	CCCGCCGGTCCCGGGCCCCA 16495	A TA G C_
		TG GGCC GA CT CGGG	
		AC CCGGG CT GG GCCC	
		C CC _ CC	
GAM2201 EGLN2	5'	TTGGGGCTCCAGAACCTC 54926	CC A
		GAGG CT GAGCTCCGG	

			CTCC GA CTCGGGGTT		
			AA C		
GAM2201	GNA11	5'	CCCAGTGA	76586	T C C__
			CTCTGGGCCTCA		
			TGAGGCC AGAG TC GGG		
			ACTCCGGG TCTC AG CCC		
			_ _ TGA		
GAM2201	LATS2	3'	GTCCCGGAGCCGGTGCCCTCA	28135	_ _ TAGA
			TGAGG C CC GCTCCGGGAC		
			ACTCC G GG CGAGGCCCTG		
			C T C__		
GAM2201	NLGN3	3'	GTCTCTCTGGCTCTAGGACC	39121	C CC_
			GG CCTAGAGCT GGGAC		
			CC GGATCTCGG CTCTG		
			A TCT		
GAM2201	NOTCH1	5'	GTCCCGGAGCCCCAAGTGCTT	92138	C AGA_
			AGGC CT GCTCCGGGAC		
			TTCG GA CGAGGCCCTG		
			T ACCC		
GAM2201	RBBP9	3'	TCCGAGTCTAGAGCCCCA	70699	A C G
			TG GGC CTAGA CTCCGGG		
			AC CCG GATCT GAGGCCT		
			C A _		
GAM2201	UBQLN1	5'	CCGAGCTCCGGGGCCCCA	26473	A TA C
			TG GGCCC GAGCTC GG		
			AC CCGGG CTCGAG CC		
			C GC _		
GAM2201	ARTN	5'	CCCGGGCCTGGAGCCCCA	15612	A C A T
			TG GGC CTAG GC CCGGG		
			AC CCG GGTC CG GGCCC		
			C A _ _		
GAM2201	CNTNAP1	3'	CCCAAAGGAGAAGCCTCATG	14641	CCTAGAG _
			TATGAGGC CTCC GGG		
			GTACTCCG GAGG CCC		
			AA_ AAA		
GAM2201	FLJ10898	5'	CCCCAAGCCAGGCACAGCCTCA	60130	_ AGA CC
	TA		TATGAGGC CCT GCT GGG		
			ATACTCCG GGA CGA CCC		
			ACAC C_ AC		
GAM2201	KIAA1977	5'	CGAAGGCTCAGGGCCTCA	74765	A C_
			TGAGGCCCT GAGCT CG		

		ACTCCGGGA CTCGG GC	
		— AA	
GAM2201 P24B	3'	TCCTGCTCTAGGGCCCCTCA 24774	___ TCC
		TGA GGCCCTAGAGC GGA	
		ACT CCGGGATCTCG TCCT	
		CC	___
GAM2201 LOC146669	3'	GTCTTTCTCCAGGGGCCTCA 78664	A_ CTCC
		TGAGGCCCT GAG GGGAC	
		ACTCCGGGG CTC TTCTG	
		AC T___	
GAM2201 LOC170127	5'	CCCGGAGCCCCAGGGGCCCA 83456	A AGA_
		TG GGCCCT GCTCCGGG	
		AC CCGGG CGAGGCC	
		— ACCC	
GAM2201 LOC256812	5'	CCCGGAGCCCCCTGGGCCCA 99406	A TAGA_
		TG GGCC GCTCCGGG	
		AC CCGGG CGAGGCC	
		C TCCCC	
GAM2201 LOC90408	5'	CCCCTCTCCGAGGCCTCATA 63342	CTA CTCC
		TATGAGGCC GAG GGG	
		ATACTCCGG CTC CCC	
		AGC TC___	
GAM2202 EPHA2	3'	CAGCCTTCGACAGACAT 16674	CC GCGG
		ATGTC TTC GAAGGCTG	
		TACAG AGG CTTCCGAC	
		AC	___
GAM2202 EPHB6	3'	AACTGGTCCGAGAAGGGACAT 16713	G AA C
G		CATGTCCCTTC CGGG GG TGT	
		GTACAGGGAAG GCCT TC ACA	
		A GG _	
GAM2202 PRPF31	3'	CTTCCCACTGAAGGGACA 32212	C_
		TGTCCCTTCG GGGAAG	
		ACAGGGAAGT CCCTTC	
		CA	
GAM2202 RHO	3'	CAGCCTGAGAAGGGACAT 6767	GCGGGA
		ATGTCCCTTC AGGCTG	
		TACAGGGAAG TCCGAC	
		AG___	
GAM2202 CHFR	3'	ACAGCCCCCTGAGGGAAGGGAC 37188	G_ AA
G		TGTCCCTTC CGGG GGCTGT	

			GCAGGGAAG GTCC CCGACA		
			GGA C_		
GAM2202	MGC11352	3'	CAACCTTCCTGGAACGTG 65425	CCCT G	C
			CATGT TC CGGGAAGG TG		
			GTGCA AG GTCCTTCC AC		
			_____ A		
GAM2202	MGC2803	3'	ACAGCCTTCCCTGAGAGGAC 44085	C C	
			GTCC TTCG GGGAAGGCTGT		
			CAGG GAGT CCCTTCCGACA		
			A _		
GAM2202	PRC1	3'	ACAGCCTTCCTCCTGAAGAGA 15625	C C_	
			TC CTTG G GGAAGGCTGT		
			AG GAAGT C CCTTCCGACA		
			A C T		
GAM2202	LOC148089	3'	ACAGCCTTCCCGCAGG 79322	TC	
			CCT GCGGGAAGGCTGT		
			GGA CGCCCTTCCGACA		

GAM2203	LDLR	3'	GGGATTGGCAATTGTCCCA 6741	A C	GT
			TGGG AC ATTGCCAA CT		
			ACCC TG TAACGGTT GG		
			C T AG		
GAM2203	NRIP1	3'	TACCAAACCTCAGGTGATTCC 60624	ACC TG A_ C	
			GGA AT CC AGT TGGTA		
			CCT TA GG TCA ACCAT		
			_____ GT AC A		
GAM2203	PSEN2	3'	ACCAGACTTTGGCTCCC 25950	ACCATT _	
			GGGA GCCAA GTCTGGT		
			CCCT CGGTT CAGACCA		
			_____ T		
GAM2203	PSEN2	3'	ACCAGACTTTGGCTCCC 6542	ACCATT _	
			GGGA GCCAA GTCTGGT		
			CCCT CGGTT CAGACCA		
			_____ T		
GAM2203	FLJ12604	3'	ACATGGTAAATGGTTCCCA 65059	_ A	
			TGGGAACCAT TGCCA GT		
			ACCCTTGGTA ATGGT CA		
			AA A		
GAM2203	FLJ13081	3'	ACATGGCAGTGGTTCCCA 46169	A	
			TGGGAACCAT TGCCA GT		

ACCCTTGGTGACGGT CA
 A
 GAM2203 FLJ23093 3' ACCAGACTCCTCAGGTTCC 45321 AT CCA
 GGAACC TG AGTCTGGT
 ||||| || |||||
 CCTTGG AC TCAGACCA
 _ TCC
 GAM2203 GP5 3' ACCAGACTCACGGTCTCCA 16857 GA AT CCA
 TGG ACC TG AGTCTGGT
 ||| ||| || |||||
 ACC TGG AC TCAGACCA
 TC C_ _
 GAM2203 KIAA0286 3' ACCAGACTTACTGGCTCACCA 68855 _ A TTGCC
 TGG GA CCA AAGTCTGGT
 ||| ||| |||||
 ACC CT GGT TTCAGACCA
 A C CA_
 GAM2203 MGC10540 3' ACCAGACTCAAAAGGACTCCA 51356 AA A GCCA
 TGGG CC TT AGTCTGGT
 |||| ||| |||||
 ACCT GG AA TCAGACCA
 CA A AC_
 GAM2203 LOC157226 5' TACCGCAGGCAAAGGTTCCCA 64640 A AAGTC
 TGGGAACC TTGCC TGGTA
 ||||| |||| |||||
 ACCCTTGG AACGG GCCAT
 A AC_
 GAM2204 ANGPT4 3' GTACCTTGAATGGGCT 32572 GGCA
 AGCCCAT T GGGGTAC
 ||||| |||||
 TCGGGTAA TTCCATG
 G_
 GAM2204 ASS 5' GGCACCCCTGCCAGTCCTGCTC 55026 CC_ A
 GAGC ATTGGCAGGGGT CC
 ||| ||||| ||||| ||
 CTCG TGACCGTCCCCA GG
 TCC C
 GAM2204 BAK1 3' TACCCTTGTGAGAGCCCA 93634 A CCA G
 TG GC TT GCAGGGGT
 || || || |||||
 AC CG GA TGTTCCCAT
 C A_ G
 GAM2204 DNASE1L1 3' GGTACCGATATGCCAATGGGCC 23018 A A_____ GGTA
 A TG GCCCATTGGC GG C
 || ||||| || |
 AC CGGGTAACCG CC G
 _ TATAG_ ATGG
 GAM2204 DUSP6 3' ACACCAAATCATGGGCTCA 66576 T CAG _
 TGAGCCCAT GG GG GT
 ||||| || |||

			ACTCGGGTA CT CC CA		
			_ AAA A		
GAM2204 MN1	3'	ACACTTTGCCAATTAGCTCA	11647	CC	_
		TGAGC ATTGGCAGGG GT			
		ACTCG TAACCGTTTC CA			
		AT A			
GAM2204 MPP2	3'	GCAGGGGCCAGTGGGCTCA	60520	AGGG	
		TGAGCCCATTGGC GT			
		ACTCGGGTGACCG CG			
		GGA			
GAM2204 SULT1A2	3'	CCCTGACCAATGGGCTCA	72672		_
		TGAGCCCATTGG CAGGG			
		ACTCGGGTAACC GTCCC			
		A			
GAM2204 SULT1A3	3'	CCCTGACCAATGGGCTCA	13483		_
		TGAGCCCATTGG CAGGG			
		ACTCGGGTAACC GTCCC			
		A			
GAM2204 TRPM2	3'	GGCACCCCTGCAGAGGCTC	13868	CATTG	A
		GAGCC GCAGGGGT CC			
		CTCGG CGTCCCCA GG			
		AGA__ C			
GAM2204 XBP1	3'	ACTTTTGCCAATGAACTC	18674	CC	
		GAG CATTGGCAGGGGT			
		CTC GTAACCGTTTTCA			
		AA			
GAM2204 BMF	3'	GGTACCGGTGCCATATGGGCTC	54286	_ A_____	GGTA
A		TGAGCCCAT TGGC GG C			
		ACTCGGGTA ACCG CC G			
		T TGG__ ATGG			
GAM2204 DKFZP727M111	5'	GCTTTTGCCAGTGAGCCCA	32061	A C	
		TG GC CATTGGCAGGGGT			
		AC CG GTGACCGTTTTCG			
		C A			
GAM2204 FLJ13162	5'	GCACCCTCCATGGGCTCA	47185	T C	_
		TGAGCCCAT GG AGGG GT			
		ACTCGGGTA CC TCCC CG			
		_ _ A			
GAM2204 GMPPB	5'	ACTTCTGCAATAAGCCCA	97429	A CC	G
		TG GC ATTG CAGGGGT			

			AC CG TAAC GTCTTCA		
			C AA _		
GAM2204	KIAA0444	3'	TGCCCCATGGGCTCA	63006	TGGCA
			TGAGCCCAT GGGGTA		
			ACTCGGGTA CCCCCT		
GAM2204	KIAA0963	3'	GACCCACAAGGGCTCA	31033	A GCAG A
			TGAGCCC TTG GGGT C		
			ACTCGGG AAC CCCA G		
			_ A _ C		
GAM2204	KIAA1649	3'	GCTTATGACCAATGGGCCA	67517	A _ GG
			TG GCCCATTGG CA GGT		
			AC CGGGTAACC GT TCG		
			_ A AT		
GAM2204	KIAA1649	5'	GCTTATGACCAATGGGCCA	51243	A _ GG
			TG GCCCATTGG CA GGT		
			AC CGGGTAACC GT TCG		
			_ A AT		
GAM2204	KIAA1813	3'	GCTTCTGCCAAGAACTCA	70825	CCCA
			TGAG TTGGCAGGGGT		
			ACTC AACCGTCTTCG		
			AAG_		
GAM2204	KIAA1813	5'	GGCTCCCCCACCACCAATGGGC	70828	CA_ TA
			GCCCATTGG GGGG CC		
			CGGGTAACC CCCC GG		
			ACC TC		
GAM2204	MAP1LC3A	3'	ACCCCTGCTGTGTGGTTCA	51679	_ T
			TGAGCC CAT GGCAGGGGT		
			ACTTGG GTG TCGTCCCCA		
			T _		
GAM2204	MGC11316	3'	GGTGCAATGCCAAGGACTCA	53047	C A GG
			TGAG CC TTGGCAG GTACC		
			ACTC GG AACCGTT CGTGG		
			A _ A_		
GAM2204	PDE8B	5'	GGCACCCCTGCCCGGCCTC	68203	C ATT A
			GAG CC GGCAGGGGT CC		
			CTC GG CCGTCCCCA GG		
			C C_ C		
GAM2204	PRO0529	3'	TACTCACCAATGGGACCA	26857	AG CAG
			TG CCCATTGG GGGTA		

AC GGGTAACC CTCAT
 CA A__
 GAM2204 RAB17 3' CCCCTGCCTGGGCCA 42617 A TT
 TG GCCCA GGCAGGGG
 || |||| |||||
 AC CGGGT CCGTCCCC

 — —
 GAM2204 UBE2G1 3' ACTCCTGCCAAGAGCCCA 13950 A CCA
 TG GC TTGGCAGGGGT
 || || |||||
 AC CG AACCGTCCTCA
 C AG_
 GAM2204 LOC115708 3' GGTACCCCTACCCCTCA 73920 CCCATT C
 TGAG GG AGGGGTACC
 ||| || |||||
 ACTC CC TCCCCATGG
 C__ A
 GAM2204 LOC150481 3' GCACCTAACAATGGGTCA 80705 G GC G
 TGA CCCATTG AGG GT
 ||| ||||| ||| ||
 ACT GGGTAAC TCC CG
 — AA A
 GAM2204 LOC153196 5' GGCAGTGCCTTGCCATCGGGCC 87171 A AT __ A
 CA TG GCCC TGGCAGGG GT CC
 || |||| ||||| |||
 AC CGGG ACCGTTCC CA GG
 C CT GT C
 GAM2204 LOC153711 5' ACCTGTTAGCCGATGGGCCCA 87342 A AG_
 TG GCCCATTGGC GGGT
 || ||||| |||
 AC CGGGTAGCCG TCCA
 C ATTG
 GAM2204 LOC157860 3' GGCACCCCCTCCTGGGCTC 87878 TT CA A
 GAGCCCA GG GGGGT CC
 ||||| || |||||
 CTCGGGT CC CCCCA GG
 — TC C
 GAM2204 LOC158014 5' GTGCCACCCATGGGCTCA 82566 T CAGG
 TGAGCCCAT GG GGTAC
 ||||| || |||||
 ACTCGGGTA CC CCGTG
 — CA_
 GAM2204 LOC158191 3' GCACCTAACAATGGGTCA 82677 G GC G
 TGA CCCATTG AGG GT
 ||| ||||| ||| ||
 ACT GGGTAAC TCC CG
 — AA A
 GAM2204 LOC203378 5' ATCTCTGCCAACAGTCTCA 92276 CCCA
 TGAG TTGGCAGGGGT
 ||| |||||

		ACTC AACCGTCTCTA			
		TGAC			
GAM2204	LOC203378 3'	GGTATTTTGCCCAAAGGCTCA	92295	CATT	G
		TGAGCC GGCAGGG TACC			
		ACTCGG CCGTTTT ATGG			
		AAAC _			
GAM2204	LOC204970 3'	GGCACCCCTGCGGGCTCA	90964	ATTG	A
		TGAGCCC GCAGGGGT CC			
		ACTCGGG CGTCCCCA GG			
		_____ C			
GAM2204	LOC219700 5'	GGCTTCCCTGCCATGGACTCA	94653	C T	TA
		TGAG CCAT GGCAGGGG CC			
		ACTC GGTA CCGTCCCT GG			
		A _ TC			
GAM2204	LOC256126 3'	GCCCCTGCCATAGGCCCA	97015	A CAT	
		TG GCC TGGCAGGGGT			
		AC CGG ACCGTCCCCG			
		C AT_			
GAM2204	LOC51246 3'	ACCTGGGCCAATGGGCCA	33636	A	AG
		TG GCCATTGGC GGGT			
		AC CGGGTAACCG TCCA			
		_ GG			
GAM2204	LOC90190 3'	ACTGTTACCAATGGGCTC	62421	C G	
		GAGCCCATTTGG AG GGT			
		CTCGGGTAACC TT TCA			
		A G			
GAM2205	MEF2D 3'	AGTGGGCAAGAGGACACC	98696	C_	AGAT
		GGGTGTCCTT GCC CACT			
		CCCACAGGAG CGG GTGA			
		AA _____			
GAM2205	PRY 3'	GTGAGGAAAAGACACCCT	60894	C CG	AGA
		AGGGTGTC TT CC TCAC			
		TCCCACAG AA GG AGTG			
		_ AA _____			
GAM2205	PTPN7 3'	AGTGATCTGGGGGTACCC	12592	GT TTCG	
		GGGT CC CCAGATCACT			
		CCCA GG GGTCTAGTGA			
		TG _____			
GAM2205	PTPN7 3'	AGTGATCTGGGGGTACCC	55458	GT TTCG	
		GGGT CC CCAGATCACT			

	CCCA GG GGTCTAGTGA	
	TG ____	
GAM2205 Apg4B	3' CTGGTAGCAGAGGACACCC 26182	C____
	GGGTGTCCTT GCCAG	
	CCCACAGGAG TGGTC	
	ACGA	
GAM2205 KIAA1244	3' GGTGATCTGAAAAAACACCCT 72448	CCTTCGC
	T AAGGGTGT CAGATCACT	
	TTCCACA GTCTAGTGG	
	AAAAA_	
GAM2205 LOC135818	3' TGAGGGACAAGGACACCCTT 75753	CG AGA
	AAGGGTGTCTT CC TCA	
	TTCCACAGGAA GG AGT	
	CA G__	
GAM2205 LOC150225	3' GTGACGCTAGGACACCCT 86203	TC CAGA
	AGGGTGTCTT GC TCAC	
	TCCACAGGA CG AGTG	
	T_ C__	
GAM2205 LOC151178	3' ATCTGGTCACACCACTT 80952	_ CCTTC
	AAG GGTGT GCCAGAT	
	TTC CCACA TGGTCTA	
	A C__	
GAM2205 LOC152286	5' GTTTGCGAAGGAAACCCTT 86813	G C
	AAGGGT TCCTTCGC AGAT	
	TTCCA AGGAAGCG TTTG	
	A _	
GAM2205 LOC159160	3' GTGAGGAAAAGACACCCT 61155	C CG AGA
	AGGGTGTCTT CC TCAC	
	TCCACAG AA GG AGTG	
	_ AA _	
GAM2205 LOC219938	3' CTGTATCAGAAGAACATCCTT 93180	C GC__
	AAGGGTGT CTTC CAG	
	TTCTACA GAAG GTC	
	A ACTAT	
GAM2206 LAMC1	3' TTGCAAAGTTTTACGTCA 11275	C CC_
	TGACGTGGA AT GCAA	
	ACTGCACTT TG CGTT	
	T AAA	
GAM2206 OPA1	3' TTGCGGGTGGAACAGTCA 56430	G GA_
	TGAC TG CATCCGCAA	

		ACTG AC GTGGGCGTT		
		_ AAG		
GAM2206	PITX2	5' TTGCGGAGGGTGCGCTCA 6161	C G A_	
		TGA GTG AC TCCGCAA		
		ACT CGC TG AGGCGTT		
		_ G GG		
GAM2206	LOC144848	3' TGGAGGATGTCCACATCA 73961	C G_	
		TGA GTGGACATCC CA		
		ACT CACCTGTAGG GT		
		A AG		
GAM2206	LOC221495	5' TTGCAGGGGCATCACGTTA 95498	ACA _	
		TGACGTGG TCC GCAA		
		ATTGCACT GGG CGTT		
		ACG A		
GAM2206	LOC256520	3' GCAGATTTTGTCTACGTCA 97667	_ _ _ C	
		TGACGTGGA CA TC GC		
		ACTGCATCT GT AG CG		
		T TTT A		
GAM2207	DJ971N18.2	3' GCCCTGTGAAATGAAAGCCAAG 41263	AT AA _ A	
		CTTG TTTCATT TC CAG GC		
		GAAC AAAGTAA AG GTC CG		
		CG _ T C		
GAM2207	FLJ10498	3' GCTCTGAAAATTGGTAAATCAA 36677	_ TTAATC	
	G	CTTGATTT TCA CAGAGC		
		GAACTAAA GGT GTCTCG		
		T TAAAA_		
GAM2207	GRSF1	3' GCTCTAGATAGGAAAAAATCA 10880	CA A_ C	
	G	TTGATTTT TT ATC AGAGC		
		GACTAAAA AG TAG TCTCG		
		AA GA A		
GAM2207	KIAA1046	3' CTGATTTTAATGAAAATCA 30661	TC_	
		TGATTTTCATTAA CAG		
		ACTAAAAGTAATT GTC		
		TTA		
GAM2207	KIAA1107	5' CTCTGGTGATATAAAAATCAA 64690	C TAAT	
		TTGATTTT AT CCAGAG		
		AACTAAAA TA GGTCTC		
		A TAGT		
GAM2207	KIAA1145	3' CTCAGGAAATGAAAACAA 66237	A AA A	
		TTG TTTTCATT TCC GAG		

AAC AAAAGTAA AGG CTC
— — A
GAM2207 LCE 3' GCTCTGGAAC TCAAAATCAA 44260 CATTAA
TTGATTTT TCCAGAGC
||||| |||||
AACTAAAA AGGTCTCG
CTCA__
GAM2207 MGC16175 3' CTCTGAATTAATGACTGT 52278 TT C
AT TCATTAAT CAGAG
|| ||||| |||||
TG AGTAATTA GTCTC
TC A
GAM2207 SPANXB1 3' CTTCGGCAATGAAAATAAAGT 51624 G AAT AG
ACTT ATTTTCATT CC AG
||| ||||| || ||
TGAA TAAAAGTAA GG TC
A C__ CT
GAM2207 TRAG3 3' TGGTGATGAAAATAAAGT 68134 G AT
ACTT ATTTTCATTA CCA
||| ||||| |||
TGAA TAAAAGTAGT GGT
A —
GAM2207 LOC221688 5' GCTCCATATAGTATGAAAATCA 95309 TAATCCA_
AGT ACTTGATTTTCAT GAGC
||||||| |||
TGA ACTAAAAGTA CTCG
TGATATAC
GAM2208 CARKL 3' TAAGATGAGAGCAAATGCCTGA 26108 CG G_ AC_
TCA TGA AGGCATTTG CT CTTA
||| ||||| || |||
ACT TCCGTAAAC GA GAAT
AG GA GTA
GAM2208 CHRNA2 5' GGGAAGCCAAATGCCTCTCA 7430 C A
TGA GAGGCATTTGGCT CCT
||| ||||| |||
ACT CTCCGTAAACCGA GGG
— A
GAM2208 HLF 3' TAAGGTAGCCCTCTCATC 10935 C CATTT
GA GAGG GGCTACCTTA
|| ||| |||||
CT CTCT CCGATGGAAT
A C__
GAM2208 FLJ10997 3' TTAAGATGTGGCAAATGCCT 37516 G _
AGGCATTTG CTAC CTTAA
||||| ||| |||||
TCCGTAAAC GGTG GAATT
— TA
GAM2208 LOC255452 3' AAGGCAGCCACGGTGTCTC 99382 _ A
GAGGCATT TGGCT CCTT
||||| ||||| |||

		CTCTGTGG ACCGA GGAA	
		C C	
GAM2208	LOC51291	3' GTGGCCAAACACCCCGCCA 33812	A A CA
		TG CG GG TTTGGCTAC	
		AC GC CC AAACCGGTG	
		C C AC	
GAM2209	ALDH1B1	3' TCCAGCAATTCCACAACCACCT 7327	CC G CA
		AGGTGGTT GGAAT GC GGA	
		TCCACCAA CCTTA CG CCT	
		CA A A_	
GAM2209	APM1	3' TCCTGGCCTAGGTGATCCACC 17793	TT_ GGAAT
		GGTGG CC GGCCAGGA	
		CCACC GG CCGGTCCT	
		TAGT AT_	
GAM2209	CLDN3	5' CCCCGCACCCGGAGCCACC 8960	AATG CA
		GGTGGTTCCGG GC GG	
		CCACCGAGGCC CG CC	
		CA_ CC	
GAM2209	DMRT2	3' CCCAGCCCAGTGGAAACCACC 22649	GAAT CA
		GGTGGTTCCG GGC GG	
		CCACCAAGGT CCG CC	
		GAC_ AC	
GAM2209	FCGR2A	3' TCCTGAGCAAACAAAACCACCT 80033	CCGGAATG _
		AGGTGGTT GC CAGGA	
		TCCACCAA CG GTCCT	
		AACAAA_ A	
GAM2209	GALR1	5' CCTGGCCACCCCGGCGCCT 9424	GTT AA_
		AGGTG CCGG TGGCCAGG	
		TCCGC GGCC ACCGGTCC	
		_ CCC	
GAM2209	HHLA1	5' TCCTGGCTCAAAAAGCACC 20339	G CCG ATG
		GGTG TT GA GCCAGGA	
		CCAC AA CT CGGTCCT	
		G AAA _	
GAM2209	KRT5	5' TCCTGGGTAACAGAGCCACCT 6463	CGGAA G
		AGGTGGTTC TG CCAGGA	
		TCCACCGAG AT GGTCT	
		ACA_ G	
GAM2209	L1CAM	3' CCCAGCCACTCCCCAGCCAGCC 43986	_ CC A CA
	T	AGG TGGTT GGA TGGC GG	

TCC ACCGA CCT ACCG CC
 G CC C AC
 GAM2209 LDOC1 3' CCTGGCCATCCCCGGGATCCC 25547 T A_
 GG GGTTCGG ATGGCCAGG
 || ||||| |||||
 CC CTAGGGCC TACCGGTCC
 _ CC
 GAM2209 LETM1 3' TCTGGAATCCCGGAACCCCT 25556 T A GG
 AGG GGTTCGG AT CCAGG
 ||| ||||| || |||||
 TCC CCAAGGCC TA GGTCT
 _ C A_
 GAM2209 MSN 3' CCTGGCCACCACCCCCCACT 60881 TTCC AA_
 GGTGG GG TGGCCAGG
 |||| | |||||
 TCACC CC ACCGGTCC
 CC_ ACC
 GAM2209 PACE 3' CCTAGCCATTCTGTGTACC 11942 T _ C
 GGT CC GGAATGGC AGG
 ||| || ||||| |||
 CCA GG CCTTACCG TCC
 T T A
 GAM2209 POLL 3' TCCTGGCCACCCAGTACTCCC 26093 TG TCC AA
 GG GT GG TGGCCAGGA
 || || || |||||
 CC CA CC ACCGGTCCT
 CT TGA C_
 GAM2209 RNH 5' TCCTGGCCATCCAAGCCTCCT 60372 T CC A
 AGG GGTT GGA TGGCCAGGA
 ||| ||| ||| |||||
 TCC CCGA CCT ACCGGTCCT
 T A_ _
 GAM2209 SLC2A3 3' TCCCGGCATGGGAAAGCCACCT 23645 _ GGAATG A
 AGGTGGT TCC GCC GGA
 ||||| ||| ||| |||
 TCCACCG AGG CGG CCT
 AA GTA_ C
 GAM2209 SLC4A7 3' CCTGGCCACAGAGCCACCT 14616 CGGAA
 AGGTGGTTC TGGCCAGG
 ||||| |||||
 TCCACCGAG ACCGGTCC
 AC_
 GAM2209 STUB1 3' TCCTGGCCACCCCGACCGCTT 76802 TC AA
 AGGTGGT CGG TGGCCAGGA
 ||||| ||| |||||
 TTCGCCA GCC ACCGGTCCT
 _ CC
 GAM2209 SULT1C1 3' TCCTGGCCATTCAGGCAACT 8324 _ G
 GGTT CC GAATGGCCAGGA
 |||| || |||||

			TCAA GG CTTACCGGTCCT		
			C A		
GAM2209	SYNGR1	3'	CCTGGCCACCCACCTCCT 17501	T	TCC AA
			AGG GGT GG TGGCCAGG		
			TCC CCA CC ACCGGTCC		
			T C__ __		
GAM2209	SYNGR3	3'	TCCTGGCCACTGTTCCCATC 16123	TTC	AA
			GGTGG CGG TGGCCAGGA		
			CTACC GTC ACCGGTCCT		
			CTT __		
GAM2209	UGDH	3'	TCCTGACCTTGTGAACCACC 14005	_	AAT C
			GGTGGTTC CGG GG CAGGA		
			CCACCAAG GTT CC GTCCT		
			T __ A		
GAM2209	WNT4	3'	CCTGCGCCGGCAACCACCT 48482	_	AATGGC
			AGGTGGTT CCGG CAGG		
			TCCACCAA GGCC GTCC		
			C GC__		
GAM2209	ATP6V1H	5'	CCCGGCGCCCCGGACCACC 32514	T	AATG A
			GGTGGT CCGG GCC GG		
			CCACCA GGCC CGG CC		
			_ CCG_ C		
GAM2209	CALN1	3'	CCTGACCCCCGAACCACC 49662	C	AAT C
			GGTGGTTC GG GG CAGG		
			CCACCAAG CC CC GTCC		
			C __ A		
GAM2209	CNNM2	5'	CCGTGGGCCGAGACCACCT 34940	TC	AATGG _
			AGGTGGT CGG CCA GG		
			TCCACCA GCC GGT CC		
			GA G__ G		
GAM2209	DKFZP761I2123	3'	TCCCAAACCTCCCCAAAACAC 49549	_	CC AAT_ CCA_
	ACCT		AGGTG GTT GG GG GGA		
			TCCAC CAA CC CC CCT		
			A AA CCCT AAAC		
GAM2209	FLJ11618	5'	CCGACCATTTCGGCCACCT 42623	TT	_ CCA
			AGGTGG CCGGAA TGG GG		
			TCCACC GGCCTT ACC CC		
			_ T AG_		
GAM2209	FLJ12649	3'	TCCTGGCCTCAAGAGATCCACC 45096	T	CGGAAT
			GGTGG TC GGCCAGGA		

		CCACC AG CCGGTCCT	
		T AGAACT	
GAM2209	FLJ12747 3'	CCTGGCTGGAAAACCACT 50665	___ GGAAT
		AGGTGGT TCC GGCCAGG	
		TCCACCA AGG TCGGTCC	
		AA _____	
GAM2209	FLJ22678 3'	CCCCAAAACCAGAGCCACCT 61117	C AA_ CCA
		AGGTGGTTC GG TGG GG	
		TCCACCGAG CC ACC CC	
		A AAA _____	
GAM2209	FLJ23420 5'	TCCTGGCCATCCTGGTCTAC 47544	TT A
		GTGG CCGG ATGGCCAGGA	
		CATC GGTC TACCGGTCCT	
		T_ C	
GAM2209	FLJ23519 5'	TCCTGGCCATCCAAGCCTCCT 50962	T CC A
		AGG GGTT GGA TGGCCAGGA	
		TCC CCGA CCT ACCGGTCCT	
		T A_ _	
GAM2209	FLJ23519 5'	TCCTGGCCATCCAAGCCTCCT 50963	T CC A
		AGG GGTT GGA TGGCCAGGA	
		TCC CCGA CCT ACCGGTCCT	
		T A_ _	
GAM2209	FLJ31300 3'	TCCTGGCCACCTGCCAGCCT 58933	_ TCC AA
		AGG TGGT GG TGGCCAGGA	
		TCC ACCG CC ACCGGTCCT	
		G T_ _	
GAM2209	GPR108 3'	TCCTTACCCCGGGACCACC 69633	AAT CC
		GGTGGTTCCGG GG AGGA	
		CCACCAGGGCC CC TCCT	
		___ AT	
GAM2209	GTF3C1 3'	CCTGGCTGGGACTGAACCACC 9506	CGGAA
		GGTGGTTC TGGCCAGG	
		CCACCAAG GTCGGTCC	
		TCAGG	
GAM2209	HBP1 3'	TCCCAGCCTAAGAGCCACCT 25321	CGGAAT CA
		AGGTGGTTC GGC GGA	
		TCCACCGAG CCG CCT	
		AAT_ AC	
GAM2209	HSPC063 3'	CCCAGCATTTCCAAAACCTACCT 27121	CC TG CA
		AGGTGGTT GGAA GC GG	

		TCCATCAA CCTT CG CC	
		AA TA AC	
GAM2209	HTCD37	3' CCTCTGTCCAGAGCCACC 68298	C A CC
		GGTGGTTC GG ATGG AGG	
		CCACCGAG CC TGTC TCC	
		A C _	
GAM2209	KIAA0444	3' CCTGACATCCCCAAAACCATCT 62997	CC A GC
		AGGTGGTT GG ATG CAGG	
		TCTACCAA CC TAC GTCC	
		AA C A_	
GAM2209	KIAA0683	3' CCTGGAGGCCTCCCCAGGACCA 32762	C AAT _
	CC	GGTGGTTC GG GGCC AGG	
		CCACCAGG CC CCGG TCC	
		A CCT AGG	
GAM2209	KIAA1001	3' TCCTTGTTTTCTCCAAAACCAC 31013	CC AT_ C
	CT	AGGTGGTT GGA GGC AGGA	
		TCCACCAA CCT TTG TCCT	
		AA CTT T	
GAM2209	KIAA1045	3' CCTGGCCACAAAACCACT 71603	CCGGAA
		GGTGGTT TGGCCAGG	
		TCACCAA ACCGGTCC	
		AAC_	
GAM2209	KIAA1274	5' CCACCTCCGGAGCCACCT 93009	A_
		AGGTGGTTCCGGA TGG	
		TCCACCGAGGCCT ACC	
		CC	
GAM2209	KIAA1719	3' TCCTGGTCAGGGCCGGAACCAT 68736	AA_
	CT	AGGTGGTTCCGG TGGCCAGGA	
		TCTACCAAGGCC ACTGGTCCT	
		GGG	
GAM2209	KIAA1887	5' CCTTCCCCCAGAACCACC 77277	C AAT CC
		GGTGGTTC GG GG AGG	
		CCACCAAG CC CC TCC	
		A _ CT	
GAM2209	MDS025	5' TCCTGTGGTGCCAGAACTACCT 41830	C A G C
		AGGTGGTTC GG AT GC AGGA	
		TCCATCAAG CC TG TG TCCT	
		A G G _	
GAM2209	MGC11134	5' CCTGCCTCCCGGACCACC 49687	T AAT C
		GGTGGT CCGG GGC AGG	

CCACCA GGCC CCG TCC
 _ CT_ _
 GAM2209 MGC13040 5' TCCTGAGTGAACCCCGAACCCAC 53044 C AATG _
 C GGTGGTTC GG GC CAGGA
 ||||| || |||||
 CCACCAAG CC TG GTCCT
 C CAAG A
 GAM2209 MGC15435 3' CCCC GTGAACCCAGACCACC 51395 CC A_ CCA
 GGTGGTT GG ATGG GG
 ||||| || ||| ||
 CCACCAG CC TGCC CC
 AC AAG _
 GAM2209 MGC4638 3' CCCCAACCCAACAACCACCT 49734 CC_ AA CCA
 AGGTGGTT GG TGG GG
 ||||| || ||| ||
 TCCACCAA CC ACC CC
 CAA CA _
 GAM2209 NTT5 3' CCTGGATCCAGAACCACTT 26731 C ATGG
 AGGTGGTTC GGA CCAGG
 ||||| ||| |||||
 TTCACCAAG CCT GGTCC
 A A_
 GAM2209 PCK2 5' TCCTGGCCACCCCGCAGCCCCT 64483 T C AA
 AGG GGTT CGG TGGCCAGGA
 ||| ||| ||| |||||
 TCC CCGA GCC ACCGGTCCT
 _ C CC
 GAM2209 PIPPIN 3' CCTGGCCACCCAGACCCC 80508 T CC AA
 GG GGTT GG TGGCCAGG
 || ||| || |||||
 CC CCAG CC ACCGGTCC
 _ AC _
 GAM2209 PRO2086 5' TCCTAGCCAGACTGAATCACCT 26921 C AA C
 AGGTGGTTC GG TGGC AGGA
 ||||| || ||| |||
 TCCACTAAG TC ACCG TCCT
 _ AG A
 GAM2209 PV1 3' CCCAACCACCCAGGGCCACC 49374 C AA CCA
 GGTGGTTC GG TGG GG
 ||||| || ||| ||
 CCACCGGG CC ACC CC
 A C_ AAC
 GAM2209 SYT6 3' CCATCTCCGAAACCACCT 79518 C _
 AGGTGGTT CGGA ATGG
 ||||| ||| |||
 TCCACCAA GCCT TACC
 A C
 GAM2209 LOC112616 3' TCCTGCTTCTAGAACCACCT 57297 CG AT C
 AGGTGGTTC GA GGC AGGA
 ||||| || ||| |||

	TCCACCAAG CT TCG TCCT	
	AT _ _	
GAM2209 LOC124216 3'	TCCTGGCCACCTCTCCTCACC 74742	TTCC A__
	GGTGG GGA TGGCCAGGA	
	CCACT CCT ACCGGTCCT	
	_ CTCC	
GAM2209 LOC135932 5'	TCCCAGCCACTGGGCTACCT 76699	T AA CA
	AGGTGGT CCGG TGGC GGA	
	TCCATCG GGTC ACCG CCT	
	_ _ AC	
GAM2209 LOC144195 3'	TCCCGGCATGGGAAAGCCACCT 60988	_ GGAATG A
	AGGTGGT TCC GCC GGA	
	TCCACCG AGG CGG CCT	
	AA GTA_ C	
GAM2209 LOC144308 3'	CCCGGCCCCAGAGGAACCCACC 83978	_ GGAAT A
T	AGGTGG TTCC GGCC GG	
	TCCACC AAGG CCGG CC	
	C AGACC C	
GAM2209 LOC145501 3'	CCTGGCCACTCATTTTTCTCCT 77766	T TTCCG A
	AGG GG GA TGGCCAGG	
	TCC CT CT ACCGGTCC	
	T TTTTA C	
GAM2209 LOC148114 5'	TCCTAACCATCCCCTCTGACCT 79365	_ TTCC A CC
	AGGT GG GG ATGG AGGA	
	TCCA TC CC TACC TCCT	
	G TC_ C AA	
GAM2209 LOC149506 5'	TCCTCCAGAGACCCCAAAGGCC 85649	CC_ AA_ CC
ACCT	AGGTGGTT GG TGG AGGA	
	TCCACCGA CC ACC TCCT	
	AAA CCAGAG _	
GAM2209 LOC150837 3'	CCTGAGCAAGAACCACCT 80802	CGGAATG _
	AGGTGGTTC GC CAGG	
	TCCACCAAG CG GTCC	
	AA_ A	
GAM2209 LOC152343 5'	TCCCAGCCTTGTAACCACCT 81437	C AAT CA
	AGGTGGTT CGG GGC GGA	
	TCCACCAA GTT CCG CCT	
	T _ AC	
GAM2209 LOC154760 5'	TCCCAGCCACTGGGCTACCT 87456	T AA CA
	AGGTGGT CCGG TGGC GGA	

	TCCATCG GGTC ACCG CCT		
	— — AC		
GAM2209 LOC159193 5'	TCCTGGCCACCCCGGAGTCACC 83055	GT	AA
	GGTG TCCGG TGGCCAGGA		
	CCAC AGGCC ACCGGTCCT		
	TG CC		
GAM2209 LOC200301 5'	CCCAGCCACTGGTGCCACC 90137	TT_	AA CA
	GGTGG CCGG TGGC GG		
	CCACC GGTC ACCG CC		
	CGT — AC		
GAM2209 LOC200940 5'	CCTGGCCACCAGTTCCACC 90391	TTCC	AA
	GGTGG GG TGGCCAGG		
	CCACC CC ACCGGTCC		
	TTGA —		
GAM2209 LOC219401 5'	CCCCAAGTCAGAGCCACCT 94385	C AA	CCA
	AGGTGGTTC GG TGG GG		
	TCCACCGAG CT ACC CC		
	A GA —		
GAM2209 LOC220954 5'	CCTGGCCACCCTCTCACCT 94758	TTCC	AA
	AGGTGG GG TGGCCAGG		
	TCCACT CC ACCGGTCC		
	CTC_ —		
GAM2209 LOC256158 5'	CCTGGCCACTGGCCCCCAC 99490	TT_	AA
	GTGG CCGG TGGCCAGG		
	CACC GGTC ACCGGTCC		
	CCC —		
GAM2209 LOC257612 5'	TCCTGTGTCCCGGAACCCCT 99738	T	AAT _
	AGG GGTTCCGG GGC CAGGA		
	TCC CCAAGGCC CTG GTCCT		
	C — T		
GAM2209 LOC90019 5'	CCTGGCCACCCCGTGCTGCCT 57527	TG TC	AA
	AGG GT CGG TGGCCAGG		
	TCC CG GCC ACCGGTCC		
	GT T_ CC		
GAM2209 LOC90190 3'	TCCCAATTTCAAACCCACCT 62432	CC	GGCCA
	AGGTGGTT GGAAT GGA		
	TCCACCAA CTTTA CCT		
	AA AC_		
GAM2209 LOC91748 3'	CCCCATACCAGAGCCACCT 67637	C A	CCA
	AGGTGGTTC GG ATGG GG		

TCCACCGAG CC TACC CC
 A A ____
 GAM2209 LOC92822 3' CCTGGAGGCGGAACCACC 71182 GAATGG
 GGTGGTTCCG CCAGG
 ||||| ||||
 CCACCAAGGC GGTCC
 GGA____
 GAM2210 ELF3 3' TGACCTTGACCTTGACCAA 16685 T GAT AAA
 TTGGT CAAGG GG GTCA
 ||||| || ||||
 AACCA GTTCC TC CAGT
 _ AGT ____
 GAM2210 JAK2 3' TGACCTTCATTCTGAGACCAA 18318 CAA AA
 TTGGTT GGGATGGA GTCA
 ||||| ||||| ||||
 AACCAG TCTTACTT CAGT
 AG_ C_
 GAM2210 SLC10A2 5' ACTCTCTGTCTTGACCAA 6590 CAA A
 TTGGTT GGGATGGA AGT
 ||||| ||||| ||||
 AACCAG TTCTGTCT TCA
 ____ C
 GAM2210 FLJ10803 3' GTGACTTTCAGTTAAAGCCAA 37205 CAAGG G
 TTGGTT GAT GAAAGTCAC
 ||||| || ||||| |||||
 AACCGA TTG CTTTCAGTG
 AA__ A
 GAM2210 KIAA1958 5' GTGACTTTGAACCCCAAACC 82788 CAA ATGG
 GGTT GGG AAAGTCAC
 |||| || ||||| |||||
 CCAA CCC TTTCAGTG
 A__ CAAG
 GAM2210 MARCKS 3' ACTTTCCACCCTGCCCA 11411 TTCA A
 TGG AGGG TGGAAAGT
 || ||||| ||||| |||||
 ACC TCCC ACCTTTCA
 CG__ _
 GAM2210 TUB 5' GTGGGACCATCCCTTAAACC 13898 C AAAG
 GGTT AAGGGATGG TCAC
 ||||| ||||| ||||
 CCAA TTCCCTACC GGTG
 A AG__
 GAM2210 LOC80298 3' ACTTTTACCTTGAACCA 48062 GATG
 TGGTTCAAGG GAAAGT
 ||||| ||||| |||||
 ACCAAGTTCC TTTTCA
 A____
 GAM2211 ELF3 3' TGACCTTGACCTTGACCAA 16685 T GAT AAA
 TTGGT CAAGG GG GTCA
 ||||| ||||| || ||||

			AACCA GTTCC TC CAGT		
			AGT		
GAM2211	JAK2	3'	TGACCTTCATTCTGAGACCAA 18318	CAA	AA
			TTGGTT GGGATGGA GTCA		
			AACCAG TCTTACTT CAGT		
			AG_ C_		
GAM2211	SLC10A2	5'	ACTCTCTGTCTTGACCAA 6590	CAA	A
			TTGGTT GGGATGGA AGT		
			AACCAG TTCTGTCT TCA		
			C		
GAM2211	FLJ10803	3'	GTGACTTTCAGTTAAAGCCAA 37205	CAAGG	G
			TTGGTT GAT GAAAGTCAC		
			AACCGA TTG CTTTCAGTG		
			AA_ A		
GAM2211	KIAA1958	5'	GTGACTTTGAACCCCAAACC 82788	CAA	ATGG
			GGTT GGG AAAGTCAC		
			CCAA CCC TTTCAGTG		
			A_ CAAG		
GAM2211	MARCKS	3'	ACTTTCCACCCTGCCCA 11411	TTCA	A
			TGG AGGG TGGAAAGT		
			ACC TCCC ACCTTTCA		
			CG_ _		
GAM2211	TUB	5'	GTGGGACCATCCCTTAAACC 13898	C	AAAG
			GGTT AAGGGATGG TCAC		
			CCAA TTCCCTACC GGTG		
			A AG_		
GAM2211	LOC80298	3'	ACTTTTACCTTGAACCA 48062	GATG	
			TGGTTCAAGG GAAAGT		
			ACCAAGTTCC TTTCA		
			A_		
GAM2212	ABCC1	3'	CCCTGGTAAACCAAGCCTC 18435	AAAA CT_	A
			GAG GC GTTTACCA GG		
			CTC CG CAAATGGT CC		
			_ AAC C		
GAM2212	ABCC1	3'	CCCTGGTAAACCAAGCCTC 39599	AAAA CT_	A
			GAG GC GTTTACCA GG		
			CTC CG CAAATGGT CC		
			_ AAC C		
GAM2212	ABCC1	3'	CCCTGGTAAACCAAGCCTC 39602	AAAA CT_	A
			GAG GC GTTTACCA GG		

		CTC CG CAAATGGT CC		
		____ AAC C		
GAM2212 ANKH	3'	TCCTCAGAGTGGCTTTTCCT 55076	A	TG ACCA
		AG GAAAAGCC TTT AGGA		
		TC CTTTTCGG AGA TCCT		
		_ TG C__		
GAM2212 BAZ2A	3'	CCCCAGTTTTCAGATTTTCTCT 26507		GC TTT CAA
		AGAGAAAA CTG AC GG		
		TCTCTTTT GAC TG CC		
		A_ TTT ACC		
GAM2212 DSG1	3'	TCCTTAGCATTTCATAAACTTTT 10451		CC__ TTTACC
CTCT		AGAGAAAAG TG AAGGA		
		TCTCTTTTC AC TTCCT		
		AAAT TTACGA		
GAM2212 DUOX2	3'	CCCTGGGCAGGCCCTCTCT 26865	AAA	TTA A
		AGAGA GCCTGT CCA GG		
		TCTCT CGGACG GGT CC		
		CCC _ C		
GAM2212 EHD2	3'	TCCTCAGATGGGCCCTC 28230	AAAA	ACCA
		GAG GCCTGTTT AGGA		
		CTC CGGGTAGA TCCT		
		CC__ C__		
GAM2212 F9	3'	TCCCCAAATCAGTTTTTCTCT 5530		C TTTACCAA
		AGAGAAAAGC TG GGA		
		TCTCTTTTGTG AC CCT		
		_ TAAACC__		
GAM2212 GBF1	5'	TCCAGGAAACAGGCTCCTTCT 16093	A_	A AA
		AGAA AGCCTGTTT CC GGA		
		TCTT TCGGACAAA GG CCT		
		CC _ A_		
GAM2212 GLUL	3'	CCTCGTGGTGGAACCTTTCTT 10808		CCTG _
		GAGAAAAG TTTACCA AGG		
		TTCTTTTC AGGTGGT TCC		
		AA__ GC		
GAM2212 HDAC4	3'	TCCTTGGACCTTTAGCCTTTT 21252		A CTGTTTA
CT		AGAGAAA GC CCAAGGA		
		TCTTTTTCG GGTCCT		
		C ATTTCCA		
GAM2212 IGF2	3'	TCCCCGAAACAGGCTACTCTC 7038	AA	ACCAA
		GAGA AGCCTGTTT GGA		

			CTCT TCGGACAAA CCT		
			CA GCC__		
GAM2212 JUP	3'	CCTCTTTGCAGGCTTTTCCT	11108	A	TTACCA
		AG GAAAAGCCTGT	AGG		
		TC CTTTTCGGACG	TCC		
		__ TTTC__			
GAM2212 KCNH3	3'	TCCCTGGGGCAGGCCTCTC	65214	AAA	TA A
		GAGA GCCTGTT CCA GGA			
		CTCT CGGACGG GGT CCT			
		C__ __ C			
GAM2212 MAZ	3'	CCTTGGTACAAGCTCCTCTC	73778	AA C TT	
		GAGA AGC TGT ACCAAGG			
		CTCT TCG ACA TGGTTCC			
		CC A __			
GAM2212 PDE7A	3'	CCCTGGTTTGCCTTTTTCT	66134	A CTGTTT	A
		AGAGAAA GC ACCA GG			
		TCTTTTT CG TGGT CC			
		C TT__ C			
GAM2212 PIK3C2B	3'	TCCTCGGCCAGAGCCCTCTCT	12112	AAA _ TTTA	A
		AGAGA GC CTG CC AGGA			
		TCTCT CG GAC GG TCCT			
		CC_ A C__ C			
GAM2212 PKP2	3'	CCTTGGTTGTTTTTCTCT	17109	CTGTTT	
		AGAGAAAAGC ACCAAGG			
		TCTCTTTTGG TGGTTCC			
		T__			
GAM2212 PPL	3'	TCCTTGGTGTGTCCTCTC	12223	AAA CTGTT	
		GAGA GC TACCAAGGA			
		CTCT TG GTGGTTCCT			
		CC_ CT__			
GAM2212 PRKAR1A	3'	TCCTCTGGCAAACCTTTTCTTT	12283	CC TTTA _	
		AGAGAAAAG TG CCA AGGA			
		TTTCTTTTC AC GGT TCCT			
		AA __ C			
GAM2212 RFNG	3'	TCCACGGGAACAGGCTT	89563	A AA_	
		AAGCCTGTTT CC GGA			
		TTCGGACAAG GG CCT			
		_ CAC			
GAM2212 SLC2A3	3'	CTTGGAGCTTTTTTCT	23640	CTGTTTA	
		AGAGAAAAGC CCAAG			

TCTTTTTTCG GGTTC
 A_____
 GAM2212 SREBF2 3' TCCTCAGTTTTTATCAGGCTTT 17190 A TTT__ CA
 CTCT AGAGAAA GCCTG AC AGGA
 ||||| ||| || ||||
 TCTCTTT CGGAC TG TCCT
 _ TATTTT AC
 GAM2212 TAF1 3' CCTTGGTCAGCCTTCCCT 17230 AA C TTT
 AG AAG CTG ACCAAGG
 || ||| ||| |||||
 TC TTC GAC TGGTTCC
 CC C ____
 GAM2212 TAF1 3' CCTTGGTCAGCCTTCCCT 57982 AA C TTT
 AG AAG CTG ACCAAGG
 || ||| ||| |||||
 TC TTC GAC TGGTTCC
 CC C ____
 GAM2212 TEAD3 3' CCTTGGTGGGCACTGTTCCCT 13669 A A CC
 AG GAA AG TGTTTACCAAGG
 || ||| || |||||
 TC CTT TC ACGGGTGGTTCC
 C G ____
 GAM2212 TMPRSS3 5' CCTTGGTGGGTGGCCCTTTCCC 51515 A A_ T TT
 T AG GAAA GCC G TACCAAGG
 || ||| ||| ||| |||||
 TC CTTT CGG T GTGGTTCC
 C CC _GG
 GAM2212 TNFRSF1A 3' CCTCGATGTACATAGCTTTTCT 8377 C T CA__
 C GAGAAAAGC TGT TAC AGG
 ||||| ||| ||| |||
 CTCTTTTCG ATA ATG TCC
 _ C TAGC
 GAM2212 VDR 3' CCTTTCCTGCGGGCTTTTC 6343 TTACC
 GAAAAGCCTGT AAGG
 ||||| ||| |||
 CTTTTCGGGCG TTCC
 TCCT_
 GAM2212 ZNF219 3' TCCCAATAAACAGGTGTCTT 33557 AAA CCAA
 GAGA GCCTGTTTA GGA
 ||| ||||| ||| |||
 TTCT TGGACAAAT CCT
 G_ AACC
 GAM2212 ALK7 3' CCTTGAATAGTGCTTTTCTC 76242 _ TAC
 GAGAAAAGC CTGTT CAAGG
 ||||| ||| ||| |||
 CTCTTTTCG GATAA GTTCC
 T ____
 GAM2212 C11orf11 3' TCCTGGGAGCAGGCCTTCCTC 94882 A A A A
 GAG AA GCCTGTTT CCA GGA
 ||| || ||||| ||| |||

		CTC TT CGGACGAG GGT CCT	
		C C _ _	
GAM2212	DKFZP564O0463	3' CCTTGGACTCCAGATCTTTCTC 27124	AGC TTTA
	T	AGAGAAA CTG CCAAGG	
		TCTCTTT GAC GGTTC	
		CTA CTCA	
GAM2212	DPCR1	3' GTAAACAGGCTCATCTCT 55997	AA
		AGAGA AGCCTGTTTAC	
		TCTCT TCGGACAAATG	
		AC	
GAM2212	FLJ10350	3' CCCTGGGGGTGGGTCCTCTCT 97247	AAA TG A A
		AGAGA GCC TTT CCA GG	
		TCTCT TGG GGG GGT CC	
		CC_ GT _ C	
GAM2212	FLJ12921	3' TCCTTGACATTTGTGCTTTTCT 46401	CTGTTTAC
	C	GAGAAAAGC CAAGGA	
		CTCTTTTCG GTTCCT	
		TGTTTACA	
GAM2212	FLJ14326	5' TCCTCCAGGGCAGGCTCCTTC 50787	A_ ACCA
		GAA AGCCTGTTT AGGA	
		CTT TCGGACGGG TCCT	
		CC ACC_	
GAM2212	FLJ23153	3' CCTTGACTTTGCTTTTCTT 45267	CT_ TTAC
		GAGAAAAGC GT CAAGG	
		TTCTTTTCG CA GTTCC	
		TTT _	
GAM2212	GAB3	3' TCCTCAGACCTGGCTTTTTCCT 55523	AG T_ ACCA
		AG AAAAGCC GTTT AGGA	
		TC TTTTCGG CAGA TCCT	
		CT TC C_	
GAM2212	GABBR1	3' TGGGAAACAGACCTTTTCT 41862	AGC A
		AGAGAAA CTGTTT CCA	
		TCTTTT GACAAA GGT	
		CCA G	
GAM2212	GABBR1	3' TGGGAAACAGACCTTTTCT 9414	AGC A
		AGAGAAA CTGTTT CCA	
		TCTTTT GACAAA GGT	
		CCA G	
GAM2212	H2AV	3' TCCCCAGTAAAAATAGGCCTTT 57637	A _ CAA
	C	GAAA GCCTGTT TAC GGA	

		CTTT CGGATAA ATG CCT		
		C AA ACC		
GAM2212	HSPC195	5' CCTCGGCAGTTGGCAGGCTCCC 81863	AAA	TA__ A
		TCT AGAG AGCCTGTT CC AGG		
		TCTC TCGGACGG GG TCC		
		CC_ TTGAC C		
GAM2212	KIAA0478	3' TCCTCTGTAGCAGACAGGCCTC 30184	AAAA	__ CA
		CCTC GAG GCCTGTT TAC AGGA		
		CTC CGGACAG ATG TCCT		
		CCTC ACG TC		
GAM2212	KIAA1016	5' TCCTTGGTAAAGTTTGACTTTT 93389	CCTG__	
		C GAAAAG TTTACCAAGGA		
		CTTTTC AAATGGTTCCT		
		AGTTTG		
GAM2212	KIAA1260	3' TCCCCAACAAAAGAGGCTTTTC 60672	G ACCAA_	
		TT GAGAAAAGCCT TTT GGA		
		TTCTTTTCGGA AAA CCT		
		G ACAACC		
GAM2212	KIAA1327	3' CCTAGGTGCAAGCTTTTTCT 72726	A C TT A	
		AGAGAAA GC TGT ACC AGG		
		TCTTTTT CG ACG TGG TCC		
		_ A _ A		
GAM2212	KIAA1668	3' CCCTGGCAGGCTCCTTCT 67062	A_ TTTA A	
		AGAA AGCCTG CCA GG		
		TCTT TCGGAC GGT CC		
		CC _ C		
GAM2212	KIAA1668	3' CCTCACTTAGGCTTTTCCTCT 67063	A TTTACCA	
		AGAG AAAGCCTG AGG		
		TCTC TTTCGGAT TCC		
		C TCAC__		
GAM2212	KIAA1877	3' TCCCCGGTTCTGGCTTTTCT 66763	TGTTT AA	
		AGAAAAGCC ACC GGA		
		TCTTTTCGG TGG CCT		
		TCT_ CC		
GAM2212	MAWBP	5' TCCTTGGTAAATTATTCCTTT 42389	A GCCTGT	
		AGAG AAA TTACCAAGGA		
		TTTC TTT AATGGTTCCT		
		C ATT__		
GAM2212	MGC24447	3' CCCC GTGAAAGCTTTTCTT 57123	CTG CAA	
		GAGAAAAGC TTTAC GG		

		TTCTTTTCG AAGTG CC		
		A__ CC_		
GAM2212	MGC2628	3' CCCTGGACCGGCTCTTCCT 44196	A A T TTA A	
		AG GAA AGCC GT CCA GG		
		TC CTT TCGG CA GGT CC		
		_ C C __ C		
GAM2212	MGC9753	5' CCTTGAGATGATTTTCTCT 54188	GCCT AC	
		AGAGAAAA GTTT CAAGG		
		TCTCTTTT TAGA GTTCC		
		AG__ _		
GAM2212	MRF2	5' CTTGGCGACTTTTTCT 77027	CCT TA	
		AGAAAAG GTT CCAAG		
		TCTTTTT CAG GGTTT		
		_ C_		
GAM2212	NDP52	3' CCTTGGTGTTGCTTTCTC 20669	A CTGTT	
		GAGAAA GC TACCAAGG		
		CTCTTT CG GTGGTTCC		
		_ TT__		
GAM2212	NET-5	3' CCCC GGCACTGATGGGCTTCT 22893	AA TA__ AA	
		AGA AGCCTGTT CC GG		
		TCT TCGGGTAG GG CC		
		_ TCAC CC		
GAM2212	NICE-3	3' CCCCAGTAGCGCTTTTTTCT 31883	CTGT CAA	
		AGAGAAAAGC TTAC GG		
		TCTTTTTTCG GATG CC		
		C__ ACC		
GAM2212	p25	3' CCAGCGGCCCTCAGGCTTTTCT 23826	TTTA AA_	
	C	GAGAAAAGCCTG CC GG		
		CTCTTTTCGGAC GG CC		
		TCCC CGA		
GAM2212	PDE8B	3' CCTTGGACAAGCTTTTCTT 68201	C TTA	
		GAGAAAAGC TGT CCAAGG		
		TTCTTTTCG ACA GGTTCC		
		A _		
GAM2212	TUSP	3' CCGATGGAGGCACAGGCTTCTG 40021	GAA _TA A_	
	TCT	AGA AAGCCTGT T CCA GG		
		TCT TTCGGACA G GGT CC		
		GTC C GA AG		
GAM2212	ZNF262	3' TCCCCAATGGCAGCTTTTCTC 18727	C TACCAA	
		GAGAAAAGC TGTT GGA		

	CTCTTTTCG ACGG CCT		
	_ TAACC_		
GAM2212 LOC115399 3'	TCCTTAGGGCCAGGCTTT 73817	TTTA _	
	AAAGCCTG CC AAGGA		
	TTTCGGAC GG TTCCT		
	CG_ A		
GAM2212 LOC127943 3'	TCCTTGGTCTCCTGCTTCCCCT 75192	AA_ CTGTTT	
C	GAG AAGC ACCAAGGA		
	CTC TTCG TGGTTCCT		
	CCC TCCTC_		
GAM2212 LOC144742 5'	CCTAGGTCCTCACCTTTTCTCT 77456	CC TTT A	
	AGAGAAAAG TG ACC AGG		
	TCTCTTTTC AC TGG TCC		
	C_ TCC A		
GAM2212 LOC144747 5'	CCTTGGTAGCTTTTCTC 77471	_ CTGTT	
	GAGAAAA GC TACCAAGG		
	CTCTTTT CG ATGGTTCC		
	T _____		
GAM2212 LOC146958 5'	TCCTTAACACCAACAGGCTTTC 84949	A TACC_	
CTC	GAG AAAGCCTGTT AAGGA		
	CTC TTTCGGACAA TTCCT		
	C CCACAA		
GAM2212 LOC147858 3'	CCTTCTGCAGAACGGGCCCTC 79268	AAAA ACC_	
	GAG GCCTGTTT AAGG		
	CTC CGGGCAAG TTCC		
	CC_ ACGTC		
GAM2212 LOC150279 3'	CCTGCTTGAACAGGCCTCTC 80481	AAA CCA	
	GAGA GCCTGTTTA AGG		
	CTCT CGGACAAGT TCC		
	C_ TCG		
GAM2212 LOC154104 5'	TCCTTGGTGAAAACCTCTC 88625	AAAGCCTG	
	GAGA TTTACCAAGGA		
	CTCT AAGTGGTTCCT		
	CAA_____		
GAM2212 LOC155036 5'	CCTTGGGCTAGATTTTCTCT 87613	GC TTTA	
	AGAGAAAA CTG CCAAGG		
	TCTCTTTT GAT GGTTC		
	A_ CG_		
GAM2212 LOC200010 3'	CCACAGAAACAGGCTCTCCTCT 91525	AAA ACCAA	
	AGAG AGCCTGTTT GG		

TCTC TCGGACAAA CC
 CTC GACA_
 GAM2212 LOC203536 3' TCCTTGGTTTATACTTTTCT 90944 CC TT
 AGAAAAG TGT ACCAAGGA
 ||||| || |||||
 TCTTTTT ATA TGGTTCCT
 C_ TT
 GAM2212 LOC220776 3' CCTCGTGTCCATGACTTTTCTC 68925 CC_ TT CA
 T
 AGAGAAAAG TG TAC AGG
 ||||| || || ||
 TCTCTTTTC AC GTG TCC
 AGT CT C_
 GAM2212 LOC255332 3' CCTTAGCAAACAGGTTTCATCTC 97948 AA ACC
 GAGA AGCCTGTTT AAGG
 ||| ||||| |||
 CTCT TTGGACAAA TTCC
 AC CGA
 GAM2212 LOC257364 5' TCCCCGGTCTGGGCAGGACCCT 96648 AAAG _ AA
 CTC
 GAGA CCTGTTT ACC GGA
 ||| ||||| ||| ||
 CTCT GGACGGG TGG CCT
 CCCA TC CC
 GAM2212 LOC92305 3' CTTGGTGCCTTTTCT 57233 A CTGTTT
 AGAGAAA GC ACCAAG
 ||||| || |||||
 TCTTTTT CG TGGTTC
 C _
 GAM2212 LOC93624 3' CTGCCTACAAGTTTTTCTCT 73100 C TTACCA
 AGAGAAAAGC TGT AGG
 ||||| || |||
 TCTCTTTTGA ACA TCC
 A TCCG_
 GAM2213 ARHGEF1 3' ACCCCCACCCCAAGTGCCT 17479 A CA AAG AA
 AG CAC TGGGG GTG GGT
 || ||| |||| ||| |||
 TC GTG ACCCC CAC CCA
 C A_ _ CC
 GAM2213 BSN 3' CCTGCCACCATGGTGTCT 14382 _ A
 AGACACCATGG GG AGG
 ||||| || |||
 TCTGTGGTACC CC TCC
 A G
 GAM2213 CHD4 3' ACCCTCACCTTCCTTCTG 8874 TG A
 CA GGGAAGGTGA GGT
 || ||||| |||
 GT TCCTTCCACT CCA
 CT C
 GAM2213 CTNS 3' ACCTCCACCTTCTCAGATG 18216 G_ A
 CAT GGGAAGGTG AGGT
 ||| ||||| |||

			GTA CTCTTCCAC TCCA		
			GA C		
GAM2213 DTNB	3'	CCAGCGGTTCTCCCCATGGTGT 53678		_ G AA	
	T	GACACCATGGGGA AG TG GG			
		TTGTGGTACCCCT TT GC CC			
		C G GA			
GAM2213 GATA4	3'	CTTCTCCCCCAGGTGCCT 10772	A A AAG T		
		AG CACC TGGGG G GAAG			
		TC GTGG ACCCC C CTTC			
		C _ _ _ T			
GAM2213 HNF4A	3'	ACCTTCACCTTCATCCATG 6605	_		
		CATGGG GAAGGTGAAGGT			
		GTACCT CTTCCACTTCCA			
		A			
GAM2213 ITGA3	3'	ACCCCTCCTCCCCCAGTGTC 19731	CA A TGAA		
		GACAC TGGGG AGG GGT			
		CTGTG ACCCC TCC CCA			
		_ C TCCC			
GAM2213 ITGA3	3'	ACCCCTCCTCCCCCAGTGTC 11027	CA A TGAA		
		GACAC TGGGG AGG GGT			
		CTGTG ACCCC TCC CCA			
		_ C TCCC			
GAM2213 ITPKB	3'	ACCCCTCTCCCCATGG 11060	_ TGAA		
		CCATGGGGA AGG GGT			
		GGTACCCCT TCC CCA			
		C _ _ _			
GAM2213 NKX3A	3'	TGCCTTCCCCAGGGTGTCT 21618	A		
		AGACACC TGGGGAAGGTG			
		TCTGTGG ACCCCTTCCGT			
		G			
GAM2213 Nrap	3'	ACCTCCACCCTCCTTGG 43621	T AA A		
		CCA GGGG GGTG AGGT			
		GGT CCTC CCAC TCCA			
		T _ C			
GAM2213 Nrap	3'	ACCTCCACCCTCCTTGG 58320	T AA A		
		CCA GGGG GGTG AGGT			
		GGT CCTC CCAC TCCA			
		T _ C			
GAM2213 SEPX1	3'	ACCCTCACCTTCTTTTCTGG 33376	T _ _ A		
		CCA GG GGAAGGTGA GGT			

GGT CC TCTTCCACT CCA
_ TTT C
GAM2213 SLC1A5 3' ACCTCCTGTCCCCATGGT 79235 _ TGA
ACCATGGGGA AGG AGGT
||||||| ||| |||
TGGTACCCCT TCC TCCA
G _
GAM2213 SLC1A5 3' ACCTCCTGTCCCCATGGT 20065 _ TGA
ACCATGGGGA AGG AGGT
||||||| ||| |||
TGGTACCCCT TCC TCCA
G _
GAM2213 TEM8 3' ACCTTCACCCCTGTG 50822 AAG
CATGGGG GTGAAGGT
||||| |||||
GTGTCCC CACTTCCA
_
GAM2213 TM6SF2 3' CCATCATCCCCCATGG 72815 AA A
CCATGGGG GGTGA GG
||||| ||| ||
GGTACCCC CTACT CC
C_ A
GAM2213 AGPAT1 3' ACCTTCACCTTCCCTCCCAGTG 22168 CAT_
T ACAC GGGGAAGGTGAAGGT
||| |||||
TGTG TCCCTTCCACTTCCA
ACCC
GAM2213 AGPAT1 3' ACCTTCACCTTCCCTCCCAGTG 52198 CAT_
T ACAC GGGGAAGGTGAAGGT
||| |||||
TGTG TCCCTTCCACTTCCA
ACCC
GAM2213 AQP10 3' ACCTTCACCTCTCGGGGATGC 55391 A _ ATG A
CT AG CA CC GGGGAAGGTGAAGGT
|| || ||| |||||
TC GT GG CTCT CCACTTCCA
C A GG_ C
GAM2213 ARHF 3' ACCCTCCAGCTCATGGTGTCT 39257 _ A
AGACACCATGG GGA GGT
||||||| ||| |||
TCTGTGGTACT CCT CCA
CGA C
GAM2213 CDC91L1 3' CCCCCACCTTGTGGCTCT 55402 CA GGGG AA
AGA CCAT AAGGTG GG
||| ||| ||||| ||
TCT GGTG TTCCAC CC
C_ _ CC
GAM2213 DKFZp547J036 3' TTGCCTTCCCCCGGTGTC 51125 AT TG
GACACC GGGGAAGG A
||||| ||||| |

CTGTGG CCCCTTCC T
 C_ GT
 GAM2213 DKFZP586B1621 3' ACCCTCACCTTCCCCCGG 32036 AT A
 CC GGGGAAGGTGA GGT
 || ||||| ||
 GG CCCCTTCCACT CCA
 C_ C
 GAM2213 DKFZP727G051 3' ACCTCAGCTCCCACAGTGCCT 70000 A CA GA G A
 AG CAC TGGG AG TGA GGT
 || ||| ||| ||| |||
 TC GTG ACCC TC ACT CCA
 C AC _ G _
 GAM2213 FLJ14810 3' ACCCCCACCCCGTTTCCCTGGT 52695 T _ AA
 G CACCA GGGGAA GGTG GGT
 ||||| ||| ||| |||
 GTGGT CCCTTT CCAC CCA
 _ GCC CC
 GAM2213 FLJ20374 5' ACCTTCACCTGCTATG 35547 GGA
 CATGG AGGTGAAGGT
 |||| |||||
 GTATC TCACTTCCA
 G_
 GAM2213 FLJ22671 3' CCCCTTCCCCAGGCATC 46311 CA A TGAA
 GA CC TGGGGAAGG GG
 || || ||||| ||
 CT GG ACCCCTTCC CC
 AC _ C_
 GAM2213 HCA4 3' ACCTTCACCCCTGTG 78037 AA
 CATGGGG GGTGAAGGT
 ||||| |||||
 GTGTCCC CCACTTCCA
 _
 GAM2213 KIAA0217 3' CCTTTACCCCCAGCAGTATCT 67599 C CA_ AAG
 AGA AC TGGGG GTGAAGG
 ||| || ||||| |||||
 TCT TG ACCCC CATTTCC
 A ACG _
 GAM2213 KIAA0240 3' ACCTTCACCCCAGCCACATG 94032 G AA_
 CATG GG GGTGAAGGT
 |||| || |||||
 GTAC CC CCACTTCCA
 A GACC
 GAM2213 KIAA1077 3' ACCTTCACCAAGTTCTGAT 73284 G A_
 AT GGGG GGTGAAGGT
 || ||| |||||
 TA TCTT CCACTTCCA
 G GAA
 GAM2213 KIAA1854 3' CCCCCACCTCGCACTGTCT 72200 CCA G GA AA
 AGACA TG G AGGTG GG
 |||| || ||||| ||

TCTGT AC C TCCAC CC
 C__ G__ CC
 GAM2213 MGC2705 5' ACCAGCGTCCCCCATGGCTTCT 52079 CA AA GT AA
 AGA CCATGGGG G G GGT
 ||| ||||| | | |||
 TCT GGTACCCC C C CCA
 TC __ TG GA
 GAM2213 SIRPB1 3' ACCTTCACAAGACCATGATG 21352 C GGAAG
 CA CATGG GTGAAGGT
 || |||| |||||
 GT GTACC CACTTCCA
 A AGAA_
 GAM2213 TRIM4 3' ACCCTCAAGTAGTCCCTGGTGT 53404 T AAGG_ A
 CT AGACACCA GGGG TGA GGT
 ||||| ||| ||| |||
 TCTGTGGT CCCT ACT CCA
 _ GATGA C
 GAM2213 LOC123745 3' ACCTCTCTCCCCATGGTGT 76139 AG TGA
 AGACACCATGGGGA G AGGT
 ||||| ||| | |||
 TTTGTGGTACCCCT C TCCA
 CT __
 GAM2213 LOC147859 5' ACCTTCACCTCCATCGTG 88516 _ A
 CATGG GGA GGTGAAGGT
 |||| | |||||
 GTGCT CCT CCACTTCCA
 A _
 GAM2213 LOC149461 3' ACCTTCACCCTCCCCAGTC 80198 ACCA A
 GAC TGGGGA GGTGAAGGT
 || |||| |||||
 CTG ACCCCT CCACTTCCA
 __ C
 GAM2213 LOC150166 5' CCGACGCTTTCCCCACGG 86036 A AA
 CC TGGGGAAGGTG GG
 || ||||| ||
 GG ACCCCTTTTCGC CC
 C AG
 GAM2213 LOC151162 5' ACCTTACCCCACTGACGTCT 86424 AC _ _
 AGAC CA TGGGG AAGGT
 ||| || |||| ||||
 TCTG GT ACCCC TTCCA
 CA C A
 GAM2213 LOC153792 3' ACCTATTTATCCTCTCCATGAT 61015 C A _
 GTCT AGACA CATGGGGA GGTGA AGGT
 |||| ||||| |||| |||
 TCTGT GTACCTCT CTATT TCCA
 A C TA
 GAM2213 LOC201158 3' ACCTCCACCTTCTCTGCGTGT 61084 CAT A
 ACAC GGGGAAGGTG AGGT
 ||| ||||| ||||

TGTG TCTCTTCCAC TCCA
 CG_ C
 GAM2213 LOC201736 5' ACCTTCACCTACCAGG 90481 A GGA
 CC TGG AGGTGAAGGT
 || ||| |||||
 GG ACC TCCA CT TCCA
 _ A_

GAM2213 LOC203377 5' ACCTTACCCCACTGACGTCT 92253 AC _ _
 AGAC CA TGGGG AAGGT
 ||| || ||| |||
 TCTG GT ACCCC TTCCA
 CA C A

GAM2213 LOC203429 3' CCTGCCGCCCATGGTATCT 90930 C GAA GA
 AGA ACCATGGG GGT AGG
 || ||||| || |||
 TCT TGGTACCC CCG TCC
 A G_ _

GAM2213 LOC206480 5' ACCCCACGTGCTCCCCATGGCC 92404 CA AG_ AA
 TCT AGA CCATGGGGA GTG GGT
 || ||||| || |||
 TCT GGTACCCCT CAC CCA
 CC CGTG C_

GAM2213 LOC256158 5' CCTTCACCCTCACC GTCC 99492 C G A
 C ATGG GA GGTGAAGG
 | ||| || |||||
 C TGCC CT CCACTTCC
 C A C

GAM2213 LOC57115 3' GCCTTCCCCTGGTGTCT 40209 T
 AGACACCA GGGGAAGGT
 ||||| |||||
 TCTGTGGT CCCCTTCCG

GAM2213 LOC91049 5' CTTCTCCCCCAGGTGCCT 65372 A A AAG T
 AG CACC TGGGG G GAAG
 || ||| ||| | |||
 TC GTGG ACCCC C CTTC
 C _ _ T

GAM2214 COL18A1 3' TGGGAGCTGAGGCCACACT 56162 CA CC G
 GG TGGCCTT GT TCCCA
 || ||||| || |||
 TC ACCGGAG CG AGGGT
 AC T_ _

GAM2214 CTMP 3' GTGAGCCAAGATCATGCCA 54953 GC CCGT CC
 TGGCATG CTT GT CAC
 ||||| || || |||
 ACCGTAC GAA CG GTG
 TA C_ A_

GAM2214 KCNJ5 3' GTGAGCCAAGATCATGCCA 7977 GC CCGT CC
 TGGCATG CTT GT CAC
 ||||| || || |||

		ACCGTAC GAA CG GTG		
		TA C__ A_		
GAM2214	C8orf2	3' GTGAGCCAAGATCATGCCA	24156	GC CCGT CC
		TGGCATG CTT GT CAC		
		ACCGTAC GAA CG GTG		
		TA C__ A_		
GAM2214	DKFZp566H0824	3' GTGAGCTGAGACCATGCCA	34491	C CCGT CC
		TGGCATGG CTT GT CAC		
		ACCGTACC GAG CG GTG		
		A T__ A_		
GAM2214	FBXO27	3' GTGAACCAAGATCATGCCA	75013	GC CCGT CC
		TGGCATG CTT GT CAC		
		ACCGTAC GAA CA GTG		
		TA C__ A_		
GAM2214	FLJ00007	3' GGGCACGAAGGCCAGGCCA	71780	A C
		TGGC TGGCCTTC GTGTCC		
		ACCG ACCGGAAG CACGGG		
		G _		
GAM2214	FLJ00026	3' TGGGACATTTGCCACCCA	65621	CA CTTCC
		TGG TGGC GTGTCCCA		
		ACC ACCG TACAGGGT		
		C_ TT__		
GAM2214	FLJ10276	3' GGCAGGGAGGGCCATGCCA	36425	G
		TGGCATGGCCTTCC TGTC		
		ACCGTACCGGGAGG ACGG		
		G		
GAM2214	FLJ10932	3' GTGAGCCAAGATCATGCCA	37430	GC CCGT CC
		TGGCATG CTT GT CAC		
		ACCGTAC GAA CG GTG		
		TA C__ A_		
GAM2214	FLJ11151	3' GTGAGCCAAGATCATGCCA	68480	GC CCGT CC
		TGGCATG CTT GT CAC		
		ACCGTAC GAA CG GTG		
		TA C__ A_		
GAM2214	FLJ11726	3' GTGAGCCGAGACCATGCCA	47028	C TC T CC
		TGGCATGG CT CG GT CAC		
		ACCGTACC GA GC CG GTG		
		A _ _ A_		
GAM2214	FLJ23537	3' GTGAGCCAAGATCATGCCA	88920	GC CCGT CC
		TGGCATG CTT GT CAC		

		ACCGTAC GAA CG GTG	
		TA C__ A_	
GAM2214 HIC2	3'	AGTGGGACGCTGGCCACGGCCA 65859	A_ TTCC
		TGGC TGGCC GTGTCCCACT	
		ACCG ACCGG CGCAGGGTGA	
		GC T__	
GAM2214 KIAA0042	3'	GTGAGCCAAGATCATGCCA 30237	GC CCGT CC
		TGGCATG CTT GT CAC	
		ACCGTAC GAA CG GTG	
		TA C__ A_	
GAM2214 KIAA0303	5'	GCAGCAGAAGGCCATGCCA 69991	C_
		TGGCATGGCCTTC G TGT	
		ACCGTACCGGAAG C ACG	
		A G	
GAM2214 KIAA0481	3'	GTGGGACCGAGCCACCCA 72325	CA CTTC T
		TGG TGGC CG GTCCAC	
		ACC ACCG GC CAGGGTG	
		C_ A__ _	
GAM2214 KIAA0738	3'	GCAGAGGAAACCCATGCCA 28886	CC G_
		TGGCATGG TTCC TGT	
		ACCGTACC AAGG ACG	
		CA AG	
GAM2214 KIAA0843	3'	TGGGACACACTGCCTGCCA 30806	T CTTCC
		TGGCA GGC GTGTCCCA	
		ACCGT CCG CACAGGGT	
		_ TCA__	
GAM2214 KIAA0971	3'	AGTAGATGCATAAGATCATGCC 30667	GC CC CC
A		TGGCATG CTT GTGTC ACT	
		ACCGTAC GAA CGTAG TGA	
		TA TA A_	
GAM2214 KIAA1257	3'	GTGAGCCAAGACCGTGCCA 63412	C CCGT CC
		TGGCATGG CTT GT CAC	
		ACCGTGCC GAA CG GTG	
		A C__ A_	
GAM2214 KIAA1958	3'	GTGAGCCGAGACCATGCCA 82790	C TC T CC
		TGGCATGG CT CG GT CAC	
		ACCGTACC GA GC CG GTG	
		A _ _ A_	
GAM2214 KLHL4	3'	ACAAGAAGGCCATCCCA 55141	C CG
		TGG ATGGCCTTC TGT	

	ACC TACCGGAAG ACA		
	C A_		
GAM2214 MGC10966 5'	AGCAGGACTGGTCAGACCATGC 49682	C T_ T CA	
TA	TGGCATGG CT CCG GTCC CT		
	ATCGTACC GA GGT CAGG GA		
	A CT _ AC		
GAM2214 NYD-SP11 3'	AGTGGGACTGAGGCCGCACCA 50054	CA CCGT	
	TGG TGGCCTT GTCCCACT		
	ACC GCCGGAG CAGGGTGA		
	AC T__		
GAM2214 X123 3'	GACAGAAGGCCACTCCA 70480	CA CG	
	TGG TGGCCTTC TGTC		
	ACC ACCGGAAG ACAG		
	TC _		
GAM2214 LOC126917 3'	AGTGGGGTTCTGAAGCCACACCA 75083	CA C C TG	
	TGG TGGC TTC G TCCCACT		
	ACC ACCG AAG C GGGGTGA		
	AC _ _ TT		
GAM2214 LOC131965 3'	GTGAGCCAAGATCATGCCA 75527	GC CCGT CC	
	TGGCATG CTT GT CAC		
	ACCGTAC GAA CG GTG		
	TA C__ A_		
GAM2214 LOC144481 3'	GTGAACTAAGATCATGCCA 84023	GC CCGT CC	
	TGGCATG CTT GT CAC		
	ACCGTAC GAA CA GTG		
	TA T__ A_		
GAM2214 LOC145978 3'	GGTGAGAAGACTATGCCA 78052	C CGTG _	
	TGGCATGG CTTC TC CC		
	ACCGTATC GAAG AG GG		
	A ____ T		
GAM2214 LOC148696 5'	AGCAGGACAGAAAAACCAACGC 85342	A_ CC_ CG CA	
CA	TGGC TGG TTC TGTCC CT		
	ACCG ACC AAG ACAGG GA		
	CA AAA _ AC		
GAM2214 LOC155006 3'	GTGAGCCAAGATCATGCCA 82175	GC CCGT CC	
	TGGCATG CTT GT CAC		
	ACCGTAC GAA CG GTG		
	TA C__ A_		
GAM2214 LOC202908 5'	AGTGAAACGTGGGACCATCCA 90710	C CC CC	
	TGG ATGG TTCCGTGT CACT		

		ACC TACC AGGGTGCA GTGA	
		— — AA	
GAM2214	LOC203378 3'	GTGAACCAAGATCATGCCA 92298	GC CCGT CC
		TGGCATG CTT GT CAC	
		ACCGTAC GAA CA GTG	
		TA C__ A_	
GAM2214	LOC220506 3'	GTGAGCCAAGATCATGCCA 74520	GC CCGT CC
		TGGCATG CTT GT CAC	
		ACCGTAC GAA CG GTG	
		TA C__ A_	
GAM2214	LOC254045 3'	GTGAACTAAGATCATGCCA 98273	GC CCGT CC
		TGGCATG CTT GT CAC	
		ACCGTAC GAA CA GTG	
		TA T__ A_	
GAM2214	LOC256979 3'	AGTTGGTACAGAAGGCCATGCC 97759	C T C
	A	TGGCATGGCCTTC GTG CC ACT	
		ACCGTACCGGAAG CAT GG TGA	
		A _ T	
GAM2214	LOC90120 5'	GGGACACGGAAGGCTCCCC 62216	CAT
		GG GGCCTTCCGTGTCCC	
		CC TCGGAAGGCACAGGG	
		CC_	
GAM2214	LOC91380 3'	GTGAGCCGAGACCATGCCA 66453	C TC T CC
		TGGCATGG CT CG GT CAC	
		ACCGTACC GA GC CG GTG	
		A __ _ A_	
GAM2214	LOC92421 3'	GTGAGCCAAGATCATGCCA 69728	GC CCGT CC
		TGGCATG CTT GT CAC	
		ACCGTAC GAA CG GTG	
		TA C__ A_	
GAM2214	LOC92578 3'	GTGGGACTGAGCCATACA 70396	GC CT CGT
		TG ATGGC TC GTCCCAC	
		AC TACCG AG CAGGGTG	
		A_ __ T__	
GAM2215	ACP2 3'	CCAACAGCCAGCCAGCCACA 9652	_ AG _
		TGTGG TGGCTGG GT GG	
		ACACC ACCGACC CA CC	
		G GA A	
GAM2215	ANKTM1 3'	CCACCCACCCACCACA 24696	C AG
		TGTGGTGG TGG GTGG	

ACACCACC ACC CACC
 C _
 GAM2215 ATF7 3' CCAGCCCCAGCCACCCCA 23399 T A _
 TG GGTGGCTGG GG TGG
 || ||||| || |||
 AC CCACCGACC CC ACC
 C _ G
 GAM2215 BDKRB2 3' GGCCCCAACCGCCACA 7111 C AGGT
 TGTGGTGG TGG GGCC
 ||||| || |||
 ACACCGCC ACC CCGG
 A _
 GAM2215 EGFL4 3' GCCACCCCCAGCCCCAC 62467 T A
 GTGG GGCTGG GGTGGC
 ||| |||| |||||
 CACC CCGACC CCACCG
 _ C
 GAM2215 ENIGMA 3' CTCCTCCACCACCACA 62868 C TG
 TGTGGTGG TGGAGG G
 ||||| ||||| |
 ACACCACC ACCTCC C
 _ CT
 GAM2215 MKI67 3' GGCACCTCCAACCACCACA 11598 C G
 TGTGGTGG TGGAGGTG CC
 ||||| ||||| ||
 ACACCACC ACCTCCAC GG
 A _
 GAM2215 TNNT3 3' TCCACATCCTCCAGCCCCCACA 23134 T _ GCC
 TGTGG GGCTGGAGG TG GA
 |||| ||||| || ||
 ACACC CCGACCTCC AC CT
 C T AC_
 GAM2215 WNT3A 3' ATTCAGCCCACCAGCCACCTCA 53609 T AGGT C
 TG GGTGGCTGG GGC GAAT
 || ||||| || |||
 AC CCACCGACC CCG CTTA
 T AC_ A
 GAM2215 BCAN 3' CTGCGCTCCCGCCACCACA 41971 T _TG
 TGTGGTGGC GGAG G G
 ||||| |||| | |
 ACACCACCG CCTC C C
 C G GT
 GAM2215 C20orf173 5' GCTCCTCCTGCCACCACA 55917 T T
 TGTGGTGGC GGAGG GGC
 ||||| |||| |||
 ACACCACCG CCTCC TCG
 T _
 GAM2215 CAPN13 3' TCGGCCACCTCCCACCA 58630 CTG
 TGGTGG GAGGTGGCCGA
 |||| | ||||| |||||

ACCACC CTCCACCGGCT

GAM2215 FLNC 3' CCACCTCCAGCCACACA 9390 G
TGTG TGGCTGGAGGTGG
|||||
ACAC ACCGACCTCCACC

GAM2215 LANCL2 3' CCTCCCCACCCACCACA 38619 C A T
TGTGGTGG TGG GG GG
||||| ||| ||
ACACCACC ACC CC CC

C _ T
GAM2215 LOC127435 3' CCAGCTCAGCCACACA 76606 G G G
TGTG TGGCTG AG TGG
||||| ||| |||
ACAC ACCGAC TC ACC

_ _ G
GAM2215 LOC127435 3' CTACCCTCCAAACCACCACA 76607 C_ _
TGTGGTGG TGGAGG TGG
||||| ||||| |||
ACACCACC ACCTCC ATC
AA C

GAM2215 LOC139840 5' TCTCCACAGCCACCACA 76777 GA T
TGTGGTGGCTG GG GG
||||||| |||
ACACCACCGAC CC CT
A_ T

GAM2215 LOC150319 3' GCCACCTCCTGCCACCACA 80473 T
TGTGGTGGC GGAGGTGGC
||||||| |||||
ACACCACCG CCTCCACCG
T

GAM2215 LOC204084 3' ATTCGGCCACCTCCACGACCA 90990 GGC
TGGT TGGAGGTGGCCGAAT
||| |||||
ACCA ACCTCCACCGGCTTA
GC_

GAM2215 LOC221477 3' TCCCCACCTCCACCACCACA 93778 C CC
TGTGGTGG TGGAGGTGG GA
||||| ||||| ||
ACACCACC ACCTCCACC CT
_ C_

GAM2215 LOC222031 3' CCACCTCCAGCCACCCA 95674 T
TG GGTGGCTGGAGGTGG
|| |||||
AC CCACCGACCTCCACC
C

GAM2216 BICD1 3' ATCTCCTGTGGACGAACAT 9935 CA _
GTG TTG CCACAGGAGAT
||| ||| |||||

		TAC AGC GGTGTCCTCTA	
		A_ A	
GAM2216 C18orf1	3'	TATCTCCTGCTGTAGCAT 60871	AT CA
		GTGC TGC CAGGAGATA	
		TACG ATG GTCCTCTAT	
		__ TC	
GAM2216 CRY2	3'	ATCTCCTGTAGCTGTCCAT 72656	C T C
		GTG AT GC ACAGGAGAT	
		TAC TG CG TGCCTCTA	
		C T A	
GAM2216 FGF7	3'	TATGTCTTGGCAATGCAC 10633	CA G
		GTGCATTGCCA GGA ATA	
		CACGTAACGGT TCT TAT	
		__ G	
GAM2216 FGF9	5'	TATCTCCTGGGTTGACAC 10635	_ TT A
		GTG CA GCC CAGGAGATA	
		CAC GT TGG GTCCTCTAT	
		A __ _	
GAM2216 GNB5	3'	ATCTTCTGACAGTGCAC 22699	CCA
		GTGCATTG CAGGAGAT	
		CACGTGAC GTCTTCTA	
		A__	
GAM2216 GNB5	3'	ATCTTCTGACAGTGCAC 33002	CCA
		GTGCATTG CAGGAGAT	
		CACGTGAC GTCTTCTA	
		A__	
GAM2216 IRS2	3'	TATTTAATGGCAATGCA 60443	CAGG
		TGCATTGCCA AGATA	
		ACGTAACGGT TTTAT	
		AA__	
GAM2216 PCSK2	3'	ATCCCCAGTCCCAATGCAC 11998	CC A A
		GTGCATTG AC GG GAT	
		CACGTAAC TG CC CTA	
		CC A C	
GAM2216 RPA3	5'	ATCTCCTGCAACAATGTA 12903	CCA
		TGCATTG CAGGAGAT	
		ATGTAAC GTCCTCTA	
		AAC	
GAM2216 RPL15	3'	TATCGGAGTGATGGCAATGC 12904	_ GGA_
		GCATTGCCA CA GATA	

			CGTAACGGT GT CTAT		
			A GAGG		
GAM2216	SMCY	3'	TATCTCCTGGCCTGGAC 17388	G TT CA	
			GT CA GCCA GGAGATA		
			CA GT CGGT CCTCTAT		
			G C_ _		
GAM2216	TRIM34	3'	TATCTCCTGCAACTGAC 41509	G _ CAC	
			GT CA TTGC AGGAGATA		
			CA GT AACG TCCTCTAT		
			_ C _		
GAM2216	TRIM34	3'	TATCTCCTGCAACTGAC 56112	G _ CAC	
			GT CA TTGC AGGAGATA		
			CA GT AACG TCCTCTAT		
			_ C _		
GAM2216	TYK2	5'	ATCTTTTGATGGCAACAC 60561	CA _	
			GTG TTGCCA CAGGAGAT		
			CAC AACGGT GTTTTCTA		
			_ A		
GAM2216	C1orf34	3'	TATCTCCTGCAGTCA 61322	C CAC	
			TG ATTGC AGGAGATA		
			AC TGACG TCCTCTAT		
			_ _		
GAM2216	C5orf6	3'	TATCTCCTGGCTAGTTAC 33956	C _ CA	
			GTG ATT GCCA GGAGATA		
			CAT TGA CGGT CCTCTAT		
			_ T _		
GAM2216	CLECSF9	3'	TATCTCCTGCCCAAGCAT 27624	A CCA	
			GTGC TTG CAGGAGATA		
			TACG AAC GTCCTCTAT		
			_ CC_		
GAM2216	EDG1	3'	TTCCTGTGAACAATGCAC 60056	C_	
			GTGCATTG CACAGGAG		
			CACGTAAC GTGTCCTT		
			AA		
GAM2216	FLJ10545	3'	TATCTCCTGATATGCAC 36769	TGCCA	
			GTGCAT CAGGAGATA		
			CACGTA GTCCTCTAT		
			TA_		
GAM2216	FLJ10656	3'	TATCTCCTATCACATGCAC 36911	_ CCAC	
			GTGCAT TG AGGAGATA		

CACGTA AC TCCTCTAT
C TA__
GAM2216 FLJ20294 3' TATCTCCTGCTGCATACTAC 35360 CAT CA
GTG TGC CAGGAGATA
||| ||| |||||
CAT ACG GTCCTCTAT
CAT TC
GAM2216 KIAA0453 3' ATCTCCTGTGATTGCAC 69601 TTGC
GTGCA CACAGGAGAT
|||| |||||
CACGT GTGTCCTCTA
TA__
GAM2216 KIAA0825 3' TATCTCCTAGTTGCCATGCA 61688 T C _
TGCAT GC AC AGGAGATA
|||| || |||||
ACGTA CG TG TCCTCTAT
C T A
GAM2216 KIAA1203 3' ATCTCCTGGTAGGCAC 72086 A CA
GTGC TTGCCA GGAGAT
||| ||||| |||||
CACG GATGGT CCTCTA
— —
GAM2216 MAFB 3' ATCCCTGACCCTGGCAGTGCAC 19589 ____ A
GTGCATTGCCA CAGG GAT
||||||| ||| |||
CACGTGACGGT GTCC CTA
CCCA _
GAM2216 PLEKHA1 5' ATCTCCTGTAGTGTA 41515 GCC
TGCATT ACAGGAGAT
||||| |||||
ATGTGA TGTCTCTA
—
GAM2216 PRRG1 3' TATCTCCTGCGGTGTAT 8152 CAC
GTGCATTGC AGGAGATA
||||||| |||||
TATGTGGCG TCCTCTAT
—
GAM2216 RACGAP1 5' TATCTCCTAGCTATGGAC 26111 G T CAC
GT CAT GC AGGAGATA
|| ||| || |||||
CA GTA CG TCCTCTAT
G T A__
GAM2216 RTCD1 3' TATCTCCTGAGAGATGGAC 14951 G GCCA
GT CATT CAGGAGATA
|| ||| |||||
CA GTAG GTCCTCTAT
G AGA_
GAM2216 SDNSF 3' ATCTCCTGGTTATATAC 58401 C T CA
GTG AT GCCA GGAGAT
||| || |||||

CAT TA TGGT CCTCTA
 A T _
 GAM2216 TP53INP1 3' TATCTTCTGTGGCAATGCAT 73322
 GTGCATTGCCACAGGAGATA
 |||||
 TACGTAACGGTGTCTTCTAT

GAM2216 TP53INP1 3' TATCTTCTGTGGCAATGCAT 53871
 GTGCATTGCCACAGGAGATA
 |||||
 TACGTAACGGTGTCTTCTAT

GAM2216 UNC5D 3' TATCTCCTTGGAATCCAC 56008 C G C
 GTG ATT CCA AGGAGATA
 ||| ||| |||
 CAC TAA GGT TCCTCTAT
 C _ _

GAM2216 USP20 3' ATCTCCTGGGCGTCAC 22897 CAT A
 GTG TGCC CAGGAGAT
 ||| ||| |||
 CAC GCGG GTCCTCTA
 T _ _

GAM2216 ZNF304 3' TATCTCCTGTGGCCAAGGC 40683 ATT_
 GC GCCACAGGAGATA
 || |||||
 CG CGGTGTCCTCTAT
 GAAC

GAM2216 LOC122553 3' TATCCCCTTTGCTAAGCAATGC 74593 ____ C A
 AT GTGCATTGC CA AGG GATA
 ||||| ||| |||
 TACGTAACG GT TCC CTAT
 AATC T C

GAM2216 LOC146961 5' TATCTCCTGCAGGGTGTGCAC 78824 _ TG A_
 GTG CAT CC CAGGAGATA
 ||| ||| ||| |||
 CAC GTG GG GTCCTCTAT
 T _ AC

GAM2216 LOC147341 3' ATCCCCCAGTTGACAATGTAC 85117 C _ A_ A
 GTGCATTG CA C GG GAT
 ||||| ||| |||
 CATGTAAC GT G CC CTA
 A T AC C

GAM2216 LOC148894 5' TATCTCCTGTTTCTGTGCAT 85422 TGCC
 GTGCAT ACAGGAGATA
 ||||| |||||
 TACGTG TGTCTCTAT
 TCCT

GAM2216 LOC154877 3' ATCTCCTGTGGCCCAACAT 87527 CATT
 GTG GCCACAGGAGAT
 ||| |||||

		TAC CGGTGTCCTCTA		
		AACC		
GAM2216	LOC158116	3' TATGTCTTGGCAATGCAC 60950	CA	G
		GTGCATTGCCA GGA ATA		
		CACGTAACGGT TCT TAT		
		___ G		
GAM2216	LOC221683	5' TATCTCCTGTGATAATCA 95332	C	C
		TG ATTG CACAGGAGATA		
		AC TAAT GTGTCCTCTAT		
		_ A		
GAM2216	LOC253868	3' TATCTTTACAGCAATGCA 97328	CACA	
		TGCATTGC GGAGATA		
		ACGTAACG TTTCTAT		
		ACA_		
GAM2217	DDX3	3' TCTGATGTTAGTAAAAACAA 9062	C___	T
		TTGT ACTAACATC GG		
		AACA TGATTGTAG CT		
		AAAA T		
GAM2217	GRP58	3' ACATTTGGAACAGTGACAAT 19205	AACA TG_	
		ATTGTCACT TC G TGT		
		TAACAGTGA AG T ACA		
		CA__ GT T		
GAM2217	NEDD4L	3' ACATCCTTTCTAATGACAATGA 31603	C	ACATCT
	A	TTCATTGTCA TA GGTGT		
		AAGTAACAGT AT CTACA		
		A CTTTC_		
GAM2217	UMOD	5' ACACCAGACATCAGAGACAG 14008	A	AACA
		TTGTC CT TCTGGTGT		
		GACAG GA AGACCACA		
		A CTAC		
GAM2217	MYH10	3' CAGACATTCAAGTGACAATGAA 69669	_	CA
		TTCATTGTCACT AA TCTG		
		AAGTAACAGTGA TT AGAC		
		C AC		
GAM2217	PPP1R1A	3' ACCCGTTAGCAACAATGGA 23092	CA	ATCT
		TTCATTGT CTAAC GGT		
		AGGTAACA GATTG CCA		
		AC C___		
GAM2217	LOC132617	3' ACTGATGTTAATGACAATGA 76406	C	T
		TCATTGTCA TAACATC GGT		

	AGTAACAGT ATTGTAG TCA	
	A _	
GAM2217 LOC144558 3'	ACTGGTAATGACAATGAA 84072	C ACAT TG
	TTCATTGTCA TA C GT	
	AAGTAACAGT AT G CA	
	A ____ GT	
GAM2217 LOC150368 3'	GGATGTTAATGAAATGAA 80516	G C
	TTCATT TCA TAACATCT	
	AAGTAA AGT ATTGTAGG	
	_ A	
GAM2217 LOC151623 5'	ACTGGTAATGACAATGAA 86630	C ACAT TG
	TTCATTGTCA TA C GT	
	AAGTAACAGT AT G CA	
	A ____ GT	
GAM2217 LOC157278 3'	ACTGGTAATGACAATGAA 87704	C ACAT TG
	TTCATTGTCA TA C GT	
	AAGTAACAGT AT G CA	
	A ____ GT	
GAM2217 LOC166660 5'	ACACTGCCCAGTGACAGTGAA 83539	AACATCT
	TTCATTGTCACT GGTGT	
	AAGTGACAGTGA TCACA	
	CCCG__	
GAM2217 LOC221962 3'	ACTGGTAATGACAATGAA 94236	C ACAT TG
	TTCATTGTCA TA C GT	
	AAGTAACAGT AT G CA	
	A ____ GT	
GAM2217 LOC253985 5'	ACACCAGACAACTGAGACAAT 98238	ACTAACA_
GAA	TTCATTGTC TCTGGTGT	
	AAGTAACAG AGACCACA	
	AGTCAAAC	
GAM2217 LOC255461 5'	ACTGGTAATGACAATGAA 99136	C ACAT TG
	TTCATTGTCA TA C GT	
	AAGTAACAGT AT G CA	
	A ____ GT	
GAM2217 LOC255516 5'	ACTGGTAATGACAATGAA 99150	C ACAT TG
	TTCATTGTCA TA C GT	
	AAGTAACAGT AT G CA	
	A ____ GT	
GAM2217 LOC57228 5'	ACCACTAGTGACAATGA 40398	ACATC
	TCATTGTCACTA TGGT	

AGTAACAGTGAT ACCA
 C____
 GAM2217 LOC92218 3' ACACCAAAGGTTAACAGTGAA 69029 CAC ATC
 TTCATTGT TAAC TGGTGT
 ||||| ||| |||||
 AAGTGACA ATTG ACCACA
 ____ GAA
 GAM2217 LOC93613 3' ACACCAGATGTCAAGCATACAA 73066 CA_ A_
 TTGT CT ACATCTGGTGT
 ||| || |||||
 AACA GA TGTAGACCACA
 TAC AC
 GAM2218 ADCY2 3' ACATAGCAAGACCCCCA 65639 AA GCC G
 TGG GGT CT TGCTATGT
 ||| ||| || |||||
 ACC CCA GA ACGATACA
 C_ ____
 GAM2218 CLCN4 3' ACATCAGGGGCACCTGCCA 10207 A GTGCT
 TGG AGGTGCCCT ATGT
 ||| ||||| |||
 ACC TCCACGGGG TACA
 G AC____
 GAM2218 FTSJ2 3' ACATAGCAACACCCCCA 26343 AA CCCTG
 TGG GGTG TGCTATGT
 ||| ||| |||||
 ACC CCAC ACGATACA
 CC A____
 GAM2218 PDE4C 3' ACATAGCAAGACCCCCA 8091 AA GCC G
 TGG GGT CT TGCTATGT
 ||| ||| || |||||
 ACC CCA GA ACGATACA
 C_ ____
 GAM2218 PDGFRB 3' AGTACAGGACACCCCCA 66580 AA C
 TGG GGTG CCTGTGCT
 ||| ||| |||||
 ACC CCAC GGACATGA
 C_ A
 GAM2218 TCF3 3' AGCACAGGACACCCCCA 71270 AA C
 TGG GGTG CCTGTGCT
 ||| ||| |||||
 ACC CCAC GGACACGA
 CC A
 GAM2218 ZFP36L1 3' GACACAAGTGCACCTTCC 18202 CCT GCTA
 GGAAGGTGC GT TGTC
 ||||| || |||
 CCTTCCACG CA ACAG
 T__ AC__
 GAM2218 FLJ10008 3' GCACGAGAGCACCTCCCA 36189 A C_
 TGG AGGTGC CT GTGC
 ||| ||||| || |||

ACC TCCACG GA CACG
 C A G
 GAM2218 LOC130813 5' ACACAGCACAGGCGGGAGTTCA 76259 AGG_ C A
 TGG TGCC TGTGCT TGT
 ||| ||| ||||| |||
 ACTT GCGG ACACGA ACA
 GAGG _ C
 GAM2218 LOC255452 3' AGAACAGGGGCATCCCCCA 99384 AA G
 TGG GGTGCCCTGT CT
 ||| ||||| |||
 ACC CTACGGGACA GA
 CC A
 GAM2218 LOC90092 3' GGCACAGGGCAGCCCCCA 62066 AA _
 TGG GG TGCCCTGTGCT
 ||| || ||||| |||
 ACC CC ACGGGACACGG
 C_ G
 GAM2218 LOC91548 5' CGACATAGGAGGGCACCACCCA 67007 AA GTG
 TGG GGTGCCCT CTATGTGCT
 ||| ||||| |||||
 ACC CCACGGGA GATACAGC
 CA G_
 GAM2218 LOC92840 3' GGCACAGGGCAGCTCCCA 57247 A G
 TGG AG TGCCCTGTGCT
 ||| || ||||| |||
 ACC TC ACGGGACACGG
 C G
 GAM2219 PRDM2 3' CCGACCTATCCCAGTTGTGTGA 25279 G GAATA
 TCACA CAACTGGGG TCGG
 |||| ||||| |||
 AGTGT GTTGACCCT AGCC
 _ ATCC_
 GAM2219 TNFRSF8 3' CCGGCATGCCCCCAGTTACTGT 8798 C A AT
 ACAG AACTGGGGG AT CGG
 |||| ||||| || |||
 TGTC TTGACCCCC TA GCC
 A G CG
 GAM2219 NR6A1 3' GTTTCGCCAGTTGCTCTGA 9448 C
 TCA AGCAACTGGGGGAAT
 ||| ||||| |||||
 AGT TCGTTGACCCCTTTG
 C
 GAM2219 NR6A1 3' GTTTCGCCAGTTGCTCTGA 54018 C
 TCA AGCAACTGGGGGAAT
 ||| ||||| |||||
 AGT TCGTTGACCCCTTTG
 C
 GAM2219 NR6A1 3' GTTTCGCCAGTTGCTCTGA 54024 C
 TCA AGCAACTGGGGGAAT
 ||| ||||| |||||

		AGT TCGTTGACCCCTTTG		
		C		
GAM2219	TA-NFKBH	3' CCAATATTTGGGGTGCTGTGA 52152	A GGGG	C
		TCACAGCA CT GAATAT GG		
		AGTGTCGT GG TTTATA CC		
		G G__ A		
GAM2219	LOC92335	3' CCGACATTCCCAGTCCTGTGA 69543	CA	AATA
		TCACAG ACTGGGGG TCGG		
		AGTGTC TGACCCTT AGCC		
		C_ AC__		
GAM2220	E2F3	3' CAAGAAAACCTCCACAGCCTTC 10464	GA_ A	CTC
	T	GGAAGG TGGA GGT CTTG		
		TCTTCC ACCT CCA GAAC		
		GAC _ AAA		
GAM2220	FECH	3' CAAGGAAGGAAGTCATCCTTCC 5553	G AAGG	_
	T	AGGAAGG ATGG TCT CCTTG		
		TCCTTCC TACT GGA GGAAC		
		_ GAA_ A		
GAM2220	GRB2	5' AGCCCTCCTCCCTCCCTTCC 10870	T _ T	
		GGAAGGGA GGA AGG CT		
		CCTTCCCT CCT TCC GA		
		C CC C		
GAM2220	HBA1	3' AGCCCCTCCTCCCCTTCCT 6901	AT A T	
		AGGAAGGG GGA GG CT		
		TCCTTCCC CCT CC GA		
		CT C C		
GAM2220	HBA2	3' GGGCCCTCCTCCCCTCCT 6715	A T A	
		AGGA GGA GGA GGTCT		
		TCCT CCCT CCT CCGGG		
		C _ C		
GAM2220	LFNG	3' GGAACCTCCCATCCCTGCC 94212	A A C	
		GG AGGGATGG AGGT TCC		
		CC TCCCTACC TCCA AGG		
		G C _		
GAM2220	MAP3K5	5' AAGGAAGCTCCGTCCCTTCC 20993	AG TC	
		GGAAGGGATGGA G TCCTT		
		CCTTCCCTGCCT C AGGAA		
		_ GA		
GAM2220	MSF	3' CAAGTCATTTCCGTCCCCCCC 89464	AA	GTCTC
		GG GGGATGGAAG CTTG		

			CC CCCTGCCTTT GAAC		
			CC ACT__		
GAM2220	NGFR	3'	AGTGGACTTTCCACCCCCTCC 11788	A A	TC
			GGA GGG TGGAAGGTC CT		
			CCT CCC ACCTTTCAG GA		
			C C GT		
GAM2220	PPP2R5E	5'	AGTCTTCCTCCCTCCCTTCC 21804	T__	T
			GGAAGGGA GGAAGG CT		
			CCTTCCCT CTTCT GA		
			CCCT _		
GAM2220	PROML1	3'	CAAGGATGACTCCCTCCCTTCC 21200	T AG	_
	T		AGGAAGGGA GGA GTC TCCTTG		
			TCCTTCCCT CCT CAG AGGAAC		
			C _ T		
GAM2220	PYGO2	5'	CAAGGGCGCCTCCATCCCCC 64684	AA	A C
			GG GGGATGGA GGT TCCTTG		
			CC CCCTACCT CCG GGGAAC		
			_ _ C		
GAM2220	RHCG	3'	CAAGGTGCCTCCACCCCTGCC 33329	A_ A A	CT
	T		AGG AGGG TGGA GGT CCTTG		
			TCC TCCC ACCT CCG GGAAC		
			CG C _ T_		
GAM2220	SALL2	3'	CAAGGAGAAGACAGCCCCCTC 64589	A AT AAGG	_
	CT		AGGA GGG GG TCTCCTTG		
			TCCT CCC CC AGAGGAAC		
			_ C_ GACAGA		
GAM2220	TRAF5	5'	GCCTCCTCCCGACCCCTTCCT 17277	AT__	_
			AGGAAGGG GGA AGGT		
			TCCTTCCC CCT TCCG		
			CAGC CC		
GAM2220	C12orf22	3'	AAGGAGACCAGCCCTACCT 48703	A	ATGGAA
			AGG AGGG GGTCTCCTT		
			TCC TCCC CCAGAGGAA		
			A GA__		
GAM2220	C22orf5	3'	GACCGCTCCATCCCCTCCT 25340	A	A_
			AGGA GGGATGGA GGTC		
			TCCT CCCTACCT CCAG		
			C CG		
GAM2220	CABYR	3'	CAAGAAGACCAGTGCCCCACCT 25170	AA	ATGGAA C
			AGG GGG GGTCT CTTG		

TCC CCC CCAGA GAAC
 AC GTGA__ A
 GAM2220 DKFZp547J036 3' AGCCCTCCACCCCTCCCT 51119 A A A T
 AGG AGGG TGGA GG CT
 ||| ||| ||| || ||
 TCC TCCC ACCT CC GA
 C C C C
 GAM2220 DKFZP564C1940 3' GCCTCCCCTCCACCACTTCCT 26744 _ A ____
 AGGAAG GG TGGA AGGT
 ||||| || ||| ||||
 TCCTTC CC ACCT TCCG
 A _ CCCC
 GAM2220 EPN2 3' CAAGAAGACAGCCCCCTGCC 31036 A AT AAG C
 GG AGGG GG GTCT CTTG
 || ||| || ||| ||||
 CC TCCC CC CAGA GAAC
 G _ GA_ A
 GAM2220 FIGN 3' AGAACCTCTCCATCTCCTCC 36574 A _ _
 GGA GGGATGGA AGGT CT
 ||| ||||| ||| ||
 CCT CTCTACCT TCCA GA
 C C A
 GAM2220 FLJ13855 3' CAAGGGAATCCATCCTTCC 43845 G AGG T
 GGAAGG ATGGA TC CCTTG
 ||||| |||| || |||||
 CCTTCC TACCT AG GGAAC
 _ A_ _
 GAM2220 GP5 5' CAAGGATACCACCCTCTTCCT 16863 AT AA C
 AGGAAGGG GG GGT TCCTTG
 ||||| || ||| |||||
 TCCTTCTC CC CCA AGGAAC
 _ A_ T
 GAM2220 KIAA0014 3' CAAGGCCCTGCCACCCCTTCCT 28537 A A TCT
 AGGAAGGG TGG AGG CCTTG
 ||||| ||| ||| ||||
 TCCTTCCC ACC TCC GGAAC
 C G C_
 GAM2220 KIAA0759 3' CAAGAACTTACATCCCCTCCC 67884 T_ ____ CTC
 TTCC GGAAGGGA GGA AGGT CTTG
 ||||| ||| ||| ||||
 CCTTCCCT CCT TTCA GAAC
 CC ACA AA_
 GAM2220 KIAA0789 5' CAAGCCCCTTCCATCCTCTCC 64427 AG TCTC
 GGA GGATGGAAGG CTTG
 ||| ||||| ||| ||||
 CCT CCTACCTTCC GAAC
 CT CC_
 GAM2220 KIAA1018 3' AAGAACATTTTCCTCCCTTCCT 31053 T CTC
 AGGAAGGGA GGAAGGT CTT
 ||||| ||||| |||

TCCTTCCCT CCTTTTA GAA
 _ CAA
 GAM2220 KIAA1181 3' CAAGTCTTTACCCACCCCTTT 68910 A AA CTC_
 CT AGGAAGGG TGG GGT CTTG
 ||||| ||| ||| |||
 TCTTTCCC ACC CCA GAAC
 C _ TTTCT
 GAM2220 KIAA1205 3' CAAGCCCCCTCCACTCCCTCCC 70580 A _ A TCTC
 GG AGGGA TGGA GG CTTG
 || |||| |||| || ||||
 CC TCCCT ACCT CC GAAC
 C C C CC_
 GAM2220 KIAA1483 3' AAGACTATCTTCCCTCCCTTCC 70429 T CTC
 GGAAGGGA GGAAGGT CTT
 ||||| ||||| |||
 CCTTCCCT CCTTCTA GAA
 C TCA
 GAM2220 KIAA1737 3' CAAGGAAACCTTCATGGATCTT 67934 GATG_ C
 CC GGAAGG GAAGGT TCCTTG
 ||||| ||||| |||||
 CCTTCT CTTCCA AGGAAC
 AGGTA A
 GAM2220 LCHN 3' AAGAAGACCTCCTTTTTCT 87465 AT A C
 GGAAGGG GGA GGTCT CTT
 ||||| ||| ||||| |||
 TCTTTTT CCT CCAGA GAA
 _ _ A
 GAM2220 MEGF10 3' CAAGGGGCCACTGCCATCCCTT 51605 AA_ T
 CCT AGGAAGGGATGG GGTC CCTTG
 ||||| ||| |||||
 TCCTTCCCTACC CCGG GGAAC
 GTCA _
 GAM2220 NUDE1 5' CAAGGAGAGTGATCTCTTCC 35052 GGAAGG
 GGAAGGGAT TCTCCTTG
 ||||| |||||
 CCTTCTCTA AGAGGAAC
 GTG_
 GAM2220 OPTC 3' AAGGACCACCTCCTTCCT 27626 AT AA TC
 AGGAAGGG GG GG TCCTT
 ||||| || || |||||
 TCCTTCCT CC CC AGGAA
 _ A _
 GAM2220 OPTC 3' AAGGACCACCTCCTTCCT 27627 AT AA TC
 AGGAAGGG GG GG TCCTT
 ||||| || || |||||
 TCCTTCCT CC CC AGGAA
 _ A _
 GAM2220 LOC115704 3' AGGCCCTTCCTCCCTTCC 73905 T TCT
 GGAAGGGA GGAAGG CCT
 ||||| ||||| |||

		CCTTCCCT CCTTC	GGA		
		— CC—			
GAM2220	LOC147646 3'	CAAGAAACATCTTCCATCCTCC	79074	AA	CTC—
		CCT			
		AGG GGGATGGAAGGT	CTTG		
		TCC TCCTACCTTCTA	GAAC		
		CC	CAAA		
GAM2220	LOC149684 5'	CAAGAAAACGCTGCAGCCCTTC	85760	A GA —	CTC
		CT			
		AGGAAGGG TG AG GT	CTTG		
		TCCTTCCC AC TC CA	GAAC		
		G G— G	AAA		
GAM2220	LOC164312 3'	CAAGGAACTGCTGCCCTCCCTT	83391	T AA—	C
		CCT			
		AGGAAGGGA GG	GGT TCCTTG		
		TCCTTCCCT CC	TCA AGGAAC		
		C GTCG —			
GAM2220	LOC199906 5'	AAGTGGCCCACCCCTTTCT	89839	A AAG	TC
		AGGAAGGG TGG	GTC CTT		
		TCTTTCCC ACC	CGG GAA		
		C — T—			
GAM2220	LOC219333 3'	AGTCCTTCCTTCCCTTCC	95182	T	T
		GGAAGGGA GGAAGG	CT		
		CCTTCCCT CCTTCC	GA		
		T	T		
GAM2220	LOC257451 5'	CAAGGGCGCCTCCATCCCCC	97296	AA	A C
		GG GGGATGGA GGT	TCCTTG		
		CC CCCTACCT CCG	GGGAAC		
		— — C			
GAM2221	IL16 3'	CATCCCAGGATCGCAAGAGCCA	16915	GTAT	CA
		TGGTTCTTG	GTCC GGATG		
		ACCGAGAAC	TAGG CCTAC		
		GC— AC			
GAM2221	KIAA1170 3'	CATCCTGGGCAACAAGAAC	70411	GTA	T
		GTTCTTG	TG CCCAGGATG		
		CAAGAAC	AC GGGTCCTAC		
		A— —			
GAM2221	MGC10966 5'	CATCCCAGAGCTCAAGGACCA	49683	—	ATG CCA
		TGGTTCTTG GT	TC GGATG		
		ACCAGGAAC CG	AG CCTAC		
		T — AC—			
GAM2221	LOC51161 5'	CCTGGGAGTGAGAGGAACCA	33039	GG	G
		TGGTTCTT TAT	TCCCAGG		

ACCAAGGA GTG AGGGTCC
 GA _
 GAM2222 CDC42 3' ACTCTGGAGAGTAATCTGGGA 10137 A TTG
 TC CAGAT TATTCTCCAGAGT
 || |||| |||||
 AG GTCTA ATGAGAGGTCTCA
 G _
 GAM2222 EIF1A 3' ACTCTGGATTAAAAATCTG 90002 G TTC
 CAGATTT TA TCCAGAGT
 ||||| || |||||
 GTCTAAA AT AGGTCTCA
 A TT_
 GAM2222 HSD17B1 5' ACTCTGGAATGAGGATC 6426 TG TC
 GATT TAT TCCAGAGT
 ||| || |||||
 CTAG GTA AGGTCTCA
 GA _
 GAM2222 SORCS3 3' CTGGAATACAAATGCATGA 31072 CAG TC
 TCA ATTTGTAT TCCAG
 ||| ||||| |||||
 AGT TAAACATA AGGTC
 ACG _
 GAM2222 ST14 3' ACCCTGGAAAACAGACGGGTCT 42041 A ATTC_ A
 GAGA TC CAGATTTGT TCCAG GT
 || ||||| |||||
 AG GTCTGGGCA AGGTC CA
 A GACAAA C
 GAM2222 C20orf12 5' ACTCTGGATGGCAGCAAACCTG 36842 A AT _
 CAG TTTGT TC TCCAGAGT
 ||| |||| || |||||
 GTC AAACG GG AGGTCTCA
 C AC T
 GAM2222 Di-Ras2 3' ACTCTGGAGTCAACAGAATCTG 34609 GTATT
 CAGATTT CTCCAGAGT
 ||||| |||||
 GTCTAAG GAGGTCTCA
 AACT
 GAM2222 HEMK 5' ACTCTGGAGAACCTTTCCCTGA 32948 A ATTTGTA
 GA TC CAG TTCTCCAGAGT
 || ||| |||||
 AG GTC AAGAGGTCTCA
 A CCTTTCC
 GAM2222 KIAA1879 5' ACCCTGGAGAAAAACCTG 73925 A GTA A
 CAG TTT TTCTCCAG GT
 ||| ||| ||||| ||
 GTC AAA AAGAGGTC CA
 C _ C
 GAM2222 LOC160646 3' ACTCTGGAAAATACTGCTCT 83100 TTT C
 AGA GTATT TCCAGAGT
 ||| ||||| |||||

		TCT CATAA AGGTCTCA		
		CGT A		
GAM2222	LOC221271 3'	ACTCTGGAAAATTC	ACTATGT 93490	GATT T C
		ACA TG ATT TCCAGAGT		
		TGT AC TAA AGGTCTCA		
		ATC_ T A		
GAM2223	CHRNA1 3'	TATCGATGGTCCAAACCGG	61156	ACC _
		CTGG TGG TTATCGATA		
		GGCC ACC GGTAGCTAT		
		AA_ T		
GAM2223	CYP1B1 3'	TGTCAACCAGGTCCAG	5450	ATC
		CTGGACCTGGTT GATA		
		GACCTGGACCAA CTGT		
GAM2223	MECP2 3'	CGACAAGCACAGTCAGGTTG	18397	ACC G A
		CAACCTGG TG TT TCG		
		GTTGGACT AC AA AGC		
		GAC G C		
GAM2223	MTNR1B 3'	ATCAACGCCATGGGTTTCAGGCT	21056	A _ TATC
	G	CA CCTGGACCT GGT GAT		
		GT GGACTTGGG CCG CTA		
		C TA CAA_		
GAM2223	KIAA0683 5'	CGGGAGCCGGGTCCAGGT	32763	AT
		ACCTGGACCTGGTT CG		
		TGGACCTGGGCCGA GC		
		GG		
GAM2223	KIAA0931 3'	TTATCGATAAATGTACCA	68023	_ CTGG
		TGG AC TTATCGATAA		
		ACC TG AATAGCTATT		
		A TA_		
GAM2223	KIAA1317 3'	TTATCAAGTGAGGTCCAGGT	87218	GG ATC
		ACCTGGACCT TT GATAA		
		TGGACCTGGA GA CTATT		
		GT A_		
GAM2223	KIAA1374 5'	TATCGATGGCACTCAGATTG	61916	C ACCTG
		CAA CTGG GTTATCGATA		
		GTT GACT CGGTAGCTAT		
		A CA_		
GAM2223	LOC219988 3'	ATGCCAGGTCTAGGCTG	93258	A T
		CA CCTGGACCTGG TAT		

			GT GGATCTGGACC GTA		
			C C		
GAM2223	LOC220020	3'	TCGTAAACCAGGTTTCAGGTCA 95055	A	AT
			C ACCTGGACCTGGTT CGA		
			A TGGACTTGGACCAA GCT		
			C AT		
GAM2224	ALDH3A2	5'	CAGCCCGCTGCCAGAGCCGGGG 69796	ATG_	A
	A		TCCCTGGCTT AGC GGCTG		
			AGGGGCCGAG TCG CCGAC		
			ACCG C		
GAM2224	CAPNS1	3'	CAGCCTGCCAGGCCAGG 10013	TA	A
			CCTGGCT TG GCAGGCTG		
			GGACCGG AC CGTCCGAC		
			— —		
GAM2224	CASP10	3'	CAGCCTGCTTTCACACTAAGGA 53245	C	CTTAT
			TCC TGG GAGCAGGCTG		
			AGG ATC TTCGTCCGAC		
			A ACACT		
GAM2224	DLEC1	3'	TGGCCCCACAAGCCAGG 24723	A	AGCA
			CCTGGCTT TG GGCTG		
			GGACCGAA AC CCGGT		
			C C_		
GAM2224	DLEC1	3'	TGGCCCCACAAGCCAGG 24724	A	AGCA
			CCTGGCTT TG GGCTG		
			GGACCGAA AC CCGGT		
			C C_		
GAM2224	DYT1	3'	CAGCCCACTCATCGCAGGG 5477	G TT	CA
			CCCTG C ATGAG GGCTG		
			GGGAC G TACTC CCGAC		
			_ C_ AC		
GAM2224	LPIN1	5'	CAGCCTGCTGAGAACTAG 67985	C	ATG
			CTGG TT AGCAGGCTG		
			GATC AA TCGTCCGAC		
			_ GAG		
GAM2224	RCV1	5'	CAGCCTGCGGCCAGGGG 12801	TATGA	
			TCCCTGGCT GCAGGCTG		
			GGGGACCGG CGTCCGAC		
			— —		
GAM2224	TNXB	5'	CTCAGCCTTGGGCCAAGCCTGG 51634	CT TA	A _
	A		TCC GGCT TG GC AGGCTGAG		

AGG CCGA AC CG TCCGACTC
 T_ _ _ GGT
 GAM2224 C20orf150 3' CAGCCTGCCCTCAAGCCAAGGA 66009 C ATGA
 TCC TGGCTT GCAGGCTG
 ||| ||||| |||||
 AGG ACCGAA CGTCCGAC
 A CTCC
 GAM2224 C20orf39 5' CAGCCTGCCGCGCCAGGCGA 46571 _ TAT A
 TC CCTGGCT G GCAGGCTG
 || ||||| | |||||
 AG GGACCGG C CGTCCGAC
 C _ _ _
 GAM2224 CBX6 3' CAGCCTGCCTGAAGCAAAGGA 27407 CTG ATGA
 TCC GCTT GCAGGCTG
 ||| ||| |||||
 AGG CGAA CGTCCGAC
 AAA GTC_
 GAM2224 CD84 3' CTCAGCCTGTAAGCAAAGCAGG 81570 G A A_
 CCTG CTT TG GCAGGCTGAG
 |||| ||| || |||||
 GGAC GAA AC TGTCCGACTC
 _ _ GAA
 GAM2224 CYP2D6 3' CAGCCTGCTCCTAGCCCAGAGG 5451 _ C T
 CC CTGG TTA GAGCAGGCTG
 || |||| || |||||
 GG GACC GAT CTCGTCCGAC
 A C C
 GAM2224 DKFZP586J0619 3' CTCAGCCTGCCCAGCAGGGA 82317 G TAT A
 TCCCTG CT G GCAGGCTGAG
 ||||| || | |||||
 AGGGAC GA C CGTCCGACTC
 _ _ C
 GAM2224 FKHL18 3' CAGCCCTGGTGAGCCAAGGA 80370 C G CA
 TCC TGGCTTAT AG GGCTG
 ||| ||||| || |||||
 AGG ACCGAGTG TC CCGAC
 A G _
 GAM2224 FLJ14800 3' CAACCTGCTCAGGCACCACAGA 52684 CC CTTA C
 TC TGG TGAGCAGG TG
 || ||| ||||| ||
 AG ACC ACTCGTCC AC
 AC ACGG A
 GAM2224 FLJ14957 3' CTCAGCCCCACTCATACCTAGAG 52816 C CT CA
 A TC CTGG TATGAG GGCTGAG
 || |||| ||||| |||||
 AG GATC ATACTC CCGACTC
 A C_ AC
 GAM2224 KIAA1023 3' CAGGCTCAGAAGCCAGGGA 34677 A AGG
 TCCCTGGCTT TGAGC CTG
 ||||| ||||| |||

AGGGACCGAA ACTCG GAC
 G ____
 GAM2224 KIAA1655 5' CTCAGCCCACTCCCAAACCAG 67183 C AT CA
 CTGG TT GAG GGCTGAG
 |||| || ||| |||||
 GACC AA CTC CCGACTC
 A CC AC
 GAM2224 MGC35521 3' CTCAGGTGTCAGTAAGCCAG 59666 GA GG
 CTGGCTTAT GCA CTGAG
 ||||| ||| ||||
 GACCGAATG TGT GACTC
 AC G_
 GAM2224 MGC5508 3' CAGCCTGCCTCACCAGGGA 44264 CTTA _
 TCCCTGG TGAG CAGGCTG
 ||||| ||| |||||
 AGGGACC ACTC GTCCGAC
 ____ C
 GAM2224 PADI1 3' CAGCCTGCACTGAGTCA 62700 TGA
 TGGCTTA GCAGGCTG
 ||||| |||||
 ACTGAGT CGTCCGAC
 CA_
 GAM2224 RIN3 5' CTCAGCCTGCCTCCCAAGGGA 46162 _ CTTAT _
 TCCCT GG GAG CAGGCTGAG
 |||| || ||| |||||
 AGGGA CC CTC GTCCGACTC
 A C ____ C
 GAM2224 SOX17 3' CAGCCTGCAGGCCAG 42630 ATGA
 CTGGCTT GCAGGCTG
 ||||| |||||
 GACCGGA CGTCCGAC

 GAM2224 SP140 3' AGTATCTCATCAGCCAGGGA 24326 T CAG
 TCCCTGGCT ATGAG GCT
 ||||| |||| |||
 AGGGACCGA TACTC TGA
 C TA_
 GAM2224 VI 3' CAGCCGCTAGGCCAGGGA 26486 ATG A
 TCCCTGGCTT AGC GGCTG
 ||||| ||| ||||
 AGGGACCGGA TCG CCGAC
 ____ -
 GAM2224 LOC112817 5' CAGTGGCCACAAGTCAGGGA 57319 A A AG
 TCCCTGGCTT TG GC GCTG
 ||||| || || ||||
 AGGGACTGAA AC CG TGAC
 C _ G_
 GAM2224 LOC129676 5' CTCAGCCTGCAGACACAGGGA 76232 GCTTATGA
 TCCCTG GCAGGCTGAG
 |||| | |||||

		AGGGAC	CGTCCGACTC		
		ACAGA__			
GAM2224	LOC134266 3'	CTCAGCCTACCAAGTAGCCAGG	75644	TATGAGC	
		CCTGGCT	AGGCTGAG		
		GGACCGA	TCCGACTC		
		TGAACCA			
GAM2224	LOC150248 3'	CCACCTCATCAGCCAGGGA	86126	T CA	
		TCCCTGGCT	ATGAG GG		
		AGGGACCGA	TACTC CC		
		C CA			
GAM2224	LOC155179 3'	CAGGCTCAGAAGCCAGGGA	82225	A AGG	
		TCCCTGGCTT	TGAGC CTG		
		AGGGACCGAA	ACTCG GAC		
		G _			
GAM2224	LOC158056 5'	CTCAGCCCAGGAGAGCCAGGGG	82589	ATGAGCA	
		TCCCTGGCTT	GGCTGAG		
		GGGGACCGAG	CCGACTC		
		AGGAC__			
GAM2224	LOC219405 3'	CAGCCTGCTCTACCCAGAGA	92450	C CTTAT	
		TC CTGG	GAGCAGGCTG		
		AG GACC	CTCGTCCGAC		
		A CAT__			
GAM2224	LOC221496 3'	TCAGCCTGCTCCCTGGGA	93643	T CTTAT	
		TCCC GG	GAGCAGGCTGA		
		AGGG CC	CTCGTCCGACT		
		T _			
GAM2224	LOC222031 3'	CAGCCTGTCTAACCCAAAGA	95672	CC C T G	
		TC TGG TTA	GA CAGGCTG		
		AG ACC AAT	CT GTCCGAC		
		AA C _ _			
GAM2224	LOC51320 3'	CTGCAACTAATAAGCCAAGGA	34028	C GA__	
		TCC TGGCTTAT	GCAG		
		AGG ACCGAATA	CGTC		
		A ATCAA			
GAM2225	DEDD 3'	TACAGCTACCTTACCACTG	53380	A C A	
		CA TG TAA	GTAGCTGTG		
		GT AC ATT	CATCGACAT		
		C C C			
GAM2225	ENAM 3'	CCTAGCACAGTGTCTTCAACAT	49927	CTA TA	
		ATG AAG	GCTGTGCTAGG		

TAC TTC TGACACGATCC
 AAC TG
 GAM2225 MAP3K14 3' CCAGAGCACAGCTCAGCATCA 15544 A AAAGT A_
 C ATGCT AGCTGTGCT GG
 ||||| ||||| ||
 A TACGA TCGACACGA CC
 C C____ GA
 GAM2225 MYH11 3' CCCAGCAGACTGTACTTAGCAT 43430 A GCTG_ A
 TG CAATGCTAA GTA TGCT GG
 ||||| || ||||| ||
 GTTACGATT CAT ACGA CC
 _ GTCAG C
 GAM2225 MYH11 3' CCCAGCAGACTGTACTTAGCAT 11739 A GCTG_ A
 TG CAATGCTAA GTA TGCT GG
 ||||| || ||||| ||
 GTTACGATT CAT ACGA CC
 _ GTCAG C
 GAM2225 USP11 5' CCCAGCACGTGCTTGGCATT 17384 AAGT _ A
 AATGCTA AGC TGTGCT GG
 ||||| || ||||| ||
 TTACGGT TCG GCACGA CC
 ____ T C
 GAM2225 FLJ20086 3' CCTAGCACAACAGAGGCA 35012 AAA AGC
 TGCT GT TGTGCTAGG
 |||| || ||||| ||
 ACGG CA ACACGATCC
 AGA ____
 GAM2225 KIAA0397 3' CCCAGCACAGCCTGCCCAGC 62346 AAA _ A
 GCT GTAG CTGTGCT GG
 || |||| ||||| ||
 CGA CGTC GACACGA CC
 CC_ C C
 GAM2225 KIAA0945 3' CCCAGCACAGCTCTGAGCTTG 30901 T AA T A
 CAA GCT AG AGCTGTGCT GG
 |||| || ||||| ||
 GTT CGA TC TCGACACGA CC
 _ G_ _ C
 GAM2225 KIAA1184 3' CCTAGCACGGTGCCTAGCA 42925 AAGTA
 TGCTA GCTGTGCTAGG
 |||| ||||| ||
 ACGAT TGGCACGATCC
 CCG____
 GAM2225 KIAA1434 3' TACAGCTACCTCAGTACTG 70212 A AAA
 CA TGCT GTAGCTGTG
 || |||| ||||| ||
 GT ATGA CATCGACAT
 C CTC
 GAM2225 KIAA1656 3' CCCAGCATGCCCTTGGCA 66363 AGTA T A
 TGCTAA GC GTGCT GG
 ||||| || ||||| ||

			ACGGTT CG TACGA CC	
			CC__ _ C	
GAM2225	LIMK2	3'	AGCACAGTTCAGCATTG 34118	AAAGT
			CAATGCT AGCTGTGCT	
			GTTACGA TTGACACGA	
			C__	
GAM2225	LIMK2	3'	AGCACAGTTCAGCATTG 19920	AAAGT
			CAATGCT AGCTGTGCT	
			GTTACGA TTGACACGA	
			C__	
GAM2225	LOC134957	3'	CTAGCACAGTCATGCACTG 58342	A TAAA AG
			CA TGC GT CTGTGCTAG	
			GT ACG TA GACACGATC	
			C ____ CT	
GAM2225	LOC147639	5'	CCTAGCACAGGTTAATTAG 79008	AG _
			CTAA TAGC TGTGCTAGG	
			GATT ATTG ACACGATCC	
			A_ G	
GAM2225	LOC150350	3'	CCAAGACTTACGTTAGCATTG 80573	A CT G A
			CAATGCTAA GTAG GT CT GG	
			GTTACGATT CATT CA GA CC	
			G _ _ A	
GAM2225	LOC151778	3'	CCTAGCACGCGCCCCAGC 71947	AAA A T
			GCT GT GC GTGCTAGG	
			CGA CG CG CACGATCC	
			CCC _ _	
GAM2225	LOC152915	3'	CCTAGCACGCGCCCCAGC 67583	AAA A T
			GCT GT GC GTGCTAGG	
			CGA CG CG CACGATCC	
			CCC _ _	
GAM2225	LOC256598	3'	CCTAGCACGCGCCCCAGC 98103	AAA A T
			GCT GT GC GTGCTAGG	
			CGA CG CG CACGATCC	
			CCC _ _	
GAM2225	LOC90625	3'	CACAGCTACCTTATCACTG 64376	A C A
			CA TG TAA GTAGCTGTG	
			GT AC ATT CATCGACAC	
			C T C	
GAM2226	NME2	3'	CTCTTCATTCCATTGACTTAGA 11813	AGTCTCCTA
			TCTAAGTCAG AAGAG	

			AGATTCAGTT	TTCTC		
			ACCTTAC__			
GAM2226	PPL	3'	CTCTCCAGATTTCTGGCTTA	12222	_	CCTAA
			TAAGTCAGAG TCT	AGAG		
			ATTCGGTCTT AGA	TCTC		
			T CC__			
GAM2226	RAB26	3'	CTTAGGAGGCTCTGGCT	27603		A
			AGTCAGAGTCTCCTA AG			
			TCGGTCTCGGAGGAT TC			
			C			
GAM2226	SCN8A	3'	CTGTGGAGACTCTAACCTGA	27214	TAA C	TAA
			TC GT AGAGTCTCC AG			
			AG CA TCTCAGAGG TC			
			TC_ A TG_			
GAM2226	CX46.6	3'	AGGCAGACTCTGCCCAGA	40307	AA T	_
			TCT G CAGAGTCT CCT			
			AGA C GTCTCAGA GGA			
			CC_ C			
GAM2226	HGC6.1.1	3'	AGGAAACTCTGACACAGA	27607	AA	C
			TCT GTCAGAGT TCCT			
			AGA CAGTCTCA AGGA			
			CA A			
GAM2226	KIAA0907	3'	CTAGAGTGAGACTCTGTCT	30873	T	_ AA
			AG CAGAGTCTC CT AG			
			TC GTCTCAGAG GA TC			
			T T GA			
GAM2226	KIAA1077	3'	CTCTTCACTCTCCTCTGATTAG	73288	G	TCTCCTA
	A		TCTAA TCAGAG AAGAG			
			AGATT AGTCTC TTCTC			
			_ CTCTCAC			
GAM2226	KIAA1456	5'	CTGAGGGGAGACTCTGTCT	67553	T	AA
			AG CAGAGTCTCCT AG			
			TC GTCTCAGAGGG TC			
			T AG			
GAM2226	KIAA1656	3'	CTCTGTTACTCTGACTCAG	66366	A	CTCCTAA
			CT AGTCAGAGT AGAG			
			GA TCAGTCTCA TCTC			
			C TTG__			
GAM2226	KIAA1970	3'	CTCTATGGGAGACCCTAAGCCA	74780	AAGTC A	A
	GA		TCT AG GTCTCCTA AGAG			

AGA TC CAGAGGGT TCTC
 CCGAA C A
 GAM2226 LCHN 3' CTCTTTAGGAGGCAGACTTG 87468 AGA
 TAAGTC GTCTCCTAAAGAG
 ||||| |||||
 GTTCAG CGGAGGATTCTC
 A__
 GAM2226 MGC11287 3' CTCTTCAGGAGACTGAGAC 49615 AG A
 GTC AGTCTCCT AAGAG
 || ||||| |||||
 CAG TCAGAGGA TTCTC
 AG C
 GAM2226 MGC2656 5' TGGGAGACCCTGACCCTGA 44722 TAA A
 TC GTCAG GTCTCCTA
 || ||||| |||||
 AG CAGTC CAGAGGGT
 TCC C
 GAM2226 MGC3047 3' CTCCCCAGGGACCTGCTGACTT 51348 _ TC AAA
 G TAAGTCAG AG TCCT GAG
 ||||| || ||||| |||||
 GTTCAGTC TC GGGA CTC
 G CA CCC
 GAM2226 MGC3771 5' CTCCTTAGAGCCGTGACTTAGG 49054 GA T C A
 TCTAAGTCA G CTC TAA GAG
 ||||| | ||||| |||||
 GGATTCAGT C GAG ATT CTC
 GC _ _ C
 GAM2226 TP53INP1 3' CTCTTTAGAACAAGAGTTAGA 53867 G AGA CTC
 TCTAA TC GT CTAAAGAG
 ||||| || ||||| |||||
 AGATT AG CA GATTCTC
 G AA_ A__
 GAM2226 VAMP3 3' CTCTTCAAGACTTTTGACTTAG 17710 _ CCTA
 A TCTAAGTCAGA GTCT AAGAG
 ||||| ||||| ||||| |||||
 AGATTCAGTTT CAGA TTCTC
 T AC__
 GAM2226 LOC144079 5' CTCTTTAGGAAGTCACTTA 77179 CA GTC
 TAAGT GA TCCTAAAGAG
 ||||| || ||||| |||||
 ATTCA CT AGGATTCTC
 _ GA_
 GAM2226 LOC144584 5' CTGTAGAAGACCCTGATCCAGA 67587 AA A C A
 TCT GTCAG GTCT CTA AG
 || ||||| ||||| ||||| |||||
 AGA TAGTC CAGA GAT TC
 CC C A G
 GAM2226 LOC146485 3' CTGTAGAAGACCCTGATCCAGA 60492 AA A C A
 TCT GTCAG GTCT CTA AG
 || ||||| ||||| ||||| |||||

AGA TAGTC CAGA GAT TC
 CC C A G
 GAM2226 LOC91035 5' CAAAGAGCTCAGCCCTGACTTA 65293 A T_____ CTAAA
 GA TCTAAGTCAG G CTC G
 ||||| | ||| |
 AGATTCAGTC C GAG C
 C GACTC__ AAAT
 GAM2227 ELF3 3' TGACCTTGACCTTGACCAA 16685 T GAT AAA
 TTGGT CAAGG GG GTCA
 ||||| || ||||
 AACCA GTTCC TC CAGT
 _ AGT _
 GAM2227 JAK2 3' TGACCTTCATTCTGAGACCAA 18318 CAA AA
 TTGGTT GGGATGGA GTCA
 ||||| ||||| ||||
 AACCAG TCTTACTT CAGT
 AG_ C_
 GAM2227 SLC10A2 5' ACTCTCTGTCTTGACCAA 6590 CAA A
 TTGGTT GGGATGGA AGT
 ||||| ||||| ||||
 AACCAG TTCTGTCT TCA
 _ C
 GAM2227 FLJ10803 3' GTGACTTTCAGTTAAAGCCAA 37205 CAAGG G
 TTGGTT GAT GAAAGTCAC
 ||||| || ||||| ||||
 AACCGA TTG CTTTCAGTG
 AA_ A
 GAM2227 KIAA1958 5' GTGACTTTGAACCCCAAACC 82788 CAA ATGG
 GGTT GGG AAAGTCAC
 |||| || ||||| ||||
 CCAA CCC TTTCAGTG
 A_ CAAG
 GAM2227 MARCKS 3' ACTTTCCACCCTGCCCA 11411 TTCA A
 TGG AGGG TGGAAAGT
 || ||||| ||||| ||||
 ACC TCCC ACCTTTCA
 CG_ _
 GAM2227 TUB 5' GTGGGACCATCCCTTAAACC 13898 C AAAG
 GGTT AAGGGATGG TCAC
 ||||| ||||| ||||
 CCAA TTCCCTACC GGTG
 A AG_
 GAM2227 LOC80298 3' ACTTTTACCTTGAACCA 48062 GATG
 TGGTTCAAGG GAAAGT
 ||||| ||||| ||||
 ACCAAGTTCC TTTTCA
 A_
 GAM2228 RP42 3' GTCAATTTCTGCTGGCTGGA 40567 TTTCC C
 TCCAGCCAGC AAAT GAC
 ||||| ||||| ||||

AGGTCGGTCG TTTA CTG
 TC___ A
 GAM2228 RRM2B 3' TTGGAAAAAGCTGGCCGAG 68437 CA ___
 TTC GCCAGCTT TCCAA
 ||| ||||| |||||
 GAG CGGTCGAA AGGTT
 C_ AA
 GAM2228 FLJ22529 3' GTCAGGGAAAGCTGACTG 45951 C AAATC
 CAG CAGCTTTCC GAC
 ||| ||||| |||
 GTC GTCGAAAGG CTG
 A GA___
 GAM2228 HSU24186 5' CGACCCTGACTGGCTGGAA 26238 CTT CAAA
 TTCCAGCCAG TC TCG
 ||||| || |||
 AAGGTCGGTC AG AGC
 ___ TCCC
 GAM2228 JDD1 3' GTCAATCTGAAAAATTCAGGCT 63918 AGC___ C A C
 GGA TCCAGCC TTT CA AT GAC
 ||||| ||| ||| |||
 AGGTCGG AAA GT TA CTG
 ACTTA A C A
 GAM2228 KIAA0090 3' TTTGAGAAAGCCTGGCTGGAA 89822 _ _
 TTCCAGCCAG CTTTC CAAA
 ||||| ||||| |||||
 AAGGTCGGTC GAAAG GTTT
 C A
 GAM2228 LOC133452 5' CGATTGGAAGGCTGCCGAA 76455 CA C C
 TTC GC AGCTTTC AAATCG
 ||| || ||||| |||||
 AAG CG TCGGAAG TTTAGC
 C_ _ _
 GAM2228 LOC151556 5' GTCGATTTAGCAAAGCTGG 81084 CC_
 CCAGCTTT AAATCGAC
 ||||| |||||
 GGTCGAAA TTTAGCTG
 CGA
 GAM2229 FASN 3' ACCAATTTGGTAAAAATGCTGC 15910 CG G TC_
 TC GAGCAGCAT TTG CG TGGT
 ||||| ||| || |||
 CTCGTCGTA AAT GT ACCA
 AA G TTA
 GAM2229 SET 3' TACCAGATAGCTCAATACTCTC 13021 C CATC _ _
 GAG AG GTTG GC GTCTGGTA
 ||| || ||| || |||||
 CTC TC TAAC CG TAGACCAT
 _ A___ T A
 GAM2229 ADG-90 5' ACCCCCCACGATGCTGCTC 53524 T CGTCT
 GAGCAGCATCGT GG GGT
 ||||| || |||

		CTCGTCGTAGCA CC CCA	
		C C_____	
GAM2229	HEF1	3' ACCAGACATATCCTGCTC 22154	CATCGT GC
		GAGCAG TG GTCTGGT	
		CTCGTC AT CAGACCA	
		CT_____ A_	
GAM2229	LOC151171	5' ACCAGACACCGAAGCTGCT 80943	ATCG C
		AGCAGC TTGG GTCTGGT	
		TCGTCTG AGCC CAGACCA	
		A_____ A	
GAM2229	LOC152641	5' ACCAGCTCGGACGCACTGC 81518	CAT GG T_
		GCAG CGTT CG CTGGT	
		CGTC GCAG GC GACCA	
		AC_ _ TC	
GAM2230	ACVRL1	5' TTTGCTCCAGCCCCCATCCCA 5241	AAATGAAA C_
		TGGGATGG TGG CAAA	
		ACCCTACC ACC GTTT	
		CCCG_____ TC	
GAM2230	ADAM19	3' TCATATCACCTCCATCCCA 53846	AA A
		TGGGATGGA TGA ATGG	
		ACCCTACCT ACT TACT	
		CC A	
GAM2230	ANK1	3' CCACATACCTCCATTCCA 40405	A_ AAA
		TGGGATGGA ATG TGG	
		ACCTTACCT TAC ACC	
		CCA _____	
GAM2230	ANK1	3' CCACATACCTCCATTCCA 40406	A_ AAA
		TGGGATGGA ATG TGG	
		ACCTTACCT TAC ACC	
		CCA _____	
GAM2230	ATP1A2	3' CCAGATCCTTTTCCATCCCA 7360	T_ AA
		TGGGATGGAAA GA TGG	
		ACCCTACCTTT CT ACC	
		TC AG	
GAM2230	AXL	3' CTATCCCACCTCCATCCCA 41883	AA AA
		TGGGATGGA TG ATGG	
		ACCCTACCT AC TATC	
		CC CC	
GAM2230	B29	3' TTATTTCAATTCCTCCCA 50039	AT
		TGGG GGAAATGAAATGG	

			ACCC CCTTTACTTTATT		
			CT		
GAM2230	CDC2L2	5'	TTTGGCCATCAAACCACCCCA 43995	A AAA AA	
			TGGG TGG TGA TGGCAAAA		
			ACCC ACC ACT ACCGGTTT		
			C AA_ _		
GAM2230	CRACC	3'	TGGAGTTTTCATTCCATCCCA 41316	A GG	
			TGGGATGGAA TGAAAT CCA		
			ACCCTACCTT ACTTTG GGT		
			_ A_		
GAM2230	EPS8	3'	TTATTTTATCCCCATCCCA 16716	AA	
			TGGGATGG ATGAAATGG		
			ACCCTACC TATTTTATT		
			CC		
GAM2230	FBXW1B	3'	TTGACCACTTTTCATCCTA 25479	TGAAA C	
			TGGGATGGAAA TGG CAA		
			ATCCTACTTTT ACC GTT		
			C_ _ A		
GAM2230	FGF20	5'	CTATCCACCTCCATCCCA 39554	AA AA	
			TGGGATGGA TG ATGG		
			ACCCTACCT AC TATC		
			CC C_		
GAM2230	IRF2	3'	CCATCCCATCCCATCCCA 11015	AA AA	
			TGGGATGG ATG ATGG		
			ACCCTACC TAC TACC		
			C_ CC		
GAM2230	IRF2	3'	CCATCCCATCCCATCCCA 11016	AA AA	
			TGGGATGG ATG ATGG		
			ACCCTACC TAC TACC		
			C_ CC		
GAM2230	IRF2	3'	CCATCCCATCCCATCCCA 11017	AA AA	
			TGGGATGG ATG ATGG		
			ACCCTACC TAC TACC		
			C_ CC		
GAM2230	IRF2	3'	CCATCCCATCCCATCCCA 11018	AA AA	
			TGGGATGG ATG ATGG		
			ACCCTACC TAC TACC		
			C_ CC		
GAM2230	IRF2	3'	CTATCCCATCCCATCCCA 11019	AA AA	
			TGGGATGG ATG ATGG		

		ACCCTACC TAC TATC		
		C_ CC		
GAM2230	JMJ	3' CATTCCATCTCCATCTCA 18320	A	A
		TGGGATGGA ATG AATG		
		ACTCTACCT TAC TTAC		
		C C		
GAM2230	KCNJ15	3' GCCATTTTCATTTCTTATCT 11160	_	
		GGATG GAAATGAAATGGC		
		TCTAT CTTTACTTTACCG		
		T		
GAM2230	MMP19	3' CCTTTCATTTCCCCCCCA 11628	AT	T
		TGGG GGAAATGAAA GG		
		ACCC CCTTTACTTT CC		
		CC _		
GAM2230	MMP19	3' CCTTTCATTTCCCCCCCA 11629	AT	T
		TGGG GGAAATGAAA GG		
		ACCC CCTTTACTTT CC		
		CC _		
GAM2230	PAP	3' TGACCACCTCATTCTTATCT 58039	GA	AA C
		GGATG AATGA TGG CA		
		TCTAT TACT ACC GT		
		TC CC A		
GAM2230	PRKACA	3' TCATAACTTCTCCCCATCCCA 12270	AAAT	___
		TGGGATGG GAA ATGG		
		ACCCTACC CTT TACT		
		CCT_ CAA		
GAM2230	RAB7L1	3' TTTGGCTTATTTTCCATCCCA 15418	TGAAAT	
		TGGGATGGAAA GGCCAAA		
		ACCCTACCTTT TCGGTTT		
		TAT___		
GAM2230	SYNGR3	3' TGGCCACTGTTCATCCCA 16126	A	AAA
		TGGGATGG AATG TGGCCA		
		ACCCTACC TTGT ACCGGT		
		C C_		
GAM2230	TFAP4	3' GGTCTCATCTTCCACCCCA 13692	A	_ AAT
		TGGG TGGAA ATGA GGCC		
		ACCC ACCTT TACT CTGG		
		C C _		
GAM2230	TP53	3' GGAAATCTCACCCCATCCCA 6803	AAA	A GG
		TGGGATGG TGA AT CC		

ACCCTACC ACT TA GG
 CC_ C AA
 GAM2230 YWHAЕ 3' TGACCACCCCTCCTCCCATC 23138 AAAT AA__ C
 CCA TGGGATGG GA TGG CA
 ||||| || |||
 ACCCTACC CT ACC GT
 CCTC CCCC A
 GAM2230 C1orf22 3' GCCATCAGCCTTACTCCATCCC 48041 AA__ AA
 A TGGGATGGA TGA TGGC
 ||||| ||| |||
 ACCCTACCT ACT ACCG
 CATTCCG _
 GAM2230 C8orf7 3' TGATGTTGCCATTTTCACCCCA 82470 A A_ GC
 TGGG TGGAAATG AATG CA
 ||| ||||| ||| ||
 ACCC ACTTTTAC TTGT GT
 C CG A_
 GAM2230 CAP 3' TTGGCCATCTAGCATTCCA 22067 GAAAT AA
 TGGGATG GA TGGCAA
 ||||| || |||||
 ACCTTAC CT ACCGGTT
 GAT__ _
 GAM2230 DKFZp434F142 3' TTGGCCACTCCAGGCCCA 51040 A_ AATGAAA
 TGGG TGGA TGGCAA
 ||| ||| |||||
 ACCC ACCT ACCGGTT
 GG C_____
 GAM2230 DKFZp434G179 3' CCGTGAATCATTTCCATTCCCA 80891 _ A_
 TGGGA TGGAAATGA ATGG
 |||| ||||| |||
 ACCCT ACCTTTACT TGCC
 T AAG
 GAM2230 DNAJA4 3' TGGCCTTATTTCCATTCCA 38363 AAT
 TGGGATGGAAATGA GGCCA
 ||||| |||||
 ACCTTACCTTTATT CCGGT
 _
 GAM2230 ERG-1 5' TTGACCACCTTCACATCC 42103 GAAA A_ C
 GGATG TGAA TGG CAA
 |||| ||| ||| |||
 CCTAC ACTT ACC GTT
 _ CC A
 GAM2230 FLJ10508 3' GCCAACATTTTCATTTCCACCC 36680 A _
 A TGGG TGGAAATGAAA TGGC
 ||| ||||| |||
 ACCC ACCTTTACTTT ACCG
 _ TACA
 GAM2230 FLJ12287 3' TGGCCATTCCAGGGACCCTCC 42565 T AAA_ A
 GGA GG TG AATGGCCA
 ||| || || |||||

		CCT CC AC TTACCGGT		
		C AGGG C		
GAM2230	FLJ12816	3' CCACTTCACCCCATCCCA	42184	AAA A
		TGGGATGG TGAA TGG		
		ACCCTACC ACTT ACC		
		CC_ C		
GAM2230	FLJ13868	3' GGCCATCCTTCCACACCCA	43029	A_ ATGAA
		TGGG TGGAA ATGGCC		
		ACCC ACCTT TACCGG		
		AC CC_		
GAM2230	FLJ20195	3' TTGGCCACCTCATGCCCATCCC	35226	AA AA
		GGGATGG ATGA TGGCCAA		
		CCCTACC TACT ACCGGTT		
		CG CC		
GAM2230	FLJ21168	3' TCAACTCATTCCCGTCCCA	47584	A AA
		TGGGATGG AATGA TGG		
		ACCCTGCC TTACT ACT		
		C CA		
GAM2230	FLJ22678	3' GCCACCCACTTCTCATCCCA	61118	_ A AAA
		TGGGATG GAA TG TGGC		
		ACCCTAC CTT AC ACCG		
		T C CC_		
GAM2230	FLJ22690	3' CTGTTTCTCTTTCCATCCCA	45574	T_
		TGGGATGGAAA GAAATGG		
		ACCCTACCTTT CTTTGTC		
		CT		
GAM2230	FLJ31890	3' TGTGCCTCAGTTCCCATCCCA	92987	A GAAAT _
		TGGGATGG AAT GGC CA		
		ACCCTACC TTG CCG GT		
		C ACT_ T		
GAM2230	KIAA0125	3' CCACCCTCACCTCCATCCCA	29563	AA AA_
		TGGGATGGA TGA TGG		
		ACCCTACCT ACT ACC		
		CC CCC		
GAM2230	KIAA1036	3' TTGACTCACCATCCCATCCCA	30499	AA AAAT C
		TGGGATGG ATG GG CAA		
		ACCCTACC TAC TC GTT		
		C_ CAC_ A		
GAM2230	KIAA1305	5' TTTGGCCAGTCCCCACTCCCA	47625	_ AAAT AA
		TGGGA TGG GA TGGCCAAA		

		ACCCT ACC CT ACCGGTTT		
		C C__ G_		
GAM2230 KIAA1691	3'	TTGGTTCCATTTCCATCC	94138	AAAT
		GGATGGAAATG GGCCAA		
		CCTACCTTTAC TTGGTT		
		C__		
GAM2230 KRTAP4-14	3'	TGAGCCCATCACCATCCCA	53516	AA AAAT _
		TGGGATGG ATG GGC CA		
		ACCCTACC TAC CCG GT		
		AC ____ A		
GAM2230 MGC4171	5'	GCCACCATGCCCCTCATCCCA	44454	AA__ AAA
		TGGGATGG ATG TGGC		
		ACCCTACT TAC ACCG		
		CCCCG C__		
GAM2230 MGC4415	3'	TGGGCAGCTCCCATCCCA	49766	AAAT AA G
		TGGGATGG GA TG CCA		
		ACCCTACC CT AC GGT		
		____ CG G		
GAM2230 NDRG4	3'	TTGACCCCTCTCATCCCA	40387	AAAT AAT C
		TGGGATGG GA GG CAA		
		ACCCTACT CT CC GTT		
		____ CC_ A		
GAM2230 PI4KII	3'	TGGCCACAGCCTCCACACCA	37956	GA AA_ AAA
		TGG TGGG TG TGGCCA		
		ACC ACCT AC ACCGGT		
		AC CCG ____		
GAM2230 PRO1866	5'	TTGGCCACCTCTGATCTCA	38150	GGAAAT AA
		TGGGAT GA TGGCCAA		
		ACTCTA CT ACCGGTT		
		GT____ CC		
GAM2230 PTPRT	3'	TCAGGTCACCTTCCATTCCA	56508	A AA
		TGGGATGGAA TGA TGG		
		ACCTTACCTT ACT ACT		
		C GG		
GAM2230 SCAM-1	3'	CCTTTCATTTCCTCCCA	20502	AT T
		TGGG GGAAATGAAA GG		
		ACCC CCTTTACTTT CC		
		CT _		
GAM2230 SDC3	5'	CCGTCTCATTTCTCCCA	28469	T A
		TGGGA GGAAATGA ATGG		

		ACCCT CCTTTACT TGCC		
		— C		
GAM2230	SLC34A2	5' GGCCGCCGCTCCATCCCA	22222	AA AAA
		TGGGATGGA TG TGGCC		
		ACCCTACCT GC GCCGG		
		CC C__		
GAM2230	SPRY4	3' CCATCTCACTCCACCCCA	49007	A AA A
		TGGG TGGA TGA ATGG		
		ACCC ACCT ACT TACC		
		C C_ C		
GAM2230	SS18L1	3' GCCACTTCATTTCTATTT	65955	A
		GGATGGAAATGAA TGGC		
		TTTATCTTTACTT ACCG		
		C		
GAM2230	TU3A	3' TCATTATCCACCCCATCCCA	24186	AAAT _
		TGGGATGG GA AATGG		
		ACCCTACC CT TTA		
		CCAC A		
GAM2230	LOC126917	3' GCCGAGATCCATTTCCAACCCA	75094	A AAA__
		TGGG TGGAAATG TGGC		
		ACCC ACCTTTAC GCCG		
		A CTAGA		
GAM2230	LOC129228	5' TGACCCCATCCTCATCCCA	76320	AA AAAT C
		TGGGATGG ATG GG CA		
		ACCCTACT TAC CC GT		
		CC C__ A		
GAM2230	LOC143173	5' CCACTTCACCTCATCCCA	61017	AAA A
		TGGGATGG TGAA TGG		
		ACCCTACT ACTT ACC		
		CC_ C		
GAM2230	LOC143187	3' TGGTCCCTTCCCATCCCA	59767	AAAT AT
		TGGGATGG GAA GGCCA		
		ACCCTACC CTT CTGGT		
		__ CC		
GAM2230	LOC144563	5' CCGTCTCCACTCTCATCCCA	77395	_ AAT A
		TGGGATG GA GA ATGG		
		ACCCTAC CT CT TGCC		
		T CAC C		
GAM2230	LOC148887	3' TGGCCGGCCACCATCCCA	85414	AAA AAA
		TGGGATGG TG TGGCCA		

	ACCCTACC AC GCCGGT	
	___ CG_	
GAM2230 LOC149372 3'	TGACCAGTGTCTTCCATCC 80107	AT AA_ C
	GGATGGAA GA TGG CA	
	CCTACCTT CT ACC GT	
	___ GTG A	
GAM2230 LOC150157 5'	CTATTTTCCATTTCCACCCA 86023	A ___
	TGGG TGGAAATG AAATGG	
	ACCC ACCTTTAC TTTATC	
	CT	
GAM2230 LOC150498 3'	TGACCACCCCCTCCTCCCCATC 80723	AAAT AA___ C
CCA	TGGGATGG GA TGG CA	
	ACCCTACC CT ACC GT	
	CCTC CCCCC A	
GAM2230 LOC151632 5'	CTGTCTCCACTCTCATCCCA 86645	_ AAT A
	TGGGATG GA GA ATGG	
	ACCCTAC CT CT TGTC	
	T CAC C	
GAM2230 LOC151871 5'	GCAATCTCCTTCCATCCCA 57978	AT A G
	TGGGATGGAA GA AT GC	
	ACCCTACCTT CT TA CG	
	C_ C A	
GAM2230 LOC152059 3'	TTGGCCATCTAGCATTCCA 81282	GAAAT AA
	TGGGATG GA TGGCCAA	
	ACCTTAC CT ACCGGTT	
	GAT___	
GAM2230 LOC158292 5'	TGGCAGGGTCTTTCCATCCCA 88059	T AATG
	TGGGATGGAAA GA GCCA	
	ACCCTACCTTT CT CGGT	
	C GGGA	
GAM2230 LOC161357 3'	CCACCTTATCCCCATCCCA 83146	AA AA
	TGGGATGG ATGA TGG	
	ACCCTACC TATT ACC	
	CC CC	
GAM2230 LOC164537 5'	GGCCACCAGTCCCCATCCCA 88575	AA GAAA
	TGGGATGG AT TGGCC	
	ACCCTACC TG ACCGG	
	CC ACC_	
GAM2230 LOC165257 3'	TGGTCTCCATCCCCATCCC 83371	AA AAAT
	GGGATGG ATG GGCCA	

	CCCTACC TAC CTGGT		
	CC CT__		
GAM2230 LOC196484 5'	TGTCCCCATCTCATCCCA 63540	AA	AAAT C
	TGGGATGG ATG GG CA		
	ACCCTACT TAC CC GT		
	C_ C__ T		
GAM2230 LOC197049 5'	GGATTTCATTCCCGCCCCA 91261	A A	GG
	TGGG TGG AATGAAAT CC		
	ACCC GCC TTA CTTTA GG		
	C C _		
GAM2230 LOC199729 3'	TTTGGCCATCCCACCTATCCC 73398	AAA	AA
	GGGATGG TG ATGGCCAAA		
	CCCTATC AC TACCGGTTT		
	C__ CC		
GAM2230 LOC200830 3'	TTTGGCTCCTCCCCACCCCA 91733	A	AAAT AAT
	TGGG TGG GA GGCCAAA		
	ACCC ACC CT TCGGTTT		
	C CC__ CC_		
GAM2230 LOC200904 5'	CTGTCTCCACTCTCATCCCA 91780	_	AAT A
	TGGGATG GA GA ATGG		
	ACCCTAC CT CT TGTC		
	T CAC C		
GAM2230 LOC203083 5'	CTGTCTCCACTCTCATCCCA 92088	_	AAT A
	TGGGATG GA GA ATGG		
	ACCCTAC CT CT TGTC		
	T CAC C		
GAM2230 LOC219919 5'	CTGTCTCCACTCTCATCCCA 94926	_	AAT A
	TGGGATG GA GA ATGG		
	ACCCTAC CT CT TGTC		
	T CAC C		
GAM2230 LOC221418 3'	GTCGTTCCAGTTCCACCCCA 95286	A	A A
	TGGG TGGAA TG AATGGC		
	ACCC ACCTT AC TTGCTG		
	C G C		
GAM2230 LOC221795 5'	CCGTCTCCACTCTCATCCCA 94073	_	AAT A
	TGGGATG GA GA ATGG		
	ACCCTAC CT CT TGCC		
	T CAC C		
GAM2230 LOC253980 3'	TTGGCCCTTCTCCACCCCA 96773	A	AAT AT
	TGGG TGGG GAA GGCCAA		

ACCC ACCT CTT CCGGTT
 _ _ _ C_
 GAM2230 LOC254176 5' CTGTCTCCACTCTCATCCCA 99169 _ AAT A
 TGGGATG GA GA ATGG
 ||||| || || ||||
 ACCCTAC CT CT TGTC
 T CAC C
 GAM2230 LOC255223 5' GGATTTCATTCCCGCCCCA 98358 A A GG
 TGGG TGG AATGAAAT CC
 |||| || ||||| ||
 ACCC GCC TTA CTTTA GG
 C C _
 GAM2230 LOC256515 5' CCGTCTCCACTCTCATCCCA 98210 _ AAT A
 TGGGATG GA GA ATGG
 ||||| || || ||||
 ACCCTAC CT CT TGCC
 T CAC C
 GAM2230 LOC256594 5' CTGTCTCCACTCTCATCCCA 98862 _ AAT A
 TGGGATG GA GA ATGG
 ||||| || || ||||
 ACCCTAC CT CT TGTC
 T CAC C
 GAM2230 LOC257000 3' TGTGCCCCATTTCCACCCC 98589 A AAAT _
 GGG TGGAAATG GGC CA
 || ||||| || ||
 CCC ACCTTTAC CCG GT
 C C _ T
 GAM2230 LOC257464 3' GCCCTCTTTCCATGCCA 91244 G T AAT
 TGG ATGGAAA GA GGC
 || ||||| || ||
 ACC TACCTTT CT CCG
 G _ C_
 GAM2230 LOC257490 5' TGTGCTCCCTTCCCCACCCCA 99562 A AAAT AT_ _
 TGGG TGG GAA GGC CA
 |||| || || || ||
 ACCC ACC CTT TCG GT
 C C _ CCC T
 GAM2230 LOC51580 3' TTGGCCATTCTCATACCA 32433 AA _
 TGG ATGA AATGGCCAA
 || |||| |||||
 ACC TACT TTACCGGTT
 A_ C
 GAM2230 LOC91040 5' TTGGCCATCCTGGCCCTCCCA 65357 T AAATGAA
 TGGGA GG ATGGCCAA
 |||| || |||||
 ACCCT CC TACCGGTT
 C GGTCC_
 GAM2231 MMP25 3' TCCTCACTCAGGGTGGGGT 42698 AT AC
 AC CGCCCTGA GAGGA
 || ||||| ||||

			TG GTGGGACT CTCCT		
			GG CA		
GAM2231	DMWD	3'	CCCGGACACGGGCGATGTA 61549	_ AA A	
			TACATCGCCC TG CG GG		
			ATGTAGCGGG AC GC CC		
			C AG _		
GAM2231	HCGIV.9	5'	TCCTCGTTCAGGACGATGTA 39136	C	
			TACATCG CCTGAACGAGGA		
			ATGTAGC GGACTTGCTCCT		
			A		
GAM2231	STX12	5'	TCCGGTAGGAGAGCGGTGTA 66953	___ AACGA	
			TACATCGC CCTG GGA		
			ATGTGGCG GGAT CCT		
			AGA GG___		
GAM2232	BACH2	3'	GCTGTCAAGCAATGGATAAACA 41787	C GGA___	
			GCTCT AGAGTTGTT ATCCA GACAGC		
			TCTCGACAA TAGGT CTGTCG		
			A AACGAA		
GAM2232	DGCR2	3'	GCTGCCTCCTGTCTCTCCACTC 18902	TGTTCATC A	
			T AGAGT CAGGAG CAGC		
			TCTCA GTCCTC GTCG		
			CCTCTCT_ C		
GAM2232	HHIP	5'	CTGTCCCACCTAAACAACCTC 42752	CATCCA A	
			GAGTTGTT GG GACAG		
			CTCAACAA CC CTGTC		
			ATCCA_ _		
GAM2232	HS3ST2	3'	CTGTCTCTGAAAACAACCTT 21277	CATCCA	
			AGAGTTGTT GGAGACAG		
			TTTCAACAA TCTCTGTC		
			AAG___		
GAM2232	MTCP1	5'	CTACATGGATAACAACCTCT 27241	C GG_	
			AGAGTTGTT ATCCA AG		
			TCTCAACAA TAGGT TC		
			_ ACA		
GAM2232	PCOLN3	3'	GCTGCCCTGTTGCCAAACAACCT 12414	___ TC AGA	
			C GAGTTGTT CA CAGG CAGC		
			CTCAACAA GT GTCC GTCG		
			ACC T_ C_		
GAM2232	PFN2	3'	CTGTCTTCATCAACAACCCT 54885	A C CCA	
			AG GTTGTT AT GGAGACAG		

		TC CAACAA TA CTTCTGTC	
		C C ____	
GAM2232 PFN2	3'	CTGTCTTCATCAACAACCCT 54886	A C CCA
		AG GTTGTT AT GGAGACAG	
		TC CAACAA TA CTTCTGTC	
		C C ____	
GAM2232 TIMP3	3'	CTCCTGAGATCCTCACCTCT 6283	T TTC _
		AGAG TG ATC CAGGAG	
		TCTC AC TAG GTCCTC	
		C TCC A	
GAM2232 AKAP11	3'	TTGTAGTCAGTTGAACAACCTCT 58468	TCCA AG
		AGAGTTGTTCA GG ACAG	
		TCTCAACAAGT CT TGTT	
		TGA_ GA	
GAM2232 FLJ10511	3'	GTCCCCTAGAAAAACAACCTCT 36690	CA C A
		AGAGTTGTT TC AGG GAC	
		TCTCAACAA AG TCC CTG	
		AA A C	
GAM2232 FLJ13102	3'	GCTGTCTGCCTGAGCAACTCT 46534	TCCA _
		AGAGTTGTTCA GG AGACAGC	
		TCTCAACGAGT CC TCTGTCG	
		____ G	
GAM2232 HAAO	3'	GCATCCCTGCCAAACAACCTCT 60171	CATC A CA
		AGAGTTGTT CAGG GA GC	
		TCTCAACAA GTCC CT CG	
		ACC_ _ AC	
GAM2232 KIAA0628	3'	CTGTCTCAAAAAACAACCTTT 29528	CATCCAG
		AGAGTTGTT GAGACAG	
		TTTCAACAA CTCTGTC	
		AAAA____	
GAM2232 KIAA0843	3'	CTGAACAACCAGACAGACAACCT 30800	CA CA AGA__
CT		AGAGTTGTT TC GG CAG	
		TCTCAACAG AG CC GTC	
		AC A_ AACAA	
GAM2232 KIAA1497	5'	CTGTCCTTGTATGAGCAAC 68120	C A
		GTTGTTTCAT CAGG GACAG	
		CAACGAGTA GTTC CTGTC	
		T _	
GAM2232 KIAA1710	3'	GCTATCTCCATACATGAACAAT 63178	G CCA_ C
CT		AGA TTGTTTCAT GGAGA AGC	

		TCT AACAAAGTA CCTCT TCG	
		— CATA A	
GAM2232	MBLL39	3' CTGTCTCTGCAGCAACAACTC 59259	CATCCA
		GAGTTGTT GGAGACAG	
		CTCAACAA TCTCTGTC	
		CGACG_	
GAM2232	MGC12972	3' CTGTCTCCTGGCGGACCAC 52053	T AT
		GT GTTC CCAGGAGACAG	
		CA CAGG GGTCTCTGTC	
		C C_	
GAM2232	MGC4308	3' CTGTCCTTTTGACAACTCT 66184	T TCC A
		AGAGTTGT CA AGG GACAG	
		TCTCAACA GT TTC CTGTC	
		— T_ —	
GAM2232	PDE7B	3' GCTGCCGAAATGAGCAACTC 38952	CCA AGA
		GAGTTGTTTCAT GG CAGC	
		CTCAACGAGTA CC GTCG	
		AAG _	
GAM2232	SEC24B	3' GCTGCATTGTTGGATGACAACT 21985	T G A_
	CT	AGAGTTGT CATCCAG AG CAGC	
		TCTCAACA GTAGGTT TT GTCG	
		— G AC	
GAM2232	LOC142948	3' CCGGGAGGAATGAATAACTC 83775	— A
		GAGTTGTTCA TCC GG	
		CTCAATAAGT AGG CC	
		AAGG G	
GAM2232	LOC145225	3' CTGTCTCCAGTTGGGCAGCTC 84266	TCCA
	T	AGAGTTGTTCA GGAGACAG	
		TCTCGACGGGT CCTCTGTC	
		TGAC	
GAM2232	LOC219914	5' CTGGGAGGAACGAACAACTC 94968	A_ AGGAGA
		GAGTTGTTCC TCC CAG	
		CTCAACAAG AGG GTC	
		CA AGG_	
GAM2232	LOC219972	3' GCTGCCCTTGATGAACACTC 93278	T C AGA
		GAGT GTTCATC AGG CAGC	
		CTCA CAAGTAG TCC GTCG	
		— T CC_	
GAM2233	NCAM2	3' AATACTTCAAATCATATCCTCA 16999	C_ TCG
		TGAGGATATG TTGG GGTATT	

ACTCCTATAC AACT TCATAA
 TA ____
 GAM2233 MPZL1 3' AATACCTAGAACATATCCTCA 15536 C GGTC
 TGAGGATATG TT GGGTATT
 ||||| || |||||
 ACTCCTATAC AG TCCATAA
 A A____
 GAM2234 ATP6V1E1 3' TGGTGGAAGCTTCATGTA 9892 ____
 TACATGAAGCT CACCA
 ||||| |||||
 ATGTACTTCGA GTGGT
 AAG
 GAM2234 EGFL4 3' CAGGGCCTTGTGGGCCCA 62457 AA C
 TG GCTCAC AAGGCCCTG
 || ||||| |||||
 AC CGGGTG TTCCGGGAC
 CC _
 GAM2234 KLHL3 3' CAGGACCTTGGTGACTGGATTC 88844 GC____ C
 A
 TGAA TCACCAAGG CCTG
 ||| ||||| |||||
 ACTT AGTGGTTCC GGAC
 AGGTC A
 GAM2234 MAP1B 3' CAGGGCCTTGACAAGTACATCA 20960 A__ CAC
 TGA GCT CAAGGCCCTG
 ||| || |||||
 ACT TGA GTTCCGGGAC
 ACA ACA
 GAM2234 RAF1 3' AGGGCCTTAACTTCATGT 81370 CTCACC
 ACATGAAG AAGGCCCT
 ||||| |||||
 TGTACTTC TTCCGGGA
 AA____
 GAM2234 SLC3A1 3' TTTGTAATAGCTTCATGTA 62924 CAC_
 TACATGAAGCT CAAG
 ||||| |||||
 ATGTACTTCGA GTTT
 TAAT
 GAM2234 SP3 3' CAGGGCCTTAAAAGCCATCATG 83382 A_ CACC
 TA
 TACATGA GCT AAGGCCCTG
 ||||| ||| |||||
 ATGTACT CGA TTCCGGGAC
 AC AAA_
 GAM2234 C20orf139 5' GGCCTTGGACTCACTGTA 85920 _ A CTCA
 TACA TGA G CCAAGGCC
 ||| ||| | |||||
 ATGT ACT C GGTTCCGG
 C _A____
 GAM2234 DKFZP564L0864 3' CAGGACCCTAGAGGAGAGCTTT 72949 A A__ C_
 AT
 ATGAAGCTC CC AGG CCTG
 ||||| || ||| |||||

TATTTTCGAG GG TCC GGAC
 A AGA CA
 GAM2234 DKFZP762D096 3' CAGGGCCTTGAGCAGCCCATG 66178 AA CA_
 CATG GCT CCAAGGCCCTG
 |||| ||| |||||
 GTAC CGA GGTTCGGGAC
 C_ CGA
 GAM2234 FLJ10432 3' CAGGGCCTGGTCTGAGCCCCA 39348 AA _ A
 TG GCTC ACCA GGCCCTG
 || |||| ||| |||||
 AC CGAG TGGT CCGGGAC
 CC TC _
 GAM2234 FLJ13188 3' GCCAGTGAGCTTCTCGTA 42192 AT CAA
 TAC GAAGCTCAC GGC
 ||| ||||| |||
 ATG CTTTCGAGTG CCG
 CT A_
 GAM2234 KIAA1804 3' CAGAAATTGTAATGAGCTTCA 70346 C_ GGCC
 TGAAGCTCA CAA CTG
 ||||| ||| |||
 ACTTCGAGT GTT GAC
 AAT AAA_
 GAM2234 KIAA1821 3' AGGAGTGAGCTTCGTGTA 72259 CAAGGC
 TACATGAAGCTCAC CCT
 ||||| ||| |||
 ATGTGCTTCGAGTG GGA
 A____
 GAM2234 KIAA1866 3' AGGGCCTCAGTCCTATGTA 61586 AA CACCA
 TACATG GCT AGGCCCT
 |||| ||| |||||
 ATGTAT TGA TCCGGGA
 CC C____
 GAM2234 LGI2 3' CAGAACCTTGGTGATTTTGT 36924 TG C CC
 A AAG TCACCAAGG CTG
 | ||| ||||| |||
 T TTT AGTGGTTCC GAC
 GT _ AA
 GAM2234 RASSF2 3' CAGGGCCTTAGATTGGCCCCAGT 29091 A AA C C
 A TAC TG GCT AC AAGGCCCTG
 ||| || ||| ||| |||||
 ATG AC CGG TG TTCCGGGAC
 _ CC T A
 GAM2234 RNF34 3' CAGGGCCTTAGACTCCACATG 47816 A_ C ACC
 CATG AG TC AAGGCCCTG
 |||| ||| |||||
 GTAC TC AG TTCCGGGAC
 ACC _ A_
 GAM2234 SDF1 3' CAGGACCAAAGCTTTTCATGTA 92514 _ CACCAA C
 TACATGAA GCT GG CCTG
 ||||| ||| || ||||

ATGTACTT CGA CC GGAC
 T AA___ A
 GAM2234 LOC126133 3' CAGGGCCTTAGGACTCTCAT 74908 _ C ACC
 ATGA AG TC AAGGCCCTG
 ||| ||| |||||
 TACT TC AG TTCCGGGAC
 C _ GA_
 GAM2234 LOC144278 3' CAGGGCCTCGGGCTCCCAGTA 77272 A A_ ACCA
 TAC TG AGCTC AGGCCCTG
 ||| ||| |||||
 ATG AC TCGGG TCCGGGAC
 _ CC C___
 GAM2234 LOC149271 3' GGCATGGTGGTGAGCCCCTGTA 80008 TGAA AG_
 TACA GCTCACCA GCC
 ||| ||||| |||
 ATGT CGAGTGGT CGG
 CCC_ GGTA
 GAM2234 LOC150111 5' CAGGGCCTCGCTGGCCCATGT 85997 AA T CCA
 ACATG GC CA AGGCCCTG
 |||| ||| |||||
 TGTAC CG GT TCCGGGAC
 C_ _ CGC
 GAM2234 LOC153205 3' CAGAACCTTGGTGAAATCTCA 87153 AGC_ CC
 TGA TCACCAAGG CTG
 ||| ||||| |||
 ACT AGTGGTTCC GAC
 CTAA AA
 GAM2234 LOC222697 5' CAGGAGTGTAGGCTTCATG 96019 TC CAAG _
 CATGAAGC AC GC CCTG
 ||||| || |||||
 GTACTTCG TG TG GGAC
 GA ___ A
 GAM2234 LOC257471 3' CAGGGCCTTAAAGCCATCATG 97388 A_ CACC
 TA TACATGA GCT AAGGCCCTG
 ||||| ||| |||||
 ATGTACT CGA TTCCGGGAC
 AC AAA_
 GAM2234 LOC257612 5' CAGTGGAGGATGAGCTTCAT 99737 _ AAGG _
 ATGAAGCTCA CC CC CTG
 ||||| || |||||
 TACTTCGAGT GG GG GAC
 A A___ T
 GAM2234 LOC90381 3' CAGGGCCTCGATGGCCTCAT 63210 A T CCA
 ATGA GC CA AGGCCCTG
 ||| ||| |||||
 TACT CG GT TCCGGGAC
 C _ AGC
 GAM2234 LOC91445 3' CAGGGCCTTGGGGAGCCCCA 61164 AA A
 TG GCTC CCAAGGCCCTG
 || ||| |||||

AC CGAG GGTTCGCGGAC
 CC G
 GAM2235 ARHC 5' GACTCGCTCACCCGCTT 18971 A G T
 AAGC GGTG AGT GGTT
 |||| |||| || ||||
 TTCG CCAC TCG TCAG
 C _ C
 GAM2235 CBFA2T3 3' GCCAACCCACCCAGCTCC 19017 A A_ A
 A AGC GGTGG GTTGGT
 | ||| |||| ||||
 C TCG CCACC CAACCG
 C AC C
 GAM2235 CD14 3' ATTCAACCCTTTGCCCCACCT 67141 A T____
 AGGTGG GT GGTTGAAT
 ||||| || |||||
 TCCACC CG CCAACTTA
 C TTTC
 GAM2235 CX3CR1 3' TCATGCATCTCCACCTGCTCC 71179 A T GT
 A AGCAGGTGGAG TG TGA
 | ||||| || |||
 C TCGTCCACCTC AC ACT
 C T GT
 GAM2235 DAG1 3' TCAGGGGCGCCCACTCTGCTT 16556 _ A_ GG
 AAGCAG GTGG GTT TTGA
 ||||| ||| ||| ||||
 TTCGTC CACC CGG GACT
 T CG G_
 GAM2235 DPYSL3 3' CAACCATTCTTCCACCTGCTT 9120 T____
 AAGCAGGTGGAG TGGTTG
 ||||| |||||
 TTCGTCCACCTT ACCAAC
 CTTT
 GAM2235 EXTL3 3' ATTCACCTTCCCCCGC 9331 A T TT T
 GC GG GGAG GGT GAAT
 || || ||| ||| ||||
 CG CC CCTT CCA CTTA
 C C _ _
 GAM2235 GPR62 3' AACTCCTCCACCTGCTT 91083 TT
 AAGCAGGTGGAG GGTT
 ||||| |||||
 TTCGTCCACCTC TCAA
 C_
 GAM2235 MSN 3' AACCCAGGAGCATCCACCTCCT 60878 C _ ____
 T AAG AGGTGGA GTT GGTT
 ||| ||||| ||| ||||
 TTC TCCACCT CGA CCAA
 C A GGAC
 GAM2235 SLC8A2 3' GACTCGGCTGCACCTGCT 66935 G _
 AGCAGGTG AGTTG GTT
 ||||| ||||| |||

			TCGTCCAC TCGGC CAG		
			G T		
GAM2235	VMD2	5'	GACCCAAGCCCACCTGCT 16081	A	__
			AGCAGGTGG GTT GGTT		
			TCGTCCACC CGA CCAG		
			_ AC		
GAM2235	BAG5	3'	TCATAACTACACCTGCTCC 18044	A	G GT
			A AGCAGGTG AGTTG TGA		
			C TCGTCCAC TCAAT ACT		
			C A __		
GAM2235	CYP4F12	3'	GACCCATCCACCTGTTTT 62187		GTT
			AAAGCAGGTGGA GGTT		
			TTTTGTCCACCT CCAG		
			AC_		
GAM2235	DIS3	3'	GATCCAGTTACCTCCACCTG 30919	T GG	A
			CAGGTGGAG T TTG ATC		
			GTCCACCTC A GAC TAG		
			C TT C		
GAM2235	ELKS	3'	GACTCACTCCACCAGCTT 31191	A	T
			AAGC GGTGGAGT GGTT		
			TTCG CCACCTCA TCAG		
			A C		
GAM2235	FLJ10297	3'	TCAAGTGATCCTCCTGC 36446	T G	G
			GCAGG GGA TTG TTGA		
			CGTCC CCT AGT AACT		
			T _ G		
GAM2235	FLJ12650	3'	TCAGTCACTCCACCCCCTT 44824	CA	T GT
			AAG GGTGGAGT G TGA		
			TTC CCACCTCA C ACT		
			CC _ TG		
GAM2235	FLJ14442	3'	GACCTCGTGATCCACCTGCTT 52383		GTT__
			AAGCAGGTGGA GGTT		
			TTCGTCCACCT CCAG		
			AGTGCT		
GAM2235	FLJ14950	3'	CAGGTAATCCACCTGCTT 52783	G	G
			AAGCAGGTGGA TTG TTG		
			TTCGTCCACCT AAT GAC		
			_ G		
GAM2235	FLJ20371	3'	AACCCCTCTCCTCACCTGCTTT 35533	_	TT_
			AAAGCAGGT GGAG GGTT		

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TTTCGTCCA CCTC CCAA
CT TCC
GAM2235 INADL 5' GACCCGGGCTCCCACCTGCTCC 20535 A _ _
A AGCAGGTGG AGTT GGTT
| ||||| ||| |||
C TCGTCCACC TCGG CCAG
C C GC
GAM2235 KIAA0337 3' TCGCCCGCCACCTGC 29483 A T T
GCAGGTGG GT GGT GA
||||| || ||| ||
CGTCCACC CG CCG CT
_ C _
GAM2235 KIAA0953 3' AACCCCCTGTGCTCCACCTCTT 67316 C T____
AAG AGGTGGAGT GGTT
||| ||||| |||
TTC TCCACCTCG CCAA
_ TGTCC
GAM2235 KIAA1069 3' TCGCCACTCCACCGGCTCC 68533 A A T T
A AGC GGTGGAGT GGT GA
| || ||||| ||| ||
C TCG CCACCTCA CCG CT
C G _ _
GAM2235 KIAA1198 3' TCAGGTAATCCACCTGC 64066 G G
GCAGGTGGA TTG TTGA
||||| ||| |||
CGTCCACCT AAT GACT
_ G
GAM2235 KIAA1199 3' GACCCTGGTGCTGCCACCTGC 72930 _ T____
GCAGGTGG AGT GGTT
||||| ||| |||
CGTCCACC TCG CCAG
G TGGTC
GAM2235 KIAA1266 3' AACCCCTCCACCTCCTCC 66688 A C TT
A AG AGGTGGAG GGTT
| || ||||| |||
C TC TCCACCTC CCAA
C C C_
GAM2235 KIAA1321 3' GATTCAACATTTTCCCCCACT 62901 A CA T TTG
CC A AG GG GGAG GTTGAATC
| || || ||| |||||
C TC CC CCTT CAACTTAG
C AC C TTA
GAM2235 KIAA1508 3' TCAGGTAATCCACCTGCTT 62562 G G
AAGCAGGTGGA TTG TTGA
||||||| ||| |||
TTCGTCCACCT AAT GACT
_ G
GAM2235 MGC3248 3' TCAACCAGGCCTCTTT 51651 C GGAG
AAAG AGGT TTGGTTGA
||| ||| |||||

```

TTTC TCCG GACCAACT

GAM2235 MOV10 3' AGCCATTCCACCCCTCC 40932 A CA T
A AG GGTGGAGT GGTT
| | ||||| |||
C TC CCACCTTA CCGA
C CC _

GAM2235 NFKBIE 3' TCAGGGCTCCACCTCTCC 17056 A C GG
A AG AGGTGGAGTT TTGA
| | ||||| |||
C TC TCCACCTCGG GACT
C _ _

GAM2235 PIB5PA 3' TTTTGCAAGCCCACCTGC 66653 A G T
GCAGGTGG GTT GT GAA
||||| ||| |||
CGTCCACC CGA CG TTT
_ A T

GAM2235 PRO1914 5' TTTAACCACCACCTACTT 26890 C AGT
AAG AGGTGG TGGTTGAA
||| ||||| |||||
TTC TCCACC ACCAATTT
A _

GAM2235 RES4-25 3' TCAGGTAATCCACCTGC 65275 G G
GCAGGTGGA TTG TTGA
||||| ||| |||
CGTCCACCT AAT GACT
_ G

GAM2235 LOC119188 5' ACCAACTCCACTGCTTT 74401 G
AAAGCAG TGGAGTTGGT
||||| |||||
TTTCGTC ACCTCAACCA

GAM2235 LOC127534 3' GACCATGTGATTCCACCTGCTT 75969
T AAAGCAGGTGGAGT TGGTT
||||||| |||||
TTTCGTCCACCTTA ACCAG
CTGT

GAM2235 LOC131308 3' TCAAGTGATCCACCAGC 75497 A G G
GC GGTGGA TTG TTGA
|| ||||| ||| |||
CG CCACCT AGT AACT
A _ G

GAM2235 LOC144558 5' TCACCCTCCCCCGCTTT 84078 A T TT T
AAAGC GG GGAG GGT GA
||||| ||| ||| |||
TTTCG CC CCTC CCA CT
C C _ _

GAM2235 LOC146059 3' TCAACCAACTGAAACCTGACTT 78089 _ GG_
T AAAG CAGGT AGTTGGTTGA
||||| |||||

		TTTC GTCCA TCAACCAACT		
		A AAG		
GAM2235	LOC148029 3'	TCTTTGCTCCCCTGCTTT	79320	T TGGTT
		AAAGCAGG GGAGT GA		
		TTTCGTCC CCTCG CT		
		_ TTT_		
GAM2235	LOC148413 3'	ATTCAAGCCAGCTGCCT	79577	GG _
		AGGT AGTTGGTT GAAT		
		TCCG TCGACCGA CTTA		
		_ A		
GAM2235	LOC150142 5'	ATTCAACCCAGAACACCACCT	80401	A _
		AGGTGG GTT GGTTGAAT		
		TCCACC CAA CCAACTTA		
		A GAC		
GAM2235	LOC152225 3'	TCAACCAACCAGGGCTTGT	86773	GGA_
		GCAGGT GTTGGTTGA		
		TGTTCG CAACCAACT		
		GGAC		
GAM2235	LOC152940 3'	TCAGCATAACTCAACCTGCTTT	81636	G _
		AAAGCAGGT GAGTTG GTTGA		
		TTTCGTCCA CTCAAT CGACT		
		A A		
GAM2235	LOC157793 5'	GACTCACTGCCCACCGGCTCC	82510	A A _ T
		A AGC GGTGG AGT GGTT		
		C TCG CCACC TCA TCAG		
		C G CG C		
GAM2235	LOC221218 3'	ACCAACCCCACTCACTTT	93415	CA A
		AAAG GGTGG GTTGGT		
		TTTC TCACC CAACCA		
		AC C		
GAM2235	LOC221756 3'	AATCCCTCCAGCTGCTTT	93755	G TT
		AAAGCAG TGGAG GGTT		
		TTTCGTC ACCTC CTAA		
		G C_		
GAM2235	LOC221931 5'	CAACCAAGTCCTCCCCTGCTTT	95629	T _
		AAAGCAGG GGAG TTGGTTG		
		TTTCGTCC CCTC AACCAAC		
		_ CTG		
GAM2235	LOC257364 3'	GATTCCATGCCACCTGC	96645	A TGGTT
		GCAGGTGG GT GAATC		

		CGTCCACC CG CTTAG	
		_ TAC_	
GAM2235	LOC51754	5' GATTACTCCACCTGCTCA 71581	A T
		A AGCAGGTGGAGT GGTT	
		A TCGTCCACCTCA TTAG	
		C _	
GAM2236	TERF1	3' CCCAAATCCTGTTCCAATGA 34391	C TA C
		TCATTGGA ACG GATT GGG	
		AGTAACCT TGT CTAA CCC	
		_ C_ A	
GAM2236	FLJ10159	3' CCATGTCACGCCATCCAATGAC 36334	CA_ A TC
		GTCATTGGA CGT GAT GG	
		CAGTAACCT GCA CTG CC	
		ACC _ TA	
GAM2236	FLJ14213	3' CCGATGCTCCCAATGACG 46216	ACAC GAT
		CGTCATTGG GTA TCGG	
		GCAGTAACC CGT AGCC	
		CT_ _	
GAM2236	MGC10715	3' ATTTACCAGACATCCAATGAC 44495	CAC_
		GTCATTGGA GTAGAT	
		CAGTAACCT CATTTA	
		ACAGAC	
GAM2236	MOST2	5' CCAGGACTGCCCAATGAC 40059	ACAC A _
		GTCATTGG GTAG TTC GG	
		CAGTAACC CGTC AGG CC	
		_ _ A	
GAM2236	LOC150370	3' CCGGGTCTACGTGCCCATGAC 86123	T A
		GTCAT GG CACGTAGATTTCGG	
		CAGTA CC GTGCATCTGGGCC	
		C _	
GAM2236	LOC152620	3' CCCAAATCCTGTTCCAATGA 60707	C TA C
		TCATTGGA ACG GATT GGG	
		AGTAACCT TGT CTAA CCC	
		_ C_ A	
GAM2236	LOC158668	3' CCCAAATCCTGTTCCAATGA 69896	C TA C
		TCATTGGA ACG GATT GGG	
		AGTAACCT TGT CTAA CCC	
		_ C_ A	
GAM2237	NME2	3' CTCTTCATTCCATTGACTTAGA 11813	AGTCTCCTA
		TCTAAGTCAG AAGAG	

			AGATTCAGTT	TTCTC		
			ACCTTAC__			
GAM2237	PPL	3'	CTCTCCAGATTTCTGGCTTA	12222	_	CCTAA
			TAAGTCAGAG TCT	AGAG		
			ATTCGGTCTT AGA	TCTC		
			T CC__			
GAM2237	RAB26	3'	CTCTAGGAGGCTCTGGCT	27602		A
			AGTCAGAGTCTCCTA AG			
			TCGGTCTCGGAGGAT TC			
			C			
GAM2237	SCN8A	3'	CTGTGGAGACTCTAACCTGA	27214	TAA C	TAA
			TC GT AGAGTCTCC AG			
			AG CA TCTCAGAGG TC			
			TC_ A TG_			
GAM2237	CX46.6	3'	AGGCAGACTCTGCCCAGA	40307	AA T	_
			TCT G CAGAGTCT CCT			
			AGA C GTCTCAGA GGA			
			CC_ C			
GAM2237	HGC6.1.1	3'	AGGAAACTCTGACACAGA	27607	AA	C
			TCT GTCAGAGT TCCT			
			AGA CAGTCTCA AGGA			
			CA A			
GAM2237	KIAA0907	3'	CTAGAGTGAGACTCTGTCT	30873	T	_ AA
			AG CAGAGTCTC CT AG			
			TC GTCTCAGAG GA TC			
			T T GA			
GAM2237	KIAA1077	3'	CTCTTCACTCTCCTCTGATTAG	73288	G	TCTCCTA
	A		TCTAA TCAGAG AAGAG			
			AGATT AGTCTC TTCTC			
			_ CTCTCAC			
GAM2237	KIAA1456	5'	CTGAGGGGAGACTCTGTCT	67553	T	AA
			AG CAGAGTCTCCT AG			
			TC GTCTCAGAGGG TC			
			T AG			
GAM2237	KIAA1656	3'	CTCTGTTACTCTGACTCAG	66366	A	CTCCTAA
			CT AGTCAGAGT AGAG			
			GA TCAGTCTCA TCTC			
			C TTG__			
GAM2237	KIAA1970	3'	CTCTATGGGAGACCCTAAGCCA	74780	AAGTC A	A
	GA		TCT AG GTCTCCTA AGAG			

AGA TC CAGAGGGT TCTC
 CCGAA C A
 GAM2237 LCHN 3' CTCTTTAGGAGGCAGACTTG 87468 AGA
 TAAGTC GTCTCCTAAAGAG
 ||||| |||||
 GTTCAG CGGAGGATTCTC
 A__
 GAM2237 MGC11287 3' CTCTTCAGGAGACTGAGAC 49615 AG A
 GTC AGTCTCCT AAGAG
 ||| ||||| |||||
 CAG TCAGAGGA TTCTC
 AG C
 GAM2237 MGC2656 5' TGGGAGACCCTGACCCTGA 44722 TAA A
 TC GTCAG GTCTCCTA
 || ||||| |||||
 AG CAGTC CAGAGGGT
 TCC C
 GAM2237 MGC3047 3' CTCCCCAGGGACCTGCTGACTT 51348 _ TC AAA
 G TAAGTCAG AG TCCT GAG
 ||||| || ||| |||
 GTTCAGTC TC GGGA CTC
 G CA CCC
 GAM2237 MGC3771 5' CTCCTTAGAGCCGTGACTTAGG 49054 GA T C A
 TCTAAGTCA G CTC TAA GAG
 ||||| | ||| |||
 GGATTCAGT C GAG ATT CTC
 GC _ _ C
 GAM2237 TP53INP1 3' CTCTTTAGAACAAGAGTTAGA 53867 G AGA CTC
 TCTAA TC GT CTAAAGAG
 ||||| || |||||
 AGATT AG CA GATTCTC
 G AA_ A__
 GAM2237 VAMP3 3' CTCTTCAAGACTTTTGACTTAG 17710 _ CCTA
 A TCTAAGTCAGA GTCT AAGAG
 ||||| ||||| |||||
 AGATTCAGTTT CAGA TTCTC
 T AC__
 GAM2237 LOC144079 5' CTCTTTAGGAAGTCACTTA 77179 CA GTC
 TAAGT GA TCCTAAAGAG
 ||||| || |||||
 ATTCA CT AGGATTCTC
 _ GA_
 GAM2237 LOC144584 5' CTGTAGAAGACCCTGATCCAGA 67587 AA A C A
 TCT GTCAG GTCT CTA AG
 ||| ||||| ||||| ||| ||
 AGA TAGTC CAGA GAT TC
 CC C A G
 GAM2237 LOC146485 3' CTGTAGAAGACCCTGATCCAGA 60492 AA A C A
 TCT GTCAG GTCT CTA AG
 ||| ||||| ||||| ||| ||

			AGA TAGTC CAGA GAT TC		
			CC C A G		
GAM2237	LOC91035	5'	CTAAAGAGCTCAGCCCTGACTT 65298	A T_____	CTAAA
			AGA TCTAAGTCAG G CTC G		
			AGATTCAGTC C GAG C		
			C GACTC___ AAATC		
GAM2238	AKAP13	3'	TCTTTAATCAAAGGATGTCTTC 91256	CCAGCGA	
			T GGAAGACATCC AAAGA		
			TCTTCTGTAGG TTTCT		
			AAACTAA		
GAM2238	ATP10C	3'	TTTCCAGAGGATGTCTTTCT 44671	CCAGC	
			AGGAAGACATCC GAAA		
			TCTTTCTGTAGG CTTT		
			AGAC_		
GAM2238	CARD15	3'	CTTCAAAGCAAATGTCTTCCT 42468	CCCCA GAA_	
			AGGAAGACAT GC AAG		
			TCCTTCTGTA CG TTC		
			AA___ AAAC		
GAM2238	CHAC	3'	CTTTTAAAATGTTTTCCT 31495	CCCCAGCG	
			AGGAAGACAT AAAAG		
			TCCTTTTGTA TTTTC		
			AAA_____		
GAM2238	CHST6	3'	TCTGGGCTGGAAGTGTCTTCC 41504	TCC GAAA	
			GGAAGACA CCAGC AGA		
			CCTTCTGT GGTCG TCT		
			CAA GG_		
GAM2238	CRYAA	3'	TTCTCTCAGACCGTCTTCCT 6368	A_ CCC C	
			AGGAAGAC TC AG GAA		
			TCCTTCTG AG TC CTT		
			CC AC_ T		
GAM2238	DDB1	5'	TCTTTTCGCTTGTGTCCCT 10400	AA CCCC	
			AGG GACAT AGCGAAAAGA		
			TCC CTGTG TCGCTTTTCT		
			_ T_		
GAM2238	DISC1	3'	TCTTGGAATGTCTTCC 38519	C C	
			GGAAGACAT CCCAG GA		
			CCTTCTGTA GGGTT CT		
			A _		
GAM2238	DYRK1A	3'	TCTTCTGCACAAAGATGTCTTC 9166	CCCA_ AA	
			T GGAAGACATC GCG AAGA		

			TCTTCTGTAG CGT TTCT	
			AAACA C_	
GAM2238	DYRK1A	3'	TCTTCTGCACAAAGATGTCTTC 56082	CCCA_ AA
	T		GGAAGACATC GCG AAGA	
			TCTTCTGTAG CGT TTCT	
			AAACA C_	
GAM2238	DYRK1A	3'	TCTTCTGCACAAAGATGTCTTC 56119	CCCA_ AA
	T		GGAAGACATC GCG AAGA	
			TCTTCTGTAG CGT TTCT	
			AAACA C_	
GAM2238	EHF	3'	TCTGATGCCAGGGCTGTCTTCC 25128	T CA AAA
	T		AGGAAGACA CCC GCG AGA	
			TCCTTCTGT GGG CGT TCT	
			C AC AG_	
GAM2238	EIF4EBP2	3'	CTGGGAGGAATGTCTTCT 15857	__
			GGAAGACAT C CCCAG	
			TCTTCTGTA G GGGTC	
			AG A	
GAM2238	FUT6	3'	TGCTGGGGATGTCTCCT 5645 A	
			AGGA GACATCCCCAGCG	
			TCCT CTGTAGGGGTCGT	
			—	
GAM2238	GALNT2	3'	TTCGCAAGTGTCTTCCT 16823	CCCCA
			AGGAAGACAT GCGAA	
			TCCTTCTGTG CGCTT	
			AA__	
GAM2238	GTF2E2	3'	TCGGGGTCTGAAGACTGTCTTC 10887	_ CC ____
	CT		AGGAAGACA TC CAG CGA	
			TCCTTCTGT AG GTC GCT	
			C AA TGGG	
GAM2238	IL2RG	3'	CTTTTCGCAGGATTCTTCCT 5779	C CCA
			AGGAAGA ATCC GCGAAAAG	
			TCCTTCT TAGG CGCTTTTC	
			_ A_	
GAM2238	KCNK4	3'	TCGAGGCCGAAAAGTCTTCCT 33989	A_ C_ AG
			AGGAAGAC TC CC CGA	
			TCCTTCTG AG GG GCT	
			AAA CC A_	
GAM2238	NEBL	3'	TCTTGGGGATATCTGCCT 22142	A C C
			AGG AGA ATCCCCAG GA	

			TCC TCT TAGGGGTT CT		
			G A _		
GAM2238	NORE1	3'	CTTTTAAATGTCTTTCT	49525	CCCCAGC
			AGGAAGACAT	GAAAAG	
			TCTTTCTGTA	TTTTTC	
			AA_____		
GAM2238	PDE4D	3'	CTTTTATAGATGTTTTCT	73964	CCCAGC
			AGGAAGACATC	GAAAAG	
			TCCTTTGTAG	TTTTTC	
			AT_____		
GAM2238	RELA	3'	TTTGTGGATGTCTTCCT	42027	CCA
			AGGAAGACATCC	GCGAA	
			TCCTTCTGTAGG	TGTTT	

GAM2238	RPL24	5'	TCTTTTCGCCATCTTTTGTCTT	8269	TCCCCA_
	TC		GGAAGACA	GCGAAAAGA	
			CTTTCTGT	CGCTTTTCT	
			TTTCTAC		
GAM2238	SRGAP2	3'	CTGGGGGCAGAGCTGTCTTCC	75110	_____
			GGAAGACA	TCCCCAG	
			CCTTCTGT	GGGGGTC	
			CGAGAC		
GAM2238	STAU2	3'	CTCTTCGCTCTGTCTTCC	27672	TCCCC A
			GGAAGACA	AGCGAA AG	
			CCTTCTGT	TCGCTT TC	
			C_____ C		
GAM2238	SUOX	5'	TTCTCTGTGTCTTCCT	6604	TCCC C
			AGGAAGACA	CAG GAA	
			TCCTTCTGT	GTC CTT	
			_____ T		
GAM2238	TRIM8	3'	CGCTGGGGAATCTTCCT	48852	CA
			AGGAAGA	TCCCCAGCG	
			TCCTTCT	AGGGGTCGC	
			A_		
GAM2238	ARPP-21	3'	TTGTTGGAGATGTCTTACC	33297	_ C
			GG AAGACATC	CCAGCGA	
			CC TTCTGTAG	GGTTGTT	
			A A		
GAM2238	CECR7	5'	TTTCTCCAGAGATGTCTTCCT	80452	CCCAGC
			AGGAAGACATC	GAAA	

TCCTTCTGTAG CTTT
 AGACCT
 GAM2238 DKFZP434K1772 3' TCAGCAGGGATGTCCTCC 68340 A CA _
 GGA GACATCCC GC GA
 ||| ||||| ||
 CCT CTGTAGGG CG CT
 C A_ A
 GAM2238 DKFZP434L0718 3' CTTTTTGTGAGAACCTCCCT 50457 A ACA CC
 AGG AG TC CAGCGAAAAG
 ||| || || |||||
 TCC TC AG GTTGTTTTTC
 C CA_ A_
 GAM2238 DNAJA4 3' TTTCGGAGTGTCTTCCT 38364 TC CAGC
 AGGAAGACA CC GAAA
 ||||| || |||
 TCCTTCTGT GG CTTT
 GA ____
 GAM2238 FLJ10761 3' TTCCAGGGATGTCTCTCC 37134 _ CAGC
 GGA AGACATCCC GAA
 ||| ||||| |||
 CCT TCTGTAGGG CTT
 C AC_
 GAM2238 FLJ12221 3' TTTCGCCTCCTGTCTTTCT 63227 TCCCCA
 AGGAAGACA GCGAAA
 ||||| |||||
 TCTTTCTGT CGCTTT
 CCTC_
 GAM2238 FLJ22415 5' CTTTCGCGCTCGCGTTTTTCCT 93119 ATCCCCA A
 AGGAAGAC GCG AAAG
 ||||| || |||||
 TCCTTTTG CGC TTTC
 CGCTC_ C
 GAM2238 FLJ22477 3' TCCTGGGAAATGTTTTCT 45678 C_ C
 AGGAAGACAT CCCAG GA
 ||||| ||||| ||
 TCCTTTTGTA GGGTC CT
 AA _
 GAM2238 GAL3ST-4 3' CTCTTCGCTGGGCTCCC 45278 A ACATC A
 GG AG CCCAGCGAA AG
 || || ||||| ||
 CC TC GGGTCGCTT TC
 C _ C
 GAM2238 HERC3 3' CTTTTCGTACCCTGTGTCTCC 28235 A CCCCCA
 GGA GACAT GCGAAAAG
 || |||| |||||
 CCT CTGTG TGCTTTTC
 C TCCCCA
 GAM2238 HTEX4 5' TCTTTTCGCTGGGAGAGGCTCC 93726 A ACA _
 C GG AG TC CCCAGCGAAAAGA
 || || || ||||| |||||

		CC TC AG GGGTCGCTTTTCT	
		C GG_ A	
GAM2238 HTEX4	5'	TCTTTTCGCTGGGAGAGGCTCC 99567	A ACA _
	C	GG AG TC CCCAGCGAAAAGA	
		CC TC AG GGGTCGCTTTTCT	
		C GG_ A	
GAM2238 HTEX4	5'	TCTTTTCGCTGGGAGAGGCTCC 99722	A ACA _
	C	GG AG TC CCCAGCGAAAAGA	
		CC TC AG GGGTCGCTTTTCT	
		C GG_ A	
GAM2238 KIAA0193	3'	TCCTGAAGAAGCTGTCTTCC 29318	___ CC C
		GGAAGACA TC CAG GA	
		CCTTCTGT AG GTC CT	
		CGA AA _	
GAM2238 KIAA0418	3'	TTCGCTGGGAGTGGATTTC 28302	GA TC
		GGAA CA CCCAGCGAA	
		CTTT GT GGGTCGCTT	
		AG GA	
GAM2238 KIAA0459	3'	TCTGAATGAAGATGTTTTCCT 61663	CC GCGAAA
		AGGAAGACATC CA AGA	
		TCCTTTTGTAG GT TCT	
		AA AAG___	
GAM2238 KIAA0546	3'	TCTTTTCACTATAGGTTTTCT 71839	ATCCCC C
		AGGAAGAC AG GAAAAGA	
		TCCTTTTG TC CTTTCT	
		GATA__ A	
GAM2238 KIAA1028	3'	TCTATGATGATGTCTTCCT 93593	CC GC
		AGGAAGACATC CA GA	
		TCCTTCTGTAG GT CT	
		TA AT	
GAM2238 KIAA1045	3'	TCCCTATGGGATGTCACCCT 71611	AA C_ C
		AGG GACATCCC AG GA	
		TCC CTGTAGGG TC CT	
		CA TA C	
GAM2238 MAPK8IP3	3'	CTTCTCATGATGTCTTTC 54139	CCCAGC A
		GGAAGACATC GA AAG	
		CTTTCTGTAG CT TTC	
		TA___ C	
GAM2238 MGC2647	3'	TCTGGGGTCAGGGATGTCCCC 74080	AA CA GAAA
		GG GACATCCC GC AGA	

		CC CTGTAGGG TG TCT	
		C_ AC GGG_	
GAM2238	MGC3035	5' TCTTCTGGTTGCTGTCTTCCT 44406	TCC_ C_
		AGGAAGACA CCAG GA	
		TCCTTCTGT GGTC CT	
		CGTT TT	
GAM2238	NYD-SP11	5' CTGACGGTGATGTCTTCC 50055	_ _
		GGAAGACATC CC CAG	
		CCTTCTGTAG GG GTC	
		T CA	
GAM2238	OS4	3' TCTTTTCCTGTTGTGTCTTCC 20397	CCC C
		GGAAGACAT CAG GAAAAGA	
		CCTTCTGTG GTC CTTTCT	
		TT_ _	
GAM2238	PDZD2	3' TTTTGCCAAAAATGTTTTCCT 81740	CCCCA
		AGGAAGACAT GCGAAA	
		TCCTTTTGTA CGTTTT	
		AAAAC	
GAM2238	REM	3' TCTTTTGTAAAAAATCTTCC 26689	CATCCCCA
	T	AGGAAGA GCGAAAAGA	
		TCCTTCT TGTTTTCT	
		AAAAAA_	
GAM2238	RNF9	3' CTAGGGAAATTGTCTTCCT 54506	_ C
		AGGAAGACA TCCC AG	
		TCCTTCTGT AGGG TC	
		TAA A	
GAM2238	RoXaN	3' CTGAGTTGGGGACTCCTCC 47289	A CA GAAA
		GGA GA TCCCCAGC AG	
		CCT CT AGGGGTTG TC	
		C C_ AG_	
GAM2238	SFXN5	3' GCTTGGGGATGCCCTTCT 58653	A_ _
		GGAAG CATCCCCA GC	
		TCTTC GTAGGGGT CG	
		CC T	
GAM2238	STK38L	3' TGTAGGAATGTCTTCCT 69689	CC A
		AGGAAGACAT CC GCG	
		TCCTTCTGTA GG TGT	
		A_ A	
GAM2238	VTI2	5' TTTCGCTGCGGCCTTCC 22069	ACAT C
		GGAAG CC CAGCGAAA	

	CCTTT GG GTCGCTTT	
	CC__ C	
GAM2238 ZAK	3' TCTTTTTTTTGGATGTCCCCT 34111 AA	CCAGC
	AGG GACATCC GAAAAGA	
	TCC CTGTAGG TTTTCT	
	C_ TTT__	
GAM2238 LOC124470 3'	CTTTCGTCATGTTTTCT 76147	CCCCA A
	AGGAAGACAT GCG AAAG	
	TCCTTTTGTA TGC TTTC	
	C____ C	
GAM2238 LOC145919 3'	TTCTCCATGTCTTCCT 78030	CCCC C
	AGGAAGACAT AG GAA	
	TCCTTCTGTA TC CTT	
	CC__ _	
GAM2238 LOC146455 5'	TCTTTTTGTGGGAAATCTTCCT 78469	CA CA
	AGGAAGA TCCC GCGAAAAGA	
	TCCTTCT AGGG TGTTTTTCT	
	AA _	
GAM2238 LOC147124 3'	TGACTGGGATTGTCTTCCT 76808	TC _
	AGGAAGACA CCCAG CG	
	TCCTTCTGT GGGTC GT	
	TA A	
GAM2238 LOC149109 3'	CTTCCAGTGAATGGTATGTCTT 85510	_ CCA_ GAA
CCT	AGGAAGACAT CC GC AAG	
	TCCTTCTGTA GG TG TTC	
	T TAAG ACC	
GAM2238 LOC158857 5'	TCTTCTGTGCTGTCTTCCT 88287	TCCCCA AA_
	AGGAAGACA GCG AAGA	
	TCCTTCTGT CGT TTCT	
	_____ GTC	
GAM2238 LOC159049 5'	TCTTCTGTGCTGTCTTCCT 88353	TCCCCA AA_
	AGGAAGACA GCG AAGA	
	TCCTTCTGT CGT TTCT	
	_____ GTC	
GAM2238 LOC162333 5'	TCTTTTCGTTCCCATTCCT 88502	CATCCCC
	AGGAAGA AGCGAAAAGA	
	TCCTTCT TTGCTTTTCT	
	TACCC__	
GAM2238 LOC202134 5'	TTGCTGGTAGGCCCTTCTT 91925	ACAT _
	AGGAAG CC CCAGCGAA	

		TTCTTC GG GGTGCTT		
		CC__ AT		
GAM2238	LOC256158 5'	TCCCTGGGTGAAGAGGTCTTCC 99515	A__ _ C	
	T	AGGAAGAC TC CCCAG GA		
		TCCTTCTG AG GGGTC CT		
		GAGA T C		
GAM2239	LDB1 3'	GGCCCTGCTGTGGCCACCCAGT 15312	AT G TA AA	
		ACT GGTGGTT AC CAG CC		
		TGA CCACCGG TG GTC GG		
		C_ _ TC CC		
GAM2239	PBX3 3'	GTCCTGTAGCTATTTTATCATA 21669	T_ A A	
		TATGGTGG TG CTACAG AC		
		ATACTATT AT GATGTC TG		
		TT C C		
GAM2239	PLG 3'	TTCTGTAGTAAGGTGACATAG 6112	GT G G	
		CTATG G TT ACTACAGAA		
		GATAC T GA TGATGTCTT		
		AG G A		
GAM2239	SSRP1 5'	GGCTCTGCCCAGGCCACCACAG 13419	A GACTA A	
		CT TGGTGGTT CAGA CC		
		GA ACCACCGG GTCT GG		
		C ACCC_ C		
GAM2239	TMEM1 3'	CTGTGGTCCCCCATA 13799	T TT	
		TATGG GG GACTACAG		
		ATACC CC CTGGTGTC		
		— —		
GAM2239	UVRAG 3'	GTTCTGTAACCCAGTAG 14026	GGT TGAC	
		CTAT GGT TACAGAAC		
		GATG CCA ATGTCTTG		
		AC_ _		
GAM2239	WNT4 3'	CTGCGCCGGCAACCACCTAGT 48483	T A A__	
		ACTA GGTGGTTG CT CAG		
		TGAT CCACCAAC GG GTC		
		_ _ CCGC		
GAM2239	CDC42BPB 3'	AGTCCTGCTGACCACCTAGT 21237	T _	
		ACTA GGTGGTT GACT		
		TGAT CCACCAG CTGA		
		_ TCGTC		
GAM2239	DCAMKL1 3'	GGTTCTGTGCATCACCACAGT 17602	A TGAC	
		ACT TGGTGGT TACAGAACC		

			TGA ACCACTA GTGTCTTGG		
			C C__		
GAM2239	FLJ10314	3'	TGTCACAACCACCATAG 36491	ACT	
			CTATGGTGGTTG ACA		
			GATACCACCAAC TGT		
			AC_		
GAM2239	FLJ21919	3'	GGCTCTGTAAAATCAGACCATA 43737	GG C__ A	
		GT	ACTATGGT TTGA TACAGA CC		
			TGATACCA GACT ATGTCT GG		
			_ AAA C		
GAM2239	KIAA0766	3'	GTTCTGTTAGCTCACCATAG 29675	_ ACT	
			CTATGGTG GTTG ACAGAAC		
			GATACCAC CGAT TGTCTTG		
			T _		
GAM2239	KIAA0918	3'	CTGTAAAGGATCACCATAG 73520	GAC	
			CTATGGTGGTT TACAG		
			GATACCACTAG ATGTC		
			GAA		
GAM2239	KIAA1130	3'	CTGACAACCACCACAGT 63092	A ACTA	
			ACT TGGTGGTTG CAG		
			TGA ACCACCAAC GTC		
			C A__		
GAM2239	KIAA1198	3'	CTGCACCAACCACCACAGT 64033	A ACTA	
			ACT TGGTGGTTG CAG		
			TGA ACCACCAAC GTC		
			C CAC_		
GAM2239	KIAA1535	3'	CTGTAGCTTGTCCCATCATA 80213	T_ _	
			TATGGTGG TGA CTACAG		
			ATACTACC GTT GATGTC		
			CT C		
GAM2239	MGC10924	3'	TTCTGTAATCATTGAATCAT 48312	GGT_ C	
			ATGGT TGA TACAGAA		
			TACTA ACT ATGTCTT		
			AGTT A		
GAM2239	MGC20235	3'	GTTCTGTTCCACCACCA 59561	T CT	
			TGGTGGT GA ACAGAAC		
			ACCACCA CT TGTCTTG		
			C _		
GAM2239	PIIB	3'	GGCCCTGTAGTCCGCCAC 8130	T AA	
			GTGGT GACTACAG CC		

CACCG CTGATGTC GG
C CC
GAM2239 Rabip4R 3' GTTCTGCAGTCATTGACTGT 36278 GGT A
ATGGT TGA CT CAGAAC
||||| ||||| |||||
TGTCA ACTGA GTCTTG
GTT C
GAM2239 SHAPY 3' GTCCTGTAGTTACCCAGC 57912 G T A
G TGG TGA CT CAG AAC
| ||| ||||| ||
C ACC ATTGATGTC TG
G C C
GAM2239 LOC148195 3' GGTTCTGTCTTTACCACCA 85285 TGACT
TGGTGGT ACAGAACC
||||| |||||
ACCACCA TGTCTTGG
TTTC_
GAM2239 LOC150837 3' GGTCCTGAGCAAGAACCACC 80805 ____ A A A
GGTGGT TG CT CAG ACC
||||| || || || ||
CCACCA AC GA GTC TGG
AGA _ _ C
GAM2239 LOC150935 3' GGTTCTGCAACCAGTTTCATATG 80836 _ _ ACTA
T AC TATGG TGGTTG CAGAACC
|| |||| ||||| |||||
TG ATACT ACCAAC GTCTTGG
T TG ____
GAM2239 LOC151248 5' TTCTGCAGATTTTAACCACTGT 81002 ____ A
ATGGTGGTTGA CT CAGAA
||||||| || |||||
TGTCACCAATT GA GTCTT
TTA C
GAM2239 LOC163682 5' GGTTCACAGTCCCACCAGAGT 88414 A TT ACA
ACT TGGTGG GACT GAACC
||| ||||| ||||| |||||
TGA ACCACC CTGA CTTGG
G _ CAC
GAM2239 LOC169505 3' TTCTGTAATCAATGCTG 83624 G C
TGGTG TTGA TACAGAA
||||| ||||| |||||
GTCGT AACT ATGTCTT
_ A
GAM2239 LOC255042 5' CTGCAGGTCAGACCACCGT 97044 _ A_
ATGGTGGT TGA CT CAG
||||||| ||||| |||
TGCCACCA ACTGG GTC
G AC
GAM2240 GAS7 3' GGCCCATCGCCACCACCT 20854 CA C
AGG GTGGCGATGG GCC
||| ||||| ||||| |||

TCC CACCGCTACC CGG
 AC _
 GAM2240 ICMT 3' GGCCACACGCCACTGCC 25737 A GC
 GGCAGTGGCG TG GCC
 ||||| || ||
 CCGTCACCGC AC CGG
 _ AC
 GAM2240 MYO1C 3' AAAGAACGCCCTTTTACTGTC 61848 C T CC
 GGCAGTGG GA GGCG CTTT
 ||||| || |||| ||||
 CTGTCATT TT CCGC GAAA
 _ C AA
 GAM2240 SLA 3' GAAAGGGCACCAGGACTGCT 23113 GGCGA C
 GGCAGT TGG GCCCTTTC
 |||| || |||||
 TCGTCA ACC CGGGAAAG
 GG_ A
 GAM2240 C20orf54 5' AAAAGGTGCATATACCACTGCC 54152 CGATG C
 GGCAGTGG GCGCC TTT
 ||||| |||| ||
 CCGTCACC CGTGG AAA
 ATATA A
 GAM2240 DKFZP434M131 3' GCCACCATCACCCTGACC 69668 _ C C_
 GG CAGTGG GATGG GC
 || ||||| |||| ||
 CC GTCACC CTACC CG
 A A AC
 GAM2240 FLJ20257 5' GAGGCCGCCACCACCACCACC 39487 CA CGA C
 GG GTGG TGGCG CCTT
 || |||| |||| ||||
 CC CACC ACCGC GGAG
 AC ACC C
 GAM2240 KIAA1853 5' GAAAGTCTCACCGCCACCGCC 69921 A A CGCC
 GGC GTGGCG TGG CTTTC
 || ||||| || ||||
 CCG CACCGC ACT GAAAG
 C C CT_
 GAM2240 KIAA1908 5' GAAAGGGCGCTGCGACCACCCC 73788 CA _ A
 C GG GTGG CG TGGCGCCCTTTC
 || |||| || |||||
 CC CACC GC GTCGCGGGAAAG
 CC A _
 GAM2240 MGC11034 3' GAAAGACTTTCACCACTGTCT 49572 C T CGCC
 AGGCAGTGG GA GG CTTTC
 ||||| || || ||||
 TCTGTCACC CT TC GAAAG
 A T A_
 GAM2240 MGC15504 3' GAAAGGACGGTAGAAACCACTG 52219 CGA_ G C
 CCT AGGCAGTGG TG CG CCTTTC
 ||||| || || ||||

		TCCGTCACC	AT GC GGAAAG		
		AAAG G A			
GAM2240	MGC35558	3'	GAAAGGGCACCTTTACTATCC	59412	CA CG T C
			GG GTGG A GG GCCCTTTC		
			CC TATC T CC CGGGAAAG		
			___ AT T A		
GAM2240	PTP4A1	5'	GCAGCCACCGCCACCGCCT	14407	A A _
			AGGC GTGGCG TGGC GC		
			TCCG CACCGC ACCG CG		
			C C A		
GAM2240	TAF6L	5'	GAGTGGGCGCCGCGCCACCGC	22386	A A T
	C		GGC GTGGCG TGGCGCCC TTC		
			CCG CACCGC GCCGCGGG GAG		
			C C T		
GAM2240	LOC146756	3'	GAAAGGGGCCACCACACCACACC	84803	CA CGA C_
			GG GTGG TGG GCCCTTTC		
			CC CACC ACC CGGGAAAG		
			A_ AC_ AC		
GAM2240	LOC158147	3'	GCCACCATCACCCTGTC	70078	C C_
			GGCAGTGG GATGG GC		
			CTGTCACC CTACC CG		
			A AC		
GAM2240	LOC166206	3'	AAGGGGCCCACCACCACTGCC	83512	CGA C
			GGCAGTGG TGG GCCCTTT		
			CCGTCACC ACC CGGGGAA		
			ACC _		
GAM2240	LOC202460	5'	AAAGGTCATCGACCACTGCC	90657	_ CGC
			GGCAGTGG CGATGG CCTTT		
			CCGTCACC GCTACT GGAAA		
			A _		
GAM2240	LOC220793	5'	GAAAGGGTGCTCACACCGCC	61009	A GCGAT
			GGC GTG GGCGCCCTTTC		
			CCG CAC TCGTGGGAAAG		
			C AC_		
GAM2240	LOC221218	5'	GAAAGGGCGCGCAGTCACTGCC	93417	GATG
	T		AGGCAGTGGC GCGCCCTTTC		
			TCCGTCACTG CGCGGGAAAG		
			ACG_		
GAM2240	LOC92080	5'	GAAAGGAGAGGAATCGCCACCC	68629	CA GGCGC_
	CCT		AGG GTGGCGAT CCTTTC		

TCC CACCGCTA GGAAAG
 CC AGGAGA
 GAM2241 ACCN2 3' AGGCCTGAGCCCCAACCCCTCT 39624 CA_ CT _
 AGA GTT GG TCAGGCCT
 ||| ||| || |||||
 TCT CAA CC AGTCCGGA
 CCC CC G
 GAM2241 BHMT2 3' GCCTGACCTGGAACCGTT 34736 A _
 GAC GTTCT GGTCAGGC
 ||| ||||| |||||
 TTG CAAGG CCAGTCCG
 C T
 GAM2241 CENPB 5' GACCAACAAGCTGTCTCCCT 70115 AA C__
 AG AGACAGTT TGGTC
 || ||||| |||||
 TC TCTGTCTGA ACCAG
 CC ACA
 GAM2241 F2RL3 3' GACCTGGAACCTCCCTTCT 15514 A AC _
 AGAA G AGTTCT GGTC
 ||||| ||||| |||||
 TCTT C TCAAGG CCAG
 _ CC T
 GAM2241 KLHL2 3' TGACCAAAACATGTCTTTCT 24339 _ C
 AGAAAGACA GTT TGGTCA
 ||||| ||| |||||
 TCTTTCTGT CAA ACCAGT
 A A
 GAM2241 NRXN3 3' GGCCTGGAAACTTCCTTCT 58075 A C CTGG
 AGAA GA AGTT TCAGGCC
 |||| || |||| |||||
 TCTT CT TCAA GGTCCGG
 C _ A__
 GAM2241 PVT1 3' AGGCCTGACCAAAGCAGATCTT 66175 CA_ C
 TT GAAAGA GTT TGGTCAGGCCT
 ||||| ||| |||||
 TTTTCT CGA ACCAGTCCGGA
 AGA A
 GAM2241 RALBP1 3' ACCAAAAATCGTCTTTCT 23268 A C_
 AGAAAGAC GTT TGGT
 ||||| ||| |||||
 TCTTTCTG TAA ACCA
 C AA
 GAM2241 RPLP0 5' AGGCCTGAGCTCCCTGTCTCTC 54974 A TTCT _
 GA AGACAG GG TCAGGCCT
 || ||||| || |||||
 CT TCTGTC TC AGTCCGGA
 C CC_ G
 GAM2241 SLC7A6 3' AGGCCTGAAATGCTACCATTTTC 15637 GAC_ TCTGG
 T AGAAA AGT TCAGGCCT
 ||||| ||| |||||

TCTTT TCG AGTCCGGA
 ACCA TAA__
 GAM2241 TMPRSS3 5' GACCTCAACGTGTCTTTCT 44024 _ CT
 AGAAAGACA GTT GGTC
 ||||| ||| |||
 TCTTTCTGT CAA CCAG
 G CT
 GAM2241 ATF3 3' GCCATTGGAGAGCTGTCTTCCT 15733 A GGTC
 AG AAGACAGTTCT GGC
 || ||||| |||
 TC TTCTGTCGAGA CCG
 C GGTTA
 GAM2241 FLJ14966 5' GGCCAAGAGCTATCTCCCT 52834 AA C GGTC
 AG AGA AGTTCT GGCC
 || ||| ||||| |||
 TC TCT TCGAGA CCGG
 CC A A__
 GAM2241 FLJ20343 3' CTGACCAGAATTACCTTCCT 35468 A AC
 AG AAG AGTTCTGGTCAG
 || ||| ||||| |||||
 TC TTC TTAAGACCAGTC
 C CA
 GAM2241 GGA2 3' AGGCCTAAAGGGAAGTGTCTTC 31157 A GGTC
 T AGAA GACAGTTCT AGGCCT
 ||| ||||| |||||
 TCTT CTGTCAAGG TCCGGA
 _ GAAA
 GAM2241 GGA2 3' AGGCCTAAAGGGAAGTGTCTTC 57651 A GGTC
 T AGAA GACAGTTCT AGGCCT
 ||| ||||| |||||
 TCTT CTGTCAAGG TCCGGA
 _ GAAA
 GAM2241 KIAA0557 3' GGCCTGAAAGTCCCTTTC 78569 AC CTGG
 GAAAG AGTT TCAGGCC
 |||| ||| |||||
 CTTTC TCAA AGTCCGG
 CC ____
 GAM2241 KIAA1887 5' TGGCACAGAGCTGTCTTCCT 77279 A _
 AG AAGACAGTTCTG GTCA
 || ||||| |||||
 TC TTCTGTCGAGAC CGGT
 C A
 GAM2241 MGC15437 3' AGGCTTTGGAGAATTGTCTTCC 52842 A GG _
 T AG AAGACAGTTCT TCAG GCCT
 || ||||| ||| |||
 TC TTCTGTTAAGA GGTT CGGA
 C _ T
 GAM2241 MRP64 5' AGGCCCAAGATGGCTGTCTTC 33663 A CTG A__
 GAA GACAGTT GTC GGCCT
 ||| ||||| ||| |||||

CTT CTGTCGG TAG CCGGA
 — — AAC
 GAM2241 MRPL50 3' CTACCAGAACTGTTCTCT 39309 AA C
 AGA GACAGTTCTGGT AG
 ||| ||||| ||
 TCT TTGTCAAGACCA TC
 C_ —
 GAM2241 PLAGL2 3' GCGCCAGAACCTCCTTCT 70962 A CA CAG
 AGAA GA GTTCTGGT GC
 |||| || ||||| ||
 TCTT CT CAAGACCG CG
 C C_ —
 GAM2241 PSKH1 3' AGGCCTGAGCCAGAACCATC 68790 CA _
 GA GTTCTGG TCAGGCCT
 || ||||| |||||
 CT CAAGACC AGTCCGGA
 AC G
 GAM2241 TIMM22 3' AGGCCTGACCACAGCTGGCCCT 78910 AAGA C
 CT AGA CAGTT TGGTCAGGCCT
 ||| |||| |||||
 TCT GTCGA ACCAGTCCGGA
 CCCG C
 GAM2241 UHRF2 3' AGGCCCATTTCTCAACTGTCTT 73828 CT TCA_
 TT GAAAGACAGTT GG GGCCT
 ||||| || ||||
 TTTTCTGTCAA CT CCGGA
 CT TTAC
 GAM2241 LOC115110 5' AGGCCTGGCCATTGCCCTC 72172 CA TC
 GA GT TGGTCAGGCCT
 || || |||||
 CT CG ACCGGTCCGGA
 CC TT
 GAM2241 LOC127281 3' AGACCTGACTGGAAGTGGCTCC 75133 AA A TG C
 CT AG AG CAGTTC GTCAGG CT
 || || |||| ||||| ||
 TC TC GTCAAG CAGTCC GA
 CC G GT A
 GAM2241 LOC146714 5' GGGCCGCCAGAACTGCCTCTTT 84750 _ CA
 AAAGA CAGTTCTGGT GGCCT
 |||| ||||| ||||
 TTTCT GTCAAGACCG CCGGG
 CC _
 GAM2241 LOC152573 3' ACCAGAGAACTGTTTTCT 81494 A _
 AGAA GACAGT TCTGGT
 |||| |||| ||||
 TCTT TTGTCA AGACCA
 _ AG
 GAM2241 LOC203083 5' GCCCCAGAACTATCTGTC 92090 A C TCA
 GA AGA AGTTCTGG GGC
 || ||||| |||

CT TCT TCAAGACC CCG
 G A ____
 GAM2241 LOC219899 3' GGCCAGAACTTCTCTCT 93133 A C
 AGA AGA AGTTCTGGTC
 ||| ||| |||||
 TCT TCT TCAAGACCGG
 C _
 GAM2241 LOC253392 5' AGGCCTGATGGGGATACCTTCC 98193 A ACA G
 T AG AAG GTTCT GTCAGGCCT
 || ||| ||||| |||||
 TC TTC TAGGG TAGTCCGGA
 C CA_ G
 GAM2241 LOC253502 3' AGGCCTACCAGAACTGCCT 96215 A C
 AG CAGTTCTGGT AGGCCT
 || ||||| |||||
 TC GTCAAGACCA TCCGGA
 C _
 GAM2241 LOC254176 5' GCCCCAGAACTATCTGTC 99171 A C TCA
 GA AGA AGTTCTGG GGC
 || ||| ||||| |||
 CT TCT TCAAGACC CCG
 G A ____
 GAM2241 LOC255565 3' AGGCCTGACCACATGGCTCCCT 96800 AA A GTTC
 AG AG CA TGGTCAGGCCT
 || ||| |||||
 TC TC GT ACCAGTCCGGA
 CC G AC_
 GAM2241 LOC256597 5' AGGCCTGAAGGTGCCGTTCCCTC 98025 AA A T GG
 GA GAC GT CT TCAGGCCT
 || ||| ||| |||||
 CT TTG CG GG AGTCCGGA
 CC C T A_
 GAM2241 LOC91263 5' GTCTCCAGGACTGTCCCTC 66001 AA TC
 GA GACAGTTCTGG AGGC
 || ||||| |||
 CT CTGTCAGGACC TCTG
 CC _
 GAM2241 LOC92558 3' AGGCCTGAGCCTCCATTCCCTC 70308 A CAGTTCT _
 GAA GA GG TCAGGCCT
 ||| || || |||||
 CTT CT CC AGTCCGGA
 C TACCT_ G
 GAM2242 BACH2 3' CTGTCAAGCAATGGATAAACAG 41782 C GGGA_
 CTCT AGAGTTGTT ATCCA GACAG
 ||||| ||||| |||||
 TCTCGACAA TAGGT CTGTC
 A AACGAA
 GAM2242 CHRNA1 3' CTGTCTCCCTGAAGAGTGAAC 5375 C_
 GTTCAT CAGGGAGACAG
 ||||| |||||

		CAAGTG GTCCCTCTGTC	
		AGAA	
GAM2242 FZD8	3'	CCATGGATAACAACCTCT 49873	C G
		AGAGTTGTT ATCCA GG	
		TCTCAACAA TAGGT CC	
		— A	
GAM2242 HHIP	5'	CTGTCCCACCTAAACAACCTC 42753	CATCCAG A
		GAGTTGTT GG GACAG	
		CTCAACAA CC CTGTC	
		ATCCA__ _	
GAM2242 MME	3'	TCCCTATGGAGGAACAACCTCT 8034	A _
		AGAGTTGTTT TCCA GGGA	
		TCTCAACAAG AGGT CCCT	
		G AT	
GAM2242 MME	3'	TCCCTATGGAGGAACAACCTCT 24437	A _
		AGAGTTGTTT TCCA GGGA	
		TCTCAACAAG AGGT CCCT	
		G AT	
GAM2242 MME	3'	TCCCTATGGAGGAACAACCTCT 24439	A _
		AGAGTTGTTT TCCA GGGA	
		TCTCAACAAG AGGT CCCT	
		G AT	
GAM2242 MME	3'	TCCCTATGGAGGAACAACCTCT 24441	A _
		AGAGTTGTTT TCCA GGGA	
		TCTCAACAAG AGGT CCCT	
		G AT	
GAM2242 MTCP1	5'	CTACATGGATAACAACCTCT 27242	C GGG
		AGAGTTGTT ATCCA AG	
		TCTCAACAA TAGGT TC	
		— ACA	
GAM2242 NR1D1	3'	TGTCTCCCCCACAACCCT 41672	A TCATCCA
		AG GTTGT GGGAGACA	
		TC CAACA CCCTCTGT	
		C CC_____	
GAM2242 NR1I2	3'	TGTCTCCCTAGGGAATTC 15304	GTTCA _
		GAGTT TCC AGGGAGACA	
		CTTAA GGG TCCCTCTGT	
		_____ A	
GAM2242 NR1I2	3'	TGTCTCCCTAGGGAATTC 42088	GTTCA _
		GAGTT TCC AGGGAGACA	

CTTAA GGG TCCCTCTGT
 _____ A
 GAM2242 PCOLN3 3' CTGCCCTGTTGCCAAACAACCTC 12411 ____ TC _
 GAGTTGTT CA CAGGG AG
 ||||| || |||||
 CTCAACAA GT GTCCC TC
 ACC T_ G
 GAM2242 PFN2 3' TGTCTTCATCAACAACCCT 12063 A CATCCAG
 AG GTTGTT GGAGACA
 || ||||| |||||
 TC CAACAA CTTCTGT
 C CTA____
 GAM2242 PFN2 3' TGTCTTCATCAACAACCCT 54890 A CATCCAG
 AG GTTGTT GGAGACA
 || ||||| |||||
 TC CAACAA CTTCTGT
 C CTA____
 GAM2242 TNS 3' CTGTCTCCCTAACTCAACTGCT 42950 _ TTCATCC
 AG AGTTG AGGGAGACAG
 || ||||| |||||
 TC TCAAC TCCCTCTGTC
 G TCAA____
 GAM2242 FLJ10511 3' CCCTAGAAAAACAACCTCT 36686 CA C
 AGAGTTGTT TC AGGG
 ||||| || |||||
 TCTCAACAA AG TCCC
 AA A
 GAM2242 FLJ20195 3' CCCGATGAACACCTCT 35216 T CA
 AGAG TGTTCATC GGG
 |||| ||||| |||||
 TCTC ACAAGTAG CCC
 C _
 GAM2242 HAAO 3' TCCCTGCCAAACAACCTCT 60173 CATC
 AGAGTTGTT CAGGGA
 ||||| |||||
 TCTCAACAA GTCCCT
 ACC_
 GAM2242 KIAA0843 3' CTGAACAACCAGACAGACAACCT 30801 CA CA GAGA_
 CT AGAGTTGTT TC GG CAG
 ||||| || || |||||
 TCTCAACAG AG CC GTC
 AC A_ AACAA
 GAM2242 KIAA1497 5' CTGTCCTTGTATGAGCAAC 68121 C GA
 GTTGTTTCAT CAGGGA CAG
 ||||| ||||| |||||
 CAACGAGTA GTTCCT GTC
 T _
 GAM2242 KIAA1710 3' TCTCCATACATGAACAATCT 63181 G CCAG
 AGA TTGTTTCAT GGAGA
 ||||| ||||| |||||

		TCT AACAAAGTA CCTCT	
		— CATA	
GAM2242	PDE7B	3' CTGCCGAAATGAGCAACTC 38949	CCA G
		GAGTTGTTTCAT GG AG	
		CTCAACGAGTA CC TC	
		AAG G	
GAM2242	SEC24B	3' CTGCATTGTTGGATGACAACTC 21984	T G GA
	T	AGAGTTGT CATCCAG GA CAG	
		TCTCAACA GTAGGTT TT GTC	
		— G AC	
GAM2242	LOC124753	5' CTGCCTCCCTGGCTTCCATCTC 74803	T TTCAT A
		GAG TG CCAGGGAG CAG	
		CTC AC GGTCCCTC GTC	
		T CTTC_ C	
GAM2242	LOC142948	3' CTACCGGGAGGAATGAATAACT 83777	_____ A G
	C	GAGTTGTTCA TCC GG AG	
		CTCAATAAGT AGG CC TC	
		AAGG G A	
GAM2242	LOC153914	5' CCACTAAAGTGAACAACTC 81898	CC_ _
		GAGTTGTTTCAT AG GG	
		CTCAACAAGTG TC CC	
		AAA A	
GAM2242	LOC219445	5' CTCCCTGGTTCAAACAATTC 93202	CAT_
		GAGTTGTT CCAGGGAG	
		CTTAACAA GGTCCCTC	
		ACTT	
GAM2242	LOC219914	5' CCACTGGGAGGAACGAACAACT 94967	A_____ _
	C	GAGTTGTTC TCCAG GG	
		CTCAACAAG GGGTC CC	
		CAAGGA A	
GAM2243	CDH12	3' CTTATCATTTAAAGTGGTGTA 15777	CCCAA GA
		TACACCACT GAA ATAAG	
		ATGTGGTGA TTT TATTC	
		AA_ AC	
GAM2243	GOCAP1	3' ATTGTTCTTGGGAGCAGTGTA 43007	CA G
		TACAC CTCCCAAGAA AAT	
		ATGTG GAGGGTTCTT TTA	
		AC G	
GAM2243	DKFZp434N2435	5' CTTATTACTGTGGGGTGGT 98090	T AGAAG
		ACCAC CCCA AATAAG	

			TGGTG GGGT TTATTC	
			_ GTCA_	
GAM2243	DKFZP564I122	3'	CTTATTCTTCTCCCTCATGTGT 63877	CACTCCCA
	A		TACAC AGAAGAATAAG	
			ATGTG TCTTCTTATTC	
			TACTCCC_	
GAM2243	FLJ21791	3'	CTTATTTGCAGAAAGTGGTGTA 62126	CCCAAGAA
			TACACCACT GAATAAG	
			ATGTGGTGA TTTATTC	
			AGACG__	
GAM2243	HMP19	3'	CTTATTCTTTGTAGGAAAATG 88860	CCAC CAA_
	TA		TACA TCC GAAGAATAAG	
			ATGT AGG TTTCTTATTC	
			AAA_ ATTG	
GAM2243	KIAA1719	3'	TCTGTCTTGGGAGTGGTGTA 68742	_
			TACACCACTCCCAAGA AGA	
			ATGTGGTGAGGGTTCT TCT	
			G	
GAM2243	KIAA1853	3'	TTTTTCTTGAAGCAGTG 69929	CA C
			CAC CT CCAAGAAGAA	
			GTG GA GGTTCTTTTT	
			AC A	
GAM2243	KIAA1877	3'	CTTATTCTTCTGCCATGAGT 66748	CCA__
			ACTC AGAAGAATAAG	
			TGAG TCTTCTTATTC	
			TACCG	
GAM2243	KIAA1906	3'	CTTATTCTTCTTGACTTTTGG 73571	CTCC_
			CCA CAAGAAGAATAAG	
			GGT GTTCTTCTTATTC	
			TTTCA	
GAM2243	OSBPL11	3'	CTTAATTTCCCAAGAGTGGTG 43206	CCAA AA
			CACCACTC GAAG TAAG	
			GTGGTGAG CTTT ATTC	
			AACC A_	
GAM2243	YME1L1	3'	TCATTCTTGATGTGGTGTA 58438	TCC _
			TACACCAC CAAGAA GA	
			ATGTGGTG GTTCTT CT	
			TA_ A	
GAM2243	ZNF262	3'	CTTATTTTGTGGGAGT 18723	A
			ACTCCCAAG AGAATAAG	

			TGAGGGTTT TTTTATTC		
			G		
GAM2243	LOC91960	3'	TGTGGCTTGGAACGTGGTGTA 68294	TC_	AAGA
			TACACCAC CCAAG ATA		
			ATGTGGTG GGTTC TGT		
			CAA GG_		
GAM2244	ANXA5	3'	CACTGCCTTCCTTCAGCACCTT 8569	TGCCA	
			AAGGTGCTGGAGG AGTG		
			TTCCACGACTTCC TCAC		
			TTCCG		
GAM2244	AREG	5'	CACTCGCTCTTCCAACACC 9762 C T CA		
			GGTG TGGAGG GC AGTG		
			CCAC ACCTTC CG TCAC		
			A T C_		
GAM2244	B3GNT3	3'	CACCTGGTACTGTTCCAGCATC 27302	_	A
	TT		AAGGTGCTGGA GGTGCCA GTG		
			TTCTACGACCT TCATGGT CAC		
			TG C		
GAM2244	CASP7	3'	TCACATCTTCCACCAGCACCTT 54034	A TGCCAA	
			AAGGTGCTGG GG GTGA		
			TTCCACGACC CC CACT		
			A TTCTA_		
GAM2244	CASP7	3'	TCACATCTTCCACCAGCACCTT 54035	A TGCCAA	
			AAGGTGCTGG GG GTGA		
			TTCCACGACC CC CACT		
			A TTCTA_		
GAM2244	CCKAR	5'	TTCACCAGCTCTCCAGCACTT 7414	T CAA	
			AGGTGCTGGAGG GC GTGAA		
			TTCACGACCTCT CG CACTT		
			_ AC_		
GAM2244	CRY1	5'	CACTGCGCCTCCAGCGCC 15808	CA	
			GGTGCTGGAGGTGC AGTG		
			CCGCGACCTCCGCG TCAC		
			_		
GAM2244	CSTA	5'	TTCACTTTGGTTCCAGCATC 19056	GGT _	
			GGTGCTGGA GCCAA GTGAA		
			CTACGACCT TGGTT CACTT		
			_ T		
GAM2244	CUBN	3'	TCACTCAGCACTTTCCCT 8424	TGCT CA	
			AGG GGAGGTGC AGTGA		

			TCC CTTTCACG TCACT		
			_____ AC		
GAM2244 DNAH9	5'	CACTTG	GATACCAGCACC 9092	AGGTG	
			GGTGCTGG CCAAGTG		
			CCACGACC GGTTCAC		
			ATA__		
GAM2244 FXD7	3'	GCCCAGCACCCCAGCATC 42097		A CAA	
			GGTGCTGG GGTGC GT		
			CTACGACC CCACG CG		
			C ACC		
GAM2244 GNA15	5'	CACCCTGTTCCCAGCACT 60585		A T CAA	
			GGTGCTGG GG GC GTG		
			TCACGACC CT TG CAC		
			__ _ TCC		
GAM2244 ISL1	5'	CACTTAGCCACAGCTCCAGCAT 11023		__ _ C	
C			GGTGCTGGAG GTG C AAGTG		
			CTACGACCTC CAC G TTCAC		
			GA C A		
GAM2244 PPP2R5B	5'	TCACCCAGCACCTCCCAGGCC 21802		T __ CAA	
			GG GCT GGAGGTGC GTGA		
			CC CGG CCTCCACG CACT		
			_ AC ACC		
GAM2244 SPN	3'	TCAGCCAGCCTCCAGCACCTT 13382		GCCAAG	
			AAGGTGCTGGAGGT TGA		
			TTCCACGACCTCCG ACT		
			ACCG__		
GAM2244 TEAD3	3'	GGCACCCCCCAGCACCTT 13672		A_	
			AAGGTGCTGG GGTGCC		
			TTCCACGACC CCACGG		
			CC		
GAM2244 TEAD3	3'	TCAGGCCACCTCCAAACC 13675		GC _ AAG	
			GGT TGGAGGTG CC TGA		
			CCA ACCTCCAC GG ACT		
			A_ C _		
GAM2244 TXNRD2	3'	CACCTCACCCCTGCACCT 22242		T A CCAA	
			AGGTGC GG GGTG GTG		
			TCCACG CC CCAC CAC		
			T _ TC__		
GAM2244 UBE2B	3'	CACCTGTAGTCCCAGCACTTT 13933		A GC A	
			AAGGTGCTGG GGT CA GTG		

TTTACGACC CTG GT CAC
 _ AT C
 GAM2244 XYLB 3' TCACTTGGCATAATTCACAACC 18831 GC G_
 T AGGT TGA GTGCCAAGTGA
 |||| ||| |||||
 TCCA ACTT TACGGTTCCT
 AC AA
 GAM2244 C20orf122 3' TCACTTGGCACCTGCCCCT 55994 T TGG
 AGG GC AGGTGCCAAGTGA
 ||| || |||||
 TCC CG TCCACGGTTCCT
 C ____
 GAM2244 C20orf150 3' TCCTGCCAGCACCCCCAGCACC 66016 A CA__ T
 T AGGTGCTGG GGTGC AG GA
 ||||| ||| |||
 TCCACGACC CCACG TC CT
 C ACCG _
 GAM2244 CSEN 3' TCACCCGCTGCCCAGCCCT 26461 T A_ CCAA
 AGG GCTGG GGTG GTGA
 ||| ||| ||| |||
 TCC CGACC TCGC CACT
 _ CG C____
 GAM2244 DKFZp434F2322 5' CACCCGCGGGACTCCAGGCACC 70298 _ G G AA__
 T AGGTGC TGGAG T CC GTG
 ||||| ||||| ||| |||
 TCCACG ACCTC A GG CAC
 G _G CGCC
 GAM2244 DKFZP434P1750 3' CAAGGTGCCACCCCCTAGCACC 32023 A_ C AG_
 TT AAGGTGCTGG GGTG CA TG
 ||||| ||| ||| |||
 TTCCACGATC CCAC GT AC
 CC C GGA
 GAM2244 FLJ12650 3' TCACTCTTCGCCCAGCATC 44826 AG CCA
 GGTGCTGG GTG AGTGAA
 ||||| ||| |||||
 CTACGACC CGC TCACTT
 _ TTC
 GAM2244 FLJ12783 3' TCACTTGGAGGAACCAGCACT 49489 AGGTG
 GGTGCTGG CCAAGTGA
 ||||| |||||
 TCACGACC GGTTCCT
 AAGGA
 GAM2244 FLJ20123 5' GGTACACATCCAGCACCTT 35072 G_
 AAGGTGCTGGA GTGCC
 ||||| |||||
 TTCCACGACCT CATGG
 ACA
 GAM2244 FLJ20413 3' CACCACACCCTCCAGCCC 35590 T _ CCAA
 GG GCTGGAGG TG GTG
 || ||||| || |||

		CC CGACCTCC AC CAC	
		— C AC—	
GAM2244	FLJ23467	3' TCACCTGGCACTAACACTTT 45013	CTGGA A
		AAGGTG GGTGCCA GTGA	
		TTTCAC TCACGGT CACT	
		AA— C	
GAM2244	GPA33	3' TCACCTGTGTGCCCAGCACCT 20572	AG TG _ A
		AGGTGCTGG G C CA GTGA	
		TCCACGACC C G GT CACT	
		— GT T C	
GAM2244	JM5	3' TCACTTCCCCCAGCACTT 23960	A TGCC
		AGGTGCTGG GG AAGTGA	
		TTCACGACC CC TTCACT	
		— CC—	
GAM2244	KIAA0478	3' CACCCAGTGGCCACGCCAGCA 30171	AG _ A—
		CC GGTGCTGG GTG CCA GTG	
		CCACGACC CAC GGT CAC	
		CG C GACC	
GAM2244	KIAA0773	3' CACCCAGGCTTCAGCATCT 28719	GGT AA_
		AGGTGCTGGA GCC GTG	
		TCTACGACTT CGG CAC	
		— ACC	
GAM2244	KIAA0830	3' TCACTCAGCATCAGCACTT 70271	GAG CA
		AGGTGCTG GTGC AGTGA	
		TTCACGAC TACG TCACT	
		— AC	
GAM2244	KIAA0843	3' TCACTGCTCCCAGCACCT 30805	AG GCCA
		AGGTGCTGG GT AGTGA	
		TCCACGACC CG TCACT	
		CT —	
GAM2244	KIAA1138	3' CACCCTCTGCCCCCAGCCCT 62818	T A T CAA—
		AGG GCTGG GG GC GTG	
		TCC CGACC CC CG CAC	
		— C _ TCTCC	
GAM2244	KIAA1196	3' CACTGGAAGTCCAGCACC 62147	GTG A
		GGTGCTGGAG CCA GTG	
		CCACGACCTC GGT CAC	
		AA_ _	
GAM2244	KIAA1727	3' TCAGAACCAACCCCCAGCATCT 64764	A GCCAAG
		AGGTGCTGG GGT TGA	

TCTACGACC CCA ACT
 C ACCAAG
 GAM2244 KIAA1755 5' CACTTGGCACCCCTCAACC 62006 GCT A
 GGT GG GGTGCCAAGTG
 ||| || |||||
 CCA CC CCACGGTTCAC
 ACT _
 GAM2244 LAK-4P 3' TCACGGGCCCCGCCAGCACC 24396 A_ T AA
 GGTGCTGG GG GCC GTGA
 ||||| || ||| |||
 CCACGACC CC CGG CACT
 CG _ G_
 GAM2244 M96 5' TCATTCTACCCCCAACCCTT 24758 TGC A CCA
 AAGG TGG GGTG AGTGA
 ||| ||| ||| |||
 TTCC ACC CCAT TTA CT
 CA_ C C_
 GAM2244 MGC15705 3' CACTTAGGGTGCCAGCACC 52246 AGGTG _
 GGTGCTGG CC AAGTG
 ||||| || |||||
 CCACGACC GG TTCAC
 GTG_ A
 GAM2244 MGC4707 3' CACCCAGCCTCCTCTCCAGCAC 44361 T_ CAA
 CTT AAGGTGCTGGAGG GC GTG
 ||||| || |||
 TTCCACGACCTCT CG CAC
 CCTC ACC
 GAM2244 MGC4737 5' TTCACCCGAGTCAGCACC 49654 AGG CCAA
 GGTGCTGG TG GTGAA
 ||||| || |||||
 CCACGACT GC CACTT
 GA_ C_
 GAM2244 NCBP2 3' TTCACCTTAGCAACAAAGTACCT 24769 GGAGG C
 T AAGGTGCT TGC AAGTGAA
 ||||| || |||||
 TTCCATGA ACG TTCACCTT
 AACA_ A
 GAM2244 NPTXR 3' TCACCTGTACCCACACCT 27444 C AG CAA
 AGGTG TGG GTGC GTGA
 ||||| ||| ||| |||
 TCCAC ACC CATG CACT
 _ _ TC_
 GAM2244 OSR2 5' CTCAGCACCCCCAGCATC 54856 A CA
 GGTGCTGG GGTGC AG
 ||||| ||||| ||
 CTACGACC CCACG TC
 C AC
 GAM2244 PCBP3 5' TCACAGCACCCCTCAGCACCTT 40445 GA CAA
 AAGGTGCTG GGTGC GTGA
 ||||| ||||| |||

TTCCACGAC CCACG CACT
 TC A__
 GAM2244 POLE3 3' CACTTGGCCCCAAAACCTT 34312 GC AGGT
 AAGGT TGG GCCAAGTG
 ||||| ||| |||||
 TTCCA ACC CGGTTCAC
 AA ____
 GAM2244 PRO1843 5' TCACTTGGTACACACCTT 38143 CTGGAG
 AAGGTG GTGCCAAGTGA
 ||||| |||||
 TTCCAC CATGGTTCCT
 A_____
 GAM2244 RAI17 3' CACGTCCCACCTCCACACC 92900 C CCAA
 GGTG TGGAGGTG GTG
 ||| ||||| |||
 CCAC ACCTCCAC CAC
 _ CCTG
 GAM2244 ZDHC8 3' CACTGCCATCACCCAGCACC 64618 A_ CCA
 GGTGCTGG GGTG AGTG
 ||||| ||| |||
 CCACGACC CTAC TCAC
 CA CG_
 GAM2244 ZIC4 5' TCACCGCCGCCTCCAGCCCCT 50544 T CCAA
 AGG GCTGGAGGTG GTGA
 ||| ||||| |||
 TCC CGACCTCCGC CACT
 C CGC_
 GAM2244 LOC124750 5' CACTTCACACCTCCAAACC 76154 GC CC
 GGT TGGAGGTG AAGTG
 ||| ||||| |||||
 CCA ACCTCCAC TTCAC
 A_ AC
 GAM2244 LOC128954 5' CACCTGGCCCATCCCTGCACCT 76299 T_ _ T A
 AAGTGC GGA GG GCCA GTG
 ||||| ||| || ||| |||
 TCCACG CCT CC CGGT CAC
 TC A _ C
 GAM2244 LOC148343 5' CACTCAGGCTTCCAGACCTT 79538 G GCCA
 AAGGT CTGGAGGT AGTG
 ||||| ||||| |||
 TTCCA GACCTTCG TCAC
 _ GAC_
 GAM2244 LOC148918 5' CACTGTCTCTCCAGCTCCTT 79818 T GT CA
 AAGG GCTGGAG GC AGTG
 ||| ||||| || |||
 TTCC CGACCTC TG TCAC
 T TC ____
 GAM2244 LOC149657 3' CACCGAGCCCTCCAGCCC 85714 T T CAA
 GG GCTGGAGG GC GTG
 || ||||| || |||

	CC CGACCTCC CG CAC	
	— — AGC	
GAM2244 LOC151512 5'	TCACCTGCCTCCAGCATCT 86619	CCAA
	AGGTGCTGGAGGTG GTGA	
	TCTACGACCTCCGT CACT	
	C—	
GAM2244 LOC152464 3'	TCACTTCCCCCAGCACTT 60650	A TGCC
	AGGTGCTGG GG AAGTGA	
	TTCACGACC CC TTCACT	
	— CC—	
GAM2244 LOC153894 5'	CACCGGACCACCTCCAGGACC 81877	G — AA
	GGT CTGGAGGTG CC GTG	
	CCA GACCTCCAC GG CAC	
	G CA C—	
GAM2244 LOC157247 5'	CACTCAAGTGTTATCCAGCACT 82288	— TG CA—
	GGTGCTGGA GG C AGTG	
	TCACGACCT TT G TCAC	
	A GT AAC	
GAM2244 LOC157623 5'	TTCACCTGGCACCCATTATCT 82417	C AG
	AGGTG TGG GTGCCAAGTGAA	
	TCTAT ACC CACGGTTCACCT	
	T —	
GAM2244 LOC165246 5'	TCACTCTACAGCTCAAACACCT 83368	CTG G CCA
T	AAGGTG GAG TG AGTGA	
	TTCCAC CTC AC TTCACT	
	AAA G ATC	
GAM2244 LOC170393 3'	CACCTCACCCCAGCACTT 83732	A CCAA
	AGGTGCTGG GGTG GTG	
	TTCACGACC CCAC CAC	
	— TC—	
GAM2244 LOC196415 5'	TTCACCTGTAATCCCAGCACTT 91193	A GC A
T	AAGGTGCTGG GGT CA GTGAA	
	TTTCACGACC CTA GT CACTT	
	— AT C	
GAM2244 LOC201475 5'	CACGCCTGCCCCCAGCACT 89618	A T CAA—
	GGTGCTGG GG GC GTG	
	TCACGACC CC CG CAC	
	— — TCCG	
GAM2244 LOC220020 5'	TCACCCTCTCCTCTCCCAGCAC 95053	— TGCCAA
C	GGTGCTGG AGG GTGA	

CCACGACC TCC CACT
 CTC TCTCC_
 GAM2244 LOC220739 3' CACCTGGCTTCACTCCAGCACC 94516 GT__ A
 GGTGCTGGAG GCCA GTG
 ||||| ||||
 CCACGACCTC CGGT CAC
 ACTT C
 GAM2244 LOC221354 3' TTCACTGTCTACCTCCAGAACC 94017 G CCA
 T AGGT CTGGAGGTG AGTGAA
 ||| ||||| ||||
 TCCA GACCTCCAT TCACTT
 A CTG
 GAM2244 LOC221474 5' CACCCAGTGCCTGCCAGCACCT 93990 _ TG CAA
 AGGTGCTGG AGG C GTG
 ||||| ||| | |||
 TCCACGACC TCC G CAC
 G GT ACC
 GAM2244 LOC253866 3' CACCTGGCACCCTATGCCACC 97332 _TGG A
 GGTG C AGGTGCCA GTG
 ||| | ||||| |||
 CCAC G TCCACGGT CAC
 C TA_ C
 GAM2244 LOC255452 3' CACTTGCCTCCACACCTT 99389 C TGC
 AAGGTG TGGAGG CAAGTG
 ||||| ||||| |||||
 TTCCAC ACCTCC GTTCAC
 _ _
 GAM2244 LOC56920 3' CACTAGCAGCCCCCAGCATCT 39795 A _ CA
 AGGTGCTGG GG TGC AGTG
 ||||| || ||| ||||
 TCTACGACC CC ACG TCAC
 C G A_
 GAM2244 LOC90139 3' CACCCACCACTGCCCAGCACC 56264 A_ CCAA
 GGTGCTGG GGTG GTG
 ||||| ||| |||
 CCACGACC TCAC CAC
 CG CACC
 GAM2244 LOC93395 5' TTCACTTGACCTGGAGAACC 61122 G GG GC
 GGT CT AGGT CAAGTGAA
 ||| || ||| |||||
 CCA GA TCCA GTTCACTT
 A GG _
 GAM2245 CARKL 3' GCTGTTCGGATATGCCA 26104 A
 TGGCATATC CGAACAGC
 ||||| |||||
 ACCGTATAG GCTTGTCG
 _
 GAM2245 C3orf4 3' CTTTGCTGTTGTAGATAGCCA 39593 A _ G
 TGGC TATC AC AACAGCAAAG
 ||| ||| || |||||

		ACCG ATAG TG TTGTCGTTTC	
		— A —	
GAM2245	FLJ10432	3' GCTTTGCCGCCCTAGCCA 39353	A TCA AACA
		TGGC TA CG GCAAAGC	
		ACCG AT GC CGTTTCG	
		— CCC —	
GAM2245	KIAA0007	3' CTTTGCTGTCCTGAGCACCCCA 80927	CATA_ C A
		TGG TCA GA CAGCAAAG	
		ACC AGT CT GTCGTTTC	
		CCACG C _	
GAM2245	KIAA1958	3' GCTGTTTGTGACATGCCA 82784	A
		TGGCAT TCACGAACAGC	
		ACCGTA AGTGTTTGTCTG	
		C	
GAM2245	KPNA6	3' TTGGTGAGTCATATGCCA 25545	C GAA G
		TGGCATAT AC CA CAA	
		ACCGTATA TG GT GTT	
		C A_ G	
GAM2245	TIMM22	3' CTTTGCTGCTCCTGGACTCCA 78912	CATA C A
		TGG TCA GA CAGCAAAG	
		ACC GGT CT GTCGTTTC	
		TCA_ C C	
GAM2245	LOC152078	3' CTTTGCAAGATGATATGTCA 81287	CGAACA
		TGGCATATCA GCAAAG	
		ACTGTATAGT CGTTTC	
		AGA_	
GAM2245	LOC158078	3' CGCTTTGCTGTTTCGTGATATG 82601	
		CATATCACGAACAGCAAAGCG	
		GTATAGTGCTTGTCTGTTTCGC	
GAM2245	LOC253890	5' TGCCATCTGTGATATGCCA 97386	AACA
		TGGCATATCACG GCA	
		ACCGTATAGTGT CGT	
		CTAC	
GAM2246	CSNK1G3	3' GCTTTAAAGTTTTGTCAAA 16509	C C T
		TTTGACAAA CTT AAG GC	
		AAACTGTTT GAA TTT CG	
		T A _	
GAM2246	ESRRG	5' AATTGCACTGTGCTCTGTCAAG 66986	AACCTTCA
		TTTGACA AGTGCAATT	

			GA	ACTGT		TC	ACGT	TAA		
				CTCGTG						
GAM2246	RYP3	3'	TG	CACTTGAAGGTTATTCA	8293	CA				
				TGA AACCTTCAAGTGCA						
				ACT TTGGAAGTTCACGT						
				TA						
GAM2246	DKFZP761E2110	3'	CA	CTTGGAAGGCTTGTTAAA	48961	A				
				TTTGACAA CCTTC AAGTG						
				AAATTGTT GGAAG TTCAC						
				C G						
GAM2246	FLJ20086	3'	A	ATTCATTGAAGGCTCATCAA	35011	CAAA			C	
				TTGA CCTTCAAGTG AATT						
				AACT GGAAGTTTAC TTAA						
				ACTC						
GAM2246	KIAA1910	3'	TG	CATATTGAAATTTGTTAAA	73718	CC				
				TTTGACAAA TTCAA GTGCA						
				AAATTGTTT AAGTT TACGT						
				A_ A						
GAM2246	KIAA1948	5'	C	AGTTGAACATTTGTCAAA	83299	CC			G	
				TTTGACAAA TTCAA TG						
				AAACTGTTT AAGTT AC						
				AC G						
GAM2246	MGC27434	3'	TG	TATTGAAGTTTTGTCAAA	59594	C			G	
				TTTGACAAA CTTCAA TGCA						
				AAACTGTTT GAAGTT ATGT						
				T						
GAM2246	NUP54	3'	AC	TGTGTAAAGGTTTGTGAAA	60722	G				
				TTT ACAAACCTT CAAGT						
				AAA TGTTTGGAA GTTCA						
				G ATGT						
GAM2246	LOC121441	3'	T	ATTTAGAAAGGTTGTCAAA	74503	A				
				TTTGACAA CCTT C AAGTG						
				AAACTGTT GGAA G TTTAT						
				_ A A						
GAM2246	LOC170409	3'	C	ATCCGGAAGGTTTGTTAAA	83742	AA				
				TTTGACAAACCTTC GTG						
				AAATTGTTTGGGAAG TAC						
				GCC						
GAM2247	AOC3	3'	TG	GCCAAGGGCTCCAGGGCCA	14962	A	TA	ATCC		
				TGGCC TGGA CC TGGCCA						

ACCGG ACCT GG ACCGGT
 G CG A___
 GAM2247 FBXL11 3' GGCCCTGTCTCCATGGCCA 25519 T CATCCT
 TGGCCATGGA AC GGCC
 ||||| || |||
 ACCGGTACCT TG CCGG
 C TC___
 GAM2247 HYAL1 5' TGGCCAGGTTGTCCTCGACCA 24604 CCAT CCAT
 TGG GGATA CCTGGCCA
 || |||| |||||
 ACC CCTGT GGACCGGT
 AGCT T___
 GAM2247 KCNS2 3' TGAGCCTGGTATCCATGGCC 68853 TCCT _
 GGCCATGGATACCA GGC CA
 ||||| ||| ||
 CCGGTACCTATGGT CCG GT
 ___ A
 GAM2247 PDAP1 3' TGGCCAGGAGCCCCCATGGCC 94057 ATACCA
 GGCCATGG TCCTGGCCA
 ||||| |||||
 CCGGTACC AGGACCGGT
 CCGG_
 GAM2247 S100A9 3' TGGCCAAGATCACAGTGGCCA 12933 GGATACC C
 TGGCCAT ATC TGGCCA
 ||||| || |||||
 ACCGGTG TAG ACCGGT
 ACAC___ A
 GAM2247 STIM1 3' TGGCCAGGAGAGCCACAGCCA 60786 CA ATACCA
 TGGC TGG TCCTGGCCA
 ||| || |||||
 ACCG ACC AGGACCGGT
 AC GAG___
 GAM2247 ZNF35 3' TGACCATTCCCTAGTCTCCATG 14241 T CATCC___ C
 GCCA TGGCCATGGA AC TGG CA
 ||||| || ||| ||
 ACCGGTACCT TG ACC GT
 C ATCCCTT A
 GAM2247 CGI-57 3' TGGCCAGGACAGTGATGCCGCC 74312 CAT A___ CA
 A TGGC GG TAC TCCTGGCCA
 ||| || ||| |||||
 ACCG CC GTG AGGACCGGT
 ___ GTA AC
 GAM2247 CLDN4 3' GGCCAGGATGGCTTAACC 8955 A ___
 GG TA CCATCCTGGCC
 || || |||||
 CC AT GGTAGGACCGG
 A TC
 GAM2247 DKFZp434N035 3' GGCTCGGTCTCCACAGCCA 51065 CA T ATCCT
 TGGC TGGA ACC GGCC
 ||| ||| || |||

		ACCG ACCT TGG TCGG	
		AC C C___	
GAM2247 DUSP9	3'	TGGCCGCCCACATCCATGGCC 9160	ACCATCC
		GGCCATGGAT TGGCCA	
		CCGGTACCTA GCCGGT	
		CACCC___	
GAM2247 FLJ11117	3'	GCCAGGATAAGCTTCAAGCCA 37635	CA TACC
		TGGC TGA ATCCTGGC	
		ACCG ACTT TAGGACCG	
		A_ CGAA	
GAM2247 FLJ14950	3'	GCCAGGATGCTGCAGGCCA 52792	A GATAC
		TGGCC TG CATCCTGGC	
		ACCGG AC GTAGGACCG	
		_ GTC___	
GAM2247 FLJ20186	5'	GGCCAGGCTTCCGTGGCCA 35203	TACCAT
		TGGCCATGGA CCTGGCC	
		ACCGGTGCCT GGACCGG	
		TC___	
GAM2247 FLJ22215	3'	TGGCCAGGATGCTCAGCTGGCC 43399	TG_ TAC
A		TGGCCA GA CATCCTGGCCA	
		ACCGGT CT GTAGGACCGGT	
		CGA C___	
GAM2247 FLJ22215	5'	TGGCCAGGATGCTCAGCTGGCC 98640	TG_ TAC
A		TGGCCA GA CATCCTGGCCA	
		ACCGGT CT GTAGGACCGGT	
		CGA C___	
GAM2247 FLJ23042	3'	GCCAGAGCTTCCATGTGCCA 47945	_ TACCATC
		TGGC CATGGA CTGGC	
		ACCG GTACCT GACCG	
		T TCGA___	
GAM2247 HPCAL4	3'	TGGCCAGAAGGGGCATGGCCA 33213	GATA ATC
		TGGCCATG CC CTGGCCA	
		ACCGGTAC GG GACCGGT	
		G___ GAA	
GAM2247 JM4	3'	GGCCAGAGCATCCATGGCCA 24261	ACCATC
		TGGCCATGGAT CTGGCC	
		ACCGGTACCTA GACCGG	
		CGA___	
GAM2247 KIAA0447	3'	GGCCTTTGGCACCCATGGTCA 72126	ATA TCCT
		TGGCCATGG CCA GGCC	

			ACTGGTACC GGT CCGG		
			CAC TT__		
GAM2247	KIAA0870	3'	GCCGCGAGACCCATGGCCA 82383	ATACCA	C
			TGGCCATGG TC TGGC		
			ACCGGTACC AG GCCG		
			CAG__ C		
GAM2247	KIAA1939	5'	TGACCAGGATGTGAGTGACCA 46186	C GGATAC	C
			TGG CAT CATCCTGG CA		
			ACC GTG GTAGGACC GT		
			A AGT__ A		
GAM2247	MGC9753	3'	GCCAGGAGCTCTCCATGGCCA 54192	TACCA	
			TGGCCATGGA TCCTGGC		
			ACCGGTACCT AGGACCG		
			CTCG_		
GAM2247	NET-5	3'	GGCTGCGACATCCATGGCCA 22894	ACCA	C
			TGGCCATGGAT TC TGGCC		
			ACCGGTACCTA AG GTCGG		
			C__ C		
GAM2247	OS4	3'	CCAGCATCCAGTGGCCA 20385	_ ACCATC	
			TGGCCA TGGAT CTGG		
			ACCGGT ACCTA GACC		
			G C_____		
GAM2247	OVCOV1	5'	GCCTTCAGAGGCACCCATGGCT 32520	ATA A CT__	
	A		TGGCCATGG CC TC GGC		
			ATCGGTACC GG AG CCG		
			CAC _ ACTT		
GAM2247	PDEF	5'	TGGCCAGGCCCCAGTGGCCA 25681	_ ATACCAT	
			TGGCCA TGG CCTGGCCA		
			ACCGGT ACC GGACCGGT		
			G CCC_____		
GAM2247	PRC1	3'	GGCCAGGTTCCATGACCA 15628	C TACCAT	
			TGG CATGGA CCTGGCC		
			ACC GTACCT GGACCGG		
			A T_____		
GAM2247	SH3BP1	3'	GGTCGGCCCCCATGGCCA 39043	ATACCATC	
			TGGCCATGG CTGGCC		
			ACCGGTACC GGCTGG		
			CCC_____		
GAM2247	TEX27	3'	GCCAGGATACCTGATGGCCA 41949	__ ATACC	
			TGGCCAT GG ATCCTGGC		

	ACCGGTA CC TAGGACCG		
	GT A_____		
GAM2247 LOC129676 5'	CAGAGTATCCATGGCC 76231	CATC	
	GGCCATGGATAC CTG		
	CCGGTACCTATG GAC		
	A_____		
GAM2247 LOC146745 5'	CAGGGTGGTATCCTGGCCA 78689	T	
	TGGCCA GGATACCATCCTG		
	ACCGGT CCTATGGTGGGAC		
	—		
GAM2247 LOC146784 5'	TGGCCAGGATGGTCTTGAACC 78720	CCAT TA	
	GG GGA CCATCCTGGCCA		
	CC TCT GGTAGGACCGGT		
	AAGT —		
GAM2247 LOC158363 3'	CCAAATGGTATCCATGTCCA 88115	C CC	
	TGG CATGGATACCAT TGG		
	ACC GTACCTATGGTA ACC		
	T A_		
GAM2247 LOC159982 5'	GGCCACCGCATCCGTGGCCA 88434	ACCATCC	
	TGGCCATGGAT TGGCC		
	ACCGGTGCCTA ACCGG		
	CGCC_____		
GAM2247 LOC160336 5'	TGTCCAGTATCCATCACCA 83087	CC CATCC C	
	TGG ATGGATAC TGG CA		
	ACC TACCTATG ACC GT		
	AC _____ T		
GAM2247 LOC197408 5'	GGCCCAGTACCCATGGCC 91318	A CATCCT	
	GGCCATGG TAC GGCC		
	CCGGTACC ATG CCGG		
	C AC_____		
GAM2247 LOC201243 5'	CAGGGTGGTATCCTGGCCA 89538	T	
	TGGCCA GGATACCATCCTG		
	ACCGGT CCTATGGTGGGAC		
	—		
GAM2247 LOC222178 3'	GGCTGGCATCCATGGCCA 95838	A TCCTG	
	TGGCCATGGAT CCA GCC		
	ACCGGTACCTA GGT CGG		
	C _____		
GAM2247 LOC51308 3'	CCAGGATGGCCAGGCCA 33962	A ATA	
	TGGCC TGG CCATCCTGG		

ACCGG ACC GGTAGGACC

GAM2247 LOC51696 5' GGCCAGGATGGCGCGGC 33085 A GATA
GCC TG CCATCCTGGCC
||| || |||||
CGG GC GGTAGGACCGG
C ____

GAM2248 ENAM 3' ACCTAGCACAGTGTCTTCAA 49925 C_ CA
TTGAAGACAC TGCT GT
||||||| ||| ||
AACTTCTGTG ACGA CA
AC TC

GAM2248 MADH3 3' CACACTGGGTGCGTCTCCAG 20920 A ACC A
TTG AGAC TGCTCAGT TG
||| ||| ||||| ||
GAC TCTG GTGGGTCA AC
C C_ C

GAM2248 PGF 3' CAGGGGAGCAGGTTCCCCAA 12064 AA C AGTA
TTG GA ACCTGCTC TG
||| || ||||| ||
AAC CT TGGACGAG AC
CC _ GGG_

GAM2248 SLC26A3 5' CATAGTTGCAAAGGTCTTCAA 5471 ACC TCAG
TTGAAGAC TGC TATG
|||||| ||| |||
AACTTCTG ACG ATAC
GAA TTG_

GAM2248 BLR1 3' ACCAAGAAGATGTCTTCAA 53110 C G CA
TTGAAGACA CT CT GT
||||||| || ||
AACTTCTGT GA GA CA
A A AC

GAM2248 CITED2 3' TCATACTGTTCACTTTCAA 21404 ACACC CT
TTGAAG TG CAGTATGA
||||| || |||||
AACTTT AC GTCATACT
C_ TT

GAM2248 CKAP2 3' TCATACTGAACAAATGTCATTC 37108 _ CC C
GAA GACA TG TCAGTATGA
||| ||| || |||||
CTT CTGT AC AGTCATACT
A AA A

GAM2248 DKFZP434K0410 5' GCTGGACAGGTGTCTCCAA 78534 A CT
TTG AGACACCTG CAGT
||| ||||| |||
AAC TCTGTGGAC GTCG
C AG

GAM2248 FBXO21 3' GTCATACTCCATGGTCTTCAA 54350 ACC CTC
TTGAAGAC TG AGTATGAC
|||||| || |||||

		AACTTCTG AC TCATACTG		
		GT_ C__		
GAM2248	FLJ20972 3'	ACAGACTAGGTGTCTCAA 47375	A	C A
		TTGA GACACCTG TC GT		
		AACT CTGTGGAT AG CA		
		_ C A		
GAM2248	KRTAP4-5 3'	GTCATACTATGAATGTCTTCA 53752		CCTGCTC
		TGAAGACA AGTATGAC		
		ACTTCTGT TCATACTG		
		AAGTA__		
GAM2248	NYD-SP16 3'	TGAGGAGCAAGGTCTTCAA 50059	ACC	AG
		TTGAAGAC TGCTC TA		
		AACTTCTG ACGAG GT		
		GA_ GA		
GAM2248	LOC144970 5'	TTGAGCAGGGGTCCCCAA 77532	AA	A
		TTG GAC CCTGCTCAG		
		AAC CTG GGACGAGTT		
		CC G		
GAM2248	LOC149086 3'	ACTGTCCAGGTGTCCCCAG 85490	AA	CT
		TTG GACACCTG CAGT		
		GAC CTGTGGAC GTCA		
		CC CT		
GAM2248	LOC221042 5'	GCCAGGCAGGTGGCTTCAA 94804	A	CA
		TTGAAG CACCTGCT GT		
		AACTTC GTGGACGG CG		
		G AC		
GAM2248	LOC222166 3'	GTCATACTAAAGGTTAATTTCA 95744	AC_	GCTC
	A	TTGAAG ACCT AGTATGAC		
		AACTTT TGGA TCATACTG		
		AAT AA__		
GAM2249	CDH12 3'	CTTATCATTTAAAGTGGTGTA 15777	CCCA	GA
		TACACCACT GAA ATAAG		
		ATGTGGTGA TTT TATTC		
		AA__ AC		
GAM2249	GOCAP1 3'	ATTGTTCTTGGGAGCAGTGTA 43007	CA	G
		TACAC CTCCCAAGAA AAT		
		ATGTG GAGGGTTCTT TTA		
		AC G		
GAM2249	DKFZp434N2435 5'	CTTATTACTGTGGGGTGGT 98090	T	AGAAG
		ACCAC CCCA AATAAG		

			TGGTG GGGT TTATTC	
			_ GTCA_	
GAM2249	DKFZP564I122	3'	CTTATTCTTCTCCCTCATGTGT 63877	CACTCCCA
	A		TACAC AGAAGAATAAG	
			ATGTG TCTTCTTATTC	
			TACTCCC_	
GAM2249	FLJ21791	3'	CTTATTTGCAGAAAGTGGTGTA 62126	CCCAAGAA
			TACACCACT GAATAAG	
			ATGTGGTGA TTTATTC	
			AGACG__	
GAM2249	HMP19	3'	CTTATTCTTTGTTAGGAAAATG 88860	CCAC CAA_
	TA		TACA TCC GAAGAATAAG	
			ATGT AGG TTTCTTATTC	
			AAA_ ATTG	
GAM2249	KIAA1719	3'	TCTGTCTTGGGAGTGGTGTA 68742	_
			TACACCACTCCCAAGA AGA	
			ATGTGGTGAGGGTTCT TCT	
			G	
GAM2249	KIAA1853	3'	TTTTTCTTGAAGCAGTG 69929	CA C
			CAC CT CCAAGAAGAA	
			GTG GA GGTTCTTTTT	
			AC A	
GAM2249	KIAA1877	3'	CTTATTCTTCTGCCATGAGT 66748	CCA_
			ACTC AGAAGAATAAG	
			TGAG TCTTCTTATTC	
			TACCG	
GAM2249	KIAA1906	3'	CTTATTCTTCTTGACTTTTGG 73571	CTCC_
			CCA CAAGAAGAATAAG	
			GGT GTTCTTCTTATTC	
			TTTCA	
GAM2249	OSBPL11	3'	CTTAATTTCCCAAGAGTGGTG 43206	CCAA AA
			CACCACTC GAAG TAAG	
			GTGGTGAG CTTT ATTC	
			AACC A_	
GAM2249	YME1L1	3'	TCATTCTTGATGTGGTGTA 58438	TCC _
			TACACCAC CAAGAA GA	
			ATGTGGTG GTTCTT CT	
			TA_ A	
GAM2249	ZNF262	3'	CTTATTTTGTGTTGGGAGT 18723	A
			ACTCCCAAG AGAATAAG	

			TGAGGGTTT TTTTATTC		
			G		
GAM2249	LOC91960	3'	TGTGGCTTGGAACGTGGTGTA 68294	TC_	AAGA
			TACACCAC CCAAG ATA		
			ATGTGGTG GGTTC TGT		
			CAA GG_		
GAM2250	AMD1	3'	CGCAAAAAGAGAACAC 9682	CC	C
			GTGTTC CTTTT TGCG		
			CACAAG GAAAA ACGC		
			A_ _		
GAM2250	APRT	3'	GCTGCCACAGGGAACAC 6666	CTTTTC	C
			GTGTTCCTC TG GCAGC		
			CACAAGGG AC CGTCG		
			AC_ C		
GAM2250	AR	5'	GGCTGCACGCGGAGAGAAC 5276	CCCT	_
			GTTC TTTCTGC GCAGCC		
			CAAG AGAGGCG CGTCGG		
			_ CA		
GAM2250	CD63	5'	GCCGCGGCGGGAGAGGAACGC 10117	CC	_ A
			GTGTTCC TTTTCTGC GC GC		
			CGCAAGG AGAGGGCG CG CG		
			_ G C		
GAM2250	DGKG	5'	GGCTGCGCAGGCGGGAAGAC 9042	G	CTTT
			GT TTCCC TCTGCGCAGCC		
			CA AAGGG GGACGCGTCGG		
			G C_		
GAM2250	DTNA	3'	GGCCACACAGAGGAGGAAGAC 53208	CC	CGCA
			GTT CCTTTTCTG GCC		
			CAG GGAGGAGAC CGG		
			AA ACAC		
GAM2250	DTNA	3'	GGCCACACAGAGGAGGAAGAC 53276	CC	CGCA
			GTT CCTTTTCTG GCC		
			CAG GGAGGAGAC CGG		
			AA ACAC		
GAM2250	DUOX1	5'	GGCCGCAGCTGGAAGAGGAAAA 34292	CC	_ _ A
	C		GTT CCTTTTCT GC GC GCC		
			CAA GGAGAAGG CG CG CGG		
			AA T A C		
GAM2250	FCN2	3'	GGCTGCACACCTGGTGGGAGAA 32346	_	TTTTC_ C
	CAC		GTGTTC CCC TG GCAGCC		

			CACAAG GGG AC CGTCGG			
			A TGGTCC A			
GAM2250	MGAM	3'	GCAAAGAAAAGGCAAACAC 72811	CC		GC
			GTGTT CCTTTTCT GC			
			CACAA GGAAAAGA CG			
			AC AA			
GAM2250	PITX2	3'	GCTATATAGAGAAAAGGAAACC 6156	—	CC	CGC
	AC		GTG TTCC TTTTCTG AGC			
			CAC AAGG AAGAGAT TCG			
			CA AA ATA			
GAM2250	PPP1R3C	3'	GGCTATGGAAAAGAAAGACAC 19424	CCC		CGC
			GTGTT CTTTCTG AGCC			
			CACAG GAAAAGGT TCGG			
			AAA A—			
GAM2250	RXRG	5'	GCTGCACAGGAGAGGAACAT 23611	CC		C
			GTGTTCC TTTTCTG GCAGC			
			TACAAGG AGAGGAC CGTCG			
			— A			
GAM2250	SDC4	3'	GCTGCGGTGAGGGGAAC 12998		TTCTG	
			GTTCCCCTT CGCAGC			
			CAAGGGGAG GCGTCG			
			TG—			
GAM2250	SORCS2	3'	GGCCACAGGACAAGGGGAGCAC 40804	—		CGCA
			GTGTTCCCCTT TTCTG GCC			
			CACGAGGGGAA AGGAC CGG			
			C AC—			
GAM2250	TLX1	3'	CTGCACCCAGGAGGGGAACAC 19821	TT	C—	
			GTGTTCCCCTT CTG GCAG			
			CACAAGGGGAG GAC CGTC			
			— CCA			
GAM2250	DKFZp586I021	3'	GCCACGCCAGGAGGAGGACAC 51083	C	CT	CA
			GTGTTT CCTTTT GCG GC			
			CACAGG GGAGGA CGC CG			
			A C— AC			
GAM2250	DKFZP586I2223	3'	GGCTGCACAGAGGGGAACAT 55768	TTT		C
			GTGTTCCCC TCTG GCAGCC			
			TACAAGGGG AGAC CGTCGG			
			— A			
GAM2250	DKFZP586I2223	3'	GGCTGCACAGAGGGGAACAT 55770	TTT		C
			GTGTTCCCC TCTG GCAGCC			

TACAAGGGG AGAC CGTCGG
 ____ A
 GAM2250 DKFZP586I2223 3' GGCTGCACAGAGGGGAACAT 31880 TTT C
 GTGTTCCCC TCTG GCAGCC
 ||||| ||| |||||
 TACAAGGGG AGAC CGTCGG
 ____ A
 GAM2250 FLJ10904 3' GCCAAAAAGGGAACAT 37382 C C C
 GTGTTCCC TTTT TG GC
 ||||| ||| || ||
 TACAAGGG AAAA AC CG
 _ A _
 GAM2250 FLJ23554 3' GTGGAGAAAAGAAACAC 46071 CCC G
 GTGTT CTTTCT CGC
 |||| ||||| |||
 CACAA GAAAAGA GTG
 A__ G
 GAM2250 HSPC155 3' GGCTGCACAGGGAAGGGAAAGA 33522 G C TT C
 C GT TT CCCTT CTG GCAGCC
 || ||||| ||| |||||
 CA AA GGGAA GAC CGTCGG
 G A GG A
 GAM2250 KIAA0649 3' GGCTGCAAGGAAGGGAAACA 29714 C T GC
 TGTT CCCTTT CT GCAGCC
 ||| ||||| || |||||
 ACAA GGGAAG GA CGTCGG
 A _ A_
 GAM2250 KIAA0711 5' GCTGCAGAGAGAGACAC 30150 CCCCT GC
 GTGTT TTTCT GCAGC
 |||| |||| |||||
 CACAG AGAGA CGTCG
 ____ GA
 GAM2250 KIAA1303 3' CGCTGAAAGGGGAAACAC 66604 C T
 GTGTT CCCTTTTC GCG
 |||| ||||| |||
 CACAA GGGGAAAG CGC
 A T
 GAM2250 KIAA1317 3' GCAGGAAAAGGGGAAGAC 87213 G GC
 GT TTCCCCTTTTCT GC
 || ||||| ||||| ||
 CA AAGGGGAAAAGG CG
 G A_
 GAM2250 KIAA1706 5' GCCGCAGGTGGAAGAGGAAC 94367 C _ CA
 GTTCC CTTT TCTGCG GC
 |||| ||| ||||| ||
 CAAGG GAAG GGACGC CG
 A GT _
 GAM2250 KIAA1908 5' GGCTGCGCCCCTGGGGACAC 73792 T TTTTCT
 GTGT CCCC GCGCAGCC
 ||| ||| |||||

			CACA GGGG CGCGTCGG			
			_ TCCC_			
GAM2250	NTPBP	3'	GCCAAGGAAAAGGGAAACAT	24393	C	GC_
			GTGTT CCCTTTTCT	GC		
			TACAA GGGAAAAGG	CG		
			A AAC			
GAM2250	NUDT11	3'	GGCTGCTATTAGAGGGGAACAC	60659		TC C
			GTGTTCCCTTT	TG GCAGCC		
			CACAAGGGGAGA	AT CGTCGG		
			TT _			
GAM2250	PDZD2	5'	CTGCGAAAAAGGGGAA	81722		CTG
			TTCCCTTTT	CGCAG		
			AAGGGGAAAA	GCGTC		
			A_			
GAM2250	PRO0899	5'	GCCGCACAGCAGGGGAGAAAC	38311	G_	TTT C A
			GT TTCCCT	CTG GC GC		
			CA GAGGGGA	GAC CG CG		
			AA C_ A C			
GAM2250	SARM	3'	GGCCACAGCAGAAAAGAGAGCA	31298	CC	GCA_
	C		GTGTTT	CTTTTCTGC GCC		
			CACGAG	GAAAAGACG CGG		
			A_ ACAC			
GAM2250	LOC139904	5'	GGCCGCGCTGGAGGGGTACAC	76368	T	TCT A
			GTGT CCCCTTT	GCGC GCC		
			CACA GGGGAGG	CGCG CGG		
			T T_ C			
GAM2250	LOC253430	5'	GGCTGCGGCGGCAGAGGAACA	97974	C TTT	_
			TGTTCC CT	CTGC GCAGCC		
			ACAAGG GA	GGCG CGTCGG		
			A C_ G			
GAM2250	LOC256015	5'	GTAAGAAAAGGAAAACAC	99454	CC	GC
			GTGTT CCTTTTCT	GC		
			CACAA GGAAAAGA	TG		
			AA A_			
GAM2250	LOC257235	3'	GCAAGAAAAGAAAAGGAACAC	98842	C_	GC
			GTGTTCC	CTTTTCT GC		
			CACAAGG	GAAAAGA CG		
			AAAA A_			
GAM2250	LOC54466	3'	CTGAGTAGAGAGGAACAC	39173	CCT	G
			GTGTTCC	TTTCTGC CAG		

		CACAAGG AGAGATG GTC		
		_____ A		
GAM2250	LOC86651	5' GGCTACAAGGAGAAAAGGAACA 69311	CC	GCGC
		TGTTCC TTTTCT AGCC		
		ACAAGG AAGAGG TCGG		
		AA AACA		
GAM2250	LOC91813	5' GCTACGCTGGGGAACAT 67844	TTTTCT	C
		GTGTTCCCC GCG AGC		
		TACAAGGGG CGC TCG		
		T_____ A		
GAM2251	CDH12	3' CTTATCATTTAAAGTGGTGTA 15777	CCCAA	GA
		TACACCACT GAA ATAAG		
		ATGTGGTGA TTT TATTC		
		AA_____ AC		
GAM2251	GOCAP1	3' ATTGTTCTTGGGAGCAGTGTA 43007	CA	G
		TACAC CTCCCAAGAA AAT		
		ATGTG GAGGGTTCTT TTA		
		AC G		
GAM2251	DKFZp434N2435	5' CTTATTACTGTGGGGTGGT 98090	T	AGAAG
		ACCAC CCCA AATAAG		
		TGGTG GGGT TTATTC		
		_ GTCA_		
GAM2251	DKFZP564I122	3' CTTATTCTTCTCCCTCATGTGT 63877	CACTCCCA	
	A	TACAC AGAAGAATAAG		
		ATGTG TCTTCTTATTC		
		TACTCCC_		
GAM2251	FLJ21791	3' CTTATTTGCAGAAAGTGGTGTA 62126	CCCAAGAA	
		TACACCACT GAATAAG		
		ATGTGGTGA TTTATTC		
		AGACG_____		
GAM2251	HMP19	3' CTTATTCTTTGTTAGGAAAATG 88860	CCAC	CAA_
	TA	TACA TCC GAAGAATAAG		
		ATGT AGG TTTCTTATTC		
		AAA_ ATTG		
GAM2251	KIAA1719	3' TCTGTCTTGGGAGTGGTGTA 68742	_	
		TACACCACTCCCAAGA AGA		
		ATGTGGTGAGGGTTCT TCT		
		G		
GAM2251	KIAA1853	3' TTTTCTTGGAAGCAGTG 69929	CA	C
		CAC CT CCAAGAAGAA		

		GTG GA GGTTCTTTTT		
		AC A		
GAM2251	KIAA1877	3' CTTATTCTTCTGCCATGAGT 66748	CCA__	
		ACTC AGAAGAATAAG		
		TGAG TCTTCTTATTC		
		TACCG		
GAM2251	KIAA1906	3' CTTATTCTTCTTGACTTTTGG 73571	CTCC_	
		CCA CAAGAAGAATAAG		
		GGT GTTCTTCTTATTC		
		TTTCA		
GAM2251	OSBPL11	3' CTTAATTTCCCAAGAGTGGTG 43206	CCAA AA	
		CACCACTC GAAG TAAG		
		GTGGTGAG CTTT ATTC		
		AACC A_		
GAM2251	YME1L1	3' TCATTCTTGATGTGGTGTA 58438	TCC _	
		TACACCAC CAAGAA GA		
		ATGTGGTG GTTCTT CT		
		TA_ A		
GAM2251	ZNF262	3' CTTATTTTGTGGGAGT 18723	A	
		ACTCCCAAG AGAATAAG		
		TGAGGGTTT TTTTATTC		
		G		
GAM2251	LOC91960	3' TGTGGCTTGGAACGTGGTGTA 68294	TC_ AAGA	
		TACACCAC CCAAG ATA		
		ATGTGGTG GGTC TGT		
		CAA GG_		
GAM2252	CDH12	3' CTTATCATTTAAAGTGGTGTA 15777	CCCAA GA	
		TACACCACT GAA ATAAG		
		ATGTGGTGA TTT TATTC		
		AA_ AC		
GAM2252	GOCAP1	3' ATTGTTCTTGGGAGCAGTGTA 43007	CA G	
		TACAC CTCCCAAGAA AAT		
		ATGTG GAGGGTTCTT TTA		
		AC G		
GAM2252	DKFZp434N2435	5' CTTATTACTGTGGGGTGGT 98090	T AGAAG	
		ACCAC CCCA AATAAG		
		TGGTG GGGT TTATTC		
		_ GTCA_		
GAM2252	DKFZP564I122	3' CTTATTCTTCTCCCTCATGTGT 63877	CACTCCCA	
	A	TACAC AGAAGAATAAG		

		ATGTG	TCTTCTTATTC		
		TACTCCC_			
GAM2252	FLJ21791	3'	CTTATTTGCAGAAAGTGGTGTA	62126	CCCAAGAA
			TACACCACT	GAATAAG	
			ATGTGGTGA	TTTATTC	
			AGACG__		
GAM2252	HMP19	3'	CTTATTCTTTGTTAGGAAAATG	88860	CCAC CAA_
	TA		TACA TCC	GAAGAATAAG	
			ATGT AGG	TTTCTTATTC	
			AAA_	ATTG	
GAM2252	KIAA1719	3'	TCTGTCTTGGGAGTGGTGTA	68742	_
			TACACCACTCCCAAGA	AGA	
			ATGTGGTGAGGGTTCT	TCT	
			G		
GAM2252	KIAA1853	3'	TTTTTCTTGGAAGCAGTG	69929	CA C
			CAC CT	CCAAGAAGAA	
			GTG GA	GGTTCTTTTT	
			AC A		
GAM2252	KIAA1877	3'	CTTATTCTTCTGCCATGAGT	66748	CCA_
			ACTC	AGAAGAATAAG	
			TGAG	TCTTCTTATTC	
			TACCG		
GAM2252	KIAA1906	3'	CTTATTCTTCTTGACTTTTGG	73571	CTCC_
			CCA	CAAGAAGAATAAG	
			GGT	GTTCTTCTTATTC	
			TTTCA		
GAM2252	OSBPL11	3'	CTTAATTTCCCAAGAGTGGTG	43206	CCAA AA
			CACCACTC	GAAG TAAG	
			GTGGTGAG	CTTT ATTC	
			AACC	A_	
GAM2252	YME1L1	3'	TCATTCTTGATGTGGTGTA	58438	TCC _
			TACACCAC	CAAGAA GA	
			ATGTGGTG	GTTCTT CT	
			TA_	A	
GAM2252	ZNF262	3'	CTTATTTTGTGTTGGGAGT	18723	A
			ACTCCCAAG	AGAATAAG	
			TGAGGGTTT	TTTTATTC	
			G		
GAM2252	LOC91960	3'	TGTGGCTTGGAACGTGGTGTA	68294	TC_ AAGA
			TACACCAC	CCAAG ATA	

ATGTGGTG GGTTC TGT
 CAA GG__
 GAM2253 EHF 3' TCCAAAACCCAAGGTTGGCT 25127 AT _ C
 AGT GCCT GGGT TTGGA
 ||| |||| |||| ||||
 TCG TGA CCA AACCT
 GT A A
 GAM2253 EPHA2 3' CCATCGGCCAAGAATACTTGAA 16675 GC G T_
 G CTTCAAGTAT CT GGTC TGG
 ||||| || |||| |||
 GAAGTTCATA GA CCGG ACC
 A_ A CT
 GAM2253 ITGA5 3' CCCAGAGACATACTTGAAG 61933 C__
 CTTCAAGTATG CTGGG
 ||||| ||||
 GAAGTTCATAC GACCC
 AGA
 GAM2253 TREM2 3' TCCAAGACTGTCATATTT 39098 CCTG
 AAGTATG GGTCTTGGA
 ||||| |||||
 TTTATAC TCAGAACCT
 TG__
 GAM2253 UQCRB 3' CCAACATAGGCATACTTAAG 21939 C GGTC
 CTT AAGTATGCCTG TTGG
 ||| ||||| ||||
 GAA TTCATACGGAT AACC
 _ AC__
 GAM2253 ATP10D 3' CAGAGACCACTTGAAG 73526 ATGCCTG _
 CTTCAAGT GGTCT TG
 ||||| |||| ||
 GAAGTTCA CCAGA AC
 _ G
 GAM2253 B3GNT7 3' CCCTTCCAGGCAACCTGAA 71678 A A TCTT
 TTCA GT TGCCTGGG GG
 |||| || ||||| ||
 AAGT CA ACGGACCT CC
 C _ TC__
 GAM2253 DKFZp547I224 3' TCCAAAATTGACCACATACTTG 39963 CCTG ____
 GA TTCAAGTATG GGTC TTGGA
 ||||| ||| ||||
 AGGTTTCATAC CCAG AACCT
 A__ TTAA
 GAM2253 FLJ22341 3' CCAAGCTCAGGCACACCCAAG 45114 CAA A T
 CTT GT TGCCTGGG CTTGG
 ||| || ||||| ||||
 GAA CA ACGGACTC GAACC
 CC_ C _
 GAM2253 KIAA0779 3' CCGAACAGCATACTTGAAG 86908 C GGTC
 CTTCAAGTATGC TG TTGG
 ||||| || ||||

GAAGTTCATACG AC AGCC
 _ A_
 GAM2253 LOC144233 3' CCAAGGCACATAATTGAA 77246 G CCTGG
 TTCAA TATG GTCTTGG
 ||||| ||| |||||
 AAGTT ATAC CGGAACC
 A A_
 GAM2253 LOC147341 3' ACCCAGGCATAACTGAAG 85116 AG
 CTTCA TATGCCTGGGT
 ||||| |||||
 GAAGT ATACGGACCCA
 CA
 GAM2253 LOC221088 5' TCCAAGGTGCTGGCCACTCGAA 94888 A AT TGGG
 G CTTC AGT GCC TCTTGGA
 ||||| ||| ||| |||||
 GAAG TCA CGG GGAACCT
 C C_ TCGT
 GAM2254 GLDC 3' TCTGTAATCACATTTCTGA 64897 A CA
 TCA AAA TGATTACAGG
 ||| ||| |||||
 AGT TTT ACTAATGTCT
 C AC
 GAM2254 IDH3A 3' ATGTCCCTAGGTCTGTTTT 19843 T AC
 AAAACA GATT AGGGACAT
 ||||| ||| |||||
 TTTTGT CTGG TCCCTGTA
 _ A_
 GAM2254 LYAAT1 3' ATGTCCCCCACCTCATGTTTT 55308 TTACA
 AAAACATGA GGGACAT
 ||||| |||||
 TTTTGTACT CCCTGTA
 CCACC
 GAM2254 PDGFRA 3' ATGCCCCCTGTTTCATGTTTTTG 21694 TT A
 CAAAAACATGA ACAGGG CAT
 ||||| ||| ||||| |||
 GTTTTTGTACT TGTCCC GTA
 _ C
 GAM2254 RPL10 3' ATGTCTTTGTATCTACATTCTT 21176 A CA AT
 GA TCAA AA TG TACAGGGACAT
 ||||| || ||| |||||
 AGTT TT AT ATGTTTCTGTA
 C AC CT
 GAM2254 WHSC1L1 3' ATGTCTCTGCAACCATATTT 35495 C A A
 AAA ATG TT CAGGGACAT
 ||| ||| || |||||
 TTT TAC AA GTCTCTGTA
 A C C
 GAM2254 ZNF9 3' TTGCTGTAATCAGTTTTT 14238 A G
 AAAAAC TGATTACAG GA
 ||||| ||||| ||| ||

TTTTGT ACTAATGTC TT
 — G
 GAM2254 BM046 3' TTTCTGTAAACATATTTCTGA 38060 A C A GG
 TCA AAA ATG TTACAG A
 ||| ||| ||| ||||| |
 AGT TTT TAC AATGTC T
 C A A TT
 GAM2254 DKFZp547I224 5' ATGTCCCTGTCTGACAGCTTTG 39950 AACA ATT_
 A TCAAA TG ACAGGGACAT
 |||| | |||||
 AGTTT AC TGTCCCTGTA
 CG__ AGTC
 GAM2254 DKFZP566K1924 3' CCTGTAATCAACTTTTGA 74196 ACA
 TCAAAA TGATTACAGG
 |||| | |||||
 AGTTTT ACTAATGTCC
 CA_
 GAM2254 KIAA0937 3' ATGTCCCTGCACTCTGTTTT 93222 T TTA
 AAAACA GA CAGGGACAT
 |||| | |||||
 TTTTGT CT GTCCCTGTA
 _ CAC
 GAM2254 KIAA1668 3' ATGTCCCTGAGCCGGCCCTTGA 67059 AAACA AT A
 TCAA TG T CAGGGACAT
 ||| | | |||||
 AGTT GC A GTCCCTGTA
 CCCG_ CG_
 GAM2254 MGC20398 3' TTTGTGTAACATGTTTTTGA 67164 A G
 TCAAAAACATG TTACA GGA
 ||||| |||| |
 AGTTTTTGTAC AATGT TTT
 — G
 GAM2254 PP35 3' TCCTAATCATGTTTTT 23800 ACA
 AAAAACATGATT GGGA
 ||||| |||
 TTTTGTACTAA TCCT
 —
 GAM2254 PPFA1 3' TCCTTTCAAATCATGTTCTT 14635 A AC_
 AA AACATGATT AGGGA
 || ||||| ||||
 TT TTGTACTAA TTCCT
 C ACT
 GAM2254 ZNF323 3' TCTAACTCATGTTTTTGA 48820 TTACAG
 TCAAAAACATGA GGA
 ||||| |||
 AGTTTTTGTACT TCT
 CAA____
 GAM2254 LOC158549 5' ATGTTGTAATAATCATGTTTTG 88215 A CAGG
 A TCAAAA CATGATTA GACAT
 |||| | |||| |


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AGTTTT GTACTAAT TTGTA
      _ AATG
GAM2254 LOC161734 3' ATGTCCTGTCTGACAGCTTTG 88460 AACA ATT_
      A      TCAAA TG ACAGGGACAT
              |||| | |||||
      AGTTT AC TGTCCCTGTA
              CG_ AGTC
GAM2254 LOC203276 3' CTTGATAATTATGTTTCTGA 92123 A _
              TCA AAACATGATTA CAGG
              || ||||| |||
      AGT TTTGTATTAAT GTTC
              C A
GAM2254 LOC203305 3' CTTGATAATTATGTTTCTGA 92176 A _
              TCA AAACATGATTA CAGG
              || ||||| |||
      AGT TTTGTATTAAT GTTC
              C A
GAM2254 LOC203339 5' CCCTGTGATACTGTTCTT 92208 A TG
              AA AACA ATTACAGGG
              || ||| |||||
      TT TTGT TAGTGTCCC
              C CA
GAM2254 LOC220758 3' TCTGTAATCACATTTCTGA 92469 A CA
              TCA AAA TGATTACAGG
              ||| ||| |||||
      AGT TTT ACTAATGTCT
              C AC
GAM2254 LOC221975 5' ATGTCAGGTGGATCTATGTTTC 94188 A _ _ AGG
      TGA      TCA AAACAT GATT AC GACAT
              ||| |||| ||| || |||
      AGT TTTGTA CTAG TG CTGTA
              C T G GA_
GAM2254 LOC254243 3' CTTGATAATTATGTTTCTGA 99262 A _
              TCA AAACATGATTA CAGG
              ||| ||||| |||
      AGT TTTGTATTAAT GTTC
              C A
GAM2254 LOC90038 3' CTTGATAATTATGTTTCTGA 61806 A _
              TCA AAACATGATTA CAGG
              ||| ||||| |||
      AGT TTTGTATTAAT GTTC
              C A
GAM2254 LOC90593 3' ATGTCCTGTCTGACAGCTTTG 64201 AACA ATT_
      A      TCAAA TG ACAGGGACAT
              |||| | |||||
      AGTTT AC TGTCCCTGTA
              CG_ AGTC
GAM2254 LOC92181 3' TTGTAACATCATGTTTCTGA 68950 A _
              TCA AAACATGAT TACAG
              ||| ||||| |||

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			AGT TTTGTACTA ATGTT		
			C CA		
GAM2255	GPD1	3'	TCATGCCACCACATTTG 60398	C	C
			TAAATG GGTGGCAT GA		
			GTTTAC CCACCGTA CT		
			A _		
GAM2255	IL5RA	5'	TCGCATGGCCACCGCATTT 6906	AT__	
			AAATGCGGTGGC CGA		
			TTTACGCCACCG GCT		
			GTAC		
GAM2255	MYO1C	3'	TGCCGATGCCAAATATTTG 61873	CGG	A
			TAAATG TGGCATCG CA		
			GTTTAT ACCGTAGC GT		
			AA_ C		
GAM2255	C6orf37	3'	TGTCACACTGCATTTA 68097	GCATC	
			TAAATGCGGTG GACA		
			ATTTACGTAC CTGT		
			A____		
GAM2255	DNAJC6	3'	TTGCAGAACCACCGCATT 29498	CA GA	
			AATGCGGTGG TC CAA		
			TTACGCCACC AG GTT		
			A_ AC		
GAM2255	FLJ11210	3'	GTCGATGTGCATGCTTTTA 60319	T GTG	
			TAAA GCG GCATCGAC		
			ATTT CGT TGTAGCTG		
			T ACG		
GAM2255	FLJ12476	3'	TCGATCTTCTGCATTTA 43270	T C	
			TAAATGCGG GG ATCGA		
			ATTTACGTC TC TAGCT		
			T _		
GAM2255	KIAA1034	3'	TCGATGGCATCCGCATTTG 63134	_ G	
			TAAATGCGG TG CATCGA		
			GTTTACGCC AC GTAGCT		
			T G		
GAM2255	KIAA1987	3'	TCATGTAAGTGCATTTA 89391	G C	
			TAAATGCGGT GCAT GA		
			ATTTACGTCA TGTA CT		
			A _		
GAM2255	MGC16063	3'	TGTCCTGGCCACTGCATT 54929	ATC	
			AATGCGGTGGC GACA		

		TTACGTCACCG CTGT		
		GTC		
GAM2255	LOC147949 3'	TGTCAGATGTCCACATTGCA	79279	— — —
		TGCG GTGG CATC GACA		
		ACGT CACC GTAG CTGT		
		TA T A		
GAM2255	LOC150577 3'	GTCCTCACCGCATTTG	86258	CATC
		TAAATGCGGTGG GAC		
		GTTTACGCCACT CTG		
		C		
GAM2255	LOC158219 3'	TGTGTGTCACCACATT	82694	C CG
		AAATG GGTGGCAT ACA		
		TTTAC CCACTGTG TGT		
		A		
GAM2255	LOC202020 3'	TGTCTCACACATTTA	90605	C CATC
		TAAATG GGTGG GACA		
		ATTTAC CCACT CTGT		
		A		
GAM2255	LOC90826 5'	TGTCGATGCAGGTTTATTTG	64788	CGGTG
		TAAATG GCATCGACA		
		GTTTAT CGTAGCTGT		
		TTGGA		
GAM2255	LOC93587 3'	TTGTCTTTACCTGCATTTA	73042	— CATC
		TAAATGC GGTGG GACAA		
		ATTTACG CCATT CTGTT		
		T T		
GAM2256	A1BG 3'	CCAGGCTGGAGTGCAATGG	56281	C
		CCA TGCACTCCAGCCTGG		
		GGT ACGTGAGGTCGGACC		
		A		
GAM2256	A1BG 3'	CCAGGCTGGAGTGCAAGTG	56282	
		CACTGCACTCCAGCCTGG		
		GTGACGTGAGGTCGGACC		
GAM2256	AASS 3'	CCAGGCTGGAGTGCAAGTG	20458	
		CACTGCACTCCAGCCTGG		
		GTGACGTGAGGTCGGACC		
GAM2256	ACADSB 3'	CCAGGCTAGAGTGCAAGTG	9644	C
		CCACTGCACTC AGCCTGG		

			GGTGACGTGAG TCGGACC	
			A	
GAM2256	ADAMTS4	3'	CCAGGCTGGAGTGCAATGG 18754	C
			CCA TGC ACTCCAGCCTGG	
			GGT ACGTGAGGTCGGACC	
			A	
GAM2256	ADCY2	3'	TCAGGCCGGGTGCAGTGG 65653	T A
			CCACTGCAC CC GCCTGG	
			GGTGACGTG GG CGGACT	
			— C	
GAM2256	ADCY6	5'	CCAGGCTGGAGTGCAATGG 31587	C
			CCA TGC ACTCCAGCCTGG	
			GGT ACGTGAGGTCGGACC	
			A	
GAM2256	AHR	3'	CCAAACTGGAGTGCAGTGG 9673	CC
			CCACTGCACTCCAG TGG	
			GGTGACGTGAGGTC ACC	
			AA	
GAM2256	AIM1	3'	TCTCAGGCTGGAGTGCAGTGG 93470	C
			CCACTGCACTCCAGCCTGG GA	
			GGTGACGTGAGGTCGGACT CT	
			—	
GAM2256	ALDH1B1	3'	CCAGGCTGGAGTGCAGTGG 7318	
			CCACTGCACTCCAGCCTGG	
			GGTGACGTGAGGTCGGACC	
GAM2256	ALOX15	3'	CCAGGCTGGAGTGCAGTGG 8542	
			CCACTGCACTCCAGCCTGG	
			GGTGACGTGAGGTCGGACC	
GAM2256	APAF1	3'	CCAGGCTGGAGTGCAGTGG 8584	
			CCACTGCACTCCAGCCTGG	
			GGTGACGTGAGGTCGGACC	
GAM2256	APAF1	3'	CCAGGCTGGAGTGCAGTGG 8585	
			CCACTGCACTCCAGCCTGG	
			GGTGACGTGAGGTCGGACC	
GAM2256	APAF1	3'	CCAGGCTGGAGTGCAGTGG 25966	
			CCACTGCACTCCAGCCTGG	

GGTGACGTGAGGTCGGACC

GAM2256 APAF1 3' CCAGGCTGGAGTGCAGTGG 25967
CCACTGCACTCCAGCCTGG
|||||
GGTGACGTGAGGTCGGACC

GAM2256 APM1 3' CCAGGCTAGAGTGCAGTGG 17770 C
CCACTGCACTC AGCCTGG
|||||
GGTGACGTGAG TCGGACC

A

GAM2256 APM1 3' CCAGGCTGGAGTACAGTG 17771 C
CACTG ACTCCAGCCTGG
|||||
GTGAC TGAGGTCGGACC

A

GAM2256 APOL1 3' GTCGCCAAGTTGGAGTGCAATG 14743 C C
G CCA TGC ACTCCAGC TGGCGAC
|||
GGT ACGTGAGGTTG ACCGCTG

A A

GAM2256 APPL 3' CCAGGCTGGAGTGCAGTGG 24944
CCACTGCACTCCAGCCTGG
|||||
GGTGACGTGAGGTCGGACC

GAM2256 AQP6 3' CCAGGCTGGAGTGCAGTGG 9726
CCACTGCACTCCAGCCTGG
|||||
GGTGACGTGAGGTCGGACC

GAM2256 AQP6 3' CCAGGCTGGAGTGCAGTGG 54992
CCACTGCACTCCAGCCTGG
|||||
GGTGACGTGAGGTCGGACC

GAM2256 ARCN1 3' CCAGGCTGGAATGCAATGG 9747 C C
CCA TGCA TCCAGCCTGG
|||
GGT ACGT AGGTCGGACC

A A

GAM2256 ATF5 3' TCTCGGCCGGGTGCAGTGG 24825 T A T C
CCACTGCAC CC GCC GG GA
|||||
GGTGACGTG GG CGG CT CT

_ C _ _

GAM2256 ATP1B2 3' CCAGGCTGGAGTGCATGG 9830 C
CCA TGC ACTCCAGCCTGG
|||

		GGT ACGTGAGGTCGGACC		
		A		
GAM2256	ATP6V1A1	3' CCAGGCTGGAGTGCAATGG	9866	C
		CCA TGCCTCCAGCCTGG		
		GGT ACGTGAGGTCGGACC		
		A		
GAM2256	ATP7A	3' GCCCAGGCTGGAGTGCAAGTGG	5327	—
		CCACTGCACTCCAGCCTGG	C	
		GGTGACGTGAGGTCGGACC	G	
		C		
GAM2256	AXL	3' CCAGGCTGGAGTGCAAGTGG	9903	
		CCACTGCACTCCAGCCTGG		
		GGTGACGTGAGGTCGGACC		
GAM2256	AXL	3' CCAGGCTGGAGTGCAAGTGG	41880	
		CCACTGCACTCCAGCCTGG		
		GGTGACGTGAGGTCGGACC		
GAM2256	BCL10	3' CCAGGCTGGAGTGCAAGTGG	15368	
		CCACTGCACTCCAGCCTGG		
		GGTGACGTGAGGTCGGACC		
GAM2256	BDKRB1	5' CCAGACTGAAGTGCAAGTGG	7384	C C
		CCACTGCACT CAG CTGG		
		GGTGACGTGA GTC GACC		
		A A		
GAM2256	BDP1	3' CCAGGCAAGAGTGCAAGTGG	37963	CA
		CCACTGCACTC GCCTGG		
		GGTGACGTGAG CGGACC		
		AA		
GAM2256	BRIP1	3' CCAGGCTGGAATGCAGTGG	50208	C
		CCACTGCA TCCAGCCTGG		
		GGTGACGT AGGTCGGACC		
		A		
GAM2256	C7	3' CCAGGCTGGAGCGCAGTGG	6982	A
		CCACTGC CTCCAGCCTGG		
		GGTGACG GAGGTCGGACC		
		C		
GAM2256	CASP10	3' CCAGACTGGAGTGCAAGG	53219	A C
		CC CTGCACTCCAG CTGG		

			GG GACGTGAGGTC GACC		
			— A		
GAM2256	CASP10	3'	CCAGACTGGAGTGCAGGG 53249	A	C
			CC CTGCACTCCAG CTGG		
			GG GACGTGAGGTC GACC		
			— A		
GAM2256	CASP2	3'	CCAGGCTGGAGGGCAGTGG 53287	A	
			CCACTGC CTCCAGCCTGG		
			GGTGACG GAGGTCGGACC		
			G		
GAM2256	CASP2	3'	CCAGGCTGGAGGGCAGTGG 53303	A	
			CCACTGC CTCCAGCCTGG		
			GGTGACG GAGGTCGGACC		
			G		
GAM2256	CASP2	3'	CCAGGCTGGAGGGCAGTGG 53324	A	
			CCACTGC CTCCAGCCTGG		
			GGTGACG GAGGTCGGACC		
			G		
GAM2256	CASP2	3'	CCAGGCTGGAGGGCAGTGG 8706	A	
			CCACTGC CTCCAGCCTGG		
			GGTGACG GAGGTCGGACC		
			G		
GAM2256	CASP8	3'	CCAGGCTGGAGTGCAGTGG 8747		
			CCACTGCACTCCAGCCTGG		
			GGTGACGTGAGGTCGGACC		
GAM2256	CASP8	3'	CCAGGCTGGAGTGCAGTGG 54071		
			CCACTGCACTCCAGCCTGG		
			GGTGACGTGAGGTCGGACC		
GAM2256	CASP8	3'	CCAGGCTGGAGTGCAGTGG 54096		
			CCACTGCACTCCAGCCTGG		
			GGTGACGTGAGGTCGGACC		
GAM2256	CASP8	3'	CCAGGCTGGAGTGCAGTGG 54112		
			CCACTGCACTCCAGCCTGG		
			GGTGACGTGAGGTCGGACC		
GAM2256	CCNF	3'	CCGGCTGGAGTGCAGTGG 10071		T
			CCACTGCACTCCAGCC GG		

GGTGACGTGAGGTCGG CC

GAM2256 CDC6 3' CCAGGCTGGAGTGCAATGG 8818 C
CCA TGC ACTCCAGCCTGG
||| |||||
GGT ACGTGAGGTCGGACC
A

GAM2256 CDH1 3' CCAGGCTGGAGTGCAGTGG 16401
CCACTGCACTCCAGCCTGG
|||||
GGTGACGTGAGGTCGGACC

GAM2256 CDH17 3' CCAGGCTGGAGTACAGTGG 15782 C
CCACTG ACTCCAGCCTGG
|||||
GGTGAC TGAGGTCGGACC
A

GAM2256 CLECSF12 3' CCAGGCTGGAGTGCAACGG 77205 AC
CC TGC ACTCCAGCCTGG
|| |||||
GG ACGTGAGGTCGGACC
CA

GAM2256 CLECSF12 3' CCAGGCTGGAGTGCAGTGG 77206
CCACTGCACTCCAGCCTGG
|||||
GGTGACGTGAGGTCGGACC

GAM2256 CMAR 5' CCAGGCTGGAGTGCAGTG 19029
CACTGCACTCCAGCCTGG
|||||
GTGACGTGAGGTCGGACC

GAM2256 CNGA1 5' CCAGGCTGGAGTGCAGTGG 60236
CCACTGCACTCCAGCCTGG
|||||
GGTGACGTGAGGTCGGACC

GAM2256 CNN2 3' CCAGGCTGGAGTGCAGTGG 16459
CCACTGCACTCCAGCCTGG
|||||
GGTGACGTGAGGTCGGACC

GAM2256 CNP 3' CCAAGCTGGAGTGCAGTGG 53617 C
CCACTGCACTCCAGC TGG
||||| |||
GGTGACGTGAGGTCG ACC
A

GAM2256 CORO2B 5' CCAAGCTGGAGTGCAGTGG 65172 C
CCACTGCACTCCAGC TGG
||||| |||


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GGTGACGTGAGGTCG ACC
      A
GAM2256 COX15  3' CCAGGCTGGAGTACAATGG  55280  C C
      CCA TG ACTCCAGCCTGG
      ||| || |||||
      GGT AC TGAGGTCGGACC
      A A
GAM2256 CPS1   3' CCAGGCTGGAGTGCAGTGG  10287
      CCACTGCACTCCAGCCTGG
      |||||
      GGTGACGTGAGGTCGGACC

GAM2256 CR1    3' CCAGGCTGGAGTGCAGTGG  6940
      CCACTGCACTCCAGCCTGG
      |||||
      GGTGACGTGAGGTCGGACC

GAM2256 CRTAP  3' CCAGGCTGGAGTGCAATGG  22075  C
      CCA TGC ACTCCAGCCTGG
      ||| |||||
      GGT ACGTGAGGTCGGACC
      A
GAM2256 CSNK2A2 5' CCAGGCTGGAGTGCAGTGG  10319
      CCACTGCACTCCAGCCTGG
      |||||
      GGTGACGTGAGGTCGGACC

GAM2256 CST    5' AGAGCTGGAGTGCAGCGG  17962  A  _
      CC CTGCACTCCAGC CT
      || ||||| ||
      GG GACGTGAGGTCG GA
      C      A
GAM2256 CTF1   3' CCAGGCTGGGGTGCAGTGG  9010
      CCACTGCACTCCAGCCTGG
      |||||
      GGTGACGTGGGGTCGGACC

GAM2256 CTSB   5' AGCGCTGGGCTGGTGTGCAGTG 65359  T  TG A
      G      CCACTGCAC CCAGCC GCG CT
      ||||| ||||| ||| ||
      GGTGACGTG GGTCGG CGC GA
      T  GT  _
GAM2256 CXCL16 3' CCAGGCTGGAGTGCAGTGG  42163
      CCACTGCACTCCAGCCTGG
      |||||
      GGTGACGTGAGGTCGGACC

GAM2256 CYP1A2 3' CCAGGCTGGAGTGCAGTGG  7507
      CCACTGCACTCCAGCCTGG
      |||||

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GGTGACGTGAGGTCGGACC

GAM2256 CYP1A2 3' CCAGGTTGGAGTGCAGTGG 7508
CCACTGCACTCCAGCCTGG
|||||||
GGTGACGTGAGGTTGGACC

GAM2256 CYP2B6 3' CCAGGCTGGAGTGCAGTGG 7553
CCACTGCACTCCAGCCTGG
|||||||
GGTGACGTGAGGTCGGACC

GAM2256 CYP2B6 3' CCAGGCTGGAGTGCTATGG 7554 CT
CCA GCACTCCAGCCTGG
||| |||||
GGT CGTGAGGTCGGACC
AT

GAM2256 CYP4F3 3' CCAGGCTGGAGTGCGGTGG 8002
CCACTGCACTCCAGCCTGG
|||||||
GGTGGCGTGAGGTCGGACC

GAM2256 CYP51 3' CCAGGCTGGAGTGCAGTGG 7613
CCACTGCACTCCAGCCTGG
|||||||
GGTGACGTGAGGTCGGACC

GAM2256 CYP8B1 3' CCAGGCTGCAGTGCAGTGG 16534 C
CCACTGCACT CAGCCTGG
||||||| |||||
GGTGACGTGA GTCGGACC
C

GAM2256 DFFB 3' CCAGGCTGGAGTGTAAGTGG 88763
CCACTGCACTCCAGCCTGG
|||||||
GGTGATGTGAGGTCGGACC

GAM2256 DFFB 3' TCAGGCTGGAGTGCAGTG 88787
CACTGCACTCCAGCCTGG
|||||||
GTGACGTGAGGTCGGACT

GAM2256 DISC1 3' CCAAGTTGGAGTGCAGTGG 38503 C
CCACTGCACTCCAGC TGG
||||||| |||
GGTGACGTGAGGTTG ACC
A

GAM2256 DNAH11 3' GCCTCTGCTGGAGTGCAGTG 15023 CT_
CACTGCACTCCAGC GGC
||||||| |||

			GTGACGTGAGGTCG CCG	
			TCT	
GAM2256	DSC3	3'	CAGGCTGGAGTGCAGTGG 10435	
			CCACTGCACTCCAGCCTG	
			GGTGACGTGAGGTCGGAC	
GAM2256	DSC3	3'	CAGGCTGGAGTGCAGTGG 44615	
			CCACTGCACTCCAGCCTG	
			GGTGACGTGAGGTCGGAC	
GAM2256	DYRK1A	5'	CCGGCTGAAGTGCAGTGG 56076	C T
			CCACTGCACT CAGCC GG	
			GGTGACGTGA GTCGG CC	
			A _	
GAM2256	EDG8	3'	CCAGGCTGGAGTGCAATGG 79146	C
			CCA TGCCTCCAGCCTGG	
			GGT ACGTGAGGTCGGACC	
			A	
GAM2256	EHD1	3'	AGTCACTGTTGAAGTTGCAGTG 70217	_ C CT C
	G		CCACTGCA CT CAGC GG GACT	
			GGTGACGT GA GTTG TC CTGA	
			T A _ A	
GAM2256	EHD2	3'	CCAGGCTGGAGTGCAGTGG 28219	
			CCACTGCACTCCAGCCTGG	
			GGTGACGTGAGGTCGGACC	
GAM2256	EIF2S3	3'	CCAGGCTGGAGTGCAGTGG 9205	
			CCACTGCACTCCAGCCTGG	
			GGTGACGTGAGGTCGGACC	
GAM2256	ELMO3	3'	GCCATGAAGGGCAGTGG 45579	A C GCC
			CCACTGC CT CA TGGC	
			GGTGACG GA GT ACCG	
			G A _	
GAM2256	ENDOGL1	3'	CCAGGCTGGAGTGCGGTGG 18821	
			CCACTGCACTCCAGCCTGG	
			GGTGGCGTGAGGTCGGACC	
GAM2256	F2RL2	3'	CCAGACTGGCGTGCAGTGG 15894	T C
			CCACTGCAC CCAG CTGG	

		GGTGACGTG GGTC GACC	
		C A	
GAM2256 F2RL3	3'	CCAGGCTGGAGTGCAGTGG 15508	
		CCACTGCACTCCAGCCTGG	
		GGTGACGTGAGGTCGGACC	
GAM2256 FABP2	3'	TCAGGCTGGAATGTAGTGG 5536	C
		CCACTGCA TCCAGCCTGG	
		GGTGATGT AGGTCGGACT	
		A	
GAM2256 FANCE	3'	CCAGGCTGGAGTGCAGTGG 41897	
		CACTGCACTCCAGCCTGG	
		GTGACGTGAGGTCGGACC	
GAM2256 FANCF	3'	CCAGTCTGGAGTGCAGTGG 42976	C
		CCACTGCACTCCAG CTGG	
		GGTGACGTGAGGTC GACC	
		T	
GAM2256 FCAR	3'	CCAGGCTGAAGTGCAGTGG 56567	C
		CCACTGCACT CAGCCTGG	
		GGTGACGTGA GTCGGACC	
		A	
GAM2256 FCAR	3'	CCAGGCTGAAGTGCAGTGG 56591	C
		CCACTGCACT CAGCCTGG	
		GGTGACGTGA GTCGGACC	
		A	
GAM2256 FCAR	3'	CCAGGCTGAAGTGCAGTGG 56603	C
		CCACTGCACT CAGCCTGG	
		GGTGACGTGA GTCGGACC	
		A	
GAM2256 FCAR	3'	CCAGGCTGAAGTGCAGTGG 56615	C
		CCACTGCACT CAGCCTGG	
		GGTGACGTGA GTCGGACC	
		A	
GAM2256 FCAR	3'	CCAGGCTGGAGTGCAGTGG 10586	
		CCACTGCACTCCAGCCTGG	
		GGTGACGTGAGGTCGGACC	
GAM2256 FCGR2A	3'	CCAGGCTGGAGTGCAGTGG 80025	
		CCACTGCACTCCAGCCTGG	

GGTGACGTGAGGTCGGACC

GAM2256 FCRH1 3' TCAATCTGGAATGCAGTGG 54734 C CC
CCACTGCA TCCAG TGG
||||||| ||||| |||
GGTGACGT AGGTC ACT
A TA

GAM2256 FEZ1 3' CCAGGCTGGAGTGCAATGG 42868 C
CCA TGCCTCCAGCCTGG
||| |||||||||
GGT ACGTGAGGTCGGACC
A

GAM2256 FGF2 3' CTAGGCCGGGTGCAGTGG 10618 T A
CCACTGCAC CC GCCTGG
||||||| || |||||
GGTGACGTG GG CGGATC
_ C

GAM2256 FGF5 3' GTCACCAGGCTGGAGTGCAGTG 53668 C
G CCACTGCACTCCAGCCTGG GAC
||||||||||| |||
GGTGACGTGAGGTCGGACC CTG
A

GAM2256 FGF5 3' GTCACCAGGCTGGAGTGCAGTG 16764 C
G CCACTGCACTCCAGCCTGG GAC
||||||||||| |||
GGTGACGTGAGGTCGGACC CTG
A

GAM2256 FHL2 5' CCAGGCTGGAGTGCAGTGG 9365
CCACTGCACTCCAGCCTGG
|||||||||||
GGTGACGTGAGGTCGGACC

GAM2256 FSHPRH1 5' CCAGGCTGGAGTGCAGTGG 23065
CCACTGCACTCCAGCCTGG
|||||||||||
GGTGACGTGAGGTCGGACC

GAM2256 FUT1 3' CCAGGCTGGAGTGCAGTGG 5587
CCACTGCACTCCAGCCTGG
|||||||||||
GGTGACGTGAGGTCGGACC

GAM2256 FUT1 3' GCCCAGGCCAGAGTGCAGTGG 5599 CA _
CCACTGCACTC GCCTGG C
||||||| ||||| |
GGTGACGTGAG CGGACC G
AC C

GAM2256 G1P3 3' CCAGGCTAGAGTGCAGTGG 43453 C
CCACTGCACTC AGCCTGG
||||||| |||||

			GGTGACGTGAG TCGGACC	
			A	
GAM2256	G1P3	3'	CCAGGCTAGAGTGCAGTGG 43457	C
			CCACTGCACTC AGCCTGG	
			GGTGACGTGAG TCGGACC	
			A	
GAM2256	G1P3	3'	CCAGGCTAGAGTGCAGTGG 10742	C
			CCACTGCACTC AGCCTGG	
			GGTGACGTGAG TCGGACC	
			A	
GAM2256	G6PC	3'	CCAGGCTGGAGTGGAGTGG 5656	G
			CCACT CACTCCAGCCTGG	
			GGTGA GTGAGGTCGGACC	
			G	
GAM2256	GHR	3'	CCAGGCTAGAGTGCAGTGG 5696	C
			CCACTGCACTC AGCCTGG	
			GGTGGCGTGAG TCGGACC	
			A	
GAM2256	GM2A	3'	GTCACCAGGCTGGAGTGCAGTG 68388	C
	G		CCACTGCACTCCAGCCTGG GAC	
			GGTGACGTGAGGTCGGACC CTG	
			A	
GAM2256	GNE	3'	CCAGGCTGGAGTGCAGTGG 19663	
			CCACTGCACTCCAGCCTGG	
			GGTGACGTGAGGTCGGACC	
GAM2256	GPR56	5'	CAGGCTGGAGTGCAGTGG 20269	
			CCACTGCACTCCAGCCTG	
			GGTGACGTGAGGTCGGAC	
GAM2256	GPR81	3'	CCAGGCTGGAGTGCAGTGG 51740	
			CCACTGCACTCCAGCCTGG	
			GGTGACGTGAGGTCGGACC	
GAM2256	GRAF	3'	CCAGGCTGGAGTGCAGTGG 31225	
			CCACTGCACTCCAGCCTGG	
			GGTGACGTGAGGTCGGACC	
GAM2256	GRAF	3'	TGCCATGGCCGGGTGCAGTGG 31253	T A _
			CCACTGCAC CC GCC TGGCG	

			GGTGACGTG GG CGG ACCGT	
			— C T	
GAM2256	GRINL1A	3'	CCAGGCTGGAGTGCAGTGG 70059	
			CCACTGCACTCCAGCCTGG	
			GGTGACGTGAGGTCGGACC	
GAM2256	GRM6	3'	TCTTAGGCTGGAGTGCAGTGG 7774	C
			CCACTGCACTCCAGCCTGG GA	
			GGTGACGTGAGGTCGGATT CT	
GAM2256	HCS	3'	CCAGGCTGAGTACAGTGG 38972	C C
			CCACTG ACTC AGCCTGG	
			GGTGAC TGAG TCGGACC	
			A —	
GAM2256	HCS	3'	CCAGGCTGGAGTGCAATGG 38973	C
			CCA TGCCTCCAGCCTGG	
			GGT ACGTGAGGTCGGACC	
			A	
GAM2256	HLCS	5'	CCAGGCTGGAGTGCAGTGG 6409	
			CCACTGCACTCCAGCCTGG	
			GGTGACGTGAGGTCGGACC	
GAM2256	HMG20A	3'	CCAGGCTGGAGTGCGGTGG 37062	
			CCACTGCACTCCAGCCTGG	
			GGTGGCGTGAGGTCGGACC	
GAM2256	HTR1D	3'	TCGCCAGGCTGGAGTGTAGTGG 7849	
			CCACTGCACTCCAGCCTGGCGA	
			GGTGATGTGAGGTCGGACCGCT	
GAM2256	HTR1E	5'	AGTCGCCCAGGCTGGAGTGCAG 7857	—
			CTGCACTCCAGCCTGG CGACT	
			GACGTGAGGTCGGACC GCTGA	
			C	
GAM2256	HUNK	3'	CCAGGCTGGAGTGCAGTGG 28181	
			CCACTGCACTCCAGCCTGG	
			GGTGACGTGAGGTCGGACC	
GAM2256	HUS1	3'	CCAGACTGGAGTGCAGTG 92737	C
			CACTGCACTCCAG CTGG	

			GTGACGTGAGGTC GACC	
			A	
GAM2256	HYAL4	5'	CCAGGCTGGAGTGTAGTGG 25366	
			CCACTGCACTCCAGCCTGG	
			GGTGATGTGAGGTCGGACC	
GAM2256	ICAM1	3'	CCAGGCTGGAGTGCAGTGG 72034	
			CCACTGCACTCCAGCCTGG	
			GGTGACGTGAGGTCGGACC	
GAM2256	IGF1	3'	CCAGGCTGGAGTGCAGTGG 7065	
			CCACTGCACTCCAGCCTGG	
			GGTGACGTGAGGTCGGACC	
GAM2256	IHPK2	3'	GCCTGGAGCTGATGTGCAGTGG 62518	TC _ _
			CCACTGCAC CAGC CT GGC	
			GGTGACGTG GTCG GG CCG	
			TA A T	
GAM2256	INMT	3'	CCAGGCTGGAGTGCAGTGG 23211	
			CCACTGCACTCCAGCCTGG	
			GGTGACGTGAGGTCGGACC	
GAM2256	ITGAM	3'	CCAGGCTGGAGTGCAATGG 72306	C
			CCA TGCACTCCAGCCTGG	
			GGT ACGTGAGGTCGGACC	
			A	
GAM2256	JAG2	3'	TGTCAGGCTGAAAACAATGG 11098	C CACTC
			CCA TG CAGCCTGGCG	
			GGT AC GTCGGA CTGT	
			A AAAA_	
GAM2256	JRK	3'	CCAGGCTGGAGTGAAGTGG 87821	G
			CCACT CACTCCAGCCTGG	
			GGTGA GTGAGGTCGGACC	
			A	
GAM2256	JRK	3'	TCAAGCTGGGTGCAGTGG 87835	T C
			CCACTGCAC CCAGC TGG	
			GGTGACGTG GGTCG ACT	
			_ A	
GAM2256	KLRD1	3'	CCAGGCTGGAGCATAGTGG 11212	CA
			CCACTG CTCCAGCCTGG	

			GGTGAT GAGGTCGGACC		
			AC		
GAM2256	KLRD1	3'	CCAGGCTGGAGCATAGTGG	24706	CA
			CCACTG CTCCAGCCTGG		
			GGTGAT GAGGTCGGACC		
			AC		
GAM2256	KMO	3'	CCAGGCTGGAGTGCAGTGG	14840	
			CCACTGCACTCCAGCCTGG		
			GGTGACGTGAGGTCGGACC		
GAM2256	LILRA3	3'	GTCACCAGGCTGGAATGCAGTG	97021	C C
	G		CCACTGCA TCCAGCCTGG GAC		
			GGTGACGT AGGTCGGACC CTG		
			A A		
GAM2256	LLGL1	3'	CCAGGCTGGAGTGCAGTGG	67416	
			CCACTGCACTCCAGCCTGG		
			GGTGACGTGAGGTCGGACC		
GAM2256	LNK	3'	CCGGGCTGGAGTGCAGTGG	19640	
			CCACTGCACTCCAGCCTGG		
			GGTGACGTGAGGTCGGGCC		
GAM2256	LTB4R	5'	TCAGGCTGGAGTGCAGTGG	7474	
			CCACTGCACTCCAGCCTGG		
			GGTGACGTGAGGTCGGACT		
GAM2256	LYZ	3'	CCAGGCTGGAGTGCAGTGG	5893	
			CCACTGCACTCCAGCCTGG		
			GGTGACGTGAGGTCGGACC		
GAM2256	LZTS1	3'	CCAGGCTGGAGTGCAGTGG	41026	
			CCACTGCACTCCAGCCTGG		
			GGTGACGTGAGGTCGGACC		
GAM2256	MAK	3'	CCAGGCTGGAGTGCAGTGG	20943	
			CCACTGCACTCCAGCCTGG		
			GGTGACGTGAGGTCGGACC		
GAM2256	MAP2K1	3'	TGCCAGGCTGAATTACAGTG	12319	CACTC
			CACTG CAGCCTGGCG		

			GTGAC GTCGGACCGT	
			ATTA	
GAM2256	MDM2	3'	CCAGGCTGGAGTGCAGTGG 11492	
			CCACTGCACTCCAGCCTGG	
			GGTGACGTGAGGTCGGACC	
GAM2256	MDM2	3'	CCAGGCTGGAGTGCAGTGG 23457	
			CCACTGCACTCCAGCCTGG	
			GGTGACGTGAGGTCGGACC	
GAM2256	MDM2	3'	CCAGGCTGGAGTGCAGTGG 23470	
			CCACTGCACTCCAGCCTGG	
			GGTGACGTGAGGTCGGACC	
GAM2256	MDM2	3'	CCAGGCTGGAGTGCAGTGG 23483	
			CCACTGCACTCCAGCCTGG	
			GGTGACGTGAGGTCGGACC	
GAM2256	MDM2	3'	CCAGGCTGGAGTGCAGTGG 23496	
			CCACTGCACTCCAGCCTGG	
			GGTGACGTGAGGTCGGACC	
GAM2256	MDM4	3'	CCAGGCTGAAGTGCAGTG 11507	C
			CACTGCACT CAGCCTGG	
			GTGACGTGA GTCGGACC	
			A	
GAM2256	MEF2A	5'	CCAGGCTGAAGTGCAGTGG 19995	C
			CCACTGCACT CAGCCTGG	
			GGTGACGTGA GTCGGACC	
			A	
GAM2256	MEFV	3'	CCAGGCTGGAGTGCAGTGG 5933	
			CCACTGCACTCCAGCCTGG	
			GGTGACGTGAGGTCGGACC	
GAM2256	MEFV	3'	CCAGGCTGGAGTGCAGTGG 5934	
			CCACTGCACTCCAGCCTGG	
			GGTGACGTGAGGTCGGACC	
GAM2256	MHC2TA	3'	CCACGCTGGAGTGCAGTG 5971	C
			CACTGCACTCCAGC TGG	

			GTGACGTGAGGTCG ACC		
			C		
GAM2256	MHC2TA	3'	CCAGGCTGGCGTGCAGTGG	5972	T
			CCACTGCAC CCAGCCTGG		
			GGTGACGTG GGTCGGACC		
			C		
GAM2256	MLANA	3'	CCAGGCTGGAGTGCAATGG	19760	C
			CCA TGCACTCCAGCCTGG		
			GGT ACGTGAGGTCGGACC		
			A		
GAM2256	MPL	3'	CCAGACTGGAGTGCAGTGG	19346	C
			CCACTGCACTCCAG CTGG		
			GGTGACGTGAGGTC GACC		
			A		
GAM2256	MPL	3'	CCAGGCTGCAGTGCAATGG	19347	C C
			CCA TGCACT CAGCCTGG		
			GGT ACGTGA GTCGGACC		
			A C		
GAM2256	MTR	3'	CCAGGCTGGAGTGCAGGG	6014	A
			CC CTGCACTCCAGCCTGG		
			GG GACGTGAGGTCGGACC		
			—		
GAM2256	NCOA6	5'	CCGAGGCTGGAGTGCAGTGG	26833	—
			CCACTGCACTCCAGCCT GG		
			GGTGACGTGAGGTCGGA CC		
			G		
GAM2256	NCOA6IP	3'	CCAGGCTGGAGTGCAGTG	46151	
			CACTGCACTCCAGCCTGG		
			GTGACGTGAGGTCGGACC		
GAM2256	NDRG3	3'	CCAGGCTGGAGTGCAATGG	50119	C
			CCA TGCACTCCAGCCTGG		
			GGT ACGTGAGGTCGGACC		
			A		
GAM2256	NEU3	5'	CCAGGCTGGAGTGCAGTGG	22828	
			CCACTGCACTCCAGCCTGG		
			GGTGACGTGAGGTCGGACC		
GAM2256	NONO	3'	CCAGGCTGGAGGTAGTGG	82885	
			CCACTGCACTCCAGCCTGG		

GGTGATGTGAGGTCGGACC

GAM2256 NPR2L 3' CCAGGCTGGAATACAGTGG 22593 CAC
CCACTG TCCAGCCTGG
||||| ||||||||
GGTGAC AGGTCGGACC
ATA

GAM2256 NQO1 3' CCAGGCTGGAGTGCAGTGG 8045
CCACTGCACTCCAGCCTGG
||||||||||||||
GGTGACGTGAGGTCGGACC

GAM2256 NT5C2 5' CCAGGCTGGAGTACAGTG 25259 C
CACTG ACTCCAGCCTGG
||||| ||||||||
GTGAC TGAGGTCGGACC
A

GAM2256 ORC1L 3' CCAGGCTGGAGTGCAGTGG 15981
CCACTGCACTCCAGCCTGG
||||||||||||||
GGTGACGTGAGGTCGGACC

GAM2256 PAICS 3' CCAGGCTGGAGTGCAGTGG 22258
CCACTGCACTCCAGCCTGG
||||||||||||||
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GAM2256 PCDHA9 3' CCAGGCTGGAGTACAGTGG 26615 C
CCACTG ACTCCAGCCTGG
||||| ||||||||
GGTGAC TGAGGTCGGACC
A

GAM2256 PCDHA9 3' CCAGGCTGGAGTGCAGTGG 26616
CCACTGCACTCCAGCCTGG
||||||||||||||
GGTGACGTGAGGTCGGACC

GAM2256 PCDHB11 3' CCTGGCTGGAGTGCAATGG 38921 C T
CCA TGCACTCCAGCC GG
||| ||||||||| ||
GGT ACGTGAGGTCGG CC
A T

GAM2256 PCDHB16 3' CCAGGCTGGAGTGCAGTGG 40904
CCACTGCACTCCAGCCTGG
||||||||||||||
GGTGACGTGAGGTCGGACC

GAM2256 PCDHB9 3' CCAGGCTGGAGTGCAGTGG 39441
CCACTGCACTCCAGCCTGG
||||||||||||||

GGTGACGTGAGGTCGGACC

GAM2256 PDE6B 3' CCAGGCTGGAGTGCCGTGG 6072 T
CCAC GCACTCCAGCCTGG
|||||
GGTG CGTGAGGTCGGACC
C

GAM2256 PDZK1 5' CCAGGCTGGAGTGCAGTGG 12033
CCACTGCACTCCAGCCTGG
|||||
GGTGACGTGAGGTCGGACC

GAM2256 PEA15 5' GCCGGGTGGAGTGAGCGG 15010 A G G
CC CT CACTCCA CCTGGC
|| |||
GG GA GTGAGGT GGGCCG
C _ _

GAM2256 PER2 3' CCAGGCTGGAGTGCAGTGG 43346
CCACTGCACTCCAGCCTGG
|||||
GGTGACGTGAGGTCGGACC

GAM2256 PIGR 3' CCAGGCTGGAGTGCAGTGG 72991
CCACTGCACTCCAGCCTGG
|||||
GGTGACGTGAGGTCGGACC

GAM2256 PIK3C2B 3' GTCGCCAGGCTGGAGTG TAGTG 12110
G CCACTGCACTCCAGCCTGGCGAC
|||||
GGTGATGTGAGGTCGGACCGCTG

GAM2256 PIK3CD 3' CCAGGCTGGAGTGCAGTGG 18487
CCACTGCACTCCAGCCTGG
|||||
GGTGACGTGAGGTCGGACC

GAM2256 PKNOX1 3' CCAGGCTGGAGGGCAATGG 17099 C A
CCA TGC CTCCAGCCTGG
||| |||
GGT ACG GAGGTCGGACC
A G

GAM2256 PMCHL1 3' CCAGGCTGGAGTGCAATGG 49913 C
CCA TGCACTCCAGCCTGG
||| |||
GGT ACGTGAGGTCGGACC
A

GAM2256 PON1 3' CCAGGCTGGAGTGCAGTGG 6534
CCACTGCACTCCAGCCTGG
|||||

GGTGACGTGAGGTCGGACC

GAM2256 POU2AF1 3' CCAGGCTGGAGTACAATGG 21734 C C
CCA TG ACTCCAGCCTGG
||| || |||||
GGT AC TGAGGTCGGACC
A A

GAM2256 PPEF2 3' CCAGGCTGGAGTGCATTGG 21773 C
CCA TGCACTCCAGCCTGG
||| |||||
GGT ACGTGAGGTCGGACC
T

GAM2256 PPID 3' CCAGGCTGGAGTGCGGTGG 88822
CCACTGCACTCCAGCCTGG
|||||
GGTGGCGTGAGGTCGGACC

GAM2256 PPP1R12B 3' CCAGGCTGGAGTGCAGTGG 50381
CCACTGCACTCCAGCCTGG
|||||
GGTGACGTGAGGTCGGACC

GAM2256 PRKR 3' CCAGGCTGGAGTGCAATG 12344 C
CA TGCACTCCAGCCTGG
|| |||||
GT ACGTGAGGTCGGACC
A

GAM2256 PRKWNK3 3' CCAGGTTGGAGTGCAGTGG 62229
CCACTGCACTCCAGCCTGG
|||||
GGTGACGTGAGGTTGGACC

GAM2256 PRKY 3' CTAGGCTAGGTGCAGTGG 12372 CC
CCACTGCACT AGCCTGG
||||| |||||
GGTGACGTGG TCGGATC
A_

GAM2256 PSEN1 5' AGCCGTCTGAACTGGAGTGGAG 24618 G CCT_ A
T ACT CACTCCAG GGCG CT
||| ||||| ||| ||
TGA GTGAGGTC CTGC GA
G AAGT C

GAM2256 PSMB2 3' GCCCAGGCTGGAGTGCTGTGG 12475 T _
CCAC GCACTCCAGCCTGG C
||| |||||
GGTG CGTGAGGTCGGACC G
T C

GAM2256 PSMD9 3' CCAGGCTGGAGTGCAGTG 12522
CACTGCACTCCAGCCTGG
|||||

GTGACGTGAGGTCGGACC

GAM2256	PTGES	3'	CCAAGCTGGAGTGAAGTGG	18058	G	C
			CCACT CACTCCAGC TGG			
			GGTGA GTGAGGTCG ACC			
			A A			
GAM2256	PTGIS	3'	CCAGGCTAGAGTGCAGTGG	8199		C
			CCACTGCACTC AGCCTGG			
			GGTGACGTGAG TCGGACC			
			A			
GAM2256	PTGIS	3'	CCAGGCTGGAGTGCAATGG	8200	C	
			CCA TGC ACTCCAGCCTGG			
			GGT ACGTGAGGTCGGACC			
			A			
GAM2256	RAB36	3'	CCAGGCTGGAGTGCAATGG	18158	C	
			CCA TGC ACTCCAGCCTGG			
			GGT ACGTGAGGTCGGACC			
			A			
GAM2256	RAB36	3'	CCAGGCTGGAGTGCAATGG	18159	C	
			CCA TGC ACTCCAGCCTGG			
			GGT ACGTGAGGTCGGACC			
			A			
GAM2256	RABL2A	3'	GTCGCCAGGCTGGAGTGCAGTG	26414		
	G		CCACTGCACTCCAGCCTGGCGAC			
			GGTGACGTGAGGTCGGACCGCTG			
GAM2256	RABL2B	3'	GTCGCCAGGCTGGAGTGCAGTG	23985		
	G		CCACTGCACTCCAGCCTGGCGAC			
			GGTGACGTGAGGTCGGACCGCTG			
GAM2256	RAI3	3'	CCAGGCTTGAGTGCAGTGG	15618		C
			CCACTGCACTC AGCCTGG			
			GGTGACGTGAG TCGGACC			
			T			
GAM2256	RHD	3'	CCAGGCTGGAGTGCAGTG	32819		
			CACTGCACTCCAGCCTGG			
			GTGACGTGAGGTCGGACC			
GAM2256	RHD	3'	CCAGGCTGGAGTGCAGTG	33139		
			CACTGCACTCCAGCCTGG			

GTGACGTGAGGTCGGACC

GAM2256	RP2	3'	CCAAGCTGGAGTGCAATGG	23598	C	C
			CCA TGC ACTCCAGC TGG			
			GGT ACGTGAGGTCG ACC			
			A A			
GAM2256	RPH3AL	3'	CCAGGCTGGGGTGCAGTGG	23732		
			CCACTGCACTCCAGCCTGG			
			GGTGACGTGGGGTCGGACC			
GAM2256	RPP30	3'	CCAGGCTGGAGTGCAGTGG	22194		
			CCACTGCACTCCAGCCTGG			
			GGTGACGTGAGGTCGGACC			
GAM2256	RPP30	3'	TCAGGCTGGAGTACAGTGG	22208	C	
			CCACTG ACTCCAGCCTGG			
			GGTGAC TGAGGTCGGA CT			
			A			
GAM2256	SAS	3'	CCAGGCTGGAGTGCAATGG	21098	C	
			CCA TGC ACTCCAGCCTGG			
			GGT ACGTGAGGTCGGACC			
			A			
GAM2256	SEDL	3'	CAGGCTGGAGTGCAGTGG	28080		
			CCACTGCACTCCAGCCTG			
			GGTGACGTGAGGTCGGAC			
GAM2256	SEDL	3'	CAGGCTGTAGTGCAGTGG	28081	C	
			CCACTGCACT CAGCCTG			
			GGTGACGTGA GTCGGAC			
			T			
GAM2256	SEDL	3'	CCAGGCTGGAGTGCAATGG	28084	C	
			CCA TGC ACTCCAGCCTGG			
			GGT ACGTGAGGTCGGACC			
			A			
GAM2256	SEDL	3'	CCAGGCTGGAGTGCAGTGG	28087		
			CCACTGCACTCCAGCCTGG			
			GGTGACGTGAGGTCGGACC			
GAM2256	SEPN1	3'	CCAGGCTGGAGTGCTATGG	66965	CT	
			CCA GCACTCCAGCCTGG			

GGT CGTGAGGTCGGACC
AT
GAM2256 SERPINB9 3' CCAGGCTGGAGTGCAGTGG 16012
CCACTGCACTCCAGCCTGG
|||||||
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GAM2256 SERPINB9 3' CCAGGCTGGAGTGTAGTGG 16013
CCACTGCACTCCAGCCTGG
|||||||
GGTGATGTGAGGTCGGACC

GAM2256 SH3BP2 3' CCAGGCTGGAGTGCAATG 13055 C
CA TGCCTCCAGCCTGG
|| |||||
GT ACGTGAGGTCGGACC
A
GAM2256 SH3BP2 3' GCCGAGGCTGGAGCACAGGG 13075 A CA _
CC CTG CTCCAGCCT GGC
|| || ||||| ||
GG GAC GAGGTCGGA CCG
_ AC G
GAM2256 SHOX 3' CCAGGCTGGAGCACACTGG 23517 C CA
CCA TG CTCCAGCCTGG
|| || |||||
GGT AC GAGGTCGGACC
C AC
GAM2256 SIL 3' GCCCAGGCTGGAGTGCAATGG 13158 C _
CCA TGCCTCCAGCCTGG C
|| ||||| |
GGT ACGTGAGGTCGGACC G
A C
GAM2256 SLA2 3' CCATGCTGGAGTGCAATGG 50884 C C
CCA TGCCTCCAGC TGG
|| ||||| ||
GGT ACGTGAGGTCG ACC
A T
GAM2256 SLC14A2 5' CCAGGCTGGAGTACACTGG 24114 C C
CCA TG ACTCCAGCCTGG
|| || |||||
GGT AC TGAGGTCGGACC
C A
GAM2256 SLC15A1 3' CCAGGCTGGAGTGCAATGG 18639 C
CCA TGCCTCCAGCCTGG
|| |||||
GGT ACGTGAGGTCGGACC
A
GAM2256 SLC19A2 3' CCAGGCTGCAGTGCAGTGG 69549 C
CCACTGCACT CAGCCTGG
||||| |||||

			GGTGACGTGA GTCGGACC		
			C		
GAM2256	SLC24A1	3'	CCAGGCTGGTGTGCAATGG 17561	C	T
			CCA TGCAC CCAGCCTGG		
			GGT ACGTG GGTCCGACC		
			A T		
GAM2256	SLC2A1	3'	GCACTGGAGTGCAGGG 22515	A	CCTG
			CC CTGCACTCCAG GC		
			GG GACGTGAGGTC CG		
			— A —		
GAM2256	SLC39A1	5'	CCAGGCTGGAGTGCGGTGG 27807		
			CCACTGCACTCCAGCCTGG		
			GGTGGCGTGAGGTCGGACC		
GAM2256	SMAC	5'	CCAGGCTGAAGTGCAGTGG 58018	C	
			CCACTGCACT CAGCCTGG		
			GGTGACGTGA GTCGGACC		
			A		
GAM2256	SMAC	5'	CCAGGCTGGAGTGCAGTGG 58019		
			CCACTGCACTCCAGCCTGG		
			GGTGACGTGAGGTCGGACC		
GAM2256	SNX15	3'	CCAGACTGGAGTGCAGTGG 74117	C	
			CCACTGCACTCCAG CTGG		
			GGTGACGTGAGGTC GACC		
			A		
GAM2256	SPN	3'	CCAGGCTGGAGTGTGCAATG 13372	C	
			CA TGCCTCCAGCCTGG		
			GT ACGTGAGGTCGGACC		
			A		
GAM2256	SS18	3'	CCAGGCTGGAGTGCAGTGG 20102		
			CCACTGCACTCCAGCCTGG		
			GGTGACGTGAGGTCGGACC		
GAM2256	STAU	5'	CCAGGCTGGAGTGCAGTGG 17196		
			CCACTGCACTCCAGCCTGG		
			GGTGACGTGAGGTCGGACC		
GAM2256	TAF11	3'	CTAGGCTGGAGTGCAGCGG 20119	A	
			CC CTGCACTCCAGCCTGG		

			GG GACGTGAGGTCGGATC		
			C		
GAM2256	TAL1	3'	TCAGGCTGGAGTACAGTGG 13532	C	
			CCACTG ACTCCAGCCTGG		
			GGTGAC TGAGGTCGGA		
			A		
GAM2256	TAPBP	3'	CCAGGCTGCAGTGCAGTGG 13553	C	
			CCACTGCACT CAGCCTGG		
			GGTGACGTGA GTCGGACC		
			C		
GAM2256	TAPBP	3'	CCAGGCTGGAGTGCAGTGG 13554		
			CCACTGCACTCCAGCCTGG		
			GGTGACGTGAGGTCGGACC		
GAM2256	TAPBP	3'	CCAGGCTGGAGTGCAGTGG 13555		
			CCACTGCACTCCAGCCTGG		
			GGTGACGTGAGGTCGGACC		
GAM2256	TAT	3'	CCATGCTGGAGTGCAGTGG 6251	C	
			CCACTGCACTCCAGC TGG		
			GGTGACGTGAGGTCG ACC		
			T		
GAM2256	TBXA2R	3'	CCAGGCTGGAGTGCAGTGG 8349		
			CCACTGCACTCCAGCCTGG		
			GGTGACGTGAGGTCGGACC		
GAM2256	TCF2	3'	CCGAGCTGGAGTGCAGTGG 22405	C	
			CCACTGCACTCCAGC TGG		
			GGTGACGTGAGGTCG GCC		
			A		
GAM2256	TDGF1	3'	CCAGGCTGGACTGCAATG 13652	C C	
			CA TGCA TCCAGCCTGG		
			GT ACGT AGGTCGGACC		
			A C		
GAM2256	TEM5	3'	GCCAAGCCCAGAGGCAGTGG 52302	A CA_ C	
			CCACTGC CTC GC TGGC		
			GGTGACG GAG CG ACCG		
			_ ACC A		
GAM2256	TERF1	3'	CCAGGCTGGAGTGCAGTGG 34390		
			CCACTGCACTCCAGCCTGG		

GGTGACGTGAGGTCGGACC

GAM2256 TERF2 3' CCAGGCTGGAGTGCAGTGG 20147
CCACTGCACTCCAGCCTGG
|||||
GGTGACGTGAGGTCGGACC

GAM2256 TIM3 3' CCAGGCTGGAGTGCAATGG 52353 C
CCA TGCCTCCAGCCTGG
||| |||||
GGT ACGTGAGGTCGGACC
A

GAM2256 TJP1 5' CCAGGCAGGAGTGCAGTGG 13762 A
CCACTGCACTCC GCCTGG
||||| |||||
GGTGACGTGAGG CGGACC
A

GAM2256 TLR5 5' CCAGGCTGGACTGCAGTG 13782 C
CACTGCA TCCAGCCTGG
||||| |||||
GTGACGT AGGTCGGACC
C

GAM2256 TMC1 5' CCAGGCTGGAGTGCAGTGG 57707
CCACTGCACTCCAGCCTGG
|||||
GGTGACGTGAGGTCGGACC

GAM2256 TMPRSS3 3' CCAGGCTGGAGTGCAGTGG 51514
CCACTGCACTCCAGCCTGG
|||||
GGTGACGTGAGGTCGGACC

GAM2256 TMPRSS3 3' CCAGGCTGGAGTGCAGTGG 51542
CCACTGCACTCCAGCCTGG
|||||
GGTGACGTGAGGTCGGACC

GAM2256 TMPRSS3 3' CCAGGCTGGAGTGCAGTGG 44021
CCACTGCACTCCAGCCTGG
|||||
GGTGACGTGAGGTCGGACC

GAM2256 TNFAIP2 3' CCAGGCTGGAGTGCAGTGG 21920
CCACTGCACTCCAGCCTGG
|||||
GGTGACGTGAGGTCGGACC

GAM2256 TNFRSF10B 3' CCAGGCTGGAGTGCAACGG 15219 AC
CC TGCCTCCAGCCTGG
|| |||||

		GG ACGTGAGGTCGGACC	
		CA	
GAM2256	TNFRSF10B 3'	CCAGGCTGGAGTGCAATGG 15220	C
		CCA TGCCTCCAGCCTGG	
		GGT ACGTGAGGTCGGACC	
		A	
GAM2256	TNFRSF11A 3'	CCAGGCTAGAGTGCAAGTGG 15191	C
		CCACTGCACTC AGCCTGG	
		GGTGACGTGAG TCGGACC	
		A	
GAM2256	TNFRSF1B 3'	TCAGGCCAGGTGCAGTGG 8401	CCA
		CCACTGCACT GCCTGG	
		GGTGACGTGG CGGACT	
		AC_	
GAM2256	TNFRSF6B 5'	AGTGGGGGGCGGAAGTGCAGTG 33595	_ A GG G
	G	CCACTGCACT CC GCCT C ACT	
		GGTGACGTGA GG CGGG G TGA	
		A _ GG _	
GAM2256	TNFRSF9 3'	CCAGGCTGGAGTGCAAGTGG 9580	
		CCACTGCACTCCAGCCTGG	
		GGTGACGTGAGGTCGGACC	
GAM2256	TP53 3'	CCAGGCTGGAGTGGAGTGG 6797	G
		CCACT CACTCCAGCCTGG	
		GGTGA GTGAGGTCGGACC	
		G	
GAM2256	TPMT 3'	CCAACCTGGAGTGCAAGTGG 6306	CC
		CCACTGCACTCCAG TGG	
		GGTGACGTGAGGTC ACC	
		CA	
GAM2256	TRAF5 3'	CCAGGCTGGAGTACAGTGG 17270	C
		CCACTG ACTCCAGCCTGG	
		GGTGAC TGAGGTCGGACC	
		A	
GAM2256	TRPM6 3'	CCAGGCTGGAGTGCAATG 35029	C
		CA TGCCTCCAGCCTGG	
		GT ACGTGAGGTCGGACC	
		A	
GAM2256	TRPV1 3'	CCAGGCTGGAATGCAGTGG 38691	C
		CCACTGCA TCCAGCCTGG	

			GGTGACGT AGGTCGGACC	
			A	
GAM2256	TRPV1	3'	CCAGGCTGGAGTGCAGTGG 38692	
			CCACTGCACTCCAGCCTGG	
			GGTGACGTGAGGTCGGACC	
GAM2256	TRPV1	3'	CCAGGCTGGAATGCAGTGG 55662	C
			CCACTGCA TCCAGCCTGG	
			GGTGACGT AGGTCGGACC	
			A	
GAM2256	TRPV1	3'	CCAGGCTGGAGTGCAGTGG 55663	
			CCACTGCACTCCAGCCTGG	
			GGTGACGTGAGGTCGGACC	
GAM2256	TRPV1	3'	CCAGGCTGGAATGCAGTGG 55707	C
			CCACTGCA TCCAGCCTGG	
			GGTGACGT AGGTCGGACC	
			A	
GAM2256	TRPV1	3'	CCAGGCTGGAGTGCAGTGG 55708	
			CCACTGCACTCCAGCCTGG	
			GGTGACGTGAGGTCGGACC	
GAM2256	TRPV1	3'	CCAGGCTGGAATGCAGTGG 55738	C
			CCACTGCA TCCAGCCTGG	
			GGTGACGT AGGTCGGACC	
			A	
GAM2256	TRPV1	3'	CCAGGCTGGAGTGCAGTGG 55739	
			CCACTGCACTCCAGCCTGG	
			GGTGACGTGAGGTCGGACC	
GAM2256	UGDH	3'	CCAGGCTGGAGTGCAGTGG 13993	
			CCACTGCACTCCAGCCTGG	
			GGTGACGTGAGGTCGGACC	
GAM2256	VENTX2	3'	CCAGGCTGGAGTGCAATG 27859	C
			CA TGCCTCCAGCCTGG	
			GT ACGTGAGGTCGGACC	
			A	
GAM2256	VHL	3'	CCAGGCTGGAGTGCAGAGG 6843	A
			CC CTGCACTCCAGCCTGG	

			GG GACGTGAGGTCGGACC		
			A		
GAM2256	VIPR2	3'	CCAGGCTGGAGTGCAGTGG 14060		
			CCACTGCACTCCAGCCTGG		
			GGTGACGTGAGGTCGGACC		
GAM2256	XRCC2	3'	CCAGGCTGGAGTGCAGTGG 19495		
			CCACTGCACTCCAGCCTGG		
			GGTGACGTGAGGTCGGACC		
GAM2256	XRCC2	3'	GCTGCTGGAGTGCAGTGG 19505	CT	
			CCACTGCACTCCAGC GGC		
			GGTGACGTGAGGTCG TCG		
GAM2256	YES1	3'	CCAGGCTGGAGTGCAGTGG 19531		
			CCACTGCACTCCAGCCTGG		
			GGTGACGTGAGGTCGGACC		
GAM2256	ZNF133	5'	CCAGGCTGGAGTGCAATGG 14293	C	
			CCA TGCCTCCAGCCTGG		
			GGT ACGTGAGGTCGGACC		
			A		
GAM2256	ZNF157	3'	CCAGGCTGGAGTGCAATGG 14329	C	
			CCA TGCCTCCAGCCTGG		
			GGT ACGTGAGGTCGGACC		
			A		
GAM2256	ZNF253	3'	CCGAGGCTGGAGTGCAATG 41077	C	—
			CA TGCCTCCAGCCT GG		
			GT ACGTGAGGTCGGA CC		
			A G		
GAM2256	ZNF264	3'	CCAGGCTGGAGTGCAGTGG 14205		
			CCACTGCACTCCAGCCTGG		
			GGTGACGTGAGGTCGGACC		
GAM2256	20D7-FC4	5'	AGTCACCCAGGCTGGAGTGCAG 61562	C_	
			TGG CCACTGCACTCCAGCCTGG GACT		
			GGTGACGTGAGGTCGGACC CTGA		
			CA		
GAM2256	AGMAT	3'	CCAGGCTGGAGTGCAGTGG 45738		
			CCACTGCACTCCAGCCTGG		

GGTGACGTGAGGTCGGACC

GAM2256 ANKRD6 3' CCAGACTGGAGTGCAGTGG 30771 C
CCACTGCACTCCAG CTGG
||||||| |||
GGTGACGTGAGGTC GACC

A

GAM2256 AP1GBP1 3' GCCACTGCAGTGTGCAGTG 24350 TC__ CC
CACTGCAC CAG TGGC
||||| ||| |||
GTGACGTG GTC ACCG

TGAC __

GAM2256 AP1GBP1 3' GCCACTGCAGTGTGCAGTG 55439 TC__ CC
CACTGCAC CAG TGGC
||||| ||| |||
GTGACGTG GTC ACCG

TGAC __

GAM2256 AP3S2 3' CCAGGCTGGAGTGCTGTGG 20647 T
CCAC GCACTCCAGCCTGG
||| |||||||||
GGTG CGTGAGGTCGGACC

T

GAM2256 APXL2 5' GTCGCCAGGCTGGAGTGCAGTG 75684
G CCACTGCACTCCAGCCTGGCGAC
|||||||||||||||
GGTGACGTGAGGTCGGACCGCTG

GAM2256 ARHF 3' TCAGGCTAGAGTGCAGTGG 39278 C
CCACTGCACTC AGCCTGG
||||||| |||||
GGTGACGTGAG TCGGACT

A

GAM2256 ARHGAP11A 3' CCAGGCTGGAGTGCAGTGG 29445
CCACTGCACTCCAGCCTGG
|||||||||||||||
GGTGACGTGAGGTCGGACC

GAM2256 ARHGAP5 5' CCAGGCTGGAGTGCAATGG 77597 C
CCA TGCACTCCAGCCTGG
||| |||||||||||
GGT ACGTGAGGTCGGACC

A

GAM2256 ASB16 3' CCAGGCTGAAGTGCAGTGG 70485 C
CCACTGCACT CAGCCTGG
||||||| |||||
GGTGACGTGA GTCGGACC

A

GAM2256 ASB16 5' CCAGGCTGGAGTGCAGTGG 70486
CCACTGCACTCCAGCCTGG
|||||||||||||||

GGTGACGTGAGGTCGGACC

GAM2256 ASB16 3' CCAGGCTGGAGTGCAGTGG 55977
CCACTGCACTCCAGCCTGG
|||||||
GGTGACGTGAGGTCGGACC

GAM2256 ASE-1 3' CCAGGCTGGAGTGCAGTGG 24972
CCACTGCACTCCAGCCTGG
|||||||
GGTGACGTGAGGTCGGACC

GAM2256 ASE-1 3' CCAGGTTGGAGTGCAGTGG 24973
CCACTGCACTCCAGCCTGG
|||||||
GGTGACGTGAGGTTGGACC

GAM2256 ATP1B4 3' CCAGGCTGGAGTGCAGTGG 24839
CCACTGCACTCCAGCCTGG
|||||||
GGTGACGTGAGGTCGGACC

GAM2256 BA108L7.2 3' CCAGGCTGGAGTGCGATGG 49069 C
CCA TGCCTCCAGCCTGG
||| |||||
GGT GCGTGAGGTCGGACC
A

GAM2256 BAG5 3' CCAGGCTGCAGTGCAGTGG 18034 C
CCACTGCACT CAGCCTGG
||||||| |||||
GGTGACGTGA GTCGGACC
C

GAM2256 BNIP-S 3' GTCGCCAGGCTGGAGTGCAGTG 57095
G CCACTGCACTCCAGCCTGGCGAC
|||||||
GGTGACGTGAGGTCGGACCGCTG

GAM2256 BY55 5' CCAGGCCAGAGTGCAGTG 60062 CA
CACTGCACTC GCCTGG
||||||| |||||
GTGACGTGAG CGGACC
AC

GAM2256 C(27)-3BETA-HSD 3' CCAGACTGGAGTGCAGTGG 48051 C
CCACTGCACTCCAG CTGG
||||||| |||||
GGTGACGTGAGGTC GACC
A

GAM2256 C11orf17 3' CCAGGCTGGAGTGCAGTGG 40578
CCACTGCACTCCAGCCTGG
|||||||

GGTGACGTGAGGTCGGACC

GAM2256 C13orf1 3' CCAGGCTAGAGTGCAGTGG 40359 C
CCACTGCACTC AGCCTGG
||||||| |||||
GGTGACGTGAG TCGGACC

A

GAM2256 C1QTNF6 3' CCAGGCTAGAGTGCAGTGG 49990 C
CCACTGCACTC AGCCTGG
||||||| |||||
GGTGACGTGAG TCGGACC

A

GAM2256 C20orf172 3' AGTTTTGAGGCTGGGCGCAATG 46762 C A T GGC
G CCA TGC C CCAGCCT GACT
||| ||| ||||| |||
GGT ACG G GGTCGGA TTGA
A C _ GTT

GAM2256 C20orf183 3' TCCCAACTGGGTGCAGTGG 48538 T CC C
CCACTGCAC CCAG TGG GA
||||||| ||| ||| ||
GGTGACGTG GGTC ACC CT

_ A _

GAM2256 C21orf25 3' CCAGGCTGGAGTGCAATGG 64286 C
CCA TGC ACTCCAGCCTGG
||| ||||| |||||
GGT ACGTGAGGTCGGACC

A

GAM2256 C21orf67 5' CCAGGCTGGAGCGCAATGG 55229 C A
CCA TGC CTCCAGCCTGG
||| ||| ||||| |||||
GGT ACG GAGGTCGGACC

A C

GAM2256 C22orf19 3' AGTCACAAGGGGGCCTGAGTGC 14816 CA GGC____
AGTGG CCACTGCACTC GCCT GACT
||||||| ||| |||
GGTGACGTGAG CGGG CTGA

TC GGAACA

GAM2256 C22orf19 3' CCAGGCTGGAGTGCAGTGG 14820
CCACTGCACTCCAGCCTGG
||||||| |||||
GGTGACGTGAGGTCGGACC

GAM2256 C22orf19 3' TGGGCTGGGCACAGTGG 14836 CA T
CCACTG C CCAGCCTG
||||| | |||||
GGTGAC G GGTCGGGT

AC _

GAM2256 C3F 3' CCACGCTGGAATGCAGTGG 20473 C C
CCACTGCA TCCAGC TGG
||||||| ||||| |||

			GGTGACGT AGGTCG ACC	
			A C	
GAM2256	C6orf33	3'	CCAGGCTGGAGTGCAGTG 56710	
			CACTGCACTCCAGCCTGG	
			GTGACGTGAGGTCGGACC	
GAM2256	C6orf5	3'	CCAGGCTGCAGTACAGTG 31979	C C
			CACTG ACT CAGCCTGG	
			GTGAC TGA GTCGGACC	
			A C	
GAM2256	C6orf5	3'	CCAGGCTGGAGTGCAGTG 31980	
			CACTGCACTCCAGCCTGG	
			GTGACGTGAGGTCGGACC	
GAM2256	C6orf5	3'	TTAGGCTGGGCGCAGTGG 32008	A T
			CCACTGC C CCAGCCTGG	
			GGTGACG G GGTCTGGATT	
			C _	
GAM2256	C8orf7	3'	GTCAGGCTTATGCAATGCAGTG 82469	CTCC__
	G		CCACTGCA AGCCTGGC	
			GGTGACGT TCGGACTG	
			AACGTAT	
GAM2256	C9orf9	3'	CCAGGCTGGAGTGCAGTGG 39011	
			CCACTGCACTCCAGCCTGG	
			GGTGACGTGAGGTCGGACC	
GAM2256	C9orf9	3'	CCAGGCTGGAGTGCGGTGG 39012	
			CCACTGCACTCCAGCCTGG	
			GGTGGCGTGAGGTCGGACC	
GAM2256	CARD6	3'	CCAGGCTGGAGTGCAATGG 51839	C
			CCA TGCACTCCAGCCTGG	
			GGT ACGTGAGGTCGGACC	
			A	
GAM2256	CDC14B	3'	CCAGGCTGGAGTGCAGTGG 54003	
			CCACTGCACTCCAGCCTGG	
			GGTGACGTGAGGTCGGACC	
GAM2256	CEACAM8	3'	CCAGGCTGGAGTGCAGTGG 10178	
			CCACTGCACTCCAGCCTGG	

GGTGACGTGAGGTCGGACC

GAM2256 CHSY1 3' CCAGGCTGGAATGCAGTGG 30565 C
CCACTGCA TCCAGCCTGG
||||||| |||||||||
GGTGACGT AGGTCGGACC

A

GAM2256 CIP29 3' CCAGCTGGAGTGCAGTGG 51372 C
CCACTGCACTCCAGC TGG
||||||||||| |||
GGTGACGTGAGGTCG ACC

GAM2256 CNNM3 3' GCCACCTTGTGAGTGCAGTTA 34808 C _ CC
C ACTGCACTC CAG TGGC
| ||||||| ||| ||||
A TGACGTGAG GTT ACCG
T T CC

GAM2256 COLEC12 3' CCAGGCTGGAGTGCAGTGG 48608
CCACTGCACTCCAGCCTGG
|||||||||||
GGTGACGTGAGGTCGGACC

GAM2256 CPSF2 3' AGTCACCCAGGCTGGAGTGCAG 62262 C_
TGG CCACTGCACTCCAGCCTGG GACT
||||||||||| ||||
GGTGACGTGAGGTCGGACC CTGA
CA

GAM2256 CPSF2 3' CCAGACTGGAGTGCAATGG 62268 C C
CCA TGCACTCCAG CTGG
||| ||||||| ||||
GGT ACGTGAGGTC GACC
A A

GAM2256 CSAD 3' GCCTTTGAGGCGGGTGCAGTG 32582 T A ____
G CCACTGCAC CC GCCT GGC
||||||| || |||| |||
GGTGACGTG GG CGGA CCG
_ C GTTT

GAM2256 DBR1 3' CTAGACTGGAGTGCAATGG 33063 C C
CCA TGCACTCCAG CTGG
||| ||||||| ||||
GGT ACGTGAGGTC GATC
A A

GAM2256 DCOHM 3' CAGACTGGAGTGCAGTGG 50513 C
CCACTGCACTCCAG CTG
||||||||||| |||
GGTGACGTGAGGTC GAC

A

GAM2256 DCOHM 3' CCAGGCTGGAGTGCAATGG 50516 C
CCA TGCACTCCAGCCTGG
||| |||||||||

		GGT ACGTGAGGTCGGACC			
		A			
GAM2256	DKFZp434A2417 3'	CCAGGCTGGAGGGCAATGG	66675	C	A
		CCA TGC CTCCAGCCTGG			
		GGT ACG GAGGTCGGACC			
		A G			
GAM2256	DKFZP434B1727 3'	CCAGGCTGGAGTACAGTGG	50476	C	
		CCACTG ACTCCAGCCTGG			
		GGTGAC TGAGGTCGGACC			
		A			
GAM2256	DKFZp434C0923 3'	CCAGGCTGGAGTACAGTGG	34646	C	
		CCACTG ACTCCAGCCTGG			
		GGTGAC TGAGGTCGGACC			
		A			
GAM2256	DKFZP434C212 3'	CCAGGCTGGAGTGCAATGG	69483	C	
		CCA TGCACTCCAGCCTGG			
		GGT ACGTGAGGTCGGACC			
		A			
GAM2256	DKFZp434E2220 5'	CCAGGCTGGAGTGCAGTGG	34710		
		CCACTGCACTCCAGCCTGG			
		GGTGACGTGAGGTCGGACC			
GAM2256	DKFZP434F0318 3'	CTAGGCTGGAGTTGCAGTGG	48751		—
		CCACTGCA CTCCAGCCTGG			
		GGTGACGT GAGGTCGGATC			
		T			
GAM2256	DKFZp434F1719 3'	CCAGGCTGGAGTGCAATGG	51014	C	
		CCA TGCACTCCAGCCTGG			
		GGT ACGTGAGGTCGGACC			
		A			
GAM2256	DKFZP564G092 5'	CCAGGCTGTAGTGCAGTGG	32155	C	
		CCACTGCACT CAGCCTGG			
		GGTGACGTGA GTCGGACC			
		T			
GAM2256	DKFZP564I122 3'	CTAGGCTGGAGTGCAGTGG	63875		
		CCACTGCACTCCAGCCTGG			
		GGTGACGTGAGGTCGGATC			
GAM2256	DKFZP564K0322 3'	CCAGGCTGGAGTGCAGTGG	50184		
		CCACTGCACTCCAGCCTGG			

GGTGACGTGAGGTCGGACC

GAM2256 DKFZP564M182 3' TGTGGGTGCTAGATGCAGTGG 78650 C C _ G
CCACTGCA TC AGC CT GCG
||||||| || ||| || |||
GGTGACGT AG TCG GG TGT
_ A T G

GAM2256 DKFZP564O0523 3' CCAGGCTGGAATGCAGTGG 50419 C
CCACTGCA TCCAGCCTGG
||||||| |||||||||
GGTGACGT AGGTCGGACC

A
GAM2256 DKFZP667O116 3' TGCCAGGCGCAGTGG 95943 ACTCCA
CCACTGC GCCTGGCG
||||||| |||||||||
GGTGACG CGGACCGT

GAM2256 DKFZP761C169 3' GCCATTTGTAGTGCAGT 68421 C CC
ACTGCACT CAG TGGC
||||||| ||| |||
TGACGTGA GTT ACCG
T T_

GAM2256 DKFZp761J139 5' CCAGGCTGGAGTGCAGTGG 51103
CCACTGCACTCCAGCCTGG
|||||||||||||||
GGTGACGTGAGGTCGGACC

GAM2256 DKFZp761N1114 3' CCAGGCTGGAATGCAGTGG 79778 C
CCACTGCA TCCAGCCTGG
||||||| |||||||||
GGTGACGT AGGTCGGACC
A

GAM2256 DKFZp761O0113 5' CCAGGCTTGAGTGCAGTG 37890 C
CACTGCACTC AGCCTGG
||||||||| |||||||
GTGACGTGAG TCGGACC
T

GAM2256 DKFZp762P2111 3' CCAGGCTGGAGTGCAATGG 87626 C
CCA TGCACTCCAGCCTGG
||| |||||||||||||
GGT ACGTGAGGTCGGACC
A

GAM2256 DSCR6 3' CCAGGCTGGAGTGCAGTG 39060
CACTGCACTCCAGCCTGG
|||||||||||||||
GTGACGTGAGGTCGGACC

GAM2256 EREG 3' CCAGGTTGGAGTGCAGTGG 9305
CCACTGCACTCCAGCCTGG
|||||||||||||||

GGTGACGTGAGGTTGGACC

GAM2256 EVI5 3' CCAGGCTGGAGTGCTGTGG 20202 T
CCAC GCACTCCAGCCTGG
|||||
GGTG CGTGAGGTCGGACC
T

GAM2256 EVI5 3' TCAGGCTGGAGTGCAGTGG 20217
CCACTGCACTCCAGCCTGG
|||||
GGTGACGTGAGGTCGGACT

GAM2256 FADS1 3' GCAAGCTGGATGCAGTGG 26380 C CTG
CCACTGCA TCCAGC GC
||||| ||
GGTGACGT AGGTGC CG
_ AA_

GAM2256 FBP17 3' TCAGACTGGAGTGCAGTGG 73161 C
CCACTGCACTCCAG CTGG
|||||
GGTGACGTGAGGTC GACT
A

GAM2256 FBXO26 3' GCCTTGCAGCCAGGTGCAGTGG 46629 CCA__ CT
CCACTGCACT GC GGC
||||| || ||
GGTGACGTGG CG CCG
ACCGA TT

GAM2256 FER1L4 3' CCAGGTTGGAGTGCAGTGG 48116
CCACTGCACTCCAGCCTGG
|||||
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GAM2256 FER1L4 3' CCAGGTTGGAGTGCAGTGG 48117
CCACTGCACTCCAGCCTGG
|||||
GGTGACGTGAGGTTGGACC

GAM2256 FKBP9 3' GTCGCCAGGCTGGAGTGCAGTG 95722
G CCACTGCACTCCAGCCTGGCGAC
|||||
GGTGACGTGAGGTCGGACCGCTG

GAM2256 FLJ00024 5' CCAGGCTGGAGTGCAATGG 64491 C
CCA TGCCTCCAGCCTGG
|||
GGT ACGTGAGGTCGGACC
A

GAM2256 FLJ00060 5' CCAGGCTGGAGTGCAGTGG 61742
CCACTGCACTCCAGCCTGG
|||||

GGTGACGTGAGGTCGGACC

GAM2256 FLJ10101 3' CCAGGCTGGAGTGCAGTGG 45592
CCACTGCACTCCAGCCTGG
|||||||
GGTGACGTGAGGTCGGACC

GAM2256 FLJ10232 3' CCAGGCTGGAGTGCGATGG 36375 C
CCA TGCCTCCAGCCTGG
||| |||||
GGT GCGTGAGGTCGGACC
A

GAM2256 FLJ10297 3' CCAGGCTAGAGTGCAGTGG 36437 C
CCACTGCACTC AGCCTGG
||||||| |||||
GGTGACGTGAG TCGGACC
A

GAM2256 FLJ10346 5' CCAGGCTGAAGTGCAGTGG 36522 C
CCACTGCACT CAGCCTGG
||||||| |||||
GGTGACGTGA GTCGGACC
A

GAM2256 FLJ10535 3' CCAGGCTGGAGTGCAGTGG 36742
CCACTGCACTCCAGCCTGG
|||||||
GGTGACGTGAGGTCGGACC

GAM2256 FLJ10560 3' CCAGGCTGGCGTGCAGTGG 36793 T
CCACTGCAC CCAGCCTGG
||||||| |||||
GGTGACGTG GGTCGGACC
C

GAM2256 FLJ10607 3' CCAGGCTGGAGTCCAGTGG 77626 C
CCACTG ACTCCAGCCTGG
||||| |||||
GGTGAC TGAGGTCGGACC
C

GAM2256 FLJ10713 3' CCAGGCTGGAGTGCAGTGG 37000
CCACTGCACTCCAGCCTGG
|||||||
GGTGACGTGAGGTCGGACC

GAM2256 FLJ10846 3' CCAGGCTGGAGTGCAGTGG 37285
CCACTGCACTCCAGCCTGG
|||||||
GGTGACGTGAGGTCGGACC

GAM2256 FLJ10847 3' CAGGCTGGAGTGCGGTGG 37297
CCACTGCACTCCAGCCTG
|||||||

GGTGGCGTGAGGTCGGAC

GAM2256 FLJ10900 3' AGTACCGGGGCTGGAGCGGAGT 37344 GCA _ CG
 G CACT CTCCAGCCT GG ACT
 |||| ||||| || |||
 GTGA GAGGTCGGG CC TGA
 GGC G A_

GAM2256 FLJ10900 3' AGTACCGGGGCTGGAGCGGAGT 66202 GCA _ CG
 G CACT CTCCAGCCT GG ACT
 |||| ||||| || |||
 GTGA GAGGTCGGG CC TGA
 GGC G A_

GAM2256 FLJ10922 3' CCAGGCTGGAATGCAATGG 37398 C C
 CCA TGCA TCCAGCCTGG
 ||| ||| |||||
 GGT ACGT AGGTCGGACC
 A A

GAM2256 FLJ10989 3' TTAGGCTGGGTGCAGTGG 37509 T
 CCACTGCAC CCAGCCTGG
 ||||| |||||
 GGTGACGTG GGTCGGATT

GAM2256 FLJ11004 5' CCAGACTGGAGTGCTGTGG 37530 T C
 CCAC GCACTCCAG CTGG
 |||| ||||| ||||
 GGTG CGTGAGGTC GACC
 T A

GAM2256 FLJ11016 3' AGTGA CTGGCTGGGTGCAGT 37539 T T CG
 ACTGCAC CCAGCC GG ACT
 ||||| ||||| || |||
 TGACGTG GGTCGG TC TGA
 _ _ AG

GAM2256 FLJ11029 3' CCAGCTGGGTGCAGTGG 61632 T C
 CCACTGCAC CCAGC TGG
 ||||| ||||| |||
 GGTGACGTG GGTCG ACC

GAM2256 FLJ11467 3' CCAGGCTGGAGTACAGTGG 46973 C
 CCACTG ACTCCAGCCTGG
 ||||| |||||
 GGTGAC TGAGGTCGGACC
 A

GAM2256 FLJ11710 3' CCAGGCTGGAGTGCAGTGG 46245
 CCACTGCACTCCAGCCTGG
 ||||| |||||
 GGTGACGTGAGGTCGGACC

GAM2256 FLJ11715 3' CCAGGCTGGAGGGCAGTG 44977 A
 CACTGC CTCCAGCCTGG
 ||||| |||||

			GTGACG GAGGTCGGACC		
			G		
GAM2256	FLJ11800	3'	CCAGGCCGAGTGCAGTGG 47038	A	
			CCACTGCACTCC GCCTGG		
			GGTGACGTGAGG CGGACC		
			C		
GAM2256	FLJ12363	3'	CCAGGCTGGAGTGCCGTGG 50633	T	
			CCAC GCACTCCAGCCTGG		
			GGTG CGTGAGGTCGGACC		
			C		
GAM2256	FLJ12448	3'	GCTTGTGGCCGGTGCAGTGG 43478	T A T__	
			CCACTGCAC CC GCC GGC		
			GGTGACGTG GG CGG TCG		
			_ C TGT		
GAM2256	FLJ12572	5'	CCAGGCTGGAGTATAGTGG 43541	C	
			CCACTG ACTCCAGCCTGG		
			GGTGAT TGAGGTCGGACC		
			A		
GAM2256	FLJ12581	3'	CCAGGCTGGAGTGCAGTGG 46332		
			CCACTGCACTCCAGCCTGG		
			GGTGACGTGAGGTCGGACC		
GAM2256	FLJ12649	3'	CCAGGCTGCAGTGCAGTGG 45087	C	
			CCACTGCACT CAGCCTGG		
			GGTGACGTGA GTCGGACC		
			C		
GAM2256	FLJ12666	3'	TTGGGCTGGGCGCAGTGG 45074	A T TG	
			CCACTGC C CCAGCC G		
			GGTGACG G GGTCGG T		
			C _ GT		
GAM2256	FLJ12668	3'	CCAGGCTGGAGTACAGTGG 47156	C	
			CCACTG ACTCCAGCCTGG		
			GGTGAC TGAGGTCGGACC		
			A		
GAM2256	FLJ12747	3'	CCAGGCTGGAGTGCAATGG 50662	C	
			CCA TGCCTCCAGCCTGG		
			GGT ACGTGAGGTCGGACC		
			A		
GAM2256	FLJ12787	3'	CCAGGCTGGAGTACAGTG 50690	C	
			CACTG ACTCCAGCCTGG		

			GTGAC TGAGGTCGGACC		
			A		
GAM2256	FLJ12876	3'	CCAGGCTGGAGTGCAGTGG 43087		
			CCACTGCACTCCAGCCTGG		
			GGTGACGTGAGGTCGGACC		
GAM2256	FLJ12888	3'	CCAGGCTAGAGTGCAGTGG 46888		C
			CCACTGCACTC AGCCTGG		
			GGTGACGTGAG TCGGACC		
			A		
GAM2256	FLJ12903	3'	CCAGGCTGGAGTGCAATGG 43065		C
			CCA TGCACTCCAGCCTGG		
			GGT ACGTGAGGTCGGACC		
			A		
GAM2256	FLJ12960	3'	CCAGGCTGGAGTGCAGTGG 45293		
			CCACTGCACTCCAGCCTGG		
			GGTGACGTGAGGTCGGACC		
GAM2256	FLJ12975	3'	CCAGGCTGGAGTGCAGTG 70188		
			CACTGCACTCCAGCCTGG		
			GTGACGTGAGGTCGGACC		
GAM2256	FLJ13072	5'	CCAGGCTGGAGTGCAGTGG 91388		
			CCACTGCACTCCAGCCTGG		
			GGTGACGTGAGGTCGGACC		
GAM2256	FLJ13102	3'	TGAGGGGCTGGAGGCAG 46536	A	GG
			CTGC CTCCAGCCT CG		
			GACG GAGGTCGGG GT		
			GA		
GAM2256	FLJ13114	3'	CCAGGCTGGAATGCAGTGG 44897		C
			CCACTGCA TCCAGCCTGG		
			GGTGACGT AGGTCGGACC		
			A		
GAM2256	FLJ13193	3'	CCAGGCTGGAGTACAGTGG 50714		C
			CCACTG ACTCCAGCCTGG		
			GGTGAC TGAGGTCGGACC		
			A		
GAM2256	FLJ13197	3'	CCAGGCTGGAGTGCAGTGG 45176		
			CCACTGCACTCCAGCCTGG		

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GAM2256 FLJ13352 3' CAGGCTGGGTGCAATGG 45048 C T
CCA TGCAC CCAGCCTG
||| |||| |||||
GGT ACGTG GGTCGGAC
A _

GAM2256 FLJ13456 3' CCAAGCTGGAGTGCAGTGG 66538 C
CCACTGCACTCCAGC TGG
||||||| |||
GGTGACGTGAGGTCG ACC
A

GAM2256 FLJ13590 5' TCAGGCTTGAGTGCAGTGG 46208 C
CCACTGCACTC AGCCTGG
||||||| |||||
GGTGACGTGAG TCGGACT
T

GAM2256 FLJ13952 3' CCAGGCTGGAATGCAGTGG 46010 C
CCACTGCA TCCAGCCTGG
||||| |||||
GGTGACGT AGGTCGGACC
A

GAM2256 FLJ13984 3' AGTTGTTAGGCCAGGTGCAATG 45800 C CCA
G CCA TGCAC GCCTGGCGACT
||| |||| |||||
GGT ACGTGG CGGATTGTTGA
A AC_

GAM2256 FLJ13984 5' CTAGGCTGGAGTGCAGTGG 45806
CCACTGCACTCCAGCCTGG
|||||||
GGTGACGTGAGGTCGGATC

GAM2256 FLJ14326 3' AGCGCTCAGGCTGGGTGCAGTG 50758 T _ A
G CCACTGCAC CCAGCCTG GCG CT
||||||| ||||| ||| ||
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_ T _

GAM2256 FLJ14351 3' CCAGGCTGGAGTGCAGTGG 45645
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GAM2256 FLJ14442 3' CCAGGCTAGAGTGTAGTGG 52378 C
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GGTGATGTGAG TCGGACC
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GAM2256 FLJ14803 3' CGCAGACTGGAGTGCAGTGG 52693 C G
CCACTGCACTCCAG CTG CG
||||||| ||| ||

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GAM2256	FLJ14950	3'	CCAGGCTGAACTGCAGTGG 52784	CTC
			CCACTGCA CAGCCTGG	
			GGTGACGT GTCGGACC	
			CAA	
GAM2256	FLJ20034	3'	CCAGGCTGGAGTACAATGG 34840	C C
			CCA TG ACTCCAGCCTGG	
			GGT AC TGAGGTCGGACC	
			A A	
GAM2256	FLJ20045	3'	CCAGGCTGGAGTGCAGTGG 34880	
			CCACTGCACTCCAGCCTGG	
			GGTGACGTGAGGTCGGACC	
GAM2256	FLJ20079	3'	CCAGGCTGGAGTGCAATGG 34968	C
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			GGT ACGTGAGGTCGGACC	
			A	
GAM2256	FLJ20136	3'	CCAGGCTGGAATGCAGTGG 35094	C
			CCACTGCA TCCAGCCTGG	
			GGTGACGT AGGTCGGACC	
			A	
GAM2256	FLJ20340	3'	CAGGCCAGGTGCAGTGG 35454	CCA
			CCACTGCACT GCCTG	
			GGTGACGTGG CGGAC	
			AC_	
GAM2256	FLJ20344	3'	CCAAACTGGAGTGCAGTGG 35478	CC
			CCACTGCACTCCAG TGG	
			GGTGACGTGAGGTC ACC	
			AA	
GAM2256	FLJ20452	3'	TCACTAAAGGCCAGGTGCAGTG 35652	CCA _ C
	G		CCACTGCACT GCCT GG GA	
			GGTGACGTGG CGGA TC CT	
			AC_ AA A	
GAM2256	FLJ20511	3'	CCAGGCTGGAGTGCAGTGG 35767	
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			GGTGACGTGAGGTCGGACC	
GAM2256	FLJ20555	3'	CAAGCCTGAGTGCAGTGG 35827	CA C
			CCACTGCACTC GC TG	

		GGTGACGTGAG CG AC		
		TC A		
GAM2256	FLJ20671	3' CCAGGCTGGAGTGCAGTGG 35936		
		CCACTGCACTCCAGCCTGG		
		GGTGACGTGAGGTCGGACC		
GAM2256	FLJ20700	3' CCAGGCTGGAGTGCAGTGG 36002		
		CCACTGCACTCCAGCCTGG		
		GGTGACGTGAGGTCGGACC		
GAM2256	FLJ20813	3' CCAGGCTGGAGTGCAGTGG 36128		
		CCACTGCACTCCAGCCTGG		
		GGTGACGTGAGGTCGGACC		
GAM2256	FLJ21162	3' AGTCTTGGGCTGGGTGCAGTGG 46366	T	TG C
		CCACTGCAC CCAGCC G GACT		
		GGTGACGTG GGTCGG T CTGA		
		— GT —		
GAM2256	FLJ21324	5' CCAGGCTGGCGTGCAGTGG 92849	T	
		CCACTGCAC CCAGCCTGG		
		GGTGACGTG GGTCGGACC		
		C		
GAM2256	FLJ21459	3' CCAGGCTGGGGTGCAGTGG 44800		
		CCACTGCACTCCAGCCTGG		
		GGTGACGTGGGGTCGGACC		
GAM2256	FLJ21603	3' CCAGGCTGGAGTACAGTGG 45769	C	
		CCACTG ACTCCAGCCTGG		
		GGTGAC TGAGGTCGGACC		
		A		
GAM2256	FLJ21777	3' CCAGGCTGGAGTGCAATGG 50838	C	
		CCA TGCACTCCAGCCTGG		
		GGT ACGTGAGGTCGGACC		
		A		
GAM2256	FLJ22029	3' GCACACGCTGGAGTGCAG 46910	C	—
		CTGCACTCCAGC TG GC		
		GACGTGAGGTCG AC CG		
		C A		
GAM2256	FLJ22167	5' TCAGGCTGCAGTGCAGTGG 44878	C	
		CCACTGCACT CAGCCTGG		

	GGTGACGTGA GTCGGACT	
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GAM2256 FLJ22316 5'	CCAGGCTGGAGTGCAGTGG 47614	
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GAM2256 FLJ22329 3'	CCAGGCTGGAGTGCAGTGG 45396	
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GAM2256 FLJ22531 5'	CCAGGCCGGAGTGCAGTGG 45370	A
	CCACTGCACTCC GCCTGG	
	GGTGACGTGAGG CGGACC	
	C	
GAM2256 FLJ22644 3'	TCAGCCTGGAGTGCAGTG 47702	C
	CACTGCACTCCAG CTGG	
	GTGACGTGAGGTC GACT	
	C	
GAM2256 FLJ23040 3'	CCAAGCCAGAGTGCAGTGG 47984	CA C
	CCACTGCACTC GC TGG	
	GGTGACGTGAG CG ACC	
	AC A	
GAM2256 FLJ23053 3'	CCAGGCTGGAGTGCAGTGG 43553	
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	GGTGACGTGAGGTCGGACC	
GAM2256 FLJ23263 5'	CCAGGCTGGAGTGCAGTGG 47800	
	CCACTGCACTCCAGCCTGG	
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GAM2256 FLJ23392 3'	CCAGACTGGAGTGCAGTGG 45884	C
	CCACTGCACTCCAG CTGG	
	GGTGACGTGAGGTC GACC	
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GAM2256 FLJ23416 3'	CCAGGCTGGAGTGCAGTGG 50930	
	CCACTGCACTCCAGCCTGG	

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GAM2256 FLJ23519 3' CCAGGCTGGAGTGCAGTGG 50945
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|||||
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GAM2256 FLJ23556 3' CCAGGCTGGAGTGCAGTGG 46435
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GAM2256 FLJ25416 5' CCAGGCTGAAGTGCCATGG 59450 CT C
CCA GCACT CAGCCTGG
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GGT CGTGA GTCGGACC
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GAM2256 FLJ25416 5' CCAGGCTGGAGTGCCATGG 59451 CT
CCA GCACTCCAGCCTGG
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GAM2256 FLJ30532 3' CCAGGCTGGAGTACAGTGG 59217 C
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GAM2256 FLJ31101 3' CCAGGCTGGAATGCAGTGG 36158 C
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GAM2256 FLJ31153 3' CCAGACTGGAGTGCAGTGG 58745 C
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GAM2256 FLJ32499 3' CCAGTCTGGAGTGCAGTGG 58776 C
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GAM2256 FLJ32865 3' CCAGGCTGGAGTACAATG 58804 C C
CA TG ACTCCAGCCTGG
|| || |||||
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A A

GAM2256 GAL3ST-4 3' CCAGGCTGGAGTGCAGTGG 45275
CCACTGCACTCCAGCCTGG
|||||

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GAM2256	GALNT6	3'	AGTACTTCAGGCTGGGCACAGT 24239	CA T	CG_
	GG		CCACTG C CCAGCCTGG ACT		
			GGTGAC G GGTCGGACT TGA		
			AC_ TCA		
GAM2256	GGA2	3'	TCAGGCTGGAGTGCGGTGG 31171		
			CCACTGCACTCCAGCCTGG		
			GGTGGCGTGAGGTCGGACT		
GAM2256	GGA2	3'	TCAGGCTGGAGTGCGGTGG 57681		
			CCACTGCACTCCAGCCTGG		
			GGTGGCGTGAGGTCGGACT		
GAM2256	GMPPB	5'	CCAGGCTGGAGTGCGATGG 97440	C	
			CCA TGCCTCCAGCCTGG		
			GGT GCGTGAGGTCGGACC		
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GAM2256	GNG4	3'	CCAGGCTGGAGTGCAATGG 16843	C	
			CCA TGCCTCCAGCCTGG		
			GGT ACGTGAGGTCGGACC		
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GAM2256	GOLGA3	3'	CCAGGCTGGAGTGCAATGG 20885		
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GAM2256	GP5	3'	CCAGGCTGGCGTGCAATGG 16869	T	
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			GGTGACGTG GGTCGGACC		
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GAM2256	GR6	5'	CCAGGCTGGAATGCAGTGG 24743	C	
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			GGTGACGT AGGTCGGACC		
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GAM2256	GREB1	3'	CCAGGCTGGAGTGCAATGG 28558	C	
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GAM2256	GREB1	3'	CCAGGCTGGAGTGCAATGG 28559		
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GAM2256	GTF2E1	3'	CCAGGCTGGAGTGCAATGG	19793	C	
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GAM2256	GTPBG3	3'	CCAGGCTGGAGTGCAAGTGG	51891		
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GAM2256	GTPBG3	3'	CCAGGCTGGAGTTCAGTGG	51892	C	
			CCACTG ACTCCAGCCTGG			
			GGTGAC TGAGGTCGGACC			
			T			
GAM2256	H2AV	3'	CCAGACTGGAGTGCGATGG	57628	C	C
			CCA TGC ACTCCAG CTGG			
			GGT GCGTGAGGTC GACC			
			A A			
GAM2256	HCA4	3'	CCAGGCTGGAGTGCAATTGG	78039	C	
			CCA TGC ACTCCAGCCTGG			
			GGT ACGTGAGGTCGGACC			
			T			
GAM2256	HSC3	3'	CTTAGCTGGGTGCAAGTGG	59731	T	CT
			CCACTGCAC CCAGC GG			
			GGTGACGTG GGTCG TC			
			— AT			
GAM2256	HSMPP8	3'	CCAGGCTGGAGTGCAATGG	95129	C	
			CCA TGC ACTCCAGCCTGG			
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GAM2256	HSPC065	3'	CCATGCTGGAGTGCAAGTGG	27146		C
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			T			
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G CC CTGCACTCCAGCCTGG GAC
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GG GACGTGAGGTCGGACC CTG
C A

GAM2256 KCNH6 3' GTGGCCGGGTGCAGTGG 48575 ACTCCA G
CCACTGC GCCTGGC AC
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GAM2256 KIAA0022 3' CCAGGCTACAGTGCAGTGG 30277 CC
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CCA TGCACTCCAGCCTGG
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GAM2256 KIAA0087 3' CCAGGCTGGAGTGCAGTGG 29341
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GAM2256 KIAA0090 3' CCAGGCTGGAGAGCAGTGG 89813 A
CCACTGC CTCCAGCCTGG
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GGTGACG GAGGTCGGACC
A
GAM2256 KIAA0161 3' CCAAGCTGGAGTACAATG 29194 C C C
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A A A
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GAM2256 KIAA0210 5' CCAGGCTGGAGTATAATGG 29152 C C
CCA TG ACTCCAGCCTGG
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GGT AT TGAGGTCGGACC
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CCA TGCACTCCAGCCTGG
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GAM2256 KIAA0426 3' CCAGGCTGGAGTGCAATGG 28922 C
CCA TGCACTCCAGCCTGG
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GGT ACGTGAGGTCGGACC
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GAM2256 KIAA0427 3' GTCGCCAACTGGCAGCAG 29389 ACT CC
CTGC CCAG TGGCGAC
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GACG GGTC ACCGCTG
AC_ A_
GAM2256 KIAA0431 3' AGTCGCCAGCAACAAGCACGT 31545 _ ACTCCA C
AC TGC GC TGGCGACT
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			C AACAA_ _	
GAM2256	KIAA0441	3'	CCAGGCCAGAGTGTAGTGG 29628	CA
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			GGTGAC TGAGGTCGGACC	
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GAM2256	KIAA0495	3'	CCAGGCTGGAGTGCAATGG 63261	C
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GAM2256	KIAA0513	5'	CCAGGCTGGAGTGCAGAGG 29022	A
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			GG GACGTGAGGTCGGACC	
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GAM2256	KIAA0513	3'	CCAGGCTGGAGTGCAGTG 29023	
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GAM2256	KIAA0513	3'	GCCTGCAGAGTGCAGTG 29039	CA CT
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			GTGACGTGAG CG CCG		
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GAM2256	KIAA0599	3'	CCAGGCTGGAGCGCAGTGG 77687	A	
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			GGTGACG GAGGTCGGACC		
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GAM2256	KIAA0599	3'	CCAGGCTGGAGTGCAATGG 77688		C
			CCA TGCACTCCAGCCTGG		
			GGT ACGTGAGGTCGGACC		
			A		
GAM2256	KIAA0668	3'	GCATGAGGCTGGATGCAGTGG 67121		C G__
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			_ GTA		
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GAM2256	KIAA0841	3'	CCAAGTTGGAGTGCAGTGG	71890	C
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GAM2256	KIAA0931	3'	AGTCGCTCAGGCTGGAGTGCAA	68005	C
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GAM2256	KIAA0961	3'	CCAGGCTGGCGTGCAGTGG	30395	T
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GAM2256	KIAA1017	3'	TGGGACTGGGTGCAGTGG	24271	T
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GAM2256	KIAA1028	3'	CCAAGCTGGAGTGCAGTGG	93587	C
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GAM2256	KIAA1041	3'	CCAGGCTGGAGTGCAGTGG	30820	
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GAM2256 KIAA1117 3' GTTGGGGCCAGGTGCAGT 61774 CCA GG
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GAM2256 KIAA1128 3' CCAGGCTGGATTACAGTGG 68998 CAC
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GAM2256 KIAA1143 3' CCAGGCTGGAGTGCAGTGG 69235
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GAM2256 KIAA1155 3' CCAGGCTGGAGTGCAGTGG 62908
CCACTGCACTCCAGCCTGG
|||||||
GGTGACGTGAGGTCGGACC

GAM2256 KIAA1161 5' CCAGGTTGGAGTGCAGTGG 82644
CCACTGCACTCCAGCCTGG
|||||||
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GAM2256 KIAA1170 3' CCAAGCTGGAGTGCAATGG 70412 C C
CCA TGCACTCCAGC TGG
||| ||||| |||
GGT ACGTGAGGTCG ACC
A A

GAM2256 KIAA1185 3' GTCGCCAGGCTGGAGTGCAGTG 63294
G CCACTGCACTCCAGCCTGGCGAC
|||||||
GGTGACGTGAGGTCGGACCGCTG

GAM2256 KIAA1193 3' GTCGCCAGGCTGGAGTGCAGTG 68277
G CCACTGCACTCCAGCCTGGCGAC
|||||||

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GAM2256 KIAA1198 3' CCAGGCTGGAGTGCAGTGG 64014
CCACTGCACTCCAGCCTGG
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GAM2256 KIAA1198 3' CCAGGCTGGAGTGCAGTGG 64015
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GAM2256 KIAA1198 3' CCAGGCTGGAGTGCAGTGG 64017
CCACTGCACTCCAGCCTGG
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GAM2256 KIAA1198 3' CCAAGCTGGACTGCAGTGG 64011 C C
CCACTGCA TCCAGC TGG
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GGTGACGT AGGTCG ACC
C A

GAM2256 KIAA1198 3' CCAGGCTGGAGTGCAGTGG 64013
CCACTGCACTCCAGCCTGG
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GAM2256 KIAA1210 3' CCAGATTGGAGTGCAGTGG 98067 GC
CCACTGCACTCCA CTGG
||||||| |||
GGTGACGTGAGGT GACC
TA

GAM2256 KIAA1254 3' GCCAGGCTGGAGTGCAGTG 70563
CACTGCACTCCAGCCTGGC
|||||||
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GAM2256 KIAA1257 3' CCAGGCTGGAGTACAATGG 63397 C C
CCA TG ACTCCAGCCTGG
||| || |||||
GGT AC TGAGGTCGGACC
A A

GAM2256 KIAA1257 3' CCAGGCTGGAGTGCAGTGG 63398
CCACTGCACTCCAGCCTGG
|||||||
GGTGACGTGAGGTCGGACC

GAM2256 KIAA1280 5' CCAGGCTGGAGTGCAGTG 70277
CACTGCACTCCAGCCTGG
|||||||

GTGACGTGAGGTCGGACC

GAM2256 KIAA1280 5' GCCAAGCTGGAGTACACGG 70282 AC C C
CC TG ACTCCAGC TGGC
|| || ||||| ||||
GG AC TGAGGTCG ACCG
C_ A A

GAM2256 KIAA1287 3' CCAGGCTGGAGTGCAGTGG 78934
CCACTGCACTCCAGCCTGG
|||||
GGTGACGTGAGGTCGGACC

GAM2256 KIAA1320 5' CCAGGCTGGAGTATAGTG 69834 C
CACTG ACTCCAGCCTGG
|||||
GTGAT TGAGGTCGGACC
A

GAM2256 KIAA1320 5' CCAGGCTGGAGTGCAGTGG 69835
CCACTGCACTCCAGCCTGG
|||||
GGTGACGTGAGGTCGGACC

GAM2256 KIAA1373 3' CCAGGCTGGAGTGCAGTGG 71503
CCACTGCACTCCAGCCTGG
|||||
GGTGACGTGAGGTCGGACC

GAM2256 KIAA1423 3' AGGGGCCAGGTGCAGTGG 62389 ACTCCA GA
CCACTGC GCCTGGC CT
||||| ||||| ||
GGTGACG TGGACCG GA
GG

GAM2256 KIAA1443 3' CCAGGCTGTAGTGCAATGG 64567 C C
CCA TGCACT CAGCCTGG
||| ||||| |||||
GGT ACGTGA GTCGGACC
A T

GAM2256 KIAA1453 5' GTCGCCAGGGCTGCGTAG 47664 ACTC _
CTGC CAGCC TGGCGAC
||| ||||| |||||
GATG GTCGG ACCGCTG
C_ G

GAM2256 KIAA1456 3' CCAGGCTGGAGTGCAGTGG 67541 C
CCA TGCACTCCAGCCTGG
||| |||||
GGT ACGTGAGGTCGGACC
C

GAM2256 KIAA1465 3' GTCGCCAGGGCTGGAGTGCAGTG 61508
G CCACTGCACTCCAGCCTGGCGAC
|||||

GGTGACGTGAGGTCGGACCGCTG

GAM2256 KIAA1467 3' CCAGGCTGGAGTGCAGTGG 72062
CCACTGCACTCCAGCCTGG
|||||
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GAM2256 KIAA1473 3' CCAGGCTGGAGTACAGTGG 71206 C
CCACTG ACTCCAGCCTGG
|||||
GGTGAC TGAGGTCGGACC

A

GAM2256 KIAA1497 5' CCAGGCTGGAGTGCAGTGG 68118
CCACTGCACTCCAGCCTGG
|||||
GGTGACGTGAGGTCGGACC

GAM2256 KIAA1530 3' CCAGGCTGAGTGCAGTGG 68552 C
CCACTGCACTC AGCCTGG
|||||
GGTGACGTGAG TCGGACC

GAM2256 KIAA1530 3' GTCGCCAGGCTGGAGTGCAATG 68569 C
G CCA TGCCTCCAGCCTGGCGAC
|||
GGT ACGTGAGGTCGGACCGCTG

A

GAM2256 KIAA1559 3' CCAGGCTGGAGTGCAGTGG 73452
CCACTGCACTCCAGCCTGG
|||||
GGTGACGTGAGGTCGGACC

GAM2256 KIAA1571 3' CCAGGCTGGAGTGCAGTGG 61613
CCACTGCACTCCAGCCTGG
|||||
GGTGACGTGAGGTCGGACC

GAM2256 KIAA1615 3' GTCACCAGGCCGGAGTGCAGTG 69282 A C
G CCACTGCACTCC GCCTGG GAC
|||||
GGTGACGTGAGG CGGACC CTG

C A

GAM2256 KIAA1655 3' CCAGGCTGGAGTGCAGTGG 67177
CCACTGCACTCCAGCCTGG
|||||
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GAM2256 KIAA1668 3' CCAGGCTGGAGTGCAGTGG 67061
CCACTGCACTCCAGCCTGG
|||||

GGTGACGTGAGGTCGGACC

GAM2256 KIAA1671 3' CCAGGCTGGAATGCAGTGG 66273 C
CCACTGCA TCCAGCCTGG
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A

GAM2256 KIAA1671 3' TCAAGCTGGAGTGGAGTGG 66289 G C
CCACT CACTCCAGC TGG
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GGTGA GTGAGGTCG ACT

G A

GAM2256 KIAA1712 3' CCAGGCTGGAGTGCAGTGG 68151 C
CCA TGCAGTCCAGCCTGG
|| |||||||||||
GGT ACGTGAGGTCGGACC

C

GAM2256 KIAA1727 3' CCAGACTGGACTGCAGTGG 64754 C C
CCACTGCA TCCAG CTGG
||||| |||| |||
GGTGACGT AGGTC GACC

C A

GAM2256 KIAA1755 3' CCAGGCTGGAGTGCAGTGG 62009
CCACTGCACTCCAGCCTGG
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GAM2256 KIAA1784 3' CTAGGCTGGAGTGCAGTGG 65747
CCACTGCACTCCAGCCTGG
|||||||||||||
GGTGACGTGAGGTCGGATC

GAM2256 KIAA1821 3' CCAGGCTGGAGTGTAAGTGG 72261
CCACTGCACTCCAGCCTGG
|||||||||||||
GGTGATGTGAGGTCGGACC

GAM2256 KIAA1829 3' CCAGGCTGGAATGCGGTG 62637 C
CACTGCA TCCAGCCTGG
||||| |||||||
GTGGCGT AGGTCGGACC

A

GAM2256 KIAA1829 3' CCAGGCTGGAGTGCAGTGG 62638
CCACTGCACTCCAGCCTGG
|||||||||||||
GGTGACGTGAGGTCGGACC

GAM2256 KIAA1877 3' CCAGGCTAGAGTGCAGTGG 66744 C
CCACTGCACTC AGCCTGG
||||||||| |||||

			GGTGACGTGAG TCGGACC	
			A	
GAM2256	KIAA1922	5'	CCAGGCTGGAGTGCAATGG 73990	C
			CCA TGC ACTCCAGCCTGG	
			GGT ACGTGAGGTCGGACC	
			A	
GAM2256	KIAA1924	3'	CTAGGCTGGAATGCAGTGG 74045	C
			CCACTGCA TCCAGCCTGG	
			GGTGACGT AGGTCGGATC	
			A	
GAM2256	KIAA1971	3'	CCAGGCTAGAGTGCAGTGG 74670	C
			CCACTGCACTC AGCCTGG	
			GGTGACGTGAG TCGGACC	
			A	
GAM2256	KIAA1971	3'	CCAGGCTGGGGTGCAGTGG 74672	
			CCACTGCACTCCAGCCTGG	
			GGTGACGTGGGGTCGGACC	
GAM2256	KIAA1971	3'	CCAGGCTGGGGTGCAGTGG 74673	
			CCACTGCACTCCAGCCTGG	
			GGTGACGTGGGGTCGGACC	
GAM2256	KIAA1987	5'	CCAGGTTAGAGTGCAGTGG 89379	C
			CCACTGCACTC AGCCTGG	
			GGTGACGTGAG TTGGACC	
			A	
GAM2256	LAMP3	3'	CCAGGCTGGAGTACAGTGG 60200	C
			CCACTG ACTCCAGCCTGG	
			GGTGAC TGAGGTCGGACC	
			A	
GAM2256	LIECG3	3'	CCAGGTTGGAGTGCAGTGG 88797	
			CCACTGCACTCCAGCCTGG	
			GGTGACGTGAGGTTGGACC	
GAM2256	LY75	3'	CCAGGCTGGAGTACAATGG 11391	C C
			CCA TG ACTCCAGCCTGG	
			GGT AC TGAGGTCGGACC	
			A A	
GAM2256	MAIL	3'	CCAGGCTGGAGTACAGTGG 49470	C
			CCACTG ACTCCAGCCTGG	

			GGTGAC TGAGGTCGGACC		
		A			
GAM2256	MAP-1	3'	CCAGGCTGGAGTGCAGTGG 42438		
			CCACTGCACTCCAGCCTGG		
			GGTGACGTGAGGTCGGACC		
GAM2256	MESDC2	3'	TGTTGGGCTGGGTACAGTGG 72925	C T	TG
			CCACTG AC CCAGCC GCG		
			GGTGAC TG GGTCGG TGT		
		A _	GT		
GAM2256	MGC10200	3'	CGCAGGCTAGAGTGCAGTGG 59640	C	G
			CCACTGCACTC AGCCTG CG		
			GGTGACGTGAG TCGGAC GC		
		A _			
GAM2256	MGC10818	3'	CCAGGCTGGAGTACAATGG 48297	C C	
			CCA TG ACTCCAGCCTGG		
			GGT AC TGAGGTCGGACC		
		A A			
GAM2256	MGC10854	3'	AGCCGCCAGGCAGTTTTACAGG 51176	A	CACTCCA A
	G		CC CTG GCCTGGCG CT		
			GG GAC CGGACCGC GA		
		_	ATTTTGA C		
GAM2256	MGC12466	3'	GCTAGGCTGAAGTGTAGTGG 79798	C	
			CCACTGCACT CAGCCTGGC		
			GGTGATGTGA GTCGGATCG		
		A			
GAM2256	MGC13138	3'	CCAGGCTGGAGTGCAGTGG 54156		
			CCACTGCACTCCAGCCTGG		
			GGTGACGTGAGGTCGGACC		
GAM2256	MGC13204	3'	CCAGGCTGGAGTGCAGTGG 49628		
			CCACTGCACTCCAGCCTGG		
			GGTGACGTGAGGTCGGACC		
GAM2256	MGC13251	3'	CGCCAGGCTGCGGACCGG 52135	CA C	
			CTG CT CAGCCTGGCG		
			GGC GG GTCGGACCGC		
		CA C			
GAM2256	MGC14289	3'	CCAGGCTGGAGTGCAGTG 55590		
			CACTGCACTCCAGCCTGG		

GTGACGTGAGGTCGGACC

GAM2256 MGC14836 3' CCAGGCTGGAGTGCAGTGG 54172
CCACTGCACTCCAGCCTGG
|||||
GGTGACGTGAGGTCGGACC

GAM2256 MGC15606 5' CCAGGCTGGAGTACATTGG 59521 C C
CCA TG ACTCCAGCCTGG
||| || |||||
GGT AC TGAGGTCGGACC
T A

GAM2256 MGC1842 3' CCAGACTGGAGTGCAGTGG 66252 C
CCACTGCACTCCAG CTGG
||||| |||
GGTGACGTGAGGTC GACC
A

GAM2256 MGC21675 3' CCAGGCTGGAGTGCAATGG 54589 C
CCA TGCACTCCAGCCTGG
||| |||||
GGT ACGTGAGGTCGGACC
A

GAM2256 MGC2474 3' CCAGGCTGGAATGCAGTGG 43953 C
CCACTGCA TCCAGCCTGG
||||| |||||
GGTGACGT AGGTCGGACC
A

GAM2256 MGC2474 3' CCAGGCTGGAGTGCAATGG 43954 C
CCA TGCACTCCAGCCTGG
||| |||||
GGT ACGTGAGGTCGGACC
A

GAM2256 MGC2477 5' CCAGCTGGAGTGCAGTGG 44294 C
CCACTGCACTCCAGC TGG
||||| |||
GGTGACGTGAGGTCG ACC

GAM2256 MGC2603 3' GTCGCCAGGCTGGAGTGCAGTG 44082
G CCACTGCACTCCAGCCTGGCGAC
|||||
GGTGACGTGAGGTCGGACCGCTG

GAM2256 MGC29891 3' CCAGGCTGGAGTGCGGTGG 58856
CCACTGCACTCCAGCCTGG
|||||
GGTGGCGTGAGGTCGGACC

GAM2256 MGC29898 3' CCAGACTGGAGTGCAGTGG 59585 C
CCACTGCACTCCAG CTGG
||||| |||

			GGTGACGTGAGGTC GACC		
			A		
GAM2256	MGC3113	3'	CCAGGCCGGAGTGCAGTGG 44059	A	
			CCACTGCACTCC GCCTGG		
			GGTGACGTGAGG CGGACC		
			C		
GAM2256	MGC3771	5'	CCATGCTGGAGTGCAATGG 49052	C	C
			CCA TGCCTCCAGC TGG		
			GGT ACGTGAGGTCG ACC		
			A T		
GAM2256	MGC4248	3'	CCAGGCTGGGTGCAGTGG 51313	T	
			CCACTGCAC CCAGCCTGG		
			GGTGACGTG GGTCGGACC		
			—		
GAM2256	MGC4638	3'	GTCACCAGGCTGGAGTGCAGTG 49744		C
			CACTGCACTCCAGCCTGG GAC		
			GTGACGTGAGGTCGGACC CTG		
			A		
GAM2256	MGC5149	3'	GTCACCAGGCTAGAGTGCAGTG 72762	C	C
	G		CCACTGCACTC AGCCTGG GAC		
			GGTGACGTGAG TCGGACC CTG		
			A A		
GAM2256	MGC9912	3'	GTCGCCAGACTGGAGTGCAGTG 55609		C
	G		CCACTGCACTCCAG CTGGCGAC		
			GGTGACGTGAGGTC GACCGCTG		
			A		
GAM2256	MKRN4	3'	CCAGGCTGGAGTGCAGTGG 48456		
			CCACTGCACTCCAGCCTGG		
			GGTGACGTGAGGTCGGACC		
GAM2256	MLZE	5'	AGTTGCCCAGGCTGGAGTGCAG 49447		—
			CTGCACTCCAGCCTGG CGACT		
			GACGTGAGGTCGGACC GTTGA		
			C		
GAM2256	MMPL1	3'	CCAGGCTGGAGTGCAATG 15961	C	
			CA TGCCTCCAGCCTGG		
			GT ACGTGAGGTCGGACC		
			A		
GAM2256	MO25	5'	GCACAGGCCGGAGTGCAGCGG 33289	A	A —
			CC CTGCACTCC GCCTG GC		

			GG GACGTGAGG CGGAC CG	
			C _ A	
GAM2256	moblak	3'	CCAGGCTGGAGTGCAGTGG 56392	
			CCACTGCACTCCAGCCTGG	
			GGTGACGTGAGGTCGGACC	
GAM2256	MOCS3	3'	CCAGGCTGGAGTGTAGTGG 27929	
			CCACTGCACTCCAGCCTGG	
			GGTGATGTGAGGTCGGACC	
GAM2256	MRAS	5'	GCCGGGGCTGGAGCGCGCGG 25237	AC A _
			CC TGC CTCCAGCCT GGC	
			GG GCG GAGGTCGGG CCG	
			C_ C G	
GAM2256	MRPL20	3'	CCAGGCTGGAGTGCAATGG 36201	C
			CCA TGC ACTCCAGCCTGG	
			GGT ACGTGAGGTCGGACC	
			A	
GAM2256	MRPL35	3'	CCAGGCTGGAGTGCAGTGG 34019	
			CCACTGCACTCCAGCCTGG	
			GGTGACGTGAGGTCGGACC	
GAM2256	MRPL44	3'	CCAGGCTGGACTGCAGTGG 43593	C
			CCACTGCA TCCAGCCTGG	
			GGTGACGT AGGTCGGACC	
			C	
GAM2256	MRPS27	3'	CCAGGCTGGAGTGCAGTGG 31326	
			CCACTGCACTCCAGCCTGG	
			GGTGACGTGAGGTCGGACC	
GAM2256	MtFMT	3'	CCAGGCTGGAATCCAGTGG 58332	CAC
			CCACTG TCCAGCCTGG	
			GGTGAC AGGTCGGACC	
			CTA	
GAM2256	MYO5C	3'	TCGCCAGGCTGGAGTGTAGTGG 38727	
			CCACTGCACTCCAGCCTGGCGA	
			GGTGATGTGAGGTCGGACCGCT	
GAM2256	NAPG	5'	CCAGGCTGGAGTGCAGTGG 98534	
			CCACTGCACTCCAGCCTGG	

GGTGACGTGAGGTCGGACC

GAM2256 NDP52 3' CCAGGCTGGCGTGCAATGG 20667 C T
CCA TGCAC CCAGCCTGG
||| ||||| |||||
GGT ACGTG GGTCTGGACC
A C

GAM2256 NDUFB1 5' CCAGGCTGGAGTGTAGTGG 17013
CCACTGCACTCCAGCCTGG
|||||||
GGTGATGTGAGGTCGGACC

GAM2256 NDUFC2 3' TCAGGCTGGAGTGCAGTGG 17037
CCACTGCACTCCAGCCTGG
|||||||
GGTGACGTGAGGTCGGACT

GAM2256 NUDC 5' GCGCGGGACTAGAGTGCAG 22749 C _ _
CTGCACTC AG CCTG GC
||||| || ||| ||
GACGTGAG TC GGGC CG
A A G

GAM2256 NXN 3' CCAGGCTGGAGTGCAGTGG 42670
CCACTGCACTCCAGCCTGG
|||||||
GGTGACGTGAGGTCGGACC

GAM2256 OCT11 3' GCCCAGGCTGGAGTGCAGTGG 27592 _
CCACTGCACTCCAGCCTGG C
||||||| |
GGTGACGTGAGGTCGGACC G
C

GAM2256 OR51E2 3' GTCACCAGGCTGGAGTGCAGTG 48516 C
G CCACTGCACTCCAGCCTGG GAC
||||||| |||
GGTGACGTGAGGTCGGACC CTG
A

GAM2256 OSBPL2 3' CCAGGCTGGAGTGCAATGG 29897 C
CCA TGCCTCCAGCCTGG
||| |||||
GGT ACGTGAGGTCGGACC
A

GAM2256 OSBPL2 3' CCAGGCTGGAGTGCAATGG 58480 C
CCA TGCCTCCAGCCTGG
||| |||||
GGT ACGTGAGGTCGGACC
A

GAM2256 PELI1 5' CCAGGCTGGAGTGCAGTGG 40631
CCACTGCACTCCAGCCTGG
|||||||

GGTGACGTGAGGTCGGACC

GAM2256 PELI1 5' CCAGGCTGGAGTGCAGTGG 40632
CCACTGCACTCCAGCCTGG
|||||||
GGTGACGTGAGGTCGGACC

GAM2256 PELI1 5' CCAGGTTGGAGTGCAGTGG 40633
CCACTGCACTCCAGCCTGG
|||||||
GGTGACGTGAGGTTGGACC

GAM2256 PIP3-E 3' CCAGGCTGGAGTGCAGTGG 67348
CCACTGCACTCCAGCCTGG
|||||||
GGTGACGTGAGGTCGGACC

GAM2256 POFUT1 3' CCAGGCTGGAGTGCAGTGG 70974
CCACTGCACTCCAGCCTGG
|||||||
GGTGACGTGAGGTCGGACC

GAM2256 POLE3 3' CCAGGCTGGAGTGCAGTGG 34313
CCACTGCACTCCAGCCTGG
|||||||
GGTGACGTGAGGTCGGACC

GAM2256 PRO0365 5' GTCGCCAGGCTGAAGTGCAGTG 26993 C
G CCACTGCACT CAGCCTGGCGAC
|||||||
GGTGACGTGA GTCGGACCGCTG
A

GAM2256 PRO0456 3' TTAGGCTGGGTGCAGTGG 27010 T
CCACTGCAC CCAGCCTGG
|||||||
GGTGACGTG GGTCCGATT

GAM2256 PRO0478 3' TCCCAGCCTGGAATGCAGTGG 27039 C C C
CCACTGCA TCCAG CTGG GA
|||||||
GGTGACGT AGGTC GACC CT
A C _

GAM2256 PRO0902 3' CCAGGCTGGAGTGTAGTGG 54964
CCACTGCACTCCAGCCTGG
|||||||
GGTGATGTGAGGTCGGACC

GAM2256 PRO1048 3' CCAGGCTGGAGTACAGTGG 38106 C
CCACTG ACTCCAGCCTGG
|||||||

			GGTGAC TGAGGTCGGACC		
			A		
GAM2256	PRO1992	5'	CCAGACTGGAGTGCAGTGG 26898		C
			CCACTGCACTCCAG CTGG		
			GGTGACGTGAGGTC GACC		
			A		
GAM2256	PRO1992	3'	CCAGGCTGGAGTGCAGTGG 26899		
			CCACTGCACTCCAGCCTGG		
			GGTGACGTGAGGTCGGACC		
GAM2256	PRO2955	3'	CCAGGCTGAAGTGCAGCGG 38236	A	C
			CC CTGCACT CAGCCTGG		
			GG GACGTGA GTCGGACC		
			C A		
GAM2256	PSPH	3'	CCAGGCTGGAGTGCAGTGG 17131		
			CCACTGCACTCCAGCCTGG		
			GGTGACGTGAGGTCGGACC		
GAM2256	PSR	3'	GCCACCAAGGCCAGGTGCAGTG 65787	CCA	_____
	G		CCACTGCACT GCCT GGC		
			GGTGACGTGG CGGA CCG		
			AC_ ACCA		
GAM2256	PSTPIP2	3'	CCAGGCTGAAGTGCAGCGG 44651	A	C
			CC CTGCACT CAGCCTGG		
			GG GACGTGA GTCGGACC		
			C A		
GAM2256	PTD011	5'	CAGGCTGGAGTGCAGTGG 26759		
			CCACTGCACTCCAGCCTG		
			GGTGACGTGAGGTCGGAC		
GAM2256	RAB21	3'	CCAGGCTGGAGTGCAGTGG 31085	C	
			CCA TGCACTCCAGCCTGG		
			GGT ACGTGAGGTCGGACC		
			C		
GAM2256	RAB33B	3'	CCAGGCTGGAGTGCAGTGG 49321		
			CCACTGCACTCCAGCCTGG		
			GGTGACGTGAGGTCGGACC		
GAM2256	RAB39	3'	CCAGGCTGGAGTGCAGTGG 77121		
			CCACTGCACTCCAGCCTGG		

GGTGACGTGAGGTCGGACC

GAM2256 RAI 5' AGTCTCGGCTGGAGTGCAGTGG 22849 T C
CCACTGCACTCCAGCC GG GACT
||||| || ||||
GGTGACGTGAGGTCGG CT CTGA

GAM2256 RAP140 3' CCAAGCTGGAGTACAGTGG 31510 C C
CCACTG ACTCCAGC TGG
||||| ||||| |||
GGTGAC TGAGGTCG ACC
A A

GAM2256 RASSF2 3' CCAGGCTGGAGTGCAGTGG 29092
CCACTGCACTCCAGCCTGG
||||| ||||| |||||
GGTGACGTGAGGTCGGACC

GAM2256 RES4-25 3' CCAGGCTGGAGTGCAATGG 65263 C
CCA TGCACCTCCAGCCTGG
||| ||||| |||||
GGT ACGTGAGGTCGGACC
A

GAM2256 SARM 3' CCAGGCTGGAGGGCAGTG 31283 A
CACTGC CTCCAGCCTGG
||||| ||||| |||||
GTGACG GAGGTCGGACC
G

GAM2256 SCAMP-4 3' CCAGGCTGGAGTGCAGTGG 55342
CCACTGCACTCCAGCCTGG
||||| ||||| |||||
GGTGACGTGAGGTCGGACC

GAM2256 SCAND2 3' CCAGGCTGGAGTGGAGTGG 42142 G
CCACT CACTCCAGCCTGG
||||| ||||| |||||
GGTGA GTGAGGTCGGACC
G

GAM2256 SCYA13 3' TCAAGCTGGAGTACGTG 19430 T C C
CAC G ACTCCAGC TGG
||| | ||||| |||
GTG C TGAGGTCG ACT
_ A A

GAM2256 SCYA16 3' CCAGGCTGGAGTGCAGTGG 17168
CCACTGCACTCCAGCCTGG
||||| ||||| |||||
GGTGACGTGAGGTCGGACC

GAM2256 SCYA22 3' CCAGGCTGGAGTGCAGTGG 92584
CCACTGCACTCCAGCCTGG
||||| ||||| |||||

GGTGACGTGAGGTCGGACC

GAM2256	SCYA22	3'	CCACGCTGGAGTGCAATGG	92583	C	C
			CCA TGC ACTCCAGC TGG			
			GGT ACGTGAGGTCG ACC			
			A C			
GAM2256	SCYA28	3'	CAGGCTGGAGGGCAGTGG	39538	A	
			CCACTGC CTCCAGCCTG			
			GGTGACG GAGGTCGGAC			
			G			
GAM2256	SDC3	3'	GTGGGGCTGGAGCCAATGG	28481	C CA	G
			CCA TG CTCCAGCCT GC			
			GGT AC GAGGTCGGG TG			
			A C_ G			
GAM2256	SERF1B	3'	CCAGGCTGGACTGCAGTGG	43692	C	
			CCACTGCA TCCAGCCTGG			
			GGTGACGT AGGTCGGACC			
			C			
GAM2256	SERF1B	3'	GTCACCAGACTGGAGTGCAGTG	43702	C C	
	G		CCACTGCACTCCAG CTGG GAC			
			GGTGACGTGAGGTC GACC CTG			
			A A			
GAM2256	SFXN2	3'	CCAGGCTGGAATGCAGTGG	74373	C	
			CCACTGCA TCCAGCCTGG			
			GGTGACGT AGGTCGGACC			
			A			
GAM2256	SIRPB1	3'	CCAGGCTGGAGTGCAATG	21359	C	
			CA TGC ACTCCAGCCTGG			
			GT ACGTGAGGTCGGACC			
			A			
GAM2256	SLC12A8	3'	CCAGGCTGGAGTCCAGTGG	45234	C	
			CCACTG ACTCCAGCCTGG			
			GGTGAC TGAGGTCGGACC			
			C			
GAM2256	SLC16A4	3'	CCAGGCTGGAGTGCAGTGG	17448		
			CCACTGCACTCCAGCCTGG			
			GGTGACGTGAGGTCGGACC			
GAM2256	SLC19A3	3'	AGTCAGAGGCTGGAGTGCAATG	48235	C	GGC
	G		CCA TGC ACTCCAGCCT GACT			

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GAM2256	SREC	3'	CCAGGCTGGAGTGCAGTGG 14900	
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GAM2256	SS-56	3'	CCAGGCTGGAGTGCAGTGG 60346	
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GAM2256	STAF65(gamma)	3'	CCAGGCTGGAGTGCAATGG 30064	C
			CCA TGCCTCCAGCCTGG	
			GGT ACGTGAGGTCGGACC	
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GAM2256	SULT1C2	3'	CCAGGCTGGAGTGCAGTGG 22710	
			CCACTGCACTCCAGCCTGG	
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GAM2256	SUN1	3'	CCAGGCTGGAGTGCAGTGG 47911	
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			GGTGACGTGAGGTCGGACC	
GAM2256	SYT12	5'	TCAGGCTGGAGTGCAGTGG 96387	
			CCACTGCACTCCAGCCTGG	
			GGTGACGTGAGGTCGGACT	
GAM2256	SYT13	3'	CCAGGCTGGAGTGCAGTGG 95099	
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GAM2256	TADA3L	3'	CCAGGCTGGAGTGCAGTGG 56806	
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GAM2256	TCL6	5'	TCAGGCTGGAATGCAGTGG 40494	C
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GAM2256	TERA	3'	CCAGGCTGGAGTGCAGTGG 41417		
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GAM2256	TGIF2	3'	CCGGGCTGGAGTGCAGTGG 41745		
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GAM2256	THEA	3'	CCAGGCTGGAGTGCAGTG 66882		
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GAM2256	TOR1B	3'	CCAAGCTGGAGTGCAGTGG 27967	C	
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			GGTGACGTGAGGTCG ACC		
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GAM2256	TRIM16	3'	CCAGGCTGGAGAGCAGTGG 22368	A	
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GAM2256	TRIM35	3'	CCAGGCTGGAGTACAGTGG 61514	C	
			CCACTG ACTCCAGCCTGG		


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GAM2256 TU12B1-TY 3' CCAGGCCGGAGTGCAATGG 33833 C A
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A C
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GAM2256 TUCAN 3' CCAGGCTGGAGTGCAGTGG 30969
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GAM2256 TXNL2 3' CCAGGCTGGAGTGCAGTGG 22578
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GAM2256 VDU1 3' CCAGGCTGGAGTGCTGTGG 31120 T
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GAM2256 VIT1 5' TGCCGGGTGCAGTGG 38609 ACTCCA G
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GAM2256 VPS33A 3' CCAGACTAGAGTGCAGTGG 43611 C C
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GAM2256	ZNF197	3'	TGGGCTGGGTGCAGTGG 23762	T	
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GAM2256	ZNF338	3'	CCAGGCTGGAGTGCAGTGG 42254		
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			GGTGACGTGAGGTCGGACC		
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GAM2256	ZNF339	3'	CCAGGCTGGAGTACAGTGG 41388	C	
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			GGTGAC TGAGGTCGGACC		
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GAM2256	ZNF347	3'	TGACTGGCTGGGTGCAGTGG 51830	T TGG	
			CCACTGCAC CCAGCC CG		
			GGTGACGTG GGTCGG GT		
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GAM2256	LOC112687	3'	CAGGCTGGGTGCAATGG 73225	C T	
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GAM2256	LOC112687	3'	CCAGGCTGGAGTGCAGTGG 73227		
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GAM2256	LOC112817	3'	CCAGGCTGGAGTGCATGG 57320	C	
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	GGT GCGTGAGGTCGGACC		
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GAM2256 LOC116411 5'	CCAGGCTGGAGTGCAGTGG 74295		
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GAM2256 LOC119504 5'	GCCGCTGAGGTGCAGTGG 74446	TC	CT
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	GGTGACGTG GTCG CCG		
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GAM2256 LOC120224 5'	CCAGGCTGGAGTGCAATGG 57884	C	
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GAM2256 LOC120939 3'	GCCCAGGCTGGGATGCAATGG 76765	C	CT
	CCA TGCA CCAGCCTGG C		
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GAM2256 LOC126661 3' AGTTGCCAGGCTGGAGTGCAAG 75049 _
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GAM2256	LOC131308	3'	TCAGGCTGGAGTGCAGTGG	75498		
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GAM2256	LOC131965	3'	CGCAGGCTGGAGTGCAGTGG	75523	G	
			CCACTGCACTCCAGCCTG CG			
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GAM2256	LOC132241	5'	CCAGGCTGGAGTGCAGTGG	75556		
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GAM2256	LOC133686	3'	CCAGGCTGGACTGCAGTGG	75613	C	
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GAM2256	LOC135154	3'	CCAGGCTGGAGTGGAGTGG	75726	G	
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GAM2256	LOC135293	3'	CCAGGCTGAAGTGTAGTGG	76679	C	
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GAM2256	LOC135293	3'	CCAGGCTGGAGTGCAGTGG	76681		
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GAM2256	LOC135763	3'	CCAGGCTGGAGTGCAGTGG	57557		
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GAM2256	LOC138050	5'	CCAGGCTGGAGTGCGGTGG	75812		
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GAM2256 LOC138199 3' CCAGGCCGGAGTGCAGTGG 75822 A
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GAM2256 LOC138241 3' GTCTGCCGGGCACAGTGG 75835 CACTCCA _
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GAM2256 LOC143241 5' CCAGGCTGGAGTGCAATGG 57972 C
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GAM2256 LOC144248 5' CCAGGCTGGAGTGCAATGG 77249 C
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GAM2256 LOC144305 3' CCAGGCTGGAGTGCAGTGG 83969
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GAM2256 LOC145009 3' CCAGGCTGGAGTGCAGTGG 60971
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GAM2256 LOC145268 5' CCAGGCTGGAGCGAAGTG 77574 GCA
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GAM2256 LOC145725 3' GTCACCAGGCTGGAGTACAGTG 77887 C C
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GAM2256 LOC145732 3' GTCACCAGGCTGGAGTACAGTG 77899 C C
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GAM2256 LOC145757 5' CCAGGCTGGAGTGCAGTGG 77922
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GAM2256 LOC145757 5' CCAGGCTGGAGTGCGGTGG 77923
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GAM2256 LOC146272 5' GCCAGCCAGGTGCAGTGG 78327 CCA C
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GAM2256	LOC146895 5'	CCAGGCTGGAGTGCAGTGG 84866	
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GAM2256	LOC146909 3'	CCAGGCTGGAGTGCAGTGG 78763	
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GAM2256 LOC151475 5' CCAGGCTGGAGTGTAGTGG 86587
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GAM2256 LOC152925 3' AGTGGCCCAGGCTGGAGTGCAG 81616 A _ G
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GAM2256 LOC153077 3' CCAGGCTGGAGTGCAGTGG 87117
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GAM2256 LOC153688 3' CCAGGCTGGAGTGCAATGG 87304 C
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GAM2256 LOC154282 5'	GTCGCCAGGTTGGAGTGCAGTG 87412	
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GAM2256 LOC155376 3'	TCAGGCTGGGTGCAGTGG 82250	T
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GAM2256 LOC157506 3' GTCACCAGGCTGGAGTGCAGT 82372 C
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GAM2256 LOC157562 5' GCCAGGCCAGGTGCAGTG 87774 CCA
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GAM2256 LOC196074 5' GCTGAGGCTGGAAACAGCGG 88971 A CAC _
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GAM2256 LOC196264 3' GTCGCCAGGCTGGAGTGCAGTG 88992
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GAM2256 LOC196529 3' CCAGGCTGGAGTGCAATG 89126 C
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GAM2256 LOC196957 3' GTCACCAGGCTGGAGTACAGTG 89193 C C
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GAM2256 LOC196961 3' GTCACCAGGCTGGAGTACAGTG 89206 C C
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GAM2256 LOC200314 3' CCAGGCTGGGGTGCAGTGG 91595
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GAM2256	LOC219673 5'		CCAGGCTGGAGGGCAGTGG 94618	A	
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GAM2256 LOC220575 3' CCAGGCCGGAGTGCAGTGG 76813 A
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GAM2256 LOC220662 3' CCAGGCTGGAGTGCGGTGG 92813
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GAM2256 LOC221060 3' CCAGGCTGGAGTGCAATGG 94830 C
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GAM2256 LOC221271 3' TCAGGCTGGAGTGCAATG 93529 C
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GAM2256	LOC221960 3'	CCAGGCTGGAATGCAATGG 92723	C	C
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GAM2256	LOC222068 3'	CCAGGCTGGAGTGCAATGG 94271	C	
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GAM2256	LOC222070 5'	CCAGGCTGGAGTGCAGTGG 95811		
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GAM2256	LOC222189 5'	GCTGAGAGCTGGAGTACAG 95835	C	_ _
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GAM2256 LOC253805 3' CCAGGCTGGAGTGCAGTG 98170
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GAM2256 LOC254013 3' CCAGGCTGGAGTGCAGTG 96531
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GAM2256 LOC254351 3' CCAGGCTGGAGTGCAATGG 96685 C
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GAM2256 LOC254381 5' AGTCGCCAGAGGGGACGCGCGG 99323 AC_ AGC
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GAM2256 LOC254655 3' CCAGGCTGGAGTGCAGTGG 97216
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GAM2256 LOC254672 3' CCAGGCTGGAGTGCAATGG 96291 C
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GAM2256	LOC256221 3'	TCAGGCTGGAGTGCAGTGG 96920	
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GAM2256 LOC256267 3' TTGTTGCCCGGGTGCAGTGG 98619 T A T
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GAM2256 LOC256306 3' CCAGGCTGGAGTGCAGAGG 98508 A
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GAM2256 LOC256405 5' GTTGGTGCTGGAATGCAGAGG 97559 A C _TG
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GAM2256 LOC256476 5' CCAGGCTGGAGTGCATG 98624 C
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GT ACGTGAGGTCGGACC

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GAM2256 LOC257054 5' CCAGGCTGGAGTGCAGTG 97370
CACTGCACTCCAGCCTGG
|||||||||||||||
GTGACGTGAGGTCGGACC

GAM2256 LOC257463 3' CCAGGCTGGAGTGCAATGG 71619 C
CCA TGCCTCCAGCCTGG
||| |||||||||||||
GGT ACGTGAGGTCGGACC

A

GAM2256 LOC257465 3' CCAGGCTGGAGTGCAGTGG 82492
CCACTGCACTCCAGCCTGG
|||||||||||||||
GGTGACGTGAGGTCGGACC

GAM2256 LOC257486 3' CCAGATTGGAGTGCAGTGG 69768 GC
CCACTGCACTCCA CTGG
|||||||||| ||||
GGTGACGTGAGGT GACC

TA

GAM2256 LOC51031 5' TCAGGCTGGAGTGCAGTGG 32711
CCACTGCACTCCAGCCTGG
|||||||||||||||
GGTGACGTGAGGTCGGACT

GAM2256 LOC51122 3' GCTAAGCTGGGTGCAGTGG 66198 T C
CCACTGCAC CCAGC TGGC
||||||| |||| ||||

		GGTGACGTG GGTCTG ATCG		
		— A		
GAM2256	LOC51193	5' CCAGGCTGGAGGACAGTG	33362	CA
		CACTG CTCCAGCCTGG		
		GTGAC GAGGTCGGACC		
		AG		
GAM2256	LOC51219	5' CCAGGCTGGAGTGCAATGG	33541	C
		CCA TGCACTCCAGCCTGG		
		GGT ACGTGAGGTCGGACC		
		A		
GAM2256	LOC51336	3' CCAGGCTGGAGTGCAATGG	34069	C
		CCA TGCACTCCAGCCTGG		
		GGT ACGTGAGGTCGGACC		
		A		
GAM2256	LOC51622	3' CCAGGCTGGAATGCAATGG	32205	C C
		CCA TGCA TCCAGCCTGG		
		GGT ACGT AGGTCGGACC		
		A A		
GAM2256	LOC55954	5' CCAGGCTGGAGTGTAAGTG	39396	
		CCACTGCACTCCAGCCTGG		
		GGTGATGTGAGGTCGGACC		
GAM2256	LOC56181	5' CCAGGTTGGAGTGCAGTGG	97271	
		CCACTGCACTCCAGCCTGG		
		GGTGACGTGAGGTTGGACC		
GAM2256	LOC57107	3' CCAGGCTGGAGTGCAATGG	40183	C
		CCA TGCACTCCAGCCTGG		
		GGT ACGTGAGGTCGGACC		
		A		
GAM2256	LOC57118	3' TCACTGGGCTGGGTGCAGTGG	40227	T TG C
		CCACTGCAC CCAGCC G GA		
		GGTGACGTG GGTCTG C CT		
		— GT A		
GAM2256	LOC57146	3' CCAGGCTGGAGTGCAACGG	40293	AC
		CC TGCACTCCAGCCTGG		
		GG ACGTGAGGTCGGACC		
		CA		
GAM2256	LOC81034	3' CCAGGCTGGAGTGCAGTGG	48586	
		CCACTGCACTCCAGCCTGG		

GGTGACGTGAGGTCGGACC

GAM2256	LOC89231	3'	CCAGGCTGGAGTGCAATGG	94294	C	
			CCA TGC ACTCCAGCCTGG			
			GGT ACGTGAGGTCGGACC			
			A			
GAM2256	LOC89932	3'	CCAGGCTGGAGGGCAATGG	61451	C	A
			CCA TGC CTCCAGCCTGG			
			GGT ACG GAGGTCGGACC			
			A G			
GAM2256	LOC89932	3'	CCAGGCTGGAGTACAATGG	61452	C	C
			CCA TG ACTCCAGCCTGG			
			GGT AC TGAGGTCGGACC			
			A A			
GAM2256	LOC90141	3'	CCTAAGCTGGAGTACAGTG	62302	C	CT_
			CACTG ACTCCAGC GG			
			GTGAC TGAGGTCG CC			
			A AAT			
GAM2256	LOC90155	3'	CCAGGCTAGAGTGCAGTGG	62364	C	
			CCACTGCACTC AGCCTGG			
			GGTGACGTGAG TCGGACC			
			A			
GAM2256	LOC90288	3'	CCAGGCTGGAGTGCAGTGG	62778		
			CCACTGCACTCCAGCCTGG			
			GGTGACGTGAGGTCGGACC			
GAM2256	LOC90333	3'	CCAGGTTGGAGTGCAGTGG	62957		
			CCACTGCACTCCAGCCTGG			
			GGTGACGTGAGGTTGGACC			
GAM2256	LOC90371	5'	CCAGGCTGGAGTGCAGTGG	63158		
			CCACTGCACTCCAGCCTGG			
			GGTGACGTGAGGTCGGACC			
GAM2256	LOC90408	5'	CCAGGCTGGAGTGCAGTGG	63340		
			CCACTGCACTCCAGCCTGG			
			GGTGACGTGAGGTCGGACC			
GAM2256	LOC90485	3'	CCAGGCTAGAGTGCAGTGG	63692	C	
			CCACTGCACTC AGCCTGG			

		GGTGACGTGAG TCGGACC	
		A	
GAM2256	LOC90485	3' CCAGGCTGGAGTGCAGTG 63693	
		CACTGCACTCCAGCCTGG	
		GTGACGTGAGGTCGGACC	
GAM2256	LOC90589	3' GTTTGCCCGGGTGCAGTGG 59777	T A TG
		CCACTGCAC CC GCC GC	
		GGTGACGTG GG CGG TG	
		_ C TT	
GAM2256	LOC90591	3' CCAGGCTGGAGTGCAGTGG 64157	
		CCACTGCACTCCAGCCTGG	
		GGTGACGTGAGGTCGGACC	
GAM2256	LOC90591	3' CCAGGCTGGAGTGCAGTGG 64158	
		CCACTGCACTCCAGCCTGG	
		GGTGACGTGAGGTCGGACC	
GAM2256	LOC90639	3' CAGGCTGGGCGCAGCGG 64405	A A T
		CC CTGC C CCAGCCTG	
		GG GACG G GGTCGGAC	
		C C _	
GAM2256	LOC90999	3' CCAGGCTGGAGTACAGTGG 65182	C
		CCACTG ACTCCAGCCTGG	
		GGTGAC TGAGGTCGGACC	
		A	
GAM2256	LOC91115	3' CCAGGCTGGAGTGCAATGG 65553	C
		CCA TGCACTCCAGCCTGG	
		GGT ACGTGAGGTCGGACC	
		A	
GAM2256	LOC91115	3' CCAGGCTGGAGTGCAATGG 65554	C
		CCA TGCACTCCAGCCTGG	
		GGT ACGTGAGGTCGGACC	
		A	
GAM2256	LOC91115	3' CCAGGCTGGAGTGCTGTGG 65555	T
		CCAC GCACTCCAGCCTGG	
		GGTG CGTGAGGTCGGACC	
		T	
GAM2256	LOC91291	5' CCAGACTAGAATGCAGTGG 66086	C C C
		CCACTGCA TC AG CTGG	

			GGTGACGT AG TC GACC		
			A A A		
GAM2256	LOC91373	3'	CCAGGCTGGAGTGAAGTGG 66409	G	
			CCACT CACTCCAGCCTGG		
			GGTGA GTGAGGTCGGACC		
			A		
GAM2256	LOC91380	3'	GTCCAGGCTGGAGTTCAGTGG 66452	C	—
			CCACTG ACTCCAGCCTGG C		
			GGTGAC TGAGGTCGGACC G		
			T T		
GAM2256	LOC91661	3'	CCAGGCTGGAATGCAATGG 57209	C	C
			CCA TGCA TCCAGCCTGG		
			GGT ACGT AGGTCGGACC		
			A A		
GAM2256	LOC91893	3'	CCAGGCGGGAGTGCAAGTGG 68069		A
			CCACTGCACTCC GCCTGG		
			GGTGACGTGAGG CGGACC		
			G		
GAM2256	LOC92148	5'	CCAGGCTAGAGTGCAAGTGG 68872		C
			CCACTGCACTC AGCCTGG		
			GGTGACGTGAG TCGGACC		
			A		
GAM2256	LOC92267	3'	CCAGGCTGGAGTGCCGTGG 69168		T
			CCAC GCACTCCAGCCTGG		
			GGTG CGTGAGGTCGGACC		
			C		
GAM2256	LOC92283	3'	CCAGGCTGGAGTCCAGTGG 69300		C
			CCACTG ACTCCAGCCTGG		
			GGTGAC TGAGGTCGGACC		
			C		
GAM2256	LOC92299	3'	TTAGGCTGGGCGCAGTGG 69376		A T
			CCACTGC C CCAGCCTGG		
			GGTGACG G GGTCCGATT		
			C _		
GAM2256	LOC92303	3'	CCGGGCTGGAGTGCAATGG 69390		C
			CCA TGCACTCCAGCCTGG		
			GGT ACGTGAGGTCGGGCC		
			A		
GAM2256	LOC92466	3'	TTGTTGGCCGGGTGCAAGTGG 69975		T A T
			CCACTGCAC CC GCC GGCGA		

GGTGACGTG GG CGG TTGTT
 _ C _
 GAM2256 LOC92568 3' GCTGGAGGCTGGGTGCAGTGG 70329 T _
 CCACTGCAC CCAGCCT GGC
 ||||| ||||| ||
 GGTGACGTG GGTGCGGA TCG
 _ GG
 GAM2256 LOC92609 3' CCAGGCTGGAGTGCATTG 73207 C
 CA TGCACTCCAGCCTGG
 || |||||
 GT ACGTGAGGTCGGACC
 T
 GAM2256 LOC92661 5' CCAGGCTGGAGTGCAGTGG 70623
 CCACTGCACTCCAGCCTGG
 |||||
 GGTGACGTGAGGTCGGACC

 GAM2256 LOC92697 5' CCAGGCTGGAGTGCAGTGG 70806
 CCACTGCACTCCAGCCTGG
 |||||
 GGTGACGTGAGGTCGGACC

 GAM2256 LOC92841 3' CCAGGCTGGAGTGCAATGG 71249 C
 CCA TGCACTCCAGCCTGG
 || |||||
 GGT ACGTGAGGTCGGACC
 A
 GAM2256 LOC93129 3' CCAGGCTGGAGTGTAGTG 71954
 CACTGCACTCCAGCCTGG
 |||||
 GTGATGTGAGGTCGGACC

 GAM2256 LOC93132 5' GTCACCAGGCTGGAGGGCAGTG 71998 A C
 G CCACTGC CTCCAGCCTGG GAC
 ||||| ||||| ||
 GGTGACG GAGGTCGGACC CTG
 G A
 GAM2256 LOC93408 5' CCAGGCTGGAGCGCAATGG 57285 C A
 CCA TGC CTCCAGCCTGG
 || || |||||
 GGT ACG GAGGTCGGACC
 A C
 GAM2256 LOC93613 5' TCACCCCGGGAGTGCAGCTGG 73081 _ AGCCT C
 CCA CTGCACTCC GG GA
 || ||||| ||
 GGT GACGTGAGG CC CT
 C GCCC_ A
 GAM2257 ADORA3 5' AAGAGCAGCAGCACTTTC 7282 AGA
 GAAGG TGCTGCTCTT
 |||| |||||

		CTTTC ACGACGAGAA	
		ACG	
GAM2257	ATP6V0E	3' AAGATGGCTCCTGCCTTCTCA 15460	_ AT C
		TGAGAAGG AG GCTG TCTT	
		ACTCTTCC TC CGGT AGAA	
		G CT _	
GAM2257	ATP7A	3' AAGAAGCATGCCTCCTTCTC 5308	AT _ _
		GAGAAGGAG GC TGCT CTT	
		CTCTTCCTC CG ACGA GAA	
		_ T A	
GAM2257	BCRP2	3' AGCCTTACCTCCTTCTCA 63067	A CT
		TGAGAAGGAG TG GCT	
		ACTCTTCCTC AT CGA	
		C TC	
GAM2257	CALR	3' AAGAACGGGGCTCTTCTCA 63656	G ATG C
		TGAGAAG AG CTG TCTT	
		ACTCTTC TC GGC AGAA	
		_ GG_ A	
GAM2257	CNGA3	3' AAGAGACATCCCCTCCTTCTCA 8937	ATGC _
		TGAGAAGGAG TG CTCTT	
		ACTCTTCCTC AC GAGAA	
		CCCT A	
GAM2257	COLQ	3' AAGAGGCTCCTCTTCTCA 20250	GA T TG
		TGAGAAG GA GC CTCTT	
		ACTCTTC CT CG GAGAA	
		TC _ _	
GAM2257	COLQ	3' AAGAGGCTCCTCTTCTCA 55409	GA T TG
		TGAGAAG GA GC CTCTT	
		ACTCTTC CT CG GAGAA	
		TC _ _	
GAM2257	COLQ	3' AAGAGGCTCCTCTTCTCA 55411	GA T TG
		TGAGAAG GA GC CTCTT	
		ACTCTTC CT CG GAGAA	
		TC _ _	
GAM2257	COLQ	3' AAGAGGCTCCTCTTCTCA 55413	GA T TG
		TGAGAAG GA GC CTCTT	
		ACTCTTC CT CG GAGAA	
		TC _ _	
GAM2257	COLQ	3' AAGAGGCTCCTCTTCTCA 55415	GA T TG
		TGAGAAG GA GC CTCTT	

			ACTCTTC CT CG GAGAA		
			TC _ _		
GAM2257 COLQ	3'	AAGAGGCTCCTCTCTCA	55417	GA T TG	
		TGAGAAG GA GC CTCTT			
		ACTCTTC CT CG GAGAA			
		TC _ _			
GAM2257 DAPK1	3'	AGCTAGTGTACCTCCTCTCA	18225	A _ _	
		TGAGA GGAG ATGCT GCT			
		ACTCT CCTC TGTGA CGA			
		_ CA T			
GAM2257 GNB3	3'	AAGAACTGCCCCATCTCCTCCC	10841	A A CT _	
A		TG GA GGAGATG GC TCTT			
		AC CT CCTCTAC CG AGAA			
		C _ CC TCA			
GAM2257 HOXD4	3'	AAGTCTCAGCTCTCCTTCTCA	28253	T CT_	
		TGAGAAGGAGA GCTG CTT			
		ACTCTTCCTCT CGAC GAA			
		_ TCT			
GAM2257 KNSL1	3'	AAGAACTGTACTCTTCTCA	16936	G A TGC	
		TGAGAAG AG TGC TCTT			
		ACTCTTC TC ATG AGAA			
		_ _ TCA			
GAM2257 MMP15	3'	AAGAGCAGCACCTCCTC	11608	A A	
		GA GGAG TGCTGCTCTT			
		CT CCTC ACGACGAGAA			
		_ C			
GAM2257 MTNR1B	3'	AAGAGCCCAACTCCTTCTCA	21055	A CT	
		TGAGAAGGAG TG GCTCTT			
		ACTCTTCCTC AC CGAGAA			
		A C_			
GAM2257 PLA2G2D	3'	AGCTCTGGCATCCCCACCTCA	25705	AA A _	
		TGAG GG GATGCT GCT			
		ACTC CC CTACGG CGA			
		CA C TCT			
GAM2257 PTP4A2	3'	AAGAGGAGTCTCTTCTCA	14434	G AT G	
		TGAGAAG AG GCT CTCTT			
		ACTCTTC TC TGA GAGAA			
		_ _ G			
GAM2257 SMOH	3'	AAGATGCATCATCTTCCTCA	20091	A C _	
		TGAG AGGAGATG TGC TCTT			

ACTC TTCTCTAC ACG AGAA
 C T T
 GAM2257 SNAI1 3' AGGACCCCACATCCTTCTCA 21120 GA CTGC
 TGAGAAGGA TG TCTT
 ||||| || |||
 ACTCTTCCT AC AGGA
 AC CCC_
 GAM2257 THY1 3' AAGGGCAGCCCTCCTTACCA 21893 AG AT
 TG AAGGAG GCTGCTCTT
 || |||| |||||
 AC TTCCTC CGACGGGAA
 CA C_
 GAM2257 TNFRSF6B 5' AAGAGCAGGCGACCCCCTC 33594 AA AGA _
 GAG GG TGC TGCTCTT
 ||| || ||| |||||
 CTC CC GCG ACGAGAA
 CC AG_ G
 GAM2257 TRHDE 5' AAGAGCAGCTCACCCTTCGCA 26311 A A_ T
 TG GAAGG GA GCTGCTCTT
 || |||| || |||||
 AC CTTCC CT CGACGAGAA
 G CA _
 GAM2257 XPNPEP1 3' AAGAACAGAAAATCTTCTTA 40199 AGATG C
 TGAGAAGG CTG TCTT
 ||||| ||| |||
 ATTCTTCT GAC AGAA
 AAAA_ A
 GAM2257 C20orf110 3' AAGAGCTGAATCTCCCTCCA 80360 A A GCT
 TG GA GGAGAT GCTCTT
 || || |||| |||||
 AC CT CCTCTA CGAGAA
 _ C AGT
 GAM2257 CAMTA1 3' AAGAAGCCATTTCTTCTCA 68502 CT _
 TGAGAAGGAGATG GCT CTT
 ||||| ||| |||
 ACTCTTCCTTTAC CGA GAA
 _ A
 GAM2257 CAMTA1 3' AAGAGGCTTCCTCTTCTCA 68503 GA T TG
 TGAGAAG GA GC CTCTT
 ||||| || || |||||
 ACTCTTC CT CG GAGAA
 TC T _
 GAM2257 D21S2056E 3' AAGACATTTCTCCTTTCA 14858 A TGC C
 TGAGA GGAGA TG TCTT
 |||| |||| || |||
 ACTTT CCTCT AC AGAA
 _ TT_ _
 GAM2257 dJ309H15.1 3' AAGATGTGTCTCCTCCCA 57565 A A TGC
 TG GA GGAGATGC TCTT
 || || ||||| |||

	AC CT CCTCTGTG AGAA	
	C _ T__	
GAM2257 FLJ10211	5' AAGAGCTGCAGCCCTTCTCA 36361	AGA_ T
	TGAGAAGG TGC GCTCTT	
	ACTCTTCT ACG CGAGAA	
	CCCG T	
GAM2257 FLJ11042	3' AAGAACATTTTTCCTTTTCA 37559	TGC C
	TGAGAAGGAGA TG TCTT	
	ACTTTTCCTTT AC AGAA	
	TT_ A	
GAM2257 FLJ11210	3' AGAAGTTCACCTTCTCA 60316	A T G
	TGAGAAGG GA GCT CT	
	ACTCTTCC CT TGA GA	
	A _ A	
GAM2257 FLJ11383	3' AGAGAAGCTCTTCTCA 46854	AGAT G
	TGAGAAGG GCT CTCT	
	ACTCTTCT CGA GAGA	
	_____ A	
GAM2257 FLJ12604	5' AGAAGTATACCTCCTTCT 65060	___ G
	AGAAGGAG ATGCT CT	
	TCTTCCTC TATGA GA	
	CA A	
GAM2257 FLJ13659	3' AAGAGTGGCACTCCATCTCA 48024	A A TG
	TGAGA GGAG TGC CTCTT	
	ACTCT CCTC ACG GAGAA	
	A _ GT	
GAM2257 FLJ14642	3' AAGAGCTGGAGCTCCCTCT 52570	A ATG _
	AGA GGAG CT GCTCTT	
	TCT CCTC GG CGAGAA	
	C GA_ T	
GAM2257 FLJ22671	3' AAGATATGCCTCCTTCTC 46308	AT TGC
	GAGAAGGAG GC TCTT	
	CTCTTCCTC CG AGAA	
	___ TAT	
GAM2257 FUSIP1	3' GAGGGCCCATCTCTTCTCA 22781	G CT
	TGAGAAG AGATG GCTCTT	
	ACTCTTC TCTAC CGGGAG	
	_ C_	
GAM2257 H2BFQ	3' AAGAGCCTTTTCCTTCTC 60074	TGCT
	GAGAAGGAGA GCTCTT	

CTCTTCCTTT CGAGAA
 TC__
 GAM2257 KIAA0594 3' AAGAGCCTTCCCTTCTTA 65502 A TGCT
 TGAGAAGG GA GCTCTT
 ||||| || |||||
 ATTCTTCC CT CGAGAA
 _ TC__
 GAM2257 KIAA0987 3' AAGAGCAGCACCCTGACA 25505 AGA AGA
 TG AGG TGCTGCTCTT
 || ||| |||||
 AC TCC ACGACGAGAA
 AG_ C__
 GAM2257 KIAA1128 3' AAGAGCAGCCTTTTTCATCA 68994 _ AT
 TGA GAAGGAG GCTGCTCTT
 ||| ||||| |||||
 ACTCTTTTC CGACGAGAA
 A _
 GAM2257 KIAA1297 5' AAGAGCAGCAGCAAGCCCTCA 72623 AA AGA__
 TGAG GG TGCTGCTCTT
 ||| || |||||
 ACTC CC ACGACGAGAA
 _ GAACG
 GAM2257 KIAA1615 3' AGTGTGATCTCCTTTCCA 69265 AG _ T
 TG AAGGAGAT GC GCT
 || ||||| || |||
 AC TTCCTCTA TG TGA
 CT G _
 GAM2257 KIAA1737 3' AAGAGCTTTTCCTTCT 67926 TGCT
 AGAAGGAGA GCTCTT
 ||||| |||||
 TCTTCCTTT CGAGAA
 T__
 GAM2257 KIAA1829 3' AAGAGCGAAACTCCTTCTCA 62623 ATGC
 TGAGAAGGAG TGCTCTT
 ||||| |||||
 ACTCTTCCTC GCGAGAA
 AAA_
 GAM2257 KRTAP1-3 3' AAGAGCCATCTGTCCTTCTCA 49043 _ CT
 TGAGAAGGA GATG GCTCTT
 ||||| ||| |||||
 ACTCTTCCT CTAC CGAGAA
 GT _
 GAM2257 LHX6 3' AAGAGCAGGCACCACTCA 27641 AA AGA _
 TGAG GG TGC TGCTCTT
 ||| || ||| |||||
 ACTC CC ACG ACGAGAA
 A_ _ G
 GAM2257 MADHIP 5' AAGATTCTAGATCCCCCTTCTC 17813 A_ G C_
 A TGAGAAGG GAT CTG TCTT
 ||||| ||| ||| |||

				ACTCTTCC	CTA	GAT	AGAA			
				CC	_	CTT				
GAM2257	MAPK8IP3	3'	AAGAGCAAGGGTTTTCCTTTCA	54134		A	G	_		
			TGAGA GGAGAT CT GCTCTT							
			ACTTT CTTTGTG GA CGAGAA							
			C	G	A					
GAM2257	MGC4309	3'	AAGAGCAGGTTCCCTGTCA	44366	GA	ATG				
			TGA AGGAG CTGCTCTT							
			ACT TCCTT GACGAGAA							
			G	G	_					
GAM2257	MGC5149	3'	AAGAGCAGTGGAGACTTCTC	72748		GAGA				
			GAGAAG TGCTGCTCTT							
			CTCTTC GTGACGAGAA							
			AGAG							
GAM2257	MGC5528	3'	AAGAACAACAGTCTTTTCTTC	44272		T	C	_		
			GAAGGAGA GCTG TCTT							
			CTTCTTTT TGAC AGAA							
			C	AACA						
GAM2257	NTSR2	3'	AAGAACAGCACCCATCTC	25629	A	AGA	C			
			GAGA GG TGCTG TCTT							
			CTCT CC ACGAC AGAA							
			A	C	_	A				
GAM2257	RA410	3'	AAGAGCAATATGTTTCCTTCTC	32753		C	_			
			GAGAAGGAGATG TGCTCTT							
			CTCTTCCTTTGT ACGAGAA							
			ATA							
GAM2257	RDHL	3'	AAGAACACATCTCCTTTTCA	60691		C	C			
			TGAGAAGGAGATG TG TCTT							
			ACTTTTCCTCTAC AC AGAA							
			_	A						
GAM2257	LOC116228	3'	AAGAGCATTTTCCCTCCCA	74221	A	A	TGC			
			TG GA GGAGA TGCTCTT							
			AC CT CCTTT ACGAGAA							
			C	C	T	_				
GAM2257	LOC118738	3'	AAGAGCTGTTTCCTTTCCA	75998	AG	GCT				
			TG AAGGAGAT GCTCTT							
			AC TTCCTTTG CGAGAA							
			CT	T	_					
GAM2257	LOC125535	5'	AAGAGCAGCTAGTGGCTTCCA	76170	A	GAGAT	_			
			TG GAAG GCTGCTCTT							

	AC CTTC CGACGAGAA	
	_ GGTGAT	
GAM2257 LOC146346 5'	AAGAGGCCTTCCCTTCCCA	78380 A AG T TG
	TG GAAGG A GC CTCTT	
	AC CTTCC T CG GAGAA	
	C CT C _	
GAM2257 LOC148397 3'	AAGATTAAATCTCCTTC	79554 GC C
	GAAGGAGAT TG TCTT	
	CTTCCTCTA AT AGAA	
	A_ T	
GAM2257 LOC150685 5'	AAGAGCTCCGTTCTTCTCA	88533 GA CT
	TGAGAAG GATG GCTCTT	
	ACTCTTC TTGC CGAGAA	
	_ CT	
GAM2257 LOC151278 5'	AGCCGGTTCACCTCCTTCTC	81009 AT_ _
	GAGAAGGAG GCTG CT	
	CTCTTCCTC TGGC GA	
	CACT C	
GAM2257 LOC157503 3'	AAGAGCAAAATCATCCTTC	87761 _ GC
	GAAGGA GAT TGCTCTT	
	CTTCCT CTA ACGAGAA	
	A AA	
GAM2257 LOC219735 3'	AAGAGCAGTCAACCACTCA	94719 AA AGAT
	TGAG GG GCTGCTCTT	
	ACTC CC TGACGAGAA	
	A_ AAC_	
GAM2257 LOC220370 3'	AAGAGCAGCAGTTTCTC	94389 GAGA
	GAGAAG TGCTGCTCTT	
	CTCTTT ACGACGAGAA	
	TG_	
GAM2257 LOC221416 3'	GGCTGCATCTCCCCTCA	95407 AA T
	TGAG GGAGATGC GCT	
	ACTC CCTCTACG CGG	
	C_ T	
GAM2257 LOC221813 5'	AGAAGTTCCCTTCTCA	95550 A T G
	TGAGAAGG GA GCT CT	
	ACTCTTCC CT TGA GA	
	_ _ A	
GAM2257 LOC256946 3'	GAGGGCCCATCTCTTCTCA	96183 G CT
	TGAGAAG AGATG GCTCTT	

	ACTCTTC TCTAC CGGGAG	
	— C—	
GAM2257 LOC90499 3'	GGAGCAGCACCTCACCTCA 63743	AAG A
	TGAG GAG TGCTGCTCT	
	ACTC CTC ACGACGAGG	
	CCA C	
GAM2257 LOC91010 3'	AAGAGCAGAGGTCTTCTC 65221	AGATG
	GAGAAGG CTGCTCTT	
	CTCTTCT GACGAGAA	
	GGA—	
GAM2258 CBFA2T1 3'	ACAATGTTCTTTATATACA 16358	TAGT A
	TGTGTAT GAA CATTGT	
	ACATATA CTT GTAACA	
	TTT— —	
GAM2258 DGKB 3'	TACAATACCTTGCTATATATAC 94110	— TG AAC
ATA	TATGTGTAT TAG A ATTGTA	
	ATACATATA ATC T TAACAT	
	T GT CCA	
GAM2258 PYGL 3'	TACAATGTCTCTAGAAAACATA 12694	GTA T AA
	TATGT TTAG GA CATTGTA	
	ATACA GATC CT GTAACAT	
	AAA T —	
GAM2258 FLJ23342 3'	ACAATGTTTCATTTTACACAT 45251	TT
	ATGTGTA AGTGAAACATTGT	
	TACACAT TTTGTAACA	
	TT	
GAM2258 KIAA1598 3'	TACAATGTTTCAGGCTACCACA 37641	TAT —
	TGTG TAGT GAAACATTGTA	
	ACAC ATCG CTTTGTAACAT	
	C— GA	
GAM2258 PANX3 3'	ATGCACACTAATACACATA 54766	AAA
	TATGTGTATTAGTG CAT	
	ATACACATAATCAC GTA	
	AC—	
GAM2258 UBE2V2 3'	ACAATGCAAAATACACAT 13972	AG AAA
	ATGTGTATT TG CATTGT	
	TACACATAA AC GTAACA	
	A— —	
GAM2258 LOC152195 5'	ACAATGTGACCACACACA 86745	ATTA AA—
	TGTGT GTG ACATTGT	

		ACACA CAC TGTAACA	
		____ CAG	
GAM2259 APP	5'	GGATCCCCTCGCACAGCAGCG 6663	A TCAAC C
		CGTTGCTG GC GGA CC	
		GCGACGAC CG CCCT GG	
		A CTCA_ A	
GAM2259 CAPN7	5'	GGCCCCAGCCCGGCAACG 27454	A CAAC AC
		CGTTGCTG GCT GGG CC	
		GCAACGGC CGA CCC GG	
		C ____ CA	
GAM2259 TACC3	5'	GGGCTCAGAGCCCGGCAACG 22020	A AAC A
		CGTTGCTG GCTC GGG CCC	
		GCAACGGC CGAG CTC GGG	
		C A__ _	
GAM2259 DD96	3'	TGGGGCTGAGGCTCAGCAAC 20466	CAA GA
		GTTGCTGAGCT CGG CCA	
		CAACGACTCGG GTC GGGT	
		A__ G__	
GAM2259 FLJ10961	3'	TGGGTCCCAATATCAGAAAC 64224	G GCTCAAC
		GTT CTGA GGGACCA	
		CAA GACT CCCTGGGT	
		A ATAA__	
GAM2259 KIAA1274	5'	GGTCCCGTCGCCGGTGAGC 93014	_ A TCA
		GTT GCTG GC ACGGGACC	
		CGA TGGC CG TGCCCTGG	
		G _ C__	
GAM2259 PSKH1	3'	TGGGTCCCCTGAGCCTCA 68803	_ AC
		TGAG CTCA GGGACCA	
		ACTC GAGT CCCTGGGT	
		C CA	
GAM2259 ZNF31	3'	GGCCACTGTGAGCTCAGCAC 65614	T ACG_ A
		GT GCTGAGCTCA GG CC	
		CA CGACTCGAGT CC GG	
		_ GTCA _	
GAM2259 LOC123872	5'	TGGATGCTCTTAACCTCAGCAA 74712	CTCAAC AC_
C		GTTGCTGAG GGG CCA	
		CAACGACTC CTC GGT	
		CAATT_ GTA	
GAM2259 LOC129831	3'	TGGAATAACCCAAGTCAGCAAC 75399	G CAAC AC__
		GTTGCTGA CT GGG CCA	

		CAACGACT GA CCC GGT		
		_ A_ AATAA		
GAM2259	LOC148397 3'	CCCGCAGTGTGAGCAACG	79567	_ CAA
		CGTTGCTGA GCT CGGG		
		GCAACGACT TGA GCCC		
		G C_		
GAM2259	LOC149707 5'	GTCCTTGAGCTCCACAAC	80298	CT AC
		GTTG GAGCTCA GGGAC		
		CAAC CTCGAGT TCCTG		
		AC _		
GAM2259	LOC158236 5'	TGGGTCCCGGGCCTCCAAAAC	88012	GCT _ CAA
		GTT GAG CT CGGGACCCA		
		CAA CTC GG GCCCTGGGT		
		AAC C _		
GAM2259	LOC169026 5'	TGGGCAGTGAGTTCAACAAC	83605	C A GGGA
		GTTG TGAGCTCA C CCCA		
		CAAC ACTTGAGT G GGGT		
		A _ AC_		
GAM2259	LOC197342 3'	GGCCCCAGGGGAGCTCAGCAGC	89372	AAC_ A
		GTTGCTGAGCTC GGG CC		
		CGACGACTCGAG CCC GG		
		GGA C		
GAM2259	LOC200227 5'	GTCCTTGAGCTCCACAAC	90043	CT AC
		GTTG GAGCTCA GGGAC		
		CAAC CTCGAGT TCCTG		
		AC _		
GAM2259	LOC202551 3'	CCATTGTGCTCAGCAACG	60748	T C
		CGTTGCTGAGC CAA GG		
		GCAACGACTCG GTT CC		
		T A		
GAM2259	LOC91942 5'	GGGTCCCGCTGCTGGCAGCG	68199	G TCAA
		CGTTGCT AGC CGGGACCC		
		GCGACGG TCG GCCCTGGG		
		_ TC_		
GAM2259	LOC92841 5'	GGGCTCCCGAGTCTCAGCAAC	71257	_ AAC _
		GTTGCTGAG CTC GGGA CCC		
		CAACGACTC GAG CCCT GGG		
		T _ C		
GAM2260	EIF2AK3 3'	GTCCCCCTGTGTGGTAAC	17902	_ ACAAGA
		GTTGCCAC CGGG GGAC		

		CAATGGTG GTCC CCTG	
		T C_____	
GAM2260 FMNL	5'	TCCTCCCCGTCGCTGTGGCAAC 20874	C _ AA_
		GTTGCCAC GG GAC GAGGA	
		CAACGGTG TC CTG CTCCT	
		_ G CCC	
GAM2260 ITGA4	5'	GGTGTGTCCCCTGGCAAC 7957	C AGAGG
		GTTGCCAC GGGACA ACC	
		CAACGGTG CCCTGT TGG	
		_ G_____	
GAM2260 KCNE1L	3'	GTTTTTCATCCCAGTGGTAAC 25390	C CAA
		GTTGCCAC GGGA GAGGAC	
		CAATGGTG CCCT CTTTGT	
		A A_	
GAM2260 MAPRE2	3'	GGGTCCTCTTTGGTGGGCAGC 27334	_ GGAC
		GTTGCC ACCG AAGAGGACCC	
		CGACGG TGGT TTCTCCTGGG	
		G _____	
GAM2260 UBTF	3'	GGGTCCTCCTCCAGGGACAGCA 27256	CA_ G CAA
AC		GTTGC CC GGA GAGGACCC	
		CAACG GG CCT CTCCTGGG	
		ACAG A C_	
GAM2260 BRD4	3'	GGGTCCTCTGGGTGGGTGGCA 55253	GGG A_
		TGCCACC AC AGAGGACCC	
		ACGGTGG TG TCTCCTGGG	
		G_ GG	
GAM2260 FLJ14451	3'	GGGTCCTCTTGTCCATCTTCAA 52397	GCCACCG
GC		GTT GGACAAGAGGACCC	
		CGA CCTGTTCTCCTGGG	
		ACTTCTA	
GAM2260 KIAA0350	3'	TTTTTGTCCTCAGTGAGAAC 61834	GC C
		GTT CAC GGGACAAGAG	
		CAA GTG CCCTGTTTTT	
		GA A	
GAM2260 MGC2848	3'	GGGCCCTGGACCAGTGGCAGC 52998	C GA A A A
		GTTGCCAC GG CA G GG CCC	
		CGACGGTG CC GT C CC GGG	
		A AG _ _ _	
GAM2260 PIG7	5'	GGGTCCTCTTACTGCTGATGGC 17971	C GAC_
A		TGCCA CGG AAGAGGACCC	

		ACGGT GTC TTCTCCTGGG		
		A GTCA		
GAM2260	SCAND2	3' GGTGGAATCCCACTGGCAAC 54420	C	CAAGAGG
		GTTGCCAC GGGA ACC		
		CAACGGTG CCCT TGG		
		A AAGG__		
GAM2260	TTYH2	3' GGCTGGTGAACCCCGGTGGGAA 51979	G	A__ AGA A
	C	GTT CCACCGGG CA GG CC		
		CAA GGTGGCCC GT TC GG		
		G CAA GG_ _		
GAM2260	LOC139941	5' GGTCCTCTGAGGGAGCAAC 75911	CA	GGGACA
		GTTGC CC AGAGGACC		
		CAACG GG TCTCCTGG		
		AG AG__		
GAM2260	LOC144100	3' GGGTCTTCCACCCCGCGGCC 77184	T A	ACAA
	AC	GT GCC CCGGG GAGGACCC		
		CA CGG GGCCC CTTCTGGG		
		C C CACC		
GAM2260	LOC148764	5' GGGTCCTCCTCATTCTGGCAGC 79739	CCGG	CAA
		GTTGCCA GA GAGGACCC		
		CGACGGT CT CTCCTGGG		
		CTTA C__		
GAM2260	LOC152274	3' GGGTCCCCTTGCGGCTAGGCA 81343	A__	GGA A
		TGCC CCG CAAG GGACCC		
		ACGG GGC GTTC CCTGGG		
		ATC __ C		
GAM2260	LOC221178	3' GGGTCCTCAGTGCAGAGCAAC 95173	CACCGGG	AA
		GTTGC AC GAGGACCC		
		CAACG TG CTCCTGGG		
		AGACG__ A_		
GAM2260	LOC253868	5' GGCCCCGTCCGGTGGAAAC 97324	G	ACAAGA A
		GTT CCACCGGG GG CC		
		CAA GGTGGCCT CC GG		
		_ GCC__ _		
GAM2260	LOC90787	5' GGATCCTCTTCTTGGTGGCAGC 64735	CA	_
		GTTGCCACCGGGA AGAGGA CC		
		CGACGGTGGTTCT TCTCCT GG		
		_ A		
GAM2260	LOC90936	5' GGATCCTCTTCTTGGTGGCAGC 65057	C	CA _
		GTTGCCA CGGGA AGAGGA CC		

			CGACGGT GTTCT TCTCCT GG		
			A _ A		
GAM2261	MADH6	3'	CGATGCCCAGAGACACAGCCC 19974	T	AT_
			GGGCT TGTCTCTGG TCG		
			CCCGA ACAGAGACC AGC		
			C CGT		
GAM2261	FLJ10276	3'	GAATCCAGAGACCAAACCC 36423	C T	
			GGG TT GTCTCTGGATTC		
			CCC AA CAGAGACCTAAG		
			A C		
GAM2261	LOC202908	5'	CCACCTTCTAAGAGACAAAGAC 90717	G	_ TTCGA
			C GG CTTTGTCTCT GGA TGG		
			CC GAAACAGAGA TCT ACC		
			A A TCC_		
GAM2261	LOC222057	5'	CCACCTTCTAAGAGACAAAGAC 94348	G	_ TTCGA
			C GG CTTTGTCTCT GGA TGG		
			CC GAAACAGAGA TCT ACC		
			A A TCC_		
GAM2261	LOC255975	5'	CCACCTTCTAAGAGACAAAGAC 97574	G	_ TTCGA
			C GG CTTTGTCTCT GGA TGG		
			CC GAAACAGAGA TCT ACC		
			A A TCC_		
GAM2261	LOC256878	5'	CCACCTTCTAAGAGACAAAGAC 98685	G	_ TTCGA
			C GG CTTTGTCTCT GGA TGG		
			CC GAAACAGAGA TCT ACC		
			A A TCC_		
GAM2262	SCAMP1	3'	GCTAAATAAATATTCTCC 54500	T C	
			GGA AATATT ATTTAGC		
			CCT TTATAA TAAATCG		
			C A		
GAM2262	SCAMP1	3'	GCTAAATAAATATTCTCC 54501	T C	
			GGA AATATT ATTTAGC		
			CCT TTATAA TAAATCG		
			C A		
GAM2262	NX-17	3'	TGAATATCAGCCCCTAATA 40706	ATA_	
			TATTAGGG ATATTCA		
			ATAATCCC TATAAGT		
			CGAC		
GAM2262	LOC161589	3'	GCTAAATGAATATTATCCCTAA 83159		
			TA TATTAGGGATAATATTCATTTAGC		

ATAATCCCTATTATAAGTAAATCG

GAM2263 ADAT1 3' CCAGCAAAGAATGAAGGC 24914 _ C
GTC CATTCTTTGC GG
||| ||||| ||
CGG GTAAGAAACG CC
AA A

GAM2263 M17S2 5' CCGGTAGCGGACGGTCCTT 20910 ATTCT
AAGGACCGTCC TTGCCGG
||||||| |||||
TTCCTGGCAGG GATGGCC
C _

GAM2263 ST14 5' CCGGCAGGGACGACGCCT 42042 AC CAT
AGG CGTC TCTTTGCCGG
||| ||| |||||
TCC GCAG AGGGACGGCC
_ C _

GAM2263 HTGN29 5' GCCAACTGTGTGGCGGTCC 39885 _ TC T
GGACCGTC CAT TT GC
||||| ||| |||
CCTGGCGG GTG AA CG
T TC C

GAM2263 PMAIP1 3' GCAAGAATGGAAGACCCTT 41211 ACCG T
AAGG TCCATTCTT GC
||| ||||| ||
TTCC AGGTAAGAA CG
CAGA _

GAM2263 LOC144278 3' GCCAGCAAAGACTGCTCGATGG 77274 _ T C
TCCT AGGACCGTC CA TCTTTGC GGC
||||| || ||||| |||
TCCTGGTAG GT AGAAACG CCG
CTC C A

GAM2263 LOC147976 3' CCGGTGAATGAAGACCCT 79287 ACC CA _ TG
AGG GTC TTC TT CCGG
||| ||| ||| |||
TCC CAG AAG AA GGCC
_ _ T GT

GAM2263 LOC254263 5' GCCGGCAGCGGACGCGCC 96367 AC ATTCT
GG CGTCC TTGCCGGC
|| |||| |||||
CC GCAGG GACGGCCG
GC C _

GAM2264 FLJ21438 5' CAAAACGCTTCCCCCATCCCA 62190 GAGATTATC
TGGGA AAGCGTTTTG
||||| |||||
ACCCT TTCGCAAAAC
ACCCCC _

GAM2264 FLJ32334 3' AAAACGCTATTCCTTCCCA 58605 A TTATCA
TGGGAG GA AGCGTTTT
||||| ||| |||||

		ACCCTT CT TCGCAAAA		
		C TA_____		
GAM2264	HHLA2	3' CAATGTACTTTGTAATCTCCCC 23953	A	C CG T
	CA	TGGG GAGATTAT AAG T TTG		
		ACCC CTCTAATG TTC G AAC		
		C T AT T		
GAM2265	ADCY8	5' GCTCACAGCGCTGCGGCTCCT 8501	A AT	CAA
		AGGA CC GGC CTGTGAGC		
		TCCT GG TCG GACACTCG		
		C CG C__		
GAM2265	CIT	5' GCTCACAGAGCTACAGCTCTCC 70304	ACCA__	CAA
		GGA TGGC CTGTGAGC		
		CCT ATCG GACACTCG		
		CTCGAC A__		
GAM2265	FAAH	5' GCGGTCTCCGGCCATGGCCCC 97238	AA	A__
		GG CCATGGCC ACTGT		
		CC GGTACCGG TGGCG		
		CC CCTC		
GAM2265	GSTM3	5' GCTCACAGTTTCCCTAGTCCT 68638	ACCAT	CC
		AGGA GG AACTGTGAGC		
		TCCT CC TTGACACTCG		
		GAT__ CT		
GAM2265	HMX1	3' GCGGTGCGCCATGGCC 38947	AA	A
		GG CCATGGCC ACTGT		
		CC GGTACCGG TGGCG		
		__ C		
GAM2265	HSD11B2	3' GCTCCGTGAGCCTTGGTTCCT 5771	T	CA T T
		AGGAACCA GGC AC G GAGC		
		TCCTTGGT CCG TG C CTCG		
		T AG __		
GAM2265	HYAL1	5' CTCCAGTGGCCATGCTCC 24603	AC	A T
		GGA CATGGCCA CTG GAG		
		CCT GTACCGGT GAC CTC		
		C_ _ _		
GAM2265	NPTX2	3' GCTGGAGTGGCCATGTCCCTT 94085	AAC	A G G
		AAGG CATGGCCA CT T AGC		
		TTCC GTACCGGT GA G TCG		
		CT_ _ G_		
GAM2265	RFX2	3' GCCCCACCAGACCATGGGTTCC 7158	_	CCAA _ A_
	TT	AAGGAACC ATGG CTG TG GC		

TTCCTTGG TACC GAC AC CG
 G A__ C CC
 GAM2265 SMAP 5' GCCCCACAGAGCCATGGTCC 22932 A CAA A_
 GGA CCATGGC CTGTG GC
 ||| ||||| |||| ||
 CCT GGTACCG GACAC CG
 _ A__ CC
 GAM2265 SMURF1 3' GCTCACAGCCCTGAGCTCTTT 94049 AC_ T CAAC
 AAGGA CA GGC TGTGAGC
 |||| || ||| |||||
 TTTCT GT CCG ACACTCG
 CGA C ____
 GAM2265 DC-TM4F2 3' ACTGTTGGCCAGGGCTCCT 48895 A A T
 AGGA CC TGGCCAAC GT
 |||| || ||||| ||
 TCCT GG ACCGGTTG CA
 C G T
 GAM2265 DKFZp566H0824 5' GCTCACAAACCCCATAGTTGCC 34488 _ C CCAAC
 T AGG AAC ATGG TGTGAGC
 ||| ||| ||| |||||
 TCC TTG TACC ACACTCG
 G A CCAA_
 GAM2265 FLJ10292 3' GCCCACAGTTGTTGTTGTTGCC 36432 C GGC A
 T AGGAAC AT CAACTGTG GC
 ||||| || ||||| ||
 TCCTTG TG GTTGACAC CG
 T GTT C
 GAM2265 FLJ20085 3' GCTCATGGTGCCACAGCCCCT 35009 AACCA CA
 AGG TGGC ACTGTGAGC
 || ||| |||||
 TCC ACCG TGGTACTCG
 CCGAC _
 GAM2265 FLJ22690 3' GCTCACAGCCGACCTGTGGCCT 45575 AA CCAA_
 AGG CCATGG CTGTGAGC
 || ||||| |||||
 TCC GGTGTC GACACTCG
 _ CAGCC
 GAM2265 FLJ32449 3' GCATTTGGCCATGGTTCCTT 59378 C
 AAGGAACCATGGCCAA TGT
 ||||| ||||| |||
 TTCCTTGGTACCGGTT ACG
 T
 GAM2265 HPIP 3' GCTCACAGCTGCCTTGGCCCC 40425 AA T CAA
 GG CCA GGC CTGTGAGC
 || ||| ||| |||||
 CC GGT CCG GACACTCG
 CC T TC_
 GAM2265 ILF3 3' GCTCACAGTCGAACTACAGCTC 25234 ACCA CCA_
 C GGA TGG ACTGTGAGC
 ||| ||| |||||

			CCT ATC TGACACTCG		
			CGAC AAGC		
GAM2265 KIAA1190	3'	GCTCACAGAGCACCCCCAGTTCC 71651		CAT CCAA	
	T	AGGAAC GG CTGTGAGC			
		TCCTTG CC GACACTCG			
		ACC ACGA			
GAM2265 MGC11266	3'	GCTCACAGTGGTCAGGGCCC 44488	AA A A		
		GG CC TGGCCA CTGTGAGC			
		CC GG ACTGGT GACACTCG			
		CG _ _			
GAM2265 MGC11352	5'	ACTGTTGGCCAGGGCTCCT 65424	A A T		
		AGGA CC TGGCCAAC GT			
		TCCT GG ACCGGTTG CA			
		C G T			
GAM2265 MKP-7	3'	GCTTCTCTTGGCCATGGTCCC 67015	A CTGT		
		GG ACCATGGCCAA GAGC			
		CC TGGTACCGGT TTCG			
		C CTC_			
GAM2265 MSP	3'	GCTCAGGCAGGCCATGGCC 50245	AA AA G		
		GG CCATGGCC CT TGAGC			
		CC GGTACCGG GG ACTCG			
		_ AC _			
GAM2265 PGR1	3'	CTCACAGTTGGAGTTCTCC 53905	A CATGG		
		A GGAAC CCAACTGTGAG			
		C TCTTG GGTGACACTC			
		C A_			
GAM2265 PTPRT	3'	GCTTCGTGTTGGCCAAGACTCC 56502	ACCA TGT		
	TT	AAGGA TGGCCAAC GAGC			
		TTCCT ACCGGTTG TTCG			
		CAGA TGC			
GAM2265 TRF4-2	3'	CTCAAACAAGCCATGGTTCCTT 42611	CAACTG		
		AAGGAACCATGGC TGAG			
		TTCCTTGGTACCG ACTC			
		AACAA_			
GAM2265 LOC122786	3'	GCCTTTGGCCATGATTCT 74622	C CT		
		GGAA CATGGCCAA GT			
		TCTT GTACCGGT CG			
		A TC			
GAM2265 LOC138428	3'	TAGTGGCCATGGCTGCCT 75862	AA_ A		
		AGG CCATGGCCA CTG			

TCC GGTACCGGT GAT
 GTC _
 GAM2265 LOC145581 3' GCTCCATTAGACCATGGTTC 77794 CCAAC T
 GAACCATGG TG GAGC
 ||||| |||||
 CTTGGTACC AC CTCG
 AGATT _
 GAM2265 LOC146268 5' GCTCACAGTCGGCTTGCTGCCT 78342 AAC T A
 AGG CA GGCC ACTGTGAGC
 || ||||| |||||
 TCC GT TCGG TGACACTCG
 GTC _ C
 GAM2265 LOC147299 3' GCTGTGAGCCGCCATGGTCCC 78981 A CAA GTG
 GG ACCATGGC CT AGC
 || ||||| || |||
 CC TGGTACCG GA TCG
 C CC_ GTG
 GAM2265 LOC159199 3' GCTCACAGCTGGCGGCCCT 83062 AA ATG A
 AGG CC GCCA CTGTGAGC
 || || ||||| |||||
 TCC GG CGGT GACACTCG
 C_ _ C
 GAM2265 LOC200982 5' AGTTGGCCATGGCTCTTT 91807 A
 AAGGA CCATGGCCAAC
 ||||| |||||
 TTTCT GGTACCGGTTGA
 C
 GAM2265 LOC253842 3' GCTCATAGAAGCCTGGTCCCT 99238 A T CAA
 AGG ACCA GGC CTGTGAGC
 || ||||| || |||||
 TCC TGGT CCG GATACTCG
 C _ AA_
 GAM2265 LOC254778 3' GCCCTGTGTTGGCCAAGGTTCC 97831 A TGTGA
 GGAACC TGGCCAAC GC
 ||||| ||||| ||
 CCTTGG ACCGGTTG CG
 A TGTCC
 GAM2265 LOC255231 3' CTCACAGTTAGCCAGCTGACC 97119 AACCA C
 GG TGGC AACTGTGAG
 || ||||| |||||
 CC ACCG TTGACACTC
 AGTCG A
 GAM2265 LOC257358 5' GCTCGTGAAGAGCATGGTTCCT 98900 G CAACTG
 T AAGGAACCATG C TGAGC
 ||||| || |||||
 TTCCTTGGTAC G GCTCG
 _ AGAAGT
 GAM2265 LOC90190 3' CGCCCACAGAGCAATTGGCCAT 62422 AC _ A _
 GCCTCC GGA CATGGCCAA CTGTG GC G
 || ||||| ||||| || |

CCT GTACCGGTT GACAC CG C
 CC AACGA C ____
 GAM2265 LOC90495 3' GCTCACAGTCAACTGCTTTCTT 63737 CCAT CA____
 T AAGGAA GGC ACTGTGAGC
 ||||| ||| |||||
 TTTCTT TCG TGACACTCG
 ____ TCAAC
 GAM2265 LOC90750 3' GCTCACAGCCCTGCCCTGCCCC 64630 AAC T CAA_
 C GG CA GGC CTGTGAGC
 || ||||| |||||
 CC GT CCG GACACTCG
 CCC C TCCC
 GAM2266 COL4A3 3' CCAGAAAGAATGTTTCAGA 49382 G AGCGA CA
 TCTGAACA TC TTC GG
 ||||| || ||| ||
 AGACTTGT AG AAG CC
 A A____ AC
 GAM2266 PCSK1 3' ACCTGGAGTATAATATTCAGA 6511 CAGTCAGCG
 TCTGAA ATTCCAGGT
 ||||| |||||
 AGACTT TGAGGTCCA
 ATAATA____
 GAM2266 CIC 3' ACCTGGAGCGTGTGACCTTCAG 31367 CA _ A
 A TCTGAA GTCA GCG TTCCAGGT
 ||||| ||||| |||||
 AGACTT CAGT TGC GAGGTCCA
 C_ G _
 GAM2266 KIAA0574 3' CCCATGCTGACTCTCAGA 69810 AC ATTCCA
 TCTGA AGTCAGCG GG
 ||||| ||||| ||
 AGACT TCAGTCGT CC
 C_ AC____
 GAM2266 KIAA1950 3' ACCTGGGAGGTAAGTGTGCCAG 94175 A_ CA GA
 A TCTG ACAGT GC TTCCAGGT
 ||||| ||||| || |||||
 AGAC TGTCA TG AGGGTCCA
 CG A_ G_
 GAM2266 LOC115265 3' ACCTAAAATGTCACTGTTCA 73740 CA G CC
 TGAACAGT GC ATT AGGT
 ||||| || ||| |||||
 ACTTGTCA TG TAA TCCA
 C_ _ AA
 GAM2266 LOC202025 5' CCTGGAACACTGTTTCAGG 91886 CAGCGA
 TCTGAACAGT TTCCAGG
 ||||| |||||
 GGAATTGTCA AAGGTCC
 C____
 GAM2266 LOC253769 5' ACCTGGTCTCTGGCTGTCCAGA 99018 A C TT
 TCTG ACAGTCAG GA CCAGGT
 ||||| ||||| || |||||

AGAC TGTCGGTC CT GGTCCA
 C T _
 GAM2267 EHF 3' TCCAAAACCCAAGGTTGGCT 25127 AT _ C
 AGT GCCT GGGT TTGGA
 ||| |||| |||| ||||
 TCG TGA CCA AACCT
 GT A A
 GAM2267 EPHA2 3' CCATCGGCCAAGAATACTTGAA 16675 GC G T_
 G CTTCAAGTAT CT GGTC TGG
 ||||| || |||| ||
 GAAGTTCATA GA CCGG ACC
 A_ A CT
 GAM2267 ITGA5 3' CCCAGAGACATACTTGAAG 61933 C_
 CTTCAAGTATG CTGGG
 ||||| ||||
 GAAGTTCATAC GACCC
 AGA
 GAM2267 TREM2 3' TCCAAGACTGTCATATTT 39098 CCTG
 AAGTATG GGTCTTGGA
 |||| |||||
 TTTATAC TCAGAACCT
 TG_
 GAM2267 UQCRB 3' CCAACATAGGCATACTTAAG 21939 C GGTC
 CTT AAGTATGCCTG TTGG
 || ||||| ||||
 GAA TTCATACGGAT AACC
 _ AC_
 GAM2267 ATP10D 3' CAGAGACCACTTGAAG 73526 ATGCCTG _
 CTTCAAGT GGTCT TG
 |||| |||| ||
 GAAGTTCA CCAGA AC
 _ G
 GAM2267 B3GNT7 3' CCCTTCCAGGCAACCTGAA 71678 A A TCTT
 TTCA GT TGCCTGGG GG
 ||| || ||||| ||
 AAGT CA ACGGACCT CC
 C _ TC_
 GAM2267 DKFZp547I224 3' TCCAAAATTGACCACATACTTG 39963 CCTG ____
 GA TTCAAGTATG GGTC TTGGA
 ||||| || ||||
 AGGTTTCATAC CCAG AACCT
 A_ TTAA
 GAM2267 FLJ22341 3' CCAAGCTCAGGCACACCCAAG 45114 CAA A T
 CTT GT TGCCTGGG CTTGG
 || || ||||| ||||
 GAA CA ACGGACTC GAACC
 CC_ C _
 GAM2267 KIAA0779 3' CCGAACAGCATACTTGAAG 86908 C GGTC
 CTTCAAGTATGC TG TTGG
 ||||| || ||||

GAAGTTCATACG AC AGCC
 _ A_
 GAM2267 LOC144233 3' CCAAGGCACATAATTGAA 77246 G CCTGG
 TTCAA TATG GTCTTGG
 ||||| ||| |||||
 AAGTT ATAC CGGAACC
 A A_
 GAM2267 LOC147341 3' ACCCAGGCATAACTGAAG 85116 AG
 CTTCA TATGCCTGGGT
 ||||| |||||
 GAAGT ATACGGACCCA
 CA
 GAM2267 LOC221088 5' TCCAAGGTGCTGGCCACTCGAA 94888 A AT TGGG
 G CTTT AGT GCC TCTTGA
 ||||| ||| ||| |||||
 GAAG TCA CGG GGAACCT
 C C_ TCGT
 GAM2268 COL5A3 3' CTCCCCACCCCTTGAACC 32316 A AA
 GGTTC AAGGG TGG AG
 ||||| ||| ||
 CCAAGTTCCC ACC TC
 C CC
 GAM2268 EN2 5' GTGACTCACACCCCTGAACCGC 9268 A A GAA
 GTGGTTCA GGG TG AGTCAC
 ||||| ||| || |||||
 CGCCAAGT CCC AC TCAGTG
 C _ AC_
 GAM2268 FKBP10 3' TTCCATCCCTAAACCAC 41939 CA
 GTGGTT AGGGATGGAA
 ||||| |||||
 CACCAA TCCCTACCTT
 A_
 GAM2268 OAS3 3' TGA CTCTATCCTCATACCAC 21658 TCAA AA
 GTGGT GGGATGGA GTCA
 ||||| ||||| |||
 CACCA TCCTATCT CAGT
 TAC_ _
 GAM2268 ZNF179 3' ACTTCTACCCTTAAAC 24087 C A A
 GTT AAGGG TGGAA GT
 ||| ||||| ||||| ||
 CAA TTCCC ATCTT CA
 A _ _
 GAM2268 ASP 3' ACTTACCCTGAATCAC 96288 A ATGGA
 GTGGTTCA GGG AAGT
 ||||| ||| |||
 CACTAAGT CCC TTCA
 _ A_
 GAM2268 ASP 3' ACTTACCCTGAATCAC 50009 A ATGGA
 GTGGTTCA GGG AAGT
 ||||| ||| |||

CACTAAGT CCC TTCA
 _ A_
 GAM2268 KIAA0669 3' TGACCTATAATCTTTGAACCAC 29433 ___ AAA
 GTGGTTCAAGGG ATGG GTCA
 ||||| ||| |||
 CACCAAGTTTCT TATC CAGT
 AA _
 GAM2268 KIAA1881 3' GTGACCTTCTTAACTGAGCCAC 97089 A GGAT A
 GTGGTTCA G GGAA GTCAC
 ||||| | ||| ||||
 CACCGAGT C TCTT CAGTG
 AAT C
 GAM2268 KIAA1958 5' GTGACTTTGAACCCCAAACC 82788 CAA ATGG
 GGTT GGG AAAGTCAC
 ||| ||| |||||
 CCAA CCC TTTCAGTG
 A_ CAAG
 GAM2268 MARCKS 3' ACTTTCCACCCTGCCCAT 11412 TTCA A
 GTGG AGGG TGGAAAGT
 ||| ||| |||||
 TACC TCCC ACCTTTCA
 CG_ _
 GAM2268 TUB 5' GTGGGACCATCCCTTAAACCC 13899 T C AAAG
 G GGTT AAGGGATGG TCAC
 | ||| ||||| |||
 C CCAA TTCCCTACC GGTG
 _ A AG_
 GAM2268 LOC253782 3' TGACTTTCCTGTTACTAAACAC 97406 GTTCA GG _
 GTG AG AT GGAAAGTCA
 ||| || |||||
 CAC TC TG CCTTTCAGT
 AAA_ AT T
 GAM2268 LOC256073 5' ACCTTCCATCCCCCATCCAT 98484 TTCAA A
 GTGG GGGATGGAA GT
 ||| ||||| ||
 TACC CCCTACCTT CA
 TACCC C
 GAM2268 LOC80298 3' ACTTTTACCTTGAACCAT 48064 GATG
 GTGGTTCAAGG GAAAGT
 ||||| |||||
 TACCAAGTTCC TTTCA
 A_
 GAM2268 LOC90620 3' ACTTCCCATTCTGAACC 64324 A GG A
 GGTTCA G ATGG AAGT
 ||||| | ||| |||
 CCAAGT C TACC TTCA
 _TT C
 GAM2269 CCNDBP1 5' TGCTCTCCCCCGCTGCATCCT 54472 AA_ T
 AGGATGCAG GGAGA CA
 ||||| ||||| ||

		TCCTACGTC CCTCT GT	
		GCCC C	
GAM2269	CHAT	5' GCAGGTCCACACCTCTGCATCC 40970	A AGATC _
		GGATGCAGA GG ACC GC	
		CCTACGTCT CC TGG CG	
		_ ACACC A	
GAM2269	COG7	5' GGCTCGCTCGCTTCTGCATCC 68256	_ ATCACC
		GGATGCAGAAG GAG GCC	
		CCTACGTCTTC CTC CGG	
		G GCT__	
GAM2269	DAP	3' GGCAGTAGGGTACCCTGCGTCC 72948	AA AGA _ C
	T	AGGATGCAG GG TC AC GCC	
		TCCTGCGTC CC GG TG CGG	
		_ ATG A A	
GAM2269	DMD	3' GGCAGCGCATTGTTTTGCATCC 5466	G GATCACC
	T	AGGATGCAGAA GA GCC	
		TCCTACGTTTT TT CGG	
		G ACGCGA_	
GAM2269	DMD	3' GGCAGCGCATTGTTTTGCATCC 15679	G GATCACC
	T	AGGATGCAGAA GA GCC	
		TCCTACGTTTT TT CGG	
		G ACGCGA_	
GAM2269	DMD	3' GGCAGCGCATTGTTTTGCATCC 15682	G GATCACC
	T	AGGATGCAGAA GA GCC	
		TCCTACGTTTT TT CGG	
		G ACGCGA_	
GAM2269	DMD	3' GGCAGCGCATTGTTTTGCATCC 15686	G GATCACC
	T	AGGATGCAGAA GA GCC	
		TCCTACGTTTT TT CGG	
		G ACGCGA_	
GAM2269	DMD	3' GGCAGCGCATTGTTTTGCATCC 15690	G GATCACC
	T	AGGATGCAGAA GA GCC	
		TCCTACGTTTT TT CGG	
		G ACGCGA_	
GAM2269	DMD	3' GGCAGCGCATTGTTTTGCATCC 15694	G GATCACC
	T	AGGATGCAGAA GA GCC	
		TCCTACGTTTT TT CGG	
		G ACGCGA_	
GAM2269	DMD	3' GGCAGCGCATTGTTTTGCATCC 15698	G GATCACC
	T	AGGATGCAGAA GA GCC	

			TCCTACGTTTT TT	CGG	
			G ACGCGA_		
GAM2269	DMD	3'	GGCAGCGCATTGTTTTGCATCC	15702	G GATCACC
	T		AGGATGCAGAA GA	GCC	
			TCCTACGTTTT TT	CGG	
			G ACGCGA_		
GAM2269	DMD	3'	GGCAGCGCATTGTTTTGCATCC	15706	G GATCACC
	T		AGGATGCAGAA GA	GCC	
			TCCTACGTTTT TT	CGG	
			G ACGCGA_		
GAM2269	DMD	3'	GGCAGCGCATTGTTTTGCATCC	15709	G GATCACC
	T		AGGATGCAGAA GA	GCC	
			TCCTACGTTTT TT	CGG	
			G ACGCGA_		
GAM2269	DMD	3'	GGCAGCGCATTGTTTTGCATCC	15712	G GATCACC
	T		AGGATGCAGAA GA	GCC	
			TCCTACGTTTT TT	CGG	
			G ACGCGA_		
GAM2269	DMD	3'	GGCAGCGCATTGTTTTGCATCC	15716	G GATCACC
	T		AGGATGCAGAA GA	GCC	
			TCCTACGTTTT TT	CGG	
			G ACGCGA_		
GAM2269	DMD	3'	GGCAGCGCATTGTTTTGCATCC	15724	G GATCACC
	T		AGGATGCAGAA GA	GCC	
			TCCTACGTTTT TT	CGG	
			G ACGCGA_		
GAM2269	FAT	3'	CGGGGACCTTCTGCATACC	19130 _	AGA A
			GG ATGCAGAAGG TC	CCG	
			CC TACGTCTTCC	AG GGC	
			A _ G		
GAM2269	GNB1	3'	GTAGTGGCTTCTCCATCCT	10839	C GAGA CG
			AGGATG AGAAG TCAC	C	
			TCCTAC TCTTC	GGTG G	
			C _ AT		
GAM2269	HAP1	3'	GACCCTCCTTCCCATCCT	15475	CA A_
			AGGATG GAAGGAG TC		
			TCCTAC CTTCTC	AG	
			C_ CC		
GAM2269	INSRR	3'	GGCCCTCCTTCCGCCTCCT	68991	T A ATCA
			AGGA GC GAAGGAG	CC	

			TCCT CG CTCCTC GG		
			C C CC__		
GAM2269	MVK	3'	GGCATGGTCTGCCCTCTGCATC 61280	A _	CC
	CT		AGGATGCAGA GG AGATCA GCC		
			TCCTACGTCT CC TCTGGT CGG		
			C G A_		
GAM2269	SIAT7D	5'	GCGGGTGA AAAACCTACGTCCT 27705	CAGA	AGA_
			AGGATG AGG TCACCGCC		
			TCCTGC TCC AGTGGCGG		
			A__ AAAA		
GAM2269	UBQLN1	5'	GCGGCGTGCTCTGCATTCT 26476	AGGA	ATCA
			AGGATGCAGA G CCGC		
			TCTTACGTCT C GGCG		
			__GTGC		
GAM2269	CALP	5'	GTCTCGTTCTGCACCCT 48173	A	_
			AGG TGCAGAAG GAGAT		
			TCC ACGTCTTC CTCTG		
			C G		
GAM2269	CECR6	3'	GGTGTCTTCTGCACCCT 49933	A	GAT
			AGG TGCAGAAGGA CACC		
			TCC ACGTCTTCCT GTGG		
			C _		
GAM2269	CENTB1	5'	GTGCCTCCACCTGCATCC 28869	AA	AT
			GGATGCAG GGAG CAC		
			CCTACGTC CCTC GTG		
			CA C_		
GAM2269	FLJ14327	3'	GCGGTACTTCTCTGCATCT 46685	A	ATC
			GGATGCAGA GGAG ACCGC		
			TCTACGTCT CTTC TGGCG		
			_ A_		
GAM2269	FLJ14800	3'	GCCCTCTATCTCCTTCTAATCC 52686	GC	CACC_
	T		AGGAT AGAAGGAGAT GC		
			TCCTA TCTTCCTCTA CG		
			A_ TCTCC		
GAM2269	GMPPB	5'	GATCACCCCCCTGCATCCT 97451	AA_	A
			AGGATGCAG GG GATC		
			TCCTACGTC CC CTAG		
			CCCC A		
GAM2269	GRIN3A	3'	GACTCTCCTTCAACATCCT 56782	CA	_
			AGGATG GAAGGAGA TC		

			TCCTAC	CTTCCTCT	AG		
			AA	C			
GAM2269	HELO1	5'	GGTGTCTCCTTCTACATCC	41797	C	T	
			GGATG	AGAAGGAGA	CACC		
			CCTAC	TCTTCCTCT	GTGG		
			A	_			
GAM2269	KCNT1	3'	GGCGGTGACCCCGCAGAGCACC	62492	A	AGAA_	AGA
	C		GG	TGC	GG	TCACCGCC	
			CC	ACG	CC	AGTGGCGG	
			C	AGACG	CC_		
GAM2269	KCNT1	3'	GGTCCTCATCCTCTTCTGCACC	62494	A	GA	C__
	CT		AGG	TGCAGAAG	GAT	ACC	
			TCC	ACGTCTTC	CTA	TGG	
			C	TC	CTCC		
GAM2269	KIAA1272	3'	GGCAGCTTGCTTCTGCACCC	70732	A	_	ATCACC
			GG	TGCAGAAG	GAG	GCC	
			CC	ACGTCTTC	TTC	CGG	
			C	G	GA__		
GAM2269	KIAA1671	3'	GCCTGCGTCTCCTTTTGCACCC	66284	A		CACC
			GG	TGCAGAAGGAGAT	GC		
			CC	ACGTTTTCTCTG	CG		
			C		CGTC		
GAM2269	MGC33345	3'	CGGTGGCCCCTGCATCT	58921	AA	AGA	
			GGATGCAG	GG	TCACCG		
			TCTACGTC	CC	GGTGGC		
			C_	__			
GAM2269	NUDEL	3'	GGCGGCTGTCCCTGTGCATCCT	48700	GA	A	CA
			AGGATGCA	AGG	GAT	CCGCC	
			TCCTACGT	TCC	CTG	GGCGG	
			G_	_	TC		
GAM2269	P450RAI-2	3'	GCGTCTCCTCCTCCTGCGCCC	39575	A	A	ATCAC
			GG	TGCAG	AGGAG	CGC	
			CC	GCGTC	TCCTC	GCG	
			C	C	CTCT_		
GAM2269	phospho1	3'	CGGTGTCTCCTTGCATCC	83245	GA	T	
			GGATGCA	AGGAGA	CACCG		
			CCTACGT	TCCTCT	GTGGC		
			_	_			
GAM2269	RPIA	3'	GCAGTGATCTCCTGATGC	58592	GA	C	
			GCA	AGGAGATCAC	GC		

CGT TCCTCTAGTG CG
AG A
GAM2269 SCRG1 5' GCCTTGTCTCCTTCCACTCC 24416 _ CA T CC
GGA TG GAAGGAGA CA GC
||| || ||||| || ||
CCT AC CTCCTCT GT CG
C _ _ TC
GAM2269 LOC123242 5' GGCGGTGACCCAGACATGCCT 76119 _ CAGAA AGA
AGG ATG GG TCACCGCC
||| || || |||||
TCC TAC CC AGTGGCGG
G AGAC _ _
GAM2269 LOC147093 5' GCGCCTCCTTCTGCACCC 85057 A ATCAC
GG TGCAGAAGGAG CGC
|| ||||| |||
CC ACGTCTTCCTC GCG
C C _
GAM2269 LOC154282 3' GGCAGCAACCTTTGCTTTCTGC 87409 A AGATCACC _
AGCCT AGG TGCAGAAGG GCC
||| ||||| |||
TCC ACGTCTTTC CGG
G GTTCCAACGA
GAM2269 LOC154881 3' GGCAGTGATCTCCTGTTCCCT 82074 AT GAA C
AGG GCA GGAGATCAC GCC
||| ||| ||||| |||
TCC TGT CCTCTAGTG CGG
CT _ A
GAM2269 LOC154881 3' GGCCTTGACCCCTTCTGCTTCC 82075 T AGA CC
GGA GCAGAAGG TCA GCC
||| ||||| ||| |||
CCT CGTCTTCC AGT CGG
T CC _ TC
GAM2269 LOC165070 5' GGCAGTGTGAGCTCTGCGTCC 83350 AGGAGAT C
GGATGCAGA CAC GCC
||||| ||| |||
CCTGCGTCT GTG CGG
CGAGT _ A
GAM2269 LOC220370 3' GGCGGCCTTCCCTGCAGTCCT 94401 _ AA ATCA
AGGA TGCAG GGAG CCGCC
||| |||| ||| ||||
TCCT ACGTC CTTC GGCGG
G CC C _
GAM2269 LOC253001 5' GGCGGTGACCCAGACATGCCT 97997 _ CAGAA AGA
AGG ATG GG TCACCGCC
||| ||| || |||||
TCC TAC CC AGTGGCGG
G AGAC _ _
GAM2269 LOC91353 3' GCGTCTCTCTCTGCATCC 61160 AG TCAC
GGATGCAGA GAGA CGC
||||| ||| |||

			CCTACGTCT CTCT GCG		
			CT ____		
GAM2269	LOC91397	5'	GCATATCCCTTCTGCATCCT 66497	A	CACC
			AGGATGCAGAAGG GAT GC		
			TCCTACGTCTTCC CTA CG		
			_ TA_		
GAM2270	MEP1B	5'	GCTACTTTCAACTGGAA 20998 G	TCGTC	
			TT CAGTTGAAG GTAGC		
			AA GTCAACTTT CATCG		
			G ____		
GAM2270	KIAA1069	3'	TGACCTACATTCAACTGCAA 68535	_ C_	
			TTGCAGTTGAA GT GTCG		
			AACGTCAACTT CA CAGT		
			A TC		
GAM2270	NICN1	3'	TGGCGACTTCATCTGCAA 51261 T		
			TTGCAG TGAAGTCGTCG		
			AACGTC ACTTCAGCGGT		
			T		
GAM2270	TEX27	3'	GCTGAACACCTGCAACTGCAA 41952	A TC CG	
			TTGCAGTTG AG GT TAGC		
			AACGTCAAC TC CA GTCG		
			G CA A_		
GAM2270	LOC142948	3'	TGGCCACCGGCCCAACTGCAG 83782	AA TC A	
			TTGCAGTTG GTCG GT GCCA		
			GACGTCAAC CGGC CA CGGT		
			C_ _ C		
GAM2270	LOC146488	5'	GCTACAACCGCTTCAACAACAA 71359	CA C C	
			TTG GTTGAAGT GT GTAGC		
			AAC CAACTTCG CA CATCG		
			AA C A		
GAM2270	LOC147080	3'	TGCACAACCTTCAGCCACAA 85053	CA C C	
			TTG GTTGAAGT GT GTA		
			AAC CGACTTCA CA CGT		
			AC A _		
GAM2270	LOC152845	5'	GCGGTGACCTCAGCTGCAA 60958	A GT	
			TTGCAGTTGA GTC CGT		
			AACGTCGACT CAG GCG		
			C TG		
GAM2270	LOC203052	3'	ACCACCATTTCAACTGCA 92073	C C	
			TGCAGTTGAAGT GT GT		

ACGTCAACTTTA CA CA
 C C
 GAM2270 LOC204084 5' GGCCAGACCTCCAAGTGCAG 91000 A TC GTA
 TTGCAGTTG AG GTC GCC
 ||||| || ||| |||
 GACGTCAAC TC CAG CGG
 C _ AC_
 GAM2271 CHAD 3' GGAAGGCTGAGCCTCTC 8855 TA CTGC
 GAGAG CTC GTCTTCC
 |||| ||| |||||
 CTCTC GAG CGGAAGG
 C_ T____
 GAM2271 DSG1 5' AGGAAGGCAGAAACACCTC 10449 A ACTC GT
 GAG GT CTGC CTCCT
 ||| || ||| |||||
 CTC CA GACG GAAGGA
 _ CAAA _
 GAM2271 MID1 3' AAGATGTAGAAGTCCCTC 6351 T_ C
 GAG ACT CTGCGTCTT
 ||| ||| |||||
 CTC TGA GATGTAGAA
 CC A
 GAM2271 OTOF 3' AGGAAGACTCCTGAAACCCTC 17828 A AC CTGC
 GAG GT TC GTCTTCCT
 ||| || ||| |||||
 CTC CA AG CAGAAGGA
 C A_ TCCT
 GAM2271 RNMT 3' AGGACATCCAAGGGTACTCTC 15047 T GCGTCT
 GAGAGTAC CCT TCCT
 ||||| ||| |||
 CTCTCATG GGA AGGA
 _ ACCTAC
 GAM2271 SCN3A 5' AGGAAGACACGTTATACCCT 23612 A CTCC C
 AG GTA TG GTCTTCCT
 || ||| || |||||
 TC CAT GC CAGAAGGA
 C ATT_ A
 GAM2271 SFRS7 3' GGAAGGCGATACTCTC 60148 CTCCTG
 GAGAGTA CGTCTTCC
 ||||| |||||
 CTCTCAT GCGGAAGG
 A_____
 GAM2271 SLC13A4 5' AAGACGAAGGAGGACTCTC 25857 A G
 GAGAGT CTCCT CGTCTT
 |||| |||| |||||
 CTCTCA GAGGA GCAGAA
 G A
 GAM2271 SSX2 3' AGGAAGATGACGAGTAACTC 97962 _ CTG
 GAGT ACTC CGTCTTCCT
 ||| ||| |||||

		CTCA TGAG GTAGAAGGA	
		A CA_	
GAM2271	TGFBR2	3' AAGATTCAAGAGTATTCTC	13725 C C
		GAGAGTACTC TG GTCTT	
		CTCTTATGAG AC TAGAA	
		A T	
GAM2271	TNFRSF11A	3' AGGAAGACCACCCGGCATTCTC	15187 A CC_ C
		GAGAGT CT TG GTCTTCCT	
		CTCTTA GG AC CAGAAGGA	
		C CCC _	
GAM2271	AP3M2	3' AGGAAGACCCGTACTCTC	23299 TCCT C
		GAGAGTAC G GTCTTCCT	
		CTCTCATG C CAGAAGGA	
		_ C	
GAM2271	CALN1	3' AGGAAGACACAGAATTCTTTC	49658 TACTC C
		GAGAG CTG GTCTTCCT	
		CTTTC GAC CAGAAGGA	
		TTAA_ A	
GAM2271	DAMS	5' AGGAAATTCAAGTACTCT	42084 CC C C
		AGAGTACT TG GT TTCCT	
		TCTCATGA AC TA AAGGA	
		_ T _	
GAM2271	DKFZP727M111	5' AGGCCAGGAGGACCCTC	32055 A A C
		GAG GT CTCCTG GTCT	
		CTC CA GAGGAC CGGA	
		C G _	
GAM2271	FLJ14486	5' AGGAAGGTTCAAGTCTCTC	52434 T CC CG
		GAGAG ACT TG TCTTCCT	
		CTCTC TGA AC GGAAGGA	
		_ _ TT	
GAM2271	FUSIP1	3' AGGAAGACAGCCATAGTCTC	22780 T CCT _
		GAG ACT GC GTCTTCCT	
		CTC TGA CG CAGAAGGA	
		_ TAC A	
GAM2271	HIC	3' GAAGATTGAGTACTCT	68048 CTGC
		AGAGTACTC GTCTTC	
		TCTCATGAG TAGAAG	
		T_	
GAM2271	IL22R	3' AGGAAATGCAGGGAAACTC	41467 AC C
		GAGT TCCTGCGT TTCCT	

			CTCA GGGACGTA AAGGA		
			AA _		
GAM2271	KIAA0472	3'	AGGAGGGGTAAGTACTCTC 72334	CC	G
			GAGAGTACT TGC TCTTCCT		
			CTCTCATGA ATG GGGAGGA		
			— —		
GAM2271	KIAA1229	3'	AGGATGTAAAAGTTCTCTC 62750	T	CC
			GAGAG ACT TGCCTCTT		
			CTCTC TGA ATGTAGGA		
			T AA		
GAM2271	LAK-4P	3'	AGGAAGACAGTTTCGCCTCTC 24394	TACTCCT	_
			GAGAG GC GTCTTCCT		
			CTCTC TG CAGAAGGA		
			CGCTT_ A		
GAM2271	MRPS35	3'	AGGTCCTCAGGAGTATTCTC 41819	CGTCTT	
			GAGAGTACTCCTG CCT		
			CTCTTATGAGGAC GGA		
			TCCT_		
GAM2271	OBTP	5'	AGGATCTGCAAGGAGGACCCTC 34663	A A	_ TCT
			GAG GT CTCCT GCG TCCT		
			CTC CA GAGGA CGT AGGA		
			C G A CT_		
GAM2271	RI58	3'	AGATCAGGAATACTCTT 25774	C	C
			GAGAGTA TCCTG GTCT		
			TTCTCAT AGGAC TAGA		
			A _		
GAM2271	SMBP	3'	AAGACAGAAGTGTAAGTCTC 72620	TC	GC_
			GAGAGTAC CT GTCTT		
			CTCTCATG GA CAGAA		
			T_ AGA		
GAM2271	SNTG1	5'	AGGACTCTGAGGAGTACTCTT 39099	G	TCT
			GAGAGTACTCCT CG TCCT		
			TTCTCATGAGGA GT AGGA		
			_ CTC		
GAM2271	SNX11	3'	AGGACCAGGAGTATCTC 26169	G	C
			GAGA TACTCCTG GTCTT		
			CTCT ATGAGGAC CAGGA		
			— —		
GAM2271	TTY7	3'	AGGAAGACACAGGTAGCT 50015	ACT	C
			AGT CCTG GTCTTCCT		

	TCG GGAC CAGAAGGA		
	AT_ A		
GAM2271 LOC123872 5'	GGAAAGAGGGTACTCTC 74710	_ GCGTC	
	GAGAGTACTC CT TTCC		
	CTCTCATGGG GA AAGG		
	A _____		
GAM2271 LOC138389 3'	AGGAAGACTTGCAAGTCTCTC 76725	T CC _	
	GAGAG ACT TGC GTCTTCCT		
	CTCTC TGA ACG CAGAAGGA		
	_ _ TT		
GAM2271 LOC143943 3'	AGGAAGATCAGCAGCCTCTC 83911	TA C C	
	GAGAG CT CTG GTCTTCCT		
	CTCTC GA GAC TAGAAGGA		
	C_ C _		
GAM2271 LOC145009 5'	AAGAAACAAAGGAGTACTTTC 60965	GCG_	
	GAGAGTACTCCT TCTT		
	CTTTCATGAGGA AGAA		
	AACAA		
GAM2271 LOC147976 5'	AGGAAGACTGGGGTACCCTC 79285	A TGC	
	GAG GTACTCC GTCTTCCT		
	CTC CATGGGG CAGAAGGA		
	C T_		
GAM2271 LOC151512 3'	AGGAAGACAATGCTTGTACCTC 86611	A TCCT _	
	GAG GTAC GC GTCTTCCT		
	CTC CATG CG CAGAAGGA		
	_ TT_ TAA		
GAM2271 LOC158801 3'	GAAAACACAAGAAGTATTCT 88255	_C C C	
	AGAGTACT C TG GT TTC		
	TCTTATGA G AC CA AAG		
	A A A A		
GAM2271 LOC206426 3'	GAAGCGAGGTGCACTCTC 91099	ACT G T	
	GAGAGT CCT CG CTTC		
	CTCTCA GGA GC GAAG		
	CGT _ _		
GAM2271 LOC254337 5'	GGAAAGGGGAGTATCTC 98012	G GCGTC	
	GAGA TACTCCT TTCC		
	CTCT ATGAGGG AAGG		
	_ GA_		
GAM2271 LOC256790 5'	AGTGCAGGAGTGCCCTC 96489	A T	
	GAG GTACTCCTGCG CT		

		CTC CGTGAGGACGT GA		
		C _		
GAM2271	LOC256946 3'	AGGAAGACAGCCATAGTCTC 96182	T	CCT _
		GAG ACT GC GTCTTCCT		
		CTC TGA CG CAGAAGGA		
		_ TAC A		
GAM2271	LOC257396 5'	GAAATGTAGGAGCATCTC 98922	GTA	C
		GAGA CTCCTGCGT TTC		
		CTCT GAGGATGTA AAG		
		AC_ _		
GAM2271	LOC257408 3'	AGGGCACCAGGAGTACCTC 97797	A	C CT
		GAG GTACTCCTG GT TCCT		
		CTC CATGAGGAC CA GGGA		
		_ _ C_		
GAM2271	LOC257453 3'	AGGAAGATGACGAGTAACTC 82927	_	CTG
		GAGT ACTC CGTCTTCCT		
		CTCA TGAG GTAGAAGGA		
		A CA_		
GAM2271	LOC51066 3'	AGGAAGATGGCCGACACTCTC 32500	AC	CTG
		GAGAGT TC CGTCTTCCT		
		CTCTCA AG GTAGAAGGA		
		C_ CCG		
GAM2272	IRS1 3'	CCATAGATGGTTCTCAATTGTA 19874	C	TGAAC
		TACA ATTGAGAACC ATGG		
		ATGT TAACTCTTGG TACC		
		_ TAGA_		
GAM2272	SERPINF1 3'	CCTGTAAGGTTTCAATG 12038	A	GA T
		CATTGAGA CCT ACA GG		
		GTAACTTT GGA TGT CC		
		_ A_ _		
GAM2272	HSA243396 3'	CCATGTTTCAGCAATGTCAATG 37844	GAAC_	
		CATTGA CTGAACATGG		
		GTAAC TACTTGACC		
		GTAAC		
GAM2272	KIAA1387 3'	CAGGAATTTTCAATATGTA 71444	C	_
		TACA ATTGAGAA CCTG		
		ATGT TAACTTTT GGAC		
		A AA		
GAM2272	MGC16063 3'	TTCAAATTCGAATGTGTA 54930	A	CC
		TACACATTG GAA TGAA		

		ATGTGTAAC CTT ACTT		
		_ AA		
GAM2272	SMCR8	3' CCATGCTCAGGTTTGACTATGT 59253	TGA_	A
		ACAT GAACCTGA CATGG		
		TGTA TTTGGA CT GTACC		
		TCAG C		
GAM2272	UPLC1	3' CCATGCTAGGCCCAATGT 35227	AGAA	AA
		ACATTG CCTG CATGG		
		TGTAAC GGAT GTACC		
		CCC_ C_		
GAM2272	ZNF334	3' CCATAAGTCAACCCTCAATGT 36637	AACC	AC_
		ACATTGAG TGA ATGG		
		TGTA ACTC ACT TACC		
		CCA_ GAA		
GAM2272	LOC145082	3' TATGGAATGCCCTTAATGTGTA 84196		AACCTGAA
		TACACATTGAG CATG		
		ATGTGTAATTC GTAT		
		CCGTAAG_		
GAM2272	LOC157723	3' CCAAGTAAGTTCTCAAATGT 82465	_	GA A
		ACATT GAGAACCT AC TGG		
		TGTAA CTCTTGGA TG ACC		
		A A_ A		
GAM2272	LOC219988	5' CCATGTTTCGGCCCCCAATG 93262	AGAAC	
		CATTG CTGAACATGG		
		GTAAC GGCTTGTACC		
		CCCC_		
GAM2273	CDH12	3' CTTATCATTTAAAGTGGTGTA 15777	CCCAA	GA
		TACACCACT GAA ATAAG		
		ATGTGGTGGA TTT TATTC		
		AA_ AC		
GAM2273	GOCAP1	3' ATTGTTCTTGGGAGCAGTGTA 43007	CA	G
		TACAC CTCCCAAGAA AAT		
		ATGTG GAGGGTTCTT TTA		
		AC G		
GAM2273	DKFZp434N2435	5' CTTATTACTGTGGGGTGGT 98090	T	AGAAG
		ACCAC CCCA AATAAG		
		TGGTG GGGT TTATTC		
		_ GTCA_		
GAM2273	DKFZP564I122	3' CTTATTCTTCTCCCTCATGTGT 63877		CACTCCCA
	A	TACAC AGAAGAATAAG		

		ATGTG TCTTCTTATTC	
		TACTCCC_	
GAM2273	FLJ21791	3' CTTATTTGCAGAAAGTGGTGTA 62126	CCCAAGAA
		TACACCACT GAATAAG	
		ATGTGGTGA TTTATTC	
		AGACG__	
GAM2273	HMP19	3' CTTATTCTTTGTTAGGAAAATG 88860	CCAC CAA_
	TA	TACA TCC GAAGAATAAG	
		ATGT AGG TTTCTTATTC	
		AAA_ ATTG	
GAM2273	KIAA1579	3' TACTCTTAGTGGTGTA 37154	CCCAAG A
		TACACCACT AAGA TA	
		ATGTGGTGA TTCT AT	
		_____ C	
GAM2273	KIAA1719	3' TCTGTCTTGGGAGTGGTGTA 68742	_
		TACACCACTCCCAAGA AGA	
		ATGTGGTGAGGGTTCT TCT	
		G	
GAM2273	KIAA1853	3' TTTTCTTGAAGCAGTG 69929	CA C
		CAC CT CCAAGAAGAA	
		GTG GA GGTTCTTTTT	
		AC A	
GAM2273	KIAA1877	3' CTTATTCTTCTGCCATGAGT 66748	CCA_
		ACTC AGAAGAATAAG	
		TGAG TCTTCTTATTC	
		TACCG	
GAM2273	KIAA1906	3' CTTATTCTTCTTGACTTTTGG 73571	CTCC_
		CCA CAAGAAGAATAAG	
		GGT GTTCTTCTTATTC	
		TTTCA	
GAM2273	OSBPL11	3' CTTAATTTCCCAAGAGTGGTG 43206	CCAA AA
		CACCACTC GAAG TAAG	
		GTGGTGAG CTTT ATTC	
		AACC A_	
GAM2273	YME1L1	3' TCATTCTTGATGTGGTGTA 58438	TCC _
		TACACCAC CAAGAA GA	
		ATGTGGTG GTTCTT CT	
		TA_ A	
GAM2273	YME1L1	3' TCATTCTTGATGTGGTGTA 27323	TCC _
		TACACCAC CAAGAA GA	

ATGTGGTG GTTCTT CT
 TA_ A
 GAM2273 ZNF262 3' CTTATTTTGTGGGAGT 18723 A
 ACTCCCAAG AGAATAAG
 ||||| |||||
 TGAGGGTTT TTTTATTC
 G
 GAM2273 LOC91960 3' TGTGGCTTGGAACGTGGTGTA 68294 TC_ AAGA
 TACACCAC CCAAG ATA
 ||||| ||| ||
 ATGTGGTG GGTTCT TGT
 CAA GG_
 GAM2274 RAB36 3' ACCCACCCACCGGGCTCA 18148 A GAC T C
 TGAG CC CG TG GGTGGGT
 ||| || || |||||
 ACTC GG GC AC CCACCCA
 _ _ C _
 GAM2274 WBP2 3' CACCCACTGCTACACTCAGCCT 73388 ACC CC T
 CA TGAG GA GT GCGGTGGGTG
 ||| || || |||||
 ACTC CT CA CGTCACCCAC
 CGA CA T
 GAM2274 GDAP1L1 3' CACCCACCCAGTCGGGTCTCA 44055 _ CGT C
 TGAGACC GAC TG GGTGGGTG
 ||||| || || |||||
 ACTCTGG CTG AC CCACCCAC
 G _ C
 GAM2274 LOC197003 3' ACCCACCGCCCAGGCTCA 89211 A GACCGTT
 TGAG CC GCGGTGGGT
 ||| || |||||
 ACTC GG CGCCACCCA
 _ ACC_
 GAM2274 LOC253868 3' CACCCACCCCTGACCACCTCA 97317 ACCGACC GC_
 TGAG GTT GGTGGGTG
 ||| || |||||
 ACTC CAG CCACCCAC
 CAC_ TCC
 GAM2274 LOC90050 3' CACCCACTCTGCGAGCCAATCT 57184 CCGAC_ TGC
 CA TGAGA CGT GGTGGGTG
 |||| || |||||
 ACTCT GCG TCACCCAC
 AACCGA TC_
 GAM2274 LOC90538 3' CACCCACTGTCTAACCAGTC 63895 C_ _
 GAC GTT GCGGTGGGTG
 || || |||||
 CTG CAA TGTCACCCAC
 AC TC
 GAM2275 ADARB1 3' GGGACACGGGGGACCACCAGGT 32338 A _ TT
 G CACCTGG TGG CT CGTGTCCC
 ||||| || |||||

			GTGGACC ACC GG GCACAGGG		
			_ A GG		
GAM2275 AICDA	3'	ATGAGAGTATCTGGGTGA	40688	TG	G
		TCACC GATG CTTTCGT			
		AGTGG CTAT GAGAGTA			
		GT _			
GAM2275 AIPL1	3'	TGGGGGTCATCTCGGTGA	60536	T	TT
		TCACC GGATGGCT CG			
		AGTGG TCTACTGG GT			
		C GG			
GAM2275 AMN	3'	GGGACATGGGAGGGGTCTAGCT	48921	C	GG TT
GG		TCA CTGGAT CT CGTGTCCC			
		GGT GATCTG GA GTACAGGG			
		C GG GG			
GAM2275 ATP11A	3'	GGGAGAGAAGAGCCGTCAGGG	77556	A	_GTG
A		TC CCTGGATGGCTTT C TCCC			
		AG GGACCTGCCGAGA G AGGG			
		_ A AG_			
GAM2275 BAK1	3'	GGGTGTGGGGTGGGGTGG	93633	GGATG	T TG
		TCACCT GCTT CG TCC			
		GGTGGG TGGG GT GGG			
		G_ _ GT			
GAM2275 CCNF	3'	GGGGCACCCACTTCCTTCTGGG	10082	TG T	CTTTC_
TGG		TCACC GA GG GTGTCCC			
		GGTGG CT CC CACGGGG			
		GT T TTCACC			
GAM2275 CDKN2D	3'	GGGGTGTGAGTGTTTGGGGGA	10159	A TG	GCT TG
		TC CC GATG TTCG TCCC			
		AG GG TTGT GAGT GGGG			
		G GT _ GT			
GAM2275 CEBPA	5'	GGGCGAGCAGGGTCTCCGGGTG	16431	T	CG_ C
G		TCACCTGGA GGCTTT TGTCC			
		GGTGGGCCT CTGGGA GCGGG			
		_ CGA			
GAM2275 CELSR3	5'	GGGGTGCGGAGAGACAGGCGG	9189	A	GATGG T TG
		TC CCTG CTT CG TCCC			
		GG GGAC GAG GC GGGG			
		C AGA_ _ GT			
GAM2275 CGTHBA	3'	GGGGCACGAGGGCCTGGGCTGG	24891	_	GAT
		TCA CCTG GGCTTTCGTGTCCC			

GGT GGGT CCGGGAGCACGGGG
C ____
GAM2275 COL9A2 3' GGGACATGGGCACCTCGGG 10255 ATG TT
CCTGG GCT CGTGTCCC
||||| ||| |||||
GGGCT CGG GTACAGGG
CCA ____
GAM2275 CRACC 3' GGGGCACGGGGGGCAGTGGGT 41315 GA G TT
ACCTG TG CT CGTGTCCC
||||| ||| |||||
TGGGT AC GG GCACGGGG
G_ G GG
GAM2275 DFFB 3' GGGATACGGGGGTTGGGCTAG 88774 A_ TT
CTGG TGGCT CGTGTCCC
||| ||||| |||||
GATC GTTGG GCATAGGG
GG GG
GAM2275 DIO3 3' GATTCGAAGGCCATTTGGTGA 9072 T T
TCACC GGATGGCTTTTCG GTC
||||| ||||| ||||| |||
AGTGG TTTACCGGAAGC TAG
_ T
GAM2275 DYT1 3' GGGGCAGTGAAGTGTTTAGGTG 5479 G CG
A TCACCTGGATG CTTT TGTCCC
||||||| ||| |||||
AGTGGATTTGT GAAG ACGGGG
_ TG
GAM2275 EGFL4 5' GGGGCTGCTGCCTCCAGGTGG 62471 T TTT T
TCACCTGGA GGC CG GTCCC
||||||| ||| || |||||
GGTGGACCT CCG GT CGGGG
_ TC_ _
GAM2275 EMP3 5' GGGGCACGGAGGCCCGAGCGAG 9245 GGAT_
G CCT GGCTTTCGTGTCCC
||| ||||| |||||
GGA CCGGAGGCACGGGG
GCGAGC
GAM2275 EN2 5' GGGGCGCGGGGGTCTCCGTGTG 9264 C T TT
CAC TGA GGCT CGTGTCCC
||| ||| ||| |||||
GTG GCCT CTGG GCGCGGGG
T _ GG
GAM2275 ESR1 3' GGGGCACGGGAGAAGGGTGG 5517 GGATGG TT
TCACCT CT CGTGTCCC
||||| || |||||
GGTGGG GA GCACGGGG
AA_ GG
GAM2275 FGF2 5' GGGGCGCGGGAGGCTGGTGGGT 10621 GA _ TT
G CACCTG TGGC T CGTGTCCC
||||| ||||| |||||

			GTGGGT GTCG A GCGCGGGG		
			G_ G GG		
GAM2275 FLNA	3'	GGGCAGAGGGAGCCATTTGGTG 9386	T TT G_ C		
G		TCACC GGATGGCT C TGTCC			
		GGTGG TTTACCGA G ACGGG			
		_ GG AG			
GAM2275 FMR2	3'	GGGATATGAGACATGTGGATGG 10697	C G GC		
		TCA CTG ATG TTTCGTGTCCC			
		GGT GGT TAC AGAGTATAGGG			
		A G _			
GAM2275 GA	3'	GGGACCAAGCAGTCATTTGGTG 26090	T TTCGT		
A		TCACC GGATGGCT GTCCC			
		AGTGG TTTACTGA CAGGG			
		_ CGAAC			
GAM2275 GOLGA4	5'	GGTACAGAAAGCCATTTGAGTG 60696	CT G _ C		
A		TCAC GGATGGCTTTC TGT CC			
		AGTG TTTACCGAAAG ACA GG			
		AG _ T			
GAM2275 HDAC8	3'	GGGCCTCAGGACCATCCAGGTG 38081	_ TCGT C		
G		TCACCTGGATGG CTT GTCC			
		GGTGGACCTACC GGA CGGG			
		A CTC_			
GAM2275 HELZ	5'	GCTCTGATGGGCTATTTGGGTG 30265	TG _ TGTCCC		
A		TCACC GATGGCTT TCG			
		AGTGG TTATCGGG AGT			
		GT T CTCG			
GAM2275 HRH2	3'	GGAGCTGCTGTTTAGGTGG 42511	TTTC G		
		TCACCTGGATGGC GT TCC			
		GGTGGATTTGTCTG CG AGG			
		T _ _			
GAM2275 IDH3B	3'	GGACAGACTGTTGGGTGG 23559	GGAT TT G		
		TCACCT GGC TC TGTCC			
		GGTGGG TTG AG ACAGG			
		_ TC _			
GAM2275 IL20RA	3'	GGGTGCAGAATTTATTTCAGGTG 27803	C TC TG C		
G		TCACCTGGATGG TT G TCC			
		GGTGGACTTATT AA C GGG			
		T GA GT			
GAM2275 IL26	3'	GGGATGTGGGGGGTGGAGGGGG 37859	A GGA G TT TG		
A		TC CCT TG CT CG TCCC			

AG GGG GT GG GT AGGG
 G AG_ G GG GT
 GAM2275 INHBB 3' GGGGCACGGAGGGCAGTCCCGG 11009 A__ G
 GTGG TCACCTGG TG CTTTCGTGTCCC
 ||||| || |||||
 GGTGGGCC AC GGAGGCACGGGG
 CTG G
 GAM2275 JUND 5' GGGGCGCGGGCCCCCGGG 19299 AT TT
 CCTGG GGCT CGTGTCCC
 |||| ||| |||||
 GGGCC CCGG GCGCGGGG
 CC _
 GAM2275 KCNA5 5' GGGGCGCGGGAGCCGGTCAGCT 60435 C GA TT
 GG TCA CTG TGGCT CGTGTCCC
 ||| ||| |||| |||||
 GGT GAC GCCGA GCGCGGGG
 C TG GG
 GAM2275 KCNN3 3' TACGGAAGCCTCTGGGTGA 11188 TG T
 TCACC GA GGCTTTCTGTG
 |||| || |||||
 AGTGG CT CCGAAGGCAT
 GT _
 GAM2275 KIF5C 3' GGGGTGTTGGGTGGTTTCTGGG 16935 TG __ G TC TG
 TGG TCACC GA T GCTT G TCCC
 |||| || | ||| | |||
 GGTGG CT G TGGG T GGGG
 GT TT G T_ GT
 GAM2275 LAMC1 5' GGGGCGCGGGGGCAGTGGTCGG 11268 ATG__ TT
 CTGG GCT CGTGTCCC
 |||| ||| |||||
 GGCT CGG GCGCGGGG
 GGTGA GG
 GAM2275 LFG 3' TGGAAGCCATCCAGCTGA 77243 C
 TCA CTGGATGGCTTTTCG
 ||| |||||
 AGT GACCTACCGAAGGT
 C
 GAM2275 LRP4 3' GGGACATGGGGGTGTGGGT 65063 GATG TT
 ACCTG GCT CGTGTCCC
 |||| ||| |||||
 TGGGT TGG GTACAGGG
 G__ GG
 GAM2275 MADH4 5' GGTAACGGAGCGGTTTGGGTGG 19307 TG G T GT
 TCACC GAT GCTT CGT CC
 |||| ||| ||| ||| ||
 GGTGG TTG CGAG GCA GG
 GT G _ AT
 GAM2275 MAX 3' GGGACGCCTGCCCTGCCCAGGT 11475 AT__ TTTC
 GG TCACCTGG GGC GTGTCCC
 ||||| ||| |||||

			GGTGGACC CCG CGCAGGG		
			CGTC TC__		
GAM2275	MLLT7	3'	GGTGGGCTGTTTAGGGGA 21042 A	TCGTGT	
			TC CCTGGATGGCTT CC		
			AG GGATTGTGCGGG GG		
			G T_____		
GAM2275	MMP2	5'	GGGGCGCGGGGGCCGGACCATG 16968	CC A_ TT	
	A		TCA TGG TGGCT CGTGTCCC		
			AGT ACC GCCGG GCGCGGGG		
			__ AG GG		
GAM2275	MN1	5'	GGGGCGCGGGGACTCCGGG 11657	TG C TT	
			CCTGGA G T CGTGTCCC		
			GGGCCT C G GCGCGGGG		
			__ A GG		
GAM2275	MYBL2	3'	AATCTGAGAGTCATTCAGGTGA 11726	TGTCCC	
			TCACCTGGATGGCTTTTCG		
			AGTGGACTTACTGAGAGT		
			CTAAG		
GAM2275	MYO1C	3'	GGCCCTGGGAGCCACCAGGTGG 61867	A TT T_	
			TCACCTGG TGGCT CG GTC		
			GGTGGACC ACCGA GT CGG		
			_ GG CC		
GAM2275	MYOD1	3'	GGGATGCACCGTTATTTGGG 65626	TG TTC	
			CC GATGGCT GTGTCCC		
			GG TTATTGG CGTAGGG		
			GT CCA		
GAM2275	NCKAP1	5'	GGGGCGCGAGGGCCATGGG 26469	GG	
			CCT ATGGCTTTCGTGTCCC		
			GGG TACCGGGAGCGCGGGG		
			__		
GAM2275	NDRG3	3'	GGGGTAGCCCTGTCCAGGT 42768	__ TTTCG GT	
			ACCTGGAT GGC T CCC		
			TGGACCTG CCG A GGG		
			TC ____ TG		
GAM2275	NFATC4	5'	GGGAGGGAGCCACCCGGGTGA 17047	A TT GTG	
			TCACCTGG TGGCT C TCCC		
			AGTGGGCC ACCGA G AGGG		
			C GG__		
GAM2275	NOTCH2	3'	GGAACAAATGAAGGTCATCCGG 44575	A G__ C	
	GAGA		TC CCTGGATGGCTTTCGT TCC		

			AG GGGCCTACTGGAAGTA AGG	
			A AACA	
GAM2275	NXT1	5'	GGGGCGCTCGCGTCTGCGTGG 26033	C G TTTC
			TCAC TGGATG C GTGTCCC	
			GGTG GTCTGC G CGCGGGG	
			C _ CT__	
GAM2275	PAX5	5'	GGGGCGCGGCGTGTCTGGGGA 34134	A TG _ TTT
			TC CC GATG GC CGTGTCCC	
			AG GG CTGT CG GCGCGGGG	
			_ GT G ____	
GAM2275	PEX10	3'	GGGGCACGGAGGCTGGCGGGT 12041	GA
			ACCTG TGGCTTTCGTGTCCC	
			TGGGC GTCGGAGGCACGGGG	
			G_	
GAM2275	PEX10	3'	GGGGTATGGGGGCTGCCAGG 12042	A TT GT
			CCTGG TGGCT CGT CCC	
			GGACC GTCGG GTA GGG	
			_ GG TG	
GAM2275	PLOD	3'	GCCCAGAAAGACTGTCTGGGTG 6115	TG _ GTGTCCC
	A		TCACC GATGG CTTTC	
			AGTGG CTGTC GAAAG	
			GT A ACCCG	
GAM2275	PPFIA3	3'	GGGGTGCGGGGCGGCACGGTGG 61673	_ GA G TT TG
			TCACC TG TG CT CG TCCC	
			GGTGG AC GC GG GC GGGG	
			C G_ G _ GT	
GAM2275	PPP1R12B	3'	GGGGTGGGGTTGGGGTTGTTTA 50362	A TG _ G GT
	GGA		TC CCTGGA GCTT TC T CCC	
			AG GGATTT TGGG GG G GGG	
			_ GT GTT G TG	
GAM2275	PTGDS	3'	GGGATCCCGGCCAGCCAGGTGA 8170	A TTCGT
			TCACCTGG TGGCT GTCCC	
			AGTGGACC ACCGG TAGGG	
			G CCC__	
GAM2275	RASAL1	5'	GGGGCGCGGAGGTTGGAGAGAG 17403	GGA__
	G		CCT TGGCTTTCGTGTCCC	
			GGA GTTGGAGGCGCGGGG	
			GAGAG	
GAM2275	RELN	3'	GGTCACAAAGCTATTTAAGTGG 95956	C C T
			TCAC TGGATGGCTTT GTG CC	

GGTG ATTTATCGAAA CAC GG
A _ T
GAM2275 REPS2 5' GGGGCGTGGGGGTGGTGGTGG 17555 TGG G TT
TCACC AT GCT CGTGTCCC
||||| || ||| |||||
GGTGG TG TGG GTGCGGGG
_ G GG
GAM2275 RFX5 3' GGAGCAGGGAGTTGCTTGGGTG 6550 TG AT TT G TC
G TCACC G GGCT C TG CC
||||| | ||| | || ||
GGTGG T TTGA G AC GG
GT CG GG _ GA
GAM2275 RGS5 3' GAGAGGCCTTCTAGGTGA 14624 T CG
TCACCTGGA GGCTTT T
||||||| ||||| |
AGTGGATCT CCGGAG G
T AT
GAM2275 RPS6KA1 5' GGGGCGCGGCGGTTCGGGT 60044 G TTT
ACCTGGAT GC CGTGTCCC
||||||| || |||||
TGGGCTTG CG GCGCGGGG
G _
GAM2275 S100B 3' GGGATGCGCCTGATCACCAGGT 21851 A CTTT_
GA TCACCTGG TGG CGTGTCCC
||||||| ||| |||||
AGTGGACC ACT GCGTAGGG
_ AGTCC
GAM2275 SCML2 3' TACGAGGGTTGTTTGGATGG 21430 C TG TG
TCA C GA GCTTTCGTG
||| | || |||||
GGT G TT TGGGAGCAT
A GT GT
GAM2275 SCNN1G 3' GGGGCATGGGTGGCTCCAGGAG 8303 A TG _
A TC CCTGGA GCT TTCGTGTCCC
|| ||||| ||| |||||
AG GGACCT CGG GGGTACGGGG
A _ T
GAM2275 SET 3' GGGGTGGGGTTTGAGATGTTTG 13018 TG GG _ G GT
GGTGG TCACC GAT CTT TC T CCC
||||| ||| ||| ||| |||
GGTGG TTG GAG GG G GGG
GT TA TTT G TG
GAM2275 SH3GL1 3' GGGTGCGGGGGGCTTATCTGGGT 13097 TG _ TT G GT C
GG TCACC GATG GCT C T CC
||||| ||||| ||| ||| |||
GGTGG CTAT CGG G G GG
GT T GG G TG
GAM2275 SIX2 3' GGGACGTGGAGTGGCGGTGTCC 34190 G _ _
AGG CCTGGAT GCT TTCGTGTCCC
||||||| ||| |||||

GGACCTG CGG AGGTGCAGGG
TGG TG
GAM2275 SLC16A2 5' GGGGTGTGGAGGAGGGGGA 22526 A GGATGG TG
TC CCT CTTTCG TCCC
|| ||| ||||| ||||
AG GGG GGAGGT GGGG
_ GA_ GT
GAM2275 SLC21A2 3' GGGGTGTGGGAGTTGGTGA 20086 TGGAT TT TG
TCACC GGCT CG TCCC
|||| | ||| || ||||
AGTGG TTGA GT GGGG
_ GG GT
GAM2275 SLC2A6 3' GGGACACGGCCCTGCTGGGTGA 34572 TG AT_ TTT
TCACC G GGC CGTGTCCC
|||| | ||| |||||
AGTGG C CCG GCACAGGG
GT GTC _
GAM2275 SLC4A4 3' GGGCTAAAGTCATCCAGTGA 14997 C CGT
TCAC TGGATGGCTTT GTCC
||| ||||| ||||
AGTG ACCTACTGAAA CGGG
_ T_
GAM2275 SMARCB1 3' GGGGTGGAGTGGGGGCTTCCAG 66187 T TT _ GT
GTGG TCACCTGGA GGCT CG T CCC
||||||| ||| || | |||
GGTGGACCT TCGG GT G GGG
_ GG GAG TG
GAM2275 STK11 3' GGGGTGTTTGGGAGCTGCTGGG 6600 TG A TT _ TG
TGG TCACC G TGGCT C G TCCC
|||| | |||| | | ||||
GGTGG C GTCGA G T GGGG
GT _ GG TT GT
GAM2275 SUFU 3' GGGGTATGAGGGCACCAGCTGG 32939 C ATG GT
TCA CTGG GCTTTCGT CCC
||| |||| | ||||| |||
GGT GACC CGGGAGTA GGG
C A_ TG
GAM2275 TARBP2 5' GGGGCGCGGAAGGAAGGAGGCG 16073 A GGATGG
G TC CCT CTTTCGTGTCCC
|| ||| |||||
GG GGA GAAGGCGCGGGG
C GGAAG_
GAM2275 TBXAS1 3' GACACAGAAGGCTGCCGGGTGG 8375 A _
TCACCTGG TGGCTTTC GTGTC
|||||| | ||||| |||||
GGTGGGCC GTCGGAAG CACAG
_ A
GAM2275 TRPV1 5' GGGGTGTGCCTGCGTCTAGCTG 55680 C G TTT TG
G TCA CTGGATG C CG TCCC
||| ||||| | || ||||

			GGT GATCTGC G GT GGGG		
			C _ TCC GT		
GAM2275	UNC5C	3'	GGGAGTCTGTGGCCGTCCAGGT 14949		TTCGTG
	GA		TCACCTGGATGGCT TCCC		
			AGTGGACCTGCCGG AGGG		
			TGTCTG		
GAM2275	USP5	3'	GGGATGTGAGGGAAATAGGG 14447	GG GG	TG
			CCT AT CTTTCG TCCC		
			GGG TA GGGAGT AGGG		
			A_ AA GT		
GAM2275	VIPR2	3'	GGGGTGCGGGATACAGCTGAGT 14069	CT A GC TT	TG
	GG		TCAC GG TG T CG TCCC		
			GGTG TC AC A GC GGGG		
			AG G AT GG GT		
GAM2275	ZNF278	3'	GCTACTGAAAGCTATCCCAGGT 50271	_	_ TCCC
	GA		TCACCTGG ATGGCTTTC GTG		
			AGTGGACC TATCGAAAG CAT		
			C T CG		
GAM2275	ZNF278	3'	GCTACTGAAAGCTATCCCAGGT 50272	_	_ TCCC
	GA		TCACCTGG ATGGCTTTC GTG		
			AGTGGACC TATCGAAAG CAT		
			C T CG		
GAM2275	54TM	5'	GGGACGTGTCGCGCGGCCGGGT 96438	A _	TTT
	GG		TCACCTGG TG GC CGTGTCCC		
			GGTGGGCC GC CG GTGCAGGG		
			G G CT_		
GAM2275	ABTB1	3'	GGGGTGCGAGGGGCTCAGTGG 51702	C GAT	_ TG
			TCAC TG GGCTT TCG TCCC		
			GGTG AC TCGGG AGC GGGG		
			_ _ G GT		
GAM2275	AF053356_CDS3	5'	GGGTGGGCGTGGCCGTCGAGGT 43984	G	TT GT_
	GG		TCACCT GATGGCT CGT CCC		
			GGTGGA CTGCCGG GCG GGG		
			G T_ GGT		
GAM2275	APELIN	3'	GGGGCATGGAAGTGCCAGGGTG 34270	_	ATG
	G		TCACC TGG GCTTTCGTGTCCC		
			GGTGG ACC TGAAGGTACGGGG		
			G G_		
GAM2275	BAG5	5'	GGGGTGCGAGGCATGCAGCTGG 18042	C G G TT	TG
			TCA CTG ATG C TCG TCCC		

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GGT GAC TAC G AGC GGGG
C G G__ GT
GAM2275 BOP1 5' GGCACGAGGGCTGTGCGGGTGG 31497 G
TCACCTG ATGGCTTTCTGTGC
||||| |||||||||
GGTGGGC TGTCGGGAGCACGG
G
GAM2275 C11orf21 3' GGCCAGGTGGAAGCCATTGGGG 27105 G __ T C
TGA TCACCT GATGGCTTTCTG TG CC
||||| ||||||| ||
AGTGGG TTACCGAAGGT AC GG
G GG C
GAM2275 C11orf21 3' GGGCAATGCTGGAGGCCGTGCA 27107 G ____ C
GGTGG TCACCTG ATGGCTTTCTG TGTCC
||||| ||||||| ||||
GGTGGAC TGCCGGAGGT ACGGG
G CGTA
GAM2275 C6orf37 5' GGGGCGGCCGCCTCCAGGTGA 68093 T TTTCG
TCACCTGGA GGC TGTCCC
||||| || ||||
AGTGGACCT CCG GCGGGG
__ CCG__
GAM2275 CBX8 3' GGGATGTGGCCTTTTGGCTGG 40608 C TG T TTT TG
TCA C GA GGC CG TCCC
||| |||| || ||||
GGT G TT CCG GT AGGG
C GT T __ GT
GAM2275 CDC16 5' GGGTGCGGGTGTGGGTGG 15338 GGATG T TG
TCACCT GC TTCG TCC
||||| || |||| ||
GGTGGG TG GGGC GGG
__ T GT
GAM2275 CECR2 3' GGGATGCGGAAGAAATGGGGG 49436 GG GG
CCT AT CTTTCGTGTCCC
||| || |||||||||
GGG TA GAAGGCGTAGGG
GG AA
GAM2275 CENTA1 3' GGGCCGTGGGGTGTGTTGGGTGG 23446 TG G TT T
TCACC GATG CT CG GTCC
||||| |||| || ||||
GGTGG TTGT GG GC CGGG
GT G GT _
GAM2275 CENTG2 3' GGGACGCGAGGGGGAGGGGA 30542 A GGATGG
TC CCT CTTTCGTGTCCC
|| || |||||||||
AG GGG GGGAGCGCAGGG
_ AGG__
GAM2275 CGI-57 3' GGGTTCAGGTGGGAGCTGCTGG 74308 TG A TT __ T_
GTGA TCACC G TGGCT CG TG CCC
||||| |||| || || |||

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AGTGG C GTCGA GT AC GGG
 GT _ GG GG TT
 GAM2275 CHRFAM7A 3' GGGCCAAGGTTGCTCGGGTGA 96721 GA CGT
 TCACCTG TGGCTTT GTCC
 ||||| ||||| |||
 AGTGGGC GTTGGA C GGG
 TC C_
 GAM2275 CLSTN3 3' GGGACGTGGGGGCCCGGGTG 28878 AT TT
 CACCTGG GGCT CGTGTCCC
 ||||| ||| |||||
 GTGGGCC CCGG GTGCAGGG
 _ GG
 GAM2275 DC-TM4F2 3' GGGCATTGTCTAGCTGG 48904 C TG CTTTC
 TCA CTGGA G GTGTCC
 || |||| | ||||
 GGT GATCT T TACGGG
 C GT _
 GAM2275 DEPP 3' GGGGTGTGAGGGTAGTGGGGGT 23808 GG G TG
 G CACCT AT GCTTTCG TCCC
 |||| || ||||| |||
 GTGGG TG TGGGAGT GGGG
 GG A GT
 GAM2275 Di-Ras2 3' GGGGCTGCATGGCTGTTGGGTG 34613 G TTCGT
 G TCACCTG ATGGCT GTCCC
 ||||| ||||| |||
 GGTGGGT TGTCGG C GGGG
 _ TACGT
 GAM2275 DKFZP434A0225 5' GGGCAACCGTCCGGGTGG 95525 CTTTCG
 TCACCTGGATGG TGTCC
 ||||| ||||| |||
 GGTGGGCCTGCC ACGGG
 A _
 GAM2275 DKFZP434C128 3' GGGGCGTGGGCCTGCCGGG 65471 AT TT
 CCTGG GGCT CGTGTCCC
 |||| ||| |||||
 GGGCC CCGG GTGCGGGG
 GT _
 GAM2275 DKFZP434O047 5' GGGACTGAGAAGCAGTCTGGGT 32123 TG G CGT
 GG TCACC GAT GCTTT GTCCC
 |||| ||| ||||| |||
 GGTGG CTG CGAAG CAGGG
 GT A AGT
 GAM2275 DKFZp547H236 3' GGGACATGGGGGCCTGAGTG 79248 CTGGAT TT
 CAC GGCT CGTGTCCC
 || ||| |||||
 GTG CCGG GTACAGGG
 AGT _ GG
 GAM2275 DKFZP564B1162 3' GGGATATGACTTAGAACCAGGT 49349 ATGGCTT
 GG TCACCTGG TCGTGTCCC
 ||||| |||||

GGTGGACC AGTATAGGG
AAGATTC
GAM2275 DKFZp761O17121 5' GGA^{CT}CCAGCCAAGGCTGTTCA 51133 C ____ C
GGTGG TCACCTGGATGGCTTT GT GTCC
||||| || |||
GGTGGACTTGTTCGAA CG CAGG
C ACCT
GAM2275 DKFZp762K222 5' GGGGTGTGGGGGGCGTGGGGA 71673 A GG G TT _TG
TC CCT ATG CT C G TCCC
|| ||| ||| || || |||
AG GGG TGC GG G T GGGG
_ _ G GG G GT
GAM2275 DNAJC5 3' GGGGTGACTGCAGCCGGTCAGG 62139 GA TTCG_ GT
TGG TCACCTG TGGCT T CCC
||||| ||| | |||
GGTGGAC GCCGA G GGG
TG CGTCA TG
GAM2275 ELF4 3' GGGCTTGGGCTGTTTGTGTGA 9233 C GG TCGT
TCAC T ATGGCTT GTCC
|||| | ||||| |||
AGTG G TGTCGGG CGGG
T TT TT_
GAM2275 FACTP140 3' GGGTTTAGGGGGCCATTTGTGT 24209 C GG TT GTGT
GG TCAC T ATGGCT C CCC
|||| | ||||| | |||
GGTG G TACCGG G GGG
T TT GG ATTT
GAM2275 FENS-1 3' GGGATATGGAAGTAAGTGGAGA 40832 A TGGATG
TC CC GCTTTCGTGTCCC
|| || ||||| |||||
AG GG TGAAGGTATAGGG
A TGAA_
GAM2275 FLJ00007 3' GGGCAGTGCTGTCCAGTGG 71781 C TTTCG
TCAC TGGATGGC TGTCC
|||| ||||| |||||
GGTG ACCTGTCTG ACGGG
_ TG_
GAM2275 FLJ10193 3' TGGGGGCCAGTTCAGGTGG 36352 _ TT
TCACCTGGA TGGCT CG
||||| |||| |||
GGTGGACTT ACCGG GT
G GG
GAM2275 FLJ10490 5' GGGACACGAGGGCTGGGCGGG 36669 GA
CCTG TGGCTTTCGTGTCCC
|||| ||||| |||||
GGGC GTCGGGAGCACAGGG
GG
GAM2275 FLJ10936 3' GGGATGTGGAGGTTGCAGTGA 37448 C GAT TG
TCAC TG GGCTTTCG TCCC
|||| || ||||| |||||

AGTG AC TTGGAGGT AGGG
 _ G_ GT
 GAM2275 FLJ11560 5' GGGGCACGAGGCATCAGTTGG 48012 C G G TT
 TCA CTG ATG C TCGTGTCCC
 ||| ||| ||| | |||||
 GGT GAC TAC G AGCACGGGG
 T _ G _
 GAM2275 FLJ12547 3' GGCTCGCTGGAGCCGTCCGGGT 47135 TC TC
 GG TCACCTGGATGGCTT GTG CC
 ||||| ||||| ||| ||
 GGTGGGCCTGCCGAG CGC GG
 GT TC
 GAM2275 FLJ13241 3' GGGACATGGAGGCATGGGTGA 47655 GGATG
 TCACCT GCTTTCGTGTCCC
 ||||| ||||| |||||
 AGTGGG CGGAGGTACAGGG
 TA_
 GAM2275 FLJ13852 3' GGGTTCTAGGGCCTTTGGGTGG 43841 TG T CGTGT
 TCACC GA GGCTTT CCC
 ||||| ||||| ||| ||
 GGTGG TT CCGGGA GGG
 GT _ TCTT_
 GAM2275 FLJ14642 3' GGGCCATCAGGTTGTTTCAGGTG 52578 TG TC T
 CACCTGGA GCTT GTG CCC
 ||||| ||| ||| |||
 GTGGACTT TGGA TAC GGG
 GT C_ C
 GAM2275 FLJ14665 3' GGGACGCGAGTGGCTGGCTGG 52586 TG AT _
 C G GGCT TTCGTGTCCC
 | | ||| |||||
 G C TCGG GAGCGCAGGG
 GT GG T
 GAM2275 FLJ20013 3' GGGATGTGAGGAGGGCAGGGA 34800 A GATGG T TG
 TC CCTG CTT CG TCCC
 || ||| ||| ||| |||
 AG GGAC GGA GT AGGG
 _ GGGA_ _ GT
 GAM2275 FLJ20211 3' GGACATGACTTCAGGTGG 35262 TGGCTT
 TCACCTGGA TCGTGTCC
 ||||| |||||
 GGTGGACTT AGTACAGG
 C_
 GAM2275 FLJ20273 3' GGGGTGTGCACATCCAGG 39250 _ TTTC TG
 CCTGGATG GC G TCCC
 ||||| || | |||
 GGACCTAC CG T GGGG
 A _ GT
 GAM2275 FLJ20548 3' GGGACACGGGCAGCTCAGGT 35820 GAT _
 ACCTG GGCT TTCGTGTCCC
 ||||| ||| |||||

TGGAC TCGA GGGCACAGGG
 ____ C
 GAM2275 FLJ20986 3' GGAATGAGGTGTTTAGGTGG 44839 G TCGTG
 TCACCTGGATG CTT TCC
 ||||| ||| |||
 GGTGGATTTGT GAG AGG
 G TA____
 GAM2275 FLJ21865 3' GGAAGAGGCCACCAGGTGG 43114 A CGTG
 TCACCTGG TGGCTTT TCC
 ||||| ||||| |||
 GGTGGACC ACCGGAG AGG
 _ A____
 GAM2275 FLJ22635 3' GGGCACGAAGGACGGGGA 47672 A GATGG
 TC CCTG CTTTCGTGTCC
 || ||| |||||
 AG GGGC GGAAGCACGGG
 _ A____
 GAM2275 FLJ23142 3' GGGATACAGGTGTTATTTTCAGG 45028 _ T TC
 TGA TCACCTGGA TGGC T GTGTCCC
 ||||| ||| | |||||
 AGTGGACTT ATTG G CATAGGG
 T TGA
 GAM2275 FLJ25422 5' CGGGTGTCTGGTGAAGGCCACT 59392 _ TGT____
 TTAGGTGA TCACCTGGA TGGCTTTCG CCC G
 ||||| ||||| ||| |
 AGTGGATTT ACCGGAAGT GGG C
 C GGTCTGT
 GAM2275 FLJ25438 3' CAGTGGGAGCCTCCAGGTGG 59121 T TT _
 TCACCTGGA GGCT CG TG
 ||||| ||| |||
 GGTGGACCT CCGA GT AC
 _ GG G
 GAM2275 FLJ30655 5' GGGGCGCGGGGGAAAGAAGCGT 58954 _ GGATGG TT
 GG TCAC CT CT CGTGTCCC
 ||| || || |||||
 GGTG GA GG GCGCGGGG
 C AGAAA_ GG
 GAM2275 GBTS1 3' GGGGTGTGGGGCCCGTGGGATG 59725 _ GG C TT TG
 G TCA CCT ATGG T CG TCCC
 ||| ||| ||| | |||
 GGT GGG TGCC G GT GGGG
 A _ C GG GT
 GAM2275 GS3955 3' GGGACACGAATTGCCTGGCTGA 41623 _ TGGAT T_
 TCA CC GGC TTCGTGTCCC
 ||| || ||| |||||
 AGT GG CCG AAGCACAGGG
 C T____ TT
 GAM2275 HBP1 5' GGGGTACGAGAGCTGCTGGTGG 25320 T A GT
 TCACC GG TGGCTTTCGT CCC
 ||||| || ||||| |||

GGTGG TC GTCGAGAGCA GGG
_ _ TG
GAM2275 HCA127 5' GGGACGTGAAATTGACAGTGA 38569 C GATGGC
TCAC TG TTTCGTGTCCC
||||| || |||||
AGTG AC AAAGTGCAGGG
_ AGTT_

GAM2275 HMP19 3' GGGATATGGGGGCGGGGCGG 88861 A GGATG TT
TC CCT GCT CGTGTCCC
|| ||| || |||||
GG GGG CGG GTATAGGG
C GG_ GG

GAM2275 HSRNAFEV 5' GGGGCGCGGGGGGCTGCCGGGT 34452 A TT_
G CACCTGG TGGCT C GTGTCCC
||||| |||| | |||||
GTGGGCC GTCGG G CGCGGGG
_ GG G

GAM2275 HTR3A 3' GGGGTACAGTCCTGGTTAGGTG 7878 AT_ _ TTC GT
G TCACCTGG GG CT GT CCC
||||| || || || |||
GGTGGATT CC GA CA GGG
GGT T _ TG

GAM2275 KCNK17 3' GGATGTGACTTTCGGGTG 49593 T CTT TG
CACCTGGA GG TCG TCC
||||| || || |||
GTGGGCTT TC AGT AGG
_ _ GT

GAM2275 KIAA0084 5' GGGGCGCGGGGAGAGCTGGGCG 68711 A TG ATGG TT_
G TC CC G CT C GTGTCCC
|| || | || | |||||
GG GG C GA G CGCGGGG
C GT GA_ GG G

GAM2275 KIAA0157 5' GAAAGAAAGTCATTGGGTGG 50749 TG A GTG
TCACC G TGGCTTTC TC
|||| | ||||| ||
GGTGG T ACTGAAAG AG
GT_ AA_

GAM2275 KIAA0229 3' GAAGGAGCCCATTTCGGGTGG 94026 _
TCACCTGGATGG CTTTC
||||||| ||||
GGTGGGCTTACC GGAAG
CGA

GAM2275 KIAA0275 3' AACCTGGGGGCCATCCTGGTGG 29321 T TT T CCC
TCACC GGATGGCT CG GT
|||| ||||| || ||
GGTGG CCTACCGG GT CA
T GG C AG

GAM2275 KIAA0515 5' GGCCTGTCGGGGGCTAGTTTGG 64553 TG _ TT T_ CC
GTGA TCACC GA TGGCT CG GTC
|||| || |||| || |||

AGTGG TT ATCGG GC CGG
 GT G GG TGTC
 GAM2275 KIAA0537 3' GGGGTACGAGGGAGGAAGGGGA 29931 A GGATGG GT
 TC CCT CTTTCGT CCC
 || ||| ||||| |||
 AG GGG GGGAGCA GGG
 _ AAGGA_ TG
 GAM2275 KIAA0561 3' GGGATATGGGAGCTGGAGCTTT 66482 CCTGGA TT
 GA TCA TGGCT CGTGTCCC
 ||| |||| |||||
 AGT GTCGA GTATAGGG
 TTCGAG GG
 GAM2275 KIAA0599 3' GGGATGCGGAGGAGAGGCTGA 77694 _ GGATGG
 TCA CCT CTTTCGTGTCCC
 ||| ||| |||||
 AGT GGA GGAGGCGTAGGG
 C GA____
 GAM2275 KIAA0721 3' GGGATGTGCAGCATCTGTGTGG 41655 C G TT TG
 TCAC TGGATG CT CG TCCC
 |||| ||||| || || ||||
 GGTG GTCTAC GA GT AGGG
 T _ C_ GT
 GAM2275 KIAA0781 3' GGGGCATGAGCTGTGTTTCAGG 68061 TG T_
 CCTGGA GC TTCGTGTCCC
 ||||| || |||||
 GGA CTT TG GAGTACGGGG
 TG TC
 GAM2275 KIAA0789 5' GGGACGCGGGAGTCGCAG 64434 GA TT
 CTG TGGCT CGTGTCCC
 ||| |||| |||||
 GAC GCTGA GCGCAGGG
 _ GG
 GAM2275 KIAA0821 5' GGGACACGGAGGCCGCC 30610 A
 GG TGGCTTTCGTGTCCC
 || |||||
 CC GCCGGAGGCACAGGG
 C
 GAM2275 KIAA0869 3' GCTAAAGTTATTTATGTGG 71420 C C
 TCAC TGGATGGCTTT GT
 |||| ||||| ||
 GGTG ATTTATTGAAA CG
 T T
 GAM2275 KIAA0884 3' GGGATGTGGAGGTTGCAGTGA 70755 C GAT TG
 TCAC TG GGCTTTCG TCCC
 |||| || ||||| ||||
 AGTG AC TTGGAGGT AGGG
 _ G_ GT
 GAM2275 KIAA0993 3' GGGGCAGACGCGATTCAGGTGA 64820 G TT G
 TCACCTGGAT GC TC TGTCCC
 ||||| || || |||||

AGTGGACTTA CG AG ACGGGG
 G C _ _
 GAM2275 KIAA1041 3' GGACACTCTGTTCAGGAGA 30824 A CTTTC
 TC CCTGGATGG GTGTCC
 || ||||| |||||
 AG GGA CTTGTC CACAGG
 A T____
 GAM2275 KIAA1655 5' GGGGTGTGGGCCAGTCTTGG 67193 T _ TT TG
 CC GGA TGGCT CG TCCC
 || ||| |||| || ||||
 GG TCT ACCGG GT GGGG
 T G _ GT
 GAM2275 KIAA1656 3' GGGGTGTGTGTCTGTGTCTAGG 66381 A _ TTT TG
 GA TC CCTGGAT GGC CG TCCC
 || ||||| || || ||||
 AG GGATCTG CTG GT GGGG
 _ TGT T__ GT
 GAM2275 KIAA1854 3' GGGCGCGTGTGTGGGTGG 72213 GGATG TTT
 TCACCT GC CGTGTCC
 ||||| || |||||
 GGTGGG TG GCGCGGG
 _ TGT
 GAM2275 KIAA1909 5' GGGCTGGTTGTCCTGGTGG 74283 T TG TTCGT
 TCACC GGA GCT GTCC
 ||||| ||| ||| ||||
 GGTGG CCT TGG CGGG
 T GT T____
 GAM2275 KIAA1940 3' GGGTCACCAAGGCTGTCTGGG 80790 TG C T
 CC GATGGCTTT GTG CCC
 || ||||| ||| |||
 GG CTGTCGGAA CAC GGG
 GT C T
 GAM2275 KIF13B 3' GGGACACGAAGGCTGCGGCCGG 31569 AT__
 G CCTGG GGCTTTTCGTGTCCC
 |||| |||||
 GGGCC TCGGAAGCACAGGG
 GGCG
 GAM2275 KIF13B 3' GGGACACGAAGGCTGCGGCCGG 31570 AT__
 G CCTGG GGCTTTTCGTGTCCC
 |||| |||||
 GGGCC TCGGAAGCACAGGG
 GGCG
 GAM2275 LTB4DH 3' GGAATCTGGAGGCCATTTAGAT 82807 C TG_ C
 GA TCA CTGGATGGCTTTCG TCC
 || ||||| ||| |||
 AGT GATTACCGGAGGT AGG
 A CTA
 GAM2275 MAPKAP1 5' GGGGCATGAGGGCTAACCCGGG 44374 A_
 CCTGG TGGCTTTTCGTGTCCC
 |||| |||||

GGGCC ATCGGGAGTACGGGG
CA
GAM2275 MEIS3 3' GGGACATGGGGGCCTGAGTG 78872 CTGGAT TT
CAC GGCT CGTGTCCC
||| ||| |||||
GTG CCGG GTACAGGG
AGT__ GG
GAM2275 MGC1127 3' GGGATTGGAAGCCATTTGGGG 54333 A TG T
A TC CC GATGGCTTTCG GTCCC
|| || ||||| |||||
AG GG TTACCGAAGGT TAGGG
_ GT T
GAM2275 MGC11352 5' GGGCATTGTCTAGCTGG 65436 C TG CTTTC
TCA CTGGA G GTGTCC
||| ||| | |||||
GGT GATCT T TACGGG
C GT ____
GAM2275 MGC15416 5' GGGACGTGGGGGCAGCCAGGGA 51404 A ATG TT
TC CCTGG GCT CGTGTCCC
|| ||| ||| |||||
AG GGACC CGG GTGCAGGG
_ GA_ GG
GAM2275 MGC16384 3' GCCTGGAGGCTGCTGGGTGG 54935 TG A T
TCACC G TGGCTTTCG GT
|||| | ||||| ||
GGTGG C GTCGGAGGT CG
GT_ C
GAM2275 MGC1842 3' GGGGTGTGGGCATCTTCAGGTG 66259 TG_ TT TG
G TCACCTGGA GCT CG TCCC
||||||| ||| || |||
GGTGGACTT CGG GT GGGG
CTA _ GT
GAM2275 MGC2452 5' GGGCCTAAGGCCGTTTGGATGA 51966 C TG CGT
TCA C GATGGCTTT GTCC
||| | ||||| |||
AGT G TTGCCGGAA CGGG
A GT TC_
GAM2275 MGC2603 3' GGAGTGAGTTTGTTTAGGTGG 44077 TG_ TCGTG
TCACCTGGA G CTT TCC
||||||| | ||| |||
GGTGGATTT T GAG AGG
GT T TG____
GAM2275 MGC29654 5' GGGGCGTGGAGTGGCGTGGCGT 67207 _ GATG _
GG TCAC CTG GCT TTCGTGTCCC
|||| ||| ||| |||||
GGTG GGT CGG AGGTGCGGGG
C G__ TG
GAM2275 MGC4701 5' GGGCACGGAGGGCGGTGG 65164 TGGAT G
TCACC G CTTTCGTGTCC
|||| | |||||

GGTGG C GGAGGCACGGG
 _____ G

GAM2275 NEU4 3' GGGGCACGAAGTGGGCCCTGGG 55791 TG AT ____
 TGA TCACC G GGCT TTCGTGTCCC
 |||| | ||| |||||
 AGTGG C CCGG AAGCACGGGG
 GT__ GTG

GAM2275 NRM 3' GGGGTATGGAAGTCATCT 99718 GT
 GGATGGCTTTCGT CCC
 ||||| |||
 TCTACTGAAGGTA GGG
 TG

GAM2275 OVCOV1 3' GGACGGGAGTCACCAGGTGG 32521 A TT GT
 TCACCTGG TGGCT C GTCC
 ||||| ||| | |||
 GGTGGACC ACTGA G CAGG
 _ GG _

GAM2275 PAXIP1L 3' GGGCTGGCTGTCTGGCTGG 70673 C TG TTCGT
 TCA C GATGGCT GTCC
 || | ||||| |||
 GGT G CTGTCCG CGGG
 C GT T____

GAM2275 PELI1 5' GGGGCATGCCCGGCCATCAGGG 40643 G TT_
 TGA TCACCT GATGGCT CGTGTCCC
 |||| | ||||| |||||
 AGTGGG CTACCGG GTACGGGG
 A CCC

GAM2275 PEX12 3' GGGATATGAGGGCCAGTGTAG 6083 G_
 CTG A TGGCTTTCGTGTCCC
 || | ||||| |||||
 GAT T ACCGGGAGTATAGGG
 G G

GAM2275 PIGQ 3' GGGGTGTGAGCGGCCTGGGG 16105 GGAT _ TG
 CCT GGCT TTCG TCCC
 || | ||| ||| |||
 GGG CCGG GAGT GGGG
 GT__ C GT

GAM2275 PISD 3' GGCCCATGAGGCCATCCAGGT 27545 T TC
 ACCTGGATGGCTT CGTG CC
 ||||| ||| ||
 TGGACCTACCGGA GTAC GG
 _ CC

GAM2275 PMI 3' GGGGTGTGGACGTGCTTTGGGG 15268 A TG TG T TG
 GA TC CC GA GC TTCG TCCC
 || || || || ||| |||
 AG GG TT TG AGGT GGGG
 G GT CG C GT

GAM2275 PP1057 3' GGCCCAAGAGCAGTCTGGGTGG 49255 TG G CGT
 TCACC GAT GCTTT GTC
 |||| || |||| |||

GGTGG CTG CGAGA CGG
GT A ACC
GAM2275 PRO0159 5' ATTCCTGAAGGCCATCCAGTGA 26945 C TGTCCC
TCAC TGGATGGCTTTTCG
|||||
AGTG ACCTACCGGAAGT
CCTTAG
GAM2275 PRO0899 3' GGGATACTGGATAGGGCTGACC 38312 A _ _
AGGTGA TCACCTGG TGGCT TTC GTGTCCC
||||| ||| |||
AGTGGACC GTCGG AGG CATAGGG
A GAT T
GAM2275 PRO1163 3' GGTGACTCTAGGGCTTTTGGGT 38324 TG T CGT _
GA TCACC GA GGCTTT GTC CC
||||| ||| |||
AGTGG TT TCGGGA CAG GG
GT _ TCT T
GAM2275 RANBP8 5' GGGGTGTGAGGTAATCCAGG 22138 G T TG
CCTGGAT GCTT CG TCCC
||||| ||| |||
GGACCTA TGGA GT GGGG
A _ GT
GAM2275 RBM12 5' GGGCTCCGGAAGCCGTTCCGGG 21283 _ GT_ C
CTGG TCA CCTGGATGGCTTTC GTCC
||| ||| ||| |||
GGT GGGCTTGCCGAAGG CGGG
C GCCT
GAM2275 RNF38 5' GGGGCGTGGGGGCGGAGAGGAT 43261 _ GGATG TT
GG TCA CCT GCT CGTGTCCC
||| ||| ||| |||
GGT GGA CGG GTGCGGGG
A GAGG_ GG
GAM2275 SDF1 3' GGGGCAGTCATTATCCAGGT 92518 CTTTCG
ACCTGGATGG TGTCCC
||||| |||
TGGACCTATT ACGGGG
ACTG_
GAM2275 SIAT9 5' GGGGCGCGGGGTACCGGGCTGG 15316 _ ATG T
TCA CCTGG GCTT CGTGTCCC
||| ||| ||| |||
GGT GGGCC TGGG GCGCGGGG
C A_ _
GAM2275 SNPH 3' GGATGTGGGAAGTGGGGA 28904 A GGATG _TG
TC CCT GCTTTC G TCC
||| ||| ||| |||
AG GGG TGAAGG T AGG
_ G GT
GAM2275 SSTK 5' GGGGTGCGGGGGTGTAGGTG 50172 GATG TT TG
CACCTG GCT CG TCCC
||||| ||| ||| |||

			GTGGAT TGG GC GGGG		
			G___ GG GT		
GAM2275	SULT4A1	3'	GGGGTTGTCTGTCAATTTATGTG 69017	C	TTT TGT
	G		TCAC TGGATGGC CG CCC		
			GGTG ATTTACTG GT GGG		
			T TCT TG_		
GAM2275	TBX21	3'	GGACATGGGAGCAGGAGA 26249	A	GGATG TT
			TC CCT GCT CGTGTCC		
			AG GGA CGA GTACAGG		
			A _____ GG		
GAM2275	TIEG	3'	GGGATGTGGAGGTAGTTGGGTA 20170	_	TG ATG TG
	GA		TC ACC G GCTTTCG TCCC		
			AG TGG T TGGAGGT AGGG		
			A GT GA_ GT		
GAM2275	TOB2	5'	GGGGCGCGGGAAGGTGCGGGT 33242	G	GGC TT
			ACCTG AT T CGTGTCCC		
			TGGGC TG A GCGCGGGG		
			G GA_ GG		
GAM2275	TOM1	3'	GGGGTGTGGAGGCAGTGGGATG 19698	_	GATG TG
	A		TCA CCTG GCTTTCG TCCC		
			AGT GGGT CGGAGGT GGGG		
			A GA_ GT		
GAM2275	USP20	3'	GGGATGTGGGGGCTGTGCAGG 22901	G	TT TG
			CCTG ATGGCT CG TCCC		
			GGAC TGTCGG GT AGGG		
			G GG GT		
GAM2275	VPS4A	5'	GGGGTGTGGGGCGGACCCAGGA 26022	A	ATG_ T TG
	GA		TC CCTGG GCTT CG TCCC		
			AG GGACC CGGG GT GGGG		
			A CAGG _ GT		
GAM2275	ZFP36L2	3'	GGGGCACGGGAGTGGGGGGGGT 23533		GGATG TT
	GA		TCACCT GCT CGTGTCCC		
			AGTGGG TGA GCACGGGG		
			GGGGG GG		
GAM2275	ZIN	3'	GGGGCATGGAGGGTGGAGTGG 26395	_	GGAT G
			TCAC CT G CTTTCGTGTCCC		
			GGTG GG T GGAGGTACGGGG		
			A _____ G		
GAM2275	ZNF333	3'	GGGCTATCAAAGTCATCTGGGT 51593	TG	C T
	GG		TCACC GATGGCTTT GTG CCC		

GGTGG CTA CTGAAA TAT GGG
GT C C
GAM2275 ZNF84 5' GGACACGGGGGACGGGCGG 14272 A GATGG TT
TC CCTG CT CGTGTCC
|| ||| || |||||
GG GGGC GG GCACAGG
C A___ GG
GAM2275 LOC115110 5' GGCTCCGGGGTACCTAGGTGG 72181 A CGT
TCACCTGG TGGCTTT GTC
||||| ||||| ||
GGTGGATC ACTGGGG CGG
C CCT
GAM2275 LOC120224 3' GGGTATGAGCCCAGGAGA 57891 A ATG TT GT
TC CCTGG GC TCGT CC
|| ||| || ||| ||
AG GGACC CG AGTA GG
A ___ TG
GAM2275 LOC125704 3' GGATGTGGGTTAGGGTGG 74880 GGA TT TG
TCACCT TGGCT CG TCC
||||| |||| || ||
GGTGGG ATTGG GT AGG
___ GT
GAM2275 LOC125875 5' GGGTGTGAGTCACTTAGGTGG 74888 GA TT TG
TCACCTG TGGC TCG TCC
||||| ||| || ||
GGTGGAT ACTG AGT GGG
TC ___ GT
GAM2275 LOC126961 3' GGGCACGGGGTGTGGGCGG 75122 A GGATG _ TT
TC CCT GC T CGTGTCC
|| ||| || | |||||
GG GGG TG G GCACGGG
C ___ T GG
GAM2275 LOC127262 3' GGATGTGGGGGCTGGGGGA 76600 A GGA TT TG
TC CCT TGGCT CG TCC
|| ||| |||| || ||
AG GGG GTCGG GT AGG
_ ___ GG GT
GAM2275 LOC130074 3' GGGGTATGTGGCCTATTTGGGT 76629 TG _ TT GT
ACC GAT GGCT CGT CCC
||| || |||| || ||
TGG TTA CCGG GTA GGG
GT T T_ TG
GAM2275 LOC130074 3' GGGTGTGGCTTGAGGTGG 76630 G AT TTT TG
TCACCT G GGC CG TCC
||||| | || || ||
GGTGGAT T TCG GT GGG
G ___ GT
GAM2275 LOC134637 3' GGGATAGGTGCCATTTGGTGG 75692 T TT G
TCACC GGATGGC TC TGTCCC
||||| ||||| || |||||

	GGTGG TTTACCG GG ATAGGG		
	— T_ —		
GAM2275 LOC135932 5'	GGGGTATGGGCTGCCTCGGGT 76698	AT T_ GT	
	ACCTGG GGC TTCGT CCC		
	TGGGCT CCG GGGTA GGG		
	— TC TG		
GAM2275 LOC136306 3'	GGGGTGTGAGAGGGAGATGGTG 75770	TGGATGG TG	
G	TCACC CTTTCG TCCC		
	GGTGG GAGAGT GGGG		
	TAGAGG_ GT		
GAM2275 LOC143286 5'	GGGGCATGAAAGAGGGCAGTGA 83847	C GATGG	
	TCAC TG CTTTCGTGTCCC		
	AGTG AC GAAAGTACGGGG		
	_ GGGA_		
GAM2275 LOC143287 3'	GCGGGGCCGACTGGGTGG 83827	TG A T	
	TCACC G TGGCTT CGT		
	GGTGG C GCCGGG GCG		
	GT A _		
GAM2275 LOC144347 3'	GGGGCATGCACTGTTAGGTGG 77308	G CTTT	
	TCACCTG ATGG CGTGTCCC		
	GGTGGAT TGTC GTACGGGG		
	_ AC_		
GAM2275 LOC144766 3'	GGGACATGGATGAAGCTAGGTG 77483	ATGGCT	
A	TCACCTGG TTCGTGTCCC		
	AGTGGATC AGGTACAGGG		
	GAAGT_		
GAM2275 LOC145231 3'	GGTTCTGGATTATCTGGGTGG 84256	TG CT TGT	
	TCACC GATGG TTCG CC		
	GGTGG CTATT AGGT GG		
	GT _ CTT		
GAM2275 LOC145601 3'	GGGAGGGGGGCTGTCAGGGTGA 84353	G TT GTG	
	TCACCT GATGGCT C TCCC		
	AGTGGG CTGTCCG G AGGG		
	A GG_		
GAM2275 LOC145678 3'	GGGCTCCAAGCCACTGGGTGG 84436	TG A TCGT	
	TCACC G TGGCTT GTCC		
	GGTGG C ACCGAA CGGG		
	GT _ CCT_		
GAM2275 LOC145989 3'	GGGAAGGGAAGCCGTCAGGTGG 60294	G GTG	
	TCACCTG ATGGCTTTC TCCC		

		GGTGGAC TGCCGAAGG AGGG		
		GA_		
GAM2275	LOC146506 3'	GGAGCATTTGGAAGTCACTGGG 78494	TG A	___ TC
	TGG	TCACC G TGGCTTTC GTG CC		
		I		
		GGTGG C ACTGAAGG TAC GG		
		GT_ TT GA		
GAM2275	LOC146517 3'	GGGAATGTTGTCATCCAGGTGG 78510	TTT	G
		TCACCTGGATGGC CGT TCCC		
		GGTGGACCTACTG GTA AGGG		
		TT_ _		
GAM2275	LOC146957 3'	GGGACACGGAATGGCAGTAGGT 78818	GATG	___
		ACCTG GCT TTCGTGTCCC		
		TGGAT CGG AGGCACAGGG		
		GA_ TA		
GAM2275	LOC147165 5'	GGGAGGGGGGTCACCCAGGTGG 85086	A	TT GTG
		TCACCTGG TGGCT C TCCC		
		I		
		GGTGGACC ACTGG G AGGG		
		C GG G_		
GAM2275	LOC147229 5'	GGGATGCGAGGGTGGCCAGTGA 78924	C	ATG
		TCAC TGG GCTTTCGTGTCCC		
		AGTG ACC TGGGAGCGTAGGG		
		_ GG_		
GAM2275	LOC147299 3'	GGAAGTCACTCTGGGTGG 78982	TG	_
		TCACC GA TGGCTTTC		
		GGTGG CT ACTGAAGG		
		GT C		
GAM2275	LOC147495 5'	GGGCACGGAAGCCGACTA 85145	A	
		TGG TGGCTTTCGTGTCC		
		ATC GCCGAAGGCACGGG		
		A		
GAM2275	LOC147649 3'	GGGATGTGTAGCATCCAGGT 79063	G TT	TG
		ACCTGGATG CT CG TCCC		
		TGGACCTAC GA GT AGGG		
		_ T_ GT		
GAM2275	LOC147965 5'	GGGGTATGGAGGTGTCCCGGG 79302	ATG	GT
		CCTGG GCTTTCGT CCC		
		GGGCC TGGAGGTA GGG		
		CTG TG		
GAM2275	LOC147976 3'	GGGATCCCTGGGGGCCATTCAG 79290	A	TT T_
	GGA	TC CCTGGATGGCT CG GTCCC		

AG GGA CTTACCGG GT TAGGG
 _ GG CCC
 GAM2275 LOC148113 3' GGGGTGTGGGGTCCAGGCTGG 79374 _ TGGC TT TG
 TCA CCTGGA T CG TCCC
 ||| ||||| | || ||||
 GGT GGACCT G GT GGGG
 C _ GG GT
 GAM2275 LOC148147 5' GGACGTGAAAGAACGGGGA 79402 A GATGG
 TC CCTG CTTTCGTGTCC
 || ||| |||||
 AG GGGC GAAAGTGCAGG
 _ AA_
 GAM2275 LOC148708 3' GGGCATGGAGGAAGGTGA 79705 GGATGG
 TCACCT CTTTCGTGTCC
 ||||| |||||
 AGTGGA GGAGGTACGGG
 A_
 GAM2275 LOC148809 5' GGTCCGGAGCTGCTGGGTGA 79758 TG A T TG
 TCACC G TGGCTT CG TC
 |||| | |||| || ||
 AGTGG C GTCGAG GC GG
 GT _ _ CT
 GAM2275 LOC149076 3' GGGGTGCGGCAGCTTCAGG 79881 AT T TG
 CCTGG GGCT TCG TCCC
 |||| ||| || |||
 GGA CT TCGA GGC GGGG
 _ C GT
 GAM2275 LOC149086 3' GGGATGCCACTGTCCAGGTG 85494 CTTTC
 CACCTGGATGG GTGTCCC
 ||||| |||||
 GTGGACCTGTC CGTAGGG
 AC_
 GAM2275 LOC149132 5' GGGCAACATGTTATTCAGGTGG 79925 TTTTCG
 TCACCTGGATGGC TGTCC
 ||||| |||||
 GGTGGACTTATTG ACGGG
 TACA_
 GAM2275 LOC149302 5' GGCTCCAGAGCCATCCAGTGG 80042 C CGT
 TCAC TGGATGGCTTT GTC
 ||| ||||| |||
 GGTG ACCTACCGAGA CGG
 _ CCT
 GAM2275 LOC149721 5' GGGGTGTGGAGGAAAAGGTG 80319 GGATGG TG
 CACCT CTTTCG TCCC
 |||| |||| |||
 GTGGA GGAGGT GGGG
 AAA_ GT
 GAM2275 LOC150147 3' AACTGGTGCGAAGGTCATTTGT 86015 C GG TG CC
 GTGA TCAC T ATGGCTTTTCG TC
 |||| | ||||| ||

	AGTG G TACTGGAAGC GG	
	T TT GT TCAA	
GAM2275 LOC150225 3'	GGGGTGCGGGGGTGTGCGGTG 86196	T G G TT TG
	CACC G ATG CT CG TCCC	
	GTGG C TGT GG GC GGGG	
	_ G _ GG GT	
GAM2275 LOC150519 3'	GGGACACTAACCATCCAGGT 80732	C TC
	ACCTGGATGG TT GTGTCCC	
	TGGACCTACC AA CACAGGG	
	_ T _	
GAM2275 LOC152633 5'	GGGGCGTGGAAGGCGGGAGGG 86997	GGA G
	CCT TG CTTTCGTGTCCC	
	GGG GC GAAGGTGCGGGG	
	AGG G	
GAM2275 LOC152762 3'	GGGTGTGGGTGCTGTGTGA 81536	CTGG T TG
	TCAC ATGGC TTCG TCC	
	AGTG TGTCG GGGT GGG	
	_____ T GT	
GAM2275 LOC153480 5'	GGGATACGGTTAAATCCAGTGA 73276	C GGCTT
	TCAC TGGAT TCGTGTCCC	
	AGTG ACCTA GGCATAGGG	
	_ AATT _	
GAM2275 LOC154092 3'	GGGATGTGGAAGAGGAGGTG 87372	GGATGG TG
	CACCT CTTTCG TCCC	
	GTGGA GAAGGT AGGG	
	GGA_____ GT	
GAM2275 LOC154760 5'	GGGGTATGGGCTGCCTCGGGT 87454	AT T_ GT
	ACCTGG GGC TTCGT CCC	
	TGGGCT CCG GGGTA GGG	
	_____ TC TG	
GAM2275 LOC154860 5'	GGAAGTAGGAGGCCACCGGGTG 87507	A GTG_ C
G	TCACCTGG TGGCTTTC TCC	
	GGTGGGCC ACCGGAGG AGG	
	_ ATGA	
GAM2275 LOC154877 3'	GGGAACACTAGCTGTCCAGGGA 87561	A TTC _
	TC CCTGGATGGCT GTGT CCC	
	AG GGACCTGTCGA CACA GGG	
	_ T_ A	
GAM2275 LOC157254 3'	GGGCACGGGCACAGGTGG 82313	GATG TT
	TCACCTG GCT CGTGTCC	

	GGTGGAC CGG GCACGGG		
	A___		
GAM2275 LOC157860 3'	GGGATCAAAGCTATCCAGGT 87879	CGT	
	ACCTGGATGGCTTT GTCCC		
	TGGACCTATCGAAA TAGGG		
	C__		
GAM2275 LOC158062 3'	GGGTGTTAAGTCAGTTTGGGTG 87966	TG _ TC TG C	
G	TCACC GA TGGCTT G TCC		
	GGTGG TT ACTGAA T GGG		
	GT G T_ GT		
GAM2275 LOC158292 5'	GGCCCTGGAGGGCTGCTAGGTG 88052	A GT_ CC	
G	TCACCTGG TGGCTTTC GTC		
	GGTGGATC GTCGGGAG CGG		
	GTCC		
GAM2275 LOC158656 5'	GCAGGAACCTATTTAGGTGG 73400	CT G	
	TCACCTGGATGG TTC TGT		
	GGTGGATTTATC AAG ACG		
	C_ G		
GAM2275 LOC163183 5'	GGACACCCTTGTCTAGGGA 83323	A TG CTTTC	
	TC CCTGGA G GTGTCC		
	AG GGATCT T CACAGG		
	_ GT CC__		
GAM2275 LOC164395 5'	GGATGGTGCCATCCAGGGA 83402	A TT GT	
	TC CCTGGATGGC TC GTCC		
	AG GGACCTACCG GG TAGG		
	_ T_ _		
GAM2275 LOC164714 3'	GGGAAGCTCAGCTACTGGGTGG 88588	TG A TTC G	
	TCACC G TGGCT GT TCCC		
	GGTGG C ATCGA CG AGGG		
	GT_ CT_ A		
GAM2275 LOC165257 3'	GGGTGCGAGGCGGGGTGG 83370	GGATG T TG	
	TCACCT GCTT CG TCC		
	GGTGGG CGGA GC GGG		
	G_ _ GT		
GAM2275 LOC200186 3'	GCAAGGGGTTTGTCCAGGTGG 91566	TG C TT G	
	TCACCTGGA G T C TGT		
	GGTGGACCT T G G ACG		
	GT T GG A		
GAM2275 LOC200225 5'	GGGCAAAGTCCTCCAGGTGA 91573	T TCG	
	TCACCTGGA GGCTT TGTCC		

		AGTGGACCT CTGAA ACGGG		
		C ____		
GAM2275	LOC200734 5'	GGACAGGCGTCTAGGTGA 90281	G	TTCGT
		TCACCTGGATG CT GTCC		
		AGTGGATCTGC GA CAGG		
		G ____		
GAM2275	LOC200830 3'	GGACATGGAGGGAGGTGA 91729	GGATGG	
		TCACCT CTTTCGTGTCC		
		AGTGGA GGAGGTACAGG		
		G ____		
GAM2275	LOC200953 3'	GGGGTGGGGGAAGCTGGCTGGG 91804	TG AT	_ G GT
	TGG	TCACC G GGCTTT C T CCC		
		GGTGG C TCGAAG G G GGG		
		GT GG G G TG		
GAM2275	LOC201475 5'	GGGAAAAAGTTATTCAGGAGA 89620	A	CGTG
		TC CCTGGATGGCTTT TCCC		
		AG GGACTTATTGAAA AGGG		
		A A ____		
GAM2275	LOC202018 3'	GGGATGTGACTATCAGGGTGG 90609	G	CTT TG
		TCACCT GATGG TCG TCCC		
		GGTGGG CTATC AGT AGGG		
		A ____ GT		
GAM2275	LOC219513 5'	GGGCGCGGGCGCTGGGCGG 95990	GA	T
		CTG TGGC TTCGTGTCC		
		GGC GTCG GGGCGCGGG		
		GG C		
GAM2275	LOC220020 5'	GGCAGACTGTTCAAGGTGG 95049	CTT	G T
		TCACCTGGATGG TC TG CC		
		GGTGGACTTGTC AG AC GG		
		____ _ C		
GAM2275	LOC220021 3'	GGGGCACGAACAGGTCTGGTGA 95024	T	GG _
		TCACC GGAT CT TTCGTGTCCC		
		AGTGG TCTG GA AAGCACGGGG		
		_ _ C		
GAM2275	LOC220595 5'	GGGGCATAAGAGTTTCCAGGTG 92779	T	CG
	G	TCACCTGGA GGCTTT TGTCCC		
		GGTGGACCT TTGAGA ACGGGG		
		_ AT		
GAM2275	LOC221501 3'	GGGGCGCGGGAAGGCAGGCGG 95434	GA	G _
		CTG TG CTTTC GTGTCCC		

GGC AC GAAGG CGCGGGG
GG G G
GAM2275 LOC221504 5' GGGACTCGCGGTGTCCGGGTGA 94021 G TT T
TCACCTGGATG CT CG GTCCC
||||||| || |||||
AGTGGGCCTGT GG GC CAGGG
_ C_ T
GAM2275 LOC245744 3' GGGGCGCGGGTCCCGGGGTGG 92789 GGA CT
TCACCT TGG TTCGTGTCCC
||||| ||| |||||
GGTGGG GCC GGGCGCGGGG
___ CT
GAM2275 LOC253868 5' GGGTCCCGGGGCTGACTGGGTG 97327 TG A T TGT
G TCACC G TGGCTT CG CCC
||||| | ||||| || |||
GGTGG C GTCGGG GC GGG
GT A _ CCT
GAM2275 LOC253926 3' GGGATGAACTTATTCAGATGG 96595 C C CGT
TCA CTGGATGG TTT GTCCC
||| ||||| ||| |||||
GGT GACTTATT AAG TAGGG
A C _
GAM2275 LOC254020 5' GGGGCGCGAGTGACCTCGGGG 97855 G T CT_
CCT GA GG TTCGTGTCCC
||| || ||| |||||
GGG CT CC GAGCGCGGGG
G _ AGT
GAM2275 LOC254431 5' GGGGTATGGGGGCTGCCAGG 98650 A TT GT
CCTGG TGGCT CGT CCC
||||| ||||| ||| |||
GGACC GTCGG GTA GGG
_ GG TG
GAM2275 LOC255031 5' GGGGTGCGGAAGAGCGCGGGGCT 99042 _ GATGG TG
GG TCA CCTG CTTTCG TCCC
||| ||||| ||||| |||||
GGT GGGC GAAGGC GGGG
C GCGA_ GT
GAM2275 LOC255189 5' GGGGTGTGGAGAGAATCAGGTG 98377 ATGG _TG
A TCACCTGG CTTTC G TCCC
||||||| ||||| | |||||
AGTGGACT GAGAG T GGGG
AA_ G GT
GAM2275 LOC255242 5' GGACATGGGGATAGTGTGG 97616 _ GATGGC TT
TCAC CTG T CGTGTCC
||||| ||| | |||||
GGTG GAT G GTACAGG
T A_ GG
GAM2275 LOC255328 3' GGGACTGATGCTGTCCAGGAGA 98344 A TT T
TC CCTGGATGGC TCG GTCCC
|| ||||| ||| |||||

AG GGACCTGTCTG AGT CAGGG
 A T _ _
 GAM2275 LOC256112 3' GAAGCCAGAGTCATCTGGGTGA 98112 TG C G
 TCACC GATGGCTTT GT TC
 |||| ||||| ||
 AGTGG CTA CTGAGA CG AG
 GT C A
 GAM2275 LOC256286 5' GGGATGTGTCCTGTTCTGTTGA 96896 CT _ TTT_ TG
 GTGG TCAC GGATGG C CG TCCC
 ||| ||||| | || ||||
 GGTG TTTGCT G GT AGGG
 AG T TCCT GT
 GAM2275 LOC256937 5' GGGATACGGTTAAATCCAGTGA 98915 C GGCTT
 TCAC TGGAT TCGTGTCCC
 ||| |||| |||||
 AGTG ACCTA GGCATAGGG
 _ AATT_
 GAM2275 LOC257054 3' GGGGCACGGGCAGGACCACGTG 97375 C ATG_ TT
 G TCAC TGG GCT CGTGTCCC
 |||| ||| ||| |||||
 GGTG ACC CGG GCACGGGG
 C AGGA _
 GAM2275 LOC257395 3' GGGCACGGGGTGTGGGCGG 97150 A GGATG _ TT
 TC CCT GC T CGTGTCC
 || ||| ||| |||||
 GG GGG TG G GCACGGG
 C _ _ T GG
 GAM2275 LOC51008 3' GGGATGTGGACATTTGGATGG 32535 C TG GCT TG
 TCA C GATG TTCG TCCC
 ||| |||| |||| ||||
 GGT G TTAC AGGT AGGG
 A GT _ _ GT
 GAM2275 LOC51241 5' GGTACTCGTCTTGGGTGA 33626 T CTTTC GT
 TCACC GGATGG GT CC
 |||| |||| || ||
 AGTGG TCTGCT CA GG
 T _ _ TG
 GAM2275 LOC51246 3' GGGGTGTGGGGCCCTGGATGG 33641 C TG AT T TG
 TCA C G GGCTT CG TCCC
 ||| | |||| || ||||
 GGT G C CCGGG GT GGGG
 A GT _ _ GT
 GAM2275 LOC51337 3' GGGTGCCCCATCTAGCTGG 34087 C CTTTC TG
 TCA CTGGATGG G TCC
 ||| ||||| | |||
 GGT GATCTACC C GGG
 C C _ _ GT
 GAM2275 LOC58525 3' GGGACCCGTTGGGAGCATTTGG 79347 TG G TT T _
 GTGG TCACC GATG CT CG GTCCC
 |||| |||| || || ||||

		GGTGG TTAC GA GT CAGGG	
		GT _ GG TGCC	
GAM2275 LOC84548	3'	GGGACGCGGAAGTGGCAGGTGA 71765	GATG
		TCACCTG GCTTTCGTGTCCC	
		AGTGGAC TGAAGGCGCAGGG	
		GG__	
GAM2275 LOC84570	5'	GGGAGTCGGAAGAGCTGTCTGG 51684	TG _ TG
		GTGG TCACC GATGGCTT TCG TCCC	
		GGTGG CTGTGAG GGC AGGG	
		GT AA TG	
GAM2275 LOC90019	3'	GGGGCATGAGCCCCTGGGTGA 57535	TG AT TT
		TCACC G GGC TCGTGTCCC	
		AGTGG C CCG AGTACGGGG	
		GT C_ _	
GAM2275 LOC90529	3'	GGGAGGCAGGAGCCACCCAGGT 63863	A TC G
		GA TCACCTGG TGGCTT GT TCCC	
		AGTGGACC ACCGAG CG AGGG	
		C GA G	
GAM2275 LOC91301	5'	GGGGTGTGGGGCCCTCAGGTAG 66149	_ AT T TG
		A TC ACCTGG GGCTT CG TCCC	
		AG TGGACT CCGGG GT GGGG	
		A C_ _ GT	
GAM2275 LOC91523	5'	GGAAGAAAGCTATCTAGGGA 57206	A GTG
		TC CCTGGATGGCTTTC TCC	
		AG GGATCTATCGAAAG AGG	
		_ A_	
GAM2275 LOC91689	5'	GGGGTGCGGGTGCCCGGGTGA 53980	ATG T TG
		TCACCTGG GC TTCG TCCC	
		AGTGGGCC CG GGGC GGGG	
		_ T GT	
GAM2275 LOC91759	5'	GGGGCATGAGACACAGGGA 67696	A GA GC
		TC CCTG TG TTTCGTGTCCC	
		AG GGAC AC AGAGTACGGGG	
		_ AC _	
GAM2275 LOC93070	3'	GGGATGTGGAGGTTGCAGTGA 71813	C GAT TG
		TCAC TG GGCTTTCG TCCC	
		AGTG AC TTGGAGGT AGGG	
		_ G_ GT	
GAM2275 LOC93276	5'	GGGCAACATGTTATTCAGGTGG 72380	TTTCG
		TCACCTGGATGGC TGTCC	

GGTGGACTTATTG ACGGG
TACA_
GAM2275 LOC93512 5' GGGAGGGGGGTCACCCAGGTGG 72877 A TT GTG
TCACCTGG TGGCT C TCCC
||||| |||| I ||||
GGTGGACC ACTGG G AGGG
C GG G_
GAM2276 FIGF 3' CCATTTTACACAGCACCACA 16771 CC_
TGTGGTGCTGT ATGG
||||||| ||||
ACACCACGACA TACC
CATT
GAM2276 IRTA2 3' TGCCAAATGGGACAGCACACA 49236 G A__ A
TGTG TGCTGTCC TGG CA
||| ||||| |||
ACAC ACGACAGG ACC GT
GTAA _
GAM2276 LTBP2 3' TGCCATGGGATACAGCACCCA 6469 T __ A
TG GGTGCTGT CCATGG CA
|| ||||| |||||
AC CCACGACA GGTACC GT
TAG _
GAM2276 PDE4B 3' CTGTTGTCCAGTCCAACTCCAC 12010 TGC TCCA
A
TGTGG TG TGGACAACAG
|||| || |||||
ACACC AC ACCTGTTGTC
TCA CTG_
GAM2276 STAR 3' CCGCTGCACAGCAACACCACA 6237 __ C _
TGTGGT GCTGT CA TGG
||||| ||||| |||
ACACCA CGACA GT GCC
CAA C C
GAM2276 ARGBP2 5' TGCTATCAGGCAGCACCA 41136 C_ A
TGGTGCTGTC ATGG CA
||||||| |||||
ACCACGACGG TATC GT
AC _
GAM2276 C20orf50 3' CTATCAAACAGCAGCCACA 70612 _ CC_
TGTGG TGCTGT ATGG
||||| ||||| |||
ACACC ACGACA TATC
G AAC
GAM2276 DKFZP434J193 3' TGCCAAGGACGGCACCACA 71565 A A
TGTGGTGCTGTCC TGG CA
||||||| |||||
ACACCACGGCAGG ACC GT
A _
GAM2276 KIAA0161 3' CTGCTGCCCATCGCATGAGCCC 29199 T GTCC__ A A
ACA
TGTGG GCT ATGG CA CAG
||||| ||| ||||| |||

			ACACC CGA TACC GT GTC		
			_ GTACGC C C		
GAM2276	KIAA1058	3'	TGTCATGTACCAGCACCACA 83141	TC_	G
			TGTGGTGCTG CATG ACA		
			ACACCACGAC GTAC TGT		
			CAT _		
GAM2276	TOR2A	3'	TGTGCTGGACAGCACCAC 56191	TGGACA	
			GTGGTGCTGTCCA ACA		
			CACCACGACAGGT TGT		
			CG____		
GAM2276	LOC125268	3'	TCCATGAGACAGCACCCA 76579	T	_
			TG GGTGCTGTC CATGGA		
			AC CCACGACAG GTACCT		
			_ A		
GAM2276	LOC148195	5'	CCATGCCAAACAGCACCCA 85274	T	C____
			TG GGTGCTGT CATGG		
			AC CCACGACA GTACC		
			_ AACC		
GAM2276	LOC149478	3'	CTGGGATTACAGACATGCACCA 80168	_	CA GACAA_
	CA		TGTGGTGCTG TG CAG		
			ACACCACG ACAG AC GTC		
			T _ ATTAGG		
GAM2276	LOC221692	3'	TGTTGCCTACAGCACCCA 93863	T	CCAT A
			TG GGTGCTGT GG CAACA		
			AC CCACGACA CC GTTGT		
			_ T____ _		
GAM2276	LOC253557	5'	CCAGAATGGTCAGCACCACA 97966	T	____
			TGTGGTGCTG CCA TGG		
			ACACCACGAC GGT ACC		
			T AAG		
GAM2276	LOC81501	3'	TGTTCCAAACAAACCACA 48633	GC CCA	_
			TGTGGT TGT TGGA CA		
			ACACCA ACA ACCT GT		
			A_ A_ T		
GAM2276	LOC91828	5'	TGTCCATGGACGTCCATA 67862	T T	
			TGTGG GC GTCCATGGACA		
			ATACC TG CAGGTACCTGT		
			_ _		
GAM2277	DNMT3B	3'	CCAGCCAGGCCCAAGCCC 23548	A	GCAGA
			GG GCT GCCTGGCTGG		

			CC CGA CGGACCGACC		
			_ ACCC_		
GAM2277 DNMT3L	5'	CCAAGTGACCCCCCGCAGCTCC 26283		AGA_____ C	
	TC		GAGGAGCTGC GC TGG		
			CTCCTCGACG TG ACC		
			CCCCCCAG A		
GAM2277 DVL3	3'	CCGATTGGCTCTGCAGCCCCCT 16640	A_ TGGC		
			AGG GCTGCAGAGCC TGG		
			TCC CGACGTCTCGG GCC		
			CC TTA_		
GAM2277 EHD2	3'	CAGCCAGGCAACACCCTCA 28216	AGC CAGA		
			TGAGG TG GCCTGGCTG		
			ACTCC AC CGGACCGAC		
			C_ AA_		
GAM2277 FCN1	3'	CAGCCAGACACACTCCCA 10607	A C CAGAGC		
			TG GGAG TG CTGGCTG		
			AC CCTC AC GACCGAC		
			_ _ ACA_		
GAM2277 FETUB	5'	CCAGCCAGTCCCTGCAGCTCC 27655	AGC		
			GGAGCTGCAG CTGGCTGG		
			CCTCGACGTC GACCGACC		
			CCT		
GAM2277 GRAF	3'	CCAGCCAGGCTCCCCTCCTT 31224	CTGCA		
			GAGGAG GAGCCTGGCTGG		
			TTCCTC CTCGGACCGACC		
			CC_		
GAM2277 HK3	3'	CCAGCCAGGCCAGCCACCCA 10924	A A_ CAGA		
			TG GG GCTG GCCTGGCTGG		
			AC CC CGAC CGGACCGACC		
			_ AC C_		
GAM2277 IL10RA	3'	CCAGCCAGGCCCTGCAGGGCT 60378	AG A		
			GG CTGCAG GCCTGGCTGG		
			TC GACGTC CGGACCGACC		
			GG C		
GAM2277 IL13	3'	CCAGCCAGCAGCCAGCTCTCA 10993	G CAGA _		
			TGAG AGCTG GC CTGGCTGG		
			ACTC TCGAC CG GACCGACC		
			_ _ AC		
GAM2277 ITGA3	3'	CCAGCCAGACCCCAGCTGAACC 11031	_ CAGAGC		
			GG AGCTG CTGGCTGG		

CC TCGAC GACCGACC
 AAG CCCA__
 GAM2277 ITGA3 3' CCAGCCAGACCCCAGCTGAACC 11032 ____ CAGAGC
 GG AGCTG CTGGCTGG
 || |||| |||||
 CC TCGAC GACCGACC
 AAG CCCA__
 GAM2277 MECP2 3' CAGGGGCCCTGCAGCTCTCA 18390 G A GG
 TGAG AGCTGCAG GCCT CTG
 ||| ||||| ||| ||
 ACTC TCGACGTC CGGG GAC
 _ C _
 GAM2277 MVK 3' CCAGCCAAGCTCTGCAGTCCC 61277 AG C
 GG CTGCAGAGC TGGCTGG
 || ||||| |||||
 CC GACGTCTCG ACCGACC
 CT A
 GAM2277 SHANK2 3' CCAGCCAGCGTGCAACTGCCCA 25525 A _ C GA C
 TG GG AG TGCA GC TGGCTGG
 || || ||| || |||||
 AC CC TC ACGT CG ACCGACC
 _ G A G _
 GAM2277 SLC9A1 5' CCAGAGTCCCAGCTCCTCA 70920 CA GC
 TGAGGAGCTG GA CTGG
 ||||| || |||
 ACTCCTCGAC CT GACC
 C_ GA
 GAM2277 SOX10 3' CCTGTTCTGCAGCCCCCA 23673 A A CT
 TG GG GCTGCAGAGC GG
 || || ||||| ||
 AC CC CGACGTCTTG CC
 C C T_
 GAM2277 STXBP1 3' CAGCGCTCCGCAGCTTCCCA 13473 A A CTG
 TG GGAGCTGC GAGC GCTG
 || ||||| ||| |||
 AC CTTGACG CTCG CGAC
 C C _
 GAM2277 TBXA2R 5' CCAGCCAGGTGGGAGCCCCGCA 8348 A A GCAGA
 TG GG GCT GCCTGGCTGG
 || ||| |||||
 AC CC CGA TGGACCGACC
 G C GGG_
 GAM2277 TCL1B 3' CCAGCCAGGCCTCCAGCACC 18192 A C A
 GG GCTG AG GCCTGGCTGG
 || ||| || |||||
 CC CGAC TC CGGACCGACC
 A C _
 GAM2277 TEL2 3' CCAGCCAGACTCTGTACCC 32850 AGC C
 GG TGCAGAG CTGGCTGG
 || ||||| |||||

CC ATGTCTC GACCGACC
 C__ A
 GAM2277 TNFRSF8 3' CCAGATGTCTGCAGCCCTCA 8796 A GC_
 TGAGG GCTGCAGA CTGG
 ||||| ||||| ||||
 ACTCC CGACGTCT GACC
 _ GTA
 GAM2277 C8orf17 5' CAGCCAGGCAGGCCCGCA 39989 A A GCAGA
 TG GG GCT GCCTGGCTG
 || ||| |||||
 AC CC CGG CGGACCGAC
 G C A__
 GAM2277 DKFZP434O047 5' CTGGGGGGGCTCTGCAGCTGCC 32122 A _ GG TG
 A TG GG AGCTGCAGAGCCT C G
 || || ||||| ||||| | |
 AC CC TCGACGTCTCGGG G C
 _ G G_ GT
 GAM2277 DOC2A 3' CCGCCCAGGCCCGCGCTCCTC 14562 T AGA C
 A TGAGGAGC GC GCCTGG TGG
 ||||| || ||||| ||||
 ACTCCTCG CG CGGACC GCC
 _ CCC C
 GAM2277 FLJ12788 3' CCAGATTACTCACAGCTCCTCA 42845 CA CCTGG
 TGAGGAGCTG GAG CTGG
 ||||| || ||||
 ACTCCTCGAC CTC GACC
 A_ ATTA_
 GAM2277 FLJ14225 3' CCAGCTGCTAAGCTCTGCAGCT 46383 A C__
 CCCCA TG GGAGCTGCAGAGC TGGCTGG
 || ||||| |||||
 AC CCTCGACGTCTCG GTCGACC
 C AATC
 GAM2277 FLJ20034 3' CCAACCACTCAATCCTAAGCTC 34839 GCA GCC__ C
 CTCA TGAGGAGCT GA TGG TGG
 ||||| || |||||
 ACTCCTCGA CT ACC ACC
 ATC AACTC A
 GAM2277 FLJ20507 3' TCAACTCTGCAGCTCCTC 35751 CC
 GAGGAGCTGCAGAG TGG
 ||||| ||||| ||||
 CTCCTCGACGTCTC ACT
 A_
 GAM2277 KIAA1100 3' CCAGCCAGGGCCCAACTCCCA 30439 A C CAGAG
 TG GGAG TG CCTGGCTGG
 || ||| || |||||
 AC CCTC AC GGACCGACC
 _ A CCG_
 GAM2277 KIAA1303 3' CCAGCCAGGCCACCTCTC 66601 G C CAGA
 A TGAG AG TG GCCTGGCTGG
 ||| || || |||||

		ACTC TC AC CGGACCGACC	
		_ C CACC	
GAM2277 KIAA1656	3'	CCAGGCTGCCCCGCAGCTCCTC 66362	AG__
A		TGAGGAGCTGC AGCCTGG	
		ACTCCTCGACG TCGGACC	
		CCCCG	
GAM2277 MAP2K3	3'	CCAGCCAGGCCCTTGTGCGGCC 59683	A _ A_
C		GG GCTG CAG GCCTGGCTGG	
		CC CGGC GTT CGGACCGACC	
		C T CC	
GAM2277 MGC26847	3'	CCAGCCAGTCAGCTACAACTCC 59398	C C AGC_
		GGAG TG AG CTGGCTGG	
		CCTC AC TC GACCGACC	
		A A GACT	
GAM2277 MMP24	3'	CCAGCCAGGCCCTTCCTCA 22916	GCTGC A
		TGAGGA AG GCCTGGCTGG	
		ACTCCT TC CGGACCGACC	
		_____ C	
GAM2277 SARM	3'	CCAGCTGGCTTCCCCAGCCCT 31281	A CA_ T
CA		TGAGG GCTG GAGCC GGCTGG	
		ACTCC CGAC TTCGG TCGACC	
		C CCC _	
GAM2277 SEEK1	5'	CCAGCCATCTATGCAGCGCCCC 26807	A A G CC
A		TG GG GCTGCA AG TGGCTGG	
		AC CC CGACGT TC ACCGACC	
		C G A T_	
GAM2277 SLC16A10	5'	CCAGGAGCCCCGCAGCTCCTC 38352	AGAG__
		GAGGAGCTGC CCTGG	
		CTCCTCGACG GGACC	
		CCCCGA	
GAM2277 LOC121219	3'	CCAGCCAGTCACAGCTCCTC 74484	CA GC
		GAGGAGCTG GA CTGGCTGG	
		CTCCTCGAC CT GACCGACC	
		A_ _	
GAM2277 LOC146445	3'	CCAGCCAGGCCTAAGGGCCCAT 84680	_ A GC_ A
CA		TGA GG GCT AG GCCTGGCTGG	
		ACT CC CGG TC CGGACCGACC	
		A _ GAA _	
GAM2277 LOC147808	3'	CCAAGCCCTTCCGCCGCTCCTC 85196	T A CCT _
A		TGAGGAGC GC GAG GGCT GG	

ACTCCTCG CG CTT CCGA CC
 C C C__ A
 GAM2277 LOC149345 3' CCAGTCTACAACCCTGCAGCTC 80083 AGCCT__
 CTC GAGGAGCTGCAG GGCTGG
 ||||| ||||
 CTCCTCGACGTC CTGACC
 CCAACAT
 GAM2277 LOC149460 5' CAGCCAGGCTCTGTCCCCT 85606 AGCT
 AGG GCAGAGCCTGGCTG
 || |||||
 TCC TGTCTCGGACCGAC
 CC__
 GAM2277 LOC149461 3' CAGCCAGGCTCTGTCCCCT 80200 AGCT
 AGG GCAGAGCCTGGCTG
 || |||||
 TCC TGTCTCGGACCGAC
 CC__
 GAM2277 LOC152271 3' CCGGCTCTGCAGGTCCCCA 81358 A G T
 TG GGA CTGCAGAGCC GG
 || ||||| ||
 AC CCT GACGTCTCGG CC
 C G _
 GAM2277 LOC153277 3' CGCTGGCAAATTCTACAGCTCC 87187 C G_____ TGGCT
 TCA TGAGGAGCTG AGA CC G
 ||||| || || |
 ACTCCTCGAC TCT GG C
 A TAAAC__ TCGG
 GAM2277 LOC169611 3' CCAGCCAGGCCTGACTCATCA 83641 G CTG A
 TGA GAG CAG GCCTGGCTGG
 || || || |||||
 ACT CTC GTC CGGACCGACC
 A A__ _
 GAM2277 LOC170281 5' CCAGGGTTTCTGCAGCTACCCA 88600 A _ _
 TG GG AGCTGCAGAG CCTGG
 || || ||||| ||||
 AC CC TCGACGTCTT GGACC
 _ A TG
 GAM2277 LOC201201 5' CCACTGGGCTCCGCAGCCCCT 91340 A A TG C
 AGG GCTGC GAGCC G TGG
 || || || || || ||
 TCC CGACG CTCGG C ACC
 C C GT_
 GAM2277 LOC201617 5' CCAGCCAACTCCACTGCC 91824 _ C CA CC
 GG AG TG GAG TGGCTGG
 || || || || |||||
 CC TC AC CTC ACCGACC
 G _ _ AA
 GAM2277 LOC219654 3' CCAGCCAGGCCGCTGCCCA 92926 A A T_ AGA
 TG GG GC GC GCCTGGCTGG
 || || || || |||||

AC CC CG CG CGGACCGACC
 _ C TC C_
 GAM2277 LOC220002 3' CCACTCTGCAGCTCACCA 93270 AG CC
 TG GAGCTGCAGAG TGG
 || ||||| ||
 AC CTCGACGTCTC ACC
 CA _
 GAM2277 LOC253917 5' CGGCTGGCTGACTCTGCAGCCC 98001 A A G_____ TGGCT
 CGCA TG GG GCTGCAGA CC G
 || ||||| || |
 AC CC CGACGTCT GG C
 G C CAGTC_____ TCGGT
 GAM2277 LOC254105 3' CCAGCCAGGCCCTAAGAGCC 96417 AG GC A
 GG CT AG GCCTGGCTGG
 || || |||||
 CC GA TC CGGACCGACC
 GA A_ C
 GAM2277 LOC51066 3' CCAACCCCTTATACAGCTCCTC 32501 CA_ CCT C
 GAGGAGCTG GAG GG TGG
 ||||| || |||
 CTCCTCGAC TTC CC ACC
 ATA C_ A
 GAM2277 LOC90139 3' CCAGCCAGACCCTGGGCCCTC 56265 A G AGC
 GAGG GCT CAG CTGGCTGG
 ||| ||| |||||
 CTCC CGG GTC GACCGACC
 _ _ CCA
 GAM2277 LOC90381 3' CCAGCCAGGCTCAGCCCTCA 63211 A GCA
 TGAGG GCT GAGCCTGGCTGG
 |||| || |||||
 ACTCC CGA CTCGGACCGACC
 _ _
 GAM2277 LOC96652 3' CCAGCCAGGCCCCACCGAGTCC 66075 GC CAGA_
 GGA TG GCCTGGCTGG
 || | |||||
 CCT GC CGGACCGACC
 GA CACCC
 GAM2278 KCNK6 3' ACAGGAATGTCCACGACACAG 17881 A_ C CG_
 C GC TGC CGTGGACA CTGT
 || ||||| |||
 CG ACG GCACCTGT GACA
 AC A AAG
 GAM2278 SEPN1 3' GGCCACAGGCATGCC 66978 C ACAC
 GGCATGCC GTGG GCT
 ||||| ||| ||
 CCGTACGG CACC CGG
 A _
 GAM2278 KIAA1879 5' ACAGCACTGACCAGGCATGCC 73923 CG A C_
 GGCATGCC TGG CA GCTGT
 ||||| ||| || |||

CCGTACGG ACC GT CGACA
 ___ A CA
 GAM2278 LOC256055 3' ACAACGTGTCTATGCATCACCA 97621 C_ CC C
 TGG ATGC GTGGACACG TGT
 ||| ||| ||||| |||
 ACC TACG TATCTGTGC ACA
 AC ___ A
 GAM2278 LOC90841 5' ACAGCGTGGTACGGATACCA 64860 C GC GA
 TGG AT CCGTG CACGCTGT
 ||| || ||||| |||||
 ACC TA GGCAT GTGCGACA
 A ___ G_
 GAM2279 GPD1 3' TCATGCCACCACATTTG 60398 C C
 TAAATG GGTGGCAT GA
 ||||| ||||| ||
 GTTTAC CCACCGTA CT
 A _
 GAM2279 IL5RA 5' TCGCATGGCCACCGCATTT 6906 AT__
 AAATGCGGTGGC CGA
 ||||| |||
 TTTACGCCACCG GCT
 GTAC
 GAM2279 MYO1C 3' TGCCGATGCCAAATATTTG 61873 CGG A
 TAAATG TGGCATCG CA
 ||||| ||||| ||
 GTTTAT ACCGTAGC GT
 AA_ C
 GAM2279 C6orf37 3' TGTCACACTGCATTTA 68097 GCATC
 TAAATGCGGTG GACA
 ||||| |||
 ATTTACGTAC CTGT
 A____
 GAM2279 DNAJC6 3' TTGCAGAACCACCGCATT 29498 CA GA
 AATGCGGTGG TC CAA
 ||||| || |||
 TTACGCCACC AG GTT
 A_ AC
 GAM2279 FLJ11210 3' GTCGATGTGCATGCTTTTA 60319 T GTG
 TAAA GCG GCATCGAC
 ||| || |||||
 ATTT CGT TGTAGCTG
 T ACG
 GAM2279 FLJ12476 3' TCGATCTTCTGCATTTA 43270 T C
 TAAATGCGG GG ATCGA
 ||||| || |||||
 ATTTACGTC TC TAGCT
 T _
 GAM2279 KIAA1034 3' TCGATGGCATCCGCATTTG 63134 _ G
 TAAATGCGG TG CATCGA
 ||||| || |||||

		GTTTACGCC AC GTAGCT		
		T G		
GAM2279	KIAA1987	3' TCATGTAAGTGCATTTA 89391	G	C
		TAAATGCGGT GCAT GA		
		ATTTACGTCA TGTA CT		
		A _		
GAM2279	MGC16063	3' TGTCCTGGCCACTGCATT 54929		ATC
		AATGCGGTGGC GACA		
		TTACGTCACCG CTGT		
		GTC		
GAM2279	LOC147949	3' TGTCAGATGTCCACATTGCA 79279	—	— —
		TGCG GTGG CATC GACA		
		ACGT CACC GTAG CTGT		
		TA T A		
GAM2279	LOC150577	3' GTCCTCACCGCATTTG 86258		CATC
		TAAATGCGGTGG GAC		
		GTTTACGCCACT CTG		
		C—		
GAM2279	LOC158219	3' TGTGTGTCACCACATTT 82694	C	CG
		AAATG GGTGGCAT ACA		
		TTTAC CCACTGTG TGT		
		A —		
GAM2279	LOC202020	3' TGTCTCACACATTTA 90605	C	CATC
		TAAATG GGTGG GACA		
		ATTTAC CCACT CTGT		
		A —		
GAM2279	LOC90826	5' TGTCGATGCAGTTTATTTG 64788		CGGTG
		TAAATG GCATCGACA		
		GTTTAT CGTAGCTGT		
		TTGGA		
GAM2279	LOC93587	3' TTGTCTTTACCTGCATTTA 73042	—	CATC
		TAAATGC GGTGG GACAA		
		ATTTACG CCATT CTGTT		
		T T—		
GAM2280	MSF	3' TCAGGTGCACACATCACCAGG 89468	C	GA AA
		CCT GGTGATGTG TGTG TGA		
		GGA CCACTACAC ACGT ACT		
		— — GG		
GAM2280	TCF3	3' TCATCCACATCCACACCTCAC 71276	—	A
		GTGA TGTGGATGTG ATGA		

CACT ACACCTACAC TACT
 CC C
 GAM2280 TEGT 3' TCATTCACATCAACAGAGCGAG 65231 G GA G
 G CCTCG T TGT GATGTGAATGA
 ||||| I ||| |||||
 GGAGC G ACA CTACACTTACT
 _AG A
 GAM2280 FLJ10815 3' CATCCCCAGACATCACCAGG 37231 C ____
 CCT GGTGATGT GGATG
 ||| ||||| |||||
 GGA CCACTACA CCTAC
 _ GACC
 GAM2280 FLJ14054 3' CACCCACATCCACATTCAGC 44965 _ AA
 GT GATGTGGATGTG TG
 || ||||| ||
 CG TTACACCTACAC AC
 AC CC
 GAM2280 FLJ20038 5' TCATTCACCAATATCCCGA 34866 T GGAT
 TCGG GATGT GTGAATGA
 ||| ||||| |||||
 AGCC CTATA CACTTACT
 _ AC_
 GAM2280 GAL3ST-4 3' CAAGGCAGATCCACATCACCGA 45274 G AA_
 TCGGTGATGTGGAT TG TG
 ||||| || ||
 AGCCACTACACCTA AC AC
 G GGA
 GAM2280 KCNT1 3' TACATCAACATCACCAAGG 62496 C G
 CCT GGTGATGT GATGTG
 ||| ||||| |||||
 GGA CCACTACA CTACAT
 A A
 GAM2280 KIAA0514 3' CACTCACCTCATCATCACTGAG 28741 TG T A
 CTCGGTGATG GA GTGA TG
 ||||| || |||||
 GAGTCACTAC CT CACT AC
 TA C C
 GAM2280 KIAA1229 3' CATTCACAATTGCCACAAAG 62754 CG AT TG A
 CT GTG G G TGTGAATG
 || ||| | |||||
 GA CAC C T ACACTTAC
 AA _GT A
 GAM2280 MGC20253 3' TCATCAAGCTCCACATCACTGA 58677 T GA_
 GG CCTCGGTGATGTGGA GT ATGA
 ||||| || |||||
 GGAGTCACTACACCT CG TACT
 _ AAC
 GAM2280 LOC146733 3' ACTCCACACCACCGGGG 84780 A T
 CCTCGGTG TGTGGA GT
 ||||| ||||| ||

GGGGCCAC ACACCT CA
C _
GAM2280 LOC147965 3' CATTACGTCAATACCAAG 79298 C ATGTG
CT GGTG GATGTGAATG
|| ||| |||||
GA CCAT CTGCACTTAC
A AA__
GAM2280 LOC152274 3' TCATTACATGGAGCCACC 81346 AT GG_
GGTG GT ATGTGAATGA
||| || |||||
CCAC CG TACACTTACT
__ AGG
GAM2280 LOC200230 3' TCACCCAGCTACCAAGG 90047 C TG AT
CCT GGTGA TGG GTGA
|| ||| || |||
GGA CCACT ACC CACT
A CG _
GAM2280 LOC220064 3' CACCCACGTCCACCTACC 95062 AT AA
GGTG GTGGATGTG TG
||| ||||| ||
CCAT CACCTGCAC AC
C_ CC
GAM2280 LOC254182 3' CACTCATCACCTCATCACCGAG 97746 T AT A
G CCTCGGTGATG GG GTGA TG
||||||| || ||| ||
GGAGCCACTAC CC TACT AC
T AC C
GAM2281 FRG1 5' CGACTCACATACTCGTCCAG 16803 CAC CCT
CTGGACGAG GTGG TCG
|||||| ||| |||
GACCTGCTC CACT AGC
ATA C__
GAM2281 C20orf18 3' GGGCCACATGCTGACCCAG 49173 ACG C
CTGG AGCA GTGGCCT
||| ||| |||||
GACC TCGT CACCGGG
CAG A
GAM2281 C20orf18 3' GGGCCACATGCTGACCCAG 49182 ACG C
CTGG AGCA GTGGCCT
||| ||| |||||
GACC TCGT CACCGGG
CAG A
GAM2281 FLJ10761 3' CGAGGAAACATGCTCCCCA 37128 AC C GG T
TGG GAGCA GT CCT CG
|| ||| || ||| ||
ACC CTCGT CA GGA GC
C_ A AA _
GAM2281 Kv6.3 3' CTCGAAGGTTTACTCACCCAG 56854 AC CACGT
CTGG GAG GGCCTTCGAG
||| || |||||

			GACC CTC TTGGAAGCTC		
			CA AT___		
GAM2281	SDF1	5'	CGACCCGCGCTCGTCC 92516	A T CCT	
			GGACGAGC CG GG TCG		
			CCTGCTCG GC CC AGC		
			C _ _ _		
GAM2281	SNRK	5'	TGGAGCCACGTGTCACCCAG 35285	AC G C	
			CTGG GA CACGTGGC TTCG		
			GACC CT GTGCACCG AGGT		
			CA _ _		
GAM2282	FMR2	3'	GAAAGCACCTGGTTTGCACCAT 10693	_ _ C	
	T		GATGGT CAG CCAGGTGC TTC		
			TTACCA GTT GGTCCACG AAG		
			C T A		
GAM2282	ARHGEF4	5'	AAGTGAACCGACCATCAA 53368	AGCCA GC_	
			TTGATGGTC GGT CTT		
			AACTACCAG CCA GAA		
			_ _ _ AGT		
GAM2282	CABP4	3'	AAAACACCTGGCCTCAAT 59747	T GTCA CC	
			ATTGA G GCCAGGTG TT		
			TAACT C CGGTCCAC AA		
			_ _ _ _ AA		
GAM2282	CDV-1	5'	ACTGTGGCTGACACCAAT 49688	ATG _	
			ATTG GTCAGCCA GGT		
			TAAC CAGTCGGT TCA		
			CA_ G		
GAM2282	FLJ23598	3'	AAGACACCCCCCTGGACCCATC 96501	_ CCA C	
	AAT		ATTGATGG TCAG GGTG CTT		
			TAACTACC GGTC CCAC GAA		
			CA CCC A		
GAM2282	PTPRR	3'	GAAGACTTGTGACACCATCAAT 56450	AGC GC	
			ATTGATGGTC CAGGT CTTC		
			TAACTACCAG GTTCA GAAG		
			ACT _		
GAM2282	RHOBTB1	3'	GCACAAGCTCACCATCAAT 93093	C CAG	
			ATTGATGGT AGC GTGC		
			TAACTACCA TCG CACG		
			C AA_		
GAM2282	LOC146181	3'	TACTCTGGCTGACCATCA 69151	_	
			TGATGGTCAGCCAG GTG		

ACTACCAGTCGGTC CAT
 T
 GAM2282 LOC255452 3' AAGTGAACCGACCATCAA 99383 AGCCA GC_
 TTGATGGTC GGT CTT
 ||||| ||| |||
 AACTACCAG CCA GAA
 _____ AGT
 GAM2282 LOC51026 3' GCATTCTTGACCATGAAT 32686 G CCA
 ATTATGGTCAG GGTGC
 ||| ||||| |||||
 TAA TACCAGTT TTACG
 G C_
 GAM2282 LOC85479 5' AAGGCACCTGGCTCCTCAG 53555 T TC
 TTGA GG AGCCAGGTGCCTT
 |||| || |||||
 GACT CC TCGGTCCACGGAA
 - -
 GAM2283 ABP1 3' GACATTCCCAACACAGCCA 63798 AA CC
 TGG CTGTGTTGGGAG TC
 ||| ||||| ||| ||
 ACC GACACAACCCTT AG
 _____ AC
 GAM2283 AUP1 3' GATGAGGCTCCCCCAATGTCAC 25024 GA TG TT
 A TG AC TG GGGAGCCTCATC
 || || || |||||
 AC TG AC CCCTCGGAGTAG
 AC TA C_
 GAM2283 C19orf7 3' AGGCTCCTATCCCACCCCA 61775 AACT T_
 TGG GTG TGGGAGCCT
 ||| ||| |||||
 ACC CAC ATCCTCGGA
 C_ CCT
 GAM2283 FLJ14810 3' GATGAGGCTTGACAAACCCCA 52702 AACTG T G
 TGG TGT G GAGCCTCATC
 ||| ||| |||||
 ACC ACA T TTCGGAGTAG
 CCCA_ _ G
 GAM2283 FLJ20342 3' ATGAGGCTCCCCCTGTCTCA 35465 GA TGTGTT
 TG AC GGGAGCCTCAT
 || || |||||
 AC TG CCCTCGGAGTA
 TC TCC_
 GAM2283 FOXJ1 3' GCCCCCAACACAGGTCCA 9377 A A_
 TGGA CTGTGTTGGG GC
 |||| ||||| ||
 ACCT GACACAACCC CG
 G CC
 GAM2283 HABP2 3' ATGAAGCTCCCCCACCCECA 15949 AACT TT C
 TGG GTG GGGAGC TCAT
 ||| ||| ||||| |||

ACC CAC CCCTCG AGTA
 CC__ C_ A
 GAM2283 MGC4840 3' ATGAAGCCTACACATCC 72016 AC TG A C
 GGA TGTGT GG GC TCAT
 ||| |||| || ||||
 CCT ACACA TC CG AGTA
 __ __ _ A
 GAM2283 MYOZ2 3' ATGAGGCTCCCATCATGCCA 33939 AAC T
 TGG TGTG TGGGAGCCTCAT
 ||| |||| |||| |||| ||||
 ACC GTAC ACCCTCGGAGTA
 __ T
 GAM2283 NASP 3' GATGAGGCAGTGGCACAGTTC 68578 GGA
 GAACTGTGTTG GCCTCATC
 |||| |||| |||| ||||
 CTTGACACGGT CGGAGTAG
 GA_
 GAM2283 TED 3' GATGAGGTGCACACAGTTGCA 32269 G TGGGA
 TG AACTGTGT GCCTCATC
 || |||| |||| ||||
 AC TTGACACA TGGAGTAG
 G CG__
 GAM2283 LOC130436 3' GAGGGAACACACAGATCCA 75437 A T GGAG
 TGG A CTGTGT G CCTC
 ||| |||| | |||
 ACCT GACACA C GGAG
 A _ AAG_
 GAM2283 LOC144289 3' ATAAGGCTCCCACTTCC 83950 CTGT T C
 GGAA GT GGGAGCCT AT
 ||| || |||| || ||
 CCTT CA CCCTCGGA TA
 __ _ A
 GAM2283 LOC163115 3' GATGAGGCAGAGCCACAGTCAC 83316 GA TTGGGA
 A TG ACTGTG GCCTCATC
 || |||| |||| ||||
 AC TGACAC CGGAGTAG
 AC CGAGA_
 GAM2283 LOC169270 3' GATGAGGCCTCTTGAACAATTC 83612 C G TG _
 CA TGGAA TGT T GGAG CCTCATC
 |||| ||| | ||| ||||
 ACCTT ACA A TCTC GGAGTAG
 A _ GT C
 GAM2283 LOC255167 3' ATGAGGCTCCTGGGAAATCCA 98939 ACTGTG TG
 TGG A T GGAGCCTCAT
 ||| | |||| ||||
 ACCT G CCTCGGAGTA
 AAAG__ GT
 GAM2284 BIKE 3' TACCATTGGACCAACAGAAACC 34608 GC_ A_ A
 TCA TGAGGTTTC TGG TAGT GGTA
 |||| ||| ||| |||

ACTCCAAAG ACC GTTA CCAT
 ACA AG _
 GAM2284 LOC221641 5' ACCTACTACCCTGACCCCT 95339 TT CT A
 AGG TCG GG TAGTAGGT
 ||| ||| || |||||
 TCC AGT CC ATCATCCA
 CC _ C
 GAM2284 LOC256158 5' TACCCACTATCCAGTGGCTGC 99513 T_ A
 GT TCGCTGGATAGT GGTA
 || ||||| |||
 CG GGTGACCTATCA CCAT
 TC C
 GAM2285 HRH1 3' AAATGTGCCCTTTTGGCCGG 7812 A A TCA
 CC GGCCAAAA GGC ACATTT
 || ||||| ||| |||||
 GG CCGGTTTT CCG TGTA
 _ C _
 GAM2285 POLD2 5' TTGAACCTCCTTGGCCTGG 21721 AA C
 CCAGGCCAA AGG TCAA
 ||||| ||| |||
 GGTCCGGTT TCC AGTT
 CC A
 GAM2285 SCN7A 3' AAATGTTGAAAGCCTAAGCC 12947 CAAAA _
 GGC AGGC TCAACATTT
 ||| ||| |||||
 CCG TCCG AGTTGTAA
 AA_ AA
 GAM2285 SHANK2 3' GTTGAACCTTCTTCTTTGGCCTC 25531 C _ C_
 A C AGGCCAAA AAGG TCAAC
 | ||||| ||| |||||
 A TCCGGTTT TTCT AGTTG
 C C TCA
 GAM2285 SIAT8E 3' TGAGCCTCCTGGCCTGG 60552 AAA
 CCAGGCCA AGGCTCA
 ||||| |||||
 GGTCCGGT TCCGAGT
 CC_
 GAM2285 SLC7A8 3' GAGCCCTTCTTGGCCTGG 25304 AA _
 CCAGGCCA AAGG CTC
 ||||| ||| |||
 GGTCCGGT TTCC GAG
 CC C
 GAM2285 TFAP2C 3' TGGGAACCCCTCCTGGCCTGG 13687 AAA ____
 CCAGGCCA AGG CTCA
 ||||| ||| |||
 GGTCCGGT TCC GGGT
 CC_ CCAA
 GAM2285 TRPM2 3' GAGCCTTGCCCTGGCCTGG 13864 AA_
 CCAGGCCA AAGGCTC
 ||||| |||||

		GGTCCGGT TTCCGAG		
		CCG		
GAM2285	FLJ13189	3' TTGAACCTTTTTGCCTGG 46498	C	C
		CCAGGC AAAAAGG TCAA		
		GGTCCG TTTTTC AGTT		
		T A		
GAM2285	FLJ20208	3' AAATGCAGGCTTTTGTAGCC 35240	C	G CAA
		GGC AAAAAG CT CATT		
		CCG TTTTTC GA GTAAA		
		A G C__		
GAM2285	FLJ22944	3' AAATGTTGGGATTGAACCC 47866	CCAA	GG
		GG AAA CTCAACATT		
		CC TTT GGGTTGTAAA		
		CAAG A_		
GAM2285	HPRP8BP	3' AAATGTTGGATGTCCAGGCT 60060	AAAAA	__
		GGCC GGC TCAACATT		
		TCGG CTG GGTGTAAA		
		AC__ TA		
GAM2285	KIAA0872	3' AAATGTTAAGCCTTTTGTATT 30731	GCCA	C
	G	CAG AAAAGGCT AACATT		
		GTT TTTTCCGA TTGTAAA		
		ATTG A		
GAM2285	KIAA1843	3' AAATGTTGACTGAACCTGACCT 62880	C	AAAA_ C
	G	CAGG CA GG TCAACATT		
		GTCC GT TC AGTTGTAAA		
		A CCAAG _		
GAM2285	KIAA1975	3' AAATGTTGATTTTCTGACC 74407	C A	C
		GG CA AAAGG TCAACATT		
		CC GT TTTT AGTTGTAAA		
		A C _		
GAM2285	MRIP2	3' AAATGTTGATTTTCTGACC 56789	C A	C
		GG CA AAAGG TCAACATT		
		CC GT TTTT AGTTGTAAA		
		A C _		
GAM2285	SLC26A10	5' TTGAACCCCTTTGGCCTG 56851	AA	C
		CAGGCCAAA GG TCAA		
		GTCCGGTTT CC AGTT		
		CC A		
GAM2285	THEG	3' TGAGCTTTTGGCCTGG 33892	G	
		CCAGGCCAAAAAG CTCA		

GGTCCGGTTTTTC GAGT

GAM2285 LOC118704 3' AAATGTTGATTTTTCTGACC 74359 C A C
GG CA AAAGG TCAACATTT
|| || |||| |||||
CC GT TTTT AGTTGTAA
A C _

GAM2285 LOC118706 3' AAATGTTGATTTTTCTGACC 74361 C A C
GG CA AAAGG TCAACATTT
|| || |||| |||||
CC GT TTTT AGTTGTAA
A C _

GAM2285 LOC123036 3' AAATGTTTGCAGTTTTGGCT 74645 AG TC
GGCCAAAA GC AACATTT
||||| || |||||
TCGGTTTT CG TTGTAA
GA T_

GAM2285 LOC123624 3' AAATGTTGGGCTTCTGTGCCT 76134 _ AAA
AGGC CA AGGCTCAACATTT
||| || |||||
TCCG GT TTCGGGTTGTAA
T C__

GAM2285 LOC128338 3' AAATATTGAGCCTTTTTAATAG 75250 AGGCC C
G CC AAAAAGGCTCAA ATTT
|| ||||| |||
GG TTTTCCGAGTT TAA
ATAA_ A

GAM2285 LOC143158 3' AAATGTTGATTTTTCTGACC 76997 C A C
GG CA AAAGG TCAACATTT
|| || |||| |||||
CC GT TTTT AGTTGTAA
A C _

GAM2285 LOC195979 3' AAATGTTGATTTTTCTGACC 88928 C A C
GG CA AAAGG TCAACATTT
|| || |||| |||||
CC GT TTTT AGTTGTAA
A C _

GAM2285 LOC219672 5' AATGGTGCTTTTTGGCTGG 92963 G G TCAA
CCAG CCAAAAAG C CATT
||| ||||| | |||
GGTC GGTTTTTC G GTAA
_ _TG_

GAM2285 LOC220466 3' AAATGTTGATTTTTCTGACC 74398 C A C
GG CA AAAGG TCAACATTT
|| || |||| |||||
CC GT TTTT AGTTGTAA
A C _

GAM2285 LOC254105 3' AGGTGTGGCCCCCTTGGCCTGG 96416 AAA CA
CCAGGCCAA GGCT ACATTT
||||| ||| |||||

GGTCCGGTT CCGG TGTGGA
CCC _
GAM2285 LOC255319 3' AAATGTTGATTTTCTGACC 96152 C A C
GG CA AAAGG TCAACATTT
|| ||||| |||||
CC GT TTTT AGTTGTAA
A C _
GAM2285 LOC91300 5' GTTGAGCTTTTCTGGCCCGG 96238 A A
CC GGCCA AAAGGCTCAAC
|| ||||| |||||
GG CCGGT TTTTCGAGTTG
C C
GAM2285 LOC91300 5' GTTGAGCTTTTCTGGCCCGG 57864 A A
CC GGCCA AAAGGCTCAAC
|| ||||| |||||
GG CCGGT TTTTCGAGTTG
C C
GAM2285 LOC91660 5' AAATGTTTATCTTCTTTTGGC 67399 CTC_
TT AGGCCAAAAAGG AACATTT
||||||| |||||
TTCGGTTTTTCT TTGTAA
TCTAT
GAM2286 SLC20A2 3' CACCCCCAGGCTCTACTC 23115 _ A A
GA TAGAGCCT GG GTG
|| ||||| |||||
CT ATCTCGGA CC CAC
C C C
GAM2286 ARP5 5' CACTCCCAGGCTCTGGGGGCTG 72031 GA A
G TCAGTCT TAGAGCCT GGAGTG
||||| ||||| |||||
GGTCGGG GTCTCGGA CCTCAC
G_ C
GAM2286 DKFZP434O125 3' CACCCTAAAACATCAGACT 65583 AGAGCC A
AGTCTGAT TAGG GTG
||||| |||||
TCAGACTA ATCC CAC
CAA_ C
GAM2286 KIAA1023 3' CACTCCCAAGCTCCATGGCTGG 34674 TGATA CTA
TCAGTC GAGC GGAGTG
||||| ||||| |||||
GGTCGG CTCG CCTCAC
TAC_ AAC
GAM2286 LOC135932 3' CACTCCTAAGCTCTGACCGCT 76696 CTGA C
AGT TAGAGC TAGGAGTG
||| ||||| |||||
TCG GTCTCG ATCCTCAC
CCA_ A
GAM2286 LOC150225 3' CACCCTAGGCTGTGGAAGC 86181 T GA G A
G CT TA AGCCTAGG GTG
|| || ||||| |||||

		C GA GT TCGGATCC CAC	
		_ AG G C	
GAM2286	LOC152573 5'	CACTCCGCAGCTATCAGAC 81495	AGCCTA
		GTCTGATAG GGAGTG	
		CAGACTATC CCTCAC	
		GACG__	
GAM2286	LOC155179 3'	CACTCCCAAGCTCCATGGCTGG 82222	TGATA CTA
		TCAGTC GAGC GGAGTG	
		GGTCGG CTCG CCTCAC	
		TAC__ AAC	
GAM2286	LOC256980 3'	CACTCCTCAAGCCTCCCAAAC 96926	C AT A CT_
		GT TG AG GC AGGAGTG	
		CA AC TC CG TCCTCAC	
		A CC _ AAC	
GAM2286	LOC90371 5'	CACTCCGTCTCCTCCAGACTGA 63157	ATA CCTA
		TCAGTCTG GAG GGAGTG	
		AGTCAGAC CTC CCTCAC	
		CTC TG__	
GAM2287	ABCD2 5'	ATGAGGGGCCTGGGAGGGA 18965	A__ G
		TCCCTCCCA CCCT GT	
		AGGGAGGGT GGGA TA	
		CCG G	
GAM2287	ADSS 3'	TTTGGTGGGGCTGGGAGGGG 72235	A G
		TCCCTCCCA CCCTG TGAG	
		GGGGAGGGT GGGGT GTTT	
		C G	
GAM2287	AES 3'	CAGGGAGGTTGGGAGGGG 8522	__
		TCCCTCCCAA CCCTG	
		GGGGAGGGT GGGAC	
		GGA	
GAM2287	ALDOB 3'	CAGTGGTAGGTTGGGAAGGA 68650	C __ G
		TCC TCCCAACC CTG TG	
		AGG AGGGTTGG GGT AC	
		A AT G	
GAM2287	AMH 5'	CTCTATCACTGGGGAGGGA 6652	AACCC _
		TCCCTCCC TGGT GAG	
		AGGGAGGG ACTA CTC	
		GTC__ T	
GAM2287	ANKRD3 3'	CTCACCAGTCTTGAGGGA 40562	CC CC
		TCCCTC AA CTGGTGAG	

			AGGGAG TT GACCACTC		
			___ CT		
GAM2287	ARHGAP6	3'	CCATGGGAGTGGGAGGGA 8611	A_ _	
			TCCCTCCCA CCC TGG		
			AGGGAGGGT GGG ACC		
			GA T		
GAM2287	AVPR1A	5'	CAATAGGGCGGGAGGGA 7374	AA G	
			TCCCTCCC CCCTG TG		
			AGGGAGGG GGGAT AC		
			C_ A		
GAM2287	B3GNT3	3'	CTCAGAAGGTTGGGGGGA 27303	T C GG	
			TCCC CCCAACC T TGAG		
			AGGG GGGTTGG A ACTC		
			_ _ AG		
GAM2287	BASP1	3'	CAATGGGAGTTGGGAGTGA 76493	C _ GG	
			TC CTCCCAAC CCT TG		
			AG GAGGGTTG GGG AC		
			T A TA		
GAM2287	BAZ2A	5'	CTCACAGTTTGGGAGG 26508	CC G	
			CCTCCCAA CTG TGAG		
			GGAGGGTT GAC ACTC		
			T_ _		
GAM2287	BCL11B	3'	CTCATTAGGTTGGAAGG 43484	C C	
			CCT CCAACC TGGTGAG		
			GGA GGTTGG ATTACTC		
			A _		
GAM2287	CACNG6	3'	CCGGGTGCGGTTGGGGGAGA 49946	C _	
			TC CTCCCAACC CTGG		
			AG GGGGGTTGG GGCC		
			A CGTG		
GAM2287	CNTN2	3'	CTCACTCCTGCCTGGGAGGGG 18660	ACCCT_	
			TCCCTCCCA GGTGAG		
			GGGGAGGGT TCACTC		
			CCGTCC		
GAM2287	COL9A1	5'	CTCACCGGGGGCAGGAGGGA 10252	CAA	
			TCCCTCC CCCTGGTGAG		
			AGGGAGG GGGGCCACTC		
			ACG		
GAM2287	DHCR24	3'	TTCATTAGTTGAAAGGGA 29305	CC CC	
			TCCCT CAAC TGGTGAG		

			AGGGA GTTG ATTACTT		
			AA _		
GAM2287	EPB49	3'	CGGCGGGTTGGGAGGGG 10527	T G	
			TCCCTCCCAACCC G TG		
			GGGGAGGGTTGGG C GC		
			_ G		
GAM2287	FCMD	3'	CTCACAGTAGGGTTGAAAGAG 23035	C_ _	
			CTC CAACCCTG GTGAG		
			GAG GTTGGGAT CACTC		
			AAA GA		
GAM2287	FLRT2	3'	CTCATCAGGGTAAGAGG 25996	CCA	
			CCTC ACCCTGGTGAG		
			GGAG TGGGACTACTC		
			AA_		
GAM2287	GGT1	3'	CTCACCAGGACCAGGAAGGG 26420	_ CAAC	
			CCCT CC CCTGGTGAG		
			GGGA GG GGACCACTC		
			A ACCA		
GAM2287	GGT1	3'	CTCACCAGGACCAGGAAGGG 26436	_ CAAC	
			CCCT CC CCTGGTGAG		
			GGGA GG GGACCACTC		
			A ACCA		
GAM2287	GGT1	3'	CTCACCAGGACCAGGAAGGG 19158	_ CAAC	
			CCCT CC CCTGGTGAG		
			GGGA GG GGACCACTC		
			A ACCA		
GAM2287	GPR17	3'	TGGTGGGGACGGGAGGGA 19182	AA_ G	
			TCCCTCCC CCCTG TG		
			AGGGAGGG GGGGT GT		
			GCA G		
GAM2287	GRIN2D	3'	CGCGTGGGTTGGGAAGGA 7735	C TG	
			TCC TCCCAACCC GTG		
			AGG AGGGTTGGG CGC		
			A TG		
GAM2287	KIAA0442	3'	CTCACACAGACTGGGGGGGA 32094	ACC _	
			TCCCTCCCA CTG GTGAG		
			AGGGGGGGT GAC CACTC		
			CA_ A		
GAM2287	LAD1	5'	CACCTGGGCTGGAAGGGG 19900	C A T	
			TCCCT CCA CCC GGTG		

		GGGGA GGT GGG CCAC	
		A C T	
GAM2287 LTF	5'	CGCGGGGAGTGGGGAGGGA 11374	A _ G
		TCCCTCCC AC CCT GTG	
		AGGGAGGG TG GGG CGC	
		G A G	
GAM2287 LYL1	5'	CTCACTTTCCCTGGGGGGGA 19950	ACCCT
		TCCCTCCCA GGTGAG	
		AGGGGGGGT TCACTC	
		CCCTT	
GAM2287 NDN	3'	CTCACCAGGGCTGTGGAAGG 11758	C _ A
		CC TCC CA CCCTGGTGAG	
		GG AGG GT GGGACCACTC	
		A T C	
GAM2287 NEDD4L	3'	TTTATTAGAATTGGAAGG 31609	C CC
		CCT CCAA CTGGTGAG	
		GGA GGTT GATTATTT	
		A AA	
GAM2287 OSCAR	5'	CTCATTTCTGGGAGGGG 56249	ACCCT
		TCCCTCCCA GGTGAG	
		GGGGAGGGT TTACTC	
		CCT__	
GAM2287 OSCAR	5'	CTCATTTCTGGGAGGGG 56477	ACCCT
		TCCCTCCCA GGTGAG	
		GGGGAGGGT TTACTC	
		CCT__	
GAM2287 OSCAR	5'	CTCATTTCTGGGAGGGG 56480	ACCCT
		TCCCTCCCA GGTGAG	
		GGGGAGGGT TTACTC	
		CCT__	
GAM2287 P53AIP1	3'	CTGTGGTGATGGGAGGGA 42336	_ C
		TCCCTCCCA ACC TGG	
		AGGGAGGGT TGG GTC	
		AG T	
GAM2287 PIP5K1A	3'	TGTTAGGGGTGGGAGGGA 14523	A GT
		TCCCTCCCA CCCTG G	
		AGGGAGGGT GGGAT T	
		G TG	
GAM2287 POV1	3'	CTCCTTGGGTTGGAGGAGA 14636	_ C T T
		TC CCTCC AACCC GG GAG	

AG GGAGG TTGGG TC CTC
 A _ T _
 GAM2287 PPP2R5D 3' CAAGTGGGGCCGGGAGGGA 21803 AA_ G_
 TCCCTCCC CCCTG TG
 ||||| ||| ||
 AGGGAGGG GGGGT AC
 GCC GA
 GAM2287 SERPINH2 3' TATTGGGGTTGGGGGGGA 8787 TG
 TCCCTCCCAACCC GTG
 ||||| |||
 AGGGGGGGTTGGG TAT
 GT
 GAM2287 SLC21A2 3' CTCACCAGCCCTGGGGGGA 20083 T ACC
 TCCC CCCA CTGGTGAG
 ||| ||| |||||
 AGGG GGGT GACCACTC
 _ CCC
 GAM2287 STK19 3' CTCAGAGTGGGCCGGGAGGGG 16097 AA TGG_
 TCCCTCCC CCC TGAG
 ||||| ||| |||
 GGGGAGGG GGG ACTC
 CC TGAG
 GAM2287 STK19 3' CTCAGAGTGGGCCGGGAGGGG 51613 AA TGG_
 TCCCTCCC CCC TGAG
 ||||| ||| |||
 GGGGAGGG GGG ACTC
 CC TGAG
 GAM2287 TSN 3' TCAGCGGTTGCCAGGAAGGG 17305 _ _ _
 CCCT CC CAACC CTGG
 ||| || ||||| |||
 GGGA GG GTTGG GACT
 A ACC C
 GAM2287 TUFT1 3' TTCATCAGATTGGGAGAGG 39681 _ CC
 CC CTCCCA CTGGTGAG
 || ||||| |||||
 GG GAGGGTT GACTACTT
 A A_
 GAM2287 BHLHB2 3' CTCACCAGACGTCGGGGAGAGA 14764 C A_ C_
 TC CTCCC AC CTGGTGAG
 || |||| || |||||
 AG GAGGG TG GACCACTC
 A GC CA
 GAM2287 BPESC1 3' CGATGGGGTTGAGAGGGG 41771 C GG
 TCCCTC CAACCCT TG
 ||||| ||||| ||
 GGGGAG GTTGGGG GC
 A TA
 GAM2287 BRPF3 5' CAGCGCGGGCCGGGAGGGG 93927 AA _ G
 TCCCTCCC CCC TG TG
 ||||| ||| |||

GGGGAGGG GGG GC AC
CC C G
GAM2287 C20orf151 3' CACCAGGGCCTGGAGAGG 90091 _ A_
CCTC CCA CCCTGGTG
||||| ||| |||||
GGAG GGT GGGACCAC
A CC
GAM2287 C20orf180 5' TGTCAGGGTTGGGGGGA 37974 T GT
TCCC CCCAACCCTG G
||||| ||||| |||
AGGG GGGTTGGGAC T
TG
GAM2287 CCT5 5' CGCCGGTTGGGGGGA 73033 T CT
TCCC CCCAACC GGTG
||||| ||||| |||
AGGG GGGTTGG CCGC

GAM2287 CECR6 5' CCGGGGTTGGCGGGGAGGGA 49931 ____
TCCCTCCC AACCTGG
||||| |||||
AGGGAGGG TTGGGGCC
GCGG
GAM2287 DGS-A 3' CCAGGGCAGGCTGGGAGGGA 86051 A____
TCCCTCCCA CCCTGG
||||| |||||
AGGGAGGGT GGGACC
CGGAC
GAM2287 DKFZp761P1010 3' CATGTGGGGTTGGAGGAGA 37942 _ C _
TC CCTCC AACCTG GTG
|| ||||| ||||| |||
AG GGAGG TTGGGGT TAC
A _ G
GAM2287 ET(B)R-LP-2 3' CAGTAGGGGTGGGGAGGGA 17672 AA_ G
TCCCTCCC CCCTG TG
||||| ||||| ||
AGGGAGGG GGGAT AC
GTG G
GAM2287 FLJ10057 3' CTCATGGAAGATGTTGGGAGAG 36251 C ____ TG
A TC CTCCAAC CC GTGAG
|| ||||| || |||||
AG GAGGGTTG GG TACTC
A TAGAA _
GAM2287 FLJ10853 3' CTCACTGGGTCAAAGGGA 37315 CCCA T
TCCCT ACCC GGTGAG
||||| ||| |||||
AGGGA TGGG TCACTC
AAC_ _
GAM2287 FLJ11000 3' CAGGAGGGTGGGGAGGGA 37525 A GG
TCCCTCCC ACCCT TG
||||| ||||| ||

			AGGGAGGG TGGGA AC		
			G GG		
GAM2287	FLJ12650	3'	CTCACCACTTGAAGG 44820	C	CC
			CCT CCAAC TGGTGAG		
			GGA GGTG ACCACTC		
			A _		
GAM2287	FLJ20489	3'	CTCACCTAACTTGGGAGGGA 35711		CCCT
			TCCCTCCCAA GGTGAG		
			AGGGAGGGTT CCACTC		
			CAAT		
GAM2287	FLJ20793	3'	CATTGTAGGTTGGGAAGGG 93448	_	CT_
			CCCT CCCAACC GGTG		
			GGGA GGGTTGG TTAC		
			A ATG		
GAM2287	FLJ21313	3'	TCAGGAAAGTGGGGAGGGA 43934	A	__
			TCCCTCCC AC CCTGG		
			AGGGAGGG TG GGA CT		
			G AAA		
GAM2287	FLJ23231	3'	CTCAGAGGGTGGGGAGGGA 47605	A	GG
			TCCCTCCC ACCCT TGAG		
			AGGGAGGG TGGGA ACTC		
			G G_		
GAM2287	FLJ32915	5'	CTCACATTTTGGGAGGGA 59432		CCCTG
			TCCCTCCCAA GTGAG		
			AGGGAGGGTT CACTC		
			TTA_		
GAM2287	FREQ	3'	CTCAAAGGCTGGGAGGGA 27370	AC	GG
			TCCCTCCCA CCT TGAG		
			AGGGAGGGT GGA ACTC		
			C_ A_		
GAM2287	GGTL4	3'	CTCACCAAGGACCAGGAAGGG 55944	_	CAAC
			CCCT CC CCTGGTGAG		
			GGGA GG GGACCACTC		
			A ACCA		
GAM2287	GMPPB	3'	CCAAGGGGTGGGAGGGA 97439	A_	_
			TCCCTCCCA CCCT GG		
			AGGGAGGGT GGGA CC		
			GG A		
GAM2287	GTPBP1	3'	CTTCCAGGGTTAGGACAGA 16266	CC	C T
			TC TCC AACCTGG GAG		

		AG AGG TTGGGACC TTC	
		AC A _	
GAM2287	HGC6.1.1	3' CAGTGGGAGCTGGGAGGGA 27609	AC_ G
		TCCCTCCCA CCTG TG	
		AGGGAGGGT GGGT AC	
		CGA G	
GAM2287	HOOK2	3' CCAGATTGGTGGGGAGGGA 26158	A ____
		TCCCTCCC ACC CTGG	
		AGGGAGGG TGG GACC	
		G TTA	
GAM2287	KIAA0140	3' CTCAGTCCTCTGGGAGGGA 28512	ACCCT ____
		TCCCTCCCA GG TGAG	
		AGGGAGGGT CC ACTC	
		CT__ TG	
GAM2287	KIAA0182	3' TACGCAGGTGGGAGGGA 72502	AC _
		TCCCTCCCA CCTG GTG	
		AGGGAGGGT GGAC CAT	
		_ G	
GAM2287	KIAA0252	3' TGGCAGGTGTGGGAGGGA 63461	AC G
		TCCCTCCCA CCTG TG	
		AGGGAGGGT GGAC GT	
		GT G	
GAM2287	KIAA0285	3' CTCAGAAGAACTGGGAGGGG 29683	ACC_ GG
		TCCCTCCCA CT TGAG	
		GGGGAGGGT GA ACTC	
		CAAA AG	
GAM2287	KIAA0677	3' CACTGTAGGTGGGAGGGA 28529	A CT_
		TCCCTCCCA CC GGTG	
		AGGGAGGGT GG TCAC	
		_ ATG	
GAM2287	KIAA0789	5' CTCACCTTCAGTTTGGGAGGG 64429	CCCT__
		CCCTCCCAA GGTGAG	
		GGGAGGGTT CCACTC	
		TGACTT	
GAM2287	KIAA0843	3' CTTTGTAGATTGGGGGGA 30802	T CC GT
		TCCC CCAA CTG GAG	
		AGGG GGGTT GAT TTC	
		_ A_ GT	
GAM2287	KIAA0853	3' TTTATTAATGGGGAGGGA 31217	AACCC
		TCCCTCCC TGGTGAG	

AGGGAGGG ATTATTT
 GTA__
 GAM2287 KIAA0864 3' CAGTGGGGGCTGGGAGGG 63938 A_ G
 CCCTCCCA CCCTG TG
 ||||| |||||
 GGGAGGGT GGGGT AC
 CG G
 GAM2287 KIAA1018 3' TTCATCAGCCAGGAGGGA 31059 CAACC
 TCCCTCC CTGGTGAG
 ||||| |||||
 AGGGAGG GACTACTT
 ACC__
 GAM2287 KIAA1061 3' CACACGGGTTGGGAGAGG 71716 _ TG
 CC CTCCCAACCC GTG
 || ||||| ||
 GG GAGGGTTGGG CAC
 A CA
 GAM2287 KIAA1171 3' GCTCACGGGGAGAGGTATGGGA 89344 _ _ G _
 GGGA TCCCTCCCA ACC CT GTGAG C
 ||||| || ||||| |
 AGGGAGGGT TGG GG CACTC G
 A AGAG G _
 GAM2287 KIAA1190 3' CTCGGGGGATTGGGGGGA 71646 T _ GG
 TCCC CCAA CCCT TGAG
 ||| ||||| ||| |||
 AGGG GGGTT GGGG GCTC
 _ A _
 GAM2287 KIAA1649 3' TGCTGGTTGGGAGTGA 67518 C CT
 TC CTCCCAACC GGTG
 || ||||| |||
 AG GAGGGTTGG TCGT
 T _
 GAM2287 KIAA1649 3' TGCTGGTTGGGAGTGA 51256 C CT
 TC CTCCCAACC GGTG
 || ||||| |||
 AG GAGGGTTGG TCGT
 T _
 GAM2287 KIAA1655 5' CTCACCTCCAGTGGGAGGGA 67182 ACCCT
 TCCCTCCCA GGTGAG
 ||||| |||||
 AGGGAGGGT CCACTC
 GACCT
 GAM2287 KIAA1750 3' CTCAGTGATAGAGTATGGGAGG 68809 _ C G_
 GA TCCCTCCCA AC CTG TGAG
 ||||| || ||| |||
 AGGGAGGGT TG GAT ACTC
 A A AGTG
 GAM2287 KIAA1944 5' CACCAGGTAGTCACTGGGCAGA 76077 C _ _ _
 GA TC CT CCAA AC CCTGGTG
 || ||||| || |||||

AG GA GGGT TG GGACCAC
 A C CAC AT
 GAM2287 KIAA1952 5' CTCTGCCGGCTGGGAGGG 73544 ACC _
 CCCTCCCA CTGGT GAG
 ||||| |||||
 GGGAGGGT GGCCG CTC
 C__ T
 GAM2287 LAGY 5' CTCAGTCCAGGGAGGGA 51658 AACCC _
 TCCCTCCC TGG TGAG
 ||||| |||||
 AGGGAGGG ACC ACTC
 _____ TG
 GAM2287 MGC10715 3' CTTATCAGGCATGGGAGGGA 44498 AC
 TCCCTCCCA CCTGGTGAG
 ||||| |||||
 AGGGAGGGT GGA CTATTC
 AC
 GAM2287 MGC15429 3' CTCAGTGGCTGGGAAGG 52211 C A CT
 CC TCCCA CC GGTGAG
 || ||||| |||||
 GG AGGGT GG TCACTC
 A C _
 GAM2287 MGC4737 5' CTCACCAGCGGAGTGGA 49640 _ CAACC
 TCC CTCC CTGGTGAG
 ||||| |||||
 AGG GAGG GACCACTC
 T C____
 GAM2287 MGC5139 5' CTTGAAAGGGTGGGGAGGGA 74571 A GG
 TCCCTCCC ACCCT TGAG
 ||||| ||||| |||||
 AGGGAGGG TGGGA GTTC
 G AA
 GAM2287 MLLT10 5' CCGGGTGGAGGTGGGGAGGGA 17351 A _____
 TCCCTCCC ACC CTGG
 ||||| ||||| |||||
 AGGGAGGG TGG GGCC
 G AGGTG
 GAM2287 MMP24 3' CTCACCAGGGTCTGAGGGG 22918 CCA
 TCCCTC ACCCTGGTGAG
 ||||| |||||
 GGGGAG TGGGACCACTC
 TC_
 GAM2287 moblak 3' CTCACCAGAATTGTCAGTGG 56396 _ CC CC
 CC CT CAA CTGGTGAG
 || ||||| |||||
 GG GA GTT GACCACTC
 T CT AA
 GAM2287 NIP30 3' CTCAGTATATTGGGAGG 46896 CCC
 CCTCCCAA TGGTGAG
 ||||| |||||

GGAGGGTT GTCACTC
ATA
GAM2287 PRO0529 3' CTCACCAGGGTGGGCAGAGA 26856 C _ A
TC CT CCCA CCCTGGTGAG
|| ||| |||||
AG GA GGGT GGGACCACTC
A C _
GAM2287 PTK6 5' CTCTGAGGGTTGGGAAGG 21076 C GGT
CC TCCCAACCCT GAG
|| ||||| |||
GG AGGGTTGGGA CTC
A GT_
GAM2287 RAB3IL1 3' CTCAGCCCTTGGGAGGGG 26365 CCCT _
TCCCTCCCAA GG TGAG
||||| |||||
GGGGAGGGTT CC ACTC
C_ G
GAM2287 RIN3 3' TTCATTAGACGGAAAGGGA 46164 C_ AACC
TCCCT CC CTGGTGAG
|||| || |||||
AGGGA GG GATTACTT
AA CA_
GAM2287 RP4-622L5 3' CTCATTTCTTGGGAGGG 39424 CCCT
CCCTCCCAA GGTGAG
||||| |||||
GGGAGGGTT TTA CTCT
CT_
GAM2287 SCMH1 3' CTCACCAGGAGTTTAGG 25283 CCC _
CCT AAC CCTGGTGAG
|| || |||||
GGA TTG GGACCACTC
T_ A
GAM2287 SERPINH1 3' TATTGGGGTTGGGGGGGA 16375 TG
TCCCTCCCAACCC GTG
||||||| |||
AGGGGGGGTTGGG TAT
GT
GAM2287 SIAT4B 5' CTCACCAGGGTGGCAGGAGA 23634 _ C A
TC CCT CCA CCCTGGTGAG
|| ||| |||||
AG GGA GGT GGGACCACTC
A C _
GAM2287 SNPH 3' CTCTGGGGGTTGGAGGGA 28902 C GGT
TCCCTCC AACCCT GAG
||||| ||||| |||
AGGGAGG TTGGGG CTC
_ GT_
GAM2287 SSH-3 5' CGCGGGGTTGAGGGA 35790 CC G
TCCCTC AACCCTG TG
||||| ||||| ||

AGGGAG TTGGGGC GC

GAM2287 SSH-3 5' CGCGGGGTTGAGGGA 37417 CC G
TCCCTC AACCTG TG
||||| ||||| ||
AGGGAG TTGGGGC GC

GAM2287 VIAAT 3' CGAGGGGGTTGGGAAGGGA 55450 _ GG
TCCCT CCCAACCT TG
||||| ||||| ||
AGGGA GGGTTGGGG GC

A GA
GAM2287 LOC114987 3' CGGGAATGAGTTGGGAGGGG 59795 _____
TCCCTCCCAAC CCTG
||||||| ||||
GGGGAGGGTTG GGGC
AGTAA

GAM2287 LOC121036 3' CAGTAGGATGGGAGGGA 74481 AC G
TCCCTCCCA CCTG TG
||||||| |||| ||
AGGGAGGGT GGAT AC
A_ G

GAM2287 LOC123346 5' CTCTGAAAGAGTCGGGGAGGGA 76127 A_ C GGT_
TCCCTCCC AC CT GAG
||||||| || || |||
AGGGAGGG TG GA CTC
GC A AAGT

GAM2287 LOC136306 3' CAAAGGGGTGTGAGAGGGA 75768 C _ GG
TCCCTC CA ACCCT TG
||||| || ||||| ||
AGGGAG GT TGGGG AC
A G AA

GAM2287 LOC144596 3' CTCACCTGGAGGCAAGAGGGA 77427 _ AAC T
TCCCTC CC CC GGTGAG
||||| || || |||||
AGGGAG GG GG CCACTC
AAC A_ T

GAM2287 LOC145497 5' CCAGGGCTTGCTGGGAGGGA 77731 A____
TCCCTCCCA CCCTGG
||||||| |||||
AGGGAGGGT GGGACC
CGTTC

GAM2287 LOC146439 5' CTCATTCTGGGAGGGG 78449 ACCCT
TCCCTCCCA GGTGAG
||||||| |||||
GGGGAGGGT TTA CTC
CC__

GAM2287 LOC147711 3' CTCAGCCTTTGGGAGGG 79116 CCCT _
CCCTCCCAA GG TGAG
||||||| || ||||

	GGGAGGGTT CC ACTC	
	T___ G	
GAM2287 LOC150150 5'	CCAGTGTGGTGGGAGGGA 86009	A ____
	TCCCTCCCA CC CTGG	
	AGGGAGGGT GG GACC	
	_ TGT	
GAM2287 LOC152667 3'	CTCACTGATATTGGGAGG 81523	CCC
	CCTCCCAA TGGTGAG	
	GGAGGGTT GTCACTC	
	ATA	
GAM2287 LOC157931 3'	CTCACGGCCTGGGAGGG 87940	AC TG
	CCCTCCCA CC GTGAG	
	GGGAGGGT GG CACTC	
	CC _	
GAM2287 LOC158055 3'	CCGGCGGCTGGTGAGGGA 82580	_ A _
	TCCCTC CCA CC CTGG	
	AGGGAG GGT GG GGCC	
	T C C	
GAM2287 LOC199927 3'	CCGGAGTGGCTGGGAGGGG 91479	A ____
	TCCCTCCCA CC CTGG	
	GGGGAGGGT GG GGCC	
	C TGA	
GAM2287 LOC201182 5'	CTCACTGGTTGAGATGGA 91336	C C CT
	TCC TC CAACC GGTGAG	
	AGG AG GTTGG TCACTC	
	T A _	
GAM2287 LOC219920 5'	CTCATTAGACTGGGAGG 94947	ACC
	CCTCCCA CTGGTGAG	
	GGAGGGT GATTACTC	
	CA_	
GAM2287 LOC220739 3'	TCAGGGCTTAGGGAGGGA 94529	_ _
	TCCCTCCC AA CCCTGG	
	AGGGAGGG TT GGGACT	
	A C	
GAM2287 LOC221424 3'	CCTGGGACTTGGGAGGGA 95271	_ T
	TCCCTCCCAA CCC GG	
	AGGGAGGGTT GGG CC	
	CA T	
GAM2287 LOC221718 5'	CTCACCAGCCTGAGGTAGGA 95280	CT _ ACC
	TCC CC CA CTGGTGAG	

AGG GG GT GACCACTC
 AT A CC_
 GAM2287 LOC253955 5' CTCACCAGGTGCAGAGGGG 96072 CCAAC
 TCCCTC CCTGGTGAG
 ||||| |||||
 GGGGAG GGACCACTC
 ACGT_
 GAM2287 LOC255328 3' CTCACCAGGTGAGGAGTGA 98338 C _ AC
 TC CTCC CA CCTGGTGAG
 || |||| || |||||
 AG GAGG GT GGACCACTC
 T A _
 GAM2287 LOC256973 3' CTCACGGCCTCCGGGAGGGG 98198 AAC__ TG
 TCCCTCCC CC GTGAG
 ||||| || ||||
 GGGGAGGG GG CACTC
 CCTCC _
 GAM2287 LOC257456 3' CTCACTAGGACCAGGAAGGG 80594 _ CAAC
 CCCT CC CCTGGTGAG
 |||| || |||||
 GGGA GG GGATCACTC
 A ACCA
 GAM2287 LOC51696 3' CATTGGAGGTTGGAAGGA 33079 C _ TG
 TCC TCCCAACC C GTG
 ||| ||||| | |||
 AGG AGGGTTGG G TAC
 A A GT
 GAM2287 LOC91496 5' CATTAGAGGTGGAAGGGA 66808 C A _
 TCCCT CCA CC CTGGTG
 ||||| ||| || |||||
 AGGGA GGT GG GATTAC
 A _ A
 GAM2287 LOC92228 5' CTCACCAGGGTGAGGG 69075 CCA
 CCCTC ACCCTGGTGAG
 ||||| |||||
 GGGAG TGGGACCACTC
 _
 GAM2287 LOC92293 3' CACACAGCTGGGGGGGA 69318 ACC _
 TCCCTCCCA CTG GTG
 ||||| ||| |||
 AGGGGGGGT GAC CAC
 C_ A
 GAM2288 ATP6V1G2 3' AAAACATCCTGACTTCAG 56192 CCTCT C
 TTGAAG TCGGGATGT TT
 ||||| ||||| || ||
 GACTTC AGTCCTACA AA
 _ A
 GAM2288 ATP6V1G2 3' AAAACATCCTGACTTCAG 57115 CCTCT C
 TTGAAG TCGGGATGT TT
 ||||| ||||| || ||

			GACTTC	AGTCCTACA AA		
			_____	A		
GAM2288	COCH	3'	ACACTGCTGAGGCTTCA	15834	TT GA	
			TGAAGCCTC	CGG TGT		
			ACTTCGGAG	GTC ACA		
			TC	__		
GAM2288	ROCK2	3'	GAAAACATCTTTTCTAGCTTCA	66618	CTCTTC	C
	A		TTGAAGC	GGGATGT TTC		
			AACTTCG	TTCTACA AAG		
			ATCTT_	A		
GAM2288	TAP2	3'	GAAGCTCAAAGAGGCTCAA	6778	A C	ATG
			TTGA GCCTCTT	GGG TC		
			AACT CGGAGAA	CTC AG		
			_	A GA_		
GAM2288	KIAA1877	3'	CATCTTGAAAGGTCCAA	66742	AA C	
			TTG GCCT TTCGGGATG			
			AAC TGGA	AAGTTCTAC		
			C_	_		
GAM2288	KIAA1884	3'	GAAGAGACCATAAAGGCTTCAA	73726	CTTCG	ATG
			TTGAAGCCT	GG TCTTC		
			AACTTCGGA	CC AGAAG		
			ATA_	AG_		
GAM2288	MGC13168	3'	AAGACATCTGCCTCAACTTCAA	52185	CCTCTTCG	
			TTGAAG	GGATGTCTT		
			AACTTC	TCTACAGAA		
			AACTCCG_			
GAM2288	LOC150481	3'	GAAGACACAGGAAGAGGCCTCA	80701	A	GGA
			TGA GCCTCTTC	TGTCTTC		
			ACT CGGAGAAG	ACAGAAG		
			C	GAC_		
GAM2288	LOC157507	5'	GAAGGCTCACAGAGGCTTCAA	82379	TCGG	T
			TTGAAGCCTCT	GA GTCTTC		
			AACTTCGGAGA	CT CGGAAG		
			CA_	_		
GAM2288	LOC158191	3'	GAAGACACAGGAAGAGGCCTCA	82674	A	GGA
			TGA GCCTCTTC	TGTCTTC		
			ACT CGGAGAAG	ACAGAAG		
			C	GAC_		
GAM2288	LOC90538	3'	AACAGAGAGGCTCAA	63889	A	CGGGA C
			TTGA GCCTCTT	TGT T		

AACT CGGAGAG ACA A
 — — A
 GAM2289 CDH12 3' CTTATCATTTAAAGTGGTGTA 15777 CCCAA GA
 TACACCACT GAA ATAAG
 ||||| ||| ||||
 ATGTGGTGA TTT TATTC
 AA__ AC
 GAM2289 GOCAP1 3' ATTGTTCTTGGGAGCAGTGTA 43007 CA G
 TACAC CTCCCAAGAA AAT
 |||| ||||| |||
 ATGTG GAGGGTTCTT TTA
 AC G
 GAM2289 DKFZp434N2435 5' CTTATTACTGTGGGGTGGT 98090 T AGAAG
 ACCAC CCCA AATAAG
 |||| ||| ||||
 TGGTG GGGT TTATTC
 _ GTCA_
 GAM2289 DKFZP564I122 3' CTTATTCTTCTCCCTCATGTGT 63877 CACTCCCA
 A TACAC AGAAGAATAAG
 |||| |||||
 ATGTG TCTTCTTATTC
 TACTCCC_
 GAM2289 FLJ21791 3' CTTATTTGCAGAAAGTGGTGTA 62126 CCCAAGAA
 TACACCACT GAATAAG
 ||||| |||||
 ATGTGGTGA TTTATTC
 AGACG__
 GAM2289 HMP19 3' CTTATTCTTTGTTAGGAAAATG 88860 CCAC CAA_
 TA TACA TCC GAAGAATAAG
 ||| ||| |||||
 ATGT AGG TTTCTTATTC
 AAA_ ATTG
 GAM2289 KIAA1579 3' TACTCTTAGTGGTGTA 37154 CCCAAG A
 TACACCACT AAGA TA
 ||||| ||| ||
 ATGTGGTGA TTCT AT
 _ C
 GAM2289 KIAA1719 3' TCTGTCTTGGGAGTGGTGTA 68742 _
 TACACCACTCCCAAGA AGA
 ||||| ||||| |||
 ATGTGGTGAGGGTTCT TCT
 G
 GAM2289 KIAA1853 3' TTTTCTTGGAAGCAGTG 69929 CA C
 CAC CT CCAAGAAGAA
 ||| || |||||
 GTG GA GGTTCTTTT
 AC A
 GAM2289 KIAA1877 3' CTTATTCTTCTGCCATGAGT 66748 CCA_
 ACTC AGAAGAATAAG
 ||| |||||

		TGAG TCTTCTTATTC	
		TACCG	
GAM2289 KIAA1906	3'	CTTATTCTTCTTGACTTTTGG 73571	CTCC_
		CCA CAAGAAGAATAAG	
		GGT GTTCTTCTTATTC	
		TTTCA	
GAM2289 OSBPL11	3'	CTTAATTTCCCAAGAGTGGTG 43206	CCAA AA
		CACCACTC GAAG TAAG	
		GTGGTGAG CTTT ATTC	
		AACC A_	
GAM2289 YME1L1	3'	TCATTCTTGATGTGGTGTA 58438	TCC _
		TACACCAC CAAGAA GA	
		ATGTGGTG GTTCTT CT	
		TA_ A	
GAM2289 YME1L1	3'	TCATTCTTGATGTGGTGTA 27323	TCC _
		TACACCAC CAAGAA GA	
		ATGTGGTG GTTCTT CT	
		TA_ A	
GAM2289 ZNF262	3'	CTTATTTTGTGGGAGT 18723	A
		ACTCCCAAG AGAATAAG	
		TGAGGGTTT TTTTATTC	
		G	
GAM2289 LOC91960	3'	TGTGGCTTGGAACGTGGTGTA 68294	TC_ AAGA
		TACACCAC CCAAG ATA	
		ATGTGGTG GGTC TGT	
		CAA GG_	
GAM2290 AIM1	3'	GACTATAGGCACACATC 93464	C _ AT
		GA GTG GCC TGTAGTC	
		CT CAC CGG ATATCAG	
		A A _	
GAM2290 ARCN1	3'	GACTACAGGTGCACGCCAC 9753	___ _
		GTGGC CAT TGTAGTC	
		CACCG GTG ACATCAG	
		CAC G	
GAM2290 COX15	3'	GACTACAGGCACAAGTC 55285	G _ AT
		GAC TG GCC TGTAGTC	
		CTG AC CGG ACATCAG	
		A A _	
GAM2290 FGF8	5'	GACCCGCGGAGCCGCGTCG 21497	CA A_
		CGACGTGGC TTGT GTC	

			GCTGCGCCG GGCG CAG		
			A_ CC		
GAM2290	FGF8	5'	GACCCGCGGAGCCGCGTCG 53712	CA	A_
			CGACGTGGC TTGT GTC		
			GCTGCGCCG GGCG CAG		
			A_ CC		
GAM2290	FGF8	5'	GACCCGCGGAGCCGCGTCG 53714	CA	A_
			CGACGTGGC TTGT GTC		
			GCTGCGCCG GGCG CAG		
			A_ CC		
GAM2290	FGF8	5'	GACCCGCGGAGCCGCGTCG 53716	CA	A_
			CGACGTGGC TTGT GTC		
			GCTGCGCCG GGCG CAG		
			A_ CC		
GAM2290	FMN2	3'	ACTACAATTCAGTGTG 80129	_	CC
			CGAC GTGG ATTGTAGT		
			GTTG CACT TAACATCA		
			T _		
GAM2290	GPR44	3'	GACTACAGCACACGTC 17698	_	CAT
			GACGTG GC TGTAGTC		
			CTGCAC CG ACATCAG		
			A _		
GAM2290	HDGF	5'	GACGCCGTGGCCGCGCCG 16898	A	T A
			CG CGTGGCCAT GT GTC		
			GC GCGCCGGTG CG CAG		
			C C _		
GAM2290	HUNK	3'	GACCACCTCTGTGGCCACCTC 28185	C	T__ A
			GA GTGGCCAT GT GTC		
			CT CACCGGTG CA CAG		
			C TCTC C		
GAM2290	PCDHB9	3'	GACTACAGTTGCATGTC 39444	G	C
			GACGTG C ATTGTAGTC		
			CTGTAC G TGACATCAG		
			_ T		
GAM2290	RPP30	3'	GACTACAGGCGCTCG 22198	C	G AT
			CGA GTG CC TGTAGTC		
			GCT CGC GG ACATCAG		
			_ _ _		
GAM2290	SIGLEC11	3'	GACTACAATTGTGAGCCAC 54652	_	_
			GTGGC CAT TGTAGTC		

			CACCG GTG ACATCAG		
			A TTA		
GAM2290	STC1	3'	GACTGCAGGGGCCACTC	13463	C A
			GA GTGGCC TTGTAGTC		
			CT CACCGG GACGTCAG		
			_ G		
GAM2290	TEM5	3'	GACGGGCTGGCCACGCG	52300	A TT A_
			CG CGTGGCCA GT GTC		
			GC GCACCGGT CG CAG		
			_ _ GG		
GAM2290	C6orf35	3'	GACTACAAAGTGACAGTC	38046	_ G CA
			GAC GT GC TTGTAGTC		
			CTG CA TG AACATCAG		
			A G A_		
GAM2290	CMG1	5'	GACTACAACATGTTG	47727	GCCA
			CGACGTG TTGTAGTC		
			GTTGTAC AACATCAG		

GAM2290	CMG2	3'	ACCATCGTGTACGTCG	55196	C T A
			CGACGTGGC AT GT GT		
			GCTGCACTG TG TA CA		
			_ C C		
GAM2290	DKFZP434C212	3'	GACTACAGGCGCATGTC	69488	_ AT
			GACGTG GCC TG TAGTC		
			CTGTAC CGG ACATCAG		
			G _		
GAM2290	DKFZP564K0322	3'	GAGTGCTGGCCACGTC	50187	TT G
			GACGTGGCCA GTA TC		
			CTGCACCGGT CGT AG		
			_ G		
GAM2290	EVI5	3'	GACTACAGGTGCACGCCAC	20208	_____
			GTGGC CAT TG TAGTC		
			CACCG GTG ACATCAG		
			CAC G		
GAM2290	FLJ10408	5'	GACACGGAGGCCTACGTCG	36582	_ A A
			CGACGT GGCC TTGT GTC		
			GCTGCA CCGG GGCA CAG		
			T A _		
GAM2290	FLJ10936	5'	GACTGCGTTCAGCCGCGTCG	37443	CAT_
			CGACGTGGC TG TAGTC		

GCTGCGCCG GCGTCAG
 ACTT
 GAM2290 FLJ12331 5' GACTATGATGGCCACATC 47112 C TG
 GA GTGGCCAT TAGTC
 || ||||| ||||
 CT CACCGGTA ATCAG
 A GT
 GAM2290 FLJ20671 3' GACTACAGGCGCACGCCG 35939 A _ AT
 CG CGTG GCC TGTAGTC
 || ||| || |||||
 GC GCAC CGG ACATCAG
 C G _
 GAM2290 GOLPH2 3' GACTACAGGCACACAGTC 33771 _ _ AT
 GAC GTG GCC TGTAGTC
 ||| ||| || |||||
 CTG CAC CGG ACATCAG
 A A _
 GAM2290 HRH4 3' GACTACAGGTACTION 41539 C G AT
 CGA GTG CC TGTAGTC
 ||| ||| || |||||
 GCT CAT GG ACATCAG
 _ _ _
 GAM2290 LBP-32 3' ACCCCAGTCAGCCATGTCG 28039 C_ TA
 CGACGTGGC ATTG GT
 ||||| ||| ||
 GCTGTACCG TGAC CA
 AC CC
 GAM2290 MGC10200 3' GACTACAAGCGTGCGCCAC 59643 _ _
 GTGGC CAT TGTAGTC
 |||| ||| |||||
 CACCG GTG ACATCAG
 C CGA
 GAM2290 MGC14859 3' GACCACCTGGCTACGCCG 62602 A TT A
 CG CGTGGCCA GT GTC
 || ||||| || |||
 GC GCATCGGT CA CAG
 C C_ C
 GAM2290 MGC3035 5' GACGCCTGGCCACGACG 44401 A TT A
 CG CGTGGCCA GT GTC
 || ||||| || |||
 GC GCACCGGT CG CAG
 A C_ _
 GAM2290 PCDH19 3' GACTGCAAAGCACGTC 64443 G CA
 GACGTG C TTGTAGTC
 ||||| | |||||
 CTGCAC G AACGTCAG
 _ A_
 GAM2290 SLI 3' GATTACGTGGCCTACGTCG 79281 _ T
 CGACGT GGCCAT GTAGTC
 ||||| ||||| |||||

GCTGCA CCGGTG CATTAG
 T _
 GAM2290 ZDHHC3 3' GACCGGCATGGCCACTC 33931 C T A_
 GA GTGGCCAT GT GTC
 || ||||| || |||
 CT CACCGGTA CG CAG
 _ _ GC
 GAM2290 LOC145622 3' GACTACAGATGCACGCCAC 77815 _ _
 GTGGC CAT TG TAGTC
 |||| | |||||
 CACCG GTA ACATCAG
 CAC G
 GAM2290 LOC150225 3' GACCCATTGGCCATGTC 86191 T TA
 GACGTGGCCA TG GTC
 ||||| || |||
 CTGTACCGGT AC CAG
 T C_
 GAM2290 LOC152698 5' GACACTGAGGCCACGTCG 61058 _ ATT A
 CGACGTGG CC GT GTC
 ||||| || |||
 GCTGCACC GG CA CAG
 C AGT _
 GAM2290 LOC152719 5' GACCACCTTGGACCCACGTCG 87025 _ TT A
 CGACGTGG CCA GT GTC
 ||||| || |||
 GCTGCACC GGT CA CAG
 CA TC C
 GAM2290 LOC152719 5' GACTACAGGCGCCCGCCG 87027 A T CA
 CG CG GGC TTGTAGTC
 || ||| |||||
 GC GC CCG GACATCAG
 C _ CG
 GAM2290 LOC157280 5' GACACTGAGGCCTACGTCG 74343 _ ATT A
 CGACGT GGCC GT GTC
 |||| ||| |||
 GCTGCA CCGG CA CAG
 T AGT _
 GAM2290 LOC163341 3' GACTACAAGGGTCATGTC 83010 A
 GACGTGGCC TTGTAGTC
 ||||| |||||
 CTGTACTGG AACATCAG
 G
 GAM2290 LOC199688 5' GACTGCGGTGGCCATGTCG 91375
 CGACGTGGCCATTGTAGTC
 ||||| |||||
 GCTGTACCGGTGGCGTCAG
 GAM2290 LOC221296 3' GACTACAGGCGCGCGCCG 93608 A _ AT
 CG CGTG GCC TG TAGTC
 || ||| || |||||

GC GCGC CGG ACATCAG
 C G ____
 GAM2290 LOC222444 3' GACTACAATATAGGCATG 96005 G ____
 CGTG CC ATTGTAGTC
 |||| || |||||||
 GTAC GG TAACATCAG
 _ ATA
 GAM2290 LOC253613 3' GACTGTCTTGGCCATGTC 97916 TT
 GACGTGGCCA GTAGTC
 ||||||| |||||
 CTGTACCGGT TGTCAG
 TC
 GAM2290 LOC255448 5' GACACTGAGGCCTACGTCG 96303 _ ATT A
 CGACGT GGCC GT GTC
 ||||| |||| |||||
 GCTGCA CCGG CA CAG
 T AGT _
 GAM2290 LOC90631 3' GACTGCGAACCAGTCG 64393 G CCA
 CGAC TGG TTGTAGTC
 |||| || |||||||
 GCTG ACC AGCGTCAG
 _ A__
 GAM2290 LOC92002 3' GACTACAATACAGGCATG 68450 G ____
 CGTG CC ATTGTAGTC
 |||| || |||||||
 GTAC GG TAACATCAG
 _ ACA
 GAM2290 LOC93070 5' GACTGCGTTTCAGCCGCGTCG 71808 CAT_
 CGACGTGGC TGTCAGTC
 ||||||| |||||||
 GCTGCGCCG GCGTCAG
 ACTT
 GAM2291 ABCB8 5' TTGCCGGCGGCTCCTG 24207 A GA
 CAGGAGCC GC GGCAG
 ||||||| || |||||
 GTCCTCGG CG CCGTT
 _ G_
 GAM2291 ADAM19 3' CTCTGCCTCAAGGCTTGGTTCC 53840 _ ____
 TG CAGGAGCCA GC GAGGCAGAG
 ||||||| || |||||||
 GTCCTTGGT CG CTCCGTCTC
 T GAA
 GAM2291 ADAR 3' CTCTGTGGAGTCTGGCTCTCTG 32360 _ _ GAG
 CAG GAGCCAG C GCAGAG
 || ||||||| | |||||
 GTC CTCGGTC G TGTCTC
 T T AGG
 GAM2291 ADCY6 3' CTCTGCCCCAGTGCTCTCTTG 40951 CCA GA_
 CAGGAG GC GGCAGAG
 ||||| || |||||||

GTTCTC TG CCGTCTC
 TCG ACC
 GAM2291 ADRA2A 5' CTGCCTCCGTCGCGGCTCCTG 7290 A ____
 CAGGAGCC GC GAGGCAG
 ||||| || |||||
 GTCCTCGG CG CTCCGTC
 _ CTGC
 GAM2291 ADRBK1 3' TTGCCTCGGCTCCTG 9670 AGC
 CAGGAGCC GAGGCAG
 ||||| |||||
 GTCCTCGG CTCCGTT

 GAM2291 ARHG 3' CTCTGCCCTCGCTGCTCTTG 77088 C _
 CAGGAGC AGCGAGG CAGAG
 ||||| ||||| |||||
 GTTCTCG TCGCTCC GTCTC
 _ C
 GAM2291 ASCL2 5' CTCTGCCTGCACCTTCCTG 18976 CCA G
 CAGGAG GC AGGCAGAG
 ||||| || |||||
 GTCCTT CG TCCGTCTC
 CCA _
 GAM2291 ASTN 3' CTCCTATGACTGGCTCCT 69869 _ _ C
 AGGAGCCAG CG AGG AG
 ||||| || ||| ||
 TCCTCGGTC GT TCC TC
 A A _
 GAM2291 ATF5 5' CTCTGCCTGCGTAGCCCC 24820 A CA _
 GG GC GCG AGGCAGAG
 || || || |||||
 CC CG TGC TCCGTCTC
 C A_ G
 GAM2291 ATRX 5' CTTTGTTCGCGGCTCCTG 57078 A _
 CAGGAGCC GCG AGGCAGAG
 ||||| || |||||
 GTCCTCGG CGC TTTGTTTC
 _ C
 GAM2291 BACH2 3' CTCAGCAGGCATTGGCTCCT 41781 _ GAG A
 AGGAGCCA GC GC GAG
 ||||| || || |||
 TCCTCGGT CG CG CTC
 TA GA_ A
 GAM2291 BCRP2 3' CTCTGGCTTATGACTCCTG 63069 C GC G
 CAGGAG CA GAG CAGAG
 ||||| || || |||||
 GTCCTC GT TTC GTCTC
 A A_ G
 GAM2291 CD34 3' CTCTGCCTCCCTCACCTG 10106 AGCC C
 CAGG AG GAGGCAGAG
 ||| || |||||

			GTCC TC CTCCGTCTC		
			CAC_ C		
GAM2291	CD80	5'	CTGCCTGTTTTGCACCTG 19024	A C_ G	
			CAGG GC AGC AGGCAG		
			GTCC CG TTG TCCGTC		
			A TT _		
GAM2291	CD81	3'	CTCTGCCTTCATGCACCTG 16384	A CAGC	
			CAGG GC GAGGCAGAG		
			GTCC CG TTCCGTCTC		
			A TAC_		
GAM2291	CHC1	3'	CTCTGAGGGCCTGGCTTCTG 8861	CGAGG	
			CAGGAGCCAG CAGAG		
			GTCTTCGGTC GTCTC		
			CGGGA		
GAM2291	CLASP1	3'	CTCTGCCTCCCTGTCTACC 65891	_ C C	
			GG AG CAG GAGGCAGAG		
			CC TC GTC CTCCGTCTC		
			A T C		
GAM2291	COLQ	3'	CTCTACCTCTTTGCCTCCTG 55423	C C C	
			CAGGAG CAG GAGG AGAG		
			GTCCTC GTT CTCC TCTC		
			C T A		
GAM2291	COLQ	3'	CTCTACCTCTTTGCCTCCTG 20256	C C C	
			CAGGAG CAG GAGG AGAG		
			GTCCTC GTT CTCC TCTC		
			C T A		
GAM2291	COLQ	3'	CTCTACCTCTTTGCCTCCTG 20257	C C C	
			CAGGAG CAG GAGG AGAG		
			GTCCTC GTT CTCC TCTC		
			C T A		
GAM2291	CRHR1	3'	CTGCCCAAGTGGCTCTTG 16503	G GA_	
			CAGGAGCCA C GGCAG		
			GTTCTCGGT G CCGTC		
			_ AAC		
GAM2291	CYP51	3'	CTCTGCCTCAGCCTCC 7615	CCA _	
			GGAG GC GAGGCAGAG		
			CCTC CG CTCCGTCTC		
			_ A		
GAM2291	DEDD	3'	CTCTGCCTGATGTGGCTCCT 53378	G _	
			AGGAGCCA CG AGGCAGAG		

			TCCTCGGT GT TCCGTCTC		
			_ AG		
GAM2291	DIAPH2	3'	CTCTATTCTTGGCTTCTG 24591	C GC	
			CAGGAGCCAG GAG AGAG		
			GTCTTCGGTT CTT TCTC		
			_ A_		
GAM2291	EBAF	5'	CTCTGCCTCCTGCTCC 66029	C C	
			GGAGC AG GAGGCAGAG		
			CCTCG TC CTCCGTCTC		
			- -		
GAM2291	EDN2	3'	CTCCAGTGCTGGCTGCTG 10482	G A_ C	
			CAG AGCCAGCG GG AG		
			GTC TCGGTCGT CC TC		
			G GA _		
GAM2291	ELL	3'	CTCTGCTGGTCTCTGGCTCT 22557	C _	
			GGAGCCAG GA GGCAGAG		
			TCTCGGTC CT TCGTCTC		
			T GG		
GAM2291	ESR1	3'	CTCTGCCTCTGGCTTTCC 5513	_ GC	
			GGA GCCA GAGGCAGAG		
			CCT CGGT CTCCGTCTC		
			TT _		
GAM2291	F2RL3	3'	CTCTGCTTCCTGGGCCCTG 15511	AG C	
			CAGG CCAG GAGGCAGAG		
			GTCC GGTC CTTCGTCTC		
			CG _		
GAM2291	FKBP1B	3'	CTCTGCCACTGGGACGGCTCCT 15926	AGCGA_	
	G		CAGGAGCC GGCAGAG		
			GTCCTCGG CCGTCTC		
			CAGGGTCA		
GAM2291	FKBP1B	3'	CTCTGCCACTGGGACGGCTCCT 15927	AGCGA_	
	G		CAGGAGCC GGCAGAG		
			GTCCTCGG CCGTCTC		
			CAGGGTCA		
GAM2291	FOS	5'	CTCTGCTTCACAGCGCCC 19135	A CA _	
			GG GC GC GAGGCAGAG		
			CC CG CG CTTCGTCTC		
			_ _ ACA		
GAM2291	G6PT1	5'	CTCTGCTTGCGGCCCTG 9401	A A G	
			CAGG GCC GCGAG CAGAG		

			GTCC CGG CGTTC GTCTC		
			C _ _		
GAM2291	GAC1	3'	CTCTGCCCAGAGGCTCCTG	22017	AGCGA
			CAGGAGCC GGCAGAG		
			GTCCTCGG CCGTCTC		
			AGAC_		
GAM2291	GNAZ	3'	CTCTGCCTCCTTGGCCCC	10826	A C
			GG GCCAG GAGGCAGAG		
			CC CGGTT CTCCGTCTC		
			C C		
GAM2291	GNL1	5'	CTCGGTGCCACTGGCTCTCA	93672	A CGA _
			C GGAGCCAG GGCA GAG		
			A TCTCGGTC CCGT CTC		
			C A_ GG		
GAM2291	HADHA	3'	CTCTGCCTGTTCTCTCC	5734	CC G
			GGAG AGC AGGCAGAG		
			CCTC TTG TCCGTCTC		
			C_ _		
GAM2291	HD	3'	CTCTGCTTCCTCAGCCCT	10915	A C_ C
			AGG GC AG GAGGCAGAG		
			TCC CG TC CTTCGTCTC		
			_ AC _		
GAM2291	IDH3A	3'	CTCTGCCTCAGCAGTACC	19845	A CA _
			GG GC GC GAGGCAGAG		
			CC TG CG CTCCGTCTC		
			A A_ A		
GAM2291	IGFBP4	3'	CTCTGCCTCCCTCTCC	9552	CC C
			GGAG AG GAGGCAGAG		
			CCTC TC CTCCGTCTC		
			_ C		
GAM2291	IL17	3'	CTCCTAGGGCCTGGCTTCTG	10997	CG__ C
			CAGGAGCCAG AGG AG		
			GTCTTCGGTC TCC TC		
			CGGGA _		
GAM2291	ITGB3	3'	CTCTGCCTCCTTTCC	5804	CC C
			GGAG AG GAGGCAGAG		
			CCTT TC CTCCGTCTC		
			_ _		
GAM2291	IVL	5'	CTCTGCCTCAGCCTTACTG	60066	_ CCA _
			CAG GAG GC GAGGCAGAG		

			GTC TTC CG CTCCGTCTC		
			A _ _ A		
GAM2291	KCNK5	3'	CTCTGCCTTCTGCCCC	14968	A C C
			GG GC AG GAGGCAGAG		
			CC CG TC TTCCGTCTC		
			C _ _		
GAM2291	MAF	5'	CTCTGCCTCGTCTTTCC	19311	CCA
			GGAG GCGAGGCAGAG		
			CCTT TGCTCCGTCTC		
			TC _		
GAM2291	MAP3K14	3'	CTTTGCTGCTGGCTACC	15546	_ GA
			GG AGCCAGC GGCAGAG		
			CC TCGGTCTG TCGTTTC		
			A _ _		
GAM2291	MGAT3	3'	CTGCCTCCTGCCGGCTCCT	11562	A _ _
			AGGAGCC GC GAGGCAG		
			TCCTCGG CG CTCCGTC		
			C TC		
GAM2291	MYO10	3'	CTCTGGCCTAGGCTGGCTCC	25612	G _ _
			GGAGCCAGC AGGC AGAG		
			CCTCGGTCTG TCCG TCTC		
			GA G		
GAM2291	NDP	5'	CTCTGCCTCCCTCTGCTG	6043	G CC C
			CAG AG AG GAGGCAGAG		
			GTC TC TC CTCCGTCTC		
			G _ _ C		
GAM2291	NEO1	3'	CTCTGTGTAGGGCTGGCTCC	11772	GAG _ _
			GGAGCCAGC GCAGAG		
			CCTCGGTCTG TGTCTC		
			GGATG		
GAM2291	NGFR	3'	CTCTGCCTGTCCCTCTCA	11794	A CCA G
			C GGAG GC AGGCAGAG		
			A TCTC TG TCCGTCTC		
			C CC _ _		
GAM2291	NRGN	5'	CTGCCGGAGGCTGCTCCTG	21624	C GA _ _
			CAGGAGC AGC GGCAG		
			GTCCTCG TCG CCGTC		
			_ GAGG		
GAM2291	PACSIN3	3'	CTCTGCTTTGGGGTTCCTG	33118	AG
			CAGGAGCC CGAGGCAGAG		

		GTCCTTGG GTTTCGTCTC	
		G_	
GAM2291 PBP	3'	CTCTGCCTTTGTGATCCTG 11937	GC GC
		CAGGA CA GAGGCAGAG	
		GTCCT GT TTCCGTCTC	
		A_ GT	
GAM2291 PDE4A	3'	CTCTGCCTCAAAGACTCTTG 21683	CCAGC
		CAGGAG GAGGCAGAG	
		GTTCTC CTCCGTCTC	
		AGAAA	
GAM2291 PDE6D	5'	CTCCATCCTCGGCTCCTG 12015	AGC CA_
		CAGGAGCC GAGG GAG	
		GTCCTCGG CTCC CTC	
		___ TAC	
GAM2291 PDGFB	3'	CTCCACCTCTGGTGGCTCCT 12024	G_ CA
		AGGAGCCA C GAGG GAG	
		TCCTCGGT G CTCC CTC	
		G T AC	
GAM2291 PFKFB1	3'	CTCTGCCTTGGCCTCACTG 12051	_ _ GCG
		CAG GAG CCA AGGCAGAG	
		GTC CTC GGT TCCGTCTC	
		A C ___	
GAM2291 PIK3R2	3'	CTCCGGCTCTGGCTCTTG 18512	CGA A_
		CAGGAGCCAG GGC GAG	
		GTTCTCGGTC TCG CTC	
		___ GC	
GAM2291 PLA2G2D	3'	CTCTGCTTGGTCTGACCCCT 25713	AGC _ G
		AGG CAG C AGGCAGAG	
		TCC GTC G TTCGTCTC	
		CCA T G	
GAM2291 POLR2E	3'	GCTCCGCCCCCATCCACGGCTC 60598	AGC ____ A ____
	C	GGAGCC GA GGC GAG C	
		CCTCGG CT CCG CTC G	
		CAC ACCC C ____	
GAM2291 PREB	3'	CTGCCTCCTTTCTTCTG 26330	CC C
		CAGGAG AG GAGGCAG	
		GTCTTC TC CTCCGTC	
		TT _	
GAM2291 PSCD4	3'	CTCTGCCTCTGACTCGCTG 26324	_ C GC
		CAG GAG CA GAGGCAGAG	

		GTC CTC GT CTCCGTCTC	
		G A _	
GAM2291 PSMD7	3'	CTCTGCCTCCGGTCACTCTTG 12519	___ AGC
		CAGGAG CC GAGGCAGAG	
		GTTCTC GG CTCCGTCTC	
		ACT C_	
GAM2291 PTHR2	3'	CTCCATGAATTGGCTCCTG 18562	___ A C
		CAGGAGCCAG CG GG AG	
		GTCCTCGGTT GT CC TC	
		AA A _	
GAM2291 RECK	3'	CTCCACCTCACTCTCCTG 41197	CC C CA
		CAGGAG AG GAGG GAG	
		GTCCTC TC CTCC CTC	
		___ A AC	
GAM2291 RFNG	3'	CTCTGCCTCCTGCTTT 89560	C C
		GGAGC AG GAGGCAGAG	
		TTTCG TC CTCCGTCTC	
		_ _	
GAM2291 RPA1	3'	CTCTGCCTTCAGGCTTCTG 12896	AGC
		CAGGAGCC GAGGCAGAG	
		GTCTTCGG TTCCGTCTC	
		AC_	
GAM2291 SCA1	3'	CTCTGCCTCACTCTCTTG 6179	CC C
		CAGGAG AG GAGGCAGAG	
		GTTCTC TC CTCCGTCTC	
		___ A	
GAM2291 SCN4A	3'	CTCTGCCTTGCCCTCCTG 6199	CCA
		CAGGAG GCGAGGCAGAG	
		GTCCTC CGTTCCGTCTC	
		C_	
GAM2291 SDC1	3'	CTCTGCTTCTCTGACTTCTG 12987	C C
		CAGGAG CAG GAGGCAGAG	
		GTCTTC GTC CTTCGTCTC	
		A T	
GAM2291 SGCB	3'	CTCTGCCTTTTAGCTTCT 5876	CAGC
		AGGAGC GAGGCAGAG	
		TCTTCG TTCCGTCTC	
		ATT_	
GAM2291 SH3BP2	3'	CTCTGCCTGCACGCCCTG 13065	A CA G
		CAGG GC GC AGGCAGAG	

			GTCC CG CG TCCGTCTC		
			_ CA _		
GAM2291	SIAT1	3'	CTCTGCCTGGCCTGACCCTG 13130	AGC _ G	
			CAGG CAG C AGGCAGAG		
			GTCC GTC G TCCGTCTC		
			CA_ C G		
GAM2291	SIRT2	3'	CTCTGTCTCCTGCCCC 48361	A C C	
			GG GC AG GAGGCAGAG		
			CC CG TC CTCTGTCTC		
			C _ _		
GAM2291	SLC22A12	3'	CTCTGCCTGCTGTCC 58688	GC G	
			GGA CAGC AGGCAGAG		
			CCT GTCG TCCGTCTC		
			_ _		
GAM2291	SLC4A2	5'	CTCCGCCTCGTTGCCCTG 13179	A C A	
			CAGG GC AGCGAGGC GAG		
			GTCC CG TTGCTCCG CTC		
			_ _ C		
GAM2291	SLC6A12	3'	CTCTGCCTCTGTCTCCTG 13191	C GC	
			CAGGAG CA GAGGCAGAG		
			GTCCTC GT CTCCGTCTC		
			T _		
GAM2291	SLC9A1	3'	CTCTGCCTGCTGGGCTCTT 70925	_ G	
			AGGAGCC AGC AGGCAGAG		
			TTCTCGG TCG TCCGTCTC		
			G _		
GAM2291	SLC9A3R1	3'	CTCTGCCTCCCTCCTCCT 70938	CC C	
			AGGAG AG GAGGCAGAG		
			TCCTC TC CTCCGTCTC		
			C_ C		
GAM2291	SLC9A5	3'	CTCTGCCTCCACTTCCTG 60473	CCAGC	
			CAGGAG GAGGCAGAG		
			GTCCTT CTCCGTCTC		
			CAC_		
GAM2291	SLC9A5	3'	CTCTGCCTCCACTTCCTG 60474	CCAGC	
			CAGGAG GAGGCAGAG		
			GTCCTT CTCCGTCTC		
			CAC_		
GAM2291	SMAC	5'	GCTCTACCTAGCGCTGCAGGCT 58003	_ _ C _	
			CCTG CAGGAGCC AGCG AGG AGAG C		

GTCCTCGG TCGC TCC TCTC G
 ACG GA A _
 GAM2291 SMARCC1 3' CTAGGCCTGCTGGCTCT 13251 G AG
 GGAGCCAGC AGGC AG
 ||||| ||| ||
 TCTCGGTCG TCCG TC
 _ GA
 GAM2291 SNL 3' CTGCCCACATGGCGGCTCCTG 13289 A GA____
 CAGGAGCC GC GGCAG
 ||||| || ||||
 GTCCTCGG CG CCGTC
 _ GTACAC
 GAM2291 SRD5A1 3' CTCTGCCTGTGTGAGTGGCTCC 8316 _ _
 TG CAGGAGCCA GCG AGGCAGAG
 ||||| ||| |||||
 GTCCTCGGT TGT TCCGTCTC
 GAG G
 GAM2291 SRM 3' CTCTGCCTTCTGTTGCCCC 13400 A _ C
 GG GC CAG GAGGCAGAG
 || || ||| |||||
 CC CG GTC TTCCGTCTC
 C TT _
 GAM2291 ST5 3' CTCTGCCAGTGCTCTCTG 58227 _ CA GA
 CAG GAGC GC GGCAGAG
 ||| ||| || |||||
 GTC CTCG TG CCGTCTC
 T _ A_
 GAM2291 STIM1 3' CTCTGGGGTTCAGCTTCTG 60778 C_ GAGG
 CAGGAGC AGC CAGAG
 ||||| ||| ||||
 GTCTTCG TTG GTCTC
 AC GG_
 GAM2291 SUFU 3' CTCCATCTCACTGGCTCT 32936 C CA
 GGAGCCAG GAGG GAG
 ||||| ||| |||
 TCTCGGTC CTCT CTC
 A AC
 GAM2291 TCF2 3' CTCTGGCCTGCTGGTTCC 6612 G _
 GGAGCCAGC AGGC AGAG
 ||||| ||| |||
 CCTTGGTCG TCCG TCTC
 _ G
 GAM2291 TCF2 3' CTCTGTTGGTGGCCTCTG 6613 GA G AG
 CAG GCCA CG GCAGAG
 ||| ||| || |||||
 GTC CGGT GT TGTCTC
 TC G _
 GAM2291 TCF21 3' CTGCCCTCAGTGCTCTCTG 13643 _ CA _ _
 CAG GAGC GC GAGG CAG
 ||| ||| || ||| |||

		GTC CTCG TG CTCC GTC	
		T _ A C	
GAM2291 TLX1	5'	CTCTATCTCTGGCTCCTG 19819	GC GC
		CAGGAGCCA GAG AGAG	
		GTCCTCGGT CTC TCTC	
		_ TA	
GAM2291 TNFRSF1B	3'	CTCTGCCCAGCTCTGGCTTC 8393	_ GA
		GGAGCCA GC GGCAGAG	
		CTTCGGT CG CCGTCTC	
		CT AC	
GAM2291 TPK1	5'	CTCCAGTCTGTGGCTCCT 42609	G G A_
		AGGAGCCA C AGGC GAG	
		TCCTCGGT G TCTG CTC	
		_ _ AC	
GAM2291 UBE2G2	3'	CTCCACGCCTGGCTTCTG 65488	_ A C
		CAGGAGCCAG CG GG AG	
		GTCTTCGGTC GC CC TC	
		C A _	
GAM2291 UBQLN1	5'	CTCTGGTGTCTGCTGGCTCCT 26474	_ G _
		AGGAGCCAGC GA GC AGAG	
		TCCTCGGTG CT TG TCTC	
		T G G	
GAM2291 VCL	3'	CTCTTTCCTTGGCTCC 14033	C GC
		GGAGCCAG GAG AGAG	
		CCTCGGTT CTT TCTC	
		C _	
GAM2291 WNT1	3'	CTCCGCCATGGGGTCGGCTCCT 19478	A GA__ A
G		CAGGAGCC GC GGC GAG	
		GTCCTCGG TG CCG CTC	
		C GGGTA C	
GAM2291 XPNPEP2	5'	CTCTGCCCACCCTGGCTCC 14143	CGA_
		GGAGCCAG GGCAGAG	
		CCTCGGTC CCGTCTC	
		CCAC	
GAM2291 XRCC3	3'	CTCTGGGTCTTGGCTCC 19517	C GG
		GGAGCCAG GA CAGAG	
		CCTCGGTT CT GTCTC	
		C GG	
GAM2291 Z39IG	3'	CTCTGCCGGGGGCTTCTG 24397	AGCGA
		CAGGAGCC GGCAGAG	

		GTCTTCGG CCGTCTC	
		GGG__	
GAM2291 ZNF74	5'	CTCCGCGTCCGATGGCTCCTG 14260	GC_ G A
		CAGGAGCCA GA GC GAG	
		GTCCTCGGT CT CG CTC	
		AGC G C	
GAM2291 AIF1	5'	CTCTGCCTGCCCCCTCCT 17925	CCA G
		AGGAG GC AGGCAGAG	
		TCCTC CG TCCGTCTC	
		CC_ _	
GAM2291 ATP6V1B1	3'	CTCCGCCCTCCGCTGGCTCC 9878	A_ A
		GGAGCCAGCG GGC GAG	
		CCTCGGTCGC CCG CTC	
		CTC C	
GAM2291 BCAA	5'	CTCTGCCTCAGCAGCCGCTG 33493	GA CA _
		CAG GC GC GAGGCAGAG	
		GTC CG CG CTCCGTCTC	
		GC A_ A	
GAM2291 BRD1	5'	CTCTGCCTGTTACTGCTG 28143	G CC G
		CAG AG AGC AGGCAGAG	
		GTC TC TTG TCCGTCTC	
		G A_ _	
GAM2291 C20orf188	3'	CTCTGCCTCATTTTCCTG 32219	CCAGC
		CAGGAG GAGGCAGAG	
		GTCCTT CTCCGTCTC	
		TTA__	
GAM2291 C21orf93	3'	GCCCCTTCCTGGCTTCTG 59745	C ____
		CAGGAGCCAG GA GGC	
		GTCTTCGGTC CT CCG	
		_ TCC	
GAM2291 C8orf13	5'	CTCTGAGGCCGCTCCTG 82474	A GAGG
		CAGGAGCC GC CAGAG	
		GTCCTCGG CG GTCTC	
		C GA__	
GAM2291 C8orf13	3'	CTCTGTGACTGGCTCTTG 82475	CGAG
		CAGGAGCCAG GCAGAG	
		GTTCTCGGTC TGTCTC	
		AG__	
GAM2291 CARD9	5'	CTCCGCGGCCAGGCTCCTG 42547	A_ GAG A
		CAGGAGCC GC GC GAG	

			GTCCTCGG CG CG CTC	
			ACC G__ C	
GAM2291	CARD9	5'	CTCCGCGGCCAGGCTCCTG 42548	A__ GAG A
			CAGGAGCC GC GC GAG	
			GTCCTCGG CG CG CTC	
			ACC G__ C	
GAM2291	CARM1	3'	CTCCGTCCTCGGCCCTG 64099	A AGC _ A
			CAGG GCC GAGG C GAG	
			GTCC CGG CTCC G CTC	
			C ____ T C	
GAM2291	CDH24	3'	CTCTGTGTCTGTCTCCTG 96601	C GC G
			CAGGAG CA GA GCAGAG	
			GTCCTC GT CT TGTCTC	
			T __ G	
GAM2291	CDKL2	5'	CTGCCTGCTTCGCCCTG 15471	A C_ G
			CAGG GC AGC AGGCAG	
			GTCC CG TCG TCCGTC	
			_ CT _	
GAM2291	CNTNAP1	3'	CTGTTTCCCCAGGCTCCTG 14643	AGC_
			CAGGAGCC GAGGCAG	
			GTCCTCGG CTTTGTC	
			ACCC	
GAM2291	CPZ	3'	CTCCGCATCCCGGGCTCCTG 14690	AGC G A
			CAGGAGCC GA GC GAG	
			GTCCTCGG CT CG CTC	
			GCC A C	
GAM2291	CYP4F12	3'	CTCTGCCTGGGCCTCACTG 62186	_ _ AGCG
			CAG GAG CC AGGCAGAG	
			GTC CTC GG TCCGTCTC	
			A C G__	
GAM2291	DAMS	3'	CTCTGCCTACATGACTACTG 42086	G C GCG
			CAG AG CA AGGCAGAG	
			GTC TC GT TCCGTCTC	
			A A ACA	
GAM2291	DDM36	3'	CTCTAGTGTCTGTCTCC 40921	C C G _
			GGAG CAG GA GC AGAG	
			CCTC GTC TT TG TCTC	
			T _ G A	
GAM2291	DGKD	3'	CTCTGGCCTGGCTGCCTG 60105	AGC G _
			CAGG CAGC AGGC AGAG	

GTCC GTCG TCCG TCTC
 ____ G G
 GAM2291 DGKD 3' CTGCCTCTGTCCTGGCTCT 60106 C____
 GGAGCCAG GAGGCAG
 ||||| |||||
 TCTCGGTC CTCCGTC
 CTGT
 GAM2291 DKFZP586M1120 3' CTCCATTGCTGTGGCTCCTG 49279 ____ _ C
 CAGGAGCCA GCGA GG AG
 ||||| ||| ||
 GTCCTCGGT CGTT CC TC
 GT A _
 GAM2291 DKFZP727G051 3' CTCTGGGCCTGCTGGCTCCT 70006 G ____
 AGGAGCCAGC AGGC AGAG
 ||||| ||| |||
 TCCTCGGTCG TCCG TCTC
 _ GG
 GAM2291 DKFZP727M111 5' CTCTGCTGGTGGCTCCTG 32057 G GA
 CAGGAGCCA C GGCAGAG
 ||||| | |||||
 GTCCTCGGT G TCGTCTC
 G ____
 GAM2291 DRF1 3' TTCTGTGCTGGGCTCCTG 47763 _ GAG
 CAGGAGCC AGC GCAGAG
 ||||| ||| |||||
 GTCCTCGG TCG TGTCTT
 G ____
 GAM2291 DSCR6 3' CTCTGTCTCCTGGGCCCTG 39066 AG C
 CAGG CCAG GAGGCAGAG
 ||| ||| |||||
 GTCC GGTC CTCTGTCTC
 CG _
 GAM2291 DXS1357E 3' CTGCCTGCAGCTGGCTTC 20432 G____
 GGAGCCAGC AGGCAG
 ||||| |||||
 CTTCGGTCG TCCGTC
 ACG
 GAM2291 EPS8R3 5' CTCTGCCTGTGGCCACT 58168 GA G G
 AG GCCA C AGGCAGAG
 || ||| | |||||
 TC CGGT G TCCGTCTC
 AC _ _
 GAM2291 EPSIN 5' CTCTGCCTAGCTCCCTCT 26210 CC G
 GGAG AGC AGGCAGAG
 ||| ||| |||||
 TCTC TCG TCCGTCTC
 CC A
 GAM2291 ERF 3' CTCTGCCTCTTGTACCCCT 22439 AGC_ C
 AGG CAG GAGGCAGAG
 ||| ||| |||||

		TCC GTT CTCCGTCTC		
		CCAT _		
GAM2291	ERMAP	3' CTCTGCCTCATCCTGCCCT 38196	A C C__	
		AGG GC AG GAGGCAGAG		
		TCC CG TC CTCCGTCTC		
		_ _ CTA		
GAM2291	ESPL1	5' CTCCGCCTTGCTCAGCCCCT 25438	A C_ A	
		AGG GC AGCGAGGC GAG		
		TCC CG TCGTTCCG CTC		
		C AC C		
GAM2291	FLB6421	5' CTCTGCCTCAGTCACCTG 39643	AGCCA _	
		CAGG GC GAGGCAGAG		
		GTCC TG CTCCGTCTC		
		AC__ A		
GAM2291	FLJ00001	5' CTGCGGCGCGGCTCCTG 82714	A AG	
		CAGGAGCC GCG GCAG		
		GTCCTCGG CGC CGTC		
		C GG		
GAM2291	FLJ10276	3' CTCCGCCTCAGCCCTTCTG 36422	CCA _ A	
		CAGGAG GC GAGGC GAG		
		GTCTTC CG CTCCG CTC		
		C_ A C		
GAM2291	FLJ10607	3' CTCTGCCTCAGCCTCC 77632	CCA _	
		GGAG GC GAGGCAGAG		
		CCTC CG CTCCGTCTC		
		_ A		
GAM2291	FLJ10709	3' CTGCCTTGCCGGCCCCTG 36988	A A	
		CAGG GCC GCGAGGCAG		
		GTCC CGG CGTTCCGTC		
		C C		
GAM2291	FLJ10815	3' CTCTGCCTCCTCCCCTG 37232	AGCC C	
		CAGG AG GAGGCAGAG		
		GTCC TC CTCCGTCTC		
		CC__ _		
GAM2291	FLJ11362	5' CTGGAGACCATCTGGCTCCTG 41963	CGA ____	
		CAGGAGCCAG GG CAG		
		GTCCTCGGTC CC GTC		
		TA_ AGAG		
GAM2291	FLJ11383	5' CTCATTTACTGGCTTCTG 46855	CG GCA	
		CAGGAGCCAG AG GAG		

GTCTTCGGTC TT CTC
 AT A__
 GAM2291 FLJ12132 5' CTCGCGGCGCTCCGGCTCCTG 47100 __ AG A
 CAGGAGCC AGCG GC GAG
 ||||| ||| |||
 GTCCTCGG TCGC CG CTC
 CC GG _
 GAM2291 FLJ12190 3' CTCTGCCTCTCTTTCTCCTG 47567 CC C
 CAGGAG AG GAGGCAGAG
 ||||| || |||||
 GTCCTC TC CTCCGTCTC
 TT T
 GAM2291 FLJ12229 3' CTCTGCCTCCCTCGCTCCT 46404 C C
 AGGAGC AG GAGGCAGAG
 ||||| || |||||
 TCCTCG TC CTCCGTCTC
 C C
 GAM2291 FLJ13102 3' CTCTGCCTCCAGGGCTCC 46530 AGC
 GGAGCC GAGGCAGAG
 ||||| |||||
 CCTCGG CTCCGTCTC
 GAC
 GAM2291 FLJ13213 3' CTCTGTGGTGTCTGGCTCT 45729 _ AG
 GGAGCCAG CG GCAGAG
 ||||| || |||||
 TCTCGGTC GT TGTCTC
 T GG
 GAM2291 FLJ13441 3' CTGTGTTACAGTGGCTCCTG 43912 G A_ G
 CAGGAGCCA CG GGCA AG
 ||||| || |||||
 GTCCTCGGT GC TTGT TC
 _ AC G
 GAM2291 FLJ13840 5' CTCTGCCTCATATTCTTG 45697 CCAGC
 CAGGAG GAGGCAGAG
 ||||| |||||
 GTTCTT CTCCGTCTC
 ATA__
 GAM2291 FLJ13848 3' GCTCTGCCTCACCCTGCTGGCT 45825 _____
 CCTG CAGGAGCCAGC GAGGCAGAG C
 ||||| ||||| |
 GTCCTCGGTG CTCCGTCTC G
 TCCA _
 GAM2291 FLJ13941 3' CTCTGCTTGCGTGACTCT 46272 C _ G
 GGAG CA GCGAG CAGAG
 ||| || ||||| |||||
 TCTC GT CGTTC GTCTC
 A G _
 GAM2291 FLJ14327 3' TTGATCGCTGGCCCTG 46690 A GG
 CAGG GCCAGCGA CAG
 ||| ||||| |||

		GTCC CGGTCGCT GTT	
		— A—	
GAM2291	FLJ14957	3' CTCTGTACTCAGCCCTCT 52817	CCA _ _
		GGAG GC GAG GCAGAG	
		TCTC CG CTC TGTCTC	
		C— A A	
GAM2291	FLJ20200	3' CTCTGCCTCAATGCCCTG 35234	A CAGC
		CAGG GC GAGGCAGAG	
		GTCC CG CTCCGTCTC	
		— TAA—	
GAM2291	FLJ20452	3' CTCCACTCCTGACTTCTG 35647	C C GCA
		CAGGAG CAG GAG GAG	
		GTCTTC GTC CTC CTC	
		A _ AC—	
GAM2291	FLJ21135	5' CTCTGCCTGCAGCTCC 46349	CA G
		GGAGC GC AGGCAGAG	
		CCTCG CG TCCGTCTC	
		A— _	
GAM2291	FLJ21432	3' CCTTGCAAACCTGGCTTCTG 44941	_____
		CAGGAGCCAG CGAGG	
		GTCTTCGGTC GTTCC	
		AAACG	
GAM2291	FLJ21939	5' CCTACGTAGCCTGGCTTCTG 42650	_____ _
		CAGGAGCCAG CG AGG	
		GTCTTCGGTC GC TCC	
		CGAT A	
GAM2291	FLJ22215	3' CTCTGCCTCCCCTCTGCCC 43398	A C C—
		GG GC AG GAGGCAGAG	
		CC CG TC CTCCGTCTC	
		— _ TCCC	
GAM2291	FLJ22349	3' CTCTGGCCAGCTGGCTTC 46108	GA _
		GGAGCCAGC GGC AGAG	
		CTTCGGTCG CCG TCTC	
		A_ G	
GAM2291	FLJ22578	5' CTCTGTGGCCCGGCTCCTG 46324	A_ GAG
		CAGGAGCC GC GCAGAG	
		GTCCTCGG CG TGTCTC	
		CC G—	
GAM2291	FLJ23233	3' CTCTGCCTTGAGCTCC 45516	CAG
		GGAGC CGAGGCAGAG	

CCTCG GTTCCGTCTC
 AG_
 GAM2291 FLJ31300 3' CTCTGCTTCCTGGCCACCTG 58929 A_ C
 CAGG GCCAG GAGGCAGAG
 |||| |||| ||||
 GTCC CGGTC CTTCGTCTC
 AC _
 GAM2291 FLJ32865 3' CTCTGAGATCTTGGTCTCCTG 58808 _ C GG_
 CAGGAG CCAG GA CAGAG
 ||||| |||| || ||||
 GTCCTC GGTT CT GTCTC
 T _ AGA
 GAM2291 FTCD 3' TTCAACCAGTGGCTCCTG 22840 G GA CA
 CAGGAGCCA C GG GAG
 ||||| || || ||
 GTCCTCGGT G CC CTT
 _ A_ AA
 GAM2291 GABBR1 3' CTCTGCCTTTGTGCTCT 9412 _ GC
 GGAGC CA GAGGCAGAG
 |||| || |||||
 TCTCG GT TTCCGTCTC
 T _
 GAM2291 GAL3ST-4 5' CTCTGCCCTCTTCCTGGCCCT 45277 A C ____
 G CAGG GCCAG GA GGCAGAG
 |||| |||| || ||||
 GTCC CGGTC CT CCGTCTC
 _ _ TCTCC
 GAM2291 HCRTR1 5' CTCTGCTGCAGCGGCTCCTG 9511 A GA_
 CAGGAGCC GC GGCAGAG
 ||||| || |||||
 GTCCTCGG CG TCGTCTC
 _ ACG
 GAM2291 IMP13 3' CTCTGCCTCCTTTCTGCTG 28457 G CC C
 CAG AG AG GAGGCAGAG
 ||| || || |||||
 GTC TC TC CTCCGTCTC
 G TT _
 GAM2291 KCNS1 3' CTCTGATATACTGGCTTCTG 11193 CGAGG
 CAGGAGCCAG CAGAG
 ||||| ||||
 GTCTTCGGTC GTCTC
 ATATA
 GAM2291 KHDRBS1 3' CTCTGCATTCTGGCTTCTG 22661 CGAG
 CAGGAGCCAG GCAGAG
 ||||| ||||
 GTCTTCGGTC CGTCTC
 TTA_
 GAM2291 KIAA0152 3' CTTTGTGGCTGGCTCC 28975 GAG
 GGAGCCAGC GCAGAG
 ||||| ||||

			CCTCGGTCG TGTTC		
			G_		
GAM2291	KIAA0222	3'	CTCATTGTTCACTGGCTCC 28394	C G _	
			GGAGCCAG GAG CA GAG		
			CCTCGGTC CTT GT CTC		
			A _ TA		
GAM2291	KIAA0356	3'	CTCTGCCTGACTGACCCCTG 66771	AGC CG	
			CAGG CAG AGGCAGAG		
			GTCC GTC TCCGTCTC		
			CCA AG		
GAM2291	KIAA0459	3'	CTCTGTGGCCTGGCTCTCA 61651	A CGAG	
			C GGAGCCAG GCAGAG		
			A TCTCGGTC TGTCTC		
			C CGG_		
GAM2291	KIAA0561	3'	CTCTGTTTGCAGGCCCTG 66475	A A G	
			CAGG GCC GCGAG CAGAG		
			GTCC CGG CGTTT GTCTC		
			_ A _		
GAM2291	KIAA0843	3'	CTCTGCTTCGTGGCCCCT 30799	A G	
			AGG GCCA CGAGGCAGAG		
			TCC CGGT GCTTCGTCTC		
			C _		
GAM2291	KIAA0939	3'	CTCCGCTCAGTGTGGCTCCT 62711	_ GA A	
			AGGAGCCA GC GGC GAG		
			TCCTCGGT TG TCG CTC		
			G AC C		
GAM2291	KIAA0997	5'	CTCCGCAGCTCTGGTTCCTG 30887	CGAG A	
			CAGGAGCCAG GC GAG		
			GTCCTTGGTC CG CTC		
			TCGA C		
GAM2291	KIAA1184	3'	CTCTGCCTCAGTGGCCTCC 42927	_ GC	
			GGAG CCA GAGGCAGAG		
			CCTC GGT CTCCGTCTC		
			C GA		
GAM2291	KIAA1274	3'	CTCTGCCTCAGTTTCC 93010	CCA _	
			GGAG GC GAGGCAGAG		
			CCTT TG CTCCGTCTC		
			_ A		
GAM2291	KIAA1322	3'	CTCTGCCTTTGAGCCCTG 73109	A _ GC	
			CAGG GC CA GAGGCAGAG		

			GTCC CG GT TTCCGTCTC		
			— A —		
GAM2291	KIAA1405	3'	CTCTGTCTGACTGGCCCC	61697	A CG
			GG GCCAG AGGCAGAG		
			CC CGGTC TCTGTCTC		
			C AG		
GAM2291	KIAA1649	5'	CTCTGCCTCCTCCTCC	51234	CC C
			GGAG AG GAGGCAGAG		
			CCTC TC CTCCGTCTC		
			C_—		
GAM2291	KIAA1742	3'	CTTTGGAAGCAGGCTCCTG	78141	A GAGG
			CAGGAGCC GC CAGAG		
			GTCCTCGG CG GTTTC		
			A AAG_		
GAM2291	KIAA1889	5'	TTCTGCATCTGGCTCCTG	73885	CGAG
			CAGGAGCCAG GCAGAG		
			GTCCTCGGTC CGTCTT		
			TA_		
GAM2291	KIAA1962	3'	CTCCATCAAGCCTGGTTCCT	82799	_ GA CA
			AGGAGCCAG C GG GAG		
			TCCTTGGTC G CT CTC		
			C AA AC		
GAM2291	KIAA1971	3'	CTCTGTCTCAGCCTCC	74678	CCA _
			GGAG GC GAGGCAGAG		
			CCTC CG CTCTGTCTC		
			— A		
GAM2291	KRTHB2	5'	CTCTGCCTCTCTCTCCTG	53452	CC C
			CAGGAG AG GAGGCAGAG		
			GTCCTC TC CTCCGTCTC		
			— T		
GAM2291	LCP	5'	CTCCGCTCGCGGCCCT	27477	A A G A
			AGG GCC GCGAG C GAG		
			TCC CGG CGCTC G CTC		
			C _ _ C		
GAM2291	LRP1B	5'	CTCTGCCTCCTCTCTCC	38274	CC C
			GGAG AG GAGGCAGAG		
			CCTC TC CTCCGTCTC		
			TC _		
GAM2291	MESDC1	5'	CTCTGCCCCGGTTCATGGTTCC	42900	G_ A
	TG		CAGGAGCCA CG GGCAGAG		

		GTCCTTGGT GC CCGTCTC	
		ACTTG C	
GAM2291	MGC10818	3' CTCTGCCTCAGCCTCCTG 48301	CCA _
		CAGGAG GC GAGGCAGAG	
		GTCCTC CG CTCCGTCTC	
		___ A	
GAM2291	MGC10870	5' CTCTGTCTGTCGGGCTCC 51177	A_ G
		GGAGCC GC AGGCAGAG	
		CCTCGG TG TCTGTCTC	
		GC _	
GAM2291	MGC13010	5' CTCCAGGTCGCTGGCTTCTG 52060	GGCA
		CAGGAGCCAGCGA GAG	
		GTCTTCGGTCGCT CTC	
		GGAC	
GAM2291	MGC20460	5' CTCTGCCCATCGGCTTCTG 54903	AGCGA
		CAGGAGCC GGCAGAG	
		GTCTTCGG CCGTCTC	
		CTAC_	
GAM2291	MGC20460	5' CTCTGCCGACCGGCTTCTG 54905	AGCGA
		CAGGAGCC GGCAGAG	
		GTCTTCGG CCGTCTC	
		CCAG_	
GAM2291	MGC35558	3' CTCCTGAGCTGGTTCCTG 59411	G_ C
		CAGGAGCCAGC AGG AG	
		GTCCTTGGTCG TCC TC	
		AG _	
GAM2291	MGC5139	5' CTCCACATCTCCTGGCTCCT 74569	C CA__
		AGGAGCCAG GAGG GAG	
		TCCTCGGTC CTCT CTC	
		_ ACAC	
GAM2291	MGC5149	3' TTCTGACCTGGCTCCTG 72764	CGAGG
		CAGGAGCCAG CAGAG	
		GTCCTCGGTC GTCTT	
		CA__	
GAM2291	MOST2	5' CTCTGCCTAGGGGGCTCCT 40061	AGCG
		AGGAGCC AGGCAGAG	
		TCCTCGG TCCGTCTC	
		GGA	
GAM2291	MRPL10	3' CTCTTGCTGCACGGGCTCCTG 59833	AGCGA _
		CAGGAGCC GGCA GAG	

GTCCTCGG TCGT CTC
 GCACG T
 GAM2291 NCKX3 3' CTGACCACTGGCTCTTG 40725 CGA _
 CAGGAGCCAG GG CAG
 ||||| || ||
 GTTCTCGGTC CC GTC
 A_ A
 GAM2291 NFKBIE 5' CTGGCCGCTGGCTCGCTG 17052 _ AGG
 CAG GAGCCAGCG CAG
 || ||||| ||
 GTC CTCGGTCGC GTC
 G CG_
 GAM2291 NIFIE14 3' CTGCCTCGCTCCAGGTTT 51947 ____
 GAGCC AGCGAGGCAG
 |||| |||||
 TTTGG TCGCTCCGTC
 ACC
 GAM2291 NMT1 3' CTAATTGCTGGCTCTCA 41146 A GC
 C GGAGCCAGCGAG AG
 | ||||| ||
 A TCTCGGTCGTTT TC
 C A_
 GAM2291 OSBPL1A 5' CTCTGCCCGACCTCGCTG 36366 _ CCAG A
 CAG GAG CG GGCAGAG
 ||| || |||||
 GTC CTC GC CCGTCTC
 G CA_ _
 GAM2291 OSBPL2 3' CTCTTCTAGGACCAGGCTCCTG 58483 AGCG_ C
 CAGGAGCC AGG AGAG
 ||||| || ||||
 GTCCTCGG TCT TCTC
 ACCAGGA _
 GAM2291 PCYT2 3' CTCTAACTGGCCTGGCTCT 12682 _ G GC
 GGAGCCAG C AG AGAG
 ||||| | || ||||
 TCTCGGTC G TC TCTC
 C G AA
 GAM2291 PEPP3 3' CTCTGCCACCTGAGGTCCTG 30706 GC_ CGA
 CAGGA CAG GGCAGAG
 |||| || |||||
 GTCCT GTC CCGTCTC
 GGA CAC
 GAM2291 PNMA5 5' CTCTACCTCTCTTGCTGCC 73971 _ C C C
 GG AGC AG GAGG AGAG
 || ||| || ||||
 CC TCG TC CTCC TCTC
 G T T A
 GAM2291 PPFIA4 3' CTCTGCCTCACTTCTTT 70841 CC C
 GGAG AG GAGGCAGAG
 |||| || |||||

			TTTC TC CTCCGTCTC		
			T_ A		
GAM2291	PPM1A	5'	CTCTGCCTCCCTCTCC	41006	CC C
			GGAG AG GAGGCAGAG		
			CCTC TC CTCCGTCTC		
			_ C		
GAM2291	PRO2289	3'	CTGCACCGCGGGCTCCTG	38412	A AG
			CAGGAGCC GCG GCAG		
			GTCCTCGG CGC CGTC		
			G CA		
GAM2291	PRO2389	3'	CTCTGCCTCCTCCTCC	64477	CC C
			GGAG AG GAGGCAGAG		
			CCTC TC CTCCGTCTC		
			C_ _		
GAM2291	RBT1	3'	CTCTGCCTCTTGCACCT	26281	A C C
			AGG GC AG GAGGCAGAG		
			TCC CG TT CTCCGTCTC		
			A _ _		
GAM2291	SCAMP5	3'	CTCTGCCTATGTCCCTCT	58057	CCA _
			GGAG GCG AGGCAGAG		
			TCTC TGT TCCGTCTC		
			CC_ A		
GAM2291	SLC26A10	5'	CTCTGCCTCAAGGCTGTCCT	56844	_ AGC
			AGGA GCC GAGGCAGAG		
			TCCT CGG CTCCGTCTC		
			GT AA_		
GAM2291	SLC38A5	5'	CTCTGCCTCTTTTCTCCTG	54309	CCAGC
			CAGGAG GAGGCAGAG		
			GTCCTC CTCCGTCTC		
			TTTT_		
GAM2291	SNT-2	3'	CTCTGCCTCACACTCCTG	22826	CCAGC
			CAGGAG GAGGCAGAG		
			GTCCTC CTCCGTCTC		
			ACA_		
GAM2291	STK25	3'	CTCTGCCTCCTCCTCC	22093	CC C
			GGAG AG GAGGCAGAG		
			CCTC TC CTCCGTCTC		
			C_ _		
GAM2291	TESK2	5'	CTGAGTCGCCGGCTTCTG	63884	A GG
			CAGGAGCC GCGA CAG		

		GTCTTCGG CGCT GTC	
		C GA	
GAM2291	TNKS1BP1 5'	CTCTGCCTCCCCGCTCTCA	54150 A CAGC
		C GGAGC GAGGCAGAG	
		A TCTCG CTCCGTCTC	
		C CCC_	
GAM2291	TOR2A 3'	CTCCGCCTCTCTGAGCCTCTG	56185 GA _ C A
		CAG GC CAG GAGGC GAG	
		GTC CG GTC CTCCG CTC	
		TC A T C	
GAM2291	TRAF3 5'	CTCCACCGTCGGCTTCTG	13850 A A_ C
		CAGGAGCC GCG GG AG	
		GTCTTCGG TGC CC TC	
		C CA _	
GAM2291	UBE3B 3'	CTGCCTCCAGGGCTCCTG	77444 AGC
		CAGGAGCC GAGGCAG	
		GTCCTCGG CTCCGTC	
		GAC	
GAM2291	LOC116173 3'	CTCTGGGGCTACCTGGCTCCT	57426 CG G__
		AGGAGCCAG AG CAGAG	
		TCCTCGGTC TC GTCTC	
		CA GGG	
GAM2291	LOC116236 3'	CTCTGTGGTTGTGGCGCCCTG	74244 A_ G G_
		CAGG GCCA CGA GCAGAG	
		GTCC CGGT GTT TGTCTC	
		CG _ GG	
GAM2291	LOC122609 3'	CTCTGTTAGCTCTGTCTCCTG	74597 C CGA_
		CAGGAG CAG GGCAGAG	
		GTCCTC GTC TTGTCTC	
		T TCGA	
GAM2291	LOC126616 3'	CTCTGGCTGCCTGGCTCC	75041 CG G
		GGAGCCAG AG CAGAG	
		CCTCGGTC TC GTCTC	
		CG G	
GAM2291	LOC126917 3'	CTCCTGGGCTGGTTCCTG	75090 G_ C
		CAGGAGCCAGC AGG AG	
		GTCCTTGGTCG TCC TC	
		GG _	
GAM2291	LOC128272 3'	CTCCATGCCTGGCTCCTG	75242 _ A C
		CAGGAGCCAG CG GG AG	

		GTCCTCGGTC GT CC TC	
		C A _	
GAM2291	LOC132241 5'	CTCTGCTTCTGGGCTCC 75560	AGC
		GGAGCC GAGGCAGAG	
		CCTCGG CTTCGTCTC	
		GT_	
GAM2291	LOC136242 3'	CTCTGCATTCCACTGGCTCT 75766	C_ _
		GGAGCCAG GAG GCAGAG	
		TCTCGGTC CTT CGTCTC	
		AC A	
GAM2291	LOC138389 5'	CTCTGCCTTCTGTTCTCTG 76736	_ C C
		CAG GAGC AG GAGGCAGAG	
		GTC CTTG TC TTCCGTCTC	
		T _ _	
GAM2291	LOC143274 3'	CTCTGCCTCCTTCCTCCT 77022	CC C
		AGGAG AG GAGGCAGAG	
		TCCTC TC CTCCGTCTC	
		CT _	
GAM2291	LOC143425 3'	CTCTGCCTCTGTTCTCTTG 89014	CC _
		CAGGAG AGC GAGGCAGAG	
		GTTCTC TTG CTCCGTCTC	
		_ T	
GAM2291	LOC143437 5'	CTCTGCCTCAGCCTCCTCC 83856	CCA _
		GGAG GC GAGGCAGAG	
		CCTC CG CTCCGTCTC	
		CTC A	
GAM2291	LOC145195 5'	CTGGTTACGGCTGGCTCCTG 84230	_ _ G
		CAGGAGCCAGC G AG CAG	
		GTCCTCGGTCG C TT GTC	
		G A G	
GAM2291	LOC145474 5'	CTCTGCCCTCTGACTCACTG 77728	_ C CGA
		CAG GAG CAG GGCAGAG	
		GTC CTC GTC CCGTCTC	
		A A TC_	
GAM2291	LOC146138 3'	CTCTGCCTCCCTAAGCTCC 84593	C_ C
		GGAGC AG GAGGCAGAG	
		CCTCG TC CTCCGTCTC	
		AA C	
GAM2291	LOC147138 5'	CTGCCTCGGAGGCTGCTG 78866	G AG
		CAG AGCC CGAGGCAG	

	GTC TCGG GCTCCGTC	
	G AG	
GAM2291 LOC148183 5'	CTCTGCCTGCCTGTTCTCTG 85264	CA G
	CAGGAGC GC AGGCAGAG	
	GTCCTTG CG TCCGTCTC	
	TC _	
GAM2291 LOC149134 5'	CTCTGTCAGCACTGGCTCT 85519	CGA_
	GGAGCCAG GGCAGAG	
	TCTCGGTC CTGTCTC	
	ACGA	
GAM2291 LOC149319 5'	CTCTGCCTTCAGGACCCTG 80070	AG AGC
	CAGG CC GAGGCAGAG	
	GTCC GG TTCCGTCTC	
	CA AC_	
GAM2291 LOC150319 3'	CTCTGCCTCCGCCTCC 80468	CCA _
	GGAG GCG AGGCAGAG	
	CCTC CGC TCCGTCTC	
	_ C	
GAM2291 LOC150445 3'	CTCTGCCTTTGTGATCCTG 80677	GC GC
	CAGGA CA GAGGCAGAG	
	GTCCT GT TTCCGTCTC	
	A_ GT	
GAM2291 LOC150838 3'	CTCTGCCTGGGTTCTTCCTG 86314	_ AGCG
	CAGGA GCC AGGCAGAG	
	GTCCT TGG TCCGTCTC	
	TCT G_	
GAM2291 LOC151429 3'	CTCTGCCTCCCTGCTCTCTG 86535	_ C C
	CAG GAGC AG GAGGCAGAG	
	GTC CTCG TC CTCCGTCTC	
	T _ C	
GAM2291 LOC151512 5'	CTCCAGCCTTGGTGGCTCCT 86615	G A_
	AGGAGCCA CGAGGC GAG	
	TCCTCGGT GTTCCG CTC	
	G AC	
GAM2291 LOC151720 5'	CTCTGCCTGGTGGTTCCTG 81154	G G
	CAGGAGCCA C AGGCAGAG	
	GTCCTTGGT G TCCGTCTC	
	_ G	
GAM2291 LOC152687 5'	CTCTGCCTCCCGTTGCTCT 81529	C _
	GGAGC AGC GAGGCAGAG	

	TCTCG TTG CTCCGTCTC	
	_ CC	
GAM2291 LOC154790 5'	CTCTGAGTCCCTGGTTCCTG 82040	C GG
	CAGGAGCCAG GA CAGAG	
	GTCCTTGGTC CT GTCTC	
	C GA	
GAM2291 LOC155370 5'	CTGGTTTGCCGGCTTCTG 72525	A G
	CAGGAGCC GCGAG CAG	
	GTCTTCGG CGTTT GTC	
	C G	
GAM2291 LOC155435 3'	CTGTTTATCACTGGCTCT 82267	C _
	GGAGCCAG GA GGCAG	
	TCTCGGTC CT TTGTC	
	A AT	
GAM2291 LOC157638 5'	CTCTGCCCAGCCTCGCTG 82422	_ CCA GA
	CAG GAG GC GGCAGAG	
	GTC CTC CG CCGTCTC	
	G _ AC	
GAM2291 LOC158156 3'	CTCTGCCATGAATTCCTG 82626	CCAG A
	CAGGAG CG GGCAGAG	
	GTCCTT GT CCGTCTC	
	AA_ A	
GAM2291 LOC158563 5'	CTCTGCCTCTCTTCTCTCTG 82846	_ CC C
	CAG GAG AG GAGGCAGAG	
	GTC CTC TC CTCCGTCTC	
	T T_ T	
GAM2291 LOC163071 5'	CTCTGCCTCACCTGCCTCCT 83284	C C_
	AGGAG CAG GAGGCAGAG	
	TCCTC GTC CTCCGTCTC	
	C CA	
GAM2291 LOC164382 5'	CTCTGCCTGGGTCCCCTG 88557	A_ AGCG
	CAGG GCC AGGCAGAG	
	GTCC TGG TCCGTCTC	
	CC G_	
GAM2291 LOC166879 5'	CTGCCGCGCCTCGGCTCCTG 88616	A_ A
	CAGGAGCC GCG GGCAG	
	GTCCTCGG CGC CCGTC	
	CTC G	
GAM2291 LOC200298 3'	CTCCGCGCCGTGGACTGGCTCC 91574	CGA_ A_
T	AGGAGCCAG GGC GAG	

	TCCTCGGTC	CCG	CTC	
	AGGTG	CGC		
GAM2291 LOC200853 3'	CTCTGCCTGGTGGCATCCT	90326	_	G G
	AGGA GCCA C AGGCAGAG			
	TCCT CGGT G TCCGTCTC			
	A _ G			
GAM2291 LOC201477 5'	CTCCACAGTTAGAGGCTCCTG	91353	___	GA_ C
	CAGGAGCC AGC GG AG			
	GTCCTCGG TTG CC TC			
	AGA ACA _			
GAM2291 LOC219731 5'	CTCTGCCTCCCCTGCCC	94702	A C C_	
	GG GC AG GAGGCAGAG			
	CC CG TC CTCCGTCTC			
	_ _ CC			
GAM2291 LOC219854 3'	CTCTGGAGTCCTGGCTTC	93115	C GG_	
	GGAGCCAG GA CAGAG			
	CTTCGGTC CT GTCTC			
	_ GAG			
GAM2291 LOC219920 5'	CTCTGCCTCGGTTTCCT	94950	_	AGC
	AGGAG CC GAGGCAGAG			
	TCCTT GG CTCCGTCTC			
	T _			
GAM2291 LOC219920 3'	CTCTGCCTGGTGGCCCTG	94951	A	G G
	CAGG GCCA C AGGCAGAG			
	GTCC CGGT G TCCGTCTC			
	_ _ G			
GAM2291 LOC220895 3'	CTCTGCCTTAGCACTCC	92491	CCA _	
	GGAG GC GAGGCAGAG			
	CCTC CG TTCCGTCTC			
	A_ A			
GAM2291 LOC245806 3'	CTCTGCCTTCTCTCC	93542	CC C	
	GGAG AG GAGGCAGAG			
	CCTC TC TTCCGTCTC			
	_ _			
GAM2291 LOC253531 5'	CTCTGCCTCAGCCTCCTCC	98222	CCA _	
	GGAG GC GAGGCAGAG			
	CCTC CG CTCCGTCTC			
	CTC A			
GAM2291 LOC253596 5'	CTGTAGCTGGTTCCTG	97231		GAG
	CAGGAGCCAGC GCAG			

	GTCCTTGGTCG	TGTC	
	A__		
GAM2291 LOC253715	5' CTCCTTGGCTGGTTCCTG	98705	_ C
	CAGGAGCCAGC GAGG AG		
	GTCCTTGGTCG TTCC TC		
	G _		
GAM2291 LOC253992	3' CTCTGCCTCTGGCCCTCCTG	98423	_ GC
	CAGGA GCCA GAGGCAGAG		
	GTCCT CGGT CTCCGTCTC		
	CC _		
GAM2291 LOC255536	3' CTCTGCCTGTTAGACTCTT	96110	CC_ G
	AGGAG AGC AGGCAGAG		
	TTCTC TTG TCCGTCTC		
	AGA _		
GAM2291 LOC256055	3' CTCTGCCTGGCCAGCCCT	97622	A CA G
	AGG GC GC AGGCAGAG		
	TCC CG CG TCCGTCTC		
	_ AC G		
GAM2291 LOC256475	5' CTCCGCCCGTGGTTCCT	99353	G A A
	AGGAGCCA CG GGC GAG		
	TCCTTGGT GC CCG CTC		
	_ C C		
GAM2291 LOC256848	5' CTCTGTATCCCCGGCTCCTG	99377	AGC G
	CAGGAGCC GA GCAGAG		
	GTCCTCGG CT TGTCTC		
	CCC A		
GAM2291 LOC257095	5' CTCTGCGTGGTGTGGCTCCT	98720	_ GAG
	AGGAGCCA GC GCAGAG		
	TCCTCGGT TG CGTCTC		
	G GTG		
GAM2291 LOC257449	3' CTTTGGAAGCAGGCTCCTG	63377	A GAGG
	CAGGAGCC GC CAGAG		
	GTCCTCGG CG GTTTC		
	A AAG_		
GAM2291 LOC257541	5' CTCGGTGCCACTGGCTCTCA	99597	A CGA _
	C GGAGCCAG GGCA GAG		
	A TCTCGGTC CCGT CTC		
	C A_ GG		
GAM2291 LOC51119	5' CTGGTTCGCCGGCTTCTG	66200	A G
	CAGGAGCC GCGAG CAG		

			GTCTTCGG CGCTT GTC		
			C G		
GAM2291	LOC89919	3'	CTCTGCCTCGGGCCTTCT 61373	_	AG
			AGGAG CC CGAGGCAGAG		
			TCTTC GG GCTCCGTCTC		
			C _		
GAM2291	LOC90371	5'	CTCTGCTGCTAGGCTTCTG 63161	_	GA
			CAGGAGCC AGC GGCAGAG		
			GTCTTCGG TCG TCGTCTC		
			A _		
GAM2291	LOC91496	5'	CTGCTTGCTGGTCCCTG 66809	AG	G
			CAGG CCAGCGAG CAG		
			GTCC GGTCGTTT GTC		
			CT _		
GAM2291	LOC91748	5'	CTCTGCCCTCCCTGGCTCCTG 67639		C _
			CAGGAGCCAG GAGG CAGAG		
			GTCCTCGGTC CTCC GTCTC		
			C C		
GAM2291	LOC96652	3'	CTCTGCTTCCAGCTGCC 66077	AGC	_
			GG CAGC GAGGCAGAG		
			CC GTCG CTTCGTCTC		
			_ AC		
GAM2292	ACP2	3'	CCAACAGCCAGCCAGCCACA 9652	_	AG _
			TGTGG TGGCTGG GT GG		
			ACACC ACCGACC CA CC		
			G GA A		
GAM2292	ANKTM1	3'	CCACCCACCCACCACA 24696	C	AG
			TGTGGTGG TGG GTGG		
			ACACCACC ACC CACC		
			C _		
GAM2292	ATF7	3'	CCAGCCCCAGCCACCCCA 23399	T	A _
			TG GGTGGCTGG GG TGG		
			AC CCACCGACC CC ACC		
			C _ G		
GAM2292	BDKRB2	3'	GGCCCCAACCGCCACA 7111	C	AGGT
			TGTGGTGG TGG GGCC		
			ACACCGCC ACC CCGG		
			A _		
GAM2292	EGFL4	3'	GCCACCCCCAGCCCCAC 62467	T	A
			GTGG GGCTGG GGTGGC		

			CACC CCGACC CCACCG		
			— C		
GAM2292	ENIGMA	3'	CTCCCTCCACCACCACA 62868	C	TG
			TGTGGTGG TGGAGG G		
			ACACCACC ACCTCC C		
			— CT		
GAM2292	MKI67	3'	GGCACCTCCAACCACCACA 11598	C	G
			TGTGGTGG TGGAGGTG CC		
			ACACCACC ACCTCCAC GG		
			A —		
GAM2292	TNNT3	3'	TCCACATCCTCCAGCCCCCACA 23134	T	— GCC
			TGTGG GGCTGGAGG TG GA		
			ACACC CCGACCTCC AC CT		
			C T AC—		
GAM2292	WNT3A	3'	ATTCAGCCCACCAGCCACCTCA 53609	T	AGGT C
			TG GGTGGCTGG GGC GAAT		
			AC CCACCGACC CCG CTTA		
			T AC— A		
GAM2292	BCAN	3'	CTGCGCTCCCGCCACCACA 41971	T	—TG
			TGTGGTGGC GGAG G G		
			ACACCACCG CCTC C C		
			C G GT		
GAM2292	C20orf173	5'	GCTCCTCCTGCCACCACA 55917	T	T
			TGTGGTGGC GGAGG GGC		
			ACACCACCG CCTCC TCG		
			T —		
GAM2292	CAPN13	3'	TCGGCCACCTCCCACCA 58630	CTG	
			TGGTGG GAGGTGGCCGA		
			ACCACC CTCCACCGGCT		
			—		
GAM2292	FLNC	3'	CCACCTCCAGCCACACA 9390	G	
			TGTG TGGCTGGAGGTGG		
			ACAC ACCGACCTCCACC		
			—		
GAM2292	KIAA1952	5'	CCCCTCCAGCCACCCA 73542	T	T
			TG GGTGGCTGGAGG GG		
			AC CCACCGACCTCC CC		
			— —		
GAM2292	LANCL2	3'	CCTCCCCACCCACCACA 38619	C	A T
			TGTGGTGG TGG GG GG		

		ACACCACC ACC CC CC		
		C _ T		
GAM2292	LOC127435 3'	CCAGCTCAGCCACACA 76606	G	G G
		TGTG TGGCTG AG TGG		
		ACAC ACCGAC TC ACC		
		_ _ G		
GAM2292	LOC127435 3'	CTACCCTCCAAACCACCACA 76607	C_ _	
		TGTGGTGG TGGAGG TGG		
		ACACCACC ACCTCC ATC		
		AA C		
GAM2292	LOC139840 5'	TCTCCACAGCCACCACA 76777	GA T	
		TGTGGTGGCTG GG GG		
		ACACCACCGAC CC CT		
		A_ T		
GAM2292	LOC150319 3'	GCCACCTCCTGCCACCACA 80473	T	
		TGTGGTGGC GGAGGTGGC		
		ACACCACCG CCTCCACCG		
		T		
GAM2292	LOC204084 3'	ATTCGGCCACCTCCACGACCA 90990	GGC	
		TGGT TGGAGGTGGCCGAAT		
		ACCA ACCTCCACCGGCTTA		
		GC_		
GAM2292	LOC221477 3'	TCCCCACCTCCACCACCACA 93778	C CC	
		TGTGGTGG TGGAGGTGG GA		
		ACACCACC ACCTCCACC CT		
		_ C_		
GAM2292	LOC222031 3'	CCACCTCCAGCCACCCCA 95674	T	
		TG GGTGGCTGGAGGTGG		
		AC CCACCGACCTCCACC		
		C		
GAM2293	ATRX 5'	ATCAGAAGAATCTGAAGAAA 57076	CG	
		TTTCTTCAGAT TTCTGAT		
		AAAGAAGTCTA AAGACTA		
		AG		
GAM2293	JAM3 3'	GAACCAGGTCTGAAAAAGTA 52489	C _	
		TATTT TTCAGATC GTTC		
		ATGAA AAGTCTGG CAAG		
		A AC		
GAM2293	UBE2L6 3'	GAGTCACAATCTGAAGAA 16161	C TCT	
		TTCTTCAGAT GT GATTC		

		AAGAAGTCTA CA CTGAG	
		A _	
GAM2293	FLJ10326	3' AATCAGAATTATAGAAGAAGTA 36499	AG C
		TATTTCTTC AT GTTCTGATT	
		ATGAAGAAG TA TAAGACTAA	
		A_ T	
GAM2293	FLJ13840	5' GAATATTTTGATCTGAAGAGA 45699	TTCTG
		TTTCTTCAGATCG ATTC	
		AGAGAAGTCTAGT TAAG	
		TTTA_	
GAM2293	KIAA0514	3' AATCAGTGCTGAGAAATA 28734	T ATCGTT
		TATTTCT CAG CTGATT	
		ATAAAGA GTC GACTAA	
		_ GT_	
GAM2293	KIAA0680	3' AATCAGAAAGAAAGAGAAATA 28895	CAGA G
		TATTTCTT TC TTCTGATT	
		ATAAAGAG AG AAGACTAA	
		AA_ A	
GAM2293	PREI3	3' TAGAATTGAAGAAATA 66928	GATC
		TATTTCTTCA GTTCTG	
		ATAAAGAAGT TAAGAT	

GAM2293	PRO0456	3' GAGAGATCTGAAGAAATA 27007	G
		TATTTCTTCAGATC TTC	
		ATAAAGAAGTCTAG GAG	
		A	
GAM2293	RA-GEF-2	3' GAACAACTGAAGAAATA 33412	ATC
		TATTTCTTCAG GTTC	
		ATAAAGAAGTC CAAG	
		AA_	
GAM2293	SULT1B1	3' AATCACAAATCTGAGAAATA 27843	T CG C
		TATTTCT CAGAT TT TGATT	
		ATAAAGA GTCTA AA ACTAA	
		_ _ C	
GAM2293	TGOLN2	3' AATCAAAAGAAATGAAGAAA 64740	GA GTTC
		TTTCTTCA TC TGATT	
		AAAGAAGT AG ACTAA	
		AA AAA_	
GAM2293	TRAD	3' AGGTCATTCTGAAGAAATA 23919	TCGT
		TATTTCTTCAGA TCT	

		ATAAAGAAGTCT	GGA		
		TACT			
GAM2293	LOC153937 5'	GAATCAGAACACAGCAGAGAA	81918	CAGATC	
		TTCTT GTTCTGATTC			
		AAGAG CAAGACTAAG			
		ACGACA			
GAM2293	LOC255131 5'	GAGAGATCTAAAGAAATA	97691	C G	
		TATTTCTT AGATC TTC			
		ATAAAGAA TCTAG GAG			
		A A			
GAM2293	LOC255621 3'	AATAATCTGAAGATAATA	98884	_ CG	
		TATT TCTTCAGAT TT			
		ATAA AGAAGTCTA AA			
		T AT			
GAM2293	LOC51131 3'	GAATCAGACTATGAAGAAAT	32783	GATC T	
		ATTTCTTCA GT CTGATTC			
		TAAAGAAGT CA GACTAAG			
		AT_ _			
GAM2294	LOX 3'	GGCAAAGCAAAACTCCCA	11346	CA CTTTA C	
		TGG AGTT GC TTTGCC			
		ACC TCAA CG AAACGG			
		C_ AA_ _			
GAM2294	NR1I2 5'	AGTCGGAGCAAAGAACTTACCA	15297	C A C C	
		TGG AAGTTCTTT GC TTTG CT			
		ACC TTCAAGAAA CG AGGC GA			
		A _ _ T			
GAM2294	PTGFRN 3'	AGGCTAAAGAAGCCA	67763	AAG	
		TGGC TTCTTTAGCCT			
		ACCG AAGAAATCGGA			

GAM2294	ST5 3'	AGGCAAAGGCCAATCAGTCCCC	19453	CAAGTTCT A	
	A	TGG TT GCCTTTGCCT			
		ACC AA CGGAAACGGA			
		CCTGACT_ C			
GAM2294	ST5 3'	AGGCAAAGGCCAATCAGTCCCC	58226	CAAGTTCT A	
	A	TGG TT GCCTTTGCCT			
		ACC AA CGGAAACGGA			
		CCTGACT_ C			
GAM2294	TCEA1 3'	AGGCAAAGATGAGAACTTCCCA	81279	C TAGC	
		TGG AAGTTCTT CTTTGCCT			

ACC TTCAAGAG GAAACGGA
 C TA__
 GAM2294 C7orf13 3' GCAGGGTCTAAAGAAATTACCA 51922 C G C
 TGG AA TTCTTTAG CTTTGC
 ||| || ||||| |||||
 ACC TT AAGAAATC GGGACG
 A A T
 GAM2294 CARD9 3' GCAAAGGCTGCCTTGCC 42549 TTCTT C
 GGCAAG TAGCCTTTG C
 ||||| ||||| |
 CCGTTC GTCGGAAAC G
 C__ A
 GAM2294 DKFZp434I1117 3' GCAAAGGCTGCTTCTCCTCCA 62845 CA_ TTCTT
 TGG AG TAGCCTTTGC
 ||| || |||||
 ACC TC GTCGGAAACG
 TCC TTC__
 GAM2294 DKFZP564P1916 5' AGACAACCCTGAAGAACCTAGC 32236 AA_ CCT C
 GC GTTCTTTAG TTG CT
 || ||||| ||| ||
 CG CAAGAAGTC AAC GA
 ATC CC_ A
 GAM2294 FLJ20034 3' GGCAAAGGCCCGCCTGGCA 34849 G A TCTTTA
 TG CA GT GCCTTTGCC
 || ||| |||||
 AC GT CG CGGAAACGG
 G C CC__
 GAM2294 FLJ25416 3' AGACAAAGGCTAAAAAACATGC 59444 A C C
 CA TGGCA GTT TTTAGCCTTTG CT
 ||||| ||| ||||| ||
 ACCGT CAA AAATCGGAAAC GA
 A A A
 GAM2294 HES6 3' CAAAAGCTTGAACCTTGCCA 38457 TTT C
 TGGCAAGTTC AGC TTTG
 ||||| ||| |||
 ACCGTTCAAG TCG AAAC
 T_ A
 GAM2294 LGP2 3' AGGCAAAAGAATTTGCCA 44377 A
 TGGCAAGTTCTTT GCCT
 ||||| ||| |||
 ACCGTTTAAGAAA CGGA
 A
 GAM2294 MGC5297 3' CAATGGAAGAACTTGC 44262 TAG T
 GCAAGTTCTT CC TTG
 ||||| || |||
 CGTTCAAGAA GG AAC
 _ T
 GAM2294 STMN4 3' AGGCCAAAGAACTTTCCA 48649 C A
 TGG AAGTTCTTT GCCT
 ||| ||||| |||

ACC TTCAAGAAA CGGA
 T C
 GAM2294 LOC145240 3' AGGCAAAGGCTAAAGAACTTGC 77562
 CA TGGCAAGTTCTTTAGCCTTTGCCT
 |||||
 ACCGTTCAAGAAATCGGAAACGGA

 GAM2294 LOC161102 5' AGGCAAAGCTAATGAAAACCTCA 88448 CAAG T C
 TGG TTC TTAGC TTTGCCT
 || ||| |||| |||||
 ACT AAG AATCG AAACGGA
 CAA_ T _
 GAM2294 LOC201203 3' GCATTAAAAAGGAACCTTACCA 89517 C AGCCTT
 TGG AAGTTCTTT TGC
 || ||||| |||
 ACC TTCAAGGAA ACG
 A AAATT_
 GAM2294 LOC203084 3' AGGCAAAGATGAAAACCTTCCCA 88875 C C GC
 TGG AAGTT TTTA CTTTGCCT
 || |||| ||| |||||
 ACC TTCAA AAGT GAAACGGA
 C _ A_
 GAM2295 ANXA8 3' TGGGCACAGGTTATACAGACCC 73466 AGCC ____
 CA TGG TCTGT ACCTGTGCCCA
 || |||| |||||
 ACC AGACA TGGACACGGGT
 CC_ TAT
 GAM2295 ANXA8 3' TGGGCACAGGTTATACAGACCC 73467 AGCC ____
 CA TGG TCTGT ACCTGTGCCCA
 || |||| |||||
 ACC AGACA TGGACACGGGT
 CC_ TAT
 GAM2295 ATP8A2 3' CACAGGTACCTATCAG 95153 _ CCTCT
 CTGG AG GTACCTGTG
 ||| || |||||
 GACT TC CATGGACAC
 A ____
 GAM2295 BHLHB3 5' TATTGTACAGAGCCCCA 48490 A C CT
 TGG GC TCTGTAC GTG
 ||| || ||||| |||
 ACC CG AGACATG TAT
 C _ T_
 GAM2295 CASP3 3' TGGGCATGGTCAAAGGCTC 16355 C T T
 GAGCCT TG ACC GTGCCCA
 ||||| || ||| |||||
 CTCGGA AC TGG TACGGGT
 A _ _
 GAM2295 CCND2 3' TGGACACAGGTGATTGGCTCC 10057 TCTG C
 GGAGCC TACCTGTG CCA
 ||||| ||||| |||

			CCTCGG GTGGACAC GGT			
			TTA_ A			
GAM2295 DPEP1	5'	GGCCAGCACAGAGGCACCAG	16620	A	AC	T
		CTGG GCCTCTGT CTG GCC				
		GACC CGGAGACA GAC CGG				
		A C_ _				
GAM2295 EPHB4	3'	TGGGGACTCACAGAGGCCCC	16710	A	ACCT	G
		GG GCCTCTGT GT CCCA				
		CC CGGAGACA CA GGGT				
		C CT_ G				
GAM2295 EVA1	5'	GGCACAGGTGAGGAACTC	20532	_	TGT	
		GAG CCTC ACCTGTGCC				
		CTC GGAG TGGACACGG				
		AA _				
GAM2295 EVA1	5'	GGCACAGGTGAGGAACTC	59235	_	TGT	
		GAG CCTC ACCTGTGCC				
		CTC GGAG TGGACACGG				
		AA _				
GAM2295 FANCC	3'	TGGGCACAGGGGCAGCCGC	71053	CT	TA	
		GC CTG CCTGTGCCCA				
		CG GAC GGACACGGGT				
		CC GG				
GAM2295 GRLF1	3'	GCAGGCAATGGCTCCAG	79260	TC	TA	
		CTGGAGCC TG CCTGT				
		GACCTCGG AC GGACG				
		TA _				
GAM2295 ITGA5	3'	CAGGGACAGAGGCCCCAG	61932	A	A	
		CTGG GCCTCTGT CCTG				
		GACC CGGAGACA GGAC				
		C G				
GAM2295 LDB3	3'	TGGGCAATTGCCAGGGCTCCAG	76928	T	TACCTG	
		CTGGAGCC CTG TGCCCA				
		GACCTCGG GAC ACGGGT				
		_ CGTTA_				
GAM2295 LZTS1	3'	TGGGCACAGTCCAGACCCA	41042	AGCC	TAC	
		TGG TCTG CTGTGCCCA				
		ACC AGAC GACACGGGT				
		C_ CT_				
GAM2295 MDM1	3'	TGAGCACATAAGCAGAGGCTGC	39684	G	ACC	C
AG		CTG AGCCTCTGT TGTGC CA				

GAC TCGGAGACG ACACG GT
 G AAT A
 GAM2295 MHC2TA 3' CACAGGCCCGGCTCCAG 5969 TCT TA
 CTGGAGCC G CCTGTG
 ||||| | |||||
 GACCTCGG C GGACAC
 ____ CC
 GAM2295 NEURL 3' GGACAGGCTGCAGAGGGCTCCA 16130 _ _ G
 G CTGGAGCC TCTGTA CCTGT CC
 ||||| ||||| ||||| ||
 GACCTCGG AGACGT GGACA GG
 G C _
 GAM2295 ONECUT2 3' GGGCACAAGTCACCTCCA 17943 CCTC T C
 TGGAG TG AC TGTGCCC
 |||| || || |||||
 ACCTC AC TG ACACGGG
 C ____ _ A
 GAM2295 PLCG1 3' GGCACAGGAGACTCCA 12159 CC GTA
 TGGAG TCT CCTGTGCC
 |||| || |||||
 ACCTC AGA GGACACGG
 _ _
 GAM2295 PLOD 3' GGCACAGGTGTTGCACCAG 6116 A CTCTG
 CTGG GC TACCTGTGCC
 |||| || |||||
 GACC CG GTGGACACGG
 A TT ____
 GAM2295 SCN4A 3' TGAGCACCACCAGGGCTCCAG 6209 T TACCT C
 CTGGAGCC CTG GTGC CA
 ||||| || |||||
 GACCTCGG GAC CACG GT
 _ CAC ____ A
 GAM2295 SYNGR3 3' GGAGAGAGGCCAGAGGCTCCA 16120 TA GTG_
 G CTGGAGCCTCTG CCT CC
 ||||| || |||||
 GACCTCGGAGAC GGA GG
 CC GAGA
 GAM2295 SYNGR3 3' GGCACAGACCAGGGCTCCA 16121 T TAC
 TGGAGCC CTG CTGTGCC
 ||||| || |||||
 ACCTCGG GAC GACACGG
 _ CA_
 GAM2295 BG1 3' TGGGCACAGGCATTTCTGCCA 88655 AGCCTCT A
 TGG GT CCTGTGCCCA
 || || |||||
 ACC TA GGACACGGGT
 GTCTT ____ C
 GAM2295 CALN1 3' TGAGCACAAGTAAACTAAGGC 49671 CT ____ C C
 TTCAG CTGGAGCCT GT AC TGTGC CA
 ||||| || || ||||| ||

GACTTCGGA CA TG ACACG GT
 AT AAA A A
 GAM2295 DGKD 3' GGGCACAGACACTGACCAG 60111 AGCC T AC
 CTGG TC GT CTGTGCCC
 ||| || |||||
 GACC AG CA GACACGGG
 ____ T CA
 GAM2295 DKFZP566G1424 3' GGGAGGGGCACAGGGCTCCAG 85944 T A GTG
 CTGGAGCC CTGT CCT CCC
 ||||| ||| ||| |||
 GACCTCGG GACA GGG GGG
 _ C GA_
 GAM2295 EMILIN-2 3' TGAGCTTGCCACAGAGGCTCC 50258 ACCTGT C
 GGAGCCTCTGT GC CA
 ||||| ||| |||
 CCTCGGAGACA CG GT
 CCGTT_ A
 GAM2295 FKSG28 3' CAGAGGTGCAGGCACCAG 48906 A CT G
 CTGG GCCT GTACCT TG
 ||| ||| ||||| ||
 GACC CGGA CGTGGA AC
 A _ G
 GAM2295 FLJ11286 3' TGGGCACAGGCATGGTACCACC 37796 AGCCT A
 AG CTGG CTGT CCTGTGCCCCA
 ||| ||| |||||
 GACC GGTA GGACACGGGT
 ACCAT C
 GAM2295 FLJ12056 3' GGGCACAGGCACGGGCACAG 46822 GA CT A
 CTG GCCT GT CCTGTGCCC
 || ||| || |||||
 GAC CGGG CA GGACACGGG
 A_ _ C
 GAM2295 FLJ13052 3' GGGCACAGGGGAAGCCCAG 43756 A C GTA
 CTGG GC TCT CCTGTGCCC
 ||| || ||| |||||
 GACC CG AGG GGACACGGG
 _ A _
 GAM2295 FLJ14103 5' GGACAGCCAGAGGCTGCAG 97938 G TAC G
 CTG AGCCTCTG CTGT CC
 || ||||| ||| ||
 GAC TCGGAGAC GACA GG
 G C_ _
 GAM2295 KIAA0321 5' GCAGCCCAGAAAGCTCCAG 63054 C_ TAC
 CTGGAGC TCTG CTGT
 ||||| ||| |||
 GACCTCG AGAC GACG
 AA CC_
 GAM2295 KIAA0476 3' GCCCAGTCAAAGGCTCCA 30040 C TAC T
 TGGAGCCT TG CTG GC
 ||||| || ||| ||

		ACCTCGGA AC GAC CG	
		A T__ C	
GAM2295 KIAA0819	5'	GGGAACCAGAGGCTCCAG 64334	TACCT G
		CTGGAGCCTCTG GT CCC	
		GACCTCGGAGAC CA GGG	
		_____ A	
GAM2295 KIAA1001	3'	GGCACAGGTGCCAGCTCCAG 31010	CTCT
		CTGGAGC GTACCTGTGCC	
		GACCTCG CGTGGACACGG	
		AC__	
GAM2295 KIAA1076	3'	TGGGCACAGTGAGGAGACCCCA 66129	AGC G C
		TGG CTCT TAC TGTGCCCA	
		ACC GAGG GTG ACACGGGT	
		CCA A _	
GAM2295 MYH7B	3'	CAGGCCACAGAGGCCCAG 71055	A A_
		CTGG GCCTCTGT CCTG	
		GACC CGGAGACA GGAC	
		_ CC	
GAM2295 NYD-SP25	3'	TGGGCAAGTCAGTGGCTCCAG 54306	T T CTG
		CTGGAGCC CTG AC TGCCCA	
		GACCTCGG GAC TG ACGGGT	
		T _ A__	
GAM2295 PDE2A	3'	TGGGGGATACAGGGGCCCCAG 12007	A _ TGTG
		CTGG GCCTCTGTA CC CCCA	
		GACC CGGGGACAT GG GGGT	
		C A _____	
GAM2295 RoXaN	3'	CACAAGTAAATGCAGGCTGCAG 47275	G CTG__ C
		CTG AGCCT TAC TGTG	
		GAC TCGGA ATG ACAC	
		G CGTAA A	
GAM2295 SPIB	3'	TGAGCACACCCGAGGCTCC 13358	TGTACC C
		GGAGCCTC TGTGC CA	
		CCTCGGAG ACACG GT	
		CCC__ A	
GAM2295 TREX1	5'	GGAGACACAATGGCTCCAG 50609	TC ACCT GC
		CTGGAGCC TGT GT CC	
		GACCTCGG ACA CA GG	
		TA ____ GA	
GAM2295 TREX1	5'	GGAGACACAATGGCTCCAG 50610	TC ACCT GC
		CTGGAGCC TGT GT CC	

			GACCTCGG ACA CA GG		
			TA ____ GA		
GAM2295	YKT6	3'	TGAGCCCACCACAGAGGCCACA	22645	GA ACC T C
	G		CTG GCCTCTGT TG GC CA		
			GAC CGGAGACA AC CG GT		
			AC CC_ C A		
GAM2295	LOC121629	5'	GGGTCACAAGAGGCTCCAG	76085	GTACC _
			CTGGAGCCTCT TGTG CCC		
			GACCTCGGAGA ACAC GGG		
			____ T		
GAM2295	LOC126006	5'	GGGCACAGCGAGGTCCA	74897	G TGTAC
			TGGA CCTC CTGTGCCC		
			ACCT GGAG GACACGGG		
			_ C_		
GAM2295	LOC127702	3'	GGGCAGCACAGAGGCCCC	75986	A ACCTG
			GG GCCTCTGT TGCCC		
			CC CGGAGACA ACGGG		
			C CG_		
GAM2295	LOC142972	3'	TGGGCACAGGTTATACAGACCC	65722	AGCC _
	CA		TGG TCTGT ACCTGTGCCCA		
			ACC AGACA TGGACACGGGT		
			CC_ TAT		
GAM2295	LOC145317	3'	GCACAGACACAGAGGCCCAG	84280	A AC
			CTGG GCCTCTGT CTGTGC		
			GACC CGGAGACA GACACG		
			_ CA		
GAM2295	LOC147160	5'	GGCACAGGGTCAGGCCCAG	85079	A CTGTA
			CTGG GCCT CCTGTGCC		
			GACC CGGA GGACACGG		
			_ CTG_		
GAM2295	LOC148114	5'	GGGCACAGACCAGCCCCA	79362	A CTC TAC
			TGG GC TG CTGTGCCC		
			ACC CG AC GACACGGG		
			C _ CA_		
GAM2295	LOC153205	3'	ATATATACTAGAAGCTCCA	87152	C _ CC
			TGGAGC TCT GTA TGT		
			ACCTCG AGA CAT ATA		
			A T AT		
GAM2295	LOC153561	3'	TGAGCACAGGAGTTGGAGGCTG	81753	G TA_ C
	CAG		CTG AGCCTCTG CCTGTGC CA		

	GAC TCGGAGGT GGACACG GT		
	G TGA A		
GAM2295 LOC158263 5'	GGGCACCACTCAGAGGCTCCAG 82730	TACCT	
	CTGGAGCCTCTG GTGCCC		
	GACCTCGGAGAC CACGGG		
	TCAC_		
GAM2295 LOC167410 3'	CAGAGGTCCTCAGAGGCTCCAG 83563	T__ G	
	CTGGAGCCTCTG ACCT TG		
	GACCTCGGAGAC TGGA AC		
	TCC G		
GAM2295 LOC170127 3'	TGGGCACAGATTCCGATTCCAG 83462	CC TGTAC	
	CTGGAG TC CTGTGCCCA		
	GACCTT AG GACACGGGT		
	_ CCTTA		
GAM2295 LOC197336 3'	TGGACACAGGCTTGGCAGAGGC 59925	A A__ C	
GCCAG	CTGG GCCTCTGT CCTGTG CCA		
	GACC CGGAGACG GGACAC GGT		
	G GTTC A		
GAM2295 LOC200282 3'	TGCTGGAACAGAGGCTCCA 90102	A T	
	TGGAGCCTCTGT CC GTG		
	ACCTCGGAGACA GG CGT		
	A T		
GAM2295 LOC201100 3'	GCCCAGCACAGAGGCTCCA 91324	AC T	
	TGGAGCCTCTGT CTG GC		
	ACCTCGGAGACA GAC CG		
	C_ C		
GAM2295 LOC203286 5'	ACAGGACAGCAGAGGCTCCAG 92139	A__	
	CTGGAGCCTCTGT CCTGT		
	GACCTCGGAGACG GGACA		
	ACA		
GAM2295 LOC203636 3'	CAGGTCTTCACAGAGGCCCGG 90975	A ____	
	CTGG GCCTCTGT ACCTG		
	GGCC CGGAGACA TGGAC		
	C CTTC		
GAM2295 LOC219513 3'	GGACACAGAGTGCAGAGACCCC 95987	AGC _ C	
GG	CTGG CTCTGTAC CTGTG CC		
	GGCC GAGACGTG GACAC GG		
	CCA A A		
GAM2295 LOC221822 5'	GGACTGGACAGAGGCACCAG 94451	A A T G	
	CTGG GCCTCTGT CC GT CC		

GACC CGGAGACA GG CA GG
 A _ T _
 GAM2295 LOC253027 3' GGCACAGGTGCCCTGCCCA 98770 A CTCT
 TGG GC GTACCTGTGCC
 ||| || |||||
 ACC CG CGTGGACACGG
 _ TCC_
 GAM2295 LOC255104 3' GCACAGGTTAGAGTCCCAG 97128 AG C T
 CTGG C TCTG ACCTGTGC
 ||| | ||| |||||
 GACC G AGAT TGGACACG
 CT _ _
 GAM2295 LOC90092 5' TGGGCACAGACACTCACAGCCC 62078 A CTCT_ AC
 CA TGG GC GT CTGTGCCCA
 ||| || || |||||
 ACC CG CA GACACGGGT
 C AACT CA
 GAM2295 LOC90917 3' GGCACAGGCCTCAGAGCCCAG 64987 A C TA_
 CTGG GC TCTG CCTGTGCC
 ||| || ||| |||||
 GACC CG AGAC GGACACGG
 _ _ TCC
 GAM2295 LOC91516 5' GCAGCTCAGAGGCTCCAG 66908 TAC
 CTGGAGCCTCTG CTGT
 ||||| |||
 GACCTCGGAGAC GACG
 TC_
 GAM2295 LOC91661 3' GGTGCACAGAGGCCCGG 57215 A ACCT TG
 CTGG GCCTCTGT G CC
 ||| ||||| | ||
 GGCC CGGAGACA C GG
 C _ _ GT
 GAM2295 LOC92340 3' TGGGCACAGGGGCTAAGTCCAG 69569 GC CT A
 CTGGA CT GT CCTGTGCCCA
 ||| || || |||||
 GACCT GA CG GGACACGGGT
 _ AT _
 GAM2296 FLJ12785 3' ATGTACAAAATGCACAAGA 46285 G G
 TCTTGTG ATTTTGTA AT
 ||||| ||||| ||
 AGAACAC TAAACAT TA
 G G
 GAM2297 ASL 3' CAGTCAGGGACTGGAGA 72394 TGAGC
 TCTCCA GTCCCTGACTG
 |||| |||||
 AGAGGT CAGGGACTGAC

 GAM2297 CFTR 3' CAGTCACCTCATGGA 6680 C CCCT
 TCCATGAG GT GACTG
 ||||| || |||

AGGTACTC CA CTGAC

```

GAM2297 HAGH 5' GGCAGTCGGGGCTCGCGGAGA 19223 A GTC
                TCTCC TGAGC CCTGACTGCC
                ||||| ||||| |||||
                AGAGG GCTCG GGGCTGACGG
                C
GAM2297 HIVEP2 3' GGCAGTCTGTCGCTGCTCATGG 23074 _ CCCT
                TCTCCATGAGC GT GACTGCC
                ||||| |||||
                AGAGGTACTCG CG CTGACGG
                T CTGT
GAM2297 KLRC1 3' CAGTCAAACCCATGGAGA 24651 AGC CCC
                TCTCCATG GT TGA CTG
                ||||| |||||
                AGAGGTAC CA ACTGAC
                C_ A_
GAM2297 KLRC1 3' CAGTCAAACCCATGGAGA 11209 AGC CCC
                TCTCCATG GT TGA CTG
                ||||| |||||
                AGAGGTAC CA ACTGAC
                C_ A_
GAM2297 KLRC2 3' CAGTCAAACCCATGGAGA 96171 AGC CCC
                TCTCCATG GT TGA CTG
                ||||| |||||
                AGAGGTAC CA ACTGAC
                C_ A_
GAM2297 NEDD4L 3' GGCAGTCAGGGGACACTAGAGA 31605 CATG C _
                TCTC AG GTCCC TGA CTG GCC
                ||| ||||| |||||
                AGAG TC CAGGG ACTGACGG
                A_ A G
GAM2297 ZNF216 3' GCAGGAAGAAATGCTCATAAAG 21173 CC CC GA
                TCT ATGAGCGT CT CTGC
                ||| ||||| |||||
                AGA TACTCGTA GA GACG
                AA AA AG
GAM2297 CNOT3 5' GGCAGTCAAGCGAGCATCAGGA 27986 A _ G C _
                TCTCC TGA GC TC CT GACTGCC
                ||||| ||||| |||||
                AGAGG ACT CG AG GA CTGACGG
                _ A _ C A
GAM2297 FKBP5 3' GCCTAAGAAACACTCATGGGA 15932 T C CC GACT
                TC CCATGAG GT CT GC
                ||||| |||||
                AG GGTACTC CA GA CG
                _ A AA ATC_
GAM2297 FLJ10159 3' CAGGGTACGCTCATGGAGA 36333 _
                TCTCCATGAGCGT CCCTG
                ||||| |||||
```


AGAGGTACTCGCA GGGAC
 T
 GAM2297 FLJ11218 3' GCAGTCAGTTTCACAGAGA 37758 CA CGTCC
 TCTC TGAG CTGACTGC
 |||| ||| |||||
 AGAG ACTT GACTGACG
 AC T____
 GAM2297 FLJ12985 3' GGTCTTCAAGAAGCTCATGGA 46799 G CC CT
 TCCATGAGC TC TGA GCC
 ||||| || ||| |||
 AGGTACTCG AG ACT TGG
 A A_ TC
 GAM2297 FLJ14957 3' CAATCAAATCGACATGGAGG 52810 AG TCCC C
 TCTCCATG CG TGA TG
 ||||| || ||| |||
 GGAGGTAC GC ACT AC
 A_ TAA_ A
 GAM2297 FLJ20060 5' TTAGGAGCTCATGGAGA 34933 GTC
 TCTCCATGAGC CCTGA
 ||||| |||||
 AGAGGTACTCG GGATT
 A____
 GAM2297 GRIP1 5' CAGTCAGGAATTCTGAGAGA 71146 _ T CGTC
 TCTC CA GAG CCTGACTG
 ||| || ||| |||||
 AGAG GT CTT GGA CTGAC
 A _ AA____
 GAM2297 KIAA1157 3' GCAGTCAGAGAGGTGGAGG 72700 ATGA G C
 TCTCC GC TC CTGACTGC
 |||| || || |||||
 GGAGG TG AG GACTGACG
 _____ G A
 GAM2297 KIAA1228 3' GCAGCAGCACTCATGGA 65675 C TCC A
 TCCATGAG G CTG CTGC
 ||||| | ||| |||
 AGGTACTC C GAC GACG
 A _____
 GAM2297 KIAA1822 3' GGCAGTCAGAGGCGCTGGAGA 68192 TGA C
 TCTCCA GCGTC CTGACTGCC
 |||| |||| |||||
 AGAGGT CGCGG GACTGACGG
 _____ A
 GAM2297 MGC12921 3' GGCAGCCAGGACCCACCCATGG 64515 AGC____ C A
 GGA TCTCCATG GTCC TG CTGCC
 ||||| ||| || |||||
 AGGGGTAC CAGG AC GACGG
 CCACC _ C
 GAM2297 MGC35558 3' CAGTCAGGGTGTGACGAGG 59409 CATG T
 TCTC AGCG CCCTGACTG
 ||| ||| |||||

			GGAG TTGT GGGACTGAC		
			CAG_ _		
GAM2297	PAK7	5'	GCAGCTGCGTACGCTCATGGA 70225	CCCTGA	
			TCCATGAGCGT CTGC		
			AGGTACTCGCA GACG		
			TGCGTC		
GAM2297	SIAT4A	3'	GCTGGGGAGACGCTCAGGGA 13139	A _ GACT	
			TCC TGAGCGTC CCT GC		
			AGG ACTCGCAG GGG CG		
			G A GT_		
GAM2297	LOC148147	3'	AGTGGAACCCTCATGGAGA 79388	CG_ _	
			TCTCCATGAG TCC CT		
			AGAGGTACTC AGG GA		
			CCA T		
GAM2297	LOC255624	3'	GGTCTTCAAGAAGCTCATGGA 96166	G CC CT	
			TCCATGAGC TC TGA GCC		
			AGGTACTCG AG ACT TGG		
			A A_ TC		
GAM2297	LOC257450	5'	CAGTCAGGGACACTCAGAAGA 91448	CCA C	
			TCT TGAG GTCCCTGACTG		
			AGA ACTC CAGGGACTGAC		
			AG_ A		
GAM2297	LOC51301	3'	CAGTCAGGATTCTACTGAAGA 33904	C TG C C	
			TCT CA AG GTCC TGA CTG		
			AGA GT TC TAGG ACTGAC		
			A CA T _		
GAM2298	SEL1L	3'	GCACATTTCAAAACAAG 18602	GGTTC	
			CTTGTTT GAATGTGC		
			GAACAAA TTTACACG		
			AC_		
GAM2298	C1orf34	3'	CACATCCGACTTCAGGTA 61300	TGTTT T A	
			TACCT GGT CG ATGTG		
			ATGGA TCA GC TACAC		
			CT_ _ C		
GAM2298	C3orf4	3'	CACATTCACCACTAAATA 39589	TC_	
			TGTTTGGT GAATGTG		
			ATAAATCA CTTACAC		
			CCA		
GAM2298	DATF1	3'	CACATTCGAACCTTCGAAGG 42324	GTTT	
			CCTT GGTTCTGAATGTG		

			GGAA TCAAGCTTACAC		
			GCT_		
GAM2298	DATF1	3'	CACATTCGAACTTCGAAGG	55848	GTTT
			CCTT GGTTCGAATGTG		
			GGAA TCAAGCTTACAC		
			GCT_		
GAM2298	DATF1	3'	CACATTCGAACTTCGAAGG	55850	GTTT
			CCTT GGTTCGAATGTG		
			GGAA TCAAGCTTACAC		
			GCT_		
GAM2298	FLJ00026	3'	ACAATGTACCAAACAAGG	65617	T AA
			CCTTGTTTGGT CG TGT		
			GGAACAAACCA GT ACA		
			T A_		
GAM2298	FLJ11186	3'	GCACGAGAAAACCAAACAG	37727	CGAA
			TTGTTTGGTT TGTGC		
			GACAAACCAA GCACG		
			AAGA		
GAM2298	FLJ11506	3'	GCACACCTGCAAAACAAGG	45435	G TCGAA
			CCTTGTTT GT TGTGC		
			GGAACAAA CG ACACG		
			A TCC_		
GAM2298	KIAA0440	5'	GCACATTTAAAACACAGATA	32085	_ C_
			TGTTTG GTT GAATGTGC		
			ATAGAC CAA TTTACACG		
			A AA		
GAM2298	MDS009	3'	GCACCTGGGAACCAAACAA	39985	GAAT
			TTGTTTGGTTC GTGC		
			AACAAACCAAG CACG		
			GGTC		
GAM2298	MDS029	3'	GCACATTTGTTTAAACAA	38064	TT
			TTGTTTGG CGAATGTGC		
			AACAAATT GTTTACACG		
			T_		
GAM2298	MGC32043	3'	GCACACCAGGATAGACAAGG	58667	G GAA
			CCTTGTTTG TTC TGTGC		
			GGAACAGAT AGG ACACG		
			_ ACC		
GAM2298	SEPT6	3'	GCACACAGTCAAACAAGGT	31392	GT CGAA
			ACCTTGTTTG T TGTGC		

TGGAACAAAC A ACACG
 TG C____
 GAM2298 SIAT8D 3' CACATTTTGAAACAAACA 20230 G _
 TGTTTG TTCGAA TGTG
 ||||| ||||| ||||
 ACAAAC AAGTTT ACAC
 A T
 GAM2298 TANK 3' CACATTTGAAAACAGACA 16076 G_
 TGTTTG TTCGAATGTG
 ||||| |||||
 ACAGAC AAGTTTACAC
 AA
 GAM2298 LOC128989 3' CACACGATGCCGAACAAGG 75312 _ AA
 CCTTGTTTGGT TCG TGTG
 ||||| ||||| ||||
 GGAACAAGCCG AGC ACAC
 T _
 GAM2298 LOC153387 5' CACACTGAAAACAAGG 87222 GGT AA
 CCTTGTTT TCG TGTG
 ||||| ||||| ||||
 GGAACAAA AGT ACAC
 _ C_
 GAM2298 LOC155006 3' GCGGGAGAACCAAATAAGG 82172 GAA
 CCTTGTTTGGTTC TGT
 ||||| ||||| ||||
 GGAATAAACCAAG GCG
 AGG
 GAM2298 LOC221975 3' GCACATTCAAAGTGGTCCAAG 94193 T_ G C
 CTTG TTG TT GAATGTGC
 |||| |||| ||||
 GAAC GGT AA CTTACACG
 CT G A
 GAM2299 SHANK2 3' ATGTCACATGGAGTTAGTCA 25523 T _
 TGAATACT CCATG GCAT
 ||||| ||||| ||||
 ACTGATTGA GGTAC TGTA
 _ AC
 GAM2299 AP3M2 3' GTGCCATGGAACTAATCA 23302 C AC
 TGA TA TTCCATGGCAT
 |||| |||||
 ACT AT AAGGTACCGTG
 A C_
 GAM2299 FLJ14260 3' ATCCATGGAAAAGTTA 47350 AAC C
 TGACT TTCCATGG AT
 |||| ||||| ||||
 ATTGA AAGGTACC TA
 A_ _
 GAM2299 KIAA0976 3' ATGCCATGAAAATTGGCCA 30548 A C C
 TG CTAA TT CATGGCAT
 || |||| |||||

AC GGTT AA GTACCGTA
 C A A
 GAM2299 KIAA1336 3' CCATGTTACAAGGAAGTTA 72785 A__
 TAACTTCC TGGCATGG
 ||||| |||||
 ATTGAAGG ATTGTACC
 AAC
 GAM2299 LOC145255 3' ATCCGTGTAAAAGTCAGT 84267 A CCATG
 ACTACTT GCATGGAT
 ||| ||| |||||
 TGA TGAA TGTGCCTA
 C AA__
 GAM2299 LOC148089 3' CCGCGCATGGGAGCCAGCCA 79328 A AA _ AT
 TGCT CTTCCATG GC GG
 || || ||||| || ||
 AC GA GAGGGTAC CG CC
 C CC G __
 GAM2299 LOC154743 3' TGTCATGGAAGCTATCA 82017 C A
 TGA TA CTTCCATGGCA
 ||| || |||||
 ACTAT GAAGGTACTGT
 _ C
 GAM2299 LOC199958 3' ATGTACACATGGAAGTTCATCA 91489 CT ____
 TGA AACTTCCATG GCAT
 ||| ||||| |||
 ACT TTGAAGGTAC TGTA
 AC ACA
 GAM2299 LOC221337 5' ATCCATGCTTCAATTAATCA 93733 C CTTCCAT
 TGA TAA GGCATGGAT
 ||| ||| |||||
 ACTATT TCGTACCTA
 A AACT__
 GAM2300 CLECSF5 3' GTCACCAAAGTACAGCACATAC 26042 C ____ G
 GTA GTGCTGTG GGTG AC
 ||| ||||| ||| ||
 CAT CACGACAT CCAC TG
 A GAAA _
 GAM2300 GAD2 5' CCGCCCGCAGCTCGCACT 7699 A T
 AGT CG GCTGTGGGTGG
 ||| || |||||
 TCA GC CGACGCCCGCC
 C T
 GAM2300 KLHL3 3' CCCCCCAGCACATACT 88845 C T T
 AGTA GTGCTG GGG GG
 ||| ||||| ||| ||
 TCAT CACGAC CCC CC
 A _ _
 GAM2300 NTSR1 3' GTCCATGCACCACAGACAC 11864 _ ____
 GTG CTGTGG GTGGAC
 ||| ||||| |||||

CAC GACACC TACCTG
A ACG
GAM2300 SCA1 3' CCACCCACGGTCACCACT 6174 AC _
AGT GTG CTGTGGGTGG
||| ||| |||||
TCA CAC GGCACCCACC
C_ T
GAM2300 DKFZP434B205 3' GTCGCCCCGACAACAGGTAC 75846 G C _ G
GTAC TG TGT GGGTG AC
|||| || ||| ||||| ||
CATG AC ACA CCCGC TG
G A G _
GAM2300 DKFZP564O0463 3' TGCTCACACACACTT 27127 AC C
AAGT GTG TGTGGGTG
|||| ||| |||||
TTCA CAC ACACTCGT
CA _
GAM2300 KIAA0182 3' CCACCCAAGACACAGTAC 72498 _ _ G
GTAC GTG CT TGGGTGG
|||| ||| || |||||
CATG CAC GA ACCCACC
A A _
GAM2300 KIAA0616 3' CGTCCACCCACCCGCCCG 47314 T T_
CG GC GTGGGTGGACG
|| || |||||
GC CG CACCCACCTGC
C CC
GAM2300 KIAA0978 3' CCACCTGTCACAGCAATAC 70992 CG ____
GTA TGCTGTG GGTGG
||| ||||| |||||
CAT ACGACAC CCACC
A_ TGT
GAM2300 NEDD5 3' CCATCCACATTTTAACAGTAC 16602 _ GC____
GTAC GT TGTGGGTGG
|||| || |||||
CATG CA ACACCTACC
A ATTTT
GAM2300 SCMH1 3' TCGCCCCACAGCTCGTAC 25285 T TG
GTACG GCTGTGGG GA
|||| ||||| ||
CATGC CGACACCC CT
T CG
GAM2300 LOC146224 5' CCAAGACACAGACACGTACT 78202 _ GG_
AGTACGTG CTGTG TGG
||||| |||| |||
TCATGCAC GACAC ACC
A AGA
GAM2300 LOC153163 3' TCATCCACCCACATATCCAATT 81655 AC C C
AAGT GTG TGTGGGTGGA GA
|||| ||| ||||| ||

TTCA TAT ACACCCACCT CT
 CC _ A
 GAM2300 LOC219793 3' CCACCTTCACAGCAGTAC 93019 G _
 GTAC TGCTGTG GGTGG
 ||| ||||| ||||
 CATG ACGACAC CCACC
 _ TT
 GAM2300 LOC222008 5' CCATCCACTCGCACGCCTT 95657 TA T_
 AAG CGTGC GTGGGTGG
 || |||| |||||
 TTC GCACG CACCTACC
 C_ CT
 GAM2300 LOC257428 3' GTCATCCACGCCTCACAC 95934 C T _ C
 GTG TG GG GTGGA GAC
 || || ||||| ||
 CAC AC CC CACCT CTG
 _ T G A
 GAM2301 ABCB8 3' GCAATCCCTCCCTCCCCTCC 24204 A_ CAGA
 GGA GGAGGGAGGG GC
 || ||||| ||
 CCT CCTCCCTCCC CG
 CC TAAC
 GAM2301 ABR 5' GCCCGCCCTCCCTCCTTT 42004 A A
 GAAGGA GGAGGG GGGC
 |||| ||||| ||
 TTTCCT CCTCCC CCG
 C G
 GAM2301 ABR 5' GCTCCCGCCCGCCCTCCCTCCT 42005 A A A_
 AGGA GGAGGG GGGC GAGC
 ||| ||||| ||| ||
 TCCT CCTCCC CCG CTCG
 C G CC
 GAM2301 ACP2 3' CTCAGCCCCCTTCCCTCC 9653 A A A
 GGA GGAGGG GGGC GAG
 || ||||| ||| ||
 CCT CCTTCC CCG CTC
 C _ A
 GAM2301 ADCY8 5' TGACCCCTCCTCCTCCT 8505 A A A G
 AG AGGA GGAGGG GG CA
 || |||| ||||| ||
 TC TCCT CCTCCC CC GT
 C _ _ A
 GAM2301 ADRA1A 3' CCCACCCCACTTCCTTCT 53950 GA A
 AGAAGGAAG GGG GGG
 ||||| ||| ||
 TCTTCCTTC CCC CCC
 AC A
 GAM2301 ADRA2A 3' GCCTGCCTGCCCTCCCCATC 7293 A AA A A
 GA GG GGAGGG GGGCAG GC
 || || ||||| ||||| ||

CT CC CCTCCC TCCGTC CG
 A _ G C
 GAM2301 AK1 3' GCCCCTCAACCCTCCGTTCTC 6639 A _ A____
 CT AG AGGAA GGAGGG GGGC
 || |||| |||| ||||
 TC TCCTT CCTCCC CCGG
 C G AACTC
 GAM2301 ALMS1 5' GCTCTCCCCTTCCCCTCCCTCC 31364 A _ C
 GGA GGAGGG AGGG AGAGC
 || |||| |||| ||||
 CCT CCTCCC TCCC TCTCG
 C CT C
 GAM2301 ALOX15 3' GCCCTGCCCTCCCAAGTCCCAC 8548 AA _ A
 C GG GGA GGGAGGGCAG GC
 || || |||| |||| ||
 CC CCT CCCTCCCGTC CG
 AC GAA C
 GAM2301 ANG 3' GCTCTGCTGTCCTTGCCCTTCC 8558 _ G
 GGAAGG AGGGA GGCAGAGC
 |||| |||| |||| ||||
 CCTTCC TTCCT TCGTCTCG
 G G
 GAM2301 ANGPT4 3' CTCTTCTCTCCCTCCCCCT 32571 AA C
 AGG GGAGGGAGGG AGAG
 || |||| |||| ||||
 TCC CCTCCCTCTC TCTC
 C_ T
 GAM2301 AP2B1 3' GCCCTGCATCCCCCCTCCTCT 8892 A A A GG A
 AGA GGA GG GGGA GCAG GC
 || || || |||| |||| ||
 TCT CCT CC CCCT CGTC CG
 _ C _ A_ C
 GAM2301 ARF3 3' CTGCCCCAGTCCTACCCCT 9775 AA A _
 AGG GG GGGA GGGCAG
 || || |||| |||| ||
 TCC CC TCCT CCGTC
 _ A GAC
 GAM2301 ARHGDIB 3' CTGTCCCTCCTCCCTGTCC 8614 _ AG _
 GGA AGG GGAGGG CAG
 || || |||| |||| ||
 CCT TCC CCTCCC GTC
 G CT T
 GAM2301 ARHGEF1 3' GCCATCTCTCCCTCCTGCCCTC 17480 A A _
 T AGA GG AGGAGGGAG GGC
 || || |||| |||| ||
 TCT CC TCCTCCCTC CCG
 C G TCTA
 GAM2301 ARIH1 5' CTCGCTCCCTCCCTCCCTCCT 20430 A CA_
 AGGA GGAGGGAGGG GAG
 |||| |||| |||| ||||

			TCCT CCTCCCTCCC CTC		
			C TCG		
GAM2301	ARIH1	5'	GCTCCCTCCCTCCCTCCTCC 20431	A	CA_
			GGA GGAGGGAGGG GAGC		
			CCT CCTCCCTCCC CTCG		
			_ TCC		
GAM2301	ASH1	3'	CTGCCCCCTCCCTACCTCT 38087	A A	AG A
			AGA GG AGG GG GGGCAG		
			TCT CC TCC CC CCCGTC		
			_ A CT _		
GAM2301	ASIC4	3'	GCCCCACCCCTAGAGTCCCTTC 38536	A_____	A GA
	T		AGAAGG AGG GG GGGC		
			TCTTCC TCC CC CCCG		
			CTGAGA _ AC		
GAM2301	ATF7	3'	CTCCTCCCCTCCCTCCTTCT 23400		CA_
			GGAAGGAGGGAGGG GAG		
			TCTTCCTCCCTCCC CTC		
			CTC		
GAM2301	ATP1B2	3'	CTGCCTGATCCCTCCCTC 9833	A	_
			GA GGAGGGA GGGCAG		
			CT CCTCCCT TCCGTC		
			C AG		
GAM2301	ATP1B2	3'	GCACTCCCTCCTTCCATTC 9836	_	G
			GAA GGAAGGAGGGAG GC		
			CTT CCTTCCTCCCTC CG		
			A A		
GAM2301	ATP2A3	3'	GCCTCACCCCTCCTCCCTCT 18978	A A	A_
			AGA GGA GGAGGG GGGC		
			TCT CCT CCTCCC TCCG		
			C _ CAC		
GAM2301	AXUD1	3'	CTGCCCCCTCCACTTCCT 53442	GA	A
			AGGAAG GGG GGGCAG		
			TCCTTC CTC CCCGTC		
			AC C		
GAM2301	BACE	3'	GCCCCCTCCTCACCCCTTC 58087	A_	AG
			GAAGG AGGAGGG GGC		
			CTTCC TCCTCCC CCG		
			CCAC _		
GAM2301	BAI2	5'	CTCCGCCCTTTCTCTCCCTCT 9912	A AG	A A
			AGA GGA GAGGG GGGC GAG		

			TCT CCT CTTTC CCCG CTC		
			C CT _ C		
GAM2301	BAK1	3'	CTCTACCCCTGCTCCCATTCCT 93627	_ AG G C_	
			AGGAA GG G AGGG AGAG		
			TCCTT CC C TCCC TCTC		
			A CT G CA		
GAM2301	BAK1	3'	CTCTGTTCCCCCACCTCC 93628	A A A	
			GGA GG GGG GGGCAGAG		
			CCT CC CCC CTTGTCTC		
			C A C		
GAM2301	BAK1	5'	GCCCTGCCCTCTGCTTCT 93631	GAA _	
			AGAAG GGAGGG AGGGC		
			TCTTC TCTCCC TCCCG		
			G_ G		
GAM2301	BAZ1B	5'	GCCCTCTCACCCCTCCCTTC 51560	A A_	
			GAAGG AGG GGGAGGGC		
			CTTCC TCC CTCTCCCG		
			C CCA		
GAM2301	BCL10	5'	GCTCCGCCTCCTCTCCTTCTTC 15370	G AG A	
			GAAG AAGGAGGG GGC GAGC		
			CTTC TTCCTCTC CCG CTCG		
			_ CT C		
GAM2301	BCL2	3'	GCCCTCCTGCCCTCCTTC 7236	A A	
			GAAGGA GG GGGAGGGC		
			CTTCCT CC TCCTCCCG		
			C G		
GAM2301	BCL2L2	5'	GCTCCCTCTCTCCCTCCCTCC 15760	A CA_	
			GGA GGAGGGAGGG GAGC		
			CCT CCTCCCTCTC CTCG		
			C TCC		
GAM2301	BMP1	3'	CTTAGCTCCCCCACTCCTCC 21531	A _ A _ A	
			GGA GGAG GG GG GC GAG		
			CCT CCTC CC CC CG TTC		
			_ A C T A		
GAM2301	BN51T	3'	GCTGGTGCTCCCCCGTCCTCC 88879	A A A G AG	
	T		AG AGGA GG GGGAG GC AGC		
			TC TCCT CC CCCTC TG TCG		
			C G C G G_		
GAM2301	BSN	3'	CTTTCCCTTCCTCCTCC 14384	A C	
			GGA GGAGGGAGGG AGAG		

CCT CTCCTTCCC TTTC
 C
 GAM2301 BTG2 3' CTCCCCTCCCCCTTCCCTTCT 23146 _ A C
 AGAAGG AAGG GGGAGGG AG
 ||||| ||| ||||| ||
 TCTTCC TTCC CCCTCCC TC
 C _ C
 GAM2301 BTRC 3' CTCCCCTCCTCTCCTCCT 54432 A _ C
 AGGA GGAG GGAGGG AG
 ||| ||| ||||| ||
 TCCT CCTC CCTCCC TC
 _ T C
 GAM2301 C4orf1 3' CTCTACAAAGTTTCCTCCTCTC 60226 _ GGC____
 CT AGGA AGGAGGGAG AGAG
 ||| ||||| ||| |||
 TCCT TCCTCCTTT TCTC
 C GAAACA
 GAM2301 CA14 5' CTCCTCCCTCCCTCTCTCT 25059 AG CA
 GGA GAGGGAGGG GAG
 ||| ||||| |||
 TCT CTCCCTCCC CTC
 CT TC
 GAM2301 CACNA1A 5' CCCTCCTTCCGCCCTCCTTCT 43783 A____
 AGAAGGA GGAGGGAGGG
 ||||| |||||
 TCTTCCT CCTTCCTCCC
 CCCCG
 GAM2301 CACNA1B 3' GCCCTCCCTCCCCCTCCT 7392 A__ _
 AGGA GGAGGGAGGG C
 ||| ||||| |||
 TCCT CCTCCCTCCC G
 CCC C
 GAM2301 CACNA1B 3' GCTCCTGTGGCCCCTCCCTCCC 7393 AA ____ _
 CCT AGG GGAGGGAGGG CAG AGC
 ||| ||||| ||| |||
 TCC CCTCCCTCCC GTC TCG
 C_ CGGT C
 GAM2301 CACNB1 3' CTGCCCTCCCTTCCCCCCTC 7408 A AA
 GA GG GGAGGGAGGGCAG
 || || |||||
 CT CC CTTCCCTCCCGTC
 C CC
 GAM2301 CACNB1 3' GCCCTCCCTTCCCCCCTC 7410 A AA
 GA GG GGAGGGAGGGC
 || || |||||
 CT CC CTTCCCTCCCG
 C CC
 GAM2301 CACNG6 5' GCTCTGCCTCCTCCCCCTTCC 49949 A ____
 GGAAGG GGGAGG GCAGAGC
 ||||| ||||| |||||

			CCTTCC CCCTCC CGTCTCG		
			— TC		
GAM2301	CACNG7	3'	GCTTTAGGCCCCGCCCTCCTCC 49942	A	A_ _
			GGA GGAGGG GGGC AGAGC		
			CCT CCTCCC CCCG TTTCG		
			— GC GA		
GAM2301	CAPN1	3'	GCCTTCCCTCCTTCGCTCCT 19010	A	_
			AG AG GAAGGAGGGAGGGC		
			TC TC CTTCTCCCTTCCG		
			C G		
GAM2301	CARP	5'	GCTTGTCCCTCCCCTCCCTCT 27668	A	_ CA
			GGA GGAGGG AGGG GAGC		
			TCT CCTCCC TCCC TTTCG		
			C C TG		
GAM2301	CASR	3'	GCCCCAGACTCCTTTCCTCT 6362	A	GGA_
			AGA GGAAGGAG GGGC		
			TCT CTTTCCTC CCCG		
			C AGAC		
GAM2301	CBFA2T3	3'	GCCCTGCCCACCCTCCCTCC 19018	A	A A
			GGA GGAGGG GGGCAG GC		
			CCT CCTCCC CCCGTC CG		
			C A C		
GAM2301	CCKBR	3'	GCCCTGCCCTCTCCTTCCTT 7416	GG	A
			AAGGAAGGA GAGGGCAG GC		
			TTCTTCCT CTCCCGTC CG		
			— C		
GAM2301	CD34	3'	CTGAGCCCCTTCCTTGCT 10107	G	A G_
			AG AAGGAGGG GG CAG		
			TC TTCCTTCC CC GTC		
			G _ GA		
GAM2301	CD34	3'	CTTCCCCTACCCCTCCT 10108	A A	_ CA
			AGGA GG GGG AGGG GAG		
			TCCT CC CCC TCCC TTC		
			— _ A C_		
GAM2301	CD3E	3'	CTGTGCTCCTCCCTCCCCC 7419	AA	_ G
			GG GGAGGGAGG GCA AG		
			CC CCTCCCTCC CGT TC		
			C_ T G		
GAM2301	CD3E	3'	GCTCCCTCCTCCCTGCCTTCT 7420	_	CA
			GGAAGG AGGGAGGG GAGC		

			TCTTCC TCCCTCCT CTCG			
			G CC			
GAM2301	CD97	3'	CTCTACTCCCTCCACCCTCC 55304	A AG	C__	
			GGA GG GGAGGG AGAG			
			CCT CC CCTCCC TCTC			
			_ CA TCA			
GAM2301	CDA	3'	GCCCCACCTTTCCTTTCCTTC 10129	__	GA	
			GAAGGAAGG AGG GGGC			
			CTTCCTTTC TCC CCCG			
			CTT AC			
GAM2301	CDC25B	5'	GCTCTTCCTCCCTCCCTCCTTC 41854	A	C	
			GAAGGA GGAGGGAGGG AGAGC			
			CTTCCT CCTCCCTCCT TCTCG			
			C _			
GAM2301	CEACAM1	3'	CTTCCCTCCCTTCCCT 9929	AA	CA	
			AGG GGAGGGAGGG GAG			
			TCC CTTCCTCCC TTC			
			C_ C_			
GAM2301	CEBPA	3'	GCTCCGCGTGTCCCCTCCCTTC 16429	A	AG A	__
	CTCT		AGA GGAAGG GG GGGCA GAGC			
			TCT CCTTCC CC CCTGT CTCG			
			_ CT _ GCGC			
GAM2301	CEP2	5'	GCTCTGCCGCCCCCCCCGCCCT 23246	AA_ A	AG	
			AGG GG GGG GGCAGAGC			
			TCC CC CCC CCGTCTCG			
			CCG C CG			
GAM2301	CHST1	3'	GCTCACCCCACTCCCTTCT 14701	A GA	A	
			AGAAGG AG GGG GGGC			
			TCTTCC TC CCC CTCG			
			C AC A			
GAM2301	CIAO1	5'	CTCTGCCCGCCCCCACCTCC 72944	A__ A	A	
			GGA GG GGG GGGCAGAG			
			CCT CC CCC CCGTCTC			
			CCA _ G			
GAM2301	CIAO1	5'	CTCTGCCCGCCCCCACCTCC 17835	A__ A	A	
			GGA GG GGG GGGCAGAG			
			CCT CC CCC CCGTCTC			
			CCA _ G			
GAM2301	CLK2	3'	GCCAGAGTTCACTCCTTCCTCC 61022	A	G	__
	T		AG AGGAAGGAG GAG GGC			

			TC TCCTTCCTC CTT CCG			
			C A GAGA			
GAM2301	CLK2	3'	GCCAGAGTTCACTCCTTCCTCC 61023	A	G	_____
	T		AG AGGAAGGAG GAG GGC			
			TC TCCTTCCTC CTT CCG			
			C A GAGA			
GAM2301	COL11A1	5'	TTTTTCCCCCTCTCCCTCC 10256	A	A	C
			GGA GGAGGG GGG AGAG			
			CCT CCTCTC CCC TTTT			
			C C T			
GAM2301	COL1A1	3'	CCTCCCCTCCACTCCTTCC 5393	_	C	A
			GGAAGGAG GGAGGG AG G			
			CCTTCCTC CCTCCC TC C			
			A C			
GAM2301	COL4A6	3'	CTCTGCCCCCTTGCCCTCCCCT 54439	AA	A	_____
			AGG GGAGGG GGGCAGAG			
			TCC CCTCCC CCCGTCTC			
			_ GTTC			
GAM2301	COL5A3	3'	GCTCTTTCTCCCCTCCCTCCCC 32319	AA	C	_____
			GG GGAGGGAGGG AGAGC			
			CC CCTCCCTCCC TCTCG			
			_ CTCTT			
GAM2301	COL6A1	3'	CTGCCCGCCCTCCCTCCT 10247	A	A	
			AGGA GGAGGG GGGCAG			
			TCCT CCTCCC CCCGTC			
			C G			
GAM2301	COL6A1	3'	CTGTCCTCCCACCCCTCC 10248	A_	A	
			GGA GG GGGAGGGCAG			
			CCT CC CCCTCCTGTC			
			CC A			
GAM2301	CRABP2	3'	CTCCGTCCCACCCCTCCTTCT 10293	A	A	A _ A
			AGAAGGA GG GGG GGG C GAG			
			TCTTCCT CC CCC CCC G CTC			
			_ _ A T C			
GAM2301	CSK	5'	CTCCCTCCCGCCCCCTTC 16505	AA	A	C
			GAAGG GG GGGAGGG AG			
			CTTCC CC CCCTCCC TC			
			C_ G _			
GAM2301	CST1	3'	CGCTCTGCCCTCCCTCCTTCCT 10331			_____
	TCT		AGAAGGAAGGAGGGAGGGCAGAGC G			

TCTTCCTTCCTCCCTCCCGTCTCG C

GAM2301 CST2 3' GACTCTGCCCTCCCTCCTTCCT 8997 C__A
TTT AGAAGGAAGGAGGGAGGGCAGAG C
|||||
TCTTCCTTCCTCCCTCCCGTCTC G

A__
GAM2301 CST3 3' CGCTCTGCCCTCCCTCCTTCCT 5435 ____
TCT AGAAGGAAGGAGGGAGGGCAGAGC G
|||||
TCTTCCTTCCTCCCTCCCGTCTCG C

GAM2301 CST4 3' CGCTCTGCCCTCCCTCCTTCCT 10336 ____
TCT AGAAGGAAGGAGGGAGGGCAGAGC G
|||||
TCTTCCTTCCTCCCTCCCGTCTCG C

GAM2301 CUL3 3' CTAGGTCCTCCCTGCCCT 14571 AA _ AG
AGG GG AGGGAGGGC AG
||| || ||||| ||
TCC CC TCCCTCCTG TC
_ G GA

GAM2301 CXCL16 3' CTTTCCACCTCCCTCCT 42166 A A C
AGGA GGAGGG GGG AGAG
|||| ||||| ||| ||||
TCCT CCTCCC CCC TTTC
C A _

GAM2301 CYP27B1 3' GCTCTGTCTACCCCTTCCTTC 7605 A A
T AGAAGGAAGG GGG GGGCAGAGC
||||||| ||| |||||
TCTTCCTTCC CCC TCTGTCTCG

_ A
GAM2301 CYP2F1 3' GCCCTTCCCCCATCCCTC 7582 A A A
GA GGA GG GGGAGGGC
|| ||| || |||||
CT CCT CC CCTTCCCG
C A C

GAM2301 CYP4A11 5' GCCCTCCCCCTTCACTCT 7589 AG A
AGA GAAGG GGGAGGGC
||| ||||| |||||
TCT CTTCC CCCTCCCG
CA _

GAM2301 DACH 5' GCCCCCTCGCTCCTTCT 55823 AG A
AGAAGGA GAGGG GGGC
||||| ||||| |||||
TCTTCCT CTCCC CCG
CG _

GAM2301 DBN1 5' CTCTTTCCCTCCCTCCTCCT 56018 A C_
AGGA GGAGGGAGGG AGAG
||||| ||||| |||||

			TCCT CCTCCCTCCC TCTC		
			— TT		
GAM2301	DBN1	5'	GCGACTCCCTCTTTCCCTC 16558	A	G_
			GA GGAAGGAGGGAG GC		
			CT CCTTTCTCCCTC CG		
			C AG		
GAM2301	DDB1	3'	CTGCTGCCCTCCCCCTCCTCT 10398	A A A	—
			AGA GGA GG GGGAGGGCAG AG		
			TCT CCT CC CCCTCCCGTC TC		
			— — — G		
GAM2301	DDX11	3'	CTTCCCCTCCTCCTTCCT 16574	GA	C
			AGGAAGGAGG GGG AG		
			TCCTTCCTCC CCC TC		
			TC T		
GAM2301	DDX11	3'	CTTCCCCTCCTCCTTCCT 16575	GA	C
			AGGAAGGAGG GGG AG		
			TCCTTCCTCC CCC TC		
			TC T		
GAM2301	DIA1	3'	CCGTCCCCTCCTTCCTC 24649	A	_ G
			GA GGAAGGAGGG A GG		
			CT CCTTCCTCCC T CC		
			C C G		
GAM2301	DLX2	3'	GCCCCGCCGCTTCTTTCCTTC 16605	— —	A_
			GAAGGAAGGA G GG GGGC		
			CTTCCTTTCT C CC CCCG		
			T G GC		
GAM2301	DLX4	3'	GCCACTCCCCCACTCCTTCT 10420	A_ A	_
			AGAAGGA GG GGGAG GGC		
			TCTTCCT CC CCCTC CCG		
			CA _ A		
GAM2301	DUSP2	3'	TCCTCCCCCGCTTCCTCCT 16629	A	GA_
			AG AGGAAG GGGAGGG		
			TC TCCTTC CCCTCCT		
			C GCC		
GAM2301	DUSP4	5'	GCCCAGTCCCCCTCCCTTCT 55128	A A	__
			AGAAGG AGG GGGA GGGC		
			TCTTCC TCC CCCT CCCG		
			C _ GA		
GAM2301	DVL3	3'	GCCCTCCCTCTCCCCTCT 16647	A AA	
			AGA GG GGAGGGAGGGC		

			TCT CC TCTCCCTCCCG			
			_ CC			
GAM2301	DYRK1A	5'	CTCTTCCCTCCCTTCCCCC	56078	AA	C
			GG GGAGGGAGGG AGAG			
			CC CTTCCCTCCC TCTC			
			CC T			
GAM2301	DYRK1A	5'	CTCTTCCCTCCCTTCCCCC	56079	AA	C
			GG GGAGGGAGGG AGAG			
			CC CTTCCCTCCC TCTC			
			CC T			
GAM2301	DYRK1A	5'	CTCTTCCCTCCCTTCCCCC	9162	AA	C
			GG GGAGGGAGGG AGAG			
			CC CTTCCCTCCC TCTC			
			CC T			
GAM2301	DYRK1B	3'	CTTGGGCCCCTCTCCCCCT	17516	AA	A A_
			AGG GGAGGG GGGC GAG			
			TCC CCTCTC CCGG TTC			
			C_ _ GG			
GAM2301	E2F3	3'	CCCGTTCCCTTCCTCT	10466	A	A _
			AGA GGAAGG GGGA GGG			
			TCT CCTTCC CCTT CCC			
			_ _ G			
GAM2301	ED1	5'	GCCCCTCCTCCTCCCTTT	9168	A	GA
			GAAGG AGGAGG GGGC			
			TTTCC TCCTCC CCGG			
			C TC			
GAM2301	EFNB1	3'	GCCCTGCCCTCCCTCGCCCC	16670	AAG	_ A
			GG GAGGGAGGG CAG GC			
			CC CTCCTCCC GTC CG			
			CCG C C			
GAM2301	EIF4EBP1	3'	CTCCCTCCCCCTCCTTCC	15851	A	CA
			GGAAGGAGGG GGG GAG			
			CCTTCCTCCC CCT CTC			
			_ CC			
GAM2301	EIF4G2	5'	CTCCTTCCTCCCCCTTCCCTC	9217	A	A CA
			GA GGAAGG GGGAGGG GAG			
			CT CCTTCC CCCTCCT CTC			
			C _ TC			
GAM2301	ELAVL3	3'	GCCTGCCCTCCCACCCCT	9227	AA	A A
			AGG GG GGGAGGGCAG GC			

			TCC CC CCCTCCCGTC CG			
			C_ A _			
GAM2301	ELMO1	3'	CCCACATCCTCCTTTCCCCT	56154	AA	A__
			AG GGAAGGAGGG GGG			
			TC CTTTCCTCCT CCC			
			CC ACA			
GAM2301	EMX2	5'	CTCTCCCTCTCCCTCCCCCTC	88954	A AA	_ C
	CT		AG AGG GGAGGGAG GG AGAG			
			TC TCC CCTCCCTC CC TCTC			
			C CC T C			
GAM2301	EN2	3'	CTAACTCCCTCCTCCTTCT	9255	A	GGC
			AGAAGGA GGAGGGAG AG			
			TCTTCCT CCTCCCTC TC			
			_ AA_			
GAM2301	ENG	3'	CCTTCCCGCCTCCCTCT	5493	A A A	
			AGA GGA GG GGGAGGG			
			TCT CCT CC CCCTTCC			
			C _ G			
GAM2301	ENSA	5'	CCCTCCCCCTTCCCTTCT	16688	_ A	
			AGAAGG AAGG GGGAGGG			
			TCTTCC TTCC CCCTCCC			
			C _			
GAM2301	EPB41	3'	CTCTGCCCTTCTCCCATCC	16690	A AG	
			GGA GG GGAGGGCAGAG			
			CCT CC CTTCCCGTCTC			
			A CT			
GAM2301	EPHA8	3'	CTGAGCCCCCTCTCCCTCCT	40432	A A AG	
			AGGA GGAGGG GGGC AG			
			TCCT CCTCTC CCG TC			
			C C AG			
GAM2301	EPHB2	3'	CTCTTCCCTCCTCCACCT	34345	AA G C	
			AGG GGAGG AGGG AGAG			
			TCC CCTCC TCCC TCTC			
			AC _ T			
GAM2301	ERBB4	3'	GCTCCAATTTCCCCACCCCCCT	19110	A AA A_	GCA
	CT		AGA GG GG GGGAGG GAGC			
			TCT CC CC CCCTTT CTCG			
			_ CC AC AAC			
GAM2301	ESRRA	3'	GCCCTCTCCTCCCCCTCCT	16719	A_ _	
			AGGA GGAGG GAGGGC			

			TCCT CCTCC CTCCCG		
			CCC T		
GAM2301 EYA2	3'	CTCAGACCCCCTCGCCTTC	19123	AAG A GCA	
		GAAGG GAGGG GG GAG			
		CTTCC CTCCC CC CTC			
		G__ _ AGA			
GAM2301 FAAH	5'	GCTCCGCCCCCGCCGCCTCCT	9342	A__ A A A	
TCT		AGAAGGA GG GGG GGGC GAGC			
		TCTTCCT CC CCC CCCG CTCG			
		CCG G _ C			
GAM2301 FAAH	3'	CTCCCACCCCCTCCGTCCT	97237	A A GCA	
		AGGA GGAGGG GG GAG			
		TCCT CCTCCC CC CTC			
		G _ ACC			
GAM2301 FANCC	3'	GCCCATGCCCTTCCTTCCTTC	71044	A_____	
T		AGAAGGAAGGAGGG GGGC			
		TCTTCCTTCCTTCC CCCG			
		CCGTA			
GAM2301 FBXL11	3'	GCTCTCCCTCCTTTCCTCT	25516	A	
		AGA GGAAGGAGGGAGGGC			
		TCT CTTTCCTCCCTCTCG			
		C			
GAM2301 FCN2	3'	GCCCCCATTTCCTCCTTC	15918	A _ A	
		GAAGGA GGAG GG GGGC			
		CTTCCT CCTT CC CCCG			
		_ TA _			
GAM2301 FCN2	3'	GCCCCCATTTCCTCCTTC	32345	A _ A	
		GAAGGA GGAG GG GGGC			
		CTTCCT CCTT CC CCCG			
		_ TA _			
GAM2301 FGF12	3'	CTCTCCCCTTCTTCCCTCT	41061	A C	
		GGA GGAGGGAGGG AGAG			
		TCT CCTTCTTCCC TCTC			
		C C			
GAM2301 FGF4	5'	CTCTGCCCCCAGCTTCC	10625	GA A	
		GGAAG GGG GGGCAGAG			
		CCTTC CCC CCCGTCTC			
		GA _			
GAM2301 FKBP10	3'	CTTTGCCCTCCTCCCTCGCC	41937	A_ AG	
		GG AGG GGAGGGCAGAG			

			CC TCC CCTCCCGTTTC			
			GC CT			
GAM2301	FLNA	3'	GCCCCGCCCTCTTCCCCTC	9385	A A	A_
			GA GG AGGAGGG GGGC			
			CT CC TTCTCCC CCG			
			C C GC			
GAM2301	FOXF2	3'	CTCTCTCCTCTCCCCTCC	9373	A A	C
			GGA GG GGGAGGG AGAG			
			CCT CC CTCTCCT TCTC			
			C _ C			
GAM2301	FOXO1A	5'	CTCCGCCGCGCCTTCCTCC	10650	A	AG_ A
			GGA GGAGGG GGC GAG			
			CCT CCTTCC CCG CTC			
			_ GCG C			
GAM2301	FXR2	3'	GCTATCCCTCCTCCCATC	17960	A A	G
			GA GG AGGAGGGA GGC			
			CT CC TCCTCCCT TCG			
			A C A			
GAM2301	FXD6	3'	CCCTACCCCTTCCAACCTTC	42090	AA	___
			GAAGG GGAGGG AGGG			
			CTTCC CTTCC TCCC			
			AA CCA			
GAM2301	GABRE	5'	GCTCTTTAGCCTCCTTCCCTTC	18285	_	___
			GAAGG AAGGAGG GAGGGC			
			CTTCC TTCCTCC TTCTCG			
			C GAT			
GAM2301	GARP	3'	GCCTGTTTCCCTCCTCCCTTC	19782	A	G A
			GAAGG AGGAGGGAGG CAG GC			
			CTTCC TCCTCCCTTT GTC CG			
			C _ _			
GAM2301	GAS7	3'	CTCTTTCCCCCCTCATCC	20848	AG	A C_
			GGA GAGGG GGG AGAG			
			CCT CTCCC CCC TCTC			
			A_ _ TT			
GAM2301	GCDH	3'	GCCCTCCCTCCCTCCCATCT	26532	A_	A
			AGA GGA GGAGGGAGGGC			
			TCT CCT CCTCCCTCCCG			
			AC C			
GAM2301	GCDH	3'	GCCCTCCCTCCCTCCCATCT	5674	A_	A
			AGA GGA GGAGGGAGGGC			

TCT CCT CCTCCCTCCCG
 AC C
 GAM2301 GFRA2 3' CTGTCTTCTCCCTCCTCCTCCT 9463 A A ____
 AG AGGA GGAGGGAG GGCAG
 || ||| ||||| ||||
 TC TCCT CCTCCCTC CTGTC
 C _ TT
 GAM2301 GJB1 3' CCCTTCCCTCTTCCCTCT 60637 A GA
 AGA GGAAG GGGAGGG
 ||| ||| |||||
 TCT CCTTC CCTTCCC
 C TC
 GAM2301 GPR17 3' CTCCCAGCCTCCTTCCCGCT 19180 AA GA C
 AG GGAAGGAGG GGG AG
 || ||||| ||| ||
 TC CCTTCCTCC CCC TC
 GC GA _
 GAM2301 GRB14 5' GCTCTCGCGCCCTCCCCGCCCC 16894 AA A_ ____
 CT AGG GG GGGAGGGC AGAGC
 ||| || ||||| ||||
 TCC CC CCCTCCCG TCTCG
 C_ GC CGC
 GAM2301 GRB2 5' GCCCTCCTCCCTCCCTTC 10871 A AG
 GAAGG AGG GGAGGGC
 ||||| ||| |||||
 CTTCC TCC CCTCCCG
 C CT
 GAM2301 GRB2 5' GCTCAGCCCTCCTCCCTCCCT 10872 A AG A
 AGG AGG GGAGGGC GAGC
 ||| ||| ||||| ||||
 TCC TCC CCTCCCG CTCG
 C CT A
 GAM2301 HAMP 3' GCCCTGCCCCCGTCCCCTCCCT 41288 _ A____ A
 TCCT AGGAAGG AGGG GGGCAG GC
 ||||| ||| ||||| ||
 TCCTTC TCCC CCGTC CG
 C CTGCC C
 GAM2301 HAP1 3' GCCCAGCCCTCTCCCCTCT 15477 A AA A_
 AGA GG GGAGGG GGGC
 ||| || ||||| |||
 TCT CC TCTCCC CCCG
 _ CC CGA
 GAM2301 HAP1 3' TCCCCCCTCCCTGCCCT 15480 AA _ CA_
 AGG GG AGGAGGG GA
 ||| || ||||| ||
 TCC CC TCCCTCCC CT
 _ G CCC
 GAM2301 HCN4 3' GCTGGGCCCTTCCCTCCTCT 19684 A AA AG
 AGA GG GGAGGGAGGGC AGC
 ||| || ||||| |||

			TCT CC CTCCTTCCCG TCG		
			— — GG		
GAM2301 HD	3'	GCTTTGTCCCTCCCCCGTTCC 10917	GA_ _		
	T	AGGAAG GGGAGGG CAGAGC			
		TCCTTC CCCTCCC GTTTCG			
		GCC T			
GAM2301 HHIP	5'	GCCCCCTCCCCTTCCCTC 42755	A A A		
		GA GGAAGG GGG GGGC			
		CT CCTTCC CTC CCG			
		C C C			
GAM2301 HHLA1	5'	GCCCCACCCTTATCTCCCTTC 20336	A _ A_		
		GAAGG AG GAGGG GGGC			
		CTTCC TC TTCCC CCG			
		C TA AC			
GAM2301 HLF	3'	CCCTCCCTCCTTCACTCCT 10933	A _		
		AG AG GAAGGAGGGAGGG			
		TC TC CTCCTCCCTCCC			
		C A			
GAM2301 HMG20A	3'	GCTTCCCTTCCTTCCCCCT 37070	AA AG		
		AG GGAAGGAGGG GGC			
		TC CCTTCCTTCC TCG			
		CC CT			
GAM2301 HOXB6	5'	CTGAATACTCCTTCCTTCCT 60539	GG_		
		AGGAAGGAGGGAG CAG			
		TCCTTCCTTCCTC GTC			
		ATAA			
GAM2301 HOXC10	3'	GCCTCTCCTCCTCCCTTC 61929	A GA		
		GAAGG AGGAGG GGGC			
		CTTCC TCCTCC TCCG			
		C TC			
GAM2301 HOXC11	3'	CTCCCCACCCTGCTCCCTTC 60811	A G A CA		
		GAAGG AG AGGG GGG GAG			
		CTTCC TC TCCC CCC CTC			
		C G A _			
GAM2301 HOXC13	3'	GCCCCTTGCCCTTCCCTTC 60418	A G_		
		GAAGG AGGAGG A GGGC			
		CTTCC TTCTCC T CCG			
		C G TC			
GAM2301 HOXC4	5'	GCTCTTCCTCCTGCCCCCT 28248	AA A		
		AG GG AGGAGGGAGGGC			

			TC CC TCCTCCTTCTCG			
			CC G			
GAM2301	HPCA	3'	GTTCCCTTCCTCCCTCC	10952	A	CA
			GGA GGAGGGAGGG GAGC			
			CCT CCTCCTTCCC CTTG			
			C			
GAM2301	HRB	5'	CCTGCCGGCCTCCTCCCT	16913	A	GAG A
			AGG AGGAGG GGCAG G			
			TCC TCCTCC CCGTC C			
			C GG_			
GAM2301	HRMT1L2	3'	GCTCCCCCTTCCTCTCCCTCCC	9517	A A	_ CA
	TC		GA GGA GGAG GGAGGG GAGC			
			CT CCT CTC CTTCC CTCG			
			C C T CC			
GAM2301	HYOU1	3'	CTCCCTGCCTCCTCCTCTCT	60385	_ A	G C
			AGA AGGA GGAGG AGGG AG			
			TCT TCCT CCTCC TCCC TC			
			C _ G _			
GAM2301	IFITM2	5'	GCCCTCAGCCCCTCTTTCCT	22235		_____
			AGGAAGGAGGG AGGGC			
			TCCTTTCTCCC TCCCG			
			CGAC			
GAM2301	IFRD2	3'	GCCCTGTGGCCCTTCCTGTC	23151	_ A G	_____
			GA AGGAAGG GG AGGGC			
			CT TCCTTCC CC TCCCG			
			G _ GGTG			
GAM2301	IGF2	5'	GCCTCCGACTCCCTCCCCCCT	7036	A AA	_____
	C		GA GG GGAGGGAG GGC			
			CT CC CCTCCCTC CCG			
			C CC AGCCT			
GAM2301	IKBKG	3'	CTATCCCTCCCTCTTCCT	14665	G	CAG
			AGGAAG AGGGAGGG AG			
			TCCTTC TCCCTCCC TC			
			_ TAA			
GAM2301	IL13RA1	3'	GCATTCTCCCTCCTTCCCTTC	9571	-	_____
			GAAGG AAGGAGGGAGG GC			
			CTTCC TTCCTCCCTCT CG			
			C TA			
GAM2301	IL1RL1	3'	GTCCTCCCCCACTCCCTCCT	15254	A	_____
			AGGA GGA GGGAGGGC			

			TCCT CCT CCCTCCTG			
			C CACC			
GAM2301	IL2RB	3'	GCCCCAGCCTCCTCCTTC	7941	A	GA_
			GAAGGA GGAGG GGGC			
			CTTCCT CCTCC CCCG			
			_ GAC			
GAM2301	INSR	3'	GCTCATCCCCCTCTCTCCTTCC	71540		CA_
		TTCT	AGAAGGAAGGAGGGAGGG		GAGC	
			TCTTCCTTCCTCTCTCCC		CTCG	
			CCTA			
GAM2301	JAG1	5'	CCCTCCCTCCCCCCTTTT	5811	AA	
			AGAAGG GGAGGGAGGG			
			TTTTCC CCTCCCTCCC			
			CC			
GAM2301	JPH2	3'	GCCCTGCCCTCCACACCCTC	96084	A AA_	_
			GA GG GGAGGG AGGGC			
			CT CC CCTCCC TCCCG			
			C ACA G			
GAM2301	KCNA5	3'	CTCCTTTCCTCCCTCCCTC	60433	A A	C
			GA GGA GGAGGGAGGG AG			
			CT CCT CCTCCTTTCC TC			
			C C _			
GAM2301	KCNC3	5'	GCCCCGCCCTCCTCCCTGCT	18332	A A	A_
			AG AGG AGGAGGG GGGC			
			TC TCC TCCTCCC CCCG			
			G C CGC			
GAM2301	KCND3	3'	CCACTCCCTCCCCCCTTT	18351	AA	_
			GAAGG GGAGGGAG GG			
			TTTCC CCTCCCTC CC			
			CC A			
GAM2301	KCND3	3'	CTGAGACCACTCCCTCCCCC	18354	AA	_ _
			GG GGAGGGAG GG CAG			
			CC CCTCCCTC CC GTC			
			CC A AGA			
GAM2301	KCNJ5	3'	TTGTCCCCTCATTCCTTC	7981	G	AG
			GAAGGAA GAGGG GGCAG			
			CTTCCTT CTCCC CTGTT			
			A _			
GAM2301	KCNK3	3'	GCCCCACTCCCCTTCCTC	11176	A	A A_
			GA GGAAGG GGG GGGC			

			CT CCTTCC CTC CCCG			
			— C AC			
GAM2301	KCNK4	3'	CTGCCCCGCCCCCTTCCT	33983	A A_	
			AGGAAGG GGG GGGCAG			
			TCCTTCC CCC CCCGTC			
			— GC			
GAM2301	KIAA0442	5'	GCTCCCCGTCCCTCCTCCCCTC	32096	A A	_ CA
	T		AGA GG AGGAGGGA GGG GAGC			
			TCT CC TCCTCCCT CCC CTCG			
			C C G —			
GAM2301	LAD1	3'	GCTTGGTTCTCCCCTCCCTTCC	19902	A_	A
			GGAAGG GGGAGGGC GAGC			
			CCTTCC CCCTCTTG TTCG			
			CTC G			
GAM2301	LAMC1	3'	GCCACACACCCCCTTCCTCCT	11267	A	A AG_
			AG AGGAAGG GGG GGC			
			TC TCCTTCC CCC CCG			
			C _ ACACA			
GAM2301	LASS2	3'	GCCTCTTCCCCCTTCCTCT	68308	A	A _
			AGA GGAAGG GGGAG GGC			
			TCT CCTTCC CCTTC CCG			
			C C T			
GAM2301	LDB1	3'	GCTCTGGGCCCTCCTCCCTGC	15311	A A	AGGG
	T		AG AGG AGGAGGG CAGAGC			
			TC TCC TCCTCCC GTCTCG			
			G C CGG_			
GAM2301	LDOC1	3'	GCTCTCCCCCTTGCCCTC	25548	A _	A
			GA GG AAGG GGGAGGGC			
			CT CC TTCC CCCTCTCG			
			C G _			
GAM2301	LPL	3'	GCTTAATCCCTCTCTCCCCCT	5882	AA	CA_
			AGG GGAGGGAGGG GAGC			
			TCC CCTCTCTCCC TTCG			
			C_ TAA			
GAM2301	LU	3'	GCCCGCCCCCGCCTTCCCTCT	19945	A	A_ A_
			AGA GGAAGG GGG GGGC			
			TCT CCTTCC CCC CCCG			
			C GC CG			
GAM2301	LU	3'	GCCTTCCCTCTTCCCTCT	19946	A	G
			AGA GGAAG AGGGAGGGC			

			TCT CCTTC TCCCTTCCG			
			C _			
GAM2301	LY9	3'	GCCCTCCCCCTCCTTCT	72146	A A	_
			AGAAGGA GG GGGAGGG C			
			TCTTCCT CC CCCTCCC G			
			_ _ C			
GAM2301	MAF	5'	CTCCCCCCTCCCTCTCCTCC	19310	A_	CA
			GGA GGAGGGAGGG GAG			
			CCT TCTCCCTCCC CTC			
			CC CC			
GAM2301	MAG	3'	GCCTGACCTCCCCCTCCTTC	11423	A A	G A
			GAAGGA GG GGGAGG CAG GC			
			CTTCCT CC CCCTCC GTC CG			
			_ _ A _			
GAM2301	MAG	3'	GCCTGACCTCCCCCTCCTTC	11424	A A	G A
			GAAGGA GG GGGAGG CAG GC			
			CTTCCT CC CCCTCC GTC CG			
			_ _ A _			
GAM2301	MAPK10	5'	CTCTTCTACTCCTTCCCCCCTT	58097	AA	_ C
	CT		AGAAGG GGAGGGAG GG AGAG			
			TCTTCC CCTTCCTC TC TCTC			
			CC A T			
GAM2301	MARK1	5'	CTCCGCGTCCTCTTCCCTCT	38470	A AG	A_
			GGA GG GGAGGGC GAG			
			TCT CC TCTCCTG CTC			
			_ CT CGC			
GAM2301	MASP1	3'	GCCCTGGCCTCCTTCCCTTCT	58214	_	G_
			AGAAGG AAGGAGG AGGGC			
			TCTTCC TTCCTCC TCCCG			
			C GG			
GAM2301	MAT1A	3'	CTCCCCCTCCCTCCCCTT	92498	AA	CA
			AAGG GGAGGGAGGG GAG			
			TTCC CCTCCCTCCC CTC			
			_ C_			
GAM2301	MDM2	3'	GCTCTGCCCTCCCCGGGTTC	11495	AGGA	
			GGA GGGAGGGCAGAGC			
			CTT CCCTCCCGTCTCG			
			GGGC			
GAM2301	MFGE8	3'	TCACCCCTCCCTCCCTCT	21009	A	CA
			GGA GGAGGGAGGG GA			

			TCT CCTCCCTCCC CT			
			C CA			
GAM2301	MGAM	3'	CTCCACATTTCCCTCTTCT 72810	G	GCA_	
			GGAAG AGGGAGG GAG			
			TCTTC TCCCTTT CTC			
			_ ACAC			
GAM2301	MGAT1	3'	GCCCTGACCCCTCCTTTCT 11554		___	
			AGGAAGGAGGG AGGGC			
			TCTTTCCTCCC TCCCG			
			CAG			
GAM2301	MMP2	3'	CTCAGCCCTCCCTGCCCT 16965	AA _	A	
			AGG GG AGGGAGGGC GAG			
			TCC CC TCCCTCCCG CTC			
			_ G A			
GAM2301	MN1	3'	CTCTTTCCCTCCCTTCTCCCC 11652	A A	C__	
	TCT		AGA GG AGGAGGGAGGG AGAG			
			TCT CC TCTTCCCTCCC TCTC			
			C C CTT			
GAM2301	MPP2	3'	CTCTGTTCTCCCTCCCTGCC 60518	AA_		
			GG GGAGGGAGGGCAGAG			
			CC CCTCCCTCTTGTCTC			
			GTC			
GAM2301	MPZ	3'	GCCTGCCCTGCCCTCACCTCC 6751	AG_ _	A	
			GGA GAGGG AGGGCAG GC			
			CCT CTCCC TCCCGTC CG			
			CCA G C			
GAM2301	MSI1	3'	CTCTGGTCCATCCCTCCCTCC 11699	A _ _		
			GGA GGAGGGA GGGC AGAG			
			CCT CCTCCCT CCTG TCTC			
			C A G			
GAM2301	MTA1L1	3'	GCTCTTTCCTTCCCTCCCCTCC 17634	A_	C_	
			GGA GGAGGGAGGG AGAGC			
			CCT CCTCCCTTCC TCTCG			
			CC TT			
GAM2301	MTMR3	3'	GCCCTGCCCTGTATTCCTCTTC 41163	G ____	A	
	C		GGAAG AGGG AGGGCAG GC			
			CCTTC TCCT TCCCGTC CG			
			_ TATG C			
GAM2301	MUC3B	3'	GCCCTAAATCCTCCCTCCTCTC 95924	_	C__ A	
	C		GGA AGGAGGGAGGG AG GC			

CCT TCCTCCCTCCT TC CG
 C AAA C
 GAM2301 MUC4 5' GCCCCGCCCTCTTTTGTCTCT 37880 _____ A_
 TC GAAG GAAGGAGGG GGGC
 ||| ||||| |||
 CTTC TTTTCTCCC CCG
 TCCTG GC
 GAM2301 MX1 3' GCTCCACCTTGCAGCTCTCCCC 11722 AA _____ CA
 TTCT AGAAGG GGAGGG AGGG GAGC
 ||||| ||||| ||| |||
 TCTTCC CCTCTC TTCC CTCG
 — GACG AC
 GAM2301 MYD88 3' CTCTCCCTCTCTCCTTCC 11731 C
 GGAAGGAGGGAGGG AGAG
 ||||| ||||| |||
 CCTTCCTCTCTCCC TCTC
 —
 GAM2301 MYEOV 3' CCCTCTCCTCTTCCTTCT 57845 GA
 AGAAGGAAG GGGAGGG
 ||||| |||||
 TCTTCCTTC CTCTCCC
 TC
 GAM2301 NAGA 3' GCTCCACCCCAACCCCTACTTC 6038 GA A GA CA_
 T AGAAG AGG GG GGG GAGC
 |||| ||| || ||| |||
 TCTTC TCC CC CCC CTCG
 A_ _ AA CAC
 GAM2301 NCOR2 3' GCTGTGTCTCCTCCCTCCCTCCCT 21960 AA_ G
 TC GAAGG GGAGGGAGGGCA AGC
 |||| | ||||| |||
 CTTCC CCTCCCTCCTGT TCG
 CTC G
 GAM2301 NESH 5' GCCCTTTCTCCCGCCTTC 33571 AA _
 GAAGG GGAGGGA GGGC
 |||| | ||||| |||
 CTTCC CTTCTT CCG
 GC T
 GAM2301 NEUD4 3' CTCTCCCTCCCTCCCTCCCTCT 17378 A A C
 AGA GGA GGAGGGAGGG AGAG
 ||| ||| ||||| |||
 TCT CCT CCTCCCTCCC TCTC
 C C _
 GAM2301 NEUROD2 3' GTTTCCTCCTCCCCCTCCT 21595 A A CA
 AGGA GG GGGAGGG GAGC
 |||| || ||||| |||
 TCCT CC CCCTCCT TTTG
 _ _ CC
 GAM2301 NF1 5' GCCCCCTTTCCCTCTCCCCCTC 6047 A AA _____
 GA GG GGAGGGA GGGC
 || || ||||| |||

			CT CC TCTCCCT CCG			
			C CC TTCC			
GAM2301	NGFR	3'	CCTCCCCTCCTTGCTCCT	11791	A _	AG
			AG AGG AAGGAGGG GG			
			TC TCC TTCCTCCC CC			
			C G CT			
GAM2301	NKX2H	5'	GCCCTGCCCGCGCTCCTTCC	27632	GA_	A
			GGAAGGAGG GGGCAG GC			
			CCTTCCTCC CCGTC CG			
			GCC C			
GAM2301	NOS1	3'	CTCTGTTCCCACTCCCTCT	7094	A _ A	
			GGA GGAG GG GGGCAGAG			
			TCT CCTC CC CTTGTCTC			
			C A _			
GAM2301	NPEPPS	5'	GCCCTCCGCTCCTCCCCTC	63785	A A	__
			GA GG AGGAGG GAGGGC			
			CT CC TCCTCC CTCCCG			
			C C GC			
GAM2301	NPEPPS	5'	GCCTCCTCCCCTCCTCCTTCT	63786	A	AG C A
			AGAAGGA GGAGGG GG AG GC			
			TCTTCCT CCTCCC CC TC CG			
			_ CT _ _			
GAM2301	NPTX1	3'	GCCCTGCCCTCGACCTTCC	11835	AGG	A
			GGAAGG GAGGGCAG GC			
			CCTTCC CTCCCGTC CG			
			AG_ C			
GAM2301	NPTX1	3'	GCTCAGTTTCCCTCTCCCCCTC	11837	A A	CA__
	C		GGA GG GGGAGGG GAGC			
			CCT CC CTCTCCC CTCG			
			C C TTTGA			
GAM2301	Nrap	3'	GCTCTGTCTCCTTCCTGCT	56309	A	G
			AG AGGAAGGAGG AGGGC			
			TC TCCTTCCTCT TCTCG			
			G G			
GAM2301	NRCAM	3'	TTCCCCCTCCCCCACCT	18457	AA A	CA
			AGG GG GGGAGGG GAG			
			TCC CC CCCTCCC CTT			
			AC _ CC			
GAM2301	NRGN	3'	GCCCTGTCGGTCCCGCCCTCCC	21625	AA	A ____ A
	CCC		GG GGAGGG GGG CAG GC			

			CC CCTCCC CCC GTC CG		
			CC G TGGCT C		
GAM2301 NRXN2	3'	CTGTCCCCACCCTCCTTCC	57819	A__	
		GGAAGGAGGG GGGCAG			
		CCTTCCTCCC CCTGTC			
		ACC			
GAM2301 NTRK3	3'	CTCTGTTGCCTCCTCTCTCC	11850	A GA _	
		GGA G GGGAGG GCAGAG			
		CCT C TCCTCC TGTCTC			
		_TC GT			
GAM2301 NXF5	3'	GCTCTGAGCCCTCCCTCTCCT	53085	AG _	
		AGGA GAGGGAGGGC AGAGC			
		TCCT CTCCCTCCCG TCTCG			
		_ AG			
GAM2301 NXF5	3'	GCTCTGAGCCCTCCCTCTCCT	53086	AG _	
		AGGA GAGGGAGGGC AGAGC			
		TCCT CTCCCTCCCG TCTCG			
		_ AG			
GAM2301 NXF5	3'	GCTCTGAGCCCTCCCTCTCCT	53087	AG _	
		AGGA GAGGGAGGGC AGAGC			
		TCCT CTCCCTCCCG TCTCG			
		_ AG			
GAM2301 NXF5	3'	GCTCTGAGCCCTCCCTCTCCT	53088	AG _	
		AGGA GAGGGAGGGC AGAGC			
		TCCT CTCCCTCCCG TCTCG			
		_ AG			
GAM2301 OCRL	3'	CTCCTACTCCCCTCGTTCT	9628	G A CA	
		GGAA GAGGG GGG GAG			
		TCTT CTCCC CTC CTC			
		G _ AC			
GAM2301 OGT	5'	GCCCTGATTAACCCTCTCCCTT	14593	AA _____	
CT		AGAAGG GGAGGG AGGGC			
		TCTTCC TCTCCC TCCCG			
		C_ AATTAG			
GAM2301 OTP	3'	GCCGCCCTCTTCCCTTC	50407	A AG	
		GAAGG AGGAGGG GGC			
		CTTCC TTCTCCC CCG			
		C CG			
GAM2301 PACSIN1	3'	GCAGATGCCCTCCTCCCTCCT	93882	A AG GA_	
		AGGA GG GGAGGGCA GC			

			TCCT CC CCTCCCGT CG			
			_ CT AGA			
GAM2301	PACSIN1	3'	GCCTGCTTCCCTTCCTCC	93883	A AG A	
			GGA GGAGGG GGCAG GC			
			CCT CCTTCC TCGTC CG			
			_ CT C			
GAM2301	PAFAH1B1	5'	CTCCCCCCTCCTTCCTC	6472	A A C	
			GA GGAAGGAGGG GGG AG			
			CT CCTTCCTCCC CCC TC			
			C _ _			
GAM2301	PAPOLA	5'	GCAGGCCCCCCCTCCCTCC	51928	A A_ AGA	
			GGA GGAGGG GGGC GC			
			CCT CCTCCC CCCG CG			
			C CC GA_			
GAM2301	PAPOLA	5'	GCCCCCCTCCCTCCCGCCT	51929	AA CAGA	
			AGG GGAGGGAGGG GC			
			TCC CCTCCCTCCC CG			
			GC CCCC			
GAM2301	PAX2	3'	GCCCTGCATCCTCCTCCCT	15658	A _	
			AGG AGGAGGG AGGGC			
			TCC TCCTCCT TCCCG			
			C ACG			
GAM2301	PAX2	3'	GCCCTGCATCCTCCTCCCT	15659	A _	
			AGG AGGAGGG AGGGC			
			TCC TCCTCCT TCCCG			
			C ACG			
GAM2301	PCDH7	5'	CCCTCCCTCCCCTCCCTCT	11988	A A_	
			AGA GGA GGAGGGAGGG			
			TCT CCT CCTCCCTCCC			
			C CC			
GAM2301	PCDH7	5'	GCTTTTGCCCCCTCCCTCCCCT	11991	A_ _ _	
	CC		GGA GGAGGGA GGGCAGA GC			
			CCT CCTCCCT CCCGTTT CG			
			CC CC T			
GAM2301	PCTK3	3'	GCCTCCCCATCCTTCCTTC	73328	_ AG	
			GAAGGAAGGA GGG GGC			
			CTTCCTTCCT CCC CCG			
			A CT			
GAM2301	PDE4A	3'	CTCTCTCCCTCCTCCCCTC	21682	A A C	
			GA GG AGGAGGGAGGG AG			

CT CC TCCTCCCTCTC TC
 C C _
 GAM2301 PDE4B 3' GCCCTGCTTCCCATCCTCCT 12013 A A_ G
 AG AGGA GGAGG AGGGC
 || ||| |||| ||||
 TC TCCT CCTTC TCCCG
 C AC G
 GAM2301 PDGFRB 5' CCCTTCCTCCATCCCTCT 66581 A A
 AGA GGA GGAGGGAGGG
 ||| ||| |||||
 TCT CCT CTCCTTCCC
 C A
 GAM2301 PFKM 5' GCCTCTCCTCCTTCCCCCT 60816 AA GA
 AG GGAAGGAGG GGGC
 || ||||| |||
 TC CCTCCTCC TCCG
 CC TC
 GAM2301 PIGR 3' CTCCATCCCTCCCTCCCGTCCT 72995 A_ CA_
 TC GAAGGA GGAGGGAGGG GAG
 ||||| ||||| |||
 CTTCT CCTCCCTCCC CTC
 GC TAC
 GAM2301 PIM1 3' GTCCTCCCTCACCCCTCCT 92690 A AAG_
 AG AGG GAGGGAGGGC
 || ||| |||||
 TC TCC CTCCTCCTG
 C CCA
 GAM2301 PLA2G2D 3' GCTCCAATCTGCCTCCTTCC 25716 G GCA
 GGAAGGAGG AGG GAGC
 ||||| ||| |||
 CCTTCCTCC TCT CTCG
 G AAC
 GAM2301 PLD2 3' GCCCTTGAACCCCTCCCTGTC 12163 _ A A ____
 GA AGG AGG GGG AGGGC
 || ||| ||| ||||
 CT TCC TCC CCC TCCCG
 G C _ AAGT
 GAM2301 PLEK 3' CTCCTGCATTCTCCTCCCCTC 12166 A A GG _
 GA GG AGGAGGGA GCAG AG
 || || ||||| ||| ||
 CT CC TCCTCCTT CGTC TC
 C C A_ C
 GAM2301 PLXNB3 3' TCCCCCTCCTTCCCCCT 19409 AA A
 AG GGAAGGAGGG GGG
 || ||||| |||
 TC CCTTCCTCCC CCT
 CC _
 GAM2301 PML 3' CTCCTCCTCCCTCCTTCC 53801 CA
 GGAAGGAGGGAGGG GAG
 ||||| |||

CCTTCCTCCCTCCT CTC
 C_
 GAM2301 PMX1 5' GCCTTCCTCTCCTTCCCTC 23568 A _
 GA GGAAGGAG GGAGGGC
 || ||||| |||||
 CT CCTTCCTC CCTTCCG
 C T
 GAM2301 POU2AF1 3' CCCTCCCTCCCTCACTTC 21737 _ A
 GAAG GA GGAGGGAGGG
 ||| || |||||
 CTTC CT CCTCCCTCCC
 A C
 GAM2301 POU2AF1 3' CCCTCCCTTCCTTCCCTC 21738 A _
 GA GGAAGGA GGGAGGG
 || ||||| |||||
 CT CCTTCCT CCCTCCC
 C T
 GAM2301 POU2AF1 3' CCCTCCCTTCCTTCCCTC 21739 A _
 GA GGAAGGA GGGAGGG
 || ||||| |||||
 CT CCTTCCT CCCTCCC
 C T
 GAM2301 POU2AF1 3' CTCCCTCCCTCCCTCGCTTCT 21742 _ A C
 AGAAG GA GGAGGGAGGG AG
 |||| || ||||| ||
 TCTTC CT CCTCCCTCCC TC
 G C _
 GAM2301 POU3F1 3' GCCCCACCCCGCTTTCCCTTT 60039 _ A A_
 CT AGAA GGAAGG GGG GGGC
 ||| ||||| ||| |||
 TCTT CCTTTC CCC CCG
 TCC G CAC
 GAM2301 PPP2R5A 5' CTCCGCCCCCGCCCTTCCCTC 21794 A AG A A
 GA GGAAGG GG GGGC GAG
 || ||||| || ||| |||
 CT CCTTCC CC CCG CTC
 C CG _ C
 GAM2301 PPP3R1 5' CTCTCCCCCTCCTTTCTTCT 76827 A GC
 AGAAGGAAGGAGGG GG AGAG
 ||||| || |||
 TCTTCTTTCCTCCC CC TCTC
 _ _
 GAM2301 PPP4C 3' GCTCCATGTTCTCCTCCTCTC 12252 GA GA _
 T AG AGGAGG GGGCA GAGC
 || ||||| ||| |||
 TC TCCTCC CTTGT CTCG
 TC TC AC
 GAM2301 PPT2 5' GCCCTTCCCCCTCCCATC 18950 A A A
 GA GG AGG GGGAGGGC
 || || || |||||

			CT CC TCC CCTTCCCG		
			A C C		
GAM2301	PRDM2	3'	CCCTCTCTCCCCACCTTC	25278	AA_
			GAAGG GGAGGGAGGG		
			CTTCC CCTCTCTCCC		
			ACC		
GAM2301	PREB	3'	CTCCCTGCCTCCTTTCTTCT	26329	G C
			AGAAGGAAGGAGG AGGG AG		
			TCTTCTTTCCTCC TCCC TC		
			G _		
GAM2301	PRex1	3'	GTCCTCCCTGCCTCCTTC	40825	A _
			GAAGGA GG AGGGAGGGC		
			CTTCCT CC TCCCTCCTG		
			_ G		
GAM2301	PRKCABP	3'	CTCCACCCTCCCTCCCCTCC	25746	A_ CA
			GGA GGAGGGAGGG GAG		
			CCT CCTCCCTCCC CTC		
			CC AC		
GAM2301	PRKCL1	5'	CTCTGGCCGCCCTCCCTCC	63174	A A_ G
			GGA GGAGGG GG CAGAG		
			CCT CCTCCC CC GTCTC		
			C CG G		
GAM2301	PSD	3'	GCTGGTTTCCCCTCCTTCCT	12439	AG AG
			AGGAAGGAGGG GGC AGC		
			TCCTTCCTCCC TTG TCG		
			CT G_		
GAM2301	PTBP1	3'	GCCCCCAGGGCCTTCCCTTCT	12541	_ AG_ A
			AGAAGG AAGG GG GGGC		
			TCTTCC TTCC CC CCCG		
			C GGGA _		
GAM2301	PTGER2	5'	GCTCTCAGACCCTCTTCCTCC	8173	A G C__
			GGA GGAGG AGGG AGAGC		
			CCT CCTTC TCCC TCTCG		
			_ _ AGAC		
GAM2301	PTPN7	5'	CTCTACCCCGAGACTGCCTTCT	55461	A GAGGGA C
			AGAAGG AG GGG AGAG		
			TCTTCC TC CCC TCTC		
			G AGAGC_ A		
GAM2301	PTPRN	3'	GCTCTGCCCTCCCTGGCCTC	12625	A AAGG
			GA GG AGGGAGGGCAGAGC		

CT CC TCCCTCCCGTCTCG
 _ GG_
 GAM2301 PXN 3' GCCCTGCCCCTGTCTCTGCCCC 12673 AA _ _ A
 CCTTC GAAGG GG AGGGA GGGCAG GC
 |||| || |||| |||| ||
 CTTCC CC TCTCT CCCGTC CG
 CC G GTC C
 GAM2301 RAB26 3' GCTTGTCCCTTCCTCCTCC 27604 A _ A
 GGA GGAGGGAGGG CAG GC
 || |||| || ||
 CCT CTCCTTCCC GTT CG
 _ T C
 GAM2301 RAB33A 5' CTCTCCTCCCTCTCTCCTCCT 17740 A AG GC
 AG AGGA GAGGGAGG AGAG
 || || || || || || || ||
 TC TCCT CTCCTCC TCTC
 C CT _
 GAM2301 RABGGTA 3' GCCCTGCCCCCTACCCTT 17153 A_ A _
 AAGG AGG GGG AGGGC
 || || || || || || || ||
 TTCC TCC CCC TCCCG
 CA _ G
 GAM2301 RAD23A 3' CTGTCCCCCGTCCTCCT 18565 A _ A
 AGGA GGA GGG GGGCAG
 || || || || || || || ||
 TCCT CCT CCC CCTGTC
 _ G C
 GAM2301 RAD50 5' GCTCCATCCCCCGCCCCCTCT 20411 A AA A A CA
 AGA GG GG GGG GGG GAGC
 || || || || || || || ||
 TCT CC CC CCC CCT CTCG
 C _ G _ AC
 GAM2301 RARA 3' GCCCTGCCCCCACCTGCCCTCC 8255 A _ GA_ A
 GGA GG AGG GGGCAG GC
 || || || || || || || ||
 CCT CC TCC CCCGTC CG
 C G ACC C
 GAM2301 RARA 3' GCTCTGCCCCGACCTCCTTC 8256 GA_
 GAAGGAGG GGGCAGAGC
 || || || || || || || ||
 CTTCTCC CCCGTCTCG
 AGC
 GAM2301 RARG 3' GCCCCTGTGACCCCTCCTTTCT 8263 A_____
 TC GAAGGAAGGAGGG GGGC
 || || || || || || || ||
 CTTCTTTCCTCCC CCCG
 CAGTGTC
 GAM2301 RARG 3' GCTCTGCCCTCTCCCCACCC 8265 AA A
 GG GG GGGAGGGCAGAGC
 || || || || || || || ||

			CC CC CTCTCCCGTCTCG		
			CA C		
GAM2301	RCV1	3'	GCCCGGTCCCACCCCTCCCTCT 12804	A A_ A _	
			AGA GGA GG GGGA GGGC		
			TCT CCT CC CCCT CCCG		
			C CC A GG		
GAM2301	RCV1	5'	GCTCCTGGGCCCCCTCCTCCCTT 12805	A _ _ _ _	
	C		GAAGG AGGAGGG AGG GC		
			CTTCC TCCTCCC TCC CG		
			C CGGG T		
GAM2301	REQ	3'	CTTCCCTTCTTCCTCCT 21840	A	
			AG AGGAAGGAGGGAGGG		
			TC TCCTTCTCCCTTTC		
			C		
GAM2301	RNASE1	3'	GCCTCTTCCCTCTTCCTTC 64602	GA _	
			GAAGGAAG GGGAG GGC		
			CTTCCTTC CCTTC CCG		
			TC T		
GAM2301	RORB	5'	GCCCTTCCTCCTCCTCCT 23590	A A	
			AG AGGA GGAGGGAGGGC		
			TC TCCT CCTCCTTCCCG		
			C _		
GAM2301	RUNX1	3'	TTTCCCTCCCTCTCTTCC 10031	_ C	
			GGAAG GAGGGAGGG AGA		
			CCTTC CTCCCTCCC TTT		
			T _		
GAM2301	RXRG	3'	CTGACCCCCTTCCTGTCC 23610	_ A _	
			GGA AGGAGGG GGG CAG		
			CCT TCCTTCC CCC GTC		
			G _ A		
GAM2301	S100A5	3'	CTGCCCTCCTCTCCCTCC 12929	A _	
			GGA GGAG GGAGGGCAG		
			CCT CCTC CCTCCCGTC		
			C T		
GAM2301	S100A5	3'	CTTTGGCCCCCTGCCCTCCT 12930	A _ A G	
			AGGA GG AGGG GG CAGAG		
			TCCT CC TCCC CC GTTTC		
			C G _ G		
GAM2301	SALL1	3'	GCCCCGCCCTTCCTTCT 12936	A GA	
			AGAAGGAAGG GG GGGC		

			TCTTCCTTCC CC CCCG			
			_ GC			
GAM2301	SALL2	3'	TTCTTCCCCCTCCTCTCTCCT 64594	A GA	A C	
			AG AG AGGAGGG GGG AGAG			
			TC TC TCCTCCC CCT TCTT			
			C TC _ _			
GAM2301	SCA2	3'	GCCAAATTCCCTCCTCCCTTCT 12942	A	___	
			AGAAGG AGGAGGGAG GGC			
			TCTTCC TCCTCCCTT CCG			
			C AAA			
GAM2301	SCA7	3'	CTTTCTCCCTCCTTCCTTTT 6191		C	
			AGAAGGAAGGAGGGAGGG AG			
			TTTTCTTCCTCCCTCTT TC			
			_			
GAM2301	SCD	3'	GCCTCTCTCTCCCTCCCTCT 18594	A A	_	
			AGA GGA GGAGGGAG GGC			
			TCT CCT CCTCTCTC CCG			
			C C T			
GAM2301	SGCA	3'	GCCCTGACTTCATCCTCCCTTC 5246	A GG	G A	
	T		AGAAGG AGGA GAGG CAG GC			
			TCTTCC TCCT CTTC GTC CG			
			C A_ A C			
GAM2301	SH3BP4	3'	CTTAACCCCTCTTCCTTCC 28001	GA	CA	
			GGAAGGAGG GGG GAG			
			CCTTCCTTC CCC TTC			
			TC AA			
GAM2301	SHANK2	3'	GCCCCGCCCCCTTCTTTC 25529	A A_		
			GAAGGAAGG GGG GGGC			
			CTTTCTTTC CCC CCCG			
			_ GC			
GAM2301	SIX2	3'	GCCCCTCCTCCTTCTCTCT 34189	AG	GA	
			AGA GAAGGAGG GGGC			
			TCT CTCCTCC CCCG			
			CT TC			
GAM2301	SIX3	5'	CTCCCCCTCCTTTCCTTCT 19440	_	A C	
			AGAAGGAA GGAGGG GGG AG			
			TCTTCCTT CCTCCC CCC TC			
			T _ _			
GAM2301	SIX3	5'	GCCCTTCCTCCTCTCCCTC 19444	A _		
			GA GGA AGGAGGGAGGGC			

			CT CCT TCCTCCTTCCCG			
			C C			
GAM2301	SLC20A1	5'	GCTCCGCCCTCCCTTTTCCCT 60096	A		A
			AGG AGGAGGGAGGGC GAGC			
			TCC TTTTCCCTCCCG CTCG			
			C C			
GAM2301	SLC21A2	3'	GCTCTTACCTCACCTCCCTCC 20085	A	_	GC
			GGA GGAGG GAGG AGAGC			
			CCT CCTCC CTCC TCTCG			
			C A AT			
GAM2301	SLC2A4	3'	CTCTCCCCTCCCTCTTCCTTC 8308	G		C
			GAAGGAAG AGGGAGGG AGAG			
			CTTCCTTC TCCCTCCC TCTC			
			_ C			
GAM2301	SLC38A3	3'	GCCCAAGCCCCTCATTCCCTC 23375	A	G	A__
			GA GGAA GAGGG GGGC			
			CT CCTT CTCCC CCCG			
			C A CGAA			
GAM2301	SLC39A1	3'	CTATCTCCCTCCTCCCATCT 27809	A	A	GC
			AGA GG AGGAGGGAGG AG			
			TCT CC TCCTCCCTCT TC			
			A C A_			
GAM2301	SLC39A1	3'	GCCCTGTTCTCCCTTCCCTCC 27812	A	_	A_
			GGA GGA GGGAGGGCAG GC			
			CCT CCT CCCTCTTGTC CG			
			C T CC			
GAM2301	SLC6A3	3'	GCTCCCTCCCTCCCTGCTCC 8312	A	G	CA_
			GGA G AGGGAGGG GAGC			
			CCT C TCCCTCCC CTCG			
			_ G TCC			
GAM2301	SLC7A4	3'	GCCCCGCCCTCCACACCTGCT 65819	A	AA__	A_
			AG AGG GGAGGG GGGC			
			TC TCC CCTCCC CCCG			
			G ACAC GC			
GAM2301	SLC7A7	5'	TTCCCCCTCCCTCACTCCTTC 15633	AG		CA
			GAAGGA GAGGGAGGG GAG			
			CTTCCT CTCCCTCCC CTT			
			CA C_			
GAM2301	SLC7A8	3'	CTCTCTCCTTCCCTCCCCCT 25303	AA		C
			AGG GGAGGGAGGG AGAG			

			TCC CCTCCTTCCT TCTC		
			C_ C		
GAM2301	SLC9A1	5'	GCTCCCAGCCCCCTCTCTCCT 70927	AG	AG A__
			AGGA GAGGG GGC GAGC		
			TCCT CTCCC CCG CTCG		
			CT _ ACC		
GAM2301	SLC9A1	3'	GCTCTGCCTCTAACTCCCTCCT 70928	A A	GG _
	C		GA GGA GGAG AG GGCAGAGC		
			CT CCT CTC TC CCGTCTCG		
			_ C AA T		
GAM2301	SLC9A3R1	3'	CCCCACCTTTTTCCTTCT 70937		GA
			AGAAGGAAGGAGG GGG		
			TCTTCCTTTTCC CCC		
			AC		
GAM2301	SMCX	3'	GCCCCACTCTCCTCCCCTCT 16087	A A	A__
			AGA GG AGGAGGG GGGC		
			TCT CC TCCTCTC CCGG		
			C C ACC		
GAM2301	SOCS5	5'	GCCCTGCCTCCCTCCTTC 26682	A	G
			GAAGGA GGAGG AGGGC		
			CTTCCT CCTCC TCCCG		
			C G		
GAM2301	SORCS2	3'	CTCCAGGCCCCCCTGCCCTCC 40801	A _	A A__
			GGA GG AGGG GGGC GAG		
			CCT CC TCCC CCG CTC		
			C G _ GAC		
GAM2301	SOX10	5'	GCTCAGGGCCCCCGCCCTCC 23678	A A_	A A__
			GGA GG GGG GGGC GAGC		
			CCT CC CCC CCG CTCG		
			C CG _ GGA		
GAM2301	SOX9	5'	GCTCTTTTTCCTCCCCTCCTCC 6232	A _	C__
			GGA GGAGGG AGGG AGAGC		
			CCT CCTCCC TCCT TCTCG		
			_ C TTT		
GAM2301	SPF30	5'	GCCCGGCGTTTCTCCCTTCCCC 20795	AA	AG G AGA
	CT		AG GGAAGG GGAG GC GC		
			TC CCTTCC CCTT CG CG		
			CC CT G GCC		
GAM2301	SPR	3'	CTCTGATGTCTCCTTCCTTC 13385		GAGGG
			GAAGGAAGGAGG CAGAG		

			CTTCCTTCCTCT	GTCTC		
			GTA__			
GAM2301	SPTBN4	3'	CTGTTTTCTCTCTCCTCCCC	48156	AA A	___
	CT		AG GG AGGAGGGAGG	GCAG		
			TC CC TCCTCTCTCC	TGTC		
			CC C	TTT		
GAM2301	SREBF1	3'	GCTCTGCCCCAGAGGCCTCTCT	96077	AG	GA___
	CT		GGA GAGG	GGGCAGAGC		
			TCT CTCC	CCCGTCTCG		
			CT	GGAGAC		
GAM2301	SSR4	3'	GCCCTGCCCTTGCTTCCTTC	21861	-	-
			GAAGGAAG GAGGG	AGGGC		
			CTTCCTTC	TTCCC TCCCG		
			G	G		
GAM2301	STAU	5'	CTCCGCCTCTTCCTCCCTTC	17198	AAG	___ A
			GAAGG	GAGGGA GGGC GAG		
			CTTCC	CTCCCT TCCG CTC		
			___	TC C		
GAM2301	STK13	5'	CCCTCTGTCTCCTTCCTTCT	13468	___	
			AGAAGGAAGGAG	GGAGGG		
			TCTTCCTTCCTC	TCTCCC		
			TG			
GAM2301	STX1A	3'	GCCCCACCCTCCCTCGGCTTT	17210	___ A	A_
			GAAG	GA GGAGGG GGGC		
			TTTC	CT CCTCCC CCG		
			GG C	AC		
GAM2301	SYT5	3'	GCCCCACCCTTAAGCTTCCTCT	13503	A	___ A_
			AGA GGAAG	GAGGG GGGC		
			TCT CCTTC	TTCCC CCG		
			___	GAA AC		
GAM2301	TAF4	3'	GCCCTCCCCTCCCCTCCCTTC	13514	A	A___
			GAAGG	AGG GGGAGGGC		
			CTTCC	TCC CCCTCCCG		
			C	CCTC		
GAM2301	TBP	3'	TTGCCTCCCCACCCCCTTCT	65373	AA A_	AG
			AGAAGG	GG GGG GGCAG		
			TCTTCC	CC CCC CCGTT		
			C_	AC CT		
GAM2301	TCF7	3'	GCCCCAGCCCCGTTTCCTTC	13622	___ A	GA_
			GAAGGAA	GG GG GGGC		

			CTTCCTT CC CC CCCG			
			G _ GAC			
GAM2301	TCF7L2	5'	CCCTCCCCTCCTCCCTCT	48438	A A _	
			AGA GGA GGAGGG AGGG			
			TCT CCT CCTCCC TCCC			
			C _ C			
GAM2301	TCTA	3'	GCCTGGACCTGCCTCCTTCC	42500	G G_ A	
			GGAAGGAGG AGG CAG GC			
			CCTTCCTCC TCC GTC CG			
			G AG C			
GAM2301	TEM7	3'	CTCCACCCTCAGCTCTTCCTT	40254	AGG CA	
			AAGGAAGG GAGGG GAG			
			TTCCTTCT CTCCC CTC			
			CGA AC			
GAM2301	TERT	3'	GCCCTGCCCTCCTTTGCCTTCC	13682	_ A	
			GGAAGG AGGGAGGGCAG GC			
			CCTTCC TTCCTCCCGTC CG			
			GT C			
GAM2301	TGFB1	5'	GCTTGCTCCCTCCCTGCCCCCT	7258	AA _ CA_	
			AGG GG AGGGAGGG GAGC			
			TCC CC TCCCTCCC TTCG			
			C_ G TCG			
GAM2301	TGFB3	5'	GCCTGGTTTTCTCCCTCCTTC	13718	A G A	
	T		AGAAGGA GGAGGGAGG CAG GC			
			TCTTCCT CTCCTTTT GTC CG			
			C G _			
GAM2301	THY1	3'	CTGCTGCCCCTCCCTGCCTCC	21897	A _ _ _	
			GGA GG AGGGAGGG CAG AG			
			CCT CC TCCCTCCC GTC TC			
			_ G C G			
GAM2301	TIMP3	3'	CTGCCCCACCTCACTTCCCTC	6284	A _ GA	
			GA GGAAG GAGG GGGCAG			
			CT CCTTC CTCC CCCGTC			
			C A AC			
GAM2301	TIMP3	3'	GCCCCACCCTGCCCTTCT	6288	AA _ A_	
			AGAAGG GG AGGG GGGC			
			TCTTCC CC TCCC CCCG			
			_ G AC			
GAM2301	TIMP3	3'	GCCCCACCTCACTTCCCTC	6289	A _ GA	
			GA GGAAG GAGG GGGC			

			CT CCTTC CTCC CCCG			
			C A AC			
GAM2301	TIRAP	5'	CTGGGTCTCCTCCCTCCTCCC	54664	A	_____
			GG AGGAGGGAGGG CAG			
			CC TCCTCCCTCCT GTC			
			C CTGG			
GAM2301	TITF1	3'	GCTCTGCCTCACCGCTTCCCTC	13891	A	GA GA
			GA GGAAG GG GGGCAGAGC			
			CT CCTTC CC TCCGTCTCG			
			C G_ AC			
GAM2301	TLE2	5'	CTCTCTCCTCCCTCTTTCT	13771		C
			GGAAGGAGGGAGGG AGAG			
			TCTTTCTCCCTCCT TCTC			
			C			
GAM2301	TMEM1	3'	GCCTGGCCTCCCTCCCCCT	13802	AA	G A
			AGG GGAGGGAGG CAG GC			
			TCC CCTCCCTCC GTC CG			
			C_ G C			
GAM2301	TMEPAI	3'	CTGCTACCCCTCCCTTC	39827	A A	AG
			GAAGG AGG GGG GGCAG			
			CTTCC TCC CCC TCGTC			
			C _ A_			
GAM2301	TNF	5'	CTCCACCCTCTCTCCCCT	92707	AA	CA
			AGG GGAGGGAGGG GAG			
			TCC CCTCTCTCCC CTC			
			AC			
GAM2301	TNFRSF10C	3'	CTCTGCCCTGCCTCCCTCT	15203	A	G
			GGA GGAGG AGGGCAGAG			
			TCT CCTCC TCCCGTCTC			
			C G			
GAM2301	TNFRSF10D	5'	TCCACCCTCCTCCCTTCT	15202	A	A
			AGAAGG AGGAGGG GGG			
			TCTTCC TCCTCCC CCT			
			C A			
GAM2301	TNFRSF1B	3'	GCCCCGCGCCTCCTTCTTGCT	8397	_	GA__
			AG AAGGAAGGAGG GGGC			
			TC TTCCTTCCTCC CCCG			
			G GCGC			
GAM2301	TOP2A	3'	GCTCTTAACCTCCTCCCCTCT	8407	A AA	GGC
			AGA GG GGAGGGAG AGAGC			

			TCT CC CTCCTTC TCTCG		
			— — AAT		
GAM2301	TRIM9	3'	CTCTGCCCTTTTCCCTTTC 31449	AG	
			GGAAGG GGAGGGCAGAG		
			CTTTCC TTTCCCGTCTC		
			CT		
GAM2301	TRPM2	3'	GCCCTACCCCCAAGTTTCT 13865	GAA A _	
			AGAAG GG GGG AGGGC		
			TCTTT CC CCC TCCCG		
			GAA _ A		
GAM2301	TXNIP	3'	GCCCTTTGAACCCCTTCCT 22383	A _ _ _	
			AGGAAGG GGG AGGGC		
			TCCTTCC CCC TCCCG		
			_ AAGTT		
GAM2301	TYRO3	5'	GCCCCGCCCTCCTCCCTCCT 21937	A A A _	
			AG AGG AGGAGGG GGGC		
			TC TCC TCCTCCC CCG		
			C C GC		
GAM2301	UBQLN2	3'	CTCCCCACTCCCTCCCTCT 26491	A _ CA	
			GGA GGAGGGAG GG GAG		
			TCT CCTCCCTC CC CTC		
			C A C _		
GAM2301	UNRIP	5'	CTGACCCCTCCCTCACCCCT 24188	AAG _ _	
			AGG GAGGGAGGG CAG		
			TCC CTCCCTCCC GTC		
			CCA CA		
GAM2301	VAT1	3'	GCTCTGCCCTCCCTCCCC 22090	AA	
			GG GGAGGGAGGGCAGAGC		
			CC CCTCCCTCCCGTCTCG		
			C _		
GAM2301	VEGF	3'	GCTCTGCCCTCCCCGATCCCCT 14042	AA _ _	
			AGG GGA GGGAGGGCAGAGC		
			TCC CCT CCCTCCCGTCTCG		
			_ AGC		
GAM2301	VTN	3'	CTCTGTAGCTCCCTCCTCCCAT 7162	A A G _	
	CT		AGA GG AGGAGGGAG GCAGAG		
			TCT CC TCCTCCCTC TGTCTC		
			A C GA		
GAM2301	WASF3	3'	GCCCTCACCTCCACCCTTC 22813	AA _	
			GAAGG GGAGG GAGGGC		

			CTTCC CCTCC CTCCCG			
			CA A			
GAM2301	WNT10B	5'	CTCCCTCCCTTCCTCCCTCC	14126	A	CA_
			GGA GGAGGGAGGG GAG			
			CCT CCTCCTTCCC CTC			
			C TCC			
GAM2301	WNT7A	5'	GCTCCTCCCTCCCTCCTCCC	17319	A	CA
			GG AGGAGGGAGGG GAGC			
			CC TCCTCCCTCCC CTCG			
			C TC			
GAM2301	WNT7A	5'	GCTCGCTCCTCCCTCCCTCCT	17320	A	_ A
			AGGA GGAGGGAGG GC GAGC			
			TCCT CCTCCCTCC CG CTCG			
			C T _			
GAM2301	YWHAG	5'	GCCCCAGTGTCTCCTCCTTCT	25943	A	A_____
			AGAAGGA GGAGGG GGGC			
			TCTTCCT CTCCT CCCG			
			_ GTGAC			
GAM2301	ZIC1	5'	CCCTCCCTCCTCCTTCT	14166	_ A	
			AGAAG G AGGAGGGAGGG			
			TCTTC C TCCTCCCTCCC			
			T C			
GAM2301	ZIC1	5'	CTCACCTCCCTCCTCCT	14167	A	CA
			AGGA GGAGGGAGGG GAG			
			TCCT CCTCCCTCCC CTC			
			_ A_			
GAM2301	ZIC3	5'	GCTCTTTCTTCCCCTCCTCCCT	14172	A A	_ C
	CCT		AG AGG AGGAGGG AGGG AGAGC			
			TC TCC TCCTCCC TTCT TCTCG			
			C C C T			
GAM2301	ZNF216	5'	GCCCCCCTCGCTTCCCTC	21174	A	_ A
			GA GGAAG GAGGG GGGC			
			CT CCTTC CTCCC CCCG			
			C G C			
GAM2301	ZNF261	3'	CTGTGCCCACTCCCTTCT	18732	A A	G
			GGAAGG GGG GGGCA AG			
			TCTTCC CTC CCCGT TC			
			_ A G			
GAM2301	ABTB1	5'	GCTCTGACCTCCTTCCTGCC	51701	A	G
			GG AGGAGGGAGG CAGAGC			

CC TCCTTCCTCC GTCTCG
 G A
 GAM2301 AF9Q34 3' GCCCTGCCCCACCCCTTCCTG 51718 _ A GA_ A
 TCT AGA AGGAAGG GG GGGCAG GC
 ||| ||||| || ||||| ||
 TCT TCCTTCC CC CCCGTC CG
 G _ ACC C
 GAM2301 AIF1 3' GCCCTTCCTCTTCCCCCT 17927 AA G
 AG GGAAG AGGGAGGGC
 || ||||| |||||
 TC CCTTC TCCTTCCCG
 CC _
 GAM2301 AKAP11 3' CTCTCTCTCCCCTCCTCCC 58459 A _ C
 GG AGGAGGG AGGG AGAG
 || ||||| ||| |||
 CC TCCTCCC TCTC TCTC
 C C _
 GAM2301 ARF6 3' GCCTTCCCCCCCCTTCCTT 9790 A__
 AAGGAAGG GGGAGGGC
 ||||| |||||
 TTCCTTCC CCCTTCCG
 CCC
 GAM2301 ARFGAP1 3' CTCTGCCCTCGTCGTTCTCCT 37138 A _____
 CCTTC GAAGGA GGAGG GAGGGCAGAG
 ||||| ||||| |||||
 CTTCTT CCTCC CTCCCGTCTC
 _ TTGCTG
 GAM2301 ARFGAP1 5' GCCTGCCCGCCCCTCCCTCC 37139 A A_ A
 GGA GGAGGG GGGCAG GC
 ||| ||||| ||||| ||
 CCT CCTCCC CCCGTC CG
 C CG C
 GAM2301 ARHGEF9 5' CCCTACTTCCTCCTCTCCT 31482 _ ____
 AGGA AGGAGGG AGGG
 ||||| ||||| |||
 TCCT TCCTCCT TCCC
 C TCA
 GAM2301 ARP3BETA 3' GCTCTCCCTCCTCCTCCT 40339 A A
 AG AGGA GGAGGGAGGGC
 || ||||| |||||
 TC TCCT CCTCCCTCTCG
 C _
 GAM2301 B3GNT7 3' GCCCTCCTCCCTTCCCTC 71680 A AG
 GA GGAAGG GGAGGGC
 || ||||| |||||
 CT CCTTCC CCTCCCG
 C CT
 GAM2301 BA108L7.2 3' CTCTGTCCCCTCCCTCACTTCC 49073 _ ____
 GGAAG GAGGGAGGG CAGAG
 ||||| ||||| |||||

CCTTC CTCCCTCCC GTCTC
 A CT
 GAM2301 BA108L7.2 3' GCTCCATTTCCCCTCCTCCTCT 49077 _ A AG CA
 CT AGA AGGA GGAGGG GG GAGC
 ||| ||| ||||| || ||||
 TCT TCCT CCTCCC TT CTCG
 C _ CT AC
 GAM2301 BCL2L1 3' CTCTACCCTCCCACCCCTTCT 57593 AA A C
 AGAAGG GG GGGAGGG AGAG
 ||||| || ||||| ||||
 TCTTCC CC CCCTCCC TCTC
 C_ A A
 GAM2301 BICD2 3' GCCCCTTCCCCTTCCCTCT 70914 A A _
 AGA GGAAGG GGGAGGG C
 ||| ||||| ||||| |
 TCT CCTTCC CCTTCCC G
 C _ C
 GAM2301 BLR1 3' CTTCCCTCTCTCCTCCT 53113 A CA
 AGGA GGAGGGAGGG GAG
 ||| ||||| |||
 TCCT CCTCTCTCCC TTC
 _ C_
 GAM2301 BLR1 3' GCTTGTCCCCTCCTCACTCC 53117 A GA CA_
 GGA G GGGAGGG GAGC
 ||| | ||||| |||
 CCT C TCCTCCC TTCG
 _AC CTG
 GAM2301 BRPF3 3' CTCTGCCTCCTTCCTTCTT 93930 G
 AGGAAGGAGGGAGG CAGAG
 ||||| ||||| |||||
 TTCTTCCTTCCTCC GTCTC
 _
 GAM2301 C11orf11 5' GCCATCCTCTCCTTCCTTCT 94878 _ G
 AGAAGGAAGGAG GGA GGC
 ||||| ||| |||
 TCTTCCTTCCTC CCT CCG
 T A
 GAM2301 C12orf22 5' CTCGCTCCTCCCTCCTTCC 48706 _ A
 GGAAGGAGGGAGG GC GAG
 ||||| ||| |||
 CCTTCCTCCCTCC CG CTC
 T _
 GAM2301 C14orf4 3' CTCGACCCTCCCTCCCCT 67915 AA CA
 AGG GGAGGGAGGG GAG
 ||| ||||| |||
 TCC CCTCCCTCCC CTC
 _ AG
 GAM2301 C14orf4 5' TTCTCGCCCCCCTCCTCC 67924 A A _
 GGA GGAGGG GGGC AGAG
 ||| ||||| ||| |||

CCT CCTCCC CCCG TCTT
 _ C C
 GAM2301 C16orf5 5' CCTGCCTTTCCTTCCCCT 26350 AA A
 AGG GGAGGGAGGGCAG G
 ||| |||||
 TCC CTCCTTTCCGTC C
 C_
 GAM2301 C17orf31 3' GCTCTGCCCTCCCTGAGGCC 34539 AAGG
 GG AGGGAGGGCAGAGC
 || |||||
 CC TCCCTCCCGTCTCG
 GGAG
 GAM2301 C1orf16 3' GCCCATCTCCATCCCTTCT 29915 AA_ GA
 AGAAGG GGAGG GGGC
 ||||| |||||
 TCTTCC CCTCT CCCG
 CTA AC
 GAM2301 C20orf103 5' CCTCCCTCCCTCCCCCTT 25325 AA C A
 AAGG GGAGGGAGGG AG G
 ||||| ||||| |||
 TTCC CCTCCCTCCC TC C
 C_ _
 GAM2301 C20orf103 5' CTCCCTCCCTCCCCCTTCT 25326 AA C
 AGAAGG GGAGGGAGGG AG
 ||||| ||||| ||
 TCTTCC CCTCCCTCCC TC
 C_ _
 GAM2301 C20orf110 3' GCTTTTAGTCTCCCCTTCCTTC 80364 AG GC_
 T
 AGAAGGAAGG GGAGG AGAGC
 ||||| ||||| |||||
 TCTTCCTTCC CCTCT TTTCCG
 _ GAT
 GAM2301 C20orf188 3' GCCCTGCCCTGTTCCCGTTCCT 32220 _ AG G A
 AGGAA GG G AGGGCAG GC
 ||||| || | ||||| ||
 TCCTT CC T TCCCGTC CG
 G CT G C
 GAM2301 C20orf27 3' CTGCCCTCCCTCGTCCT 35824 AG _
 AGGA GAGGGAGGG CAG
 ||||| ||||| |||
 TCCT CTCCTCCC GTC
 G_ C
 GAM2301 C20orf55 3' GCTCTGTTTCCTCCTTCCTTCC 49477 _
 T
 AGGAAGGAGGGAGG GCAGAGC
 ||||| ||||| |||||
 TCCTTCCTTCCTCC TGTCTCG
 TT
 GAM2301 C22orf5 3' GCTCCATCCCCTCCTCCTCCT 25341 A GA CA_
 AGGA GGAGG GGG GAGC
 ||||| ||||| ||| |||||

			TCCT CCTCC CCC CTCG			
			— TC TAC			
GAM2301	C6orf9	3'	GCCCTGCCCCACCCTCCCTCC 42327	A	A	A
			GGA GGAGGG GGGCAG GC			
			CCT CCTCCC CCGTC CG			
			C A C			
GAM2301	CBX3	5'	GCCCCGCCTCCCCCTTCCCTC 24408	A	A	—
			GA GGAAGG GGA GGGC			
			CT CCTTCC CCCT CCG			
			C — CCGC			
GAM2301	CBX8	3'	GCCCCTTTTCATCCCTCCTTCCT 40607			—
			AGGAAGGAGGGA GGGC			
			TCCTTCCTCCCT CCG			
			ACTTTC			
GAM2301	CDH24	3'	GCCCCAGGCCTCCTCCCTGTC 96604	—	A	GA—
			GA AGG AGGAGG GGGC			
			CT TCC TCCTCC CCG			
			G C GGAC			
GAM2301	CDH24	3'	GCTCTCACCTCCCTCCTCCT 96605	A		GC
			AGGA GGAGGGAGG AGAGC			
			TCCT CCTCCCTCC TCTCG			
			— AC			
GAM2301	CENTB1	5'	GTCCCTCTCCTCCTTCCCCCT 28868	AA		— —
			AG GGAAGGAGG GAGGG C			
			TC CCTTCCTCC CTCCC G			
			CC T T			
GAM2301	CENTG2	5'	GCTCCGCCCCGCGCCTTTCTTCT 30541			AGGGA A
			AGAAGGAAGG GGGC GAGC			
			TCTTCTTTCC CCG CTCG			
			GCG— C			
GAM2301	CLSTN3	3'	CCCTCTCCTCTCCCCTTC 28875	AA		—
			GAAGG GGAGG GAGGG			
			CTTCC TCTCC CTCCC			
			CC T			
GAM2301	COPS7B	3'	CTCACCCACTCCCTCCTTCC 42997			— CA
			GGAAGGAGGGAG GG GAG			
			CCTTCCTCCCTC CC CTC			
			A CA			
GAM2301	CXorf2	3'	GCTAGCTCCCTCCCTCCTCCT 9626	A		CAG—
			AGGA GGAGGGAGGG AGC			

			TCCT CCTCCCTCCC	TCG		
			—	TCGA		
GAM2301	D15Wsu75e 5'	GCTCGGTCCCCCCTCTCCCTC	67224	A	_	A A A
		GA GGA AGG GGG GGGC GAGC				
		CT CCT TCC CCC CCTG CTCG				
		C C _ _ G				
GAM2301	dA141H5.1 3'	CTCCCTCCCTCCCTCCTTCTCT	59779	AG		CA_
	CT	AGA GAAGGAGGGAGGG GAG				
		TCT CTCCTCCCTCCC CTC				
		CT TCC				
GAM2301	dA141H5.1 3'	GCTCCCCATCCTCCCTCCTCAC	59781	—		CA_
	TCC	GGA AGGAGGGAGGG GAGC				
		CCT TCCTCCCTCCT CTCG				
		CAC ACCC				
GAM2301	DDM36 3'	CTCTTCCCCTCCTTCCTTGCC	40922	_		C_
		GG AAGGAGGGAGGG AGAG				
		CC TTCCTTCCTCCC TCTC				
		G CT				
GAM2301	DDX12 3'	CTTCCCCTCCTCCTTCCT	60422	GA		C
		AGGAAGGAGG GGG AG				
		TCCTTCCTCC CCC TC				
		TC T				
GAM2301	DDX39 3'	GCCCTCCCACCTCCCTTC	58118	A A		_
		GAAGG AGG GGGAGGG C				
		CTTCC TCC CCCTCCC G				
		C A C				
GAM2301	DGKD 3'	GCTCCTCCCTCCTCCATC	60110	A A		_
		GA GGA GGAGGGAGG GC				
		CT CCT CCTCCCTCC CG				
		A _ T				
GAM2301	DJ726C3.2 3'	CTTTCCTTCCTCCTCCT	48209	A		C
		AGGA GGAGGGAGGG AGAG				
		TCCT CCTCCTTCCC TTTC				
		— —				
GAM2301	DJ726C3.2 3'	TCTCCCCCTCCTTCCTCT	48210	A		A C
		AGA GGAAGGAGGG GGG AGA				
		TCT CCTTCCTCCC CCC TCT				
		— — —				
GAM2301	DJ726C3.2 3'	TCTCCCTCCCTCACTTCT	48211	_		C
		GGAAG GAGGGAGGG AGA				

TCTTC CTCCCTCCC TCT
 A _
 GAM2301 DKFZP434J037 3' GCCCCACCTAACCCTTCCTT 48949 ____ GA
 AAGGAAGG AGG GGGC
 ||||| ||| ||||
 TTCCTTCC TCC CCCG
 CAA AC
 GAM2301 DKFZp434J0617 3' GCCCCCCTCTCCCTTCT 50978 AA A
 AGAAGG GGAGGG GGGC
 ||||| ||||| ||||
 TCTTCC TCTCCC CCCG
 C_ C
 GAM2301 DKFZp434N035 3' GCCCCGCCCTAGCTCTTCT 51063 _ AA A A_
 AGAAG G GG GGG GGGC
 ||||| | ||| ||||
 TCTTC C TC CCC CCCG
 T GA _ GC
 GAM2301 DKFZP434N1817 5' CTCCACCCTCTCTCCCACC 68721 AA CA
 GG GGAGGGAGGG GAG
 || ||||| |||
 CC CCTCTCTCCC CTC
 AC AC
 GAM2301 DKFZp547H236 3' CTGTCCCCCCTACCTCCCTTCT 79246 A _ A
 AGAAGG AGG AGGG GGGCAG
 ||||| ||| ||| |||||
 TCTTCC TCC TCCC CCTGTC
 C A C
 GAM2301 DKFZp547I094 3' CTCTGCAGCCCCTGCTCCT 50556 A G AGG
 AGGA G AGGG GCAGAG
 ||||| ||| |||||
 TCCT C TCCC CGTCTC
 _G CGA
 GAM2301 DKFZp547I094 5' GCCTCATCCCCCTTCCCTC 50563 A A _
 GA GGAAGG GGGG GGGC
 || ||||| ||| ||||
 CT CCTTCC CCCT TCCG
 C _ AC
 GAM2301 DKFZp547J036 3' GCTCAGCCCCTCCACCCCTCC 51122 A AG _A
 GGA GG GGAGGG C GAGC
 ||| || ||||| | ||||
 CCT CC CCTCCC G CTCG
 C CA C A
 GAM2301 DKFZp564A176 3' GCTCCGTGTCTCCCTCTCCCC 50974 AA _
 GG GGAGGGAGGGCA GAGC
 || ||||| ||||| ||||
 CC TCTCCCTCCTGT CTCG
 CC GC
 GAM2301 DKFZP564C103 3' GCCAGTTCCCTTCTCCCCTC 32240 A A _
 GA GG AGGAGGGAG GGC
 || || ||||| ||| |||

			CT CC TCTTCCCTT CCG			
			C C GA			
GAM2301	DKFZP566K1924	5'	GCTCCACCACCTCCCTCACCT	74198	AAG	GCA__
			AGG GAGGGAGG GAGC			
			TCC CTCCCTCC CTCG			
			CA_ ACCAC			
GAM2301	DKFZP586C1324	3'	CTCTCCCTTCCTTCCTTCT	70356	_	
			AGAAGGAAGGA GGGAGGG			
			TCTTCCTTCCT CCCTCTC			
			T			
GAM2301	DKFZP586G1122	3'	CTGCCTTTCCCTCTCCCT	61939	AA	_
			AGG GGAGGGAG GGCAG			
			TCC TCTCCCTT CCGTC			
			CC T			
GAM2301	DKFZp761B0514	3'	CCCTTTCTCCTCCTCCTTC	51145	_	GG
			GAAGGA AGGAG AGGG			
			CTTCCT TCCTC TCCC			
			CC TT			
GAM2301	DRG1	3'	CCCTACCCAGTTCTTTCT	15972	GGA	_
			AGAAGGAA GGG AGGG			
			TCTTTCTT CCC TCCC			
			GAC A			
GAM2301	EDR2	3'	GCCCCGCTCTTCCCTCT	61112	A A	A_
			AGA GG AGGAGGG GGGC			
			TCT CC TTCTCTC CCCG			
			C C GC			
GAM2301	EDR2	3'	GCCCTTGCCTTCCTTCCT	61113	_	
			AGGAAGGAGGG AGGGC			
			TCCTTCCTTCC TCCCG			
			GT			
GAM2301	EFS2	3'	CTCTGCTCCTCCCTGCC	20772	AA A	_
			GG GG GGGAGG GCAGAG			
			CC TC CCCTCC CGTCTC			
			G_ _ T			
GAM2301	ELF4	3'	GCTCCCTGCTTCCCCCTTCCT	9232	A A	G _
	CT		AGA GGAAGG GGGAGG CA GAGC			
			TCT CCTTCC CCCTTC GT CTCG			
			C _ _ CC			
GAM2301	ELF4	3'	TCCTCCCCTCTCCCTTCT	9235	A GA	
			AGAAGG AG GGGAGGG			

TCTTCC TC CCCTCCT
 C TC
 GAM2301 ELOVL2 3' CTTCTCTCTCCCTCCCTCC 35437 A CA
 GGA GGAGGGAGGG GAG
 ||| ||||| |||
 CCT CCTCCCTCTC TTC
 C TC
 GAM2301 ENDO180 3' GCCCCTTCTCTCCCACCCCTTC 21266 A__ C A_
 CTTCT AGAAGGAAGG GGGAGGG AG GC
 ||||| ||||| || ||
 TCTTCCTTCC CCCTCTC TC CG
 CCA T CC
 GAM2301 ESAM 3' CTCTGCCCCACCTCTCT 58046 GA AG A
 AG AGG GG GGGCAGAG
 || ||| |||||
 TC TCC CC CCCGTCTC
 TC A_ _
 GAM2301 ESDN 5' GCTTCCTTCCCTCCCCTCC 56058 A_ CA
 GGA GGAGGGAGGG GAGC
 ||| ||||| |||
 CCT CCTCCCTTCC TTCG
 CC _
 GAM2301 EZF-2 3' CTCAGCCCCCCCCTTCTCCCT 37674 AA A A A
 AG GGAAGG GGG GGGC GAG
 || ||||| ||| ||| |||
 TC TCTTCC CCC CCCG CTC
 CC _ _ A
 GAM2301 EZF-2 3' CTCTTCCTCTCCTTCCCTC 37675 A _ C
 GA GGAAGGAGG GAGGG AGAG
 || ||||| |||| |||
 CT CTTCTTCC CTCCT TCTC
 C T _
 GAM2301 FLJ00058 5' GCTCCGCCTCCCCTGCCCTCCT 79507 A _ AG A
 AGGA GG AGGG GGC GAGC
 |||| ||| ||| |||
 TCCT CC TCCC CCG CTCG
 C G CT C
 GAM2301 FLJ10035 3' CTGCCCTTCCCTTTCCTCCT 36212 A AG
 AG AGGA GAGGGAGGGCAG
 || ||| |||||
 TC TCCT TTCCTTCCCGTC
 C _
 GAM2301 FLJ10142 3' GCTTGCCCTTCCCTTCCCTCC 36321 A _ A
 GGA GGAGGGA GGGCAG GC
 ||| ||||| ||||| ||
 CCT CCTTCCT CCCGTT CG
 C T C
 GAM2301 FLJ10330 5' CTCCCCCCCCTCCTTCCCTC 36505 A A CA
 GA GGAAGGAGGG GGG GAG
 || ||||| ||| |||

		CT CCTTCCTCCC CCC CTC		
		C _ C_		
GAM2301	FLJ10330	5' GCTTGGCCCCCTCCCCCCCCTC 36508	A A_	CA__
		C GGA GG GGGAGGG GAGC		
		CCT CC CCCTCCC TTCG		
		C CC CCGG		
GAM2301	FLJ10375	3' GCCCCACCCTGTCTGCTCCTTC 36558	_ _	A_
		GAAGGA AGG AGGG GGGC		
		CTTCCT TCT TCCC CCCG		
		CG G AC		
GAM2301	FLJ10743	3' TCTGCCCCCTACCTTCCCTC 37090	A	A A
		GA GGAAGG GGG GGGCAGA		
		CT CCTTCC TCC CCCGTCT		
		C A _		
GAM2301	FLJ10781	3' GCCCTGCCATATTCTTCCT 37172	_ _	G
		AGGAAGGA GG AGGGC		
		TCCTTCTT CC TCCCG		
		ATA G		
GAM2301	FLJ10922	3' GCCCTACGCCCTCCTTGCT 37403	G	_ _ _
		AG AAGGAGGG AGGGC		
		TC TTCCTCCC TCCCG		
		G CGCA		
GAM2301	FLJ11078	3' GCCCTCCCTCCCTCCTTC 37595	A	_
		GAAGGA GGAGGGAGGG C		
		CTTCCT CCTCCCTCCC G		
		C T		
GAM2301	FLJ11099	3' CTCTGCCACATCACTTCCTTCT 37604	GA	GAG
		AGAAGGAAG GG GGCAGAG		
		TCTTCCTTC CT CCGTCTC		
		A_ ACA		
GAM2301	FLJ11783	5' CTGAACCCCTCCTCCCTTTC 46548	AG	_ _
		GGAAGG GGAGGG CAG		
		CTTTCC CCTCCC GTC		
		CT CAA		
GAM2301	FLJ11783	5' TTCCTCCCTCCCTCCCTCCT 46552	A	CA
		AGGA GGAGGGAGGG GAG		
		TCCT CCTCCCTCCC CTT		
		C TC		
GAM2301	FLJ12089	3' CCCGCCCTTCTTCCCTCT 44949	A	A
		AGA GGAAGGAGGG GGG		

TCT CTTCTTCCC CCC
 C G
 GAM2301 FLJ12132 3' GCCTGCCTTGCCTTGCCTTCC 47102 _ _ A
 GGAAGG AGGG AGGGCAG GC
 ||||| ||| ||||| ||
 CCTTCC TTCC TTCCGTC CG
 G G C
 GAM2301 FLJ12529 3' GCCCCACCCCTTCCCTTTC 46086 _ A A_
 GAA GGAAGG GGG GGGC
 ||| ||||| ||| ||||
 CTT CCTTCC CCC CCCG
 TC _ AC
 GAM2301 FLJ12650 3' CTTTCCCCACCTCCCTCC 44821 A GA C
 GGA GGAGG GGG AGAG
 ||| ||||| ||| ||||
 CCT CCTCC CCC TTTC
 C AC _
 GAM2301 FLJ13102 3' CTCCACTCCCCTTCTTTT 46529 AG GGCA
 AGAAGGAAGG GGAG GAG
 ||||| ||| |||
 TTTTCCTTCC CTC CTC
 _ AC_
 GAM2301 FLJ13491 5' CTCCCTCCTCCTCCTTCC 45217 G CA
 GGAAGGAGG AGGG GAG
 ||||| ||| |||
 CCTTCCTCC TCCT CTC
 _ CC
 GAM2301 FLJ13491 5' GCCCCGCTCCCTCCTCCTCCT 45219 A A _
 AG AGGA GGAGGGA GGGC
 || ||||| ||||| ||||
 TC TCCT CCTCCCT CCCG
 C _ CGC
 GAM2301 FLJ13798 3' GCTCCTAGAAGCCTCCCTCCTA 88475 A GCA____
 CC GG AGGAGGGAGG GAGC
 || ||||| ||||| ||||
 CC TCCTCCCTCC CTCG
 A GAAGATC
 GAM2301 FLJ13855 3' CTCTGGAGGCTCCTCCCCTTCT 43848 AA _ AGGG
 AGAAGG GGAGG G CAGAG
 ||||| ||||| ||| ||||
 TCTTCC CCTCC C GTCTC
 _ T GGAG
 GAM2301 FLJ13855 3' CTTTTCCTCCCTGCCTTCCTTC 43850 _ C
 GAAGGAAGG AGGGAGGG AGAG
 ||||| ||||| ||||| ||||
 CTTTCCTTCC TCCCTCCT TTTC
 G _
 GAM2301 FLJ13881 3' GCTCCCTGTCCTCCTTTCTTCC 45642 _
 GGAAGGAGGGAGGGCA GAGC
 ||||| ||||| ||||| ||||

			CCTTCTTTCTCCTGT CTCG		
			CC		
GAM2301	FLJ14100	5'	GCTCTATGTCCCCTCGCCCTCT 47336	A A A	___
			GGA GG GGG GGGCA GAGC		
			TCT CC CTC CCTGT CTCG		
			C G C AT		
GAM2301	FLJ14154	3'	CTTGGGTCTCTCCCCGCCCTCC 46230	A A_	A_
			GGA GG GGGAGGGC GAG		
			CCT CC CCCTCCTG TTC		
			C GC GG		
GAM2301	FLJ14249	3'	GTTCTTCCTCCTTCCCCCT 42645	AA	
			AG GGAAGGAGGGAGGGC		
			TC CCTTCCTCCTTCTTG		
			CC		
GAM2301	FLJ14249	3'	GTTCTTCCTCCTTCCCCCT 42646	AA	
			AG GGAAGGAGGGAGGGC		
			TC CCTTCCTCCTTCTTG		
			CC		
GAM2301	FLJ14299	3'	CTCCCTCTCCCTCCTCCT 47552	A	CA
			AGGA GGAGGGAGGG GAG		
			TCCT CCTCCCTCTC CTC		
			_ C_		
GAM2301	FLJ14299	3'	GCCCCCTCACCTCCTCCCTCT 47553	A A	A___
			AGA GGA GGAGGG GGGC		
			TCT CCT CCTCCC CCG		
			C _ ACTCC		
GAM2301	FLJ14326	3'	CCCGTCCCCCTTCCTTGCT 50767	_	A _
			AG AAGGAAGG GGGA GGG		
			TC TTCCTTCC CCCT CCC		
			G _ G		
GAM2301	FLJ14442	3'	GCCCTCCTCCTCCCTCCT 52385	A	___
			AGGA GGAGG GAGGGC		
			TCCT CCTCC CTCCCG		
			C TC		
GAM2301	FLJ14816	3'	CTCTAGCCTCCCTCTCCCT 52710	AA	GC
			AGG GGAGGGAGG AGAG		
			TCC TCTCCCTCC TCTC		
			C_ GA		
GAM2301	FLJ20079	3'	CCCTCCCCGCCCCCTTCT 34969	AA A_	
			AGAAGG GG GGGAGGG		

TCTTCC CC CCCTCCC
 C_ GC
 GAM2301 FLJ20079 3' TCTCCCCCCTCCCCGCCCCCT 34980 AA AA_ A C
 AG GG GGAGGG GGG AGA
 || || ||||| ||| |||
 TC CC CCTCCC CCC TCT
 CC GCC _ _
 GAM2301 FLJ20294 3' CTGCCCTCTTCCTCCCCT 35353 AA _
 AGG GGAGG GAGGGCAG
 ||| ||||| |||||
 TCC CCTCC CTCCCGTC
 _ TT
 GAM2301 FLJ20337 3' CTCCTGGCCCCCTCTTCCCTCT 35442 A GA A_ C
 AGA GGAAG GGG GGG AG
 ||| ||||| ||| ||| ||
 TCT CCTTC CCC TCC TC
 C TC GG _
 GAM2301 FLJ20359 3' GCCCTGGGTCTCTCCACCTCT 35517 A AA _
 AGA GG GGAGGG AGGGC
 ||| || ||||| |||||
 TCT CC CCTCCT TCCCG
 C AC GGG
 GAM2301 FLJ20450 3' GCTTCCATCCCTCCTTCCTTCT 35639 G CA
 AGAAGGAAGGAGGGA GG GAGC
 ||||| ||||| || |||||
 TCTTCCTTCCTCCCT CC TTCG
 A _
 GAM2301 FLJ20548 3' GCCCCACCCCTGCCCTTTT 35819 A_ A GA
 AGAAGG AGG GG GGGC
 ||||| ||| || |||||
 TTTTCC TCC CC CCG
 CCG _ AC
 GAM2301 FLJ20568 3' GCCCTCCCACCTTCCTTCT 35846 A _
 AGAAGGAAGG GGGAGGG C
 ||||| ||||| ||||| |
 TCTTCCTTCC CCCTCCC G
 A C
 GAM2301 FLJ20920 3' GCCAGGCCCTCCCTCCTGTCC 47889 _ AGA_
 GGA AGGAGGGAGGGC GC
 ||| ||||| ||||| ||
 CCT TCCTCCCTCCCG CG
 G GACC
 GAM2301 FLJ20967 5' CTTTCCCTCCCTCCCTTCC 42207 _ C
 GGAAGG AGGGAGGG AGAG
 ||||| ||||| ||||| |||||
 CCTTCC TCCCTCCC TTTC
 C _
 GAM2301 FLJ21156 3' GCTCTTTTCCCCTCTCCCTCC 45121 A A C_
 GGA GGAGGG GGG AGAGC
 ||| ||||| ||| |||||

CCT CCTCTC CCC TCTCG
 C _ TTT
 GAM2301 FLJ21324 5' CTCTGCCCCGTCCACCTTCC 92853 A GA
 GGAAGG GG GGGCAGAG
 ||||| || |||||
 CCTTCC CC CCCGTCTC
 A TG
 GAM2301 FLJ21736 3' GCGGGTCCTCCCTCCCTTCC 46785 _ AGA
 GGAAGG AGGGAGGGC GC
 ||||| ||||| ||
 CCTTCC TCCCTCCTG CG
 C GGC
 GAM2301 FLJ21919 3' GCCCCTAGCCCCTTCCCTCCTC 43736 A _ _ A_
 CT AGGA GGAGGGA GGGC AG GC
 ||| ||||| ||| || ||
 TCCT CCTCCCT CCCG TC CG
 _ TC A CC
 GAM2301 FLJ21940 3' CTCTTTCCTCCCTCTCTTCCT 43385 _ C
 AGGAAG GAGGGAGGG AGAG
 ||||| ||||| ||||
 TCCTTC CTCCCTCCT TCTC
 T T
 GAM2301 FLJ21940 3' TTCTCCCTCCCTCCTTCC 43388 C
 GGAAGGAGGGAGGG AGAG
 ||||| ||||| ||||
 CCTTCCTCCCTCCC TCTT
 _
 GAM2301 FLJ22127 3' GCCTGCCCTCACCCACCCTCT 43200 A A_ _ A
 GGA GG GG GAGGGCAG GC
 ||| || || ||||| ||
 TCT CC CC CTCCCGTC CG
 C AC A C
 GAM2301 FLJ22169 3' CCTGCGCTCCTTCTCCCC 44231 AA G A
 GG GGAGGGAG GCAG G
 || ||||| |||| |
 CC TCTTCCTC CGTC C
 CC G
 GAM2301 FLJ22408 3' TGTCCCACCTCCTCCCTTC 45989 A GA
 GAAGG AGGAGG GGGCA
 ||||| ||||| ||||
 CTTCC TCCTCC CCTGT
 C AC
 GAM2301 FLJ22477 3' CTCCACCCCACTCCTTTT 45673 _ A GCA
 GGAAGGAG GG GG GAG
 ||||| || || |||
 TTTTCCTC CC CC CTC
 A _ AC_
 GAM2301 FLJ22570 3' GCCTGCCCTGCCCTCCTC 46362 A _ A
 GA GGAGGG AGGGCAG GC
 || ||||| ||||| ||

CT CCTCCC TCCCGTC CG
 _ G C
 GAM2301 FLJ22582 3' GCCCCCTAACCTCTTTCCCCCT 47457 AA GA____
 AG GGAAGGAGG GGGC
 || ||||| |||
 TC CCTTTCTCC CCG
 CC AATCC
 GAM2301 FLJ22795 3' GCTCAGATTCCCACCCCCCTC 47635 A A A A CA____
 CCTCT AGA GGA GG GGG GGG GAGC
 ||| ||| ||| ||| |||
 TCT CCT CC CCC CCC CTCG
 C C C A TTAGA
 GAM2301 FLJ22938 3' CTGTCCACCCCTCCTTCC 45484 A_
 GGAAGGAGGG GGGCAG
 ||||| |||||
 CCTTCCTCCC CCTGTC
 CA
 GAM2301 FLJ22969 3' GCCCTCCCACTTCCCTCT 69207 A GA
 AGA GGAAG GGGAGGGC
 ||| ||| |||||
 TCT CCTTC CCCTCCCG
 C A_
 GAM2301 FLJ23306 5' GCTCCGCCTTTCCCCACCCT 44849 AA A A
 AGG GG GGGAGGGC GAGC
 ||| ||| ||||| |||
 TCC CC CCTTTCCG CTCG
 CA C C
 GAM2301 FLJ23451 3' CTCTCCAGCTCCCTCCCCGCCT 45787 A AA_ _ C
 CT AGA GG GGAGGGAG GG AGAG
 ||| ||| ||||| ||| |||
 TCT CC CCTCCCTC CC TCTC
 _ GCC GA _
 GAM2301 FLJ23519 3' GCCCTGCCCTTTTCGTCTTCCT 50953 A GA GG_ A
 C GA GGAAG G A GGGCAG GC
 || ||||| ||| ||||| ||
 CT CCTTC C T CCGTC CG
 _ TG TT T C
 GAM2301 FLJ31300 3' GCCCTGCCTCCCTTCCTCC 58931 A AG A_
 GGA GGAGGG GGCAG GC
 ||| ||||| ||||| ||
 CCT CCTTCC CCGTC CG
 _ CT CC
 GAM2301 FLJ32468 3' CTCTTCCCCACCCCTCT 59708 A AA AG A C
 AGA GG GG GG GGG AGAG
 ||| ||| ||| ||| |||
 TCT CC CC CC CCC TCTC
 _ CA _ T
 GAM2301 FN3K 3' GCCCTGCCCTCCCTTCCCCT 42463 AA A_
 AGG GGAGGGAGGGCAG GC
 ||| ||||| ||||| ||

			TCC CTTCCTCCCGTC CG			
			C_ CC			
GAM2301	FOXH1	5'	GCCTCTTCCCTCCCTTCCCTC 15378 A _ _			
			GA GGAAGG AGGGAG GGC			
			CT CCTTCC TCCTTC CCG			
			C C T			
GAM2301	FREQ	3'	CTCTGCCTTGCCCTCGTCC 27372 AG _			
			GGA GAGGG AGGGCAGAG			
			CCT CTCCC TTCCGTCTC			
			G_ G			
GAM2301	FREQ	3'	GCTCTGCCTTCCCTCCTTCCTA 27375 _			
	TCT		AGA AGGAAGGAGGGAGGGCAGAGC			
			TCT TCCTTCCTCCCTTCCGTCTCG			
			A			
GAM2301	FZD9	3'	CTGCCCCCTCCTTGCCCTC 14509 A _ AG			
			GA GG AAGGAGGG GGCAG			
			CT CC TTCCTCCC CCGTC			
			C G _			
GAM2301	GAPCENA	3'	CTCTGCTCTCCTCCCTGCC 25177 A AG			
			GG AGG GGAGGGCAGAG			
			CC TCC CCTCTCGTCTC			
			G CT			
GAM2301	GEMIN7	3'	CTTCACTCCCTCCTCTCTTCT 45558 GA GGCA			
			AGAAG AGGAGGGAG GAG			
			TCTTC TCCTCCCTC TTC			
			TC AC_			
GAM2301	GGTLA4	5'	CTGTGCCCCCTCCCCACCCTC 56050 A AA AG A G			
			GA GG GG GG GGGCA AG			
			CT CC CC CC CCCGT TC			
			C AC CT _ G			
GAM2301	GPA33	3'	GCCTGTTCTCCTGTCCCTCC 20570 A _ A			
			GGA GGA GGGAGGGCAG GC			
			CCT CCT TCCTCTTGTC CG			
			C G C			
GAM2301	GPR88	3'	CCGTGCGCTCCTTCCCTC 42134 A _ G			
			GA GGAAGGAGG GA GG			
			CT CCTTCCTCC CT CC			
			C G G			
GAM2301	GTF2A1	5'	GCCCCCTCCTCCTCCTCT 32404 A _ A			
			AGA GGA AGGAGGG GGGC			

			TCT CCT TCCTCCC CCG			
			— CC —			
GAM2301	GTPBP1	3'	GCTGGTCCCCTCTCCTTCCCTC 16267	A	A	AG
			GA GGAAGGAGGG GGGC AGC			
			CT CCTTCCTCTC CCTG TCG			
			C C G_			
GAM2301	H11	3'	CCTAGGTCCCCCCTTTCTTCT 27635	A	—	
			AGAAGGAAGG GGGA GGG			
			TCTTCTTTCC CCCT TCC			
			C GGA			
GAM2301	HA-1	3'	CCTGCCCTGCCCTCTCCT 66155	AG	—	A
			AGGA GAGGG AGGGCAG G			
			TCCT CTCCC TCCCGTC C			
			— G			
GAM2301	HAAO	3'	CCCACCCTCCTGCCCTTCT 60170	A_		A
			AGAAGG AGGAGGG GGG			
			TCTTCC TCCTCCC CCC			
			CG A			
GAM2301	HAND1	3'	CTCACAGCCCCCTCCCTTC 17878	AAG	A	A_
			GAAGG GAGGG GGGC GAG			
			CTTCC CTCCC CCG CTC			
			— — ACA			
GAM2301	HCRTR1	5'	GCCCAAGCTCCCTCCTCTCCCT 9513	A	—	—
	CT		AGA GGA AGGAGGGA GGGC			
			TCT CCT TCCTCCCT CCG			
			C C CGAA			
GAM2301	HEI10	5'	GCTCCACTTTCTTTCCCTCT 41297	A		A _
			AGA GGAAGGAGGG GG GC			
			TCT CCTTTCTTTC CC CG			
			C A T			
GAM2301	HEMK	3'	GCCCTATCCCCTCCCTTGCT 32957	—	A	A _
			AG AAGG AGG GGG AGGGC			
			TC TTCC TCC CCT TCCCG			
			G C _ A			
GAM2301	HERC3	3'	TTCTCCTTCCTCCCTTCC 28238	AG		C
			GGAAGG GGAGGG AGAG			
			CCTTCC CCTTCC TCTT			
			CT _			
GAM2301	HHLA3	3'	GCCCCACCCCTATCTCCCTTC 23950	A	—	A_
			GAAGG AGG AGGG GGGC			

CTTCC TCT TCCC CCG
 C A CAC
 GAM2301 HIF1AN 3' GCCCTGTGTCTCCTCACCTCT 62669 A A_ G_
 AGA GG AGGAGG AGGGC
 ||| || ||||| ||||
 TCT CC TCCTCT TCCCG
 _ AC GTG
 GAM2301 HIF3A 3' CCCTCCCTCCTCCCTCT 42653 A A
 AGA GGA GGAGGGAGGG
 ||| ||| ||||| ||||
 TCT CCT CCTCCCTCCC
 C _
 GAM2301 HNRPA0 5' GCTCCCCTTCCCTCCCCCTTC 23305 AA CA
 GAAGG GGAGGGAGGG GAGC
 |||| ||||| ||||
 CTTCC CCTCCCTTCC CTCG
 C_ C_
 GAM2301 HRH3 3' GCTCCCACGCCCTCCTCCCTCC 24318 A AG A____
 GGA GG GGAGGGC GAGC
 ||| || ||||| ||||
 CCT CC CCTCCCG CTCG
 _ CT CACC
 GAM2301 HSJ1 3' CTCCCTTCTTCCTTCCTTC 23079 C
 GAAGGAAGGAGGGAGGG AG
 ||||| ||||| ||
 CTTCTTCCTTCTTCCC TC
 _
 GAM2301 HSJ1 3' GCTAGGACTCCCTTCTTCCTTC 23081 GGCAG
 GAAGGAAGGAGGGAG AGC
 ||||| ||||| |||
 CTTCTTCTTCCCTC TCG
 AGGA_
 GAM2301 HSPC182 3' GCCTTCCCTCCCTCCTCCC 27200 A C A
 GG AGGAGGGAGGG AG GC
 || ||||| || ||
 CC TCCTCCCTCCC TC CG
 C T _
 GAM2301 HSPC189 5' GCCCCGCCCAACCTTCCTTC 96989 A_ A_
 GAAGGAAGG GGG GGGC
 ||||| ||| ||||
 CTTCTTCC CCC CCG
 AAC GC
 GAM2301 HZFW1 3' GCTATTTCCCTCTCTCCTCCT 48221 A CAG_
 AGGA GGAGGGAGGG AGC
 ||| ||||| |||
 TCCT CCTCTCTCCC TCG
 _ CTTTA
 GAM2301 ISL2 3' GCTCTGCCCTCTCCTCTCCTCT 71400 _ AG _
 CT AGA AGGA GAGG GAGGGCAGAGC
 ||| ||| ||| ||||| ||||

TCT TCCT CTCC CTCCCGTCTCG
 C _ T
 GAM2301 ITGA10 3' CTCTGCTTCCCTCCTCCT 60088 A G
 AGGA GGAGGGAGG CAGAG
 ||| ||||| ||||
 TCCT CCTCCCTTC GTCTC

_ _
 GAM2301 ITM3 3' GCCCTCCTCCTTCCCCCT 48891 AA G
 AG GGAAGGAGG AGGGC
 || ||||| ||||
 TC CCTTCCTCC TCCCG
 CC _

GAM2301 ITM3 3' GCTCTCTGGCCCTCCTCCTTCC 48892 G _
 GGAAGGAGG AGGGC AGAGC
 ||||| |||| ||||
 CCTTCCTCC TCCCG TCTCG
 _ GTC

GAM2301 K6HF 3' GCTCCACCTCCCTCCCTCCCTC 17438 A CA_
 C GGA GGAGGGAGGG GAGC
 ||| ||||| ||||
 CCT CCTCCCTCCC CTCG
 C TCCAC

GAM2301 KCNK15 3' GCTAAGTCCCCTCCCTCCTTTC 42553 CAG_
 GGAAGGAGGGAGGG AGC
 ||||| |||| ||||
 CTTTCCTCCCTCCC TCG
 CTGAA

GAM2301 KIAA0057 3' CCCTCCCTGCCTCCTCCT 25407 A A _
 AG AGGA GG AGGGAGGG
 || |||| || |||||
 TC TCCT CC TCCCTCCC
 C _ G

GAM2301 KIAA0125 5' TTCTTCCCTCGCTCCTCCT 61129 A G C
 AGGA GGAG GAGGG AGAG
 ||| |||| |||| ||||
 TCCT CCTC CTCCC TCTT
 _ G T

GAM2301 KIAA0153 3' GCCTGCCCTCACCCCTCACC 31398 A_ A _ A
 GG AGG GG GAGGGCAG GC
 || |||| || ||||| ||
 CC TCC CC CTCCCGTC CG
 AC _ A C

GAM2301 KIAA0194 3' GCTTTTTTCCCTCCCTCTTCC 66592 G C_
 GGAAG AGGGAGGG AGAGC
 |||| ||||| ||||
 CCTTC TCCCTCCC TTTCG
 _ TTTT

GAM2301 KIAA0211 3' TTGCCCTCCTCCCTGTCT 28290 A AA GA
 AGA GG GGAGG GGGCAG
 ||| || |||| |||||

		TCT TC CCTCC CCCGTT			
		G _ TC			
GAM2301	KIAA0222	3' CTTTGCCTCCCCGCCCCT	28396	AA A AG	
		AGG GG GGG GGCAGAG			
		TCC CC CCC CCGTTTC			
		_ G CT			
GAM2301	KIAA0226	3' CTCCGTTCTCTCCCCTTCC	64257	A A	
		GGAAGG GGGAGGGC GAG			
		CCTTCC CTCTCTTG CTC			
		C C			
GAM2301	KIAA0227	3' CTTAGCCCCTGCCTCCTTCC	61348	G _ A	
		GGAAGGAGG AGGG C GAG			
		CCTTCCTCC TCCC G TTC			
		G C A			
GAM2301	KIAA0237	3' CTTTCCCTCCCTCCCCTCC	29222	A_ C	
		GGA GGAGGGAGGG AGAG			
		CCT CCTCCCTCCC TTTC			
		CC _			
GAM2301	KIAA0247	5' CTCCTCCCTCCCTCCCGCC	29068	AA CA	
		GG GGAGGGAGGG GAG			
		CC CCTCCCTCCC CTC			
		GC TC			
GAM2301	KIAA0247	3' GCCCTTCCTCCCTCTCCCT	29072	AA A	
		AG GGA GGAGGGAGGGC			
		TC TCT CCTCCTTCCCG			
		CC C			
GAM2301	KIAA0265	3' CTCACATACTCCCTCTTCCTTC	70439	G GGCA_	
	T	AGAAGGAAG AGGGAG GAG			
		TCTTCCTTC TCCCTC CTC			
		_ ATACA			
GAM2301	KIAA0275	3' TCTGCCCTTCTCCCTCCT	29334	A AG	
		AGGA GG GGAGGGCAGA			
		TCCT CC CTTCCCGTCT			
		_ CT			
GAM2301	KIAA0280	3' CTCTATCCCCTTCCTCCT	93296	C_	
		AGGAGGGAGGG AGAG			
		TCCTCCTTCCC TCTC			
		CTA			
GAM2301	KIAA0285	3' GCTCCTCATCCCTCCCTCCCC	29685	AA CA_	
	TT	AAGG GGAGGGAGGG GAGC			

TTCC CCTCCCTCCC CTCG
 C_ TACTC
 GAM2301 KIAA0293 3' CCCTGGTAACTACCTTCCTTCT 61237 _ GG____
 AGAAGGAAGG AG AGGG
 ||||| || |||
 TCTTCCTTCC TC TCCC
 A AATGG
 GAM2301 KIAA0296 3' CCCTACTCCCTGTCCCTCT 28771 A _ A _
 AGA GGA AGG GGG AGGG
 ||| ||| ||| ||| |||
 TCT CCT TCC CTC TCCC
 C G _ A
 GAM2301 KIAA0356 3' CTCTTCCCGCCTCCCCTCC 66772 A_ GA C
 GGA GGAGG GGG AGAG
 ||| |||| ||| |||
 CCT CCTCC CCC TCTC
 CC G_ T
 GAM2301 KIAA0356 3' GCCCTCCCCCACCCCTCT 66776 A AA A
 AGA GG GG GGGAGGGC
 ||| || ||| |||||
 TCT CC CC CCCTCCCG
 C CA C
 GAM2301 KIAA0397 3' GCCATCCCCACTTCCTCCT 62350 A GA G
 AG AGGAAG GGGG GGC
 || |||| ||| |||
 TC TCCTTC CCCT CCG
 C AC A
 GAM2301 KIAA0415 3' GCTCCGCCCCCGGTCTCCTCTT 94166 A ____ A A
 AGGA GGAG GG GGGC GAGC
 |||| |||| || |||| |||
 TTCT CCTC CC CCGG CTCG
 _ TGG _ C
 GAM2301 KIAA0427 5' CCCTCCCTCCCTCCCCTCT 29376 A_ A
 AGA GGA GGAGGGAGGG
 ||| ||| ||||| |||
 TCT CCT CCTCCCTCCC
 CC C
 GAM2301 KIAA0427 5' CTCGTCCCTCCCTTCCCCT 29377 AA CA
 AGG GGAGGGAGGG GAG
 ||| ||||| ||| |||
 TCC CTTCCCTCCC CTC
 C_ TG
 GAM2301 KIAA0427 3' CTGCCTTCTTCCTCCCTCC 29379 A _
 GGA GGAGG GAGGGCAG
 ||| |||| |||||
 CCT CCTCC CTTCCGTC
 C TT
 GAM2301 KIAA0427 3' GCCCTGGCCCTCCCCTTC 29384 AA _
 GAAGG GGAGGG AGGGC
 |||| |||| ||||

CTTCC CCTCCC TCCCG
 — GG
 GAM2301 KIAA0447 3' CTGCCCTCCTATCCCTTCC 72119 A__
 GGAAGG GGGAGGGCAG
 ||||| |||||
 CCTTCC TCCTCCCGTC
 CTA
 GAM2301 KIAA0447 3' CTTCCCCTCCCTCTCCCT 72121 AA CAG
 AGG GGAGGGAGGG AG
 ||| ||||| ||
 TCC TCTCCCTCCC TC
 C_ CTG
 GAM2301 KIAA0450 5' CTCTCCTCCCCTCCCCTCC 28349 A_ AG C
 GGA GGAGGG GG AGAG
 ||| ||||| || ||||
 CCT CCTCCC CC TCTC
 CC CT _
 GAM2301 KIAA0450 5' CTGGCCTCTCCTCCCCTCC 28353 A_ _ G
 GGA GGAGG GAGG CAG
 ||| ||||| ||| |||
 CCT CCTCC CTCC GTC
 CC T G
 GAM2301 KIAA0450 5' CTGTGCCCTCCTATCCCCCT 28355 AA _ _ G
 AGG GGA GGGAGGG CA AG
 ||| ||| ||||| || ||
 TCC CCT TCCTCCC GT TC
 C_ A C G
 GAM2301 KIAA0450 3' GCCCTGCCTCCCTCCTGCC 28359 A G A_
 GG AGGAGGGAGG CAG GC
 || ||||| ||| ||
 CC TCCTCCCTCC GTC CG
 G _ CC
 GAM2301 KIAA0450 5' CTATCCCCCTCCTTCTCTCT 28347 AG A GC
 AGA GAAGGAGGG GG AG
 ||| ||||| || ||
 TCT CTCCTCCC CC TC
 CT _ TA
 GAM2301 KIAA0450 3' CTCTCCCTGCCTCCCTCT 28348 A G C
 GGA GGAGG AGGG AGAG
 ||| ||||| ||| |||
 TCT CCTCC TCCC TCTC
 C G _
 GAM2301 KIAA0495 5' GCCCGGTTCCCTCCCCCTTCT 63269 AA ____
 AGAAGG GGAGGGA GGGC
 ||||| ||||| ||||
 TCTTCC CCTCCCT CCCG
 C_ TGC
 GAM2301 KIAA0513 3' GCGGGGCTCTCCCTCCTCCT 29041 A AGA
 AGGA GGAGGGAGGGC GC
 ||||| ||||| ||| ||

TCCT CCTCCCTCTCG CG
 _ GGG
 GAM2301 KIAA0514 5' CTCCACTCCCTCCCTTTCT 28744 AA _ C
 AGAAGG GGAGGGAG GG AG
 ||||| ||||| || ||
 TCTTTC CCTCCCTC CC TC
 _ A _
 GAM2301 KIAA0522 3' GCTCCTGCCTCCCTCTCCCCTC 72424 A AA G _
 T AGA GG GGAGGGAGG CAG AGC
 ||| || ||||| || |||
 TCT CC TCTCCCTCC GTC TCG
 _ CC _ C
 GAM2301 KIAA0544 3' GCTCCCCCGCTCCCTCCT 71467 _ CA
 AGGAGGGAG GG GAGC
 ||||| || |||
 TCCTCCCTC CC CTCG
 G CC
 GAM2301 KIAA0544 3' GCTCCCCCGCTCCCTCCTTCC 71468 _ CA
 GGAAGGAGGGAG GG GAGC
 ||||| || |||
 CCTTCCTCCCTC CC CTCG
 G CC
 GAM2301 KIAA0545 3' GCCTGCTGCCTCTCTCCCTCC 63845 A _ A
 GGA GGAGGGAGG GCAG GC
 ||| ||||| ||| ||
 CCT CCTCTCTCC CGTC CG
 C GT C
 GAM2301 KIAA0552 3' GCTCCAGACCTCTCTCCCTCCT 28993 A GCA_
 AGGA GGAGGGAGG GAGC
 ||| ||||| |||
 TCCT CCTCTCTCC CTCG
 C AGAC
 GAM2301 KIAA0553 3' CTGCCCTCCCACCCTCCT 70448 A A
 AGGA GG GGGAGGGCAG
 ||| || |||||
 TCCT CC CCCTCCCGTC
 C A
 GAM2301 KIAA0574 3' GCCTTCCCCCCTCCTCT 69817 A A A
 AGA GGA GG GGGAGGGC
 ||| ||| || |||||
 TCT CCT CC CCCTTCCG
 _ C C
 GAM2301 KIAA0638 3' GCTCTGCCCCATTGTTCTCCTT 72830 A____
 TC GGAAGGAGGG GGGCAGAGC
 ||||| |||||
 CTTTCCTCTT CCGTCTCG
 GTTAC
 GAM2301 KIAA0648 3' CTCTGTTCTCCCCCTTCC 83540 A
 GGAAGG GGGAGGGCAGAG
 ||||| |||||

CCTTCC CCCTCTTGTCTC

GAM2301 KIAA0668 3' CTCCCTTCTTCCCTTCCCTCT 67120 A C
AGA GGAAGGAGGGAGGG AG
||| ||||| ||
TCT CCTTCTTCTTCCC TC
C _

GAM2301 KIAA0668 3' GCTCCAGCAGCTCCCTTCTTCC 67122 G_ A_
TTC GAAGGAAGGAGGGAG GC GAGC
||||| || ||||
CTTCTTCTTCCCTC CG CTCG
GA AC

GAM2301 KIAA0669 5' GCTCTGCCCTCCCCGGTTTCC 29432 GA_
GGAAG GGGAGGGCAGAGC
|||| |||||
CCTTT CCCTCCCGTCTCG
GGC

GAM2301 KIAA0721 3' CCCTCCTCCTCCCCTCT 41650 A A G
AGA GG AGGAGG AGGG
||| || |||||
TCT CC TCCTCC TCCC
C C _

GAM2301 KIAA0748 3' GCCCCACCCCTATCTCCCTTT 29616 A _ A__
GAAGG AGG AGGG GGGC
|||| || |||||
TTTCC TCT TCCC CCGG
C A CAC

GAM2301 KIAA0759 3' CCCTCCCTTCCCCCTCCT 67885 A AA
AG AGG GGAGGGAGGG
|| ||| |||||
TC TCC CTTCCCTCCC
C CC

GAM2301 KIAA0767 3' CCTGCCCTTCTCCGTTCC 61254 _ G A
GGAA GGAGG AGGGCAG G
|||| ||||| |||||
CCTT CCTCT TCCCGTC C
G _

GAM2301 KIAA0773 3' GCCCTATCTCCTTCTTTC 28724 GG
GAAGGAAGGAG AGGGC
||||| |||||
CTTTCTTCTCCTC TCCCG
TA

GAM2301 KIAA0794 3' TTCTGCCTCCCCCTCCCCC 81239 AA A_
GG GGAGGG GGGCAGAG
|| ||||| |||||
CC CCTCCC TCCGTCTT
CC CC

GAM2301 KIAA0819 3' GCGACTCCCGCCCTTCCTTC 64331 A_ G_
GAAGGAAGG GGGAG GC
||||| ||||| ||

			CTTCCTTCC CCCTC CG		
			CG AG		
GAM2301	KIAA0821	3'	CTCCTTCCTCTCTCCTCT 30606	A	CA
			AGGA GGAGGGAGGG GAG		
			TCCT CCTCTCTCCT CTC		
			TC		
GAM2301	KIAA0843	3'	GCTCCTTAACCCTCCTCCTTCT 30803	A	___
			AGAAGGA GGAGGG AGG GC		
			TCTTCCT CCTCCC TCC CG		
			AAT T		
GAM2301	KIAA0844	3'	CTGTCTTCCCCTCCTTCCCTC 30891	A	___
			GA GGAAGGAGGG AGGGCAG		
			CT CCTTCCTCCC TTCTGTC		
			C C		
GAM2301	KIAA0903	3'	CTTTTCCTCCCTCCTTTC 71912	C	
			GGAAGGAGGGAGGG AGAG		
			CTTTCCTCCCTCCT TTTC		

GAM2301	KIAA0937	3'	CCCTGACCCCTTTCCTTCT 93224	A	___
			AGAAGGAAGG GGG AGGG		
			TCTTCCTTTC CCC TCCC		
			AG		
GAM2301	KIAA0953	3'	CTTTGCCCCCTCCCCTCCCCT 67327	AA	A___
			AGG GGAGGG GGGCAGAG		
			TCC CCTCCC CCCGTTTC		
			CTCC		
GAM2301	KIAA1016	5'	GCCCACACCCTCCTCCCCTC 93386	A A	A___
			GA GG AGGAGGG GGGC		
			CT CC TCCTCCC CCCG		
			C C ACA		
GAM2301	KIAA1026	5'	GCTCCTCCTCCTCCTTCT 71740	A	GA
			AGAAGGA GGAGG GGGC		
			TCTTCCT CCTCC CTCG		
			TC		
GAM2301	KIAA1032	3'	CTCCATTCCCTCCCCTCT 66724	A AA	___ C
			AG AGG GGAGGGAG GG AG		
			TC TCC CCTCCCTT CC TC		
			A		
GAM2301	KIAA1034	3'	GCCCTGGCCCCATCCTTCC 63131	___	___
			GGAAGGA GGG AGGGC		

CCTTCCT CCC TCCCG
 A CGG
 GAM2301 KIAA1037 3' TTCTGCCCTCCTTCCCATCC 31139 A_
 GGA GGAGGGAGGGCAGAG
 ||| |||||
 CCT CCTTCCTCCCGTCTT
 AC
 GAM2301 KIAA1042 3' GCTCCCACCTCCCTCTCTTCC 31050 _ GCA
 GGAAG GAGGGAGG GAGC
 ||||| ||||| ||||
 CCTTC CTCCCTCC CTCG
 T ACC
 GAM2301 KIAA1128 3' GCTCCGCCCCCCCTCAGGCTCT 69008 AG__ A A
 TTC GAAGGA GAGGG GGGC GAGC
 ||||| ||||| ||||| |||||
 CTTTCT CTCCC CCG CTCG
 CGGA C C
 GAM2301 KIAA1130 3' GCTCAGTCTTCCCTCCCCCTCC 63094 A__ A
 GGA GGAGGGAGGGC GAGC
 ||| ||||| ||||| |||||
 CCT CCTCCCTTCTG CTCG
 CCC A
 GAM2301 KIAA1130 3' GCTCCGCCCTGCCTTCC 63095 AG A A
 GGAAGG GG GGGC GAGC
 ||||| || ||||| |||||
 CCTTCC TC CCG CTCG
 G_ _ C
 GAM2301 KIAA1157 3' TCTGCCCCCGCCCCCCTTCT 72706 AA A A
 AGAAGG GG GGG GGGCAGA
 ||||| || ||||| |||||
 TCTTCC CC CCC CCGTCT
 CC G _
 GAM2301 KIAA1183 3' GCCCTCCCCTCCCCTCTTC 63197 AA _
 GAAGG GGAGGG AGGGC
 ||||| ||||| |||||
 CTTCT CCTCCC TCCCG
 CC C
 GAM2301 KIAA1193 3' GCCCTGCAGGTCTTCCTTCT 68273 AGGG_
 AGAAGGAAGG AGGGC
 ||||| ||||| |||||
 TCTTCCTTCT TCCCG
 GGACG
 GAM2301 KIAA1238 5' CTCCCCCTCCTCTCCTTCC 71634 _ CA
 GGAAGGAG GGAGGG GAG
 ||||| ||||| ||||| |||||
 CCTTCCTC CCTCCC CTC
 T C_
 GAM2301 KIAA1240 3' CTCTGGCCCTCCTTCCCTC 67289 A _
 GA GGAGGGAGGGC AGAG
 || ||||| ||||| |||||

		CT CCTTCCTCCCG TCTC		
		C G		
GAM2301	KIAA1246	5' CTTTTCCTCCCTTCTTCT 93683	A	C
		GGAAGGAGGG GGG AGAG		
		TCTTCTTCCC CCC TTTC		
		- T		
GAM2301	KIAA1266	3' CCCTCCACCTCCTCCCTTCT 66694	A	-
		AGAAGG AGGAGG GAGGG		
		TCTTCC TCCTCC CTCCC		
		C AC		
GAM2301	KIAA1359	5' CTCTGCCCTTTTCTTCTTCT 91081	G	A
		AGAAG AAGGAGGG GGGCAGAG		
		TCTTC TTCTTTTC CCCGTCTC		
		- -		
GAM2301	KIAA1388	5' GCTCCTCTCCTCCCTCCCTTCC 95229	-	CA-
		GGAAGG AGGGAGGG GAGC		
		CCTTCC TCCCTCCT CTCG		
		C CTC		
GAM2301	KIAA1462	3' CCCTCCCTCCCTCCCTTC 93026	AA-	
		GAAGG GGAGGGAGGG		
		CTTCC CCTCCCTCCC		
		CTC		
GAM2301	KIAA1465	3' CTCGACCCCTCCTCCTCCCT 61491	A	GA CA
		AGG AGGAGG GGG GAG		
		TCC TCCTCC CCC CTC		
		C TC AG		
GAM2301	KIAA1465	3' GCCCGGCCCTCCTCCCTTT 61500	A	A-
		GAAGG AGGAGGG GGGC		
		TTTCC TCCTCCC CCCG		
		C CGG		
GAM2301	KIAA1530	5' GCCCTGCCGGGCCCTTCTTTC 68563	A	GAG A
		GAAGGAAGG GG GGCAG GC		
		CTTTCTTCC CC CCGTC CG		
		- GGG C		
GAM2301	KIAA1535	3' CCCTAAGTCTCCTTTCCTTCT 80210	-	G-
		AGAAGGAA GGAGG AGGG		
		TCTTCCTT CCTCT TCCC		
		T GAA		
GAM2301	KIAA1535	3' CTCTGCCTGTCCCCTCTCCT 80211	AG	A -
		AGGA G GGGA GGGCAGAG		

TCCT C CCCT TCCGTCTC
 CT _ G
 GAM2301 KIAA1600 3' TTTTCCCCCTCTCCCTCT 71945 A AG A C
 AGA GGA GAGGG GGG AGAG
 ||| ||| ||||| ||| |||||
 TCT CCT CTCCC CCC TTTT
 C _ _ T
 GAM2301 KIAA1602 3' CCCGCCCTTGGTCCCTTCT 65238 _ AG A
 AGAAGG A GAGGG GGG
 ||||| | ||||| |||
 TCTTCC T TTCCC CCC
 C GG G
 GAM2301 KIAA1656 3' GCCTGCGCTCACCTTCCTCCT 66370 A _ G A
 AGGA GGAGG GAG GCAG GC
 ||| ||||| ||| ||||| ||
 TCCT CTTCC CTC CGTC CG
 C A G C
 GAM2301 KIAA1674 3' GCTCTCGTCCGCCTCCCTTCC 69345 AG A _
 GGAAGG GG GGGC AGAGC
 ||||| || ||| |||||
 CCTTCC CC CCTG TCTCG
 CT G C
 GAM2301 KIAA1691 3' GCTCTGCCCTGGCCTTCCTCT 94131 A AGGG
 AGA GGAAGG AGGGCAGAGC
 ||| ||||| ||||| |||||
 TCT CCTTCC TCCCGTCTCG
 _ GG_
 GAM2301 KIAA1691 3' GCTGGCACCCCCCTTCCCTC 94132 A A AGG AG
 GA GGAAGG GGG GC AGC
 || ||||| ||| || |||
 CT CCTTCC CCC CG TCG
 C _ CA_ G_
 GAM2301 KIAA1718 3' CCTTATATCCCACCTTCCCTCT 64973 A A ____
 AGA GGAAGG GGGA GGG
 ||| ||||| ||||| |||
 TCT CCTTCC CCCT TCC
 C A ATAT
 GAM2301 KIAA1751 3' GCCCTGCCCTCCCCATGCCTCC 72159 A A____ A
 T AGGA GG GGGAGGGCAG GC
 ||||| || ||||| ||||| ||
 TCCT CC CCCTCCCGTC CG
 _ GTAC C
 GAM2301 KIAA1828 5' CCCTCCCTCTTCCTCCT 74203 A G
 AG AGGAAG AGGGAGGG
 || ||||| ||||| |||||
 TC TCCTTC TCCCTCCC
 C _
 GAM2301 KIAA1828 5' GCTTTCCTCCCTCCCTCTTCC 74206 A A C
 T AG AGGA GGAGGGAGGG AGAGC
 || ||||| ||||| ||||| |||||

			TC TTCT CCTCCCTCCC TTTCG			
			C C _			
GAM2301	KIAA1878	3'	CTCTCTCTCCCTCCCCC	93366	AA	C
			GG GGAGGGAGGG AGAG			
			CC CCTCCCTCTC TCTC			
			CC _			
GAM2301	KIAA1884	3'	CTGCTCCCTTCCCCCTTCT	73725	AA	A
			AGAAGG GGAGGG GGGCAG			
			TCTTCC CCTTCC CTCGTC			
			C _ _			
GAM2301	KIAA1904	3'	CTCCCTTCCTCCCTCCCTCT	73866	A A	C
			AGA GGA GGAGGGAGGG AG			
			TCT CCT CCTCCTTCCC TC			
			C C _			
GAM2301	KIAA1904	3'	CTTCCCTCCCTCCCTCCCTTC	73870	AA_	C
			GAAGG GGAGGGAGGG AG			
			CTTCC CCTCCCTCCC TC			
			CTC T			
GAM2301	KIAA1922	3'	GCCCTGCCCCCTGCCCTCTCCC	73996	AA	A__ A
	CT		AGG GGAGGG GGGCAG GC			
			TCC TCTCCC CCGTC CG			
			CC GTCC C			
GAM2301	KIAA1949	5'	GCCTCTTTCCCTCCTCCTCTC	99696	_ A	C A
			GA AGGA GGAGGGAGGG AG GC			
			CT TCCT CCTCCCTTTC TC CG			
			C _ _ _			
GAM2301	KIAA1949	5'	GCTCTCCGCCCCTCCTTGCCT	99698	_	AG C
			AGG AAGGAGGG GG AGAGC			
			TCC TTCCTCCC CC TCTCG			
			G CG _			
GAM2301	KIF13B	5'	GCCTGAGCCCCCCCATCCCTCC	31566	A _ A _ A	
	T		AGGA GGA GGG GGGC AG GC			
			TCCT CCT CCC CCG TC CG			
			C A C AG _			
GAM2301	KIF13B	3'	GCCTGAGCCCCCCCATCCCTCC	31567	A _ A _ A	
	T		AGGA GGA GGG GGGC AG GC			
			TCCT CCT CCC CCG TC CG			
			C A C AG _			
GAM2301	KPNA6	3'	CTCTGCTTTTCCTTCCTCT	25542	A	
			GGA GGAGGGAGGGCAGAG			

TCT CTCCTTTTCGTCTC
 C
 GAM2301 LBP-9 3' GCTCCTGATTCCTCTTCCTTCT 28048 G GGGCA
 AGAAGGAAG AGGGA GAGC
 ||||| ||| |||
 TCTTCCTTC TCCTT CTCG
 _ AGTC_
 GAM2301 LGALS8 3' CTCTGCCCTCTCTCCTACT 22448 A
 GG AGGAGGGAGGGCAGAG
 || |||||
 TC TCCTCTCTCCCGTCTC
 A
 GAM2301 LGP2 3' CTCCAGGCCCTCCTTCCT 44378 AG__ C
 AGGAAGGAGGG GG AG
 ||||| ||
 TCCTTCCTCCC CC TC
 CGGA _
 GAM2301 LR8 3' GCTCTCCAGACCCTCCTCCTTT 26702 A AG_ C
 CT AGAAGG AGGAGGG GG AGAGC
 ||||| ||| |||
 TCTTTC TCCTCCC CC TCTCG
 C AGA _
 GAM2301 LY6G5B 5' GCCTCCATCCCTCCTTCT 41402 _
 GGAAGGAGGGA GGGC
 ||||| |||
 TCTTCCTCCCT TCCG
 ACC
 GAM2301 MEIS3 3' CTGTCCCCCCCCACCTCCCTTCT 78870 A A A _
 AGAAGG AGG GGG GGG CAG
 ||||| ||| ||| |||
 TCTTCC TCC CCC CCC GTC
 C A C T
 GAM2301 MG61 3' GCCTCCCCGCCTTCCTTCT 43382 A AG
 AGAAGGAAGG GGG GGC
 ||||| ||| |||
 TCTTCCTTCC CCC CCG
 G CT
 GAM2301 MGC10818 5' CCCTCACCTCCTTCATTC 48298 G _
 GAA GAAGGAGG GAGGG
 ||| ||||| |||||
 CTT CTCCTCC CTCCC
 A A
 GAM2301 MGC10986 3' GCTCCAGGACTCCTTCCTTCTT 48326 GGCA_
 AGGAAGGAGGGAG GAGC
 ||||| |||
 TTCTTCCTTCCTC CTCG
 AGGAC
 GAM2301 MGC10986 3' TCCTTCCTTCTTCCTTCT 48328
 AGAAGGAAGGAGGGAGGG
 |||||

TCTTCCTTCTTCCTTCCT

GAM2301 MGC11082 3' GCTAGAGCCCACTCCTTCCT 52073 GGA AG_
AGGAAGGAG GGGC AGC
||||||| ||| |||
TCCTTCCTC CCCG TCG
A__ AGA

GAM2301 MGC11115 3' CTGCCCCTCCCTCTCTCT 51206 AG _
GGA GAGGGAGGG CAG
||| ||||||| |||
TCT CTCCCTCCC GTC
CT C

GAM2301 MGC11266 3' CTCTGCCACCCTCCTGCT 44487 A AG
GG AGGAGGG GGCAGAG
|| ||||||| |||||||
TC TCCTCCC CCGTCTC
G A_

GAM2301 MGC13090 3' GCCCTGCCCTTCTTCCACCCC 52121 AA AA A
CT AG GG GGAGGGAGGGCAG GC
|| || ||||||||| ||
TC CC CTTTCTTCCCGTC CG
CC AC C

GAM2301 MGC15437 5' GCCCGACTCCCTCCTCCTTC 52847 A ____
GAAGGA GGAGGGA GGGC
||||| ||||||| |||
CTTCCT CCTCCCT CCCG
_ CAG

GAM2301 MGC15437 3' GCCCTATCCCCCTCCTTGCTT 52848 G ____
CT AGAAG AAGGAGGG AGGGC
||||| ||||||| |||
TCTTC TTCCTCCC TCCCG
G CCCTA

GAM2301 MGC20255 3' GCTCTGGGCCCTTCTTCCCCC 54538 AA ____
T AGG GGAGGGAGGG CAGAGC
||| ||||||| |||||||
TCC CTTTCTTCCC GTCTCG
C_ CGG

GAM2301 MGC2474 5' GCTCTACTGACGTCCCTCCTTC 43961 G__ C
C GGAAGGAGGGA GG AGAGC
||||||| || |||
CCTTCCTCCCT TC TCTCG
GCAG A

GAM2301 MGC2574 3' GCTCCCATCCCTCCTTCCTCTC 44284 _ G CA
GA AGGAAGGAGGGA GG GAGC
|| ||||||||| || |||
CT TCCTTCCTCCCT CC CTCG
C A _

GAM2301 MGC2668 3' GCTTTGCCCCTCCTCCCCTTC 61195 AA GA
GAAGG GGAGG GGGCAGAGC
||||| ||| |||||||

CTTCC CCTCC CCCGTTTCG
 — TC
 GAM2301 MGC2817 5' GCCCTTCCTCCTCCTCT 70739 A A
 AG AGGA GGAGGGAGGGC
 || ||| |||||
 TC TCCT CCTCCTTCCCG
 C _
 GAM2301 MGC3020 5' CTGCTCTTTCTCCTTCATTC 44122 G GG
 GAA GAAGGAG AGGGCAG
 ||| ||||| |||||
 CTT CTTCTC TCTCGTC
 A TT
 GAM2301 MGC32043 3' GCCCTACTTTCCTCCCTCT 58668 A A _
 AGA GGA GGAGGG AGGGC
 ||| ||| ||||| |||||
 TCT CCT CTTTC TCCCG
 C _ A
 GAM2301 MGC3222 3' CTCTGCACTCCCTCTCCTCT 44543 A AG G
 AGA GGA GAGGGAG GCAGAG
 ||| ||| ||||| |||||
 TCT CCT CTCCCTC CGTCTC
 _ _ A
 GAM2301 MGC3329 3' CTCCCCCGCCTCCTTCC 44245 GA CA
 GGAAGGAGG GGG GAG
 ||||| ||| |||
 CCTTCCTCC CCC CTC
 G_ CC
 GAM2301 MGC3731 3' CTCCAGTTCCTTCTCCCTCT 44477 A A G_ C
 AGA GG AGGAGGGA GG AG
 ||| || ||||| |||
 TCT CC TCTTCCTT CC TC
 C C GA _
 GAM2301 MGC4342 3' GCCCTCCCCGCTCCCTTC 44516 A GA _
 GAAGG AG GGGAGGG C
 ||||| || ||||| |
 CTTCC TC CCCTCCC G
 C GC C
 GAM2301 MGC4415 3' GCTTCTGGCTGCCCCCTTCCCT 49763 A A A G _
 C GA GGAAGG GGG GG CAGA GC
 || ||||| ||| || ||| ||
 CT CTTCC CCC TC GTCT CG
 C _ G G T
 GAM2301 MGC4604 3' GCTCTGCCCCATACCCCTGCC 49796 A A GA__
 GG AGG GG GGGCAGAGC
 || ||| || |||||
 CC TCC CC CCCGTCTCG
 G _ ATAC
 GAM2301 MGC4796 3' GCTTCCCCTCCTCCCTGCT 62167 A A AG
 AG AGG AGGAGGG GGC
 || ||| ||||| |||

			TC TCC TCCTCCC TCG		
			G C CT		
GAM2301	MGC9753	5'	CTGCTGGCCTCCCTTCTCC	54190	A G _
			GGA GGAGGGAGG CAG AG		
			CCT CTTCCCTCC GTC TC		
			_ G G		
GAM2301	MGC9753	3'	GCTCTGCCCCCTGACCCCTT	54194	A GA__
			AAGG GG GGGCAGAGC		
			TTCC CC CCCGTCTCG		
			_ AGTC		
GAM2301	MKP-7	3'	GCCATGGTCCCCCTTCCTTCT	67014	A G__
			AGAAGGAAGG GGGA GGC		
			TCTTCCTTCC CCCT CCG		
			_ GGTA		
GAM2301	MSTP032	3'	GCCCCTGTTCTCCCTTCCTCT	48205	A AG ____
			AGA GGAAGG GGA GGGC		
			TCTCCTTCC CCT CCG		
			_ CT TGTC		
GAM2301	N4BP3	3'	GCCCCACCCTCTACCCATTCC	66855	_____ A_
	TTC		GAAGGAA GGAGGG GGGC		
			CTTCCTT TCTCCC CCG		
			ACCCCA AC		
GAM2301	NAV1	3'	GCTCCTCCTCTCCCCTCT	40324	A AA _ _
			AGA GG GGAG GGAGG GC		
			TCT CC CCTC CCTCC CG		
			_ _ T T		
GAM2301	NFAT5	3'	CCCTCCCTGCCTCCCTTCT	57767	A _
			AGAAGG AGG AGGGAGGG		
			TCTTCC TCC TCCCTCCC		
			C G		
GAM2301	NFAT5	5'	GCCGCTCCCCCCTCCCGCT	57773	AA A A _
			AG GGA GG GGGAG GGC		
			TC CCT CC CCCTC CCG		
			GC C C G		
GAM2301	NFAT5	5'	GCCGCTCCCCCCTCCCGCT	57774	AA A A _
			AG GGA GG GGGAG GGC		
			TC CCT CC CCCTC CCG		
			GC C C G		
GAM2301	NFAT5	3'	TTCTCCCTCCCTCTCCCCT	57780	AA C
			AGG GGAGGGAGGG AGAG		

			TCC TCTCCCTCCC TCTT CC _		
GAM2301	NFAT5	3'	TTCCTCCCTCCCTCCTTTCT 22747	CA	
			AGGAAGGAGGGAGGG GAG 		
			TCTTTCCTCCCTCCC CTT TC		
GAM2301	NINJ2	3'	CTCTACCCCACTGCTTCCTTCT 33723	G GGA C	
			AGAAGGAAG AG GGG AGAG 		
			TCTTCCTTC TC CCC TCTC G AC_ A		
GAM2301	NIR3	3'	GCCCCACCACCTGCCTTCT 66828	A A GA	
			AGAAGG AGG GG GGGC 		
			TCTTCC TCC CC CCG G A AC		
GAM2301	NKX2B T	3'	GCTCTGCCCATGCCTCTCCTTC 11812	A__	
			GGAAGGAGGG GGGCAGAGC 		
			TCTTCCTCTC CCGTCTCG CGTA		
GAM2301	NOVA2	3'	CTGACCCCTCCTTCCTCCCT 11819	A _	
			AGG AGGAGGGAGGG CAG 		
			TCC TCCTTCCTCCC GTC C CA		
GAM2301	NR5A1	3'	GCCCCGCCCCCTCCCTGCT 18274	A A A A_	
			AG AGG AGG GGG GGGC 		
			TC TCC TCC CCC CCG G C _ GC		
GAM2301	NUDT3	5'	CTCCCCCTCCCTGCTTCC 22951	G CA	
			GGAAG AGGGAGGG GAG 		
			CCTTC TCCCTCCC CTC G C_		
GAM2301	NXN	3'	CTCCCCCTCCTTCCTTCC 42673	CA	
			GGAAGGAGGGAGGG GAG 		
			CCTTCCTTCCTCCC CTC C_		
GAM2301	NXN TC	3'	GCCTTCTCCTCCTCCCCCTCCT 42677	_____ -	
			GAAGGA AGGAGG GAGGGC 		
			CTTCCT TCCTCC CTTCCG CCCC T		
GAM2301	OCIA	5'	TTCTCCCTCCCTGCCCCCT 35657	AA _ C	
			AGG GG AGGGAGGG AGAG 		

		TCC CC TCCCTCCC TCTT		
		C_ G _		
GAM2301	OSBPL7	5' GCTCTGACATCTCCTTCCTTCC 35305	G__	
		GGAAGGAGGGAGG CAGAGC		
		CCTTCCTTCCTCT GTCTCG		
		ACA		
GAM2301	P311	3' GCTGAGAGTCCCCCCCCCACC 17677	AA A A AG__	
	T	AGG GG GGG GGGC AGC		
		TCC CC CCC CCTG TCG		
		AC C C AGAG		
GAM2301	P5326	3' GCTATACCTCCCCTTCCTCCT 49551	A AG GCAG	
		AG AGGAAGG GGAGG AGC		
		TC TCCTTCC CCTCC TCG		
		C _ ATA_		
GAM2301	P66	3' CCTTCCACCTCCTCCCTTC 40737	A _	
		GAAGG AGGAGG GAGGG		
		CTTCC TCCTCC CTTCC		
		C AC		
GAM2301	P66	3' CTCCTCCCTTCCCTCCTCCT 40739	A _ CA	
		AGGA GGAGGGA GGG GAG		
		TCCT CCTCCCT CCC CTC		
		_ T TC		
GAM2301	PAK6	3' GCCCCACCTCTGCCCTTC 39809	AA A_	
		GAAGG GGAGGG GGGC		
		CTTCC TCTCCC CCG		
		CG AC		
GAM2301	PAK7	5' GCTCTGCCTCTCACCCCCTCC 70226	A A _ _	
		GGA GG GG GAG GGCAGAGC		
		CCT CC CC CTC CCGTCTCG		
		C _ A T		
GAM2301	PALM	3' CTGGCCCTCCTTCCTCCT 11965	A AG	
		AGGA GGAGGGAGGGC AG		
		TCCT CCTTCCTCCCG TC		
		_ GG		
GAM2301	PARVB	3' GCCCCACCCCTGCCTCT 26191	A A A A_	
		AGA GG AGG GGG GGGC		
		TCT CC TCC CCC CCG		
		_ G _ AC		
GAM2301	PDEF	3' CTCCATCCCCCTGCCTCC 25679	A _ A CA	
		GGA GG AGGG GGG GAG		

			CCT CC TCCC CCT CTC		
			_ G _ AC		
GAM2301	PFTK1	3'	CTCCCTCCCTCCCTCTCTCCTT 25686	AG	CA_
	C		GAAGGA GAGGGAGGG GAG		
			CTTCCT CTCCCTCCC CTC		
			CT TCC		
GAM2301	PFTK1	3'	CTCTCACTCCCTCCCTCCCTCT 25687	A	C__
			GGA GGAGGGAGGG AGAG		
			TCT CCTCCCTCCC TCTC		
			C TCAC		
GAM2301	phospho1	3'	CCCAAGCCCCTCCTTCCTCT 83243	A	A__
			AGA GGAAGGAGGG GGG		
			TCT CCTTCCTCCC CCC		
			_ CGAA		
GAM2301	PHYHIP	3'	CTCTGCCCAGCTGCCCTCCCCT 29288	A AA	A__
	C		GA GG GGAGGG GGGCAGAG		
			CT CC CCTCCC CCCGTCTC		
			_ _ GTCGA		
GAM2301	PIP5K2B	5'	GCCCAGCCCTCCTCCCCTTC 57696	A_	A_
			GAAGG AGGAGGG GGGC		
			CTTCC TCCTCCC CCG		
			CC GA		
GAM2301	PLA2G3	5'	CTCCAGCCTCTTTCCTCCT 32309	A	GCA
			AGGA GGAGGGAGG GAG		
			TCCT CCTTTCTCC CTC		
			_ GAC		
GAM2301	PMF1	3'	GCTCTGCCCCTCCGCCCCCTC 24286	A AA A GA	
	CT		AG AGG GG GG GGGCAGAGC		
			TC TCC CC CC CCCGTCTCG		
			C CC G TC		
GAM2301	PP3501	3'	CTGACCACTCCCTCCTCC 41681	A	_ _
			GGA GGAGGGAG GG CAG		
			CCT CCTCCCTC CC GTC		
			_ A A		
GAM2301	PPM1A	5'	GCTCTTCCTCCTCCTTCT 41008	A	
			AGAAGGA GGAGGGAGGGC		
			TCTTCCT CTCCTTCTCG		
			_		
GAM2301	PPP1R1B	3'	GCTCTGCCCCTTTCCCCTTCTT 50791	A__	
	CC		GGAAGGAGGG GGGCAGAGC		

			CCTTCTTCCC	CCCGTCTCG				
			CTTTC					
GAM2301	PRKRI	5'	CTGCTGGGATCCCTTCCTTC	21829	A	GAG_		
			GAAGGAAGG GG GGCAG					
			CTTCCTTCC CT TCGTC					
			_ AGGG					
GAM2301	PRO2389	3'	CTCTGCCTCCTCCTCCCT	64478	A	GA		
			AGG AGGAGG GGGCAGAG					
			TCC TCCTCC TCCGTCTC					
			C _					
GAM2301	PRO2958	3'	CCCTCTCTCCCTCCTTCT	38248	A			
			AGAAGGA GGAGGGAGGG					
			TCTTCCT CCTCTCTCCC					
			C					
GAM2301	PSK	5'	GCTTTGCCCTCCTCCTTTCT	32878		GA		
			AGGAAGGAGG GGGCAGAGC					
			TCTTTCCTCC CCCGTTTCG					
			TC					
GAM2301	PSKH1	3'	CTCTGTTGCTCCCTCCTCT	68796	A	_		
			GGA GGAGGGAG GGCAGAG					
			TCT CCTCCCTC TTGTCTC					
			_ G					
GAM2301	PTD004	5'	GTTCTCTCCTCCTTCCTCC	26237	A	C		
			GGA GGAGGGAGGG AGAGC					
			CCT CCTTCCTCCT TCTTG					
			_ C					
GAM2301	PTD008	3'	CTTACCCCTCCTGCCTCC	32866	A A	CA		
			GGA GG GGGAGGG GAG					
			CCT CC TCCTCCC TTC					
			_ G CA					
GAM2301	PTGES2	3'	CTCTGCCGCCCTCTTCCT	47576		GA AG		
			AGGAAG GGG GGCAGAG					
			TCCTTC CCC CCGTCTC					
			TC G_					
GAM2301	PTPRT	3'	GCTCCCCTGCCCTCCTTCT	56498	_	CA		
			GGAAGGAGGG AGGG GAGC					
			TCTTCCTCCC TCCC CTCG					
			G _					
GAM2301	QSCN6	3'	GCTCCGCCCACCTGCTCCCTT	12568	A G	A A		
	C		GAAGG AG AGGG GGGC GAGC					

CTTCC TC TCCC CCG CTCG
 C G A C
 GAM2301 RAB1B 3' CTCTGCTAGCACCTCCTCCCTT 49117 A GAG_
 T GAAGG AGGAGG GGCAGAG
 |||| |||| ||||
 TTTCC TCCTCC TCGTCTC
 C ACGA
 GAM2301 RAB3IL1 3' CCCTTCCTCCCTCCCCCT 26364 AA A
 AG GGA GGAGGGAGGG
 || |||||
 TC CCT CCTCCTTCCC
 CC C
 GAM2301 RAB6B 5' CTCTCCCCTCCCTGCTCCT 33873 A G C
 AGGA G AGGGAGGG AGAG
 ||| | ||||| |||
 TCCT C TCCCTCCC TCTC
 _ G C
 GAM2301 RAB6B 5' GCTCCGCCCGCGCCTCTCTCC 33874 AG GA_ A
 GGA GAGG GGGC GAGC
 ||| ||| |||||
 CCT CTCC CCG CTCG
 CT GCG C
 GAM2301 RAB6C 5' CTCCGCCACCCTCCGTCT 50483 A AG A
 GGA GGAGGG GGC GAG
 ||| ||||| ||| |||
 TCT CCTCCC CCG CTC
 G A_ C
 GAM2301 RALGPS1A 3' CTTTGGCCCCCTCCCTCC 28330 A A G
 GGA GGAGGG GG CAGAG
 ||| ||||| || |||||
 CCT CCTCCC CC GTTTC
 C _ G
 GAM2301 RBPMS 5' GCCCTGCCCGTCTCTCC 23431 _ A
 GGAGGGA GGGCAG GC
 ||||| ||||| ||
 CCTCTCT CCGTC CG
 GC C
 GAM2301 RBPMS 5' GCTCCTCCTCCTCCTCT 23434 A A GA
 AG AGGA GGAGG GGGC
 || ||||| |||||
 TC TCCT CCTCC CTCG
 _ _ TC
 GAM2301 RBPMS 5' GCTCCTCCTCCTCCTTC 23435 _ A GA
 GAAG G AGGAGG GGGC
 |||| | ||||| |||
 CTTT C TCCTCC CTCG
 T C TC
 GAM2301 RER1 5' GCCCCGCCGTCTCCTTC 23845 A G A_
 GAAGGA GGA GG GGGC
 ||||| ||| || |||||

CTTCCT CCT CC CCCG
 _ G GC
 GAM2301 RHOBTB2 3' TTCTCCCTCACCCCCTCCT 61607 A A _ C
 AGGA GG GG GAGGG AGAG
 |||| || || |||| ||||
 TCCT CC CC CTCCC TCTT
 C _ A _
 GAM2301 RIP60 3' CTCTTACCTCTCCCTTCC 26361 A GC
 GGAAGG GGGAGG AGAG
 ||||| ||||| ||||
 CCTTCC CTCTCC TCTC
 _ AT
 GAM2301 RNF24 3' CTTTGGCCTCTCCCCCTCCT 24279 A A G
 AGGA GG GGGAGG CAGAG
 |||| || ||||| ||||
 TCCT CC CTCTCC GTTTC
 C C G
 GAM2301 RNF24 3' GCCTCTCCCCCTCCTTCCATCT 24281 A A C A
 AGA GGAAGGAGGG GGG AG GC
 ||| ||||| ||| || ||
 TCT CCTTCCTCCC CCT TC CG
 A _ C _
 GAM2301 RNPC1 3' CTCTCTCCTTCCTTCCTTC 34409 C
 GAAGGAAGGAGGGAGGG AG
 ||||| ||||| || ||
 CTTCCTTCCTTCCTCTC TC
 _
 GAM2301 SARM 3' CTCTTACCTCCCTCCCTCCT 31286 A GC
 AGGA GGAGGGAGG AGAG
 |||| ||||| ||||
 TCCT CCTCCCTCC TCTC
 C AT
 GAM2301 SCYA1 3' GCCCTACACCATTCCTTCT 12950 _ AGGG
 AGAAGGAA GG AGGGC
 ||||| || ||||
 TCTTCCTT CC TCCCG
 A ACA_
 GAM2301 SDC3 5' CTTCTCCCTCCCCCATCC 28474 A A CA
 GGA GG GGGAGGG GAG
 ||| || ||||| |||
 CCT CC CCCTCCC TTC
 A _ TC
 GAM2301 SDFR1 5' CTCCTCCCTCCCCTCCCTTC 25791 AA__ C
 GAAGG GGAGGGAGGG AG
 |||| ||||| || ||
 CTTCC CCTCCCTCCC TC
 CTCC _
 GAM2301 SDFR1 5' CTCGCCCGCCCCCTCCCTCC 25792 A A__ A
 GGA GGAGGG GGGC GAG
 ||| ||||| |||| |||

			CCT CCTCCC CCG CTC			
			C CCG _			
GAM2301	SDS3	3'	CTCCGCCATTGCCTTCTCCT 69745	A	G _ A	
			AGGA GGAGG AG GGC GAG			
			TCCT CTTCC TT CCG CTC			
			_ G A C			
GAM2301	SELM	3'	GCTCCACTAAATTCCTCCTGC 55399	A	__ CA	
	CT		AGG AGGAGGGAG GG GAGC			
			TCC TCCTCCCTT TC CTCG			
			G AAA AC			
GAM2301	SEMA6C	3'	CTCCCACTCCCCGCTCCCTTC 48859	A GA	_ CA	
			GAAGG AG GGGAG GG GAG			
			CTTCC TC CCCTC CC CTC			
			C GC A _			
GAM2301	SH3BP1	3'	CTCAGCACCCCCTCCCTCC 39042	A	A _ A	
			GGA GGAGGG GG GC GAG			
			CCT CCTCCC CC CG CTC			
			C _ A A			
GAM2301	SHANK1	3'	GCCCTGCCCTCATCTTCC 32872	_	_	
			GGAAG GAGGG AGGGC			
			CCTTC CTCCC TCCCG			
			TA G			
GAM2301	SIMRP7	3'	CTGCAGAGTTCTCCCCTCT 93971	A AA	AGG_	
			AG AGG GGAGGG GCAG			
			TC TCC CCTCTT CGTC			
			_ _ GAGA			
GAM2301	SLC2A11	3'	GCCTGGTCCTCACTCCCTCCT 48694	A G	_ A	
			AGGA GGAG GAGGGC AG GC			
			TCCT CCTC CTCCTG TC CG			
			C A G C			
GAM2301	SLC5A7	5'	CCCGCACCCCTCCCTTTCT 41805	AA	A__	
			AGAAGG GGAGGG GGG			
			TCTTTC CCTCCC CCC			
			_ ACG			
GAM2301	SNPH	3'	GCCTGCACCCTCCCTGCTCC 28903	A G	_ A	
			GGA G AGGGAGG GCAG GC			
			CCT C TCCCTCC CGTC CG			
			_ G CA C			
GAM2301	SNPH	3'	GTTCCCCCCTCCCTTCTCC 28908	A	CA	
			GGA GGAGGGAGGG GAGC			

CCT CTTCCCTCCC CTTG
 _ CC
 GAM2301 SP192 5' CTCTTTCCCCTTCCCCC 41616 AA A C
 GG GGAGGG GGG AGAG
 || ||||| || ||||
 CC CCTTC CCT TCTC
 CC _ T
 GAM2301 SP2 3' GCTCTGCCTTGGCCCTTCCCCT 13332 AA _
 AGG GGAGGG AGGGCAGAGC
 ||| ||||| |||||
 TCC CTTCCC TTCCGTCTCG
 C_ GG
 GAM2301 SPRY4 3' TTCTCCCTCCCTCCCTCC 49039 A C
 GGA GGAGGGAGGG AGAG
 ||| ||||| ||||
 CCT CCTCCCTCCC TCTT
 C _
 GAM2301 SR-A1 3' GCTCCACCTCCCCACCTCCCTC 70584 A A A_ GCA
 GA GGA GG GGGAGG GAGC
 || ||| || ||||| ||||
 CT CCT CC CCCTCC CTCG
 C _ AC AC_
 GAM2301 STAT5A 5' TTTTCCCTCCTCCCTTTT 13444 A
 AGAAGG AGGAGGGAGGG
 ||||| |||||
 TTTTCC TCCTCCCTTTT
 C
 GAM2301 STK25 3' CTGCCCTCCTCCCTCTCC 22094 _ AG
 GGA AGG GGAGGGCAG
 ||| ||| |||||
 CCT TCC CCTCCCGTC
 C CT
 GAM2301 STK39 3' TTCAACCCTCCCTCTTTCT 26012 CA
 GGAAGGAGGGAGGG GAG
 ||||| ||||| |||
 TCTTTCTCCCTCCC CTT
 AA
 GAM2301 SYT12 3' CTCTCCCCTCTCTCCCTCCCC 96380 AA A C
 T AG GGA GGAGGGAGGG AGAG
 || ||| ||||| ||||
 TC CCT CCTCTCTCCC TCTC
 CC C C
 GAM2301 SYT12 3' CTGACTCCCCCCTGCCCTCT 96382 A A A A _
 AGA GG AGG GGG GGG CAG
 ||| || ||| ||| |||
 TCT CC TCC CCC CTC GTC
 C G _ C A
 GAM2301 TBCA 5' CTCTCCGCCCTCCTTCT 17231 AG C
 GGAAGGAGGG GG AGAG
 ||||| || |||

			TCTTCCTCCC CC TCTC			
			CG _			
GAM2301	TERE1	5'	GCCCCGTCCTTCCTCCTTCC 26168		AGA	
			GGAAGGAGGGAGGGC GC			
			CCTTCCTCCTTCCTG CG			
			CCC			
GAM2301	TINF2	3'	GCTCTCCCTGCTCCCTTCT 25873	A G		
			AGAAGG AG AGGGAGGGC			
			TCTTCC TC TCCCTCTCG			
			C G			
GAM2301	TJP4	3'	CTGTCTCCTCCCTCCCTCT 55505	A	__	
			GGA GGAGGGAGG GCAG			
			TCT CCTCCCTCC TGTC			
			C TC			
GAM2301	TM9SF2	5'	CTCCCCACCCCTCCTTCCCTCT 17823	A	AG CA	
			AGA GGAAGGAGGG GG GAG			
			TCT CCTTCCTCCC CC CTC			
			C CA C_			
GAM2301	TMPRSS5	3'	CTCTCCCCTCCCTGCCCCT 48495	AA _	C	
			AGG GG AGGGAGGG AGAG			
			TCC CC TCCCTCCC TCTC			
			_ G C			
GAM2301	TMPRSS5	3'	TTCTGCCCTCTCCCCTCC 48497	A A		
			GGA GG GGGAGGGCAGAG			
			CCT CC CTCTCCCGTCTT			
			C _			
GAM2301	TOB2	3'	GCCCCACCCACCATTCCTCT 33239	A _	A A__	
			AGA GGAA GG GGG GGGC			
			TCT CCTT CC CCC CCG			
			C A A CAC			
GAM2301	TOB2	3'	GCTCCCTGCTCCTCCCTTCCTC 33240	A	- -	
	CT		AGGA GGAGGGAGG GCA GAGC			
			TCCT CTTCCCTCC CGT CTCG			
			C T CC			
GAM2301	TOMM40	3'	GCCCCCTCCCTTCCCTC 21484	A	- A	
			GA GGAAGG AGGG GGGC			
			CT CCTTCC TCCC CCG			
			C C _			
GAM2301	TPSG1	3'	GCTCCGCCCTCCCTCTCCCT 25891	AA	- A	
			AGG GGAGGGA GGGC GAGC			

			TCC TCTCCCT CCCG CTCG		
			C_ CC C		
GAM2301	TRAF3	3'	GCCCCATTCCACCACCCCTTC 13851	AA_ A _	
			GAAGG GG GGA GGC		
			CTTCC CC CCTT CCCG		
			CCA A AC		
GAM2301	TRAF3	3'	GCCTCTCCCTCCTTTCTCCT 13852	A _	
			AG AGGAAGGAGGGAG GGC		
			TC TCTTTCCTCCCTC CCG		
			C T		
GAM2301	TUBB5	3'	CTACCCTCCCTCCCCGCTTC 21413	GAA C	
			GAAG GGAGGGAGGG AG		
			CTTC CCTCCCTCCC TC		
			GCC A		
GAM2301	USP2	3'	GCCACGTCCCTTCTCCCTTC 16111	A G_	
			GAAGG AGGAGGGA GGC		
			CTTCC TCTTCCCT CCG		
			C GCA		
GAM2301	VELI1	5'	CCTTCCTTCCTTCCCCCT 17418	AA	
			AG GGAAGGAGGGAGGG		
			TC CCTTCCTTCCTTCC		
			CC		
GAM2301	VPS4A	3'	GCTCTTCCTACTTCCTCCT 26021	A G	
			AG AGGAAG AGGGAGGGC		
			TC TCCTTC TCCTTCTCG		
			C A		
GAM2301	WNT8A	5'	CTGCCCTCTCCTCACTCCT 50032	AG _	
			AGGA GAGG GAGGGCAG		
			TCCT CTCC CTCCCGTC		
			CA T		
GAM2301	ZNRD1	3'	CTCTACAGTCCCTCCCTCCTTT 97693	_____	
	C		GGAAGGAGGGAGGG C AGAG		
			CTTTCCTCCCTCCC G TCTC		
			T ACA		
GAM2301	ZNRD1	3'	CTCTACAGTCCCTCCCTCCTTT 97694	_____	
	C		GGAAGGAGGGAGGG C AGAG		
			CTTTCCTCCCTCCC G TCTC		
			T ACA		
GAM2301	ZSIG11	3'	CTCTCCAGCCCTCTTCCTCCT 32492	A G AG C	
			AG AGGAAG AGGG GG AGAG		

		TC TCCTTC TCCC CC TCTC			
		C _ GA _			
GAM2301	ZSIG11	3' GCCCTCTTCCTCCTTCCTCT	32493	A	___
		AGA GGAAGGAGG GAGGGC			
		TCT CCTTCCTCC CTCCCG			
		_ TT			
GAM2301	LOC112473	5' GCTCCGCCCGAGTCCCACCTTC	73579	A	___ A
	C	GGAAGG GGGA GGGC GAGC			
		CCTTCC CCCT CCCG CTCG			
		A GAG C			
GAM2301	LOC112476	3' CTCAGTCCTCTCTTCCTTCC	59786	_	A
		GGAAGGAGG GAGGGC GAG			
		CCTTCCTTC CTCCTG CTC			
		T A			
GAM2301	LOC112840	3' GCTCTGCCCCTTTAACTCCTCA	55614	GA	___ A
	CT	AG AGGAG GG GGGCAGAGC			
		TC TCCTC TC CCCGTCTCG			
		AC AATT _			
GAM2301	LOC115704	3' GCCTCCCCTCACTTCCTCCT	73908	A	_ AG
		AG AGGAAG GAGGG GGC			
		TC TCCTTC CTCCC CCG			
		C A CT			
GAM2301	LOC115708	3' GCTCTGCCCCTGGTCCCTGCTC	73919	A G	___
	CT	AGGA G AGGGA GGGCAGAGC			
		TCCT C TCCCT CCCGTCTCG			
		_ G GGTC			
GAM2301	LOC116113	3' GCCCTGCCCCCCTCCCTTCCGC	93840	A _	_ A A
	TC	GA GGAAGG AGGG GGGCAG GC			
		CT CCTTCC TCCC CCCGTC CG			
		CG C _ C			
GAM2301	LOC118738	3' GCTCTGATGTCCTCGCTCCCTC	76005	A G	___
	C	GGA GGAG GAGGGCA GAGC			
		CCT CCTC CTCCTGT CTCG			
		C G AGT			
GAM2301	LOC122664	5' CTCTAAGTCCTCCCTCCCCCTT	74616	AA	___
	CT	AGAAGG GGAGGGAGGGC AGAG			
		TCTTCC CCTCCCTCCTG TCTC			
		C_ AA			
GAM2301	LOC122792	5' GCTCCGCCGGCCCTCCTTCCTT	59825	AG	A
	C	GAAGGAAGGAGGG GGC GAGC			

		CTTCCTTCCTCCC CCG CTCG		
		GG C		
GAM2301	LOC123096 3'	CTCACCCCGCCCTCCTTCC 74652	A	CA
		GGAAGGAGGG GGG GAG		
		CCTTCCTCCC CCC CTC		
		G CA		
GAM2301	LOC124245 3'	GCCTTCTCTTCCTCCTCCT 58769	A	C A
		AGGA GGAGGGAGGG AG GC		
		TCCT CCTCCTTCTC TC CG		
		— T —		
GAM2301	LOC124369 5'	CTCTGCTGGCCCTCCTTCC 74762	AG	
		GGAAGGAGGG GGCAGAG		
		CCTTCCTCCC TCGTCTC		
		GG		
GAM2301	LOC124446 5'	CTCTGCCCTCCCCTCCCTTT 74773	AA	GA
		GAAGG G GGGAGGGCAGAG		
		TTTCC C CCCTCCCGTCTC		
		— TC		
GAM2301	LOC126364 3'	GCTCTGCCGCCCTCCCTGTC 76193	— A A AG	
		GA AGG AGG GGG GGCAGAGC		
		CT TCC TCC CCC CCGTCTCG		
		G C _ G_		
GAM2301	LOC126917 3'	GCTATGCCCTCCCTTCCTCCT 75095	A	G
		AGGA GGAGGGAGGGCA AGC		
		TCCT CTTCCCTCCCGT TCG		
		C A		
GAM2301	LOC128989 3'	GCCTGCTCTCTCCCTCTTCC 75318	GA _ A	
		GGAAG GG GAGGGCAG GC		
		CCTTC CC CTCTCGTC CG		
		TC T C		
GAM2301	LOC129080 3'	CTGTGCCCTCCCTCCTT 56793	_ G	
		AAGGAGGGAGGG CA AG		
		TTCTCCCTCCC GT TC		
		C G		
GAM2301	LOC129198 3'	GCCCTGTGACCTCCCTCCTGTC 76614	GA _ A	
	T	AG AGGAGGGAGG GCAG GC		
		TC TCCTCCCTCC TGTC CG		
		TG AG C		
GAM2301	LOC129303 3'	CCCACCCCATATCTTCTTTC 75370	A_ A	
		GAAGGAAGG GGG GGG		

		CTTTCTTCT	CCC CCC		
		ATAC	A		
GAM2301	LOC129303 3'	CTCTGCCCCTCACTTCCTTT	75372	GA	A
		GAAGGAAG GGG GGGCAGAG			
		TTTCCTTC CTC CCCGTCTC			
		A_ _			
GAM2301	LOC130574 5'	CTGCGCTCCCTCGCTCCTTC	75461	AG	G
		GAAGGA GAGGGAG GCAG			
		CTTCCT CTCCCTC CGTC			
		CG G			
GAM2301	LOC131034 5'	CTCCACTCCCTCCCTCTT	56419	A	_ C
		AGGA GGAGGGAG GG AG			
		TTCT CCTCCCTC CC TC			
		C A _			
GAM2301	LOC133688 3'	GCCCTGCCTCCTCCTTTCT	75608	A	G
		AGAAGG AGGAGG AGGGC			
		TCTTTC TCCTCC TCCCG			
		C G			
GAM2301	LOC138389 5'	CCCTCCCTCCCTCTTTCT	76730	A	
		AGAAGGA GGAGGGAGGG			
		TCTTTCT CCTCCCTCCC			
		C			
GAM2301	LOC138623 3'	GCCCTGCCCAACGGTCCTGCCT	76487	A	_____ _
	TCT	AGAAGG AGGA GGG AGGGC			
		TCTTCC TCCT CCC TCCCG			
		G GGCAA G			
GAM2301	LOC140380 5'	CTCCCCCTCTCCCTCCTCC	76490	A	_ CA
		GGA GGAGGGAG GG GAG			
		CCT CCTCCCTC CC CTC			
		_ T CC			
GAM2301	LOC142955 3'	GCTCTCCTCCCCTTCCTTC	76961	A_	
		GAAGGAAGG GGGAGGGC			
		CTTCCTTCC TCCTCTCG			
		CC			
GAM2301	LOC143188 5'	GCTCCAGGCCTCCCTTCTTCT	83792	GCA_	
		GGAAGGAGGGAGG GAGC			
		TCTTCTTCCCTCC CTCG			
		GGAC			
GAM2301	LOC143274 3'	CTCTGCCTCCTTCCTCCT	77021	A	G
		AGGA GGAGGGAGG CAGAG			

TCCT CCTTCCTCC GTCTC

GAM2301 LOC143677 5' CTTCTCCTCCTTCCCTCC 83896 A CA
GGA GGAGGGAGGG GAG
||| ||||| |||
CCT CCTTCCTCCT TTC
C CC

GAM2301 LOC143879 3' GCTCTCTCTCTCTCTCCT 77160 AG C
AGGA GAGGGAGGG AGAGC
||| ||||| |||||
TCCT CTCTCTCTC TCTCG
CT

GAM2301 LOC143903 5' CTCCGCGCCCTCCCCCCGCT 77113 AA A A__
AGG GG GGGAGGGC GAG
||| ||||| |||
TCC CC CCCTCCCG CTC
GC C CGC

GAM2301 LOC144231 5' GCCCTATCCATTCTCTCCTTCC 83939 A _____
CTCT AGA GGAAGGAGGGA GGGC
||| ||||| |||
TCT CCTTCCTCTCT CCCG
C TACCTAT

GAM2301 LOC144347 3' CTCTGAGCCTTCCTCCCCCT 77306 AA G_
AGG GGAGGGAGG CAGAG
||| ||||| |||||
TCC CTCCTTCC GTCTC
CC GA

GAM2301 LOC144373 3' CTTCCCCTCCTCCTTCT 77311 GA C
AGGAAGGAGG GGG AG
||| ||||| ||| ||
TCCTTCCTCC CCC TC
TC T

GAM2301 LOC144501 3' CTCCTTCCCCTTCCTCCCTCC 84027 A CA__
GGA GGAGGGAGGG GAG
||| ||||| |||
CCT CTCCTTCCC CTC
C CTC

GAM2301 LOC144501 3' CTCTCCCCTCCCTGCCCCT 84028 AA _ C
AGG GG AGGGAGGG AGAG
||| ||||| |||||
TCC CC TCCCTCCC TCTC
_ G C

GAM2301 LOC144776 3' GCTCTAACCCTCCTCCCTT 77492 A _
AAGG AGGAGGG AGGGC
||| ||||| |||||
TTCC TCCTCCC TCTCG
C AA

GAM2301 LOC144810 5' GCCTGGCCTACCTCCCTCC 77499 A G G A
GGA GGAGG AGG CAG GC
||| ||||| ||| ||| ||

CCT CCTCC TCC GTC CG
 C A G C
 GAM2301 LOC145468 3' CTGACCCCCCTCCCTTCC 74252 _ A _
 GGAAGG AGGG GGG CAG
 ||||| |||| ||| |||
 CCTTCC TCCC CCC GTC
 C _ A
 GAM2301 LOC145717 3' GCTCAGATTCCCACCCCCCTCC 67375 A A A A CA____
 CTCT AGA GGA GG GGG GGG GAGC
 ||| ||| || ||| ||| ||||
 TCT CCT CC CCC CCC CTCG
 C C _ A TTAGA
 GAM2301 LOC145719 5' GCCATCCCTCCCGCCCTTCT 84466 AA_ G
 AGAAGG GGAGGGA GGC
 ||||| ||||| |||
 TCTTCC CCTCCCT CCG
 CGC A
 GAM2301 LOC145720 5' GCCATCCCTCCCGCCCTTCT 84452 AA_ G
 AGAAGG GGAGGGA GGC
 ||||| ||||| |||
 TCTTCC CCTCCCT CCG
 CGC A
 GAM2301 LOC145786 5' CTGGGAACCCCTCCTTCCATCT 84492 A AGGG_
 AGA GGAAGGAGGG CAG
 ||| ||||| |||
 TCT CCTTCCTCCC GTC
 A CAAGG
 GAM2301 LOC146210 5' CTCAGTCCTCCCTCCCTCT 84602 A A
 GGA GGAGGGAGGGC GAG
 ||| ||||| |||
 TCT CCTCCCTCCTG CTC
 C A
 GAM2301 LOC146237 3' CTTTTCCCCACCTCCTCCT 84610 A GA C
 AGGA GGAGG GGG AGAG
 |||| |||| ||| ||||
 TCCT CCTCC CCC TTTC
 _ AC T
 GAM2301 LOC146243 3' CTCCACTCTCCTCTCTTCC 84620 GA CA
 GGAAG GGGAGGG GAG
 |||| ||||| |||
 CCTTC TCCTCTC CTC
 TC AC
 GAM2301 LOC146268 3' CTCCCAGACCTCCCTCATTCT 78337 G GCA____
 GGAA GAGGGAGG GAG
 |||| ||||| |||
 TCTT CTCCCTCC CTC
 A AGACC
 GAM2301 LOC146336 3' CTCCTCCCTCCCTCTCTCT 78370 AG CA
 GGA GAGGGAGGG GAG
 ||| ||||| |||

	TCT CTCCCTCCC CTC		
	CT TC		
GAM2301 LOC146378 3'	GCCCCCACCTCCTCCCTTC 78420	A	GA__
	GAAGG AGGAGG GGGC		
	CTTCC TCCTCC CCCG		
	C ACCC		
GAM2301 LOC146667 5'	GCCCCTGTCCCCCTTCTCTTCT 84712	_	A ____
	AGAAG GAAGG GGA GGGC		
	TCTTC CTTCC CCCT CCCG		
	T _ GTC		
GAM2301 LOC146856 5'	CTTTTCCTTCCTCCTTCCT 83701		C
	AGGAAGGAGGGAGGG AGAG		
	TCCTTCCTCCTTCCT TTTC		
	-		
GAM2301 LOC147160 5'	CTGCCCCGACCCTCCCTCCTGCT 85074	A	A A_
	AG AGGA GGAGGG GGGCAG		
	TC TCCT CCTCCC CCGTC		
	G C AG		
GAM2301 LOC147229 5'	GCTCTGCTGCTGCCCCTTCC 78923	A	G _
	GGAAGG GG AG GGCAGAGC		
	CCTTCC CC TC TCGTCTCG		
	_ G G		
GAM2301 LOC147353 3'	CTGTATTCCCCTCCTTCC 85136	AG	_
	GGAAGGAGGG G GCAG		
	CCTTCCTCCC T TGTC		
	CT A		
GAM2301 LOC147917 3'	GCTCAACCCCTCCTTTCT 79264	A	GCA
	AGGAAGGAGGG GG GAGC		
	TCTTTCCTCCC CC CTCG		
	_ AA_		
GAM2301 LOC147990 5'	GCCCCGTCGGCCTCCTTCC 85225	__	__
	GGAAGGAGG GA GGGC		
	CCTTCCTCC CT CCCG		
	GG GC		
GAM2301 LOC148137 3'	GCCTGCCCCCACCCTTCCT 59102	A__	A A
	AGGAAGG GGG GGGCAG GC		
	TCCTTCC CCC CCGTC CG		
	CCA _ C		
GAM2301 LOC148137 3'	GCTCTGCCCTGCCCCCACC 59103	AA	A _
	GG GG GGG AGGGCAGAGC		

		CC CC CCC TCCCGTCTCG			
		CA C G			
GAM2301	LOC148142 5'	GCTCTGCCCTAAGGCCTTCCCT 79377	A	AGGG	
	CT	AGA GGAAGG AGGGCAGAGC			
		TCT CCTTCC TCCCGTCTCG			
		C GGAA			
GAM2301	LOC148223 3'	GCCCCTGACCCCACTTCCTTCT 79486	GA	A__	
		AGAAGGAAG GGG GGGC			
		TCTTCCTTC CCC CCG			
		AC AGTC			
GAM2301	LOC148696 5'	GCTTTTGCCCCCCTTCCCCT 85346	AA	A _	
		AGG GGAGGG GGGCAGA GC			
		TCC CTTCCC CCGTTT CG			
		C_ C T			
GAM2301	LOC149664 5'	CTCTCTCCCTCCCCTCCTTCT 80287	A_	C	
		AGAAGGA GGAGGGAGGG AG			
		TCTTCCT CCTCCCTCTC TC			
		CC _			
GAM2301	LOC149670 5'	GCCCTGCCACTCCTTCCTC 80305	A	_ _	
		GA GGAAGGAG GG AGGGC			
		CT CCTTCCTC CC TCCCG			
		_ A G			
GAM2301	LOC149670 5'	GCCTGCTCCCCTCCCTTCCT 80306	_	A A	
		AGGAAGG AGGG GGGCAG GC			
		TCCTTCC TCCC CTCGTC CG			
		C _ C			
GAM2301	LOC149706 3'	CTTTCCTCATTCCCTCT 85804	A	G	
		AGA GGAA GAGGGAGGG			
		TCT CCTT CTCCCTTTC			
		C A			
GAM2301	LOC149711 3'	CCTATCCCTCCTTTCCTTC 85848	_	_	
		GAAGGAA GGAGGGA GGG			
		CTTCCTT CCTCCCT TCC			
		T A			
GAM2301	LOC149711 3'	CTAACTCCCTCCATCCCCCT 85850	AA	A GGC	
		AG GGA GGAGGGAG AG			
		TC CCT CCTCCCTC TC			
		CC A AA_			
GAM2301	LOC149832 5'	GCCCCGAGCCCTCCTGTCCTT 85864	_	A__	
	CT	AGAAGGA AGGAGGG GGGC			

		TCTTCCT TCCTCCC CCG		
		G GAGCC		
GAM2301	LOC149911 3'	CTGTGTTGCCTCCTCCCTGTCT 85873	_ A	G G
		AGA AGG AGGAGG AG GCAG		
		TCT TCC TCCTCC TT TGTC		
		G C G G		
GAM2301	LOC150005 3'	CTCCCTCCCCACTCCCTCCT 85961	A _	C
		AGGA GGA GGGAGGG AG		
		TCCT CCT CCCTCCC TC		
		C CAC _		
GAM2301	LOC150135 3'	CTTCTCCCTCCCTCCTGCC 80394	A	CA
		GG AGGAGGGAGGG GAG		
		CC TCCTCCCTCCC TTC		
		G TC		
GAM2301	LOC150135 3'	TTCCCCCTTCCTCCTTCCCTC 80395	A	CA
		GA GGAAGGAGGGAGGG GAG		
		CT CCTTCCTCCCTTCC CTT		
		C CC		
GAM2301	LOC150142 5'	GCTCTGCTTCCTGCCCCCTTCC 80407	A _ _	
		GGAAGG GGG AGG GCAGAGC		
		CCTTCC CCC TCC CGTCTCG		
		_ G TT		
GAM2301	LOC150155 3'	CTGACCCCCCTCCCTTCC 71411	_ A _	
		GGAAGG AGGG GGG CAG		
		CCTTCC TCCC CCC GTC		
		C _ A		
GAM2301	LOC150236 5'	CTCTGTGCCCTCCTTCCT 80499		AGG
		AGGAAGGAGGG GCAGAG		
		TCCTTCCTCCC TGTCTC		
		CG_		
GAM2301	LOC150271 3'	GCTCTGGTGTCTCCTCCTTTC 86141	GA _	GGG
	T	AGAAG AGGAGG GA CAGAGC		
		TCTTC TCCTCC CT GTCTCG		
		_ T GTG		
GAM2301	LOC150319 3'	CTCTGCCTCCGCCTCCCTTCT 80469	A AG	G
		AGAAGG AGG GGAGG CAGAG		
		TCTTCC TCC CCTCC GTCTC		
		C G_ _		
GAM2301	LOC150319 3'	GCTCTGCCACCCCTTACCCCT 80475	AAG	A
		AGG GAGGG GGGCAGAGC		

TCC TTCCC CCCGTCTCG
 CCA A
 GAM2301 LOC150372 3' GCCCTGCCCTCCTAGGTCTTCC 80615 A__ A
 GGAAGG GGGAGGGCAG GC
 ||||| ||||| ||
 CCTTCT TCCTCCCGTC CG
 GGA C
 GAM2301 LOC151178 5' GCCCTCTCCTCTCCCCTCT 80960 A AA _
 AGA GG GGAGG GAGGGC
 ||| || ||||| |||||
 TCT CC TCTCC CTCCCG
 _ CC T
 GAM2301 LOC151193 5' CTCCGCCCATGACTCACTTCT 80974 _ GGA_ A
 GGAAG GAG GGGC GAG
 ||||| ||| ||||| |||
 TCTTC CTC CCG CTC
 A AGTA C
 GAM2301 LOC151414 5' GCCCTCACCTTCTCCCTC 81037 A A _
 GA GGA GGAGG GAGGGC
 || ||||| |||||
 CT CCT CTTCC CTCCCG
 C C A
 GAM2301 LOC151512 5' CTGCCCTCCTGGTCACCCT 86617 AA A_
 AGG GG GGGAGGGCAG
 ||| || ||||| |||||
 TCC CT TCCTCCCGTC
 CA GG
 GAM2301 LOC151517 5' GCCCGACCCGTCCCCTCT 86620 A AA _ A_
 AGA GG GGA GGG GGGC
 ||| || ||||| |||||
 TCT CC CCT CCC CCG
 _ _ G AGC
 GAM2301 LOC151701 5' CCCTCATGGCCTCCTTTCTTCT 86668 ____
 AGAAGGAAGGAGG GAGGG
 ||||| ||||| |||||
 TCTTCTTCTCTCC CTCCC
 GGTA
 GAM2301 LOC151736 5' GCTTGTTCCCTCTCCTCCTCCC 83498 A _ CA_
 TTCT AGAAGG AGGAGG GAGGG GAGC
 ||||| ||||| ||||| |||||
 TCTTCC TCCTCC CTCCC TTCG
 C T TTG
 GAM2301 LOC151742 3' CTGCCCTCTCCCCTCCTGCT 58346 A A A
 AG AGGA GG GGGAGGGCAG
 || ||||| || ||||| |||||
 TC TCCT CC CTCTCCCGTC
 G C _
 GAM2301 LOC152220 3' GCCCTCCCTTCTCCCCTC 86765 A A
 GA GG AGGAGGGAGGGC
 || || ||||| |||||

CT CC TCTTCCCTCCCG
 C C
 GAM2301 LOC152245 5' CCCTCCCCCTCTTCCCTC 86777 A _ A
 GA GGAAG G GGGAGGG
 || |||| | |||||
 CT CCTTC C CCCTCCC
 C T C
 GAM2301 LOC152245 5' GTCCCCCTCCCCCTCTTC 86782 AA_ A
 GAAGG GGAGGG GGC
 |||| |||| |||
 CTTCT CCTCCC CTG
 CCC C
 GAM2301 LOC152317 5' GCTCTGTTCTCCATCCTTCC 86833 G _
 GGAAGGA GGAGGG CAGAGC
 ||||| ||||| |||||
 CCTTCCT CCTCCT GTCTCG
 A T
 GAM2301 LOC152328 3' GCTCTGTTTCCCCCTCTCC 81368 AG A AG
 GGA G GGG GGCAGAGC
 || | || |||||
 CCT C CCC TTGTCTCG
 CT _ CT
 GAM2301 LOC152667 3' GCCATTCCCTCTCCCCTCT 81524 A AA _
 AGA GG GGAGGGAG GGC
 ||| || ||||| |||
 TCT CC TCTCCCTT CCG
 _ CC A
 GAM2301 LOC152851 5' GCTCTGCCCCCGCTCTCCTTG 81592 _ AG A A
 CT AG AAGGA G GGG GGGCAGAGC
 || |||| | ||| |||||
 TC TTCCT C CCC CCCGTCTCG
 G CT G _
 GAM2301 LOC153205 3' CTCTGCCCCACTTCCGCCCT 87156 AA GA
 AGG GGAGG GGGCAGAG
 || |||| |||||
 TCC CCTTC CCCGTCTC
 CG A_
 GAM2301 LOC153811 3' CCCAAATCTCCTCCTTCCTCCT 81827 A _ _
 AG AGGAAGGAGG GA GGG
 || ||||| || |||
 TC TCCTTCCTCC CT CCC
 C T AAA
 GAM2301 LOC153910 3' CGCCCTGCTTTTCTCCCTCCCC 81905 _ _ A _
 TTCCTTC GAAGGAA GGAGGGAG GGCAG GC G
 ||||| ||||| |||| || |
 CTTCTT CCTCCCTC TCGTC CG C
 CC TTT C _
 GAM2301 LOC157349 3' CTGACCCCTCTCCCTTCT 82339 AA A G
 AGAAGG GGAGGG GG CAG
 ||||| ||||| || |||

TCTTCC TCTCCC CC GTC
 C _ _ A
 GAM2301 LOC157349 3' CTGCCTCCCCTCCCTCCT 82340 A AG
 AGGA GGAGGG GGCAG
 ||| ||||| ||||
 TCCT CCTCCC CCGTC
 C CT
 GAM2301 LOC157349 3' GCCTCCCCTCCCTCCTTCCTGC 82345 A C A
 T AG AGGAAGGAGGGAGGG AG GC
 || ||||| ||||| || ||
 TC TCCTTCCTCCCTCCC TC CG
 G C _
 GAM2301 LOC157638 3' GCTCCCTTTCTCCCTCTCTTCC 82424 _ CA_
 T AGGAAG GAGGGAGGG GAGC
 ||||| ||||| ||||
 TCCTTC CTCCCTCTT CTCG
 T TCC
 GAM2301 LOC157931 3' CCTTCCCTCCTTTCTCT 87938 A
 AGA GGAAGGAGGGAGGG
 ||| ||||| |||||
 TCT CTTTCTCCCTTCC
 C
 GAM2301 LOC158549 3' CTCCCTCCTTTCCTTCCTTC 88223 _ C
 GAAGGAAGGAG GGAGGG AG
 ||||| ||||| ||||| ||
 CTTCTTCCTT CCTCCC TC
 T _
 GAM2301 LOC158819 5' GCCTATCCCTACCTCCCTCCT 88278 A A _ _
 AG AGG AGG AGGGA GGGC
 || ||| ||| ||||| ||||
 TC TCC TCC TCCCT TCCG
 C C A A
 GAM2301 LOC159090 5' CCCTCCCTCTTCCCTCCT 82958 A A
 AG AGG AGGAGGGAGGG
 || ||| ||||| |||||
 TC TCC TTCTCCCTCCC
 C C
 GAM2301 LOC159090 5' CTCTGTCCTCCTCCCTCCCTC 82960 A A AG
 T AGA GG AGG GGAGGGCAGAG
 ||| || ||| ||||| |||||
 TCT CC TCC CCTCCTGTCTC
 C C CT
 GAM2301 LOC161158 5' GCCCTCCCCTCCCCCTCT 88450 A AA _
 AGA GG GGAGGG AGGGC
 ||| || ||||| |||||
 TCT CC CCTCCC TCCG
 C _ C
 GAM2301 LOC163724 5' CTCCCCCTCCCTCCACCT 83032 AA CA
 AGG GGAGGGAGGG GAG
 ||| ||||| ||||| |||

TCC CCTCCCTCCC CTC
 A_ C_
 GAM2301 LOC164312 3' CTGCCCTCCCTTCCTTCT 83393 _
 GGAAGGA GGGAGGGCAG
 ||||| |||||
 TCTTCCT CCCTCCCGTC
 T
 GAM2301 LOC164945 5' CTCCTTCCCTCCTGCCTCCT 88540 A A C
 AG AGG AGGAGGGAGGG AG
 || ||| ||||| ||
 TC TCC TCCTCCCTTCC TC
 C G _
 GAM2301 LOC166968 3' TCTTCCCCACTCCCTTCT 83559 A GA
 AGAAGG AG GGGAGGG
 ||||| || |||||
 TCTTCC TC CCCTTCT
 C AC
 GAM2301 LOC197044 3' GCTCCGATCCCCTCCTCCCTCT 89218 _ A A GCA
 CT AGA AGG AGGAGGG GG GAGC
 ||| ||| ||||| || |||
 TCT TCC TCCTCCC CT CTCG
 C C _ AGC
 GAM2301 LOC197114 3' CCCATCCCCGCCTCCTTC 91266 A A_ _
 GAAGGA GG GGGG GGG
 ||||| || ||| |||
 CTTCT CC CCCT CCC
 _ GC A
 GAM2301 LOC197114 5' GCCATCCCTCCCGCCCTTCT 91272 AA_ G
 AGAAGG GGAGGGA GGC
 ||||| ||||| |||
 TCTTCC CCTCCCT CCG
 CGC A
 GAM2301 LOC197117 3' CCCATCCCCGCCTCCTTC 91279 A A_ _
 GAAGGA GG GGGG GGG
 ||||| || ||| |||
 CTTCT CC CCCT CCC
 _ GC A
 GAM2301 LOC197117 3' GCCATCCCTCCCGCCCTTCT 91282 AA_ G
 AGAAGG GGAGGGA GGC
 ||||| ||||| |||
 TCTTCC CCTCCCT CCG
 CGC A
 GAM2301 LOC197201 3' GCCTGCAGCCCCTCTTCCCTC 89276 A GA AGG A
 GA GGAAG GGG GCAG GC
 || |||| ||| |||| ||
 CT CCTTC CCC CGTC CG
 C TC GA_ _
 GAM2301 LOC197202 5' GCTCCGCCCGAGTCCCACCTTC 89294 A _ _ A
 C GGAAGG GGGG GGGC GAGC
 ||||| |||| |||| ||||

CCTTCC CCCT CCCG CTCG
 A GAG C
 GAM2301 LOC197342 3' CTCTGCCCTGCCACCCC 89365 AA A _
 GG GG GGG AGGGCAGAG
 || || || |||||
 CC CC CCC TCCCGTCTC
 _ A G
 GAM2301 LOC199782 3' GCTCCGTCTCACCTTCCCTCC 91445 A A_ A
 GGA GGAGGG GGGC GAGC
 ||| ||||| ||| ||||
 CCT CCTTCC TCTG CTCG
 C CAC C
 GAM2301 LOC199786 3' CTCTGCCACCGCCTTCT 89751 A GA
 GGAAGG GG GGGCAGAG
 ||||| || |||||
 TCTTCC CC CCCGTCTC
 G A_
 GAM2301 LOC199886 3' GCCCTCACCTTCCCCCTCCT 89824 A AA _
 AG AGG GGAGG GAGGGC
 || ||| ||||| |||||
 TC TCC CTTCC CTCCCG
 C CC A
 GAM2301 LOC199986 5' GCCCTGCCCTCCTGACCTT 91510 A_ _
 AAGG AGGAGGG AGGGC
 |||| ||||| |||||
 TTCC TCCTCCC TCCCG
 AG G
 GAM2301 LOC199998 3' CTCTGAGGCTCCCTCTCCT 91517 AG GG_
 AGGA GAGGGAG CAGAG
 |||| ||||| |||||
 TCCT CTCCCTC GTCTC
 _ GGA
 GAM2301 LOC200634 5' CTGCCCTCCCCCGTGCTTT 90263 AA_ A
 AAGG GG GGGAGGGCAG
 |||| || |||||
 TTTC CC CCCTCCCGTC
 GTG _
 GAM2301 LOC200734 3' CTCCCTTCCCCACTCCTTCT 90275 A_ A CA
 AGAAGGA GG GGGAGGG GAG
 ||||| || ||||| |||
 TCTTCCT CC CCTTTCC CTC
 CA _ _
 GAM2301 LOC200734 3' CTCTCATCTTCTCCCCGCTCC 90276 AA_ A C_
 CTTC GAAGG GG GGGAGGG AGAG
 |||| || ||||| |||||
 CTTCC CC CCCTCTT TCTC
 CTCG _ CTAC
 GAM2301 LOC202126 3' GCTCCACTCTCCTGCCCTTCC 91908 A_ CA
 GGAAGG GGGAGGG GAGC
 ||||| ||||| |||||

CCTTCC TCCTCTC CTCG
 CG AC
 GAM2301 LOC202134 5' CCTTCCCTCCTTCCTATCT 91919 _
 AGA AGGAAGGAGGGAGGG
 ||| |||||
 TCT TCCTTCCTCCCTTCC
 A
 GAM2301 LOC219404 5' GCTCCTCCTCCCTCCTTCCGTC 95148 A CA
 GA GGAAGGAGGGAGGG GAGC
 || ||||| ||||
 CT CCTTCCTCCCTCCT CTCG
 G C_
 GAM2301 LOC219649 3' CTGCCTGGGTCTCCTCCCTC 94551 A A GA_
 GA GGA GGAGG GGGCAG
 || ||| |||| |||||
 CT CCT CCTCT TCCGTC
 C _ GGG
 GAM2301 LOC219653 3' CTCTGCCTGCCTCCCTCC 92915 A GA
 GGA GGAGG GGGCAGAG
 ||| |||| |||||
 CCT CCTCC TCCGTCTC
 C G_
 GAM2301 LOC219654 3' GCCCACTCCCTTTCCTTC 92936 AG ____
 GAAGGA GAGGGA GGGC
 ||||| ||||| ||||
 CTTCTT TTCCCT CCGG
 _ CAC
 GAM2301 LOC219688 5' GCCCCCCTCCTCCTCCTCT 94641 A _ A
 AGA GGA AGGAGGG GGGC
 ||| ||| ||||| ||||
 TCT CCT TCCTCCC CCGG
 _ CC _
 GAM2301 LOC219920 5' CCTTTCCTCCTTCCCTCT 94945 A
 AGA GGAAGGAGGGAGGG
 ||| |||||
 TCT CCTTCCTCCTTTCC
 C
 GAM2301 LOC219920 3' GCTCTGCCAAGCTGCCCTTCCT 94954 A AG____
 CCT AGGA GGAGGG GGCAGAGC
 |||| ||||| |||||
 TCCT CTTCCC CCGTCTCG
 C GTCGAA
 GAM2301 LOC219942 3' GCCCGTCTCCCCCTTCTTCCCT 94993 A A____
 C GA GGAAGGAGGG GGGC
 || ||||| ||||
 CT CCTTCTTCCC CCGG
 C CCTCTG
 GAM2301 LOC219997 3' CTCCACTCTCCCTGCTTCC 93255 G CA
 GGAAG AGGGAGGG GAG
 ||||| ||||| |||

CCTTC TCCCTCTC CTC
 G AC
 GAM2301 LOC220537 3' GCTCAGATTCCCACCCCCCTC 92425 A A A A CA____
 CCTCT AGA GGA GG GGG GGG GAGC
 ||| ||| || ||| ||| ||||
 TCT CCT CC CCC CCC CTCG
 C C C A TTAGA
 GAM2301 LOC220595 3' GCCCTCCCCCACCCTCT 92776 A AA A
 AGA GG GG GGGAGGGC
 ||| || || |||||
 TCT CC CC CCCTCCCG
 C CA C
 GAM2301 LOC220753 3' GCCCTCCCCCTTTCTTCT 94534 A
 AGAAGGAAGG GGGAGGGC
 ||||| |||||
 TCTTCCTTTC CCCTCCCG
 C
 GAM2301 LOC220827 3' CTGCCCTCAACTCCCCTT 92880 AA G_
 AAGG GGAG GAGGGCAG
 ||| ||| |||||
 TTCC CCTC CTCCCGTC
 _ AA
 GAM2301 LOC221218 3' CTCTACCAAGTCTCTTCTCCTC 93416 A _ _ C
 CT AGGA GGAGGGAG GG AGAG
 ||| ||||| || |||
 TCCT CTTCTCTC CC TCTC
 C TGAA A
 GAM2301 LOC221337 5' GCTTCTTACCCTCCCTCCCTTC 93736 _ CA_
 C GGAAGG AGGGAGGG GAGC
 ||||| ||||| |||
 CCTTCC TCCCTCCC TTCG
 C ATTC
 GAM2301 LOC221486 3' GCTCCATGCACCTCCCTTCCCT 92657 A _ _ _
 CC GGA GGA GGGAGG GCA GAGC
 ||| ||| ||||| ||| |||
 CCT CCT CCCTCC CGT CTCG
 C T A AC
 GAM2301 LOC221632 5' CTCTTTCCTCCCCTCTCC 95447 AG A C
 GGA G GGGAGGG AGAG
 ||| | ||||| |||
 CCT C CCCTCCT TCTC
 CT _ T
 GAM2301 LOC221763 5' GCTTTCCCCTCCTCCCGTCT 95437 A A _
 AGA GG AGGAGGG AGGGC
 ||| || ||||| |||||
 TCT CC TCCTCCC TTTCG
 G C C
 GAM2301 LOC221876 5' GCTCTTCTTCCCCACCTTCCCT 95541 A A_ C
 CT AGA GGAAGG GGGAGGG AGAGC
 ||| ||||| ||||| |||||

TCT CCTTCC CCCTTCT TCTCG
 C AC _
 GAM2301 LOC221893 5' GCTCCGCGCTCCTTCCCTC 94096 A G A
 GA GGAGGGAG GC GAGC
 || ||||| || ||||
 CT CCTTCCTC CG CTCG
 C G C
 GAM2301 LOC221915 3' CTCTGTGCTCCCTTCCCTCT 95568 A AA G
 AGA GG GGAGGGAG GCAGAG
 ||| || ||||| |||||
 TCT CC CTTCCCTC TGTCTC
 _ _ G
 GAM2301 LOC221935 3' CCCTCCCTCCCTTCCTCT 94200 A _
 AGA GGAAGG AGGGAGGG
 ||| ||||| |||||
 TCT CCTTCC TCCCTCCC
 _ C
 GAM2301 LOC221935 3' CCCTCCTTTCTTCCTTC 94201 _
 GAAGGAAGGAG GGAGGG
 ||||| |||||
 CTTCTTCCTT CCTCCC
 T
 GAM2301 LOC221975 5' GCATTCCCCTCTCTCCCTCCCT 94194 A A C A
 CT AGA GGA GGAGGGAGGG AG GC
 ||| ||| ||||| || ||
 TCT CCT CCTCTCTCCC TT CG
 C C C A
 GAM2301 LOC222166 3' CTCCCTCCTCCCTCCCCT 95734 AA CA
 AGG GGAGGGAGGG GAG
 ||| ||||| |||
 TCC CCTCCCTCCT CTC
 _ CC
 GAM2301 LOC222166 3' CTCTGCTCCCTCCTCCCTCC 95735 A GA _
 GGA GGAGG GG GCAGAG
 ||| |||| || |||||
 CCT CCTCC CC CGTCTC
 C TC T
 GAM2301 LOC222183 5' GCCCAGCCCCTCTTCCTCCT 95829 A GA A_
 AG AGGAAG GGG GGGC
 || ||||| ||| ||||
 TC TCCTTC CCC CCCG
 C TC GA
 GAM2301 LOC222183 3' GTCCCCCTCCCTCTTTCT 95830 A A
 AGAAGGA GGAGGG GGGC
 ||||| ||||| ||||
 TCTTTCT CCTCCC CCTG
 C C
 GAM2301 LOC253264 5' GCTCAGACACCCCCCTTCCT 96338 A A GCA_
 AGGAAGG GGG GG GAGC
 ||||| ||| || ||||

			TCCTTCC CCC CC	CTCG		
			— — ACAGA			
GAM2301	LOC253609 3'	CCCTTCCTCCTCCCTCT	98565	A A		
		AGA GGA GGAGGGAGGG				
		TCT CCT CTCCTTCCC				
		C —				
GAM2301	LOC253609 3'	CTCAACCCCTTCCTCCTCC	98566	A	CA_	
		GGA GGAGGGAGGG GAG				
		CCT CTCCTTCCC CTC				
		— CAA				
GAM2301	LOC253629 5'	GCTCTGCGGACGCTCCTTCC	99463		GGAGG	
		GGAAGGAG GCAGAGC				
		CCTTCCTC CGTCTCG				
		GCAGG				
GAM2301	LOC253962 5'	GCTCCATCCTCCCTCTCTTCC	98480	—	CA	
		GGAAG GAGGGAGGG GAGC				
		CCTTC CTCCTCCT CTCG				
		T AC				
GAM2301	LOC253980 3'	GCCCTGCGTCCTTCCCTCT	96772	A	GGG	
		AGA GGAAGGA AGGGC				
		TCT CCTTCCT TCCCG				
		C GCG				
GAM2301	LOC253992 3'	GCTCTGATCCCCCTCCTTCCTC	98426	—	A —	
	TC	GA AGGAAGGAGGG GGG CAGAGC				
		CT TCCTTCCTCCC CCT GTCTCG				
		C — A				
GAM2301	LOC254181 3'	CTCAAGCCCCCTTCCTCCT	99441	A	A A_	
		AGGA GGAGGG GGGC GAG				
		TCCT CTTCC CCG CTC				
		— — AA				
GAM2301	LOC254532 5'	CTTAGCCTCCCCTCCCTCC	98454	A	AG A	
		GGA GGAGGG GGC GAG				
		CCT CCTCCC CCG TTC				
		C CT A				
GAM2301	LOC254532 5'	GCCTTCTCCCGTCCTCCCCTC	98456	A A	— —	
		GA GG AGGA GGGAG GGC				
		CT CC TCCT CCCTC CCG				
		C C G TT				
GAM2301	LOC254532 3'	CCCTCCCTCCCTTCCTTC	98451	—		
		GAAGGAAGG AGGGAGGG				

		CTTCCTTCC TCCCTCCC			
		C			
GAM2301	LOC254557 5'	CTCCGCCCCCTTCCTATCC	97978	_	A A
		GGA AGGAGGG GGGC GAG			
		CCT TCCTTCC CCGC CTC			
		A _ C			
GAM2301	LOC254842 5'	CTCTGTCCTCCCTGCTTCC	99449	G	
		GGAAG AGGGAGGGCAGAG			
		CCTTC TCCCTCCTGTCTC			
		G			
GAM2301	LOC254873 3'	CTCTCCCCTCCCTCTTCCTTC	96212	G	C
		GAAGGAAG AGGGAGGG AGAG			
		CTTCCTTC TCCCTCCC TCTC			
		_ C			
GAM2301	LOC254945 5'	CCCTTCCTCCCTCCTTCT	98677	A	
		AGAAGGA GGAGGGAGGG			
		TCTTCCT CCTCCTTCCC			
		C			
GAM2301	LOC255042 3'	CTGACCCCTTCCCTTCC	97043	_	A _
		GGAAGG AGGG GGG CAG			
		CCTTCC TTCC CCC GTC			
		C _ A			
GAM2301	LOC255147 3'	GCTGTTTCCTCCTTCCCCCT	97408	AA	_
		AG GGAAGGAGGGAG GGC			
		TC CCTTCCTCCTTT TCG			
		CC G			
GAM2301	LOC255158 3'	CTCCATTGTCCTCTTCCTTCT	97879	G	___
		GGAAGGAGG AGGGCA GAG			
		TCTTCCTTC TCCTGT CTC			
		_ TAC			
GAM2301	LOC255270 3'	CTGCCCTCCTCTCCCTCC	96242	A	_
		GGA GGAG GGAGGGCAG			
		CCT CCTC CCTCCCGTC			
		C T			
GAM2301	LOC255270 3'	CTTTGGCCCCCTGCCCTCCT	96243	A _	A G
		AGGA GG AGGG GG CAGAG			
		TCCT CC TCCC CC GTTTC			
		C G _ G			
GAM2301	LOC255316 3'	GCCCCTGCCACCTCCTTCCCTC	99095	A	GAG A_
		GA GGAAGGAGG GGCAG GC			

CT CCTTCCTCC CCGTC CG
 C A__ CC
 GAM2301 LOC255739 3' TCCTCCCTCCTGCCCTCCT 97906 A A_
 AG AGG AGGAGGGAGGG
 || ||| |||||
 TC TCC TCCTCCCTCCT
 C CG
 GAM2301 LOC256416 3' GCCCTTCCTCCTCCTCTTC 96060 _ A _
 GAAG G AGGAGGGAGGG C
 |||| | |||||
 CTTC C TCCTCCTTCCC G
 T C C
 GAM2301 LOC256416 3' GCTCTGCGGCCCTTCCTCCTC 96061 A ____
 CT AGGA GGAGGGAGG GCAGAGC
 |||| ||||| |||||
 TCCT CCTCCTTCC CGTCTCG
 _ CCGG
 GAM2301 LOC256663 5' CTCTACTCCCTTCCCCCT 98747 AA GGC
 AGG GGAGGGAG AGAG
 || ||||| |||||
 TCC CTTCCCTC TCTC
 CC A__
 GAM2301 LOC256942 3' CTACTGCCCCCCCCCTCTT 96186 A A A _
 AGGA GG GGG GGGCAG AG
 |||| || ||| ||||| ||
 TTCT CC CCC CCGTC TC
 C _ C A
 GAM2301 LOC256950 3' GCTCTGCTGTTCCCTCCTCCT 97156 A _
 AGGA GGAGGGAG GGCAGAGC
 |||| ||||| |||||
 TCCT CCTCCCTT TCGTCTCG
 _ G
 GAM2301 LOC257019 5' GCGTCCCCTCCCTCCTCCCCTC 97868 A A CAGA
 GA GG AGGAGGGAGGG GC
 || || ||||| ||
 CT CC TCCTCCCTCCC CG
 C C CTG_
 GAM2301 LOC257203 5' CCCCACCGTTTCCTTCCATTCT 98714 _ ____ GA
 AGAA GGAAGGA GG GGG
 |||| ||||| || |||
 TCTT CCTTCCT CC CCC
 A TTG AC
 GAM2301 LOC257358 3' GCTCCAAAGCTCCCTCTCTTCC 98899 _ GGCA_
 GGAAG GAGGGAG GAGC
 |||| ||||| |||||
 CCTTC CTCCCTC CTCG
 T GAAAC
 GAM2301 LOC257364 3' GCCTGGGCCCCCTCCTTCC 96646 A G_ A
 GGAAGGAGGG GG CAG GC
 ||||| || ||| ||

			CCTTCCTCCC CC GTC CG		
			_ GG _		
GAM2301	LOC257459 3'	GCCTCCCCTCCTTTCTCCT	91530	A	AG
		AG AGGAAGGAGGG GGC			
		TC TCTTTCCTCCC CCG			
		C CT			
GAM2301	LOC257551 5'	CTCCACCCTCTCTCCCCT	99556	AA	CA
		AGG GGAGGGAGGG GAG			
		TCC CCTCTCTCCC CTC			
		_ AC			
GAM2301	LOC257601 5'	CTCCACCCTCTCTCCCCT	99650	AA	CA
		AGG GGAGGGAGGG GAG			
		TCC CCTCTCTCCC CTC			
		_ AC			
GAM2301	LOC51035 5'	CCTTCCCGCCCTCCTTCT	32392	A A	
		AGAAGGA GG GGGAGGG			
		TCTTCCT CC CCCTTCC			
		C G			
GAM2301	LOC51107 3'	CTGCCCAAGACTCACCTCCCTT	32609	A A A	_
	C	GAAGG AGG GGG GGGCAG			
		CTTCC TCC CTC CCGTC			
		C A AGAA			
GAM2301	LOC51195 3'	TTCTGCTCCCTGCCCCCTCC	33411	A A	_ _
		GGA GG GGG AGG GCAGAG			
		CCT CC CCC TCC CGTCTT			
		_ _ G CT			
GAM2301	LOC51634 3'	GCTCCCCGTTTCCTCCCTCCTC	32612	A	CA
	C	GGA GGAGGGAGGG GAGC			
		CCT CCTCCCTCCT CTCG			
		_ TTGCCC			
GAM2301	LOC51634 3'	TCCTCCCTCCTCCCTGTC	32613	_ A	
		GA AGG AGGAGGGAGGG			
		CT TCC TCCTCCCTCCT			
		G C			
GAM2301	LOC51673 3'	GCCCTTCCTCCTCCTCTTC	96208	_ A	_
		GAAG G AGGAGGGAGGG C			
		CTTC C TCCTCCTTCCC G			
		T C C			
GAM2301	LOC51673 3'	GCTCTGCGGCCCTTCCTCCTC	96209	A	_
	CT	AGGA GGAGGGAGG GCAGAGC			

			TCCT CCTCCTTCC CGTCTCG			
			— CCGG			
GAM2301	LOC51762	5'	GCCCGCGGCCCTCCCGCCT 33707	A	AA_	A_____
		CT	AGA GG GGAGGG GGGC			
			TCT CC CCTCCC CCGG			
			_ GCC CCGGCG			
GAM2301	LOC55580	5'	CTTTCCTTCCTCCTCCT 34534	A		C
			AGGA GGAGGGAGGG AGAG			
			TCCT CCTCCTTCCC TTTC			
			— —			
GAM2301	LOC56961	5'	TTCCCCCTCCCCTCCTTCT 63580		_	CA
			GGAAGGAGGG AGGG GAG			
			TCTTCCTCCC TCCC CTT			
			C C_			
GAM2301	LOC57100	3'	CCCTGCCTCCTCCCTGCT 40161	A	A	G
			AG AGG AGGAGG AGGG			
			TC TCC TCCTCC TCCC			
			G C G			
GAM2301	LOC57149	5'	CTCTTCCTCCCTCCCTCT 40302	A		C
			GGA GGAGGGAGGG AGAG			
			TCT CCTCCCTCCC TCTC			
			C T			
GAM2301	LOC58512	3'	GCTTTGTCCCCACCTCCTCC 65284	A	GA	_
			GGA GGAGG GGG CAGAGC			
			CCT CCTCC CCC GTTTCG			
			_ AC T			
GAM2301	LOC59346	5'	GCGTCTCCCCGCCTTCCCTC 41572	A	A_	_
			GA GGAAGG GGGAGG GC			
			CT CCTTCC CCCTCT CG			
			C GC G			
GAM2301	LOC90019	5'	GCCCGCCCCACCTTCCTTC 57530	A	A_	
			GAAGGAAGG GGG GGGC			
			CTTCCTTCC CCC CCGG			
			A CG			
GAM2301	LOC90092	5'	CTCTGCCCCCGTCCTCCCTTC 62061	A	G	A
			GAAGG AGGA GG GGGCAGAG			
			CTTCC TCCT CC CCCGTCTC			
			C G _			
GAM2301	LOC90288	3'	CTCTTAGTCCCTCCTTCCTTC 62785			GGGC
			GAAGGAAGGAGGGA AGAG			

		CTTCCTTCCTCCCT	TCTC		
		GAT_			
GAM2301	LOC90342	5'	TTGTCCTGCCCTCCTTCT	63019	_
			GGAAGGAGGG AGGGCAG		
			TCTTCCTCCC TCCTGTT		
			G		
GAM2301	LOC90494	5'	CTGATCCTCTCCCTCCTTCC	63733	___
			GGAAGGAGGGAGGG CAG		
			CCTTCCTCCCTCTC GTC		
			CTA		
GAM2301	LOC90719	5'	GCCCCCTCCCTCCTCTC	64608	_ A A
			GA AGGA GGAGGG GGGC		
			CT TCCT CCTCCC CCCG		
			C C _		
GAM2301	LOC90925	3'	CTCTTACTCCCTCCTTCT	65055	GGC
			GGAAGGAGGGAG AGAG		
			TCTTCCTCCCTC TCTC		
			AT_		
GAM2301	LOC91040	5'	CTCCACCCTCTTCCTGCC	65345	A G CA
			GG AGGAGG AGGG GAG		
			CC TCCTTC TCCC CTC		
			G _ AC		
GAM2301	LOC91064	5'	GCCCTCCACCCCTCCTTCCT	65387	___
			AGGAAGGAGGG AGGGC		
			TCCTTCCTCCC TCCCG		
			CCACC		
GAM2301	LOC91266	5'	CTGCCCTTCTCCCTCCT	66020	A GA
			AGGA GGAGG GGGCAG		
			TCCT CCTCT CCCGTC		
			C TC		
GAM2301	LOC91301	5'	CTGCCTGGACCCCCCTTCC	66146	A A___
			GGAAGG GGG GGGCAG		
			CCTTCC CCC TCCGTC		
			C CAGG		
GAM2301	LOC91397	5'	CTGCCCTCCCCCTTCC	66496	A_ _
			GGAAGG GGGAGGG CAG		
			CCTTCC CCCTCCC GTC		
			CC C		
GAM2301	LOC91397	5'	GCCCTCCCCCTTCCTCT	66499	A A_ _
			AGA GGAAGG GGGAGGG C		

		TCT CCTTCC CCCTCCC G	
		— CC C	
GAM2301	LOC91445 3'	CTCTGTTCTCTTTCCTTCC 61168	
		GGAAGGAGGGAGGGCAGAG	
		CCTTCCTTTCTCTTGTCTC	
GAM2301	LOC91571 3'	GCTCCTGATCCCCCTTCTCCT 67103	A A _ _
		AGGA GGAGGG GGG CAG AGC	
		TCCT CTTCCC CCT GTC TCG	
		— — A C	
GAM2301	LOC91748 5'	GCTCTGCCCTCCCTGGCTCCT 67640	AGG
		AGGA AGGGAGGGCAGAGC	
		TCCT TCCCTCCCGTCTCG	
		CGG	
GAM2301	LOC92148 5'	GCCCCACCCACCCCTTCCTGTC 68882	_ A_ A_
		GA AGGAAGG GGG GGGC	
		CT TCCTTCC CCC CCG	
		G CCA AC	
GAM2301	LOC92293 3'	GCCCTGCCCAGATGCCTTCCTT 69322	AGGGA A
		AAGGAAGG GGGCAG GC	
		TTCCTTCC CCGTC CG	
		GTAGA C	
GAM2301	LOC92799 3'	CTAGGTCCCCACCTTCCTCT 57242	A AG A AG
		AGA GGAAGG GG GGGC AG	
		TCT CCTTCC CC CCTG TC	
		C A_ _ GA	
GAM2301	LOC93259 5'	GCTCTGCTTCCCTTCCCACCT 72287	AA AG
		AGG GGAGGG GGCAGAGC	
		TCC CCTTCC TCGTCTCG	
		AC CT	
GAM2301	LOC93380 5'	GCTCCGCCGTCCTTCGCTTCT 72654	_ G A
		GGAAG GAGGGA GGC GAGC	
		TCTTC CTTCTT CCG CTCG	
		G G C	
GAM2302	ANPEP 3'	TGAGCACCTCCAGCCCCT 8566	G G
		AGGGG TGGGAGGTGT CA	
		TCCCC ACCCTCCACG GT	
		G A	
GAM2302	ATP2B2 5'	CTCGGCCACCCCCACCCCC 9849	A T ATA
		GGGGGTGGG GGTG GC AG	

CCCCCACCC CCAC CG TC
 _ _ GC_
 GAM2302 BACH2 3' CACCTTCCTCCCACCCACC 41776 _ T__
 GG GGGTGGGAGG GTG
 || ||||| ||
 CC CCCACCCTCC CAC
 A TTC
 GAM2302 C18orf2 3' CACATCCCGCCACCCCC 49459 A__
 GGGGGTGGG GGTGTG
 ||||| ||||
 CCCCCACCC CTACAC
 GCC
 GAM2302 CST3 3' ATCTTATGCACACCTCCCACCC 5433 ____
 CCT AGGGGGTGGGAGGTGTGCATAAGA T
 ||||| ||||| |
 TCCCCACCCCTCCACACGTATTCT A
 GAM2302 DNM1 3' GCATCCCTCCCACCCCT 16613 TG _
 AGGGGGTGGGAGG TG C
 ||||| ||
 TCCCCACCCCTCC AC G
 CT C
 GAM2302 EGFL4 3' CACCACCTCCACCACCCCT 62452 _ _
 AGGGGGTGG GAGGTG TG
 ||||| |||| ||
 TCCCCACC CTCCAC AC
 AC C
 GAM2302 EIF2C1 3' CTATGTCCCCACCCCT 25187 A TGT A
 GGGGGTGGG GG GCAT AG
 ||||| || ||||
 TCCCCACCC CC TGTA TC
 _ _ C
 GAM2302 FUS1 3' CTTACAGTAACCCCCACCCCTT 24405 A G A_
 AGGGGGTGGG GGT TGC TAAG
 ||||| |||| ||||
 TTCCCCACCC CCA ATG ATTC
 _ _ AC
 GAM2302 KPNB1 5' CACCCGACCCCAACCCCC 11217 _ A ____
 GGGGGT GGG GGT GTG
 |||| |||| ||
 CCCCCA CCC CCA CAC
 A _ GCC
 GAM2302 LTBR 3' GCAGACCCACCCACCCCT 11373 A_ G
 AGGGGGTGGG GGT TGC
 ||||| ||||
 TCCCCACCC CCA ACG
 AC G
 GAM2302 MEIS1 3' ATGCAACAACCACCACCT 11533 G GAG G
 AGG GGTGG GT TGCAT
 || |||| || ||||

		TCC CCACC CA ACGTA		
		A AA_ _		
GAM2302	MSX2	3' TCTATCTCTCCCCGCCCCC 66173	A TGTGC	A
		GGGGGTGGG GG ATA GA		
		CCCCCGCCC CC TAT CT		
		_ TCTC_ C		
GAM2302	NPTX1	3' CTCATGCACACGAAGCAGCCCC 11833	G GGAG	A
	T	AGGGG TG GTGTGCAT AG		
		TCCCC AC CACACGTA TC		
		G GAAG C		
GAM2302	PLP2	3' GCAGACCAACTCCCACCCCT 12175	___ G	
		AGGGGGTGGGA GGT TGC		
		TCCCCACCT CCA ACG		
		CAA G		
GAM2302	PPP2R4	3' CTTGTCCTCCACCTCCCT 61180	_ TGTGC	
		AGGG GGTGGGAGG ATAAG		
		TCCC CCACCCTCC TGTTT		
		T		
GAM2302	TBX6	3' CTTGATTTCACCTCCACCCCC 55812	G TGCA	
		GGGGGTGGGAG TG TAAG		
		CCCCCACCTC AC GTTC		
		_ TTTA		
GAM2302	TCF7L2	3' TCTTAATTTGCCCCCCACCCCC 48442	A TGCA	
		GGGGGTGGG GGTG TAAGA		
		CCCCCACCC CCGT ATTCT		
		C TTA_		
GAM2302	TNFRSF6	3' TCTTATTTTTCCCCACCCCC 5268	A TGTGC	
		GGGGGTGGG GG ATAAGA		
		CCCCCACCC CC TATTCT		
		_ TTTT_		
GAM2302	TNFSF12	3' TCTTACAACTCCCCACCGCCC 15084	_ A T GCA	
		GGG GGTGGG GG GT TAAGA		
		CCC CCACCC CC CA ATTCT		
		G _ T AC_		
GAM2302	TP53	3' TGACAGCCTCCCACCCCC 6807	GTG	
		GGGGGTGGGAGGT CA		
		CCCCCACCTCCG GT		
		ACA		
GAM2302	UCP3	3' ATGCAGCCTCTTCCCCACCCCC 13980	___ G	
		GGGGGTGGG AGGT TGCAT		

CCCCCACCC TCCG ACGTA
 CTTC _
 GAM2302 ABT1 3' TCTTAGAGCCCCCTCCCCCT 26306 T A T GCA
 AGGGGG GGG GG GT TAAGA
 ||||| ||| || || |||||
 TCCCCC CCC CC CG ATTCT
 T _ _ AG_
 GAM2302 C1orf34 3' ATGGCCCCACACCCCT 61298 _ A T G
 AGGGGGTG GG GG GT CAT
 ||||| || || || |||
 TCCCCAC CC CC CG GTA
 A _ _ _
 GAM2302 CAMTA2 3' CACGCCTTGCTCCCACACCCCT 61881 _ ____
 AGGGG GTGGGA GGTGTG
 |||| ||||| |||||
 TCCCC CACCCT CCGCAC
 A CGTT
 GAM2302 CCR1 3' TCTTCCATCACCTCCCCCCCC 8931 T _ CAT
 GGGGG GGGAGGTG TG AAGA
 |||| ||||| || |||||
 CCCCC CCCTCCAC AC TTCT
 _ T C_
 GAM2302 COP9 3' TCTTTTCACCCCCACCTCCT 22965 A T CAT
 AGGGGGTGGG GG GTG AAGA
 ||||| || || || |||||
 TCCTCCACCC CC CAC TTCT
 _ _ TT_
 GAM2302 DKFZP564O0423 3' TACGCTTCCCCACGCCCT 93358 G ____
 AGGG GT GGGAGGTGTG
 |||| || ||||| |||||
 TCCC CA CCCTTCGCAT
 G CC
 GAM2302 DKFZP727M111 3' TCTTACCTAACTCCCAACCCCT 32063 G GTGTGCA
 AGGGG TGGGAG TAAGA
 |||| ||||| |||||
 TCCCC ACCCTC ATTCT
 A AATCC_
 GAM2302 DMWD 3' GCGCCACCTCCACCCCC 61551 GA _
 GGGGGTGG GGTG TGC
 ||||| |||| |||||
 CCCCCACC CCAC GCG
 TC C
 GAM2302 FLJ00058 5' CACCCCTCTCCACCCCTC 79506 T__
 GGGGGTGGGAGG GTG
 ||||| ||||| |||||
 CTCCACCCCTCT CAC
 CCC
 GAM2302 FLJ20625 3' CATCTCTACCCACCCCT 35897 ____
 AGGGGGTGGG AGGTG
 ||||| ||||| |||||

		TCCCCACCC TCTAC	
		CATC	
GAM2302	FLJ21736	3' TGACCCTCCCCCACCCCC 46788	___ T G
		GGGGGT GGGAGG GT CA	
		CCCCCA CCCTCC CA GT	
		CCC _ _	
GAM2302	HTR3A	3' TACACCCTTGTCCCACCCCC 7879	___
		GGGGGTGGGA GGTGTG	
		CCCCCACCT CCACAT	
		GTTC	
GAM2302	IKKE	3' TACGCCTTCCCACTCCCT 26595	_
		AGGGGGTGGGA GGTGTG	
		TCCCTCACCT CCGCAT	
		T	
GAM2302	KCND1	5' CTTTCAACACCCACCCCC 18344	AG GCAT
		GGGGGTGGG GTGT AAG	
		CCCCACCC CACA TTC	
		_ ACT_	
GAM2302	KIAA0757	3' GCTGGACTCCCCACCCCT 21258	AG G _
		AGGGGGTGGG GT T GC	
		TCCCCACCC CA G CG	
		CT G T	
GAM2302	KIAA1402	5' CACGCCTCCGCCCGCCCCCT 66991	___
		AGGGGGTGGG AGGTGTG	
		TCCCCGCCC TCCGCAC	
		CGCC	
GAM2302	KIAA1553	3' TATACCTGGCCACCCCCT 93570	G_
		AGGGGGTGG AGGTGTG	
		TCCCCACC TCCATAT	
		GG	
GAM2302	KIAA1822	3' GCATCCCCCCCACCCCCT 68185	A TG
		AGGGGGTGGG GG TGC	
		TCCCCACCC CC ACG	
		C CT	
GAM2302	LR8	5' CACACCTCGACCCCTCACCCCC 26700	___
	T	AGGGGGTGG GAGGTGTG	
		TCCCCACT CTCCACAC	
		CCCCAG	
GAM2302	MGC10986	3' TGTAACCTTCCACCCCCT 48329	G
		AGGGGGTGGGAGGT TGCA	

TCCCCCACCTTCCA ATGT

GAM2302 MGC15476 3' CTATGACCCCCACTCCCT 59609 A GTG A
AGGGGGTGGG GGT CAT AG
||||||| ||| ||| ||
TCCCTCACCC CCA GTA TC
_ _ _ C
GAM2302 NXPH3 3' CTATGCACACTGCCGCCT 66341 GA A
GGGTGG GGTGTGCAT AG
||||| ||||| ||
TCCGCC TCACACGTA TC
G _ C
GAM2302 P450RAI-2 3' TATGCCACGGTTCCCACCCTC 39578 G _
GGGGGTGGGAG TGTG CATA
||||||| ||| |||
CTCCCACCCTT GCAC GTAT
G C
GAM2302 PARVB 3' CACGCCTGCCCCACCCCCT 26189 _
AGGGGGTGGG AGGTGTG
||||||| |||||
TCCCCACCC TCCGCAC
CG
GAM2302 PLA2G6 3' CACACTGGCCCAGCCCCT 67087 G A_
AGGGG TGGG GGTGTG
||||| ||| |||||
TCCCC ACCC TCACAC
G GG
GAM2302 PLSR3 3' ATGCACTCTCTCCCACCCCCT 40151 _ T
AGGGGGTGGGAG G GTGCAT
||||||| ||| |||||
TCCCCACCCTC C CACGTA
T T
GAM2302 SDS3 3' ATGCCCTGCCTACCCCCT 69742 _ TGT
AGGGGGTGGG AGG GCAT
||||||| ||| |||
TCCCCATCC TCC CGTA
G _
GAM2302 SPTLC2 3' GTAACACGTCCCACCCCCT 18000 G _
AGGGGGTGGGA GTGT GC
||||||| ||| ||
TCCCCACCCT CACA TG
G A
GAM2302 STRAIT11499 3' TCTATGGCACCCCCACCCC 41432 A G A
GGGGTGGG GGTGT CATA GA
||||| ||||| ||| ||
CCCCACCC CCACG GTAT CT
_ _ C
GAM2302 XPO5 3' CACAAGCCCTCCCACCCCC 92872 _
GGGGGTGGGAGG TGTG
||||||| |||

	CCCCCACCTCC ACAC		
	CGA		
GAM2302 LOC144473 3'	CTTATTTCCACCCCCACCCC 83995	A	TGC
	GGGGGTGGG GGTG ATAAG		
	CCCCCACCC CCAC TATTC		
	C CTT		
GAM2302 LOC149876 3'	TGCTGCCCCCACCACCCT 80352	_	A T
	AGGG GGTGGG GGTG GCA		
	TCCC CCACCC CCGT CGT		
	A C _		
GAM2302 LOC170396 3'	CTCATGTTTTGTCCCACTCCC 83730		GGTGT A
	GGGGGTGGGA GCAT AG		
	CCCTCACCT TGTA TC		
	GTTT_ C		
GAM2302 LOC200014 3'	CATCTTCCCCACCCCCT 89925	___	
	AGGGGGTGGG AGGTG		
	TCCCCCACCC TCTAC		
	CCT		
GAM2302 LOC95633 3'	CACCTTGGCCCCACCCCCT 60557	A	___
	AGGGGGTGGG GGT GTG		
	TCCCCCACCC CCG CAC		
	_ GTTC		
GAM2303 ACPT 3'	TCTTGCCCAGATCTCGGCT 55829	T	A_
	AGCCG AGATCTGG AAGA		
	TCGGC TCTAGACC TTCT		
	_ CG		
GAM2303 B3GAT1 3'	CTGCTCTTCCCAAAGCTGC 38454	ATC	A
	GTAG TGG AAGAGCAG		
	CGTC ACC TTCTCGTC		
	GAA C		
GAM2303 B3GAT1 3'	CTGCTCTTCCCGAGAGCT 55055	A _	A
	AG TCT GG AAGAGCAG		
	TC AGA CC TTCTCGTC		
	G G C		
GAM2303 CNTN2 3'	TCTGCTCTCCCAGCACTG 18665	AT	AA
	TAG CTGG AGAGCAGA		
	GTC GACC TCTCGTCT		
	AC C_		
GAM2303 KCNC3 3'	CTGCTCTTTCCCTAC 18331	ATCT	___
	GTAG GGAA AGAGCAG		

			CATC CCTT TCTCGTC		
			_____ TC		
GAM2303	KRT3	3'	CTCCTTCCAGATCCCCGGC 55103	TA	A
			GCCG GATCTGGAA GAG		
			CGGC CTAGACCTT CTC		
			CC C		
GAM2303	LANCL1	3'	TCTACTCTTTCTATTACTGC 21335	ATC	C
			GTAG TGGAAAGAG AGA		
			CGTC ATCTTTCTC TCT		
			ATT A		
GAM2303	MDM1	3'	TCTGCTCTCTTATGTCACAGCT 39683	C A	CTG A
			AGC GT GAT GA AGAGCAGA		
			TCG CA CTG TT TCTCGTCT		
			A _ TA_ C		
GAM2303	OAS3	3'	TCTGCTCTCCCAGCTCAC 21657	A T	AA
			GT GA CTGG AGAGCAGA		
			CA CT GACC TCTCGTCT		
			_ C C_		
GAM2303	PFKFB3	3'	CTGCTCTTCCCAGGTGGGG 83750	G AG	A
			CC T ATCTGG AAGAGCAG		
			GG G TGGACC TTCTCGTC		
			G__ C		
GAM2303	PKP1	5'	TCTGCTCTCCTAGGCCCGGC 6108	TAGA	AA
			GCCG TCTGG AGAGCAGA		
			CGGC GGATC TCTCGTCT		
			CCC_ C_		
GAM2303	PTGER3	5'	TCTGCCCCCTCCCGCTGCGGCT 8175	ATCT	AAGA
			AGCCGTAG GGA GCAGA		
			TCGGCGTC CCT CGTCT		
			GC__ CCCC		
GAM2303	TLE2	3'	TCTGCTCTCTGGCCAACGGCT 13772	AGATC	AA__
			AGCCGT TGG AGAGCAGA		
			TCGGCA ACC TCTCGTCT		
			_____ GGTC		
GAM2303	VTN	5'	TCTGCCCTCCAGATCCACGGT 7166	A	AA A
			GCCGT GATCTGGA G GCAGA		
			TGGCA CTAGACCT C CGTCT		
			C _ C		
GAM2303	C9orf7	3'	TCTGCCCTTTCCAGAGGGGT 34587	GTAGA	A
			GCC TCTGGAAAG GCAGA		

TGG AGACCTTTC CGTCT
 GG__ C
 GAM2303 DKFZP564J157 3' CTGCTCTCCCATCAAGCT 38053 CGTA TC AA
 AGC GA TGG AGAGCAG
 ||| || ||| |||||
 TCG CT ACC TCTCGTC
 AA__ C_

GAM2303 HA-1 3' CTGCCCTCTCCTCACAGGT 66157 _ A TCT A A
 GCC GT GA GGA AG GCAG
 ||| || ||| |||||
 TGG CA CT CCT TC CGTC
 A _ C C

GAM2303 KIAA0280 3' TCTGCTCTTTTCCTCCACGGAC 93311 _ A TCT
 T AG CCGT GA GGAAAGAGCAGA
 || ||| || |||||
 TC GGCA CT CTTTCTCGTCT
 A C C_

GAM2303 KIAA1817 5' CTGCCCTTCCGGATCCAGAGCT 68778 CGTA A A
 AGC GATCTGGAA G GCAG
 ||| ||||| |||
 TCG CTAGGCCTT C CGTC
 AGAC _ C

GAM2303 MGC16179 3' CTGCCCTCCAGTTCTGCGGC 52281 T AAAGA
 T AGCCGTAGA CTGG GCAG
 ||||| ||| |||
 TCGGCGTCT GACC CGTC
 T CTCCC

GAM2303 MGC16372 3' CTGCTCTCTGGATTTCCAGGG 59530 GT__ TG AA
 CT AGCC AGATC GA GAGCAG
 ||| ||| || |||||
 TCGG TTTAG CT CTCGTC
 GACCT GT _

GAM2303 MGC2452 3' TCTGCCTAGAAAGATCTATGAC 51969 C GGAA A
 T AG CGTAGATCT AG GCAGA
 || ||||| || |||||
 TC GTATCTAGA TC CGTCT
 A AAGA _

GAM2303 NBR2 5' TCTACTCTTCCAGTTGCGGCT 20623 AT A C
 AGCCGTAG CTGGAA GAG AGA
 ||||| ||||| ||| |||
 TCGGCGTT GACCTT CTC TCT
 _ _ A

GAM2303 PCYT2 3' TCCGCTCTTCCAGCAAAGCTG 12685 C AGAT A
 CT AGC GT CTGGAAAGAGC GA
 ||| || ||||| ||| |||
 TCG CG GACCTTTCTCG CT
 T AAAC C

GAM2303 PEX16 3' TCTGCCCTTCTCCGCAGGGC 55159 GTAGATC _ A_

GCC TGGA AAG GCAGA
 ||| ||| ||| |||||

CGG GCCT TTC CGTCT
 GAC___ C CC
 GAM2303 PI4KII 3' TCTGCTCTCTGCTGGCCTACAG 37955 C AT TG AA_
 CT AGC GTAG C G AGAGCAGA
 ||| ||| | | |||||
 TCG CATC G C TCTCGTCT
 A C_ GT GTC
 GAM2303 PTK6 3' CTGCTCTTCCCAGTTCAGC 21077 A T A
 GT GA CTGG AAGAGCAG
 || || ||| |||||
 CG CT GACC TTCTCGTC
 A T C
 GAM2303 SEMA4G 5' CTGCTCTTTCTGGGCACAGCT 96327 C AGA TG
 AGC GT TC GAAAGAGCAG
 ||| || || |||||
 TCG CA GG CTTTCTCGTC
 A C_ GT
 GAM2303 LOC145255 5' TCTGCTCTCCAGGCACTAC 84270 A_ AA
 GTAG TCTGG AGAGCAGA
 ||| ||| |||||
 CATC GGACC TCTCGTCT
 AC C_
 GAM2303 LOC149483 3' CTATTTCCAGACCTACAGGT 80186 _ A G
 GCC GTAG TCTGGAAA AG
 ||| ||| ||||| ||
 TGG CATC AGACCTTT TC
 A C A
 GAM2303 LOC151475 3' TCTGCCCTGTTCATCTACGG 86606 TC A A
 CCGTAGA TGGA AG GCAGA
 ||||| ||| || |||
 GGCATCT ACTT TC CGTCT
 _ G C
 GAM2303 LOC222962 3' GCTTCCAGATCCCCGGC 94455 TA AAG
 GCCG GATCTGGA AGC
 ||| ||||| ||
 CGGC CTAGACCT TCG
 CC _
 GAM2303 LOC253502 3' CTGCCAGGGTCCAGCTCTACG 96218 T AAGA_
 GC GCCGTAGA CTGGA GCAG
 ||||| ||| |||
 CGGCATCT GACCT CGTC
 C GGGACC
 GAM2303 LOC254824 3' CTGCTCTTCCAGCTGCCAGGCT 98411 _ AT A
 AGCC GTAG CTGGAA GAGCAG
 ||| ||| ||||| |||||
 TCGG CGTC GACCTT CTCGTC
 AC _ _
 GAM2303 LOC255736 3' CTGCTCTCCCATCAAGCT 97074 CGTA TC AA
 AGC GA TGG AGAGCAG
 ||| || ||| |||||

		TCG CT ACC TCTCGTC		
		AA__ C_		
GAM2303	LOC256812 5'	GCTCTCGGAGGCCTGCGGCT 99407	AT	GGAA
		AGCCGTAG CT AGAGC		
		TCGGCGTC GA TCTCG		
		CG GGC_		
GAM2304	CDH12 3'	CTTATCATTTAAAGTGGTGTA 15777	CCCAA	GA
		TACACCACT GAA ATAAG		
		ATGTGGTGA TTT TATTC		
		AA__ AC		
GAM2304	GOCAP1 3'	ATTGTTCTTGGGAGCAGTGTA 43007	CA	G
		TACAC CTCCCAAGAA AAT		
		ATGTG GAGGGTTCTT TTA		
		AC G		
GAM2304	DKFZp434N2435 5'	CTTATTACTGTGGGGTGGT 98090	T	AGAAG
		ACCAC CCCA AATAAG		
		TGGTG GGGT TTATTC		
		_ GTCA_		
GAM2304	DKFZP564I122 3'	CTTATTCTTCTCCCTCATGTGT 63877	CACTCCCA	
	A	TACAC AGAAGAATAAG		
		ATGTG TCTTCTTATTC		
		TACTCCC_		
GAM2304	FLJ21791 3'	CTTATTTGCAGAAAGTGGTGTA 62126	CCCAAGAA	
		TACACCACT GAATAAG		
		ATGTGGTGA TTTATTC		
		AGACG__		
GAM2304	HMP19 3'	CTTATTCTTTGTTAGGAAAATG 88860	CCAC	CAA_
	TA	TACA TCC GAAGAATAAG		
		ATGT AGG TTTCTTATTC		
		AAA_ ATTG		
GAM2304	KIAA1719 3'	TCTGTCTTGGGAGTGGTGTA 68742	_	
		TACACCACTCCCAAGA AGA		
		ATGTGGTGAGGGTTCT TCT		
		G		
GAM2304	KIAA1853 3'	TTTTTCTTGGAAGCAGTG 69929	CA	C
		CAC CT CCAAGAAGAA		
		GTG GA GGTTCTTTTT		
		AC A		
GAM2304	KIAA1877 3'	CTTATTCTTCTGCCATGAGT 66748	CCA__	
		ACTC AGAAGAATAAG		

		TGAG TCTTCTTATTC	
		TACCG	
GAM2304 KIAA1906	3'	CTTATTCTTCTTGACTTTTGG 73571	CTCC_
		CCA CAAGAAGAATAAG	
		GGT GTTCTTCTTATTC	
		TTTCA	
GAM2304 OSBPL11	3'	CTTAATTTCCCAAGAGTGGTG 43206	CCAA AA
		CACCACTC GAAG TAAG	
		GTGGTGAG CTTT ATTC	
		AACC A_	
GAM2304 YME1L1	3'	TCATTCTTGATGTGGTGTA 58438	TCC _
		TACACCAC CAAGAA GA	
		ATGTGGTG GTTCTT CT	
		TA_ A	
GAM2304 ZNF262	3'	CTTATTTTGTTTGGGAGT 18723	A
		ACTCCCAAG AGAATAAG	
		TGAGGGTTT TTTTATTC	
		G	
GAM2304 LOC91960	3'	TGTGGCTTGGAACGTGGTGTA 68294	TC_ AAGA
		TACACCAC CCAAG ATA	
		ATGTGGTG GGTC TGT	
		CAA GG_	
GAM2305 MEIS2	3'	CCAATGCATTCATATTTG 39724	CCCAA
		CAAATATGA GCATTGG	
		GTTTATACT CGTAACC	
		TA_	
GAM2305 FLJ22555	3'	CGTTGTTGGTGTCATATTCAAT 44795	CA _ G T
A		TAT AATATGAC CCAA CA TG	
		ATA TTATACTG GGTT GT GC	
		AC T _ T	
GAM2305 KIAA1884	3'	CCAATGTTCCGGGCCACATTTGA 73720	A A A
		TCAAAT TG CCC AGCATTGG	
		AGTTTA AC GGG TTGTAACC	
		C C C	
GAM2305 KIAA1915	3'	CCAATGTTTAACCATATTTG 73665	ACCC
		CAAATATG AAGCATTGG	
		GTTTATAC TTTGTAACC	
		CAA_	
GAM2305 LOC147949	3'	CCAATGCACATTAATATATTTG 79277	ACCCAA_
A		TCAAATATG GCATTGG	

			AGTTTATAT	CGTAACC		
			AATTACA			
GAM2306	CRACC	3'	ACCATAAAAAAGTGCTT	41303	CTG	GAA
			AAGCACTTTT TA GGT			
			TTCGTGAAAA AT CCA			
			AA_ A__			
GAM2306	GNB5	3'	ACCTTCCTCTGGAAGTGCTGA	22698	A	CTGTA
			TCA GCACTTTT GAAGGT			
			AGT CGTGAAGG CTTCCA			
			_ TCTC_			
GAM2306	GNB5	3'	ACCTTCCTCTGGAAGTGCTGA	33001	A	CTGTA
			TCA GCACTTTT GAAGGT			
			AGT CGTGAAGG CTTCCA			
			_ TCTC_			
GAM2306	NEUROD1	3'	ACCAGCAGAAAAGTGCTT	11777		AGAA
			AAGCACTTTTCTGT GGT			
			TTCGTGAAAAGACG CCA			
			A__			
GAM2306	NGFR	3'	GACCTTCTGGGAAATGGCTTGA	11796	ACT	G
			TCAAGC TTTCT TAGAAGGTC			
			AGTTCG AAAGG GTCTTCCAG			
			GT_ _			
GAM2306	DKFZp547I224	5'	ACCAATACAGAGAAGTGCTT	39947		GAA
			AAGCACTTTTCTGTA GGT			
			TTCGTGAAGAGACAT CCA			
			AA_			
GAM2306	FKBP5	3'	ACCTTTTAAAAAAAATGCTT	15929	C	CTG
			AAGCA TTTT TAGAAGGT			
			TTCGT AAAA ATTTTCCA			
			A AAA			
GAM2306	FLJ10803	3'	ACTAAAGACAGAAAAAAGCTTG	37193	AC	AGAA
	A		TCAAGC TTTTCTGT GGT			
			AGTTCG AAAAGACA TCA			
			AA GAAA			
GAM2306	MGC11324	3'	ATAGAAAAAAGTGCTTGA	52148	__	
			TCAAGCACTTT TCTGT			
			AGTTCGTGAAA AGATA			
			AA			
GAM2306	MGC3113	3'	ACCTCCCAAAGTGCTGGA	44056	A	CTGTA A
			TC AGCACTTTT GA GGT			

AG TCGTGAAAA CT CCA
 G CC___ _
 GAM2306 MRPS18C 3' ACCTTTGGATAGAAAAGTGTTT 32679 A_
 GA TCAAGCACTTTTCTGT GAAGGT
 |||||
 AGTTTGTGAAAAGATA TTTCCA
 GG
 GAM2306 PDZD2 3' ACCTGTCTTGATAAGTGCTTGA 81714 T TGT _
 TCAAGCACTT TC AGA AGGT
 ||||| || |||
 AGTTCGTGAA AG TCT TCCA
 T T___ G
 GAM2306 PTPN21 3' ACCTGGGAAAGGTGCT 23862 GTAGA
 AGCACTTTTCT AGGT
 ||||| |||
 TCGTGGAAAGG TCCA
 G___
 GAM2306 LOC133418 3' ACCTTAAATAGGAAAAGTACT 75593 C GTAG_
 AG ACTTTTCT AAGGT
 || ||||| |||
 TC TGAAAAGG TTCCA
 A ATAAA
 GAM2306 LOC134265 3' ACCTTTTACAAACACTTGA 75651 CACTTTTC
 TCAAG TGTAGAAGGT
 |||| |
 AGTTC ACATTTTCCA
 ACAA___
 GAM2306 LOC144766 3' ACCTTCCGAAAAGTGCTGGA 77478 A TA
 TC AGCACTTTTCTG GAAGGT
 || ||||| |||||
 AG TCGTGAAAAGGC CTTCCA
 G _
 GAM2306 LOC153603 5' CTTAGACAGAAAATACTTGA 81776 CAC AG
 TCAAG TTTTCTGT AAG
 |||| |
 AGTTC AAAAGACA TTC
 AT_ GA
 GAM2306 LOC204285 5' ACCTCCTACAGAATTGTG 91011 TT A
 CAC TTCTGTAG AGGT
 || ||||| |||
 GTG AAGACATC TCCA
 TT C
 GAM2306 LOC256597 5' ACCCCCTACAAGGCCTGA 98024 A A TTTC AA
 TCA GC CT TGTAG GGT
 ||| || ||| |||
 AGT CG GA ACATC CCA
 C _ _ CC
 GAM2306 LOC89932 5' GACCCTCTAGCCCCAAAAGTGC 61460 A CT_ _ A
 CTG CA GCACTTTT GT AGA GGTC
 || ||||| || ||| |||

			GT CGTGAAAA CG TCT CCAG		
			C CCC A C		
GAM2307 CSRP1	3'	CCCCACAGAGCTCTGTTCTT	15813	T _	
		GAG GCA AGCTCTGTGGGG			
		TTC TGT TCGAGACACCCC			
		T C			
GAM2307 FOXF2	5'	CCCGGGGCCCGCCCTCGCGG	9372	A T AA T	
		CC CGAG GC GCTCTG GG			
		GG GCTC CG CGGGGC CC			
		C C CC _			
GAM2307 GALGT	3'	CCCCACAGAGAGAACTTGTGG	9418	GCAAG	
		CCACGAGT CTCTGTGGGG			
		GGTGTTCAGAGACACCCC			
		AGA_			
GAM2307 PFKFB4	3'	CCCCTTCAGGCCTGCTCTC	17082	T A T T_	
		GAG GCA GC CTG GGGG			
		CTC CGT CG GAC CCCC			
		T C _ TT			
GAM2307 PTGS1	3'	CCTTATGGAGCTCACACTC	8241	CA	
		GAGTG AGCTCTGTGGGG			
		CTCAC TCGAGGTATTCC			
		AC			
GAM2307 PTGS1	3'	CCTTATGGAGCTCACACTC	55472	CA	
		GAGTG AGCTCTGTGGGG			
		CTCAC TCGAGGTATTCC			
		AC			
GAM2307 PVRL2	5'	CCCCACAGAGTGGCCCGCGG	12651	A AGT AA	
		CC CG GC GCTCTGTGGGG			
		GG GC CG TGAGACACCCC			
		C C_ G_			
GAM2307 RASD1	5'	CCCCGCGCCCGCCCTCGCGG	32726	A T AA TCT	
		CC CGAG GC GC GTGGGG			
		GG GCTC CG CG CGCCCC			
		C C CC _			
GAM2307 SMN1	5'	CCCCACGCTGCGCACCCGCGG	43460	A A AA TC	
		CC CG GTGC GC TGTGGGG			
		GG GC CACG CG GCACCCC			
		C C _ TC			
GAM2307 SMN1	5'	CCCCACGCTGCGCACCCGCGG	6225	A A AA TC	
		CC CG GTGC GC TGTGGGG			

GG GC CACG CG GCACCCC
C C _ TC
GAM2307 TCF7 3' CCCCACAGAACTGCTTACT 13618 CA_ C
AGTG AG TCTGTGGGG
|||| | |||||
TCAT TC AGACACCCC
TCG A
GAM2307 UBTF 3' CCCCACCCACTTCTGCACTTGC 27254 A AGCTCT_
GGT ACC CGAGTGCA GTGGGG
||| ||||| |||||
TGG GTTCACGT CACCCC
C CTTACC
GAM2307 A 5' CCCCACAGAGCTCAAGGGGGTG 39568 GAGTGCA
G CCAC AGCTCTGTGGGG
|||| | |||||
GGTG TCGAGACACCCC
GGGGAAC
GAM2307 C20orf11 3' CAGAGCCTGCACTCTGG 35865 C A
CCA GAGTGCA GCTCTG
||| ||||| |||||
GGT CTCACGT CGAGAC
_ C
GAM2307 ELOVL1 3' CCCCACAAAGGGTCTCGTGG 43370 TGCAA _
CCACGAG GCTCT GTGGGG
||||| |||| | |||||
GGTGCTC TGGGA CACCCC
_ AA
GAM2307 EPSIN 5' CCCCTGGGCTTACATCATGG 26207 C G C TGT
CCA GA TG AAGCTC GGGG
||| || ||||| |||||
GGT CT AC TTCGGG CCCC
A _ A T_
GAM2307 FLJ12800 3' CCCACTCTGCTCTCGTGG 43527 T AGCTCT
CCACGAG GCA GTGGG
||||| ||| |||||
GGTGCTC CGT CACCC
T CT_
GAM2307 FLJ22637 5' CCCCGTGCTGCTTGCACTCG 47967 TC GT
CGAGTGCAAGC T GGGG
||||||| | |||||
GCTCACGTTTCG G CCCC
TC TG
GAM2307 KIAA0258 3' CCCCACAGAGCCCTTTTCAGTG 29467 _ TGCAA
G CCAC GAG GCTCTGTGGGG
|||| ||| |||||
GGTG CTT CGAGACACCCC
A TCCC_
GAM2307 KIAA0469 3' CCTCACAGCTTACATC 29976 G C CT
GA TG AAGCT GTGGGG
|| || |||| | |||||

		CT AC TTCGA CACTCC		
		_ A _		
GAM2307 KIAA1118	3'	CCCACAGAGGCTGGTGGT 70209	G	GCAAG
		ACCAC AGT CTCTGTGGG		
		TGGTG TCG GAGACACCC		
		G _		
GAM2307 KIAA1679	3'	CCCCACAGAGCTTACCCAGG 70710	ACGA	CA
		CC GTG AGCTCTGTGGGG		
		GG CAT TCGAGACACCCC		
		ACC _		
GAM2307 LRP1B	5'	CCCCACAGAACCAGCTTCG 38273	T	AAGC
		CGAG GC TCTGTGGGG		
		GCTT CG AGACACCCC		
		_ ACCA		
GAM2307 MGC4415	3'	CCCCTTCCCTCCCGCCCCGTGG 49758	A_	CA CTCTGT
	T	ACCACG GTG AG GGGG		
		TGGTGC CGC TC CCCC		
		CC CC CCTT_		
GAM2307 SFRS6	5'	CCCGCACCCGACCCGCGGT 21857	A A	AAGCTC
		ACC CG GTGC TGTGGG		
		TGG GC CACG ACGCCC		
		C _ CCC_		
GAM2307 SLC22A6	5'	CCCACAGAGCAGCTCG 17736	GCAA	
		CGAGT GCTCTGTGGG		
		GCTCG CGAGACACCC		
		A_		
GAM2307 LOC145826	5'	CCTTTTGCACCTGCACTCGTGG 84528	A_	TCTGT
		CCACGAGTGCA GC GGG		
		GGTGCTCACGT CG TCC		
		CCA TTT_		
GAM2307 LOC150951	5'	CCCACAGAGAGGCTGTG 86343	AGT	AAG
		CACG GC CTCTGTGGG		
		GTGT CG GAGACACCC		
		_ GA_		
GAM2307 LOC153328	3'	CCCCGCTCCTGCACCCGTGG 81677	A	AGCTCT
		CCACG GTGCA GTGGGG		
		GGTGC CACGT CGCCCC		
		C CCT_		
GAM2307 LOC164395	3'	CCTGGAGCTTACACCTGTG 83401	A C	GT
		CACG GTG AAGCTCT GGG		

GTGT CAC TTCGAGG TCC
 C A _
 GAM2307 LOC199936 3' CCCACAGGCCTGCAGCCCATGG 91481 CGA_ A T
 T ACCA G TGCA GC CTGTGGG
 ||| | ||| || |||||
 TGGT C ACGT CG GACACCC
 ACC G C _
 GAM2308 BHLHB3 3' TTGAGAAATTGACCATGAA 48493 G CACCA
 TTCATGGT AA TTCAA
 ||||| || ||||
 AAGTACCA TT GAGTT
 G AAA_
 GAM2308 HTR2C 3' TTGTCAAATGGTATTTTTTTGTG 7875 TG T C CA
 AA TTCA G GAA ACCATT ACAA
 ||| | ||| ||||| ||||
 AAGT T TTT TGGTAA TGTT
 GT T A AC
 GAM2308 LILRB4 3' TTGTTGAGGATCAATTCACCAT 23390 CACCA_
 ATGGTGAA TTCAACAA
 ||||| |||||
 TACCACTT GAGTTGTT
 AACTAG
 GAM2308 FJX1 3' GATGATGTTCCACCAGAA 27566 A C
 TTC TGGTGAACA CATT
 || ||||| ||||
 AAG ACCACTTGT GTAG
 _ A
 GAM2308 FLJ14075 3' TTGTGAAATGTACACCATGAA 46585 A CCA A
 TTCATGGTG ACA TTCA CAA
 ||||| || ||||| ||||
 AAGTACCAC TGT AAGT GTT
 A A_ _
 GAM2308 KIAA1024 3' TGCTGAATGGTGCTCTGACA 69620 GT_ A A
 TG GA CACCATTCA CA
 || || ||||| ||
 AC CT GTGGTAAGT GT
 AGT C C
 GAM2308 KIAA1497 3' GTTGAATGATGTTAGTTGA 68128 TGGTG C
 TCA AACA CATTCAAC
 || ||||| |||||
 AGT TTGT GTAAGTTG
 TGA_ A
 GAM2308 MGC2752 5' TGCTGGTGTTCACCATGAA 79084 TT
 TTCATGGTGAACACCA CA
 ||||| ||||| ||
 AAGTACCACTTGTGGT GT
 CG
 GAM2308 MGC2752 5' TGCTGGTGTTCACCATGAA 79085 TT
 TTCATGGTGAACACCA CA
 ||||| ||||| ||

		AAGTACCACTTGTGGT GT	
		CG	
GAM2308	PRO1598	5' GTTGAATTTAGCACCATGAA 38130	AACACC
		TTCATGGTG ATTCAAC	
		AAGTACCAC TAAGTTG	
		GATT__	
GAM2308	LOC133283	3' TGTGAAATGCACCATGAA 75591	AACACCA A
		TTCATGGTG TTC ACA	
		AAGTACCAC AAG TGT	
		GTA____ C	
GAM2308	LOC143916	3' TTGTTGAATGATTGACTCAC 77151	A_ C_
		GTGA CA CATTCAACAA	
		CACT GT GTAAGTTGTT	
		CA TA	
GAM2308	LOC161589	3' TGTCAAAAGGCACCATGAA 83161	AACA A CA
		TTCATGGTG CC TT ACA	
		AAGTACCAC GG AA TGT	
		____ A AC	
GAM2308	LOC254211	3' TGGCAGATGTTACCAGAA 98139	A ____
		TTC TGGTGAACA CCA	
		AAG ACCACTTGT GGT	
		_ AGAC	
GAM2308	LOC91907	3' GTTGAATGATGTTAGTTGA 68102	TGGTG C
		TCA AACA CATTCAAC	
		AGT TTGT GTAAGTTG	
		TGA__ A	
GAM2309	LDLR	3' GGGATTGGCAATTGTCCCCA 6741	A C GT
		TGGG AC ATTGCCAA CT	
		ACCC TG TAACGGTT GG	
		C T AG	
GAM2309	NRIP1	3' TACCAAACCTCAGGTGATTCC 60624	ACC TG A_ C
		GGA AT CC AGT TGGTA	
		CCT TA GG TCA ACCAT	
		____ GT AC A	
GAM2309	PSEN2	3' ACCAGACTTTGGCTCCC 25950	ACCATT _
		GGGA GCCAA GTCTGGT	
		CCCT CGGTT CAGACCA	
		_____ T	
GAM2309	PSEN2	3' ACCAGACTTTGGCTCCC 6542	ACCATT _
		GGGA GCCAA GTCTGGT	

CCCT CGGTT CAGACCA
 _____ T
 GAM2309 FLJ12604 3' ACATGGTAAATGGTTCCCA 65059 ____ A
 TGGGAACCAT TGCCA GT
 ||||| |||||
 ACCCTTGGTA ATGGT CA
 AA A
 GAM2309 FLJ13081 3' ACATGGCAGTGGTTCCCA 46169 A
 TGGGAACCATTGCCA GT
 ||||| |||||
 ACCCTTGGTGACGGT CA
 A
 GAM2309 FLJ23093 3' ACCAGACTCCTCAGGTTCC 45321 AT CCA
 GGAACC TG AGTCTGGT
 ||||| || |||||
 CCTTGG AC TCAGACCA
 ____ TCC
 GAM2309 GP5 3' ACCAGACTCACGGTCTCCA 16857 GA AT CCA
 TGG ACC TG AGTCTGGT
 ||| ||| || |||||
 ACC TGG AC TCAGACCA
 TC C_ ____
 GAM2309 KIAA0286 3' ACCAGACTTACTGGCTCACCA 68855 _ A TTGCC
 TGG GA CCA AAGTCTGGT
 ||| ||| |||||
 ACC CT GGT TTCAGACCA
 A C CA____
 GAM2309 MGC10540 3' ACCAGACTCAAAAGGACTCCA 51356 AA A GCCA
 TGGG CC TT AGTCTGGT
 |||| ||| |||||
 ACCT GG AA TCAGACCA
 CA A AC____
 GAM2309 LOC157226 5' TACCGCAGGCAAAGGTTCCCA 64640 A AAGTC
 TGGGAACC TTGCC TGGTA
 ||||| ||||| |||||
 ACCCTTGG AACGG GCCAT
 A AC____
 GAM2310 ACP2 3' CTCCCCAGCCCATGGACA 9654 C AG
 TG CTATGGGCTGG GGAG
 || ||||| |||||
 AC GGTACCCGACC CCTC
 A ____
 GAM2310 FTL 3' GCCTCTCCCTCCAGCCAATAGG 5573 G
 CA TGCCTAT GGCTGGAGGGAGAGGC
 ||||| ||||| |||||
 ACGGATA CCGACCTCCCTCTCCG
 A
 GAM2310 MAD1L1 3' CTCTCCAGCCCCACAGGGCA 88870 AT____
 TGCCT GGGCTGGAGGG
 ||||| ||||| |||||

ACGGG CCCGACCTCTC
 ACAC
 GAM2310 MECP2 3' GCCCCCTGTACCCATG 18405 C _ AGA
 TATGGG TGG AGGG GGC
 ||||| ||| ||| |||
 GTACCC ACT TCCC CCG
 _ G C_
 GAM2310 OGDH 3' CCCCTCCCTCTGCTCTCATAGG 92746 CT_ A
 CCTATGGG GGAGGGAG GG
 ||||| ||||| ||
 GGATACTC TCTCCCTC CC
 TCG C
 GAM2310 VTN 5' GCCTCTCCCTCCCTTCCTCAGG 7164 AT CT
 CA TGCCT GGG GGAGGGAGAGGC
 |||| ||| |||||
 ACGGA CCT CCTCCCTCTCCG
 CT TC
 GAM2310 ZNF215 3' CCTCTCCCTAGTTCATA 26034 GG
 TATGGGCT AGGGAGAGG
 ||||| |||||
 ATACTTGA TCCCTCTCC
 —
 GAM2310 DKFZP667O116 3' GCCTCTTCTGCCAGCCACAGGC 95941 ATG A
 A TGCCT GGCTGG GGGAGAGGC
 |||| ||||| |||||
 ACGGA CCGACC TCTTCTCCG
 CA_ G
 GAM2310 FLJ21438 5' CCTCCCAAACCCAGCCCACAGC 62191 C A AG_ A
 CA TG CT TGGGCTGG GG GAGG
 || || ||||| || ||||
 AC GA ACCCGACC CC CTCC
 C C CAAA _
 GAM2310 FLJ22477 3' GCCCTTCCCCCAGCCCACAGCC 45675 C A A A
 A TG CT TGGGCTGG GGGAG GGC
 || || ||||| ||||| |||
 AC GA ACCCGACC CCCTT CCG
 C C _ C
 GAM2310 FLJ23058 3' CCTCCCCTTCTCCCACAGCCA 45523 C A CT A
 TG CT TGGG GGAGGG GAGG
 || || ||| ||||| ||||
 AC GA ACCC CTTCCC CTCC
 C C T_ _
 GAM2310 FOXN4 3' CCAGGTCCAGCCCCAGGCA 76088 AT _
 TGCCT GGGCTGGA GG
 |||| ||||| ||
 ACGGA CCCGACCT CC
 C_ GGA
 GAM2310 KIAA0337 3' GCCTCTCCCTAGCCCACACGCA 29477 CTA GG
 TGC TGGGCT AGGGAGAGGC
 || ||||| |||||

ACG ACCCGA TCCCTCTCCG
 CAC ____
 GAM2310 KIAA1320 3' GCCTAAATGCAACCCATAGGCA 69843 C GAGGGAG
 TGCCTATGGG TG AGGC
 ||||| || ||||
 ACGGATACCC AC TCCG
 A GTAAA__
 GAM2310 MGC7036 3' CTCCCTGTGCCACACAGACA 59616 C A _ T G
 TG CT TG GGC G AGGGAG
 || || || || || || || ||
 AC GA AC CCG T TCCCTC
 A C A _ G
 GAM2310 N4BP3 3' GCCCCTCCCTCCAGCTGGCGGG 66856 ATG_ A
 GC GCCT GGCTGGAGGGAG GGC
 ||| ||||| ||||| |||
 CGGG TCGACCTCCCTC CCG
 GCGG C
 GAM2310 PPI5PIV 3' GCCTCTCCCTCCACACCCGAAG 39584 CTA C_
 CA TGC TGGG TGGAGGGAGAGGC
 ||| ||| ||||| ||||| |||||
 ACG GCCC ACCTCCCTCTCCG
 AA_ AC
 GAM2310 PRO0097 3' TTCCACCCAGCCCACAGGCA 26935 A AG
 TGCCT TGGGCTGG GGAG
 ||||| ||||| |||||
 ACGGA ACCCGACC CCTT
 C CA
 GAM2310 RPIA 3' CCTTGAGTCTCCAGCCCACAGC 58590 C A GA_
 CA TG CT TGGGCTGGAGG GAGG
 || || ||||| ||||| |||||
 AC GA ACCCGACCTCT TTCC
 C C GAG
 GAM2310 LOC145255 3' CCTCTCCCTCCCCACCAGCA 84268 CTA GCT
 TGC TGG GGAGGGAGAGG
 ||| ||| ||||| |||||
 ACG ACC CCTCCCTCTCC
 ____ ACC
 GAM2310 LOC147299 5' GCCTCTCTGCACCTCATAGACA 78980 C C GAG
 TG CTATGGG TG GGAGAGGC
 || ||||| || ||||| |||||
 AC GATACTC AC TCTCTCCG
 A C G__
 GAM2310 LOC220776 3' CCATCCCTCCAGCCCACAGCA 68921 CTA GA
 TGC TGGGCTGGAGGGA GG
 ||| ||||| ||||| || |||||
 ACG ACCCGACCTCCCT CC
 AC_ A_
 GAM2310 LOC253805 3' GCCTCTCCCCCAGGATCAGGG 98178 A G_ A
 CCT TGG CTGG GGGAGAGGC
 ||| ||| ||||| ||||| |||||

GGG ACT GACC CCCTCTCCG
_ AG C
GAM2310 LOC253842 3' CCTCTCCCCGCTCATAG 99235 TGGA
CTATGGGC GGGAGAGG
||||| |||||
GATACTCG CCCTCTCC
C__
GAM2310 LOC254423 3' CCCCCCCTCCAGCAGGGACA 99301 _ ATGG AGA
TG CCT GCTGGAGGG GG
|| ||| ||||| ||
AC GGG CGACCTCCC CC
A A__ CCC
GAM2310 LOC90246 5' GCCTCTCCCTCCAGCACA 62586 G
TG GCTGGAGGGAGAGGC
|| |||||
AC CGACCTCCCTCTCCG
A
GAM2311 CD5 3' GCTGGGCGAGTGCATTTTGA 27222 AGA
TCGAAG TACTCGCCCAGC
||||| |||||
AGTTTT GTGAGCGGGTCG
AC_
GAM2311 CSNK1G2 3' GCCAGGCGGGTGCTTCTCGA 8988 AG A CA
TCGA AG TACTCGCC GC
||| || ||||| ||
AGCT TC GTGGGCGG CG
CT _ AC
GAM2311 EFEMP1 5' CTGGAAGATTGCTCTCCGA 38773 A A C GC
TCG AGAG TA TC CCAG
||| ||| || |||
AGC TCTC GT AG GGTC
C _ T AA
GAM2311 ICA1 3' CTGGGAAAATTCTTTCGA 18311 ACTCG
TCGAAGAGAT CCCAG
||||| |||
AGCTTCTTTA GGGTC
AAA_
GAM2311 NTSR1 5' GCTGGGCGCTGTCTCCG 11859 A A CT
TCGA G GATA CGCCCAGC
||| ||| |||||
GGCT C CTGT GCGGGTCG
__ C_
GAM2311 SEZ6L 5' GCTGGGCGAGCTGGTGCTGGA 41206 GA AGA _
TC AG TA CTCGCCCAGC
|| || |||||
AG TC GT GAGCGGGTCG
G_ GTG C
GAM2311 SOD3 5' CTGGGCGAGTAATGATCTC 13300 ____
GAGA TACTCGCCCAG
||| |||||

CTCT ATGAGCGGGTC
 AGTA
 GAM2311 TEM6 3' GCTGGGCGAGCTGGGCGA 43037 AAG ATA
 TCG AG CTCGCCCAGC
 ||| || |||||
 AGC TC GAGCGGGTCG
 GGG ____
 GAM2311 TEM6 3' GCTGGGCGAGCTGGGCGA 43038 AAG ATA
 TCG AG CTCGCCCAGC
 ||| || |||||
 AGC TC GAGCGGGTCG
 GGG ____
 GAM2311 DKFZP564O1664 3' GCTTTTGGTATCTCTTGA 48667 G CGCC
 TC AAGAGATACT AGC
 || ||||| |||
 AG TTCTCTATGG TCG
 _ TTT__
 GAM2311 FLJ13725 5' GCTGGGCGAGTTTCATCTCCG 68832 A _ T
 CG AGA GA ACTCGCCCAGC
 || ||| || |||||
 GC TCT CT TGAGCGGGTCG
 C A T
 GAM2311 FLJ14457 5' GCTGGGTGTGTCCCTCCGA 52409 A A TC
 TCG AG GATAC GCCCAGC
 ||| || |||| |||||
 AGC TC CTGTG TGGGTCG
 C C ____
 GAM2311 FLJ20730 3' GCTAGGTTGTCTCTTGA 36051 G CTC C
 TC AAGAGATA GCC AGC
 || ||||| ||| |||
 AG TTCTCTGT TGG TCG
 _ ____ A
 GAM2311 FLJ32940 5' GCTGGGCGGGGCACTCTTC 58878 ATA
 GAAGAG CTCGCCCAGC
 ||||| |||||
 CTTCTC GGGCGGGTCG
 ACG
 GAM2311 GRM5 3' GCTGACAAGGCGTCTCTTC 63243 TACT ____
 GAAGAGA CGCC CAGC
 ||||| ||| |||
 CTTCTCT GCGG GTCG
 ____ AACA
 GAM2311 HSMPP8 3' CTGGGCGGAGTTCTCTTC 95132 T _
 GAAGAGA ACTC GCCAG
 ||||| ||| |||||
 CTTCTCT TGAG CGGGTC
 _ G
 GAM2311 KIAA0847 3' GCCAGGCTGCATCTCTTTGA 78075 ACTC CA
 TCGAAGAGAT GCC GC
 ||||| ||| ||

		AGTTTCTCTA CGG CG	
		CGT_ AC	
GAM2311 KIAA0960	3'	GCTGGACAAGTACTAGTGTCTT 94225	C__ ____
		GAGATACT GC CCAGC	
		TTCTGTGA TG GGTCG	
		TCA AACA	
GAM2311 KIAA1854	3'	GCTGCCCCGAGATCTCTTCGA 72211	A CC
		TCGAAGAGAT CTCG CAGC	
		AGCTTCTCTA GAGC GTCG	
		_ CC	
GAM2311 KLHL6	3'	GCCAGTCTGTAGCTCTTCGA 56173	A TC CCA
		TCGAAGAG TAC GC GC	
		AGCTTCTC ATG TG CG	
		G TC AC_	
GAM2311 MCAM	3'	GCTGGGCGCTGTTTTTCGA 22462	GATACT
		TCGAAGA CGCCCAGC	
		AGCTTTT GCGGGTCG	
		GTC____	
GAM2311 SBB103	5'	CTGGGAGAATCTCTTC 20522	AC G
		GAAGAGAT TC CCCAG	
		CTTCTCTA AG GGGTC	
		_ A	
GAM2311 SLC26A9	3'	CTGGGAACCTTATCTCTTGA 54712	G CTCG_
		TC AAGAGATA CCCAG	
		AG TTCTCTAT GGGTC	
		_ TCCAA	
GAM2311 SLC26A9	3'	CTGGGAACCTTATCTCTTGA 54713	G CTCG_
		TC AAGAGATA CCCAG	
		AG TTCTCTAT GGGTC	
		_ TCCAA	
GAM2311 STRAIT11499	5'	GCCGGGCGAGTGTTACTCG 41429	A A A
		CGA G GATACTCGCCC GC	
		GCT C TTGTGAGCGGG CG	
		_ A C	
GAM2311 USP15	3'	CTGCGGCAGCATTCTTCGA 21961	ATA C _
		TCGAAGAG CT GCC CAG	
		AGCTTCTT GA CGG GTC	
		AC_ _ C	
GAM2311 LOC129566	5'	GCTGGGGCGCCCTCTTCGA 76225	ATACT _
		TCGAAGAG CGCCC AGC	

	AGCTTCTC GCGGG TCG	
	CC__ G	
GAM2311 LOC150837 3'	CTCTGTCAGCCTCTCTTCGA 80803	TA C CC
	TCGAAGAGA CT GC AG	
	AGCTTCTCT GA TG TC	
	CC C TC	
GAM2311 LOC152445 3'	GCTGGGGCTTCCTCTTTGA 86952	ATACTC
	TCGAAGAG GCCCAGC	
	AGTTTCTC CGGGTCG	
	CTT__	
GAM2311 LOC200940 3'	GCTGGGATTCTCTTTGA 90393	TACTCG
	TCGAAGAGA CCCAGC	
	AGTTTCTCT GGGTCG	
	TTA__	
GAM2311 LOC201456 3'	CTGGACCGAGTCTCTTC 89615	TA C_
	GAAGAGA CTCG CCAG	
	CTTCTCT GAGC GGTC	
	_ CA	
GAM2311 LOC201516 5'	GCTGGAACAGTTCTTCGA 89631	GAT CGC
	TCGAAGA ACT CCAGC	
	AGCTTCT TGA GGTCG	
	_ CAA	
GAM2311 LOC202134 3'	GCTGTGGCACCTCTTTGA 91923	ATACTC _
	TCGAAGAG GCC CAGC	
	AGTTTCTC CGG GTCG	
	CA__ T	
GAM2311 LOC221271 3'	GCTGGGGTGGAAGTATCTC 93521	_ _
	GAGATACT CGCCC AGC	
	CTCTATGA GTGGG TCG	
	AG G	
GAM2311 LOC222133 5'	GCTGAGAGCCCTTTTCGA 95761	ATA GCC
	TCGAAGAG CTC CAGC	
	AGCTTTTC GAG GTCG	
	CC_ A__	
GAM2311 LOC254122 3'	GCCGGGTCTCCTCTTTTCGA 96395	TACTC A
	TCGAAGAGA GCCC GC	
	AGCTTTTCT TGGG CG	
	CCTC_ C	
GAM2311 LOC96652 5'	GCCAAGCAGCTCTCTTCGG 66080	TA C CCA
	TCGAAGAGA CT GC GC	

GGCTTCTCT GA CG CG
C_ _ AAC
GAM2312 B3GALT3 3' AAGAGAAGAGTGAAGATCCA 53717 T GGC C
TG GAT CAC CTTCTCTT
|| ||| ||| |||||
AC CTA GTG GAAGAGAA
_ GAA A
GAM2312 DCT 3' AAGAGAAGAGGCTGGCCA 10395 _ _
TGGCCA CC CTTCTCTT
||||| || |||||
ACCGGT GG GAAGAGAA
C A
GAM2312 DPYSL3 3' AAGAGAAGAGCAGGCCTCA 9119 T ACC_
TGA GGCC CTTCTCTT
||| ||| |||||
ACT CCGG GAAGAGAA
_ ACGA
GAM2312 DTNA 3' AAGAGAGGAACCACCACA 9137 A CCACC
TGTG TGG CTTCTCTT
|||| ||| |||||
ACAC ACC GGAGAGAA
C AA_
GAM2312 DTNA 3' AAGAGAGGAACCACCACA 9138 A CCACC
TGTG TGG CTTCTCTT
|||| ||| |||||
ACAC ACC GGAGAGAA
C AA_
GAM2312 EGFL5 5' AAGAGAAAAGCCATCATA 87899 CACCC
TGTGATGGC TTCTCTT
||||||| |||||
ATACTACCG AAGAGAA
AA_
GAM2312 GALNT7 3' AAGAGAATTTTGGCCATCA 55085 CCC
TGATGGCCA TTCTCTT
||||||| |||||
ACTACCGGT AAGAGAA
TTT
GAM2312 GOLGA4 5' AAGAGAAAAGGGAAGTTCACA 60693 TG CA _
TGTGA GC CCCTT CTCTT
|||| ||| |||||
ACACT TG GGGAA GAGAA
_ AA A
GAM2312 MAML1 3' AAGAAAAGGGTGCTCAGAC 29271 GA GC C
GT TG CACCCTT TCTT
|| || ||||| |||
CA AC GTGGGAA AGAA
G_ TC A
GAM2312 MEST 3' AAGAGGTCCTGGCCATCA 70456 CCCT
TGATGGCCA TCTCTT
||||||| |||||

			ACTACCGGT GGAGAA		
			CCT_		
GAM2312	PAG	3'	AAGAGAAGAAGTGACACA 38012	ATGGC	C_
			TGTG CAC CTTCTCTT		
			ACAC GTG GAAGAGAA		
			A____ AA		
GAM2312	PCDH9	5'	AGGAGACAGCCATTCACA 83690	_	CACCCT
			TGTGA TGGC TCTCTT		
			ACACT ACCG AGAGGA		
			T AC____		
GAM2312	RRAS	3'	GAGAGAAGCAACCACCACA 21844	A	CCACC
			TGTG TGG CTTCTCTT		
			ACAC ACC GAAGAGAG		
			C AAC__		
GAM2312	SRGAP2	3'	AGGAGCTGGCCATCCA 75105	T	CC
			TG GATGGCCA CTTCT		
			AC CTACCGGT GAGGA		
			_ C_		
GAM2312	SYNGR2	3'	AAGACTCGTGGGGGCCATCACA 17489	A	TTC__
			TGTGATGGCC CCC TCTT		
			ACACTACCGG GGG AGAA		
			_ TGCTC		
GAM2312	UBQLN3	5'	AAGAGAAGGACGGGACCACA 34370	A	_ AC_
			TG TGG CC CCTTCTCTT		
			AC ACC GG GGAAGAGAA		
			_ A GCA		
GAM2312	C5orf4	3'	AAGAGAAGGGTAGGAGAT 33422	GG	_
			AT CC ACCCTTCTCTT		
			TA GG TGGGAAGAGAA		
			GA A		
GAM2312	C5orf4	3'	AAGAGAAGGGTAGGAGAT 51485	GG	_
			AT CC ACCCTTCTCTT		
			TA GG TGGGAAGAGAA		
			GA A		
GAM2312	CDH9	5'	AAGAGAAGGACCGAGACA 33255	GA	CCAC
			TGT TGG CCTTCTCTT		
			ACA GCC GGAAGAGAA		
			GA A__		
GAM2312	CHRA1	3'	AAGAGAAAACCTATCATA 34326		CCACCC
			TGTGATGG TTCTCTT		

			ATACTATC	AAGAGAA		
			CAA__			
GAM2312	FLJ10826	5'	AAGAGAAGAGAGCCTCACA	37238	T	CACC
			TGTGA GGC CTTCTCTT			
			ACACT CCG GAAGAGAA			
			_ AGA_			
GAM2312	FLJ14624	3'	AAGAGCAGGCAGCCTCACA	71841	T	CAC T
			TGTGA GGC CCT CTCTT			
			ACACT CCG GGA GAGAA			
			_ AC_ C			
GAM2312	FLJ20420	3'	AAGAGAAGGGCAGCCCTC	35611	T	CA
			GA GGC CCCTTCTCTT			
			CT CCG GGG AAGAGAA			
			C AC			
GAM2312	FLJ20972	3'	AAGAGAAGAACTCCATCTCA	47374	T	CCACC
			TG GATGG CTTCTCTT			
			AC CTACC GAAGAGAA			
			T TCAA			
GAM2312	FSCN3	3'	AAGAGAAGAACATCTGTTACA	40156		CCACC
			TGTGATGG CTTCTCTT			
			ACATTGTC GAAGAGAA			
			TACAA			
GAM2312	GBL	3'	GAGAGAGTATGGCGGCCACCA	42571	A	A C__
			TG TGGCC CC TTCTCTT			
			AC ACCGG GG GAGAGAG			
			C C TAT			
GAM2312	HARC	3'	AAGAGAAGAGTGGTACCATA	35915	ATG	C
			TGTG GCCAC CTTCTCTT			
			ATAC TGGTG GAAGAGAA			
			CA_ A			
GAM2312	HIP-55	3'	AGGGGTGGTGGCCACCAC	26773	A	_
			GTG TGGCCACC CTTCT			
			CAC ACCGGTGG GGGGA			
			C T			
GAM2312	KIAA0227	3'	AAGAGAAGGGTAGAGGTCA	61342		__
			TGGCC ACCCTTCTCTT			
			ACTGG TGGGAAGAGAA			
			AGA			
GAM2312	KIAA0390	3'	AAGAGAAGAATGTATACACA	28870	A	GC CC
			TGTG TG CA CTTCTCTT			

ACAC AT GT GAAGAGAA
 _ AT AA
 GAM2312 KIAA0953 3' AAGAAAGGCATGCTGGTCATCA 67317 C____ C
 TGATGGCCA CCTT TCTT
 ||||| ||| |||
 ACTACTGGT GGAA AGAA
 CGTAC _
 GAM2312 KIAA1024 3' AAGAGCAGTGGCATCACA 69612 G CCTT
 TGTGATG CCAC CTCTT
 ||||| ||| ||||
 ACACTAC GGTG GAGAA
 _ AC_
 GAM2312 KIAA1853 5' AAGAGAAGGAGGTCCTCA 69916 T AC
 TGA GGCC CCTTCTCTT
 ||| ||| |||||
 ACT CTGG GGAAGAGAA
 C A_
 GAM2312 KIAA1855 3' AAGGGAAGTAGCCATCACA 93944 CACC
 TGTGATGGC CTTCTCTT
 ||||| |||||
 ACACTACCG GAAGGGAA
 AT_
 GAM2312 LANCL2 3' AAGAGAAGCAGACACCGTCACA 38616 CCACC_
 TGTGATGG CTTCTCTT
 ||||| |||||
 ACACTGCC GAAGAGAA
 ACAGAC
 GAM2312 MAWBP 3' AAGAGAAGGAGGAATACA 42370 ATGG AC
 TGTG CC CCTTCTCTT
 ||| || |||||
 ACAT GG GGAAGAGAA
 AA_ A_
 GAM2312 NYD-SP11 3' AAGAATCTGAAGTGGCCATCA 50052 CC ____
 TGATGGCCAC TTC TCTT
 ||||| ||| |||
 ACTACCGGTG AAG AGAA
 _ TCTA
 GAM2312 PPP1R1A 3' AAGAGAAGAACTGTCTCA 23091 T CCACC
 TG GATGG CTTCTCTT
 || ||| |||||
 AC CTGTC GAAGAGAA
 T AAA_
 GAM2312 PRO2012 5' AAGCAGAAATAGCCATTACA 38385 CACCC _
 TGTGATGGC TTCT CTT
 ||||| ||| |||
 ACATTACCG AAGA GAA
 ATA_ C
 GAM2312 PRO2533 3' AAGAAAAGGGTGATCAGC 38421 GA GC C
 GT TG CACCCTT TCTT
 || || ||||| |||

CG AC GTGGGAA AGAA
 _ TA A
 GAM2312 TSPAN-2 3' AAGAGAAGGGTTCTGTTCCA 20372 TG CC
 TG ATGG ACCCTTCTCTT
 || ||| |||||
 AC TGTC TGGGAAGAGAA
 CT T_

GAM2312 LOC123591 3' AGGGGAGACAGCCATCTCA 76128 T CACC
 TG GATGGC CTTCTCT
 || ||||| |||||
 AC CTACCG GAGGGGA
 T ACA_

GAM2312 LOC143465 5' AAGAGAAGGAGATGCTCACA 83862 TG CAC_
 TGTGA GC CCTTCTCTT
 ||||| || |||||
 ACACT CG GGAAGAGAA
 _ TAGA

GAM2312 LOC150319 3' AGTAGGGGTGGCCATCAC 80463 _
 GTGATGGCCACCCTT CT
 ||||| ||||| ||
 CACTACCGGTGGGGA GA
 T

GAM2312 LOC158293 3' AAGAGAAGAGTTGTTCTCA 82742 TG C C
 TGA GC AC CTTCTCTT
 ||| ||| |||||
 ACT TG TG GAAGAGAA
 CT T A

GAM2312 LOC196478 5' AAGAGAATCATCCCATCGCA 89066 CCACCC
 TGTGATGG TTCTCTT
 ||||| |||||
 ACGCTACC AAGAGAA
 CTA CT_

GAM2312 LOC200382 5' AAGCCGGGTGGTGGCCACGACA 90235 GA _ CT
 TGT TGGCCACC CTT CTT
 ||| ||||| ||| |||
 ACA ACCGGTGG GGG GAA
 GC T CC

GAM2312 LOC220143 5' AAGAGAAGGCACCCACCACA 95232 A CCAC
 TGTG TGG CCTTCTCTT
 ||||| ||| |||||
 ACAC ACC GGAAGAGAA
 C CAC_

GAM2312 LOC222161 5' AAGAGAAGAGTGCTTTCA 94373 T C C
 TGA GGC AC CTTCTCTT
 ||| ||| || |||||
 ACT TCG TG GAAGAGAA
 T _ A

GAM2312 LOC51027 3' AAGAGAAGAATCACTCAC 60080 _ CCACC
 GTGA TGG CTTCTCTT
 ||||| ||| |||||

CACT ACT GAAGAGAA
 C AA____
 GAM2312 LOC83693 5' AAGAGAAGGACGGAGCCACA 49603 ATGG AC
 TGTG CC CCTTCTCTT
 |||| || |||||
 ACAC GG GGAAGAGAA
 CGA_ CA
 GAM2312 LOC91650 5' AAGAGAAGGAACCTCACA 67392 T CCAC
 TGTGA GG CCTTCTCTT
 |||| || |||||
 ACACT CC GGAAGAGAA
 C AA____
 GAM2313 ADAM19 3' GGACGGTTTTTGC AAAGCACCT 53843 ____ TCT_ A
 GGAGA TCTCCAGGTGCT CA CC TCC
 ||||| || || |||
 AGAGGTCCACGA GT GG AGG
 AAC TTTT C
 GAM2313 ARF4L 3' GGATGGAAGTGACTTGGAGA 70389 TGC TC
 TCTCCAGG TCA TCCATCC
 ||||| || |||||
 AGAGGTTC AGT AGGTAGG
 ____ GA
 GAM2313 CASP10 3' ATGGAGATGGTCCTGCAGA 53199 C T T
 TCT CAGG GC CATCTCCAT
 || ||| || |||||
 AGA GTCC TG GTAGAGGTA
 C _ _
 GAM2313 CD1D 5' GAGATGAGTTGGAGA 80269 GGT
 TCTCCA GCTCATCTC
 |||| |||||
 AGAGGT TGAGTAGAG

 GAM2313 CNTFR 3' GGACATGCAGAGCACCTGCAGA 10238 C ____ C
 TCT CAGGTGCTC AT TCC
 || ||||| || |||
 AGA GTCCACGAG TA AGG
 C ACG C
 GAM2313 EGLN2 5' GGATGGAGTGAAGACCTGGAGA 54917 GC T
 TCTCCAGGT TCA CTCCATCC
 ||||| || |||||
 AGAGGTCCA AGT GAGGTAGG
 GA _
 GAM2313 EPO 3' GACAGGATGACCTGGAGA 7684 TGC CCA
 TCTCCAGG TCATCT TC
 ||||| |||| ||
 AGAGGTCC AGTAGG AG
 ____ AC_
 GAM2313 FBXL11 3' GGACAGAGGAACCTGGGGA 25518 G_ ATC
 TCTCCAGGT CTC TCC
 ||||| || |||

			AGGGGTCCA GAG AGG		
			AG AC_		
GAM2313	GAS11	3'	GATGGAGAGGCCAGGAGA 9429	A	GCT A
			TCTCC GGT C TCTCCATC		
			AGAGG CCG G AGAGGTAG		
			A ____		
GAM2313	GNA11	3'	GGATGGAGACACGGGGCAGGA 10813	AGG	A ____
			TCC TGCTC TCTCCATCC		
			AGG ACGGG AGAGGTAGG		
			____ GCAC		
GAM2313	GNA14	3'	GGACAGAGATGGGTGATGGA 16284	GG	CA
			TCCA TGCTCATCTC TCC		
			AGGT GTGGGTAGAG AGG		
			A_ AC		
GAM2313	KCNK10	3'	GGACCTGAGAGCACCTGGA 41268	A	____
			TCCAGGTGCTC TC TCC		
			AGGTCCACGAG AG AGG		
			_ TCC		
GAM2313	KCNK10	3'	GGACCTGAGAGCACCTGGA 57161	A	____
			TCCAGGTGCTC TC TCC		
			AGGTCCACGAG AG AGG		
			_ TCC		
GAM2313	KCNK10	3'	GGACCTGAGAGCACCTGGA 57162	A	____
			TCCAGGTGCTC TC TCC		
			AGGTCCACGAG AG AGG		
			_ TCC		
GAM2313	KCNS2	3'	GGACAGAGTAGAACTGGAGA 68849	G____	ATC
			TCTCCAG TGCTC TCC		
			AGAGGTC ATGAG AGG		
			AAAG AC_		
GAM2313	KRT16	5'	GATGGAGATGGAAGGCCTG 96890	GC_	
			CAGGT TCATCTCCATC		
			GTCCG GGTAGAGGTAG		
			GAA		
GAM2313	LRRC2	3'	GGATGGAGTTCACATGAAGA 44753	C G	CTCAT
			TCT CA GTG CTCCATCC		
			AGA GT CAC GAGGTAGG		
			A A TT____		
GAM2313	LZTR1	3'	GGATATGTCAGCACCTGGA 23174	____	C
			TCCAGGTGCT CAT TCC		

AGGTCCACGA GTA AGG
 CT T
 GAM2313 MID2 5' GATGGCTGGCACCTGGGA 54482 T T TCT
 TC CCAGGTGC CA CCATC
 || ||||| || ||||
 AG GGTCCACG GT GGTAG
 _ _ C_
 GAM2313 NHLH1 5' GGATGAGCCTTGAGCACCCAGA 20020 CA T_ C
 GG TCTC GGTGCTCA CTC ATCC
 ||| ||||| || ||||
 GGAG CCACGAGT GAG TAGG
 AC TCC _
 GAM2313 POLH 3' ATGGAGATAATACCTTACAGA 22472 CC_ CTC
 TCT AGGTG ATCTCCAT
 || |||| |||||
 AGA TCCAT TAGAGGTA
 CAT AA_
 GAM2313 PTGFRN 5' GGAGCTTGCAAGCACCTGGG 67769 _ T_
 TCCAGGTGCT CA CTCC
 ||||| || ||||
 GGGTCCACGA GT GAGG
 AC TC
 GAM2313 RAD51C 3' GAAGGTTCTTGAGCACCCGGA 12750 A TCT_ A
 TCC GGTGCTCA CC TC
 || ||||| || ||
 AGG CCACGAGT GG AG
 C TCCTT A
 GAM2313 RNF6 5' GAAGGCCCAAGACCTGGAGA 21086 G CATCT A
 TCTCCAGGT CT CC TC
 ||||| || || ||
 AGAGGTCCA GA GG AG
 _ ACCC_ A
 GAM2313 RPA1 3' GGTCATGAGCACCTGGGGA 12898 CT
 TCTCCAGGTGCTCAT CC
 ||||| || ||
 AGGGGTCCACGAGTA GG
 CT
 GAM2313 SLC6A12 3' GGATGAGGAACCTGGAGA 13195 G_
 TCTCCAGGT CTCATCT
 ||||| |||||
 AGAGGTCCA GAGTAGG
 AG
 GAM2313 SYNGR1 3' GGATGGAGATGAGAGAGGGTGA 17506 T AGGTG
 TC CC CTCATCTCCATCC
 || || ||||| |||||
 AG GG GAGTAGAGGTAGG
 T GAGA_
 GAM2313 TNNT1 3' GGACAGTGGCACCTGGGA 13821 T T C_
 TC CCAGGTGC CAT TCC
 || ||||| || || ||

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AG GGTCCACG GTG AGG
  _ _ AC
GAM2313 TULP1 3' GGACGGAGATGAAGAACATCTG 13904 C__ A
      GAG      CTCCAGGTG TCATCTCC TCC
      ||||| ||||| |||
      GAGGTCTAC AGTAGAGG AGG
      AAGA C
GAM2313 ZNFN2A1 5' GATGGAGATGAGGATGGA 61393 GGTG
      TCCA CTCATCTCCATC
      ||| |||||
      AGGT GAGTAGAGGTAG
      AG__
GAM2313 AP1GBP1 3' GACATAAGCATCTGAAGA 24349 C C C
      TCT CAGGTGCT AT TC
      || ||||| |||
      AGA GTCTACGA TA AG
      A A C
GAM2313 DKFZp434A171 3' ATGGAAATGTTTACACCTGAAG 71341 C CT__ C
      CT CAGGTG CAT TCCAT
      || ||||| |||
      GA GTCCAC GTA AGGTA
      A ATTT A
GAM2313 DKFZP434K2235 3' GGATGGAGATGCATTT 84497 TC
      AGGTGC ATCTCCATCC
      ||||| |||||
      TTTACG TAGAGGTAGG
      _
GAM2313 EDG1 3' GATGAAGATGGTTTGGAGG 60050 GT T C
      TCTCCAG GC CATCT CATC
      ||||| || |||||
      GGAGGTT TG GTAGA GTAG
      _ _ A
GAM2313 FLJ10898 3' ATGGCTAAGGGAACATCTGGA 60125 C A __
      TCCAGGTG TC TCT CCAT
      ||||| || ||| |||
      AGGTCTAC AG GGA GGTA
      A _ ATC
GAM2313 FLJ11110 3' GATGGAGATGATTGTAGA 37627 C GTGC
      TCT CAG TCATCTCCATC
      ||| ||| |||||
      AGA GTT AGTAGAGGTAG
      T ____
GAM2313 FLJ14442 3' GGACAGAGAGCTGCCTGGA 52386 _ A __
      TCCAGGT GCTC TC TCC
      ||||| ||| |||
      AGGTCCG CGAG AG AGG
      T _ AC
GAM2313 FLJ20551 3' AGATGAAGTCCTACCTGGA 35825 __ _
      TCCAGGT GCT CATCT
      ||||| ||| |||||

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AGGTCCA TGA GTAGA
 TCC A
 GAM2313 FLJ21820 3' GATGAAGATGAGCCCAGG 41918 A T C
 CC GG GCTCATCT CATC
 || || ||||| ||||
 GG CC CGAGTAGA GTAG
 A _ A
 GAM2313 FLJ23356 5' GGATGGAGACCTGAGCTGGAGA 50925 GGT _
 TCTCCA GCTCA TCTCCATCC
 ||||| |||| |||||
 AGAGGT CGAGT AGAGGTAGG
 _ CC
 GAM2313 KIAA0182 3' GATGGAGATGGTCAGCAC 72500 _
 GTGCT CATCTCCATC
 |||| |||||
 CACGA GTAGAGGTAG
 CTG
 GAM2313 KIAA0586 5' ATGGAAGAGCACCAGAGA 29237 CA ATC
 TCTC GGTGCTC TCCAT
 ||| ||||| ||||
 AGAG CCACGAG AGGTA
 A_ A_
 GAM2313 KIAA1024 3' ATGGAGATGAAATCATGGAGG 69615 _ GC
 TCTCCA GGT TCATCTCCAT
 ||||| ||| |||||
 GGAGGT CTA AGTAGAGGTA
 A A_
 GAM2313 KIAA1095 3' GGATGGAGACGGTTTGTGGA 68088 GGT CA
 TCCA GCT TCTCCATCC
 |||| ||| |||||
 AGGT TGG AGAGGTAGG
 GTT C_
 GAM2313 KIAA1155 3' GGACAGTGAGCACCTGGAGA 62914 C_
 TCTCCAGGTGCTCAT TCC
 ||||| ||||| |||
 AGAGGTCCACGAGTG AGG
 AC
 GAM2313 KIAA1183 3' GATGAAATGACCTGGGGA 63196 TGC CTC
 TCTCCAGG TCAT CATC
 ||||| ||| |||
 AGGGGTCC AGTA GTAG
 _ AA_
 GAM2313 KIAA1238 3' ATGGAGATGCTGCAGAG 71631 CAGG T_
 CTC TGC CATCTCCAT
 ||| ||| |||||
 GAG ACG GTAGAGGTA
 _ TC
 GAM2313 KIAA1376 3' GGACAGAGAAGTATCTTGGAGA 64387 _ CA CA
 TCTCCA GGTGCT TCTC TCC
 ||||| ||||| ||| |||

			AGAGGT CTATGA AGAG AGG		
			T _ AC		
GAM2313	KIAA1655	3'	GAAGGGCGAGCACCTGCAGA 67186	C	ATC A
			TCT CAGGTGCTC TCC TC		
			AGA GTCCACGAG GGG AG		
			C C_ A		
GAM2313	KIAA1808	3'	GGATGGAGATAGGATGGAGA 87050	GGTG	C
			TCTCCA CT ATCTCCATCC		
			AGAGGT GA TAGAGGTAGG		
			AG_ _		
GAM2313	KIAA1808	3'	GGATGGAGATAGGATGGAGA 87051	GGTG	C
			TCTCCA CT ATCTCCATCC		
			AGAGGT GA TAGAGGTAGG		
			AG_ _		
GAM2313	MPZL1	3'	GGATGGAGATGCTATGATGGA 15537	GGTGCT	
			TCCA CATCTCCATCC		
			AGGT GTAGAGGTAGG		
			AGTATC		
GAM2313	MRPL35	3'	GATGGAAATGGTGCCTGCAGA 34020	C	TG T C
			TCT CAGG C CAT TCCATC		
			AGA GTCC G GTA AGGTAG		
			C GT_ A		
GAM2313	SDR1	3'	GGATGAAGACATGCTTGAGGA 17647	TC	CTCA C
			TC CAGGTG TCT CATCC		
			AG GTTCGT AGA GTAGG		
			GA AC_ A		
GAM2313	SLC21A14	3'	GGATGGAGCAGAACATGGAGA 34296	G G	CAT
			TCTCCA GT CT CTCCATCC		
			AGAGGT CA GA GAGGTAGG		
			A A C_		
GAM2313	LOC115004	3'	GGAGCTACTATGAGCACGTGAA 73550	C G	_____
	GA		TCT CA GTGCTCAT CTCC		
			AGA GT CACGAGTA GAGG		
			A G TCATC		
GAM2313	LOC139770	3'	GATGGAGGATGAACCTATAGA 75905	CC	GC _
			TCT AGGT TCATC TCCATC		
			AGA TCCA AGTAG AGGTAG		
			TA _ G		
GAM2313	LOC146229	3'	GATGGAGATGATTTG 78287	TGC	
			CAGG TCATCTCCATC		

GTTT AGTAGAGGTAG

GAM2313 LOC147650 5' GGACAGAGATGAGGCAGAGA 79020 CAGG _ CA
TCTC TGC TCATCTC TCC
|||| ||| ||||| |||
AGAG ACG AGTAGAG AGG
_ G AC

GAM2313 LOC148932 5' ATGGAGATGGCAAATGAAG 79847 C GG T
CT CA TGC CATCTCCAT
|| || ||| |||||
GA GT ACG GTAGAGGTA
A AA _

GAM2313 LOC149013 3' GGACCTATAGGCACCTGAAGA 79858 C TC C_
TCT CAGGTGC AT TCC
||| ||||| || |||
AGA GTCCACG TA AGG
A GA TCC

GAM2313 LOC149705 3' GGATGGAGATGATAGTGATG 85785 GG _
CA TGC TCATCTCCATCC
|| ||| |||||
GT GTG AGTAGAGGTAGG
A_ AT

GAM2313 LOC150481 5' GGATGGAGACTGTACTGAGA 80710 CA TCA
TCTC GGTGC TCTCCATCC
||| |||| |||||
AGAG TCATG AGAGGTAGG
_ TC_

GAM2313 LOC152317 5' GGATGCACCAAGCACCTGGG 86834 CATCTC
TCCAGGTGCT CATCC
||||||| |||||
GGGTCCACGA GTAGG
ACCAC_

GAM2313 LOC154282 3' GGACAGAGCACCTGGGGA 87408 ATC
TCTCCAGGTGCTC TCC
||||||| |||
AGGGGTCCACGAG AGG
AC_

GAM2313 LOC197414 3' GATGGAGATGGTGCTAGAAGA 89458 CCA TG T
TCT GG C CATCTCCATC
||| || | |||||
AGA TC G GTAGAGGTAG
AGA GT_

GAM2313 LOC200047 5' ATGGGGGGACACTTGGAGA 89951 C A
TCTCCAGGTG TC TCTCCAT
||||||| || |||||
AGAGGTTTAC AG GGGGGTA

GAM2313 LOC219917 3' GGAAAGATGACACCTGGAGA 93166 C _
TCTCCAGGTG TCATC TCC
||||||| |||| |||

AGAGGTCCAC AGTAG AGG
 _ AA
 GAM2313 LOC220729 3' GACCTGAAGCATCTGAAGA 72051 C _ TC
 TCT CAGGTGCT CA TC
 ||| ||||| || ||
 AGA GTCTACGA GT AG
 A A CC
 GAM2313 LOC256310 3' GGACGAGGAGCAGCACCTGGAG 98101 CAT A__
 G TCTCCAGGTGCT CTCC TCC
 ||||| ||| |||
 GGAGGTCCACGA GAGG AGG
 C__ AGC
 GAM2313 LOC256364 5' GGATGGAGACATTCTCACTGGA 96446 GTGCTCA_
 G CTCCAG TCTCCATCC
 |||| |||||
 GAGGTC AGAGGTAGG
 ACTCTTAC
 GAM2313 LOC256642 3' ATGGAAATGACGCTACAGGA 98042 A__ C C
 TCC GGTG TCAT TCCAT
 || ||| ||| ||||
 AGG TCGC AGTA AGGTA
 ACA _ A
 GAM2313 LOC256925 5' GGACAAAAGCAACAACCTGGAG 99470 ____ CATC
 A TCTCCAGGT GCT TCC
 ||||| ||| |||
 AGAGGTCCA CGA AGG
 ACAA AAAC
 GAM2313 LOC257031 3' GGACCTATAGGCACCTGAAGA 96249 C TC C__
 TCT CAGGTGC AT TCC
 ||| ||||| || |||
 AGA GTCCACG TA AGG
 A GA TCC
 GAM2313 LOC257095 5' ATGGAGATCTGCCCCGGGGA 98716 A T TC
 TCTCC GG GC ATCTCCAT
 |||| || || |||||
 AGGGG CC CG TAGAGGTA
 C _ TC
 GAM2313 LOC257475 3' AGATGAAAATACTTGGGA 72852 T C__
 TC CCAGGTG TCATCT
 || ||||| |||||
 AG GGTTCAT AGTAGA
 _ AAA
 GAM2313 LOC51301 3' GGATGGAAATAAGAGGGTGCCT 33908 TG A ____
 G CAGG CTC TC TCCATCC
 ||| ||| || |||||
 GTCC GGG AG AGGTAGG
 GT _ AATAA
 GAM2313 LOC90133 3' ATGGAGGTGCGCCACCTACAGA 62289 CC CTC
 TCT AGGTG ATCTCCAT
 || |||| |||||

			AGA TCCAC TGGAGGTA		
			CA CGC		
GAM2313	LOC90668	3'	GAGGGAGCCACCTGGAGA	83143	_ A
			TCTCCAGGTG CTC TCTC		
			AGAGGTCCAC GAG GGAG		
			C _		
GAM2313	LOC96597	5'	GATGGATGAGCACCCGGA	67461	A TC
			TCC GGTGCTCA TCCATC		
			AGG CCACGAGT AGGTAG		
			C _		
GAM2314	ADCY1	5'	ACGACAATGTGAGCATC	94336	AG
			GATGCTCACAT GTTGT		
			CTACGAGTGTA CAGCA		
			A_		
GAM2314	C8orf1	3'	ATAGCATGATGTGAGCATC	16343	AG_
			GATGCTCACAT GTTGT		
			CTACGAGTGTA CGATA		
			GTA		
GAM2314	CDH12	3'	ATAGCTATGTGGCATCA	15776	T G
			TGATGC CACATAG TTGT		
			ACTACG GTGTATC GATA		
			- -		
GAM2314	HIP1	3'	ACAAACTTGTGAGCATCA	19242	T G
			TGATGCTCACA AG TTGT		
			ACTACGAGTGT TC AACA		
			- A		
GAM2314	DKFZp547I224	5'	ATGGCCTATGTGAGATCA	39948	G TG
			TGAT CTCACATAGGT T		
			ACTA GAGTGTATCCG A		
			- GT		
GAM2314	DKFZp761P1010	3'	GGCACAAATAAGCTCA	37943	T CACA GG
			TGA GCT TA TTGTGCC		
			ACT CGA AT AACACGG		
			- _ _ A_		
GAM2314	FLJ13114	3'	ACAGGCCAGGTGAGCATCA	44889	ATA _
			TGATGCTCAC GGT TGT		
			ACTACGAGTG CCG ACA		
			GA_ G		
GAM2314	FLJ23024	3'	TGGCACAACTCAGCTCA	46851	T CACAT
			TGA GCT AGGTTGTGCCA		

ACT CGA TCCAACACGGT
 _ C_
 GAM2314 HNK-1ST 5' ACAGCAAGGAAATGTGAGCCCC 17946 AT AG_
 A TG GCTCACAT GTTGT
 || ||||| ||||
 AC CGAGTGTA CGACA
 CC AAGGAA
 GAM2314 KIAA0459 3' ACAATCATGTGAGCTCA 61639 T A
 TGA GCTCACAT GGTGT
 ||| ||||| |||||
 ACT CGAGTGTA CTAACA
 _ _
 GAM2314 KIAA1466 3' ATAACCTATGAAACATCA 72405 CTCA
 TGATG CATAGGTTGT
 |||| |||||
 ACTAC GTATCCAATA
 AAA_
 GAM2314 KIAA1954 5' ACAGCTTACTGAGCATCA 78220 CA
 TGATGCTCA TAGGTTGT
 ||||| |||||
 ACTACGAGT ATTCGACA
 C_
 GAM2314 PACSIN2 3' ATGGCACAGATTGATGCGCACC 24296 A T _ TAGG
 A TG TGC CA CA TTGTGCCAT
 || ||| || |||||
 AC ACG GT GT GACACGGTA
 C C A TA_
 GAM2314 PARVA 3' GGCCCATGTGAGCATCA 37183 A TTGT
 TGATGCTCACAT GG GCC
 ||||| || |||
 ACTACGAGTGTA CC CGG
 _ _
 GAM2314 RoXaN 3' GCACACATGTGAGCACA 47292 A AGGT
 TG TGCTCACAT TGTGC
 || ||||| ||||
 AC ACGAGTGTA ACACG
 _ C_
 GAM2314 LOC148638 3' ATGGCCATGTGAGCACA 79665 A A TG
 TG TGCTCACAT GGT T
 || ||||| ||| |
 AC ACGAGTGTA CCG A
 _ _ GT
 GAM2314 LOC148696 5' GGCCAGCATTGAGCATCA 85348 CATAG T
 TGATGCTCA GTTG GCC
 ||||| ||| |||
 ACTACGAGT CGAC CGG
 TA_ _
 GAM2314 LOC200609 5' ATAACACTGTGCAATCATCA 91658 CTCA _
 TGATG CATAG GTTGT
 |||| |||| ||||

			ACTAC	GTGTC	CAATA		
			TAAC	A			
GAM2314	LOC203235	3'	ATGACACAACCTGAGAGGCACC	92097	A	CACA	C
		A	TG TGCT	TAGGTTGTG	CAT		
			AC ACGG	GTCCAACAC	GTA		
			C	AGA_	A		
GAM2314	LOC219667	3'	GCCAGCCTATGCAACATCA	92948	CTCA	T	
			TGATG	CATAGGTTG	GC		
			ACTAC	GTATCCGAC	CG		
			AAC_	_			
GAM2314	LOC220514	3'	ATGGCACAGATTGATGCGCACC	61072	A	T _	TAGG
		A	TG TGC	CA CA	TTGTGCCAT		
			AC ACG	GT GT	GACACGGTA		
			C	C A	TA_		
GAM2314	LOC221463	3'	GGCATGGCACGTGAGCAGCA	93706	A	ATAG	TG
			TG TGCTCAC	GT TGCC			
			AC ACGAGTG	CG ACGG			
			G	CA_	GT		
GAM2315	ASL	3'	GTTTGACACAGCCTGGGCAACA	72396	GA	A	C
			TGT	CCCA	GCTGTGTC	AAT	
			ACA	GGGT	CGACACAG	TTG	
			AC	C	T		
GAM2315	DHFR	3'	GACCAGCTTGGGCAACA	7647	GA	T	
			TGT	CCCAAGCTG	GTC		
			ACA	GGGTTCGAC	CAG		
			AC	_			
GAM2315	MMP19	3'	GACCAGCTTGGGCAACA	11630	GA	T	
			TGT	CCCAAGCTG	GTC		
			ACA	GGGTTCGAC	CAG		
			AC	_			
GAM2315	MMP19	3'	GACCAGCTTGGGCAACA	43304	GA	T	
			TGT	CCCAAGCTG	GTC		
			ACA	GGGTTCGAC	CAG		
			AC	_			
GAM2315	NR1I2	5'	AGATCAAAGTGGTGGGGTCACA	15294	AA	TG	GTCCA
			TGTGACCC	GC T	ATCT		
			ACACTGGG	TG G	TAGA		
			G_	GT AAAC_			
GAM2315	PRKY	3'	GACCAGCTTGGGCAACA	12375	GA	T	
			TGT	CCCAAGCTG	GTC		

ACA GGGTTCGAC CAG
 AC _
 GAM2315 RAD54B 3' AGATTGTCAGCTTGGTCCACA 57062 AC TGTC
 TGTG CCAAGCTG CAATCT
 ||| ||||| |||||
 ACAC GGTTCGAC GTTAGA
 CT T__
 GAM2315 RCE1 3' GATTTAAGTTGGGTAACA 18890 G C T
 TGT ACCCAAG TG GTC
 ||| ||||| || |||
 ACA TGGGTTC AT TAG
 A A T
 GAM2315 SFRS2IP 5' GACCAGCTTGGGCAACA 17540 GA T
 TGT CCAAGCTG GTC
 ||| ||||| |||
 ACA GGGTTCGAC CAG
 AC _
 GAM2315 TEM7 3' GACCAGCTTGGGCAACA 40259 GA T
 TGT CCAAGCTG GTC
 ||| ||||| |||
 ACA GGGTTCGAC CAG
 AC _
 GAM2315 FLJ13263 3' AGATTGCTCCTTCAGCTCAGGG 47809 A A_ TGTC__
 CCACA TGTG CCC AGCTG CAATCT
 ||| ||| ||||| |||||
 ACAC GGG TCGAC GTTAGA
 C AC TTCCTC
 GAM2315 FLJ14327 3' GACCAGCTTGGGCAACA 46679 GA T
 TGT CCAAGCTG GTC
 ||| ||||| |||
 ACA GGGTTCGAC CAG
 AC _
 GAM2315 KIAA0172 3' GACTGCTAGCCTGGGCACA 65596 A A _ _
 TGTG CCA GCT GT GTC
 ||| ||| ||| || |||
 ACAC GGGT CGA CG CAG
 _ C T T
 GAM2315 KIAA1833 3' GGACCACAGCCTGGGCACA 90753 A A _
 TGTG CCA GCTGTG TCC
 ||| ||| ||||| |||
 ACAC GGGT CGACAC AGG
 _ C C
 GAM2315 KIAA1870 3' GACCAGCTTGGGCAACA 52901 GA T
 TGT CCAAGCTG GTC
 ||| ||||| |||
 ACA GGGTTCGAC CAG
 AC _
 GAM2315 MEGF11 3' ATTGGACAAATGTGGATACA 51599 AC AGCTG
 TGTG CCA TGTCCAAT
 ||| ||| |||||

ACAT GGT ACAGGTTA
 A_ GTAA_
 GAM2315 MGC15631 3' GACCAGCCTGGGTGACA 52230 G A T
 TGT ACCCA GCTG GTC
 ||| ||||| ||||| |||
 ACA TGGGT CGAC CAG
 G C _
 GAM2315 MGC32043 3' GACCAGGTCTTGGGCACA 58665 A _ T
 TGTG CCAAG CTG GTC
 ||||| ||||| ||| |||
 ACAC GGGTTC GAC CAG
 _ TG _
 GAM2315 PLP1 3' ATTGGACATTAAGCATCACA 6755 CCAA _
 TGTGA GCT GTGTCCAAT
 ||||| ||| ||||| |||||
 ACACT CGA TACAGGTTA
 A_ AT
 GAM2315 PTD012 3' GACCAGCTTGGGCAACA 26738 GA T
 TGT CCAAGCTG GTC
 ||| ||||| ||||| |||
 ACA GGGTTCGAC CAG
 AC _
 GAM2315 STAF42 3' ATTGAATGTTTTTTGGGTCCA 54942 T CT TG C
 TG GACCCAAG G T CAAT
 || ||||| | | |||||
 AC CTGGGTTT T A GTTA
 _ TT GT A
 GAM2315 TRIM31 3' ACGCCAGCCTGGGTCACA 92649 A _
 TGTGACCCA GCTG TGT
 ||||| ||||| ||| |||
 ACACTGGGT CGAC GCA
 C C
 GAM2315 LOC142893 5' ATTGGAACATTTTTGGGTCCA 83757 T CT _
 TG GACCCAAG GTGT CCAAT
 || ||||| ||||| |||||
 AC CTGGGTTT TACA GGTTA
 _ T_ A
 GAM2315 LOC143503 5' AGACTGGACAAAGGGGGTCACA 83882 AAGCTG A
 TGTGACCC TGTCCA TCT
 ||||| ||||| ||||| |||
 ACACTGGG ACAGGT AGA
 GGAA_ C
 GAM2315 LOC145824 5' GACTTGCAGCTTGGATACACA 77986 AC_ _
 TGTG CCAAGCTGT GTC
 ||||| ||||| ||||| |||
 ACAC GGTTCGACG CAG
 ATA TT
 GAM2315 LOC157603 3' GACCAGCTTGGGCAACA 87786 GA T
 TGT CCAAGCTG GTC
 ||| ||||| ||||| |||

		ACA GGGTTCGAC CAG		
		AC _		
GAM2315	LOC221300	3' GACCAGCTTGGGTAACA	93576	G T
		TGT ACCCAAGCTG GTC		
		ACA TGGGTTTCGAC CAG		
		A _		
GAM2315	LOC257608	3' ACGCCAGCCTGGGTCACA	99664	A _
		TGTGACCCA GCTG TGT		
		ACACTGGGT CGAC GCA		
		C C		
GAM2315	LOC51337	3' GACCAGAGCATCCTGGGTACA	34081	A A__ G _
		TGTG CCCA GCT TG TC		
		ACAT GGGT CGA AC AG		
		_ CCTA G C		
GAM2316	ALPP	3' TGAAGCAGGATAATCGCTTGA	69421	A GC
		TCGAGC ATTG TCTGCTTCA		
		AGTTCG TAAT GGACGAAGT		
		C A_		
GAM2316	FGF2	3' AAGCAGGAGGATCGCTTGAGC	10610	A GG T
		GCTCGAGC ATT C CTGCTT		
		CGAGTTCG TAG G GACGAA		
		C GA _		
GAM2316	FLRT2	5' TGAAGCAGGAGGACCACTCGAG	26005	CAAT _ _
	C	GCTCGAG TGG CT CTGCTTCA		
		CGAGCTC ACC GG GACGAAGT		
		_ _ A AG		
GAM2316	KLF8	3' AAGCAGCCCACTGAGC	24367	G CAAT CT
		GCTC AG TGG CTGCTT		
		CGAG TC ACC GACGAA		
		_ _ _ C_		
GAM2316	MMP19	3' TGAAGCAGGAGGATCACTTGAG	11643	CA GG T
	C	GCTCGAG ATT C CTGCTTCA		
		CGAGTTC TAG G GACGAAGT		
		AC GA _		
GAM2316	MMP19	3' TGAAGCAGGAGGATCACTTGAG	43307	CA GG T
	C	GCTCGAG ATT C CTGCTTCA		
		CGAGTTC TAG G GACGAAGT		
		AC GA _		
GAM2316	PLDN	5' TGGGGCAGAGCCAACTCTCGAG	25677	CAA
	C	GCTCGAG TTGGCTCTGCTTCA		

			CGAGCTC AACCGAGACGGGGT		
			TC_		
GAM2316	PRKY	3'	TGAAGCAGAAAGATTGCTTGAG 12388	GGC	
	C		GCTCGAGCAATT TCTGCTTCA		
			CGAGTTCGTTAG AGACGAAGT		
			AA_		
GAM2316	PTGS1	3'	AAGCAGAGGCAACACTGGA 8239	G CAA G	
			TC AG TTG CTCTGCTT		
			AG TC AAC GAGACGAA		
			G AC_ G		
GAM2316	PTGS1	3'	AAGCAGAGGCAACACTGGA 55468	G CAA G	
			TC AG TTG CTCTGCTT		
			AG TC AAC GAGACGAA		
			G AC_ G		
GAM2316	DRF1	3'	TGAAGCAGAAGAATCACTTGA 47759	CA GGC	
			TCGAG ATT TCTGCTTCA		
			AGTTC TAA AGACGAAGT		
			AC GA_		
GAM2316	FBXO5	5'	TGAAGCAGGCAGGTTGCTCAGC 25156	C TG T	
			GCT GAGCAAT GC CTGCTTCA		
			CGA CTCGTTG CG GACGAAGT		
			_ GA _		
GAM2316	FLJ12425	3'	TGAAGCAGTACATCATTGCTC 87095	_ GCT	
			GAGCAAT TG CTGCTTCA		
			CTCGTTA AC GACGAAGT		
			CT AT_		
GAM2316	FLJ13456	3'	TGAAGCAGGAGGATTGCTTGAG 66566	GG T	
	C		GCTCGAGCAATT C CTGCTTCA		
			CGAGTTCGTTAG G GACGAAGT		
			GA_		
GAM2316	FLJ20211	3'	TGAAGCAGGAGAATTGCCTGA 35268	A GG T	
			TCG GCAATT C CTGCTTCA		
			AGT CGTTAA G GACGAAGT		
			C GA_		
GAM2316	FLJ20340	3'	TGAAGCAGGAGAATCGCTTGA 35461	A GG T	
			TCGAGC ATT C CTGCTTCA		
			AGTTCG TAA G GACGAAGT		
			C GA_		
GAM2316	FLJ23209	3'	TGAAGCAGCAAGATCACTTGAG 46588	CA GGCT	
	C		GCTCGAG ATT CTGCTTCA		

	CGAGTTC TAG GACGAAGT	
	AC AAC_	
GAM2316 KIAA0355	3' TGAAGCAGAAGAATCGCTTGA 28711	A GGC
	TCGAGC ATT TCTGCTTCA	
	AGTTCG TAA AGACGAAGT	
	C GA_	
GAM2316 KIAA1958	3' TGAAGCAGGAGAATTGCTTGA 82794	GG T
	TCGAGCAATT C CTGCTTCA	
	AGTTCGTTAA G GACGAAGT	
	GA_	
GAM2316 MGC13017	3' TGAAGCAGAAGAAGTCTTGA 55580	A GGC
	TCGAGCA TT TCTGCTTCA	
	AGTTCGT AA AGACGAAGT	
	C GA_	
GAM2316 MGC13198	5' AAGCAGGAGAATTGCTTGA 52068	GG T
	TCGAGCAATT C CTGCTT	
	AGTTCGTTAA G GACGAA	
	GA_	
GAM2316 MGC16385	3' AAGCAGGAGAATTGCTTGA 59531	GG T
	TCGAGCAATT C CTGCTT	
	AGTTCGTTAA G GACGAA	
	GA_	
GAM2316 MGC4562	3' TGAAGCAGGAGAATTGCCTGA 56744	A GG T
	TCG GCAATT C CTGCTTCA	
	AGT CGTTAA G GACGAAGT	
	C GA_	
GAM2316 PAFAH2	3' TGAAGCAGAAGAATCACTTGA 6509	CA GGC
	TCGAG ATT TCTGCTTCA	
	AGTTC TAA AGACGAAGT	
	AC GA_	
GAM2316 PRO0478	5' TGAAGCAGGAGAATCGCTTGAG 27042	A GG T
C	GCTCGAGC ATT C CTGCTTCA	
	CGAGTTCG TAA G GACGAAGT	
	C GA_	
GAM2316 PRO2859	3' TGAAGCAGGAGAATCACTTGA 38215	CA GG T
	TCGAG ATT C CTGCTTCA	
	AGTTC TAA G GACGAAGT	
	AC GA_	
GAM2316 RES4-25	3' TGAAGCAGGAGGACTGCTTGAG 65278	A GG T
C	GCTCGAGCA TT C CTGCTTCA	

			CGAGTTCGT AG G GACGAAGT	
			C GA _	
GAM2316 SSR3	3'	TGAAGCAGGAGAACTGCCTGA 24040	A A GG T	
		TCG GCA TT C CTGCTTCA		
		AGT CGT AA G GACGAAGT		
		C C GA _		
GAM2316 TMG4	3'	TGAAGCAGGAGAATTGCTCGA 44218	GG T	
		TCGAGCAATT C CTGCTTCA		
		AGCTCGTTAA G GACGAAGT		
		GA _		
GAM2316 TRAF3	5'	GAAGCAGAACCCTCTGAGC 60454	_ CAATT C	
		GCTC GAG GG TCTGCTTC		
		CGAG CTC CC AGACGAAG		
		T _ _ _ _ A		
GAM2316 VIT1	5'	TGAAGCAGGAGAATTGCTTGA 38607	GG T	
		TCGAGCAATT C CTGCTTCA		
		AGTTCGTTAA G GACGAAGT		
		GA _		
GAM2316 ZFD25	3'	TGAAGCAGGAGAATTGCTC 33116	GG T	
		GAGCAATT C CTGCTTCA		
		CTCGTTAA G GACGAAGT		
		GA _		
GAM2316 LOC130589	3'	TGAAGCAGGAGAATCGCTTGA 57935	A GG T	
		TCGAGC ATT C CTGCTTCA		
		AGTTCG TAA G GACGAAGT		
		C GA _		
GAM2316 LOC144347	3'	TGAAGCAGAGAACAGCCCCGAG 77309	A_ AATTGG	
C		GCTCG GC CTCTGCTTCA		
		CGAGC CG GAGACGAAGT		
		CC ACAA_		
GAM2316 LOC150299	3'	TGAAGCAGGAGAATCGCTGGA 86171	G A GG T	
		TC AGC ATT C CTGCTTCA		
		AG TCG TAA G GACGAAGT		
		G C GA _		
GAM2316 LOC152283	3'	TGAAACAGGAGAATTGCTTGA 86877	GG T C	
		TCGAGCAATT C CTG TTCA		
		AGTTCGTTAA G GAC AAGT		
		GA _ A		
GAM2316 LOC153338	3'	TGAAGCAGTAGAATCGCTT 87200	A GG _	
		GAGC ATT CT CTGCTTCA		

		TTCG TAA GA GACGAAGT		
		C _ T		
GAM2316	LOC154092 3'	TGAAGCAGGAGGATCACTTGAG 87374	CA	GG T
	C	GCTCGAG ATT C CTGCTTCA		
		CGAGTTC TAG G GACGAAGT		
		AC GA _		
GAM2316	LOC157292 5'	GAAGCAGAATAGCTTGA 87698	A	TGGC
		TCGAGC AT TCTGCTTC		
		AGTTCG TA AGACGAAG		
		A _ _ _		
GAM2316	LOC201895 3'	AAGCAGGAGAATTGCTTGA 90536	GG	T
		TCGAGCAATT C CTGCTT		
		AGTTCGTTAA G GACGAA		
		GA _		
GAM2316	LOC219722 5'	TGAAGCAGAAGAATCACTTGA 94687	CA	GGC
		TCGAG ATT TCTGCTTCA		
		AGTTC TAA AGACGAAGT		
		AC GA _		
GAM2317	BMP1 3'	CTGAATACCCCAATGGCT 21530	_	C
		AGCCATTGGG AT CAG		
		TCGGTAACCC TA GTC		
		CA A		
GAM2317	ISGF3G 3'	GATGAGGGTCCCATGGC 21407	T	AGA
		GCCAT GGGATCC CATC		
		CGGTA CCCTGGG GTAG		
		_ A _		
GAM2317	NR5A2 5'	TCTGATGTGTCCTTCCCAAGGC 15118	A	TCCAG
		GCC TTGGGA ACATCAGA		
		CGG AACCT TGTAGTCT		
		_ TCCTG		
GAM2317	PKD2 3'	TCTGATGTCTGTGGGACTAA 60720	GA	_
		TTGG TC CAGACATCAGA		
		AATC GG GTCTGTAGTCT		
		AG T		
GAM2317	SLA 3'	CTGATGTCTGCAGCCATGGCT 23112	TG	ATC
		AGCCAT GG CAGACATCAG		
		TCGGTA CC GTCTGTAGTC		
		_ GAC		
GAM2317	SPINT2 5'	CTGATCGCGAGACCCCAACGGC 63849	A	A CAGAC
	T	AGCC TTGGG TC ATCAG		

TCGG AACCC AG TAGTC
C C AGCGC
GAM2317 DKFZP434G1411 3' CTGATGTCTAAATTGCAGTG 93731 G CC
CATTG GAT AGACATCAG
||||| ||| |||||
GTGAC TTA TCTGTAGTC
G AA
GAM2317 DKFZp434G179 3' TCTGATGTCTTCAAACAAACAG 80893 CA_ GGATCC
CT AGC TTG AGACATCAGA
||| ||| |||||
TCG AAC TCTGTAGTCT
ACA AAAC T_

GAM2317 DUSP9 3' TCGTTGCACTGGATCCCAGTGG 9158 A_ TCA
CT AGCCATTGGGATCCAG CA GA
||||| ||| ||| |||
TCGGTGACCCTAGGTC GT CT
AC TG_

GAM2317 FLJ10111 3' GATGAGGGTCCCATGGC 36302 T AGA
GCCAT GGGATCC CATC
||||| ||| |||
CGGTA CCCTGGG GTAG
_ A_

GAM2317 FLJ21135 5' ATGGCCCGGATCCCGACGGC 46347 A AGA_
GCC TTGGGATCC CAT
||| ||||| |||
CGG AGCCCTAGG GTA
C CCG

GAM2317 FLJ21865 3' TGTCTGGACCCACGGC 43115 AT A
GCC TGGG TCCAGACA
||| ||| |||||
CGG ACCC AGGTCTGT
C_ C

GAM2317 KIAA0542 5' GTCAGGCCCGATGGCT 66666 AT A
AGCCATTGGG CC GAC
||||| ||| |||
TCGGTAGCCC GG CTG
_ A

GAM2317 KIAA0644 3' CTAATGCCTGGATCTGTG 29725 TG A C
CAT GGATCCAG CAT AG
||| ||||| ||| |||
GTG TCTAGGTC GTA TC
_ C A

GAM2317 MIG2 3' CTAATGCCTGGACTGGC 72858 TTGG A A C
GCCA G TCCAG CAT AG
||||| ||| ||| |||
CGGT C AGGTC GTA TC
_ _ C A

GAM2317 LOC126767 3' CTGATGTCCAGAGGACGTGGT 75959 T GGA CA
GCCAT G TC GACATCAG
||||| ||| ||| |||

TGGTG C AG CTGTAGTC
 _AGG AC
 GAM2317 LOC146562 5' TCTGATGCCCCGCGGTAGCCAAT 58256 _ GAT AGA__
 GAGCT AGC CATTGG CC CATCAGA
 ||| ||||| || |||||
 TCG GTAACC GG GTAGTCT
 A GAT CGCCC
 GAM2317 LOC146957 3' CTGATTTTGACCCCAGTGGC 78814 ATC C
 GCCATTGGG CAGA ATCAG
 ||||| ||| |||||
 CGGTGACCC GTTT TAGTC
 CA_ _
 GAM2317 LOC220980 5' TCTGATGTCTATTGTGAATTGG 94774 _ G CC
 CT AGCCA TTG GAT AGACATCAGA
 |||| ||| ||| |||||
 TCGGT AGT TTA TCTGTAGTCT
 TA G _
 GAM2317 LOC221486 3' TCTGATGTCCATTTGTCCCAAT 92662 C CCA__
 AGCT AGC ATTGGGAT GACATCAGA
 ||| ||||| |||||
 TCG TAACCCTG CTGTAGTCT
 A TTTAC
 GAM2317 LOC221496 3' TCTGATGTCTGGATGATCGGC 93644 _ GGG
 GCC ATT ATCCAGACATCAGA
 ||| ||| |||||
 CGG TAG TAGGTCTGTAGTCT
 C _
 GAM2317 LOC91050 3' CTGAGACTAGATCCCAAAGCT 65374 CA C ACA
 AGC TTGGGATC AG TCAG
 ||| ||||| || |||
 TCG AACCTAG TC AGTC
 A_ A AG_
 GAM2318 ATP1B2 3' CATTCGCCTTCCCAGAATATCC 9828 ACCGCG A
 T AGGA GGGAA GGCGAATG
 |||| ||||| |||||
 TCCT CCCTT CCGCTTAC
 ATAAGA _
 GAM2318 ATP1B2 3' TCGCCTTTCCCACTTCT 9842 ACCGCG
 AGGA GGGAAAGGCGA
 |||| |||||
 TCTT CCCTTCCGCT
 CAACCA
 GAM2318 EGFL3 3' CGCTCTCCCCGCGGCTCT 63299 A AA
 GGA CCGCGGGGA GGCG
 ||| ||||| |||
 TCT GCGCCCCCT TCGC
 C C_
 GAM2318 EGR3 3' CCTTCCCCTCGCGGTCCC 60302 A _ A
 GG ACCGCG GGG AAGG
 || ||||| ||| |||

CC TGGCGC CCC TTCC
 C T C
 GAM2318 GTF2IRD1 5' ATTCCCCCCCCGCGCCCCCT 33346 AAC AAA C
 AGG CGCGGGG GG GAAT
 ||| ||||| || ||||
 TCC GCGCCCC CC CTTA
 CCC C__ _
 GAM2318 MARK3 5' CGCCCTCCCCACGGCGCCT 11462 AA C AA
 AGG CCG GGGGA GGCG
 ||| || ||||| ||||
 TCC GGC CCCCT CCGC
 GC A C_
 GAM2318 PCSK2 3' CATCCGCCTTTCCACCGCCCT 12000 AC_ CG A
 CC GGA CG GGGAAAGGCG ATG
 ||| || ||||| ||||
 CCT GC CCCTTTCCGC TAC
 CCC CA C
 GAM2318 SHANK2 3' TCTTTCCCGGAGTCCCT 25534 A CG
 AGG AC CGGGGAAAGG
 ||| || ||||| ||||
 TCC TG GCCCCTTTCT
 C AG
 GAM2318 ABTB1 5' CATCCGCCGGGTGCGCGGTTT 51698 GGGAAA A
 GAACCGCG GGCG ATG
 ||||| ||||| ||||
 CTTGGCGC CCGC TAC
 GTGGG_ C
 GAM2318 C20orf18 3' TCTCTCCCCTGCGGCTCC 49174 A _ A
 GGA CCGC GGGGA AGG
 ||| ||||| ||||
 CCT GGCG CCCCT TCT
 C T C
 GAM2318 C20orf18 3' TCTCTCCCCTGCGGCTCC 49183 A _ A
 GGA CCGC GGGGA AGG
 ||| ||||| ||||
 CCT GGCG CCCCT TCT
 C T C
 GAM2318 CDC42BPB 3' ATTCGCTTCCACGGCTTCT 21238 A C GAAA
 AGGA CCG GGG GGCGAAT
 ||||| ||||| |||||
 TCTT GGC CCT TCGCTTA
 C A ____
 GAM2318 DKFZP434A0131 3' GCCTTCCTCGCGGCCCT 39152 AA A
 AGG CCGCGGGGAA GGC
 ||| ||||| ||||
 TCC GGCGCTCCTT CCG
 CC _
 GAM2318 FENS-1 3' CATTCTTCCTTTCCCCAAAT 40831 CCGC C__
 TCCT AGGAA GGGGAAAGG GAATG
 ||||| ||||| |||||

			TCCTT	CCCCTTTCC	CTTAC			
			AAAC	CTT				
GAM2318	FLJ22494	5'	CCTTTCCCCCAGCTCCT	46096	ACC	___		
			AGGA	GC	GGGGAAAGG			
			TCCT	CG	CCCCTTTCC			
			___	AC				
GAM2318	LBP-9	3'	ATCGCCTTTCCTGTTCTT	28043	CGCG	A		
			AGGAAC	GGGAAAGGCG	AT			
			TTCTTG	TCCTTTCCGC	TA			
			___	C				
GAM2318	OCIA	5'	CCCCTCCCCGCGGTACCT	35655	A	AA		
			AGG	ACCGCGGGGA	GG			
			TCC	TGGCGCCCCT	CC			
			A	CC				
GAM2318	LOC126669	3'	CATTTCCCTTCCCCGCACCCCT	75927	AACC	A	C	
			AGG	GCGGGGAA	GG	GAATG		
			TCC	CGCCCCTT	CC	TTTAC		
			CCA_	_	C			
GAM2318	LOC132617	5'	TCGCCCGCTTTCCCTCGACT	76422	AC	C	___	
	CC		GGA	CG	GGGGAAA	GGCGA		
			CCT	GC	CCCCTTT	CCGCT		
			CA	T	CGCC			
GAM2318	LOC146434	5'	CGGCTTTTCCCGCAGCTCCT	78454	ACC	G		
			AGGA	GCGGGGAAAG	CG			
			TCCT	CGCCCTTTTC	GC			
			CGA	G				
GAM2318	LOC146603	3'	TCACCCCTCCCCTGGTTTCT	78607	C	AA	C	
			AGGAACCG	GGGGA	GG	GA		
			TCTTTGGT	CCCCT	CC	CT		
			_	CC	A			
GAM2318	LOC157958	3'	TCACCTTTCTCTAGTTCT	82531	CGC	C		
			GGAAC	GGGGAAAGG	GA			
			TCTTG	TCTCTTTCC	CT			
			A_	A				
GAM2318	LOC255223	3'	TCACCCTCTCTGTGCTCC	98359	AC	AA	C	
			GGA	CGCGGGGA	GG	GA		
			CCT	GTGTCTCT	CC	CT		
			C_	C_	A			
GAM2319	FGFR2	5'	CCACCGCAGCTGAAGGCATTG	43677	T	A	AA	
			CA	ATG	TTTCAGCTGC	TGG		

			GT TAC GAAGTCGACG ACC			
			_ G CC			
GAM2319	FGFR2	5'	CCACCGCAGCTGAAGGCATTG 43766	T A	AA	
			CA ATG TTTCAGCTGC TGG			
			GT TAC GAAGTCGACG ACC			
			_ G CC			
GAM2319	FGFR2	5'	CCACCGCAGCTGAAGGCATTG 43770	T A	AA	
			CA ATG TTTCAGCTGC TGG			
			GT TAC GAAGTCGACG ACC			
			_ G CC			
GAM2319	STAT1	3'	CCATCACAGCTGAACTTGTTG 58366	T TG T	CA	
			CA A A TTCAGCTG ATGG			
			GT T T AAGTCGAC TACC			
			_ GT C AC			
GAM2319	BPESC1	3'	CACCACAGCTGCTTATGTG 41770	TTT	CAA	
			CATATGA CAGCTG TG			
			GTGTATT GTCGAC AC			
			C_ ACC			
GAM2319	ST13	3'	CATTTCTGAAATCATA 15430	CTGC		
			TATGATTTTCAG AATG			
			ATACTAAAGTC TTAC			
			T_			
GAM2319	LOC139274	5'	CCATTGCTAGTGAAATCATAGT 76333	A	G _	
	A		TAC TATGATTTCA CT GCAATGG			
			ATG ATACTAAAGT GA CGTTACC			
			_ _ T			
GAM2319	LOC145781	3'	CAGCTGAAATCACTGTA 77956	TA		
			TACA TGATTTTCAGCTG			
			ATGT ACTAAAGTCGAC			
			C_			
GAM2319	LOC200933	3'	CATTCGCAAATCATATG 91790	TCAGC	_	
			CATATGATT TGC AATG			
			GTATACTAA ACG TTAC			
			_ _ C			
GAM2319	LOC202934	3'	CCATCGTAGCCTAAAAGCATAT 92035	A_ CA	A	
	GTA		TACATATG TTT GCTGC ATGG			
			ATGTATAC AAA CGATG TACC			
			GA TC C			
GAM2319	LOC56902	3'	CATTTATCTGAAATCACATGTA 39717	A	C C	
			TACAT TGATTTTCAG TG AATG			

ATGTA ACTAAAGTC AT TTAC
 C T _
 GAM2320 CORT 5' GTGGGAGAGAAGCTCCAGTCA 8943 ACC____
 TGACTGGAGC CCCAT
 ||||| ||||
 ACTGACCTCG GGGTG
 AAGAGA
 GAM2320 DRD5 3' AATGGCTTGTTCAGTCA 7681 G CCC
 TGACTG AGCA CCATT
 ||||| ||||
 ACTGAC TTGT GGTAA
 _ TC_
 GAM2320 LFNG 3' GTGAATAAAGGTGCTCTTTGCA 94214 ACT CCC
 TG GGAGCACC ATTCAC
 || ||||| |||||
 AC TCTCGTGG TAAGTG
 GTT AAA
 GAM2320 PTPRN 3' ATGGGGGTGCTGCAGCCA 12623 A G
 TG CTG AGCACCCCCAT
 || ||| |||||
 AC GAC TCGTGGGGGTA
 C G
 GAM2320 SORCS1 3' AATGGGGGTCTTGTC 54673 TG C
 GAC GAG ACCCCCATT
 ||| ||| |||||
 CTG TTC TGGGGGTAA
 _ _
 GAM2320 TRIM14 3' TGAATGGGAGTCATCCAGTC 29519 GC C
 GACTGGA AC CCCATTCA
 ||||| || |||||
 CTGACCT TG GGGTAAGT
 AC A
 GAM2320 APOBEC3G 5' GTGAAACCCTGGTGCTCCAG 41822 CCCA_
 CTGGAGCACC TTCAC
 ||||| ||||
 GACCTCGTGG AAGTG
 TCCCA
 GAM2320 FLJ14564 3' GTGAATGGAGAGCTTCAG 77016 ACCC
 CTGGAGC CCATTCAC
 ||||| |||||
 GACTTCG GGTAAGTG
 AGA_
 GAM2320 FLJ32734 3' GTGAGCCTGCGGTCCAGTCA 59037 GCAC C _
 TGACTGGA CC CA TTCAC
 ||||| || || |||||
 ACTGACCT GG GT GAGTG
 _ C CC
 GAM2320 GRIN3A 3' GTGAACGGGCTGTTTGTCTCCA 56787 A CC____ A
 GCCA TG CTGGAGCA CCC TTCAC
 || ||||| || |||||

AC GACCTCGT GGG AAGTG
 C TTTGTC C
 GAM2320 KIAA0317 5' GTGAATAGGAGTGCTCTA 29746 C C
 TGGAGCAC CC ATTCAC
 ||||| || |||||
 ATCTCGTG GG TAAGTG
 A A
 GAM2320 KIAA0596 3' GTGAATGAATGCTCCAGCG 63496 A CCCC
 TG CTGGAGCA CATTAC
 || ||||| |||||
 GC GACCTCGT GTAAGTG
 _ AA_
 GAM2320 KIAA1649 5' TGAATGGGAATGTTATCA 51254 _ CC
 TGG AGCA CCCATTCA
 ||| ||| |||||
 ACT TTGT GGGTAAGT
 A AA
 GAM2320 LANO 3' GTGAATGGGAAGCTAAAGCCAG 47974 _ ACC
 CTGG AGC CCCATTAC
 ||| ||| |||||
 GACC TCG GGGTAAGTG
 GAAA AA_
 GAM2320 MGC26768 3' GTGAATGAAGGTGCTTTTC 58913 CT CC
 GA GGAGCACC CATTAC
 || ||||| |||||
 CT TTTCGTGG GTAAGTG
 _ AA
 GAM2320 PAK6 3' GTGAATGGCCTGCTCCAG 39810 CCC
 CTGGAGCA CCATTAC
 ||||| |||||
 GACCTCGT GGTAAGTG
 CC_
 GAM2320 SEC14L2 5' GAGTCTGTGCTCCATCA 25795 C CCCC
 TGA TGGAGCAC ATTC
 ||| ||||| |||
 ACT ACCTCGTG TGAG
 _ TC_
 GAM2320 LOC146237 3' TGAATGGGAAAGGCTCAGGCA 84617 A G ACC_
 TG CT GAGC CCCATTCA
 || || ||| |||||
 AC GG CTCG GGGTAAGT
 _ A GAAA
 GAM2320 LOC150606 5' ATGGGAGGCCTCCAGCCA 86265 A CA _
 TG CTGGAG CC CCCAT
 || ||||| || |||||
 AC GACCTC GG GGGTA
 C C_ A
 GAM2320 LOC159053 3' TGAATGGGGGAATCTCCAGTCA 88379 CA_
 TGA CTGGAG CCCCCATTCA
 ||||| |||||

ACTGACCTC GGGGGTAAGT
 TAA
 GAM2320 LOC220739 3' GTGAACAGGGCTTCAGTCA 94526 A CCCA
 TGA CTGGAGC CC TTCAC
 ||||| || ||||
 ACTGACTTCG GG AAGTG
 _ AC_
 GAM2320 LOC253820 5' GTGAATGGAGGCTGCCAGCA 97423 A _ ACCC
 TG CTGG AGC CCATTAC
 || ||| || |||||
 AC GACC TCG GGTAAGTG
 _ G GA_
 GAM2320 LOC90785 3' TGAATGGGGGTGCCTGGTGA 64721 G TG A
 T AC G GCACCCCCATTCA
 | || |||||
 A TG C CGTGGGGGTAAGT
 G GT_
 GAM2320 LOC90829 5' GTGAATGGGAGTTCACTCA 64793 CTG ACC
 TGA GAGC CCCATTAC
 || ||| |||||
 ACT CTTG GGGTAAGTG
 CA_ A_
 GAM2320 LOC91812 5' GTGAATGGCTCTGTCTCCAGCA 67820 A _ CCC
 TG CTGGAG CA CCATTAC
 || |||| || |||||
 AC GACCTC GT GGTAAGTG
 _ T CTC
 GAM2320 LOC91813 5' GTGAATGGCTCTGTCTCCAGCA 67846 A _ CCC
 TG CTGGAG CA CCATTAC
 || |||| || |||||
 AC GACCTC GT GGTAAGTG
 _ T CTC
 GAM2321 ASC 5' GACGGCCTGGGGCCCCAATCCA 26068 T CT _
 TGGATTGG GCCCA GGCT TC
 ||||| |||| ||| ||
 ACCTAACC CGGGGT CCGG AG
 C _ C
 GAM2321 CDC6 3' TGAAGCCAATGAATTTAATCT 8830 TGCCC C
 A TGGATTGG CA TGGCTTCA
 ||||| || |||||
 ATCTAATT GT ACCGAAGT
 TTAA_ A
 GAM2321 DES 3' TGAAGCCAGCCTTCTTCCATCC 72593 AT TGCCCCA
 CA TGG TGG CTGGCTTCA
 || || |||||
 ACC ACC GACCGAAGT
 CT TTCTTCC
 GAM2321 DUX4 5' CGGCGGGGCACCACCCA 73194 AT A
 TGG TGGTGCCCC CTG
 || ||||| |||

		ACC ACCACGGGG GGC	
		C_ C	
GAM2321	PLXNA1	3' GAGGCCGGAGCACCACATCCA 72771	_ CCCA
		TGGAT TGGTGC CTGGCTTC	
		ACCTA ACCACG GGCCGGAG	
		C A__	
GAM2321	PPARGC1	3' AAGCCAGTGGAATTTTCTA 26074	TT GCC
		TGGA GGT CCACTGGCTT	
		ATCT TTA GGTGACCGAA	
		T_ AA_	
GAM2321	SCO1	3' TGAAGCCAGTGAAGAGCCCA 17162	T CC__
		TGG GC CACTGGCTTCA	
		ACC CG GTGACCGAAGT	
		_ AGAA	
GAM2321	TTC3	5' TGAACTTTAGCACCAATCC 13887	CCCACT C
		GGATTGGTGC GG TTCA	
		CCTAACCACG TC AAGT	
		ATT__ A	
GAM2321	CAPS2	3' AAGCCAGTGAGATAATTCA 71124	GTGCCC
		TGGATTG CACTGGCTT	
		ACTTAAT GTGACCGAA	
		AGA__	
GAM2321	FLJ21736	3' GTTTGTGAATGCACCAATCCA 46787	CC_ TG
		TGGATTGGTGC CAC GC	
		ACCTAACCACG GTG TG	
		TAA TT	
GAM2321	FLJ23790	5' AAGCCAGTGGAATTGCCA 59273	CC__
		TGGTG CCACTGGCTT	
		ACCGT GGTGACCGAA	
		TAAA	
GAM2321	KIAA0493	5' AAGCCAGTGGAATTGCCA 64923	CC__
		TGGTG CCACTGGCTT	
		ACCGT GGTGACCGAA	
		TAAA	
GAM2321	KIAA1808	3' TGAAGCCAGCAGGGCATCCC 87053	ATT CA
		GG GGTGCCC CTGGCTTCA	
		CC CTACGGG GACCGAAGT	
		__ AC	
GAM2321	LOXL4	3' TGATGGCAAGATCACCAATCCA 50862	CCCCA G _
		TGGATTGGTG CT GCT TCA	

ACCTAACCAC GA CGG AGT
 TA__ A T
 GAM2321 MAP1LC3A 3' CAGAGGGGCACCAACCCA 51680 A CA
 TGG TTGGTGCCC CTG
 ||| ||||| |||
 ACC AACCACGGG GAC
 C A_
 GAM2321 PRO0245 5' AGGCGTGAGGCACCACACCCA 26954 AT_ C TG
 TGG TGGTGCC CAC GCTT
 ||| ||||| ||| ||||
 ACC ACCACGG GTG CGGA
 CAC A _
 GAM2321 LOC118851 5' TGAAGACATTTAAGACCCAATC 76019 TGCCCCAC G
 CA TGGATTGG TG CTTCA
 ||||| || |||||
 ACCTAACC AC GAAGT
 CAGAATTT A
 GAM2321 LOC146435 5' TGAAGCCAACAGAGTCCCAACC 78453 A TG CCCAC
 A TGG TTGG C TGGCTTCA
 ||| ||| | |||||
 ACC AACC G ACCGAAGT
 _ CT AGACA
 GAM2321 LOC152851 5' TGAAGCCAGTGGGCTGGGGACT 81598 GA GG GC
 CA TG TT T CCCACTGGCTTCA
 || || | |||||
 AC AG G GGGTGACCGAAGT
 TC GG TC
 GAM2321 LOC163104 5' CCAGTGGGGGCCAGCACA 88519 GA GT
 TG TTG GCCCCACTGG
 || ||| |||||
 AC GAC CGGGGTGACC
 AC _
 GAM2321 LOC220469 3' AAGCCAGTGGGCTAATACA 76890 G TGCC
 TG ATTGG CCACTGGCTT
 || |||| |||||
 AC TAATC GGTGACCGAA
 A _
 GAM2321 LOC253181 3' GTCCGTGGGGCACAACCCA 99417 ATTG T
 TGG GTGCCCCAC GGC
 ||| ||||| |||
 ACC CACGGGGTG CTG
 CAA_ C
 GAM2321 LOC253841 3' TGGACCACGGGGCACCATCCA 98094 AC C
 TGGATTGGTGCCCC TGG TTCA
 ||||| ||| ||||
 ACCTAACCACGGGG ACC AGGT
 C_ _
 GAM2321 LOC91445 3' TGAAGCCAGTGGGGGCTCC 61174 T _
 GG GCCCC ACTGGCTTCA
 || |||| |||||

			CC CGGGG TGACCGAAGT		
			T G		
GAM2322	A1BG	3'	AGATGAGTCTCACTATGTTGCC 56278	AC	A C
	CA		TG CAACATGGTGA AC CATCT		
			AC GTTGTATCACT TG GTAGA		
			CC C A		
GAM2322	ADAMTS4	3'	AGACAGGGTTTCACCATGTTGG 18746	A	A_
	CCA		TG CCAACATGGTGAAACCC TCT		
			AC GGTTGTACCACTTTGGG AGA		
			C AC		
GAM2322	ADAMTS4	3'	AGACGGGGTTTCACCATGTTGG 18749	A	A_
	CCA		TG CCAACATGGTGAAACCC TCT		
			AC GGTTGTACCACTTTGGG AGA		
			C GC		
GAM2322	ADCY6	5'	AGACGAGGTTTCACCATCTTGG 31585	A C	CA_
	CCA		TG CCAA ATGGTGAAACC TCT		
			AC GGTT TACCACTTTGG AGA		
			C C AGC		
GAM2322	ALDH1B1	3'	AGATGAGGTTTCACCATTTTGG 7314	A C	_
	CCA		TG CCAA ATGGTGAAACC CATCT		
			AC GGTT TACCACTTTGG GTAGA		
			C T A		
GAM2322	APAF1	3'	AGACGGGGTTTCACCATGTTGG 8578	A	A_
	CCG		TG CCAACATGGTGAAACCC TCT		
			GC GGTTGTACCACTTTGGG AGA		
			C GC		
GAM2322	APAF1	3'	AGACGGGGTTTCACCATGTTGG 25959	A	A_
	CCG		TG CCAACATGGTGAAACCC TCT		
			GC GGTTGTACCACTTTGGG AGA		
			C GC		
GAM2322	APM1	3'	AGACAGGGTTTCACCATATTGG 17756	A C	A_
	CCA		TG CCAA ATGGTGAAACCC TCT		
			AC GGTT TACCACTTTGGG AGA		
			C A AC		
GAM2322	APM1	3'	AGACGGGGTTTCACCACATTCG 17757	C CA	A_
	TCA		TGAC AA TGGTGAAACCC TCT		
			ACTG TT ACCACTTTGGG AGA		
			C AC GC		
GAM2322	APOL1	3'	AGATGGGGTTTCACCATGTTGG 14726	A	_
	CCA		TG CCAACATGGTGAAACCC ATCT		

			AC GGTGTGACCACTTTGGG TAGA		
			C G		
GAM2322	APPL	3'	AGACGGGGTTTCACCGTGTT 24941	A_	
			AACATGGTGAAACCC TCT		
			TTGTGCCACTTTGGG AGA		
			GC		
GAM2322	AQP6	3'	AGATGGGGTTTCATCATATTGG 9722	C	-
	TCA		TGACCAA ATGGTGAAACCC ATCT		
			ACTGGTT TACTACTTTGGG TAGA		
			A G		
GAM2322	AQP6	3'	AGATGGGGTTTCATCATATTGG 54981	C	-
	TCA		TGACCAA ATGGTGAAACCC ATCT		
			ACTGGTT TACTACTTTGGG TAGA		
			A G		
GAM2322	ARSF	5'	AGACAGGCTCTCACCATGTTG 65207	AA_ CA	
			CAACATGGTGA CC TCT		
			GTTGTACCACT GG AGA		
			CTC AC		
GAM2322	ATM	3'	GGTTTCACCATATTGCCCA 57147	AC C	
			TG CAA ATGGTGAAACC		
			AC GTT TACCACTTTGG		
			CC A		
GAM2322	ATP6V1A1	3'	GGGTTTCACCATATTGGTCA 9872	C	
			TGACCAA ATGGTGAAACCC		
			ACTGGTT TACCACTTTGGG		
			A		
GAM2322	AXL	3'	AGACAGGGTTTCACCATGTTGG 9899	A	A_
	CCA		TG CCAACATGGTGAAACCC TCT		
			AC GGTGTGACCACTTTGGG AGA		
			C AC		
GAM2322	AXL	3'	AGACAGGGTTTCACCATGTTGG 41874	A	A_
	CCA		TG CCAACATGGTGAAACCC TCT		
			AC GGTGTGACCACTTTGGG AGA		
			C AC		
GAM2322	BRIP1	3'	AGATGGGGTTTCACCATGTTGG 50205	A	-
	CCA		TG CCAACATGGTGAAACCC ATCT		
			AC GGTGTGACCACTTTGGG TAGA		
			C G		
GAM2322	C7	3'	AGATGGGGTTTCACCATGTTGGC 6979	A	
	CA		TG CCAACATGGTGAAACCCATCT		

			AC GGTGTGACCACTTTGGGTAGA		
			C		
GAM2322	CAMLG	3'	AGACAGGGTTTCTCCATGTTGG 9995	T	A_
	TCA		TGACCAACATGG GAAACCC TCT		
			ACTGGTTGTACC CTTTGGG AGA		
			T AC		
GAM2322	CASP2	3'	AGACAGGGTTTCACCATGTT 8702	A_	
			AACATGGTGAAACCC TCT		
			TTGTACCACTTTGGG AGA		
			AC		
GAM2322	CASP2	3'	AGACAGGGTTTCACCATGTT 53283	A_	
			AACATGGTGAAACCC TCT		
			TTGTACCACTTTGGG AGA		
			AC		
GAM2322	CASP2	3'	AGACAGGGTTTCACCATGTT 53299	A_	
			AACATGGTGAAACCC TCT		
			TTGTACCACTTTGGG AGA		
			AC		
GAM2322	CASP2	3'	AGACAGGGTTTCACCATGTT 53317	A_	
			AACATGGTGAAACCC TCT		
			TTGTACCACTTTGGG AGA		
			AC		
GAM2322	CCNF	3'	AGACGGGATTTACCATGTTGG 10065	A	_ A
	CCA		TG CCAACATGGTGAAA CCC TCT		
			AC GGTGTGACCACTTT GGG AGA		
			C A C		
GAM2322	CDC6	3'	AGACAGGGTTTTACCATGTTGG 8815	A	A_
	CCA		TG CCAACATGGTGAAACCC TCT		
			AC GGTGTGACCATTTTGGG AGA		
			C AC		
GAM2322	CLECSF11	5'	AGATGGGGTTTCACTATGTTGG 56145	A	_
	CCA		TG CCAACATGGTGAAACCC ATCT		
			AC GGTGTATCACTTTGGG TAGA		
			C G		
GAM2322	CNGA1	5'	AGATGGGATTTACCATGTTGG 60232	A	_
	CCA		TG CCAACATGGTGAAA CCCATCT		
			AC GGTGTGACCACTTT GGGTAGA		
			C A		
GAM2322	CNN2	3'	AGATGGGGTTTCCCATGTTGG 16453	A	T _
	CCA		TG CCAACATGG GAAACCC ATCT		

			AC GGTGTACC CTTTGGG TAGA		
			C C G		
GAM2322	COX15	3'	GGGTTTCACCACATTGGCCG 55287	A CA	
			TG CCAA TGGTGAAACCC		
			GC GGTT ACCACTTTGGG		
			C AC		
GAM2322	CR1	3'	AGACGGGGTTTCACCATGTT 6934	A_	
			AACATGGTGAAACCC TCT		
			TTGTACCACTTTGGG AGA		
			GC		
GAM2322	CXCL16	3'	AGACGGGGTTTCACCATGTTG 42158	A_	
			CAACATGGTGAAACCC TCT		
			GTTGTACCACTTTGGG AGA		
			GC		
GAM2322	CYP1A2	3'	AGACGGGGTTTCACCATGTTGGT 7496	A	
	CA		TGACCAACATGGTGAAACCC TCT		
			ACTGGTTGTACCACTTTGGG AGA		
			C		
GAM2322	CYP1A2	3'	AGATGGGGTTTCACCATGTTGG 7501	A	
	CCA		TG CCAACATGGTGAAACCC ATCT		
			AC GGTGTACCACTTTGGG TAGA		
			C G		
GAM2322	DFFB	3'	AGACGGGGTTTCACCATGTTGG 88756	A_	
	TCA		TGACCAACATGGTGAAACCC TCT		
			ACTGGTTGTACCACTTTGGG AGA		
			GC		
GAM2322	DFFB	3'	GGGTTTCACCATGTTGGCCA 88780	A	
			TG CCAACATGGTGAAACCC		
			AC GGTGTACCACTTTGGG		
			C		
GAM2322	DHFR	3'	AGATGGGGTTTCACCATGTTGG 7640		
	TCA		TGACCAACATGGTGAAACCC ATCT		
			ACTGGTTGTACCACTTTGGG TAGA		
			G		
GAM2322	DISC1	3'	AGACAGGGCTTCACCATGTTGG 38499	A A_	
			CCAACATGGTGAA CCC TCT		
			GGTTGTACCACTT GGG AGA		
			C AC		
GAM2322	DSCR3	3'	AGACGGGGCTTCACCATCTTGG 21306	A C A_ A	
	CCA		TG CCAA ATGGTGAA CCC TCT		

			AC GGTT TACCACTT GGG AGA		
			C C CG C		
GAM2322	EDNRA	3'	AGATGAGTTTATCATGTCAGT 64798	CA	A C
			AC ACATGGTGAA C CATCT		
			TG TGTACTATTT G GTAGA		
			AC _ A		
GAM2322	EHD2	3'	AGACGGGGTTTCACCATGTTGG 28212	A	A_
	CCA		TG CCAACATGGTGAAACCC TCT		
			AC GGTTGTACCACTTTGGG AGA		
			C GC		
GAM2322	EPB72	3'	AGACGGGGTTTCACCATGTTGG 15867	A	A_
	CCA		TG CCAACATGGTGAAACCC TCT		
			AC GGTTGTACCACTTTGGG AGA		
			C GC		
GAM2322	F2RL2	3'	AGACGGGGTTTCACCATGTTG 15890		A_
			CAACATGGTGAAACCC TCT		
			GTTGTACCACTTTGGG AGA		
			GC		
GAM2322	F2RL3	3'	AGACGGAGTTTCACCATGTTGG 15491	A	_ A
	CCA		TG CCAACATGGTGAAAC CC TCT		
			AC GGTTGTACCACTTTG GG AGA		
			C A C		
GAM2322	F3	3'	AGATGGGGTTTCACCATCTTGG 67672	A C	_
	CCA		TG CCAA ATGGTGAAACCC ATCT		
			AC GGTT TACCACTTTGGG TAGA		
			C C G		
GAM2322	FANCF	3'	AGACGGGGTTTCACCATGCTGG 42972	A A	A_
	CCA		TG CCA CATGGTGAAACCC TCT		
			AC GGT GTACCACTTTGGG AGA		
			C C GC		
GAM2322	FCAR	3'	AGACAGGGTTTCACCATGTTGG 56630	A	A_
	CCA		TG CCAACATGGTGAAACCC TCT		
			AC GGTTGTACCACTTTGGG AGA		
			C AC		
GAM2322	FEZ1	3'	AGATGGGAGTTTCACCATGTTG 42866	A	—
	GCCA		TG CCAACATGGTGAAA CCCATCT		
			AC GGTTGTACCACTTT GGGTAGA		
			C GA		
GAM2322	FGF5	3'	AGACGGGGTTTCACCATGTTGG 16756		A_
	TCA		TGACCAACATGGTGAAACCC TCT		

			ACTGGTTGTACCACTTTGGG AGA	
			GC	
GAM2322	FGF5	3'	AGACGGGGTTTCACCATGTTGG 53649	A_
	TCA		TGACCAACATGGTGAAACCC TCT	
			ACTGGTTGTACCACTTTGGG AGA	
			GC	
GAM2322	FUT1	3'	AGACAGGGTTTCACCATGTTGG 5579 A	A_
	CCG		TG CCAACATGGTGAAACCC TCT	
			GC GGTGTACCACTTTGGG AGA	
			C AC	
GAM2322	G6PC	3'	AGATGGGATTTCATCATGTTGG 5652 A	_
	CCA		TG CCAACATGGTGAAA CCCATCT	
			AC GGTGTACTACTTT GGGTAGA	
			C A	
GAM2322	GHR	3'	AGACGGGGTTTCACCATGTTGG 5690 A	A_
	CCA		TG CCAACATGGTGAAACCC TCT	
			AC GGTGTACCACTTTGGG AGA	
			C GC	
GAM2322	GM2A	3'	AGATGGGGTTTCACCATGTTGG 68373 A	_
	CCA		TG CCAACATGGTGAAACCC ATCT	
			AC GGTGTACCACTTTGGG TAGA	
			C G	
GAM2322	GNE	3'	GGGTTTCACCATGTTGGCCA 19675 A	
			TG CCAACATGGTGAAACCC	
			AC GGTGTACCACTTTGGG	
			C	
GAM2322	GRM7	5'	AGATTGGGTTTCACCATGTTGG 7781 A	_
	CCA		TG CCAACATGGTGAAACCCA TCT	
			AC GGTGTACCACTTTGGGT AGA	
			C T	
GAM2322	HCS	3'	AGATGGTGTTCACCATGTTGG 38964 A	_
	CCA		TG CCAACATGGTGAAAC CCATCT	
			AC GGTGTACCACTTTG GGTAGA	
			C T	
GAM2322	HDC	3'	AGATGGGTTTCATCAGTCTGGTC 10920 ACA	A
	A		TGACCA TGGTGAA CCCATCT	
			ACTGGT ACTACTT GGGTAGA	
			CTG _	
GAM2322	HTR1D	3'	AGACGGGGTTTCATCATGTTGG 7837 A	A_
	CCA		TG CCAACATGGTGAAACCC TCT	

			AC GGTGTACTACTTTGGG AGA		
			C GC		
GAM2322	HTR1E	5'	AGACGGGATTTACCATGTTGG 7856 A	_	A
	CCA		TG CCAACATGGTGAAA CCC TCT		
			AC GGTGTACCACTTT GGG AGA		
			C A C		
GAM2322	HYAL4	5'	AGATGGGGTTTCACCGTGTGG 25363 A	_	
	CCA		TG CCAACATGGTGAAACCC ATCT		
			AC GGTGTGCCACTTTGGG TAGA		
			C G		
GAM2322	IFNAR2	3'	AGACAGGATTTTACCATGTTGG 7895 A	_	CA
	CCA		TG CCAACATGGTGAAA CC TCT		
			AC GGTGTACCATTTT GG AGA		
			C A AC		
GAM2322	IGF1	3'	AGACGGGGTTTTACCATGTTGG 7058 A	A_	
	CCA		TG CCAACATGGTGAAACCC TCT		
			AC GGTGTACCATTTTGGG AGA		
			C GC		
GAM2322	IL11	3'	AGACAGGGTTTCACCATGTTGG 7176 A	A_	
	CCA		TG CCAACATGGTGAAACCC TCT		
			AC GGTGTACCACTTTGGG AGA		
			C AC		
GAM2322	INMT	3'	AGATATGGGGTTTCACCGTGT 23206	—	
			AACATGGTGAAACCC ATCT		
			TTGTGCCACTTTGGG TAGA		
			GTA		
GAM2322	JAK3	3'	AGATGAGGTTTCACCATGATGG 5825 A A	_	
	CCA		TG CCA CATGGTGAAACC CATCT		
			AC GGT GTACCACTTTGG GTAGA		
			C A A		
GAM2322	LLGL1	3'	AGATGGGGTTTCACCATGTT 67412	_	
			AACATGGTGAAACCC ATCT		
			TTGTACCACTTTGGG TAGA		
			G		
GAM2322	LNK	3'	AGACAGGGTTTCACCATGTTGG 19630 A	A_	
	CCA		TG CCAACATGGTGAAACCC TCT		
			AC GGTGTACCACTTTGGG AGA		
			C AC		
GAM2322	LTB4R	5'	AGACGGGGTTTCACCATGTTGG 7458 A	A_	
	CCA		TG CCAACATGGTGAAACCC TCT		

			AC GGTGTGACCACTTTGGG AGA	
			C GC	
GAM2322	LYZ	3'	AGACAGGGTTTCACCGTGTT 5890	A_
			AACATGGTGAAACCC TCT	
			TTGTGCCACTTTGGG AGA	
			AC	
GAM2322	MAK	3'	AGACAGGGTTTCACCATGTTGG 20939	A_
	TCA		TGACCAACATGGTGAAACCC TCT	
			ACTGGTTGTACCACTTTGGG AGA	
			AC	
GAM2322	MDM2	3'	AGACAGGGTTTCACCGTGTT 11489	A_
			AACATGGTGAAACCC TCT	
			TTGTGCCACTTTGGG AGA	
			AC	
GAM2322	MDM2	3'	AGACAGGGTTTCACCGTGTT 23455	A_
			AACATGGTGAAACCC TCT	
			TTGTGCCACTTTGGG AGA	
			AC	
GAM2322	MDM2	3'	AGACAGGGTTTCACCGTGTT 23468	A_
			AACATGGTGAAACCC TCT	
			TTGTGCCACTTTGGG AGA	
			AC	
GAM2322	MDM2	3'	AGACAGGGTTTCACCGTGTT 23481	A_
			AACATGGTGAAACCC TCT	
			TTGTGCCACTTTGGG AGA	
			AC	
GAM2322	MDM2	3'	AGACAGGGTTTCACCGTGTT 23494	A_
			AACATGGTGAAACCC TCT	
			TTGTGCCACTTTGGG AGA	
			AC	
GAM2322	MEF2A	5'	AGATGGAGTTTCACCATGTTGG 19990	A
	CCA		TG CCAACATGGTGAAAC CCATCT	_
			AC GGTGTGACCACTTTG GG TAGA	
			C A	
GAM2322	MEFV	3'	GGTTTCATCATGTTGGCCA 5943	A
			TG CCAACATGGTGAAACC	
			AC GGTGTACTACTTTGG	
			C	
GAM2322	MF12	3'	GGTCTCACCATGTTGCCCA 53973	AC A
			TG CAACATGGTGACC	

			AC GTTGTACCACT TGG			
			CC C			
GAM2322 MLANA	3'	AGACGGGGTTTCTCCATGTTGG 19757		T	A_	
	TCA		TGACCAACATGG GAAACCC TCT			
			ACTGGTTGTACC CTTTGGG AGA			
			T GC			
GAM2322 MPL	3'	AGACCGGTTTTACCACGTTGG 19337	A A		_ CA	
	CCA		TG CCAAC TGGTGAAA CC TCT			
			AC GGTG ACCACTTT GG AGA			
			C C T CC			
GAM2322 MRPL49	3'	AGATGGGGTTTCACCATGTTGG 70159	A		_	
	CCA		TG CCAACATGGTGAAACCC ATCT			
			AC GGTGTACCACTTTGGG TAGA			
			C G			
GAM2322 MYCL2	3'	AGATGGGGTTTCACCACATTGG 19369	A CA		_	
	CCA		TG CCAA TGGTGAAACCC ATCT			
			AC GGTT ACCACTTTGGG TAGA			
			C AC G			
GAM2322 NCOA6	5'	GGTTTCATCATGTTGGCCA 26842	A			
			TG CCAACATGGTGAAACC			
			AC GGTGTACTACTTTGG			
			C			
GAM2322 NCOA6IP	3'	AGACGAGGTCCCACCATGTTGC 46150	AC		AA CA_	
	CCA		TG CAACATGGTG ACC TCT			
			AC GTTGTACCAC TGG AGA			
			CC CC AGC			
GAM2322 NDRG3	3'	AGATGGAGTTTCACCATGTTGG 50116	A		_	
	CCA		TG CCAACATGGTGAAAC CCATCT			
			AC GGTGTACCACTTTG GG TAGA			
			C A			
GAM2322 NQO1	3'	AGACGGCGTTTCACCATGTTGG 8041	A		_ A	
	CCA		TG CCAACATGGTGAAAC CC TCT			
			AC GGTGTACCACTTTG GG AGA			
			C C C			
GAM2322 NRCAM	3'	ATGAGTTCATTATGACAGTCA 18454	CAA		A C	
			TGAC CATGGTGAA C CAT			
			ACTG GTATTACTT G GTA			
			ACA _ A			
GAM2322 ORC1L	3'	AGACAGGGCTTCACCATGTTG 15978	A A_			
			CAACATGGTGAA CCC TCT			

		GTTGTACCACTT GGG AGA			
		C AC			
GAM2322	PCDHA9	3'	AGATGGGGTTTCACCGTGTAG 26608	C	—
	TCA		TGAC AACATGGTCAAACCC ATCT		
		ACTG TTGTGCCACTTTGGG TAGA			
		A G			
GAM2322	PCDHA9	3'	AGATGGGGTTTCATCATGTTGG 26610	A	—
	CCA		TG CCAACATGGTCAAACCC ATCT		
		AC GGTGTACTACTTTGGG TAGA			
		C G			
GAM2322	PCDHB11	3'	AGACGGGGTTTCACCACGTTGG 38915	A A	A_
	CCG		TG CCAAC TGGTCAAACCC TCT		
		GC GGTG ACCACTTTGGG AGA			
		C C GC			
GAM2322	PCDHB9	3'	AGACGGGGTTTCATCATGGTGGC 39435	A A	A
	CA		TG CCA CATGGTCAAACCC TCT		
		AC GGT GTACTACTTTGGG AGA			
		C G C			
GAM2322	PDE6B	3'	AGATGGGGTTTCACCATATTGG 6069	C	—
			CCAA ATGGTCAAACCC ATCT		
		GGTT TACCACTTTGGG TAGA			
		A G			
GAM2322	PER2	3'	AGACAGGGTTTCACCATGTTGG 43341	A	A_
	CCA		TG CCAACATGGTCAAACCC TCT		
		AC GGTGTACCACTTTGGG AGA			
		C AC			
GAM2322	PIGR	3'	AGACAGGGTTTCACCGTGTT 72985	A_	
			AACATGGTCAAACCC TCT		
		TTGTGCCACTTTGGG AGA			
		AC			
GAM2322	PIK3C2B	3'	AGACGGGGTTTCACCATGTTGG 12089	A	A_
	CCA		TG CCAACATGGTCAAACCC TCT		
		AC GGTGTACCACTTTGGG AGA			
		C GC			
GAM2322	PMCHL1	3'	GGTTTCACCATCTTGGTCA 49919	C	
			TGACCAA ATGGTCAAACC		
		ACTGGTT TACCACTTTGG			
		C			
GAM2322	POU2AF1	3'	AGACGGGGTTTCACCATGTTGG 21730	A	A_
	CCA		TG CCAACATGGTCAAACCC TCT		

			AC GGTGTGACCACTTTGGG AGA		
			C GC		
GAM2322	PPEF2	3'	GGGTTTCTCCATGTTGGTCA 21776	T	
			TGACCAACATGG GAAACCC		
			ACTGGTTGTACC CTTTGGG		
			T		
GAM2322	PPID	3'	AGATGGGGTTTCACCATATTGG 88819	C	—
	TCA		TGACCAA ATGGTGAAACCC ATCT		
			ACTGGTT TACCACTTTGGG TAGA		
			A G		
GAM2322	PRKR	3'	AGACAGGGTTTCACCATGTTGG 12343	A	A_
	CCA		TG CCAACATGGTGAAACCC TCT		
			AC GGTGTGACCACTTTGGG AGA		
			C AC		
GAM2322	PRKWNK3	3'	GGTTTCACTATGTTGGCCA 62236	A	
			TG CCAACATGGTGAAACC		
			AC GGTGTATCACTTTGG		
			C		
GAM2322	PSMB2	3'	AGACAGGGTCTCACCATGTCAT 12459	CCA	A A_
	TCA		TGA ACATGGTGA ACCC TCT		
			ACT TGTACCACT TGGG AGA		
			TAC C AC		
GAM2322	PTGES	3'	AGACGGGTTTCACCATGTTGCCC 18054	AC	A A
	A		TG CAACATGGTGAA CCC TCT		
			AC GTTGTACCACTT GGG AGA		
			CC — C		
GAM2322	PTGIS	3'	AGACGGGGTTTCCCCATGTTGG 8189	T	A_
	TCA		TGACCAACATGG GAAACCC TCT		
			ACTGGTTGTACC CTTTGGG AGA		
			C GC		
GAM2322	PTPN18	3'	ATGAGTTTTTTGCCATGTTGCCC 27648	AC	TG _ C
	A		TG CAACATGG AAA C CAT		
			AC GTTGTACC TTT G GTA		
			CC GT T A		
GAM2322	RAB36	3'	AGATGGGGTTTCTCCATGTTGG 18154	T	—
	TCA		TGACCAACATGG GAAACCC ATCT		
			ACTGGTTGTACC CTTTGGG TAGA		
			T G		
GAM2322	RABL2A	3'	AGACGGGGTTTTCACCATGTTGC 26403	AC	A_
	CCA		TG CAACATGGTGAAACCC TCT		

			AC GTTGTACCACTTTGGG AGA		
			CC GC		
GAM2322	RABL2B	3'	AGACGGGGTTTCACCATGTTGC 23971	AC	A_
	CCA		TG CAACATGGTGAAACCC TCT		
			AC GTTGTACCACTTTGGG AGA		
			CC GC		
GAM2322	RBBP9	3'	AGACAGGGTTTCACCATGTTGG 70679	A	A_
	CCA		TG CCAACATGGTGAAACCC TCT		
			AC GGTGTACCACTTTGGG AGA		
			C AC		
GAM2322	RHD	3'	AGATGGGGTTTCACCATGTTGG 32814	A	_
	CCA		TG CCAACATGGTGAAACCC ATCT		
			AC GGTGTACCACTTTGGG TAGA		
			C G		
GAM2322	RHD	3'	AGATGGGGTTTCACCATGTTGG 33134	A	_
	CCA		TG CCAACATGGTGAAACCC ATCT		
			AC GGTGTACCACTTTGGG TAGA		
			C G		
GAM2322	RPH3AL	3'	AGATGGGGTTTCTCCATGTTGG 23728	A T	_
	CCA		TG CCAACATGG GAAACCC ATCT		
			AC GGTGTACC CTTTGGG TAGA		
			C T G		
GAM2322	RPP30	3'	AGACGGGGTTTCACCGTGTT 22189	A_	
			AACATGGTGAAACCC TCT		
			TTGTGCCACTTTGGG AGA		
			GC		
GAM2322	SAS	3'	AGACAGGGTTTCACCATGTTAG 21094	C	A_
	TCA		TGAC AACATGGTGAAACCC TCT		
			ACTG TTGTACCACTTTGGG AGA		
			A AC		
GAM2322	SCML2	3'	AGATGGGGTTTCTCCATGTTGG 21422	T	_
	TCA		TGACCAACATGG GAAACCC ATCT		
			ACTGGTTGTACC CTTTGGG TAGA		
			T G		
GAM2322	SED1	3'	AGACAGGGTTTCACCATATTGG 28075	C	A_
	TCA		TGACCAA ATGGTGAAACCC TCT		
			ACTGGTT TACCACTTTGGG AGA		
			A AC		
GAM2322	SED1	3'	AGACAGGGTTTCACCATATTGG 28076	C	A_
	TCA		TGACCAA ATGGTGAAACCC TCT		

			ACTGGTT TACCACTTTGGG AGA		
			A AC		
GAM2322	SEPN1	3'	AGATGGGGTTTCACCATATTGG 66959	C	—
	TCA		TGACCAA ATGGTGAAACCC ATCT		
			ACTGGTT TACCACTTTGGG TAGA		
			A G		
GAM2322	SERPINB9	3'	AGACGGGGTTTCACCGTGTT 16007	A_	
			AACATGGTGAAACCC TCT		
			TTGTGCCACTTTGGG AGA		
			GC		
GAM2322	SH3BP2	3'	GGTTTCACCATGTTGGCCA 13082	A	
			TG CCAACATGGTGAAACC		
			AC GGTTGTACCACTTTGG		
			C		
GAM2322	SH3GL3	5'	AGATGGGGTTTCACCATGTTGGC 13103	A	
	CA		TG CCAACATGGTGAAACCCATCT		
			AC GGTTGTACCACTTTGGGTAGA		
			C		
GAM2322	SHOX	3'	AGACGGCGTTTCACCGTGTTGG 6560	A	— A
	CCA		TG CCAACATGGTGAAAC CC TCT		
			AC GGTTGTGCCACTTTG GG AGA		
			C C C		
GAM2322	SHOX	3'	AGATGGGGTTTGACCATGTTGG 23514	A	G —
	CCA		TG CCAACATGGT AAACCC ATCT		
			AC GGTTGTACCA TTTGGG TAGA		
			C G G		
GAM2322	SIL	5'	AGACGGGGTTTCACCATGTTGG 13151	A_	
	TC		GACCAACATGGTGAAACCC TCT		
			CTGGTTGTACCACTTTGGG AGA		
			GC		
GAM2322	SIL	3'	AGACTGGTTTCTCCATGTTGGT 13152	T CA	
	CA		TGACCAACATGG GAAACC TCT		
			ACTGGTTGTACC CTTTGG AGA		
			T TC		
GAM2322	SLA2	3'	GGGTTTCACCACATTGGCCA 50892	A CA	
			TG CCAA TGGTGAAACCC		
			AC GGTT ACCACTTTGGG		
			C AC		
GAM2322	SLC14A2	5'	AGACGGGGTTTCACCACATTGG 24108	A CA A_	
	CCA		TG CCAA TGGTGAAACCC TCT		

			AC GGTT ACCACTTTGGG AGA		
			C AC GC		
GAM2322	SLC15A1	3'	AGATGGGGTTTCACCATGTT 18634	—	
			AACATGGTGAAACCC ATCT		
			TTGTACCACTTTGGG TAGA		
			G		
GAM2322	SMAC	5'	AGATGGGGTTTCACCATGTTGG 58013	—	
	TCA		TGACCAACATGGTGAAACCC ATCT		
			ACTGGTTGTACCACTTTGGG TAGA		
			G		
GAM2322	SNX15	3'	GGTTACACCATGTTGGCCA 74128 A A		
			TG CCAACATGGTG AACC		
			AC GGTTGTACCAC TTGG		
			C A		
GAM2322	SPN	3'	AGATGGGGTTTCACCATGTTGG 13367	—	
			CCAACATGGTGAAACCC ATCT		
			GGTTGTACCACTTTGGG TAGA		
			G		
GAM2322	SRGAP2	3'	AGACAGGTTTTTCATTATCAGGT 75104 AAC	—	CA
	CA		TGACC ATGGTGAAA CC TCT		
			ACTGG TATTACTTT GG AGA		
			AC_ T AC		
GAM2322	SULT2B1	5'	GGTTTCACCATGTTGGCCA 17224 A		
			TG CCAACATGGTGAAACC		
			AC GGTTGTACCACTTTGG		
			C		
GAM2322	TAPBP	3'	AGACGGGGTTTCACCATGTTGG 13545 A		A_
	CCA		TG CCAACATGGTGAAACCC TCT		
			AC GGTTGTACCACTTTGGG AGA		
			C GC		
GAM2322	TAPBP	3'	AGACGGGGTTTCACCGTGTT 13546		A_
			AACATGGTGAAACCC TCT		
			TTGTGCCACTTTGGG AGA		
			GC		
GAM2322	TAPBP	3'	AGACGGGGTTTCACCGTGTT 13547		A_
			AACATGGTGAAACCC TCT		
			TTGTGCCACTTTGGG AGA		
			GC		
GAM2322	TAT	3'	AGACAGGGTTTCACCATGTT 6247		A_
			AACATGGTGAAACCC TCT		

			TTGTACCACTTTGGG AGA		
			AC		
GAM2322	TBXA2R	3'	AGACGGGGTTTCACCGTGTGG 8341	A	A_
	CCA		TG CCAACATGGTGAAACCC TCT		
			AC GGTTGTGCCACTTTGGG AGA		
			C GC		
GAM2322	TDGF1	3'	AGATGGGGTTTCACCATATTG 13651	A C	—
	GCCA		TG CCAA ATGGTGAAACCC ATCT		
			AC GGTT TACCACTTTGGG TAGA		
			C A GG		
GAM2322	TERF1	3'	GGTTTCACCATGCTGGTCA 34396	A	
			TGACCA CATGGTGAAACC		
			ACTGGT GTACCACTTTGG		
			C		
GAM2322	TERF2	3'	AGACGGGGTTTCACCGTGT 20143	A_	
			AACATGGTGAAACCC TCT		
			TTGTGCCACTTTGGG AGA		
			GC		
GAM2322	TES	3'	AGACAGGTTTTTCACCATGTT 72458	_ CA	
			AACATGGTGAAA CC TCT		
			TTGTACCACTTT GG AGA		
			T AC		
GAM2322	TIM3	3'	AGACAGGGTTTCACCATGTTGG 52349	A	A_
	CCA		TG CCAACATGGTGAAACCC TCT		
			AC GGTTGTACCACTTTGGG AGA		
			C AC		
GAM2322	TMPRSS3	3'	AGACAGGGTTTCACCATGTTGG 51510	A	A_
	CCA		TG CCAACATGGTGAAACCC TCT		
			AC GGTTGTACCACTTTGGG AGA		
			C AC		
GAM2322	TMPRSS3	3'	AGACAGGGTTTCACCATGTTGG 51538	A	A_
	CCA		TG CCAACATGGTGAAACCC TCT		
			AC GGTTGTACCACTTTGGG AGA		
			C AC		
GAM2322	TMPRSS3	3'	AGACAGGGTTTCACCATGTTGG 44013	A	A_
	CCA		TG CCAACATGGTGAAACCC TCT		
			AC GGTTGTACCACTTTGGG AGA		
			C AC		
GAM2322	TNFRSF10B	3'	AGACGGGGTTTCACCATGTTGG 15213	A_	
	TCA		TGACCAACATGGTGAAACCC TCT		

		ACTGGTTGTACCACTTTGGG AGA	
		GC	
GAM2322	TNFRSF11A 3'	AGACACGGTCCCACCATGTT 15184	AA CA_
		AACATGGTG ACC TCT	
		TTGTACCAC TGG AGA	
		CC CAC	
GAM2322	TP53BP2 5'	AGATAGAGTTTCATCATGTTGG 19458 A	CC_
	CCA	TG CCAACATGGTGAAAC ATCT	
		AC GGTTGTACTACTTTG TAGA	
		C AGA	
GAM2322	TPMT 3'	AGACGGGGTTTCACCATGTTGG 6303	A_
	TCA	TGACCAACATGGTGAAACCC TCT	
		ACTGGTTGTACCACTTTGGG AGA	
		GC	
GAM2322	TRIM9 5'	AGACGGGGTTTCACCATACTGG 31439 AC	A_
		CCA ATGGTGAAACCC TCT	
		GGT TACCACTTTGGG AGA	
		CA GC	
GAM2322	TRPM6 3'	AGATGGGGTTTCACCATGTTGG 35025 A	_
	CCA	TG CCAACATGGTGAAACCC ATCT	
		AC GGTTGTACCACTTTGGG TAGA	
		C G	
GAM2322	TRPV1 3'	AGACGGGGTTTCACCATGTTGG 38684 A	A_
	CCA	TG CCAACATGGTGAAACCC TCT	
		AC GGTTGTACCACTTTGGG AGA	
		C GC	
GAM2322	TRPV1 3'	AGATATGGGGTTTCGCCATGTT 38687 A	___
	GGCCA	TG CCAACATGGTGAAACCC ATCT	
		AC GGTTGTACCGCTTTGGG TAGA	
		C GTA	
GAM2322	TRPV1 3'	AGACGGGGTTTCACCATGTTGG 55654 A	A_
	CCA	TG CCAACATGGTGAAACCC TCT	
		AC GGTTGTACCACTTTGGG AGA	
		C GC	
GAM2322	TRPV1 3'	AGATATGGGGTTTCGCCATGTT 55657 A	___
	GGCCA	TG CCAACATGGTGAAACCC ATCT	
		AC GGTTGTACCGCTTTGGG TAGA	
		C GTA	
GAM2322	TRPV1 3'	AGACGGGGTTTCACCATGTTGG 55700 A	A_
	CCA	TG CCAACATGGTGAAACCC TCT	

				AC GGTGTACCACTTTGGG AGA		
				C GC		
GAM2322	TRPV1	3'	AGATATGGGGTTTCGCCATGTT 55703	A		_____
			GGCCA TG CCAACATGGTGAAACCC ATCT			
			AC GGTGTACCGCTTTGGG TAGA			
			C GTA			
GAM2322	TRPV1	3'	AGACGGGGTTTCACCATGTTGG 55731	A		A_
			CCA TG CCAACATGGTGAAACCC TCT			
			AC GGTGTACCACTTTGGG AGA			
			C GC			
GAM2322	TRPV1	3'	AGATATGGGGTTTCGCCATGTT 55734	A		_____
			GGCCA TG CCAACATGGTGAAACCC ATCT			
			AC GGTGTACCGCTTTGGG TAGA			
			C GTA			
GAM2322	TUFT1	3'	AGATGGGGTTTCACCATACTGG 39666	AC		_
			CCA ATGGTGAAACCC ATCT			
			GGT TACCACTTTGGG TAGA			
			CA G			
GAM2322	UGDH	3'	AGACAGGGTTTCACCATGT 13989	A_		
			ACATGGTGAAACCC TCT			
			TGTACCACTTTGGG AGA			
			AC			
GAM2322	VHL	3'	AGACAGTGTTCGCCATGTTGG 6825	A		CCA_
			CCA TG CCAACATGGTGAAAC TCT			
			AC GGTGTACCGCTTTG AGA			
			C TGAC			
GAM2322	VHL	3'	AGACGGGGTTTCACCATGTTGT 6828	AC		A_
			CCA TG CAACATGGTGAAACCC TCT			
			AC GTTGTACCACTTTGGG AGA			
			CT GC			
GAM2322	VIPR2	3'	AGACAGGGTTTCACCATGTT 14055	A_		
			AACATGGTGAAACCC TCT			
			TTGTACCACTTTGGG AGA			
			AC			
GAM2322	WASF3	3'	AGATGGCACCTTTCACCACTTG 22810	CA		C_____
			GTCA TGACCAA TGGTGAAA CCATCT			
			ACTGGTT ACCACTTT GG TAGA			
			C_ CCAC			
GAM2322	WHSC1	3'	AGACAGGGTTTCGCCATATTGG 56687	A C		A_
			CCA TG CCAA ATGGTGAAACCC TCT			

			AC GGT TACCGCTTTGGG AGA		
			C A AC		
GAM2322	XRCC2	3'	AGACGGGGTTTCACCATGTTGG 19490	A	A_
	CCA		TG CCAACATGGTGAACCC TCT		
			AC GGTGTACCACTTTGGG AGA		
			C GC		
GAM2322	YES1	3'	AGACGCAGTTTCACCGTGTT 19526	CCA_	
			AACATGGTGAAC TCT		
			TTGTGCCACTTTG AGA		
			ACGC		
GAM2322	ZNF157	3'	AGACGGGGTTTCACCATGTTGGC 14326	A	A
	CA		TG CCAACATGGTGAACCC TCT		
			AC GGTGTACCACTTTGGG AGA		
			C C		
GAM2322	ZNF264	3'	AGACGGGGTTTCACCATCTTGG 14189	A C	A_
	CCA		TG CCAA ATGGTGAACCC TCT		
			AC GGT TACCACTTTGGG AGA		
			C C GC		
GAM2322	ZNF264	3'	AGACGGGGTTTCACCATGTTGC 14192	C	A_
	TCA		TGA CAACATGGTGAACCC TCT		
			ACT GTTGTACCACTTTGGG AGA		
			C GC		
GAM2322	AAK1	3'	AGATGGGGTTTCTCCATGTTGG 30515	T	_
	TCA		TGACCAACATGG GAAACCC ATCT		
			ACTGGTTGTACC CTTTGGG TAGA		
			T G		
GAM2322	AP3S2	3'	AGACAGGGTTTCACCATGTTGG 20641	A	A_
	CCA		TG CCAACATGGTGAACCC TCT		
			AC GGTGTACCACTTTGGG AGA		
			C AC		
GAM2322	ARHF	3'	AGACAGGGTTTCACCATGTTGG 39260	A	A_
	CCA		TG CCAACATGGTGAACCC TCT		
			AC GGTGTACCACTTTGGG AGA		
			C AC		
GAM2322	ARHGAP11A	3'	AGACGGTTTCACCGTGTT 29440	CA	
			AACATGGTGAAC TCT		
			TTGTGCCACTTTGG AGA		
			C_		
GAM2322	ASB16	3'	AGACGGGGTCTCGCCATGTTGG 55970	A	A A_
	CCA		TG CCAACATGGTGA ACCC TCT		

			AC GGTGTACCGCT TGGG AGA		
			C C GC		
GAM2322 ASE-1	3'	AGATGGGGTTTCACCACGTT	24966	A	—
		AAC TGGTGAAACCC ATCT			
		TTG ACCACTTTGGG TAGA			
		C G			
GAM2322 ASE-1	3'	GGGTTTCACCATATTGGCCA	24986	A C	
		TG CCAA ATGGTGAAACCC			
		AC GGTT TACCACTTTGGG			
		C A			
GAM2322 ATP1B4	3'	AGACAGGGTTTCACCATGTTGG	24832	A	A_
CCA		TG CCAACATGGTGAAACCC TCT			
		AC GGTGTACCACTTTGGG AGA			
		C AC			
GAM2322 BA108L7.2	3'	AGATGGGGGTTTCACCATGTTG	49065	A	—
GCCA		TG CCAACATGGTGAAACCC ATCT			
		AC GGTGTACCACTTTGGG TAGA			
		C GG			
GAM2322 BNIP-S	3'	AGACGGGGTTTCACCATGTTGG	57085	A	A_
CCA		TG CCAACATGGTGAAACCC TCT			
		AC GGTGTACCACTTTGGG AGA			
		C GC			
GAM2322 BTN3A1	3'	AGATGAGGGTTCACTATGTTGG	23883	A	A _
CCA		TG CCAACATGGTGAA CC CATCT			
		AC GGTGTATCACTT GG GTAGA			
		C G A			
GAM2322 C11orf17	3'	AGACGGGGTTTAACCATGTTGG	40574	A	G A_
CCA		TG CCAACATGGT AAACCC TCT			
		AC GGTGTACCA TTTGGG AGA			
		C A GC			
GAM2322 C13orf1	3'	AGATGGGGTTTCACCATGTTGT	40351	AC	—
CCA		TG CAACATGGTGAAACCC ATCT			
		AC GTTGTACCACTTTGGG TAGA			
		CT G			
GAM2322 C1orf16	5'	AGATGAGCAGCTATGTTGG	29909	GAAACC	
		CCAACATGGT CATCT			
		GGTTGTATCG GTAGA			
		ACGA_			
GAM2322 C1orf24	3'	AGATGGGGTTTCACCATGTTGG	54780	A	—
CCA		TG CCAACATGGTGAAA CCCATCT			

			AC GGTGTACCACTTT GGGTAGA		
			C T		
GAM2322	C1QTNF6	3'	AGATGGGGTTTCACCATATTGG 49984	A C	_
	CCA		TG CCAA ATGGTGAAACCC ATCT		
			AC GGTT TACCACTTTGGG TAGA		
			C A G		
GAM2322	C20orf142	3'	AGATGGGGTTTCTCCATGTTGG 75271	T	_
	TCA		TGACCAACATGG GAAACCC ATCT		
			ACTGGTTGTACC CTTTGGG TAGA		
			T G		
GAM2322	C21orf25	3'	ATGGAGTCTCACCATGTTGGTC 64282	A	_
	A		TGACCAACATGGTGA AC CCAT		
			ACTGGTTGTACCACT TG GGTA		
			C A		
GAM2322	C21orf93	3'	AGACAGGCCCTGCTGTGTCCGT 59744	CA	AAA CA
	CA		TGAC ACATGGTG CC TCT		
			ACTG TGTGTCGT GG AGA		
			CC CCC AC		
GAM2322	C3F	3'	GGGATTTCACCACGTTGGCCA 20478	A A	_
			TG CCAAC TGGTGAAA CCC		
			AC GGTTG ACCACTTT GGG		
			C C A		
GAM2322	C6orf5	3'	AGACAGGGTTTCATATTGGCCA 31966	A	CATG A_
			TG CCAA GTGAAACCC TCT		
			AC GGTT TACTTTGGG AGA		
			C A__ AC		
GAM2322	C9orf14	5'	GGTTTCACCCTGTTGGCCA 87960	A	T
			TG CCAACA GGTGAAACC		
			AC GGTTGT CCACTTTGG		
			C C		
GAM2322	CARD6	3'	GGGTTTCTCCATGTTGGTCA 51845		T
			TGACCAACATGG GAAACCC		
			ACTGGTTGTACC CTTTGGG		
			T		
GAM2322	CCRN4L	3'	AGACGGGGTTTCACCGTGTT 25065		A_
			AACATGGTGAAACCC TCT		
			TTGTGCCACTTTGGG AGA		
			GC		
GAM2322	CDC14B	3'	AGACAGGGTTTCACCATGTTGG 53998	A	A_
	CCA		TG CCAACATGGTGAAACCC TCT		

			AC GGTGTACCACTTTGGG AGA		
			C AC		
GAM2322	CHRA1	3'	AGACGGGGTTCACCATGTTGGC 34330	A	A A
	CA		TG CCAACATGGTGAA CCC TCT		
			AC GGTGTACCACTT GGG AGA		
			C G C		
GAM2322	CIP29	3'	AGACGGGGTTTCACCATGTTGC 51369	AC	A_
	CCA		TG CAACATGGTGAAACCC TCT		
			AC GTTGTACCACTTTGGG AGA		
			CC GC		
GAM2322	CPSF2	3'	AGACAGGGTTTCACCATGTTGG 62258	A	A_
	CCA		TG CCAACATGGTGAAACCC TCT		
			AC GGTGTACCACTTTGGG AGA		
			C AC		
GAM2322	DBR1	3'	GGGTTTCACCGTGTGGCCA 33069	A	
			TG CCAACATGGTGAAACCC		
			AC GGTGTGCCACTTTGGG		
			C		
GAM2322	DKFZP434C212	3'	GGGTTTCACCATGTTGGCCA 69495	A	
			TG CCAACATGGTGAAACCC		
			AC GGTGTACCACTTTGGG		
			C		
GAM2322	DKFZP434D146	3'	AGACAGGGTTTCATCATGTTGG 32130	A	A_
	CCA		TG CCAACATGGTGAAACCC TCT		
			AC GGTGTACTACTTTGGG AGA		
			C AC		
GAM2322	DKFZP434F0318	3'	AGACAGGGTTTCGCCATGTTGG 48742	A	A_
	CCA		TG CCAACATGGTGAAACCC TCT		
			AC GGTGTACCGCTTTGGG AGA		
			C AC		
GAM2322	DKFZp434F1719	3'	AGATGGGATTTCGCCATGTTGG 51010	A	_
	CCA		TG CCAACATGGTGAAA CCCATCT		
			AC GGTGTACCGCTTT GGGTAGA		
			C A		
GAM2322	DKFZP434J037	3'	AGACAGGGTTTCTCCATGTTGG 48938		T A_
	TCA		TGACCAACATGG GAAACCC TCT		
			ACTGGTTGTACC CTTTGGG AGA		
			T AC		
GAM2322	DKFZp547H025	3'	AGATGAGGTTTCACCATGTTGG 39769	A	_
	CCA		TG CCAACATGGTGAAACC CATCT		

			AC GGTGTGACCACTTTGG GTAGA		
			C A		
GAM2322	DKFZP564G092 5'	AGACAGGATTTACCATGTTGG 32150	A		_ CA
	CCA	TG CCAACATGGTGAAA CC TCT			
		AC GGTGTGACCACTTT GG AGA			
		C A AC			
GAM2322	DKFZP564O0523 3'	AGATGGGTTTTACCATATTGG 50416	C		_
	TCA	TGACCAA ATGGTGAAA CCCATCT			
		ACTGGTT TACCACTTT GGGTAGA			
		A T			
GAM2322	DKFZp761F2014 3'	GGTTTCACCATGCGATCA 39941	CCAA		
		TGA CATGGTGAAACC			
		ACT GTACCACTTTGG			
		AGC_			
GAM2322	DKFZp761J139 5'	AGATGGGGTTTGACCATGTTGG 51098	A	G	_
	CCA	TG CCAACATGGT AAACCC ATCT			
		AC GGTGTACCA TTTGGG TAGA			
		C G G			
GAM2322	DKFZp761N1114 3'	AGACGGGATTTACCGTGTT 79773		_ A	
		AACATGGTGAAA CCC TCT			
		TTGTGCCACTTT GGG AGA			
		A C			
GAM2322	DKFZp761O0113 5'	AGACGGGGTTTCTCCATGTTGG 37887		T	A_
	TCA	TGACCAACATGG GAAACCC TCT			
		ACTGGTTGTACC CTTTGGG AGA			
		T GC			
GAM2322	DRIM 3'	GGATTTCGCCATGTTGGCCA 27952	A	C	
		TG CCAACATGGTGAAA CC			
		AC GGTGTACCGCTTT GG			
		C A			
GAM2322	DSCR6 3'	AGACTCGGTTTCACCATGTTGG 39056		CA_	
	TCA	TGACCAACATGGTGAAACC TCT			
		ACTGGTTGTACCACTTTGG AGA			
		CTC			
GAM2322	EREG 3'	GGTTTCACCATGTTGGCCA 9313	A		
		TG CCAACATGGTGAAACC			
		AC GGTGTACCACTTTGG			
		C			
GAM2322	FBP17 3'	AGACAGGGTTTCACCGTGTTGG 73142		A_	
	TCA	TGACCAACATGGTGAAACCC TCT			

		ACTGGTTGTGCCACTTTGGG AGA	
		AC	
GAM2322 FER1L4	3'	AGACAGGGTTTCACCATGTTGT 48109 AC	A_
CCA		TG CAACATGGTGAAACCC TCT	
		AC GTTGTACCACTTTGGG AGA	
		CT AC	
GAM2322 FKBP9	3'	AGACGGGGTTTCACCGTGTTGG 95711 A	A_
CCA		TG CCAACATGGTGAAACCC TCT	
		AC GGTGTGCCACTTTGGG AGA	
		C GC	
GAM2322 FLJ00060	5'	AGATGGAATTTACCATGTT 61733 C_	
		AACATGGTGAAA CCATCT	
		TTGTACCACTTT GGTAGA	
		AA	
GAM2322 FLJ10298	3'	AGACGGGGTTTCACCATGTTGG 36452 A_	
TCA		TGACCAACATGGTGAAACCC TCT	
		ACTGGTTGTACCACTTTGGG AGA	
		GC	
GAM2322 FLJ10535	3'	AGATGGGGTTTCACCATGTTGG 36737 A	-
CCA		TG CCAACATGGTGAAACCC ATCT	
		AC GGTGTACCACTTTGGG TAGA	
		C G	
GAM2322 FLJ10560	3'	AGACGGGGTTTCACCGTGTTAG 36790 C	A_
TCA		TGAC AACATGGTGAAACCC TCT	
		ACTG TTGTGCCACTTTGGG AGA	
		A GC	
GAM2322 FLJ10713	3'	AGATGGGGTTTCACCATGTTGG 36997 A	-
CCA		TG CCAACATGGTGAAACCC ATCT	
		AC GGTGTACCACTTTGGG TAGA	
		C G	
GAM2322 FLJ10846	3'	AGACAGGGTCTCACCATGTT 37283 A A_	
		AACATGGTGA ACCC TCT	
		TTGTACCACT TGGG AGA	
		C AC	
GAM2322 FLJ10901	3'	AGATGGGGTTTCATCATGTTGG 37352 A	-
CCA		TG CCAACATGGTGAAACCC ATCT	
		AC GGTGTACTACTTTGGG TAGA	
		C G	
GAM2322 FLJ10956	3'	AGACGGGGTTTCACCATGTTGG 37461 A	A_
CCA		TG CCAACATGGTGAAACCC TCT	

AC GGTGTGACCACTTTGGG AGA
 C GC
 GAM2322 FLJ11193 3' AGATGGGGTCTCACCATGTT 37744 AA_
 AACATGGTGA CCCATCT
 ||||| |||||
 TTGTACCACT GGGTAGA
 CTG
 GAM2322 FLJ11700 3' AGATGGGCTTGGCTATTGTCA 46555 CAAC G A
 TGAC ATGGT AA CCCATCT
 ||| |||| |||||
 ACTG TATCG TT GGGTAGA
 T__ G C
 GAM2322 FLJ12363 3' GGTTCACCATGTTGGCCA 50638 A
 TG CCAACATGGTGAACCC
 || |||||
 AC GGTGTGACCACTTTGG
 C
 GAM2322 FLJ12668 3' AGATGAGGTTTCACCTTGTGG 47153 T _
 TCA TGACCAACA GGTGAAACC CATCT
 ||||| ||||| |||||
 ACTGGTTGT CCACTTTGG GTAGA
 T A
 GAM2322 FLJ12687 3' AGACAGGGTTTCACCATGTTGG 46742 A A_
 CCA TG CCAACATGGTGAACCC TCT
 || ||||| ||||| |||||
 AC GGTGTGACCACTTTGGG AGA
 C AC
 GAM2322 FLJ12903 3' AGACAGGATTTCTCCATGTTGG 43061 T _ CA
 TCA TGACCAACATGG GAAA CC TCT
 ||||| |||| |||||
 ACTGGTTGTACC CTTT GG AGA
 T A AC
 GAM2322 FLJ12973 3' AGATGGGGTTTCATCATGTTGG 46638 A _
 CCA TG CCAACATGGTGAACCC ATCT
 || ||||| ||||| |||||
 AC GGTGTACTACTTTGGG TAGA
 C G
 GAM2322 FLJ13072 5' AGACAGGGTTTCACCATGTTGG 91384 A_
 CCAACATGGTGAACCC TCT
 ||||| ||||| |||||
 GGTGTACCACTTTGGG AGA
 AC
 GAM2322 FLJ13114 3' AGATGGAGTTTCACCATGTT 44892 _
 AACATGGTGAAAC CCATCT
 ||||| ||||| |||||
 TTGTACCACTTTG GGTAGA
 A
 GAM2322 FLJ13197 3' GTTTCACCATGTTGGCCA 45184 A
 TG CCAACATGGTGAAC
 || ||||| |||||

				AC GGTGTACCACTTTG		
				C		
GAM2322	FLJ13305	5'	AGATGGGGTTTCACCATGTTGG	91705	A	—
	CCA		TG CCAACATGGTGAAACCC	ATCT		
			AC GGTGTACCACTTTGGG	TAGA		
			C	G		
GAM2322	FLJ13952	3'	AGACGGGGTTTCACCACGTTGGC	46002	A A A	
	CA		TG CCAAC TGGTGAAACCC	TCT		
			AC GGTG ACCACTTTGGG	AGA		
			C C C			
GAM2322	FLJ14442	3'	AGATGGGGTTTTACCATGTTGG	52375		—
	TCA		TGACCAACATGGTGAAACCC	ATCT		
			ACTGGTTGTACCATTTTGGG	TAGA		
			G			
GAM2322	FLJ14950	3'	AGACAGGGTTTCACCATGTTGG	52780	A	A_
	CCA		TG CCAACATGGTGAAACCC	TCT		
			AC GGTGTACCACTTTGGG	AGA		
			C	AC		
GAM2322	FLJ14957	3'	AGACGGGGTTTCACCATGTTGG	52807		A_
	TCA		TGACCAACATGGTGAAACCC	TCT		
			ACTGGTTGTACCACTTTGGG	AGA		
			GC			
GAM2322	FLJ20034	3'	AGATGGGGTCTCTCCATGTTGG	34833		T AA_
	TCA		TGACCAACATGG GA CCCATCT			
			ACTGGTTGTACC CT GGGTAGA			
			T CTG			
GAM2322	FLJ20045	3'	ATGGGGATTTCACCATGTTGGTC	34872		A_
	A		TGACCAACATGGTGAA CCCAT			
			ACTGGTTGTACCACTT GGGTA			
			AG			
GAM2322	FLJ20136	3'	AGATGAGTTTCACCATGTTGGT	35091		C
	CA		TGACCAACATGGTGAAAC CATCT			
			ACTGGTTGTACCACTTTG GTAGA			
			A			
GAM2322	FLJ20344	3'	AGACAGGGTTTCACCATGTTGG	35475	A	A_
	CCA		TG CCAACATGGTGAAACCC	TCT		
			AC GGTGTACCACTTTGGG	AGA		
			C	AC		
GAM2322	FLJ20452	3'	AGATGAGGTTTCTCCATGTTGG	35644		T _
	TCA		TGACCAACATGG GAAACC CATCT			

				ACTGGTTGTACC CTTTGG GTAGA		
				T A		
GAM2322	FLJ20507	3'	AGACAGGGTTTCACCATGTTGG 35729	A		A_
	CCA		TG CCAACATGGTCAAACCC TCT			
			AC GGTTGTACCACTTTGGG AGA			
			C AC			
GAM2322	FLJ20507	3'	AGACAGGGTTTCACCATGTTGG 60838	A		A_
	CCA		TG CCAACATGGTCAAACCC TCT			
			AC GGTTGTACCACTTTGGG AGA			
			C AC			
GAM2322	FLJ20700	3'	AGACGGGGTTTCACCATATTG 35995	C	A	
			CAA ATGGTCAAACCC TCT			
			GTT TACCACTTTGGG AGA			
			A C			
GAM2322	FLJ20813	3'	AGATGGGGCTTTCACCTACGTT 36125	A	_	
			AAC TGGTGAAA CCCATCT			
			TTG ATCACTTT GGGTAGA			
			C C			
GAM2322	FLJ21302	3'	AGACAGGGTTTCACCATGTTGG 43502	A		A_
	CCA		TG CCAACATGGTCAAACCC TCT			
			AC GGTTGTACCACTTTGGG AGA			
			C AC			
GAM2322	FLJ21324	5'	AGATGGGGTTTCACCATGTTGG 92841	A	_	
	CCA		TG CCAACATGGTCAAACCC ATCT			
			AC GGTTGTACCACTTTGGG TAGA			
			C G			
GAM2322	FLJ21459	3'	GGGTGTTACCATGTTGGCCA 44807	A	A	
			TG CCAACATGGTGA ACCC			
			AC GGTTGTACCATT TGGG			
			C G			
GAM2322	FLJ21603	3'	AGATGGGGTTTCACCCTGTT 45765	T	_	
			AACA GGTCAAACCC ATCT			
			TTGT CCACTTTGGG TAGA			
			C G			
GAM2322	FLJ22329	3'	AGACGGGGTTTCACCATGTTGG 45392	A		A_
	CCA		TG CCAACATGGTCAAACCC TCT			
			AC GGTTGTACCACTTTGGG AGA			
			C GC			
GAM2322	FLJ22529	3'	AGACAGGGTTTCACCACATTGG 45936	A	CA	A_
	CCA		TG CCAA TGGTCAAACCC TCT			

			AC GGT ACCACTTTGGG AGA		
			C AC AC		
GAM2322	FLJ22529	3'	AGACAGGGTTTCATCATGTTGG 45938	A	A_
	CCA		TG CCAACATGGTCAAACCC TCT		
			AC GGTGTACTACTTTGGG AGA		
			C AC		
GAM2322	FLJ22684	3'	AGACAGGGTTTCACCATGTTGG 47464	A	A_
	CCA		TG CCAACATGGTCAAACCC TCT		
			AC GGTGTACCACTTTGGG AGA		
			C AC		
GAM2322	FLJ22794	3'	AGACAGGGTTTCACCATGTTGG 93236		A_
	TCA		TGACCAACATGGTCAAACCC TCT		
			ACTGGTGTACCACTTTGGG AGA		
			AC		
GAM2322	FLJ22969	3'	AGACAGGGTTTCACCATGTTGC 69196	AC	A_
	CCA		TG CAACATGGTCAAACCC TCT		
			AC GTTGTACCACTTTGGG AGA		
			CC AC		
GAM2322	FLJ23024	3'	AGACGGGGTTTCACCATGTTGG 46836	A	A_
	CCA		TG CCAACATGGTCAAACCC TCT		
			AC GGTGTACCACTTTGGG AGA		
			C GC		
GAM2322	FLJ23392	3'	AGACAGGGTTTCACCATGTTGG 45874	A	A_
	CCA		TG CCAACATGGTCAAACCC TCT		
			AC GGTGTACCACTTTGGG AGA		
			C AC		
GAM2322	FLJ23392	3'	AGACAGGGTTTCACCGTGTT 45875		A_
			AACATGGTCAAACCC TCT		
			TTGTGCCACTTTGGG AGA		
			AC		
GAM2322	FLJ23392	3'	AGACGGGGTTTCACCGTGTTAG 45877	C	A_
	TCA		TGAC AACATGGTCAAACCC TCT		
			ACTG TTGTGCCACTTTGGG AGA		
			A GC		
GAM2322	FLJ23519	3'	AGATGGGGTTTCACCGTGTT 50943		_
			AACATGGTCAAACCC ATCT		
			TTGTGCCACTTTGGG TAGA		
			G		
GAM2322	FLJ23556	3'	AGACCGGGCTTCACCATGTTGG 46422	A	A A_
	CCA		TG CCAACATGGTCAA CCC TCT		

			AC GGTGTACCACTT GGG AGA		
			C C CC		
GAM2322	FLJ23556	3'	AGACGGGGTTTCACCGTGTT 46423	A_	
			AACATGGTGAAACCC TCT		
			TTGTGCCACTTTGGG AGA		
			GC		
GAM2322	FLJ25416	5'	AGATGGGGTTTCACCATGTTGG 59447 A	_	
	CCA		TG CCAACATGGTGAAACCC ATCT		
			AC GGTGTACCACTTTGGG TAGA		
			C G		
GAM2322	FLJ30532	3'	AGACAGGATTTCATGTTGG 59213 A	_ CA	
	CCA		TG CCAACATGGTGAAA CC TCT		
			AC GGTGTATCACTTT GG AGA		
			C A AC		
GAM2322	FLJ31101	3'	GGGATTTCACCATGTTGGCCA 36164 A	_	
			TG CCAACATGGTGAAA CCC		
			AC GGTGTACCACTTT GGG		
			C A		
GAM2322	FLJ31153	3'	AGATGGGGTTTCACCATGCTGG 58742 A A	_	
	CCA		TG CCA CATGGTGAAACCC ATCT		
			AC GGT GTACCACTTTGGG TAGA		
			C C G		
GAM2322	GGA2	3'	AGACAGGATTTCACCATGTTGG 57650 A	_ CA	
	CCA		TG CCAACATGGTGAAA CC TCT		
			AC GGTGTACCACTTT GG AGA		
			C A AC		
GAM2322	GGA2	3'	AGACAGGATTTCACCATGTTGG 31156 A	_ CA	
	CCA		TG CCAACATGGTGAAA CC TCT		
			AC GGTGTACCACTTT GG AGA		
			C A AC		
GAM2322	GMPPB	5'	AGACAGGGTTTCACCAAGTTGG 97431 A A	A_	
	CCA		TG CCAAC TGGTGAAACCC TCT		
			AC GGTG ACCACTTTGGG AGA		
			C G AC		
GAM2322	GNG4	3'	AGACGGGGTTTCACCATGTTGG 16841	A_	
	TCA		TGACCAACATGGTGAAACCC TCT		
			ACTGGTTGTACCACTTTGGG AGA		
			GC		
GAM2322	GOLGA3	3'	GGGTTTCACCATGTTGGCCA 20892 A		
			TG CCAACATGGTGAAACCC		

			AC GGTGTACCACTTTGGG		
			C		
GAM2322	GP5	3'	AGACGGGCTTTGCCATATTGG 16859	C	TG A A
			CCAA ATGG AA CCC TCT		
			GGTT TACC TT GGG AGA		
			A GT C C		
GAM2322	GREB1	3'	AGACGGGGTTTCACCATGTT 28552	A_	
			AACATGGTGAAACCC TCT		
			TTGTACCACTTTGGG AGA		
			GC		
GAM2322	GRWD	3'	AGACGGGGTTTCACCATGTTGG 49773	A	A_
	CCA		TG CCAACATGGTGAAACCC TCT		
			AC GGTGTACCACTTTGGG AGA		
			C GC		
GAM2322	GTPBG3	3'	AGACAAGGTTTCACCATGTTG 51887	CA_	
			CAACATGGTGAAACC TCT		
			GTTGTACCACTTTGG AGA		
			AAC		
GAM2322	H2AV	3'	GGGTTTCACCATGTTGGCCA 57631	A	
			TG CCAACATGGTGAAACCC		
			AC GGTGTACCACTTTGGG		
			C		
GAM2322	HARS2	3'	AGACGGGGTTTACCATGTT 55861	A_	
			AACATGGTGAAACCC TCT		
			TTGTACCATTTTGGG AGA		
			GC		
GAM2322	HSMPP8	3'	AGATGGGGTTTATCCATGTTGG 95125	_	A
	TCA		TGACCAACATGG TGAA CCCATCT		
			ACTGGTTGTACC ATTT GGGTAGA		
			T G		
GAM2322	HSNOV1	3'	GGGTTTCACCATGTTGCCCA 34438	AC	
			TG CAACATGGTGAAACCC		
			AC GTTGTACCACTTTGGG		
			CC		
GAM2322	HSPC065	3'	AGATGGGGTTTACCATGTTGG 27136	A	_
	CCA		TG CCAACATGGTGAAACCC ATCT		
			AC GGTGTACCACTTTGGG TAGA		
			C G		
GAM2322	HSPC065	3'	AGATGGGGTTTACGATGTTGG 27138	A	G _
	CCA		TG CCAACAT GTGAAACCC ATCT		

			AC GGTGTGTA CACTTTGGG TAGA		
			C G G		
GAM2322	HSPC232	3'	AGATGGGGTTTCACCATGTTGGC 33654	A	A
	CA		TG CCAACATGGTGAA CCCATCT		
			AC GGTGTACCACTT GGGTAGA		
			C G		
GAM2322	HT002	3'	GGGTTTCACCGTGTGGCCA 26797	A	
			TG CCAACATGGTGAAACCC		
			AC GGTGTGCCACTTTGGG		
			C		
GAM2322	JAM1	3'	AGACAGGGTTTCACCATGTTGG 34211		A_
	TC		GACCAACATGGTGAAACCC TCT		
			CTGGTTGTACCACTTTGGG AGA		
			AC		
GAM2322	JAM1	3'	AGACAGGGTTTCACCATGTTGG 58504		A_
	TC		GACCAACATGGTGAAACCC TCT		
			CTGGTTGTACCACTTTGGG AGA		
			AC		
GAM2322	JAM1	3'	AGACAGGGTTTCACCATGTTGG 58532		A_
	TC		GACCAACATGGTGAAACCC TCT		
			CTGGTTGTACCACTTTGGG AGA		
			AC		
GAM2322	JAM1	3'	AGACAGGGTTTCACCATGTTGG 58559		A_
	TC		GACCAACATGGTGAAACCC TCT		
			CTGGTTGTACCACTTTGGG AGA		
			AC		
GAM2322	JM11	3'	AGACAAGGTTTCACCATATTGG 54352	A C	CA_
	CCA		TG CCAA ATGGTGAAACC TCT		
			AC GGTT TACCACTTTGG AGA		
			C A AAC		
GAM2322	KIAA0063	3'	AGATGGGGTTTCTCCATGTTGG 30250	T	_
	TCA		TGACCAACATGG GAAACCC ATCT		
			ACTGGTTGTACC CTTTGGG TAGA		
			T G		
GAM2322	KIAA0087	3'	AGATGGGGTTTCACCATCTTGG 29338	A C	_
	CCA		TG CCAA ATGGTGAAACCC ATCT		
			AC GGTT TACCACTTTGGG TAGA		
			C C G		
GAM2322	KIAA0161	3'	AGACGGGGTTTCACCATGTTGG 29189	A	A_
	CCA		TG CCAACATGGTGAAACCC TCT		

				AC GGTGTACCACTTTGGG AGA			
				C GC			
GAM2322	KIAA0186	3'	AGACAGAGTTTTACCATGTTGG	41093	A		CCA_
	CCA		TG CCAACATGGTGAAC		TCT		
			AC GGTGTACCATTTTG		AGA		
			C AGAC				
GAM2322	KIAA0186	3'	AGATGGGGTTTCACCATGTTGG	41096	A		_
	CCA		TG CCAACATGGTGAACCC		ATCT		
			AC GGTGTACCACTTTGGG		TAGA		
			C G				
GAM2322	KIAA0205	3'	AGATGGGGTTTCACCATGTTGG	30201	A		_
	CCA		TG CCAACATGGTGAACCC		ATCT		
			AC GGTGTACCACTTTGGG		TAGA		
			C G				
GAM2322	KIAA0210	5'	AGACGGGGTTTCACTATATTGG	29146	A	C	A_
	CCA		TG CCAA ATGGTGAACCC		TCT		
			AC GGT TATCACTTTGGG		AGA		
			C A GC				
GAM2322	KIAA0210	5'	GGAGGAGTTTCACCATGTTGGC	29165	A		_ A
	CA		TG CCAACATGGTGAAC		CC TCT		
			AC GGTGTACCACTTTG		GG AGG		
			C A _				
GAM2322	KIAA0426	3'	AGACGGGGTTTCACCATGTTGG	28917	A		A_
	CCA		TG CCAACATGGTGAACCC		TCT		
			AC GGTGTACCACTTTGGG		AGA		
			C GC				
GAM2322	KIAA0438	3'	ATGAATTTTCACTGTTGGCA	29731	A	TG	CC_
			TG CCAACA GTGAAA		CAT		
			AC GGTTGT CACTTT		GTA		
			_ _ TAA				
GAM2322	KIAA0459	3'	AGACGGGGTTTCACCATGTT	61641			A_
			AACATGGTGAACCC		TCT		
			TTGTACCACTTTGGG		AGA		
			GC				
GAM2322	KIAA0475	3'	GGTTTCACCATGTTGGCCA	30125	A		
			TG CCAACATGGTGAAC				
			AC GGTGTACCACTTTGG				
			C				
GAM2322	KIAA0495	3'	AGATGGGATTTACCATGTTGG	63258	A		_
	CCA		TG CCAACATGGTGAAA		CCCATCT		

			AC GGTGTACCACTTT GGGTAGA		
			C A		
GAM2322	KIAA0513	5'	AGACAGGGTTTCGCCATGTTGG 29009	A	A_
		CCA	TG CCAACATGGTGAAACCC TCT		
			AC GGTGTACCGCTTTGGG AGA		
			C AC		
GAM2322	KIAA0513	3'	AGATGGGGTTTCACCATGCTGG 29016	A A	_
		CCA	TG CCA CATGGTGAAACCC ATCT		
			AC GGT GTACCACTTTGGG TAGA		
			C C G		
GAM2322	KIAA0527	3'	AGATGGAGTTTCACCATGTTGG 97488	A	_
		CCA	TG CCAACATGGTGAAAC CCATCT		
			AC GGTGTACCACTTTG GGTAGA		
			C A		
GAM2322	KIAA0544	3'	GGGATTTACCATGTTGGCCG 71472	A	_
			TG CCAACATGGTGAAA CCC		
			GC GGTGTACCACTTT GGG		
			C A		
GAM2322	KIAA0555	3'	AGACAGGGTTTCACTATGCTGG 29543	A	A_
		TCA	TGACCA CATGGTGAAACCC TCT		
			ACTGGT GTATCACTTTGGG AGA		
			C AC		
GAM2322	KIAA0557	3'	AGATGGGGTTTCTCCATGTTGG 78545	T	_
		TCA	TGACCAACATGG GAAACCC ATCT		
			ACTGGTTGTACC CTTTGGG TAGA		
			T G		
GAM2322	KIAA0561	3'	AGACGGGGTTTCACCATGTTGG 66465		A_
		TCA	TGACCAACATGGTGAAACCC TCT		
			ACTGGTTGTACCACTTTGGG AGA		
			GC		
GAM2322	KIAA0562	3'	AGACGGGGTTTCACCATATTGG 28815	A C	A_
		CCA	TG CCAA ATGGTGAAACCC TCT		
			AC GGT TACCACTTTGGG AGA		
			C A GC		
GAM2322	KIAA0563	5'	GTTTCGCCATGTTGGTCA 29888		
			TGACCAACATGGTGAAAC		
			ACTGGTTGTACCGCTTTG		
GAM2322	KIAA0594	3'	AGATGGGGTTTCAGCATATTGG 65504	A C G	_
		CCA	TG CCAA ATG TGAAACCC ATCT		

			AC GGTT TAC ACTTTGGG TAGA		
			C A G G		
GAM2322	KIAA0682	3'	AGACGGGGTTTCACCATGTGGG 30013	A A	A_
		CCA	TG CC ACATGGTGAAACCC TCT		
			AC GG TGTACCACTTTGGG AGA		
			C G GC		
GAM2322	KIAA0682	3'	AGACTGGGTTTCACCATGT 30014		_
			ACATGGTGAAACCCA TCT		
			TGTACCACTTTGGGT AGA		
			C		
GAM2322	KIAA0720	3'	AGACGGGCATTTACCATATTGG 62973	C	C_ A
		TCA	TGACCAA ATGGTGAAA CC TCT		
			ACTGGTT TACCACTTT GG AGA		
			A AC C		
GAM2322	KIAA0737	3'	AGACAGGGTTTCACCATGTTGG 29796	A	A_
		CCA	TG CCAACATGGTGAAACCC TCT		
			AC GGTTGTACCACTTTGGG AGA		
			C AC		
GAM2322	KIAA0831	5'	GGGTTTCACCATGTTGGCCA 30648	A	
			TG CCAACATGGTGAAACCC		
			AC GGTTGTACCACTTTGGG		
			C		
GAM2322	KIAA0831	3'	GGGTTTTCACCATGTTGGCCA 30649	A	_
			TG CCAACATGGTGAAA CCC		
			AC GGTTGTACCACTTT GGG		
			C T		
GAM2322	KIAA0841	3'	GGTTTCATCATGTTGGCCA 71901	A	
			TG CCAACATGGTGAAACC		
			AC GGTTGTACTACTTTGG		
			C		
GAM2322	KIAA0884	3'	GGTTTCACCATGTTGCCCA 70756	AC	
			TG CAACATGGTGAAACC		
			AC GTTGTACCACTTTGG		
			CC		
GAM2322	KIAA0924	3'	AGATGGGGTTTCACCATATTGG 30353	A C	_
		CCA	TG CCAA ATGGTGAAACCC ATCT		
			AC GGTT TACCACTTTGGG TAGA		
			C A G		
GAM2322	KIAA0931	3'	AGACGGGGTTTCACCATGTTGG 68003	A	A_
		CCA	TG CCAACATGGTGAAACCC TCT		

			AC GGTGTACCACTTTGGG AGA		
			C GC		
GAM2322	KIAA0961	3'	AGATGGGGTTTCACCATGTTGG 30388 A	—	
	CCA		TG CCAACATGGTGAAACCC ATCT		
			AC GGTGTACCACTTTGGG TAGA		
			C G		
GAM2322	KIAA1026	3'	AGATGAGATTTACCATGTTGG 71729 A	CC_	
	CCA		TG CCAACATGGTGAAA CATCT		
			AC GGTGTACCACTTT GTAGA		
			C AGA		
GAM2322	KIAA1028	3'	AGATGGGGTTTCACCCTATTGG 93585 CAT	—	
	TCA		TGACCAA GGTGAAACCC ATCT		
			ACTGGTT CCACTTTGGG TAGA		
			ATC G		
GAM2322	KIAA1040	3'	AGATGGGGTTTCACCATTTTGG 72678 A C	—	
	CCA		TG CCAA ATGGTGAAACCC ATCT		
			AC GGT TACCACTTTGGG TAGA		
			C T G		
GAM2322	KIAA1054	3'	GGTTTCACCGTGTTGGTCA 68967		
			TGACCAACATGGTGAAACC		
			ACTGGTTGTGCCACTTTGG		
GAM2322	KIAA1161	5'	AGATGGGGTTTACCATGTTGGC 82637 A	A	
	CA		TG CCAACATGGTGAA CCCATCT		
			AC GGTGTACCATTT GGGTAGA		
			C G		
GAM2322	KIAA1185	3'	AGACGGGGTTTCACCATTTTG 63282 C	A_	
			CAA ATGGTGAAACCC TCT		
			GTT TACCACTTTGGG AGA		
			T GC		
GAM2322	KIAA1198	3'	AGACAGTGTTCACCATGTTG 63985	CCA_	
			CAACATGGTGAAAC TCT		
			GTTGTACCACTTTG AGA		
			TGAC		
GAM2322	KIAA1198	3'	AGACGGGGTTTCACCATGTTGG 63990 A	A_	
	CCA		TG CCAACATGGTGAAACCC TCT		
			AC GGTGTACCACTTTGGG AGA		
			C GC		
GAM2322	KIAA1198	3'	AGACGGGGTTTCACCATGTTGG 63991 A	A_	
	CCA		TG CCAACATGGTGAAACCC TCT		

		AC GGTGTACCACTTTGGG AGA	
		C GC	
GAM2322 KIAA1198	3'	AGACGGGGTTTCACCGTGTT 63992	A_
		AACATGGTGAAACCC TCT	
		TTGTGCCACTTTGGG AGA	
		GC	
GAM2322 KIAA1198	3'	AGATGGGGTTTCACCATGTTG 63999	_
		CAACATGGTGAAACCC ATCT	
		GTTGTACCACTTTGGG TAGA	
		G	
GAM2322 KIAA1198	3'	AGATGGGGTTTCTCCATGTTGG 64002	T _
	TCA	TGACCAACATGG GAAACCC ATCT	
		ACTGGTTGTACC CTTTGGG TAGA	
		T G	
GAM2322 KIAA1200	3'	AGACGGGGTTTCACCATGTTGG 63028 A	A_
	CCA	TG CCAACATGGTGAAACCC TCT	
		AC GGTGTACCACTTTGGG AGA	
		C GC	
GAM2322 KIAA1209	3'	GGTTTCATCATGTTGGCCA 61408 A	
		TG CCAACATGGTGAAACC	
		AC GGTGTACTACTTTGG	
		C	
GAM2322 KIAA1210	3'	AGACGGGGTTTCACCATGTTGG 98063 A	A_
	CCA	TG CCAACATGGTGAAACCC TCT	
		AC GGTGTACCACTTTGGG AGA	
		C GC	
GAM2322 KIAA1254	3'	AGATGGGGTTTCACCATGTTGG 70553 A	_
	CCA	TG CCAACATGGTGAAACCC ATCT	
		AC GGTGTACCACTTTGGG TAGA	
		C G	
GAM2322 KIAA1443	3'	AGACGGGGTTTCATCATGTT 64564	A
		AACATGGTGAAACCC TCT	
		TTGTACTACTTTGGG AGA	
		C	
GAM2322 KIAA1456	3'	AGACGGGGTTTCACCGTGTT 67526	A_
		AACATGGTGAAACCC TCT	
		TTGTGCCACTTTGGG AGA	
		GC	
GAM2322 KIAA1465	3'	AGACGGGGTTTCACCATGTTGG 61484 A	A_
	CCA	TG CCAACATGGTGAAACCC TCT	

			AC GGTGTACCACTTTGGG AGA		
			C GC		
GAM2322	KIAA1467	3'	AGACGGGGTTTCACCATGTTGG 72059	A	A_
	CCA		TG CCAACATGGTGAAACCC TCT		
			AC GGTGTACCACTTTGGG AGA		
			C GC		
GAM2322	KIAA1493	3'	AGATGGGGTTTCACCTTGTTGG 64833	T	_
	TCA		TGACCAACA GGTGAAACCC ATCT		
			ACTGGTTGT CCACTTTGGG TAGA		
			T G		
GAM2322	KIAA1497	5'	AGACAGGGTTTCACCATGTTGG 68109		A_
	TCA		TGACCAACATGGTGAAACCC TCT		
			ACTGGTTGTACCACTTTGGG AGA		
			AC		
GAM2322	KIAA1508	3'	GGTTTCACCATGTTGGTCA 62556		
			TGACCAACATGGTGAAACC		
			ACTGGTTGTACCACTTTGG		
GAM2322	KIAA1571	3'	GGTTTCACTATGTTGGCCA 61621	A	
			TG CCAACATGGTGAAACC		
			AC GGTGTATCACTTTGG		
			C		
GAM2322	KIAA1615	3'	GTTTCACCACGTTGGCCA 69284	A A	
			TG CCAAC TGGTGAAAC		
			AC GGTG ACCACTTG		
			C C		
GAM2322	KIAA1617	3'	AGACAGGGTTTCACCATGTTGG 93069		A_
	TCA		TGACCAACATGGTGAAACCC TCT		
			ACTGGTTGTACCACTTTGGG AGA		
			AC		
GAM2322	KIAA1655	3'	AGACAGGTTTCACCATGTTGGC 67171	A	CA
	CA		TG CCAACATGGTGAAACC TCT		
			AC GGTGTACCACTTTGG AGA		
			C AC		
GAM2322	KIAA1668	3'	AGACGGGGTTTCACCGTGTT 67056		A_
			AACATGGTGAAACCC TCT		
			TTGTGCCACTTTGGG AGA		
			GC		
GAM2322	KIAA1712	3'	AGACAGGGTTTCACCATGTTGC 68148	AC	A_
	CCA		TG CAACATGGTGAAACCC TCT		

			AC GTTGTACCACTTTGGG AGA		
			CC AC		
GAM2322	KIAA1784	3'	GGGTTTCACCATGTTGCTCA 65753 C		
			TGA CAACATGGTGAAACCC		
			ACT GTTGTACCACTTTGGG		
			C		
GAM2322	KIAA1829	3'	AGACGGGGTTTCACCACATTGG 62628 CA A_		
			TCA TGACCAA TGGTGAAACCC TCT		
			ACTGGTT ACCACTTTGGG AGA		
			AC GC		
GAM2322	KIAA1877	3'	AGACAGGGTTTCACCGTGTT 66737 A_		
			AACATGGTGAAACCC TCT		
			TTGTGCCACTTTGGG AGA		
			AC		
GAM2322	KIAA1922	5'	AGATGGGGTTTCGCCATATTGA 73982 C C _		
			TCA TGA CAA ATGGTGAAACCC ATCT		
			ACT GTT TACCGCTTTGGG TAGA		
			A A G		
GAM2322	KIAA1971	3'	AGACGAGGTTTCACCGTGTT 74667 CA_		
			AACATGGTGAAACC TCT		
			TTGTGCCACTTTGG AGA		
			AGC		
GAM2322	KIAA1975	5'	AGATGGGGTTTCACCATGTT 74411 _		
			AACATGGTGAAACCC ATCT		
			TTGTACCACTTTGGG TAGA		
			G		
GAM2322	KIAA1987	5'	GGTTTCACCATATTGGCCA 89385 A C		
			TG CCAA ATGGTGAAACC		
			AC GGTT TACCACTTTGG		
			C A		
GAM2322	KLK7	3'	AGACAGGGTTTCACCATGTTGG 58386 A A_		
			CCA TG CCAACATGGTGAAACCC TCT		
			AC GGTTGTACCACTTTGGG AGA		
			C AC		
GAM2322	KLK7	3'	AGACAGGGTTTCACCATGTTGG 18539 A A_		
			CCA TG CCAACATGGTGAAACCC TCT		
			AC GGTTGTACCACTTTGGG AGA		
			C AC		
GAM2322	LAMP3	3'	AGACGGGGTTTCACCATGTTGG 60197 A A_		
			CCA TG CCAACATGGTGAAACCC TCT		

			AC GGTGTACCACTTTGGG AGA		
			C GC		
GAM2322	LY75	3'	AGATGGGGTTTCACCATGTTGG 11387 A	—	
	CCA		TG CCAACATGGTGAAACCC ATCT		
			AC GGTGTACCACTTTGGG TAGA		
			C G		
GAM2322	MAP-1	3'	AGACGGGGTTTCACCATGTTGG 42433 A	A_	
	CCA		TG CCAACATGGTGAAACCC TCT		
			AC GGTGTACCACTTTGGG AGA		
			C GC		
GAM2322	MCLC	3'	AGATGGGGTTTCACCATGTTGG 31377	—	
	TCA		TGACCAACATGGTGAAACCC ATCT		
			ACTGGTTGTACCACTTTGGG TAGA		
			G		
GAM2322	MEF-2	3'	AGACTGGGGTTTCACCATGTTGG 65015	—	
	TCA		TGACCAACATGGTGAAACCCA TCT		
			ACTGGTTGTACCACTTTGGGT AGA		
			C		
GAM2322	MGC12518	3'	GGGTTTCACCATGTTGGCCA 64778 A		
			TG CCAACATGGTGAAACCC		
			AC GGTGTACCACTTTGGG		
			C		
GAM2322	MGC13204	3'	AGATGTGGTTTCTCCATGTTGG 49623 A	T _	
	CCA		TG CCAACATGG GAAACC CATCT		
			AC GGTGTACC CTTTGG GTAGA		
			C T T		
GAM2322	MGC15563	3'	AGATGGGATCTCACCATGTTGC 52859 AC	AA_	
	CCA		TG CAACATGGTGA CCCATCT		
			AC GTTGTACCACT GGGTAGA		
			CC CTA		
GAM2322	MGC1842	3'	AGACCAGGCTTCGCCATGTTGG 66245 A	A CA_	
	CCA		TG CCAACATGGTGAA CC TCT		
			AC GGTGTACCGCTT GG AGA		
			C C ACC		
GAM2322	MGC21675	3'	AGATGGGGTTTCACCATGTTGG 54585	—	
	TCA		TGACCAACATGGTGAAACCC ATCT		
			ACTGGTTGTACCACTTTGGG TAGA		
			G		
GAM2322	MGC2474	3'	AGATGGGGTTCCCACTATGTTG 43945 C	AAA_	
	ATCA		TGA CAACATGGTG CCCATCT		

			ACT GTTGTATCAC	GGGTAGA		
			A	CCTTG		
GAM2322	MGC2474	3'	AGATGGGGTTTCACCATGTTGG	43948		—
			CCAACATGGTGAAACCC	ATCT		
			GGTTGTACCACTTTGGG	TAGA		
			G			
GAM2322	MGC4638	3'	GGTTTCAACATGTTGGCCA	49740	A	G
			TG CCAACATG	TGAAACC		
			AC GGTGTAC	ACTTTGG		
			C	A		
GAM2322	MGC4766	5'	AGACGGGGTTTCACCGTGTT	49553		A_
			AACATGGTGAAACCC	TCT		
			TTGTGCCACTTTGGG	AGA		
			GC			
GAM2322	MGC5149	3'	AGATGGGGTTTCACCACATTGG	72752	A	CA
			CCA	TG CCAA	TGGTGAAACCC	ATCT
			AC GGT	ACCACTTTGGG	TAGA	
			C	AC	G	
GAM2322	MKRN4	3'	GGGTTTCACCATATTGGTCA	48471		C
			TGACCAA	ATGGTGAAACCC		
			ACTGGTT	TACCACTTTGGG		
			A			
GAM2322	moblak	3'	AGACAGGGTTTCACCGTGTT	56382		A_
			AACATGGTGAAACCC	TCT		
			TTGTGCCACTTTGGG	AGA		
			AC			
GAM2322	MOCS3	3'	AGGGGGTTTCACCATGTTTGTC	27926	C	A
			A	TGAC AACATGGTGAAACCC	TCT	
			ACTG TTGTACCACTTTGGG	GGA		
			T			
GAM2322	MRPL20	3'	AGACCGGGTTCCGCCATGTTGG	36198		A
			TCA	TGACCAACATGGTG AACCC	TCT	A_
			ACTGGTTGTACCGC	TTGGG	AGA	
			C	CC		
GAM2322	MRPS27	3'	AGATGGGGTTTCACCATGTTGG	31319		—
			TCA	TGACCAACATGGTGAAACCC	ATCT	
			ACTGGTTGTACCACTTTGGG	TAGA		
			G			
GAM2322	MtFMT	3'	AGATGGGGTTTCACCATGTTGG	58329		—
			TCA	TGACCAACATGGTGAAACCC	ATCT	

		ACTGGTTGTACCACTTTGGG TAGA		
		G		
GAM2322	MYO5C	3' AGACAGGTTTTCACCATGTTGGC 38712	A	CA
	CA	TG CCAACATGGTGAAACC TCT		
		AC GGTTGTACCACTTTGG AGA		
		C AC		
GAM2322	NDP52	3' AGACAGGGTTTTCACATGTTGG 20663	A	A_
	CCA	TG CCAACATGGTGAAACCC TCT		
		AC GGTTGTATCACTTTGGG AGA		
		C AC		
GAM2322	NDUFC2	3' AGACGGGGTTTTCACCATGTTGG 17024	A	A_
	CCA	TG CCAACATGGTGAAACCC TCT		
		AC GGTTGTACCACTTTGGG AGA		
		C GC		
GAM2322	NINJ2	3' AGACGGGGTTTCTCCATGTTGG 33716	T	A_
	TCA	TGACCAACATGG GAAACCC TCT		
		ACTGGTTGTACC CTTTGGG AGA		
		T GC		
GAM2322	Nup43	3' GGGTTTCACCATGTTGGCCA 45350	A	
		TG CCAACATGGTGAAACCC		
		AC GGTTGTACCACTTTGGG		
		C		
GAM2322	NXN	3' AGATGGGGTTTTCACCATGTTGG 42665		_
		CCAACATGGTGAAACCC ATCT		
		GGTTGTACCACTTTGGG TAGA		
		G		
GAM2322	OCT11	3' AGATGGGGTTTTCACCATGTTGG 27582		_
	TCA	TGACCAACATGGTGAAACCC ATCT		
		ACTGGTTGTACCACTTTGGG TAGA		
		G		
GAM2322	OR51E2	3' AGACAGAGTTTTCACCATGTTGG 48501	A	CCA_
	CCA	TG CCAACATGGTGAAAC TCT		
		AC GGTTGTACCACTTTG AGA		
		C AGAC		
GAM2322	OSBPL2	3' GGGTTTTCACCATGTTGGTCA 58488		_
		TGACCAACATGGTGAAA CCC		
		ACTGGTTGTACCACTTT GGG		
		T		
GAM2322	OSBPL2	3' GGGTTTTCACCATGTTGGTCA 29902		_
		TGACCAACATGGTGAAA CCC		

		ACTGGTTGTACCACTTT GGG		
		T		
GAM2322	PASK	5' AGACGGGGTTTCTCCATGTTGG 31404	T	A_
	TCA	TGACCAACATGG GAAACCC TCT		
		ACTGGTTGTACC CTTTGGG AGA		
		T GC		
GAM2322	PELI1	5' AGACGGGGTTTCACCATGTTGC 40620 AC		A_
	CCA	TG CAACATGGTGAAACCC TCT		
		AC GTTGTACCACTTTGGG AGA		
		CC GC		
GAM2322	PELI1	5' AGATGGGGTTTCACCATGTTGG 40624 A		_
	CCA	TG CCAACATGGTGAAACCC ATCT		
		AC GGTGTACCACTTTGGG TAGA		
		C G		
GAM2322	PRO0365	5' AGACGGGGTTTCACCATGTTGG 26976 A		A_
	CCA	TG CCAACATGGTGAAACCC TCT		
		AC GGTGTATCACTTTGGG AGA		
		C GC		
GAM2322	PRO2955	3' AGACAGGGTTTTACCATGTTGG 38232		A_
	TCA	TGACCAACATGGTGAAACCC TCT		
		ACTGGTTGTACCATTTTGGG AGA		
		AC		
GAM2322	PSTPIP2	3' AGACAGGGTTTTACCATGTTGG 44648		A_
	TCA	TGACCAACATGGTGAAACCC TCT		
		ACTGGTTGTACCATTTTGGG AGA		
		AC		
GAM2322	RAB33B	3' AGATGGGGTTTCACCATGTTGG 49318 A		_
	CCA	TG CCAACATGGTGAAACCC ATCT		
		AC GGTGTACCACTTTGGG TAGA		
		C G		
GAM2322	RAI	5' AGACAGGGTTCTTACCATGTTG 22848 A	_	A_
	GCCA	TG CCAACATGGTGA AACCC TCT		
		AC GGTGTACCATT TTGGG AGA		
		C C AC		
GAM2322	RASSF2	3' GGTTTCACCATCTTGGCCA 29107 A C		
		TG CCAA ATGGTGAAACC		
		AC GGTT TACCACTTTGG		
		C C		
GAM2322	RES4-25	3' AGACGGGGTTTCTCCATGTTGG 65259	T	A_
	TCA	TGACCAACATGG GAAACCC TCT		

		ACTGGTTGTACC CTTTGGG AGA			
		T GC			
GAM2322	RNF8	3'	AGACAGGGTTTCACCATGTTGG 15558	A	A_
	CCA		TG CCAACATGGTGAAACCC TCT		
		AC GGTGTACCACTTTGGG AGA			
		C AC			
GAM2322	RNO2	5'	AGATGGGGTGTACCATGTTGG 53917	A	AA_
	CCA		TG CCAACATGGTGA CCCATCT		
		AC GGTGTACCACT GGGTAGA			
		C GTG			
GAM2322	SCAMP-4	3'	AGATGGGGTTCACCATGTTGG 55336	A	_
	CCA		TG CCAACATGGTGAAACCC ATCT		
		AC GGTGTACCACTTTGGG TAGA			
		C G			
GAM2322	SCYA22	3'	AGACAGGTTTCACCATATTGGC 92570	A C	CA
	CA		TG CCAA ATGGTGAAACC TCT		
		AC GGT TACCACTTTGG AGA			
		C A AC			
GAM2322	SCYA22	3'	AGACGAGGCTTCACCATGTTGG 92572	A	A CA_
	CCA		TG CCAACATGGTGAA CC TCT		
		AC GGTGTACCACTT GG AGA			
		C C AGC			
GAM2322	SERF1B	3'	AGATGGGGTTCACCATGTTGG 43689	A	_
	CCA		TG CCAACATGGTGAAACCC ATCT		
		AC GGTGTACCACTTTGGG TAGA			
		C G			
GAM2322	SFXN2	3'	AGACGGGGTTTCACCATGCTGG 74371	A A	A_
	CCA		TG CCA CATGGTGAAACCC TCT		
		AC GGT GTACCACTTTGGG AGA			
		C C GC			
GAM2322	SIRPB1	3'	AGATGGGGTTTCTCCATGTTGA 21355	C T	_
	TCA		TGA CAACATGG GAAACCC ATCT		
		ACT GTTGTACC CTTTGGG TAGA			
		A T G			
GAM2322	SLC12A8	3'	AGACAGGGTTTCACCATGTTGG 45232	A	A_
	CCA		TG CCAACATGGTGAAACCC TCT		
		AC GGTGTACCACTTTGGG AGA			
		C AC			
GAM2322	SLC19A3	3'	AGATGAGTTCTCTATGT 48232	T A C	
		ACATGG GAA C CATCT			

			TGTATC CTT G GTAGA		
			T _ A		
GAM2322	SLC19A3	3'	AGATGGGGTTTCACAATGTTGG 48234	A	G _
	CCA		TG CCAACAT GTGAAACCC ATCT		
			AC GGTTGTA CACTTTGGG TAGA		
			C A G		
GAM2322	SLC6A14	3'	GTTTCCCCATGTTGGCCA 24311	A	T
			TG CCAACATGG GAAAC		
			AC GGTTGTACC CTTTG		
			C C		
GAM2322	SREC	3'	AGACAGGGTTTCACCATGTT 14895		A_
			AACATGGTGAAACCC TCT		
			TTGTACCACTTTGGG AGA		
			AC		
GAM2322	SS-56	3'	AGACGGAGTTTCACCATGTT 60342		_ A
			AACATGGTGAAAC CC TCT		
			TTGTACCACTTTG GG AGA		
			A C		
GAM2322	STAF65(gamma)	3'	AGATGAGGTTTCACCGTGTTGG 30060	A	_
	CCA		TG CCAACATGGTGAAACC CATCT		
			AC GGTTGTGCCACTTTGG GTAGA		
			C A		
GAM2322	SULT1C2	3'	AGACGAGGTTTCACCGTGTT 22707		CA_
			AACATGGTGAAACC TCT		
			TTGTGCCACTTTGG AGA		
			AGC		
GAM2322	SYT13	3'	AGATGGGGTTTCACCATGTTGG 95094	A	_
	CCA		TG CCAACATGGTGAAACCC ATCT		
			AC GGTTGTACCACTTTGGG TAGA		
			C G		
GAM2322	TADA3L	3'	AGACGGGGTTTCACCGTGTT 56803		A_
			AACATGGTGAAACCC TCT		
			TTGTGCCACTTTGGG AGA		
			GC		
GAM2322	TCL6	5'	AGACGAGGTTTCACCATGTTGG 40505	A	CA_
	CCA		TG CCAACATGGTGAAACC TCT		
			AC GGTTGTACCACTTTGG AGA		
			C AGC		
GAM2322	TCL6	5'	AGACGAGGTTTCACCATGTTGG 40459	A	CA_
	CCA		TG CCAACATGGTGAAACC TCT		

			AC GGTGTGACCACTTTGG	AGA		
			C	AGC		
GAM2322	TCL6	3'	AGACAGGGTTTCACCGTGTT	25897	A_	
			AACATGGTGAAACCC	TCT		
			TTGTGCCACTTTGGG	AGA		
			AC			
GAM2322	TCL6	5'	AGACGAGGTTTCACCATGTTGG	25899	A	CA_
	CCA		TG CCAACATGGTGAAACC	TCT		
			AC GGTGTGACCACTTTGG	AGA		
			C	AGC		
GAM2322	TCL6	3'	AGACAGGGTTTCACCGTGTT	27749	A_	
			AACATGGTGAAACCC	TCT		
			TTGTGCCACTTTGGG	AGA		
			AC			
GAM2322	TCL6	5'	AGACGAGGTTTCACCATGTTGG	27751	A	CA_
	CCA		TG CCAACATGGTGAAACC	TCT		
			AC GGTGTGACCACTTTGG	AGA		
			C	AGC		
GAM2322	TERA	3'	AGACGGGGTTTCACCACGTTGG	41415	A A	A_
	CCA		TG CCAAC TGGTGAAACCC	TCT		
			AC GGTG ACCACTTTGGG	AGA		
			C C	GC		
GAM2322	TGIF2	3'	AGACGGGGTTTCACCATCTTGG	41741	A C	A_
	CCA		TG CCAA ATGGTGAAACCC	TCT		
			AC GGT TACCACTTTGGG	AGA		
			C C	GC		
GAM2322	TRIM16	3'	AGATGGGGTTTCACCATGTTGG	22364	A	_
	CCA		TG CCAACATGGTGAAACCC	ATCT		
			AC GGTGTGACCACTTTGGG	TAGA		
			C	G		
GAM2322	TRIM6	3'	AGATAGGGTTTCACCGTGTTGG	55173	A	_
	CCA		TG CCAACATGGTGAAACCC	ATCT		
			AC GGTGTGCCACTTTGGG	TAGA		
			C	A		
GAM2322	TU12B1-TY	3'	AGACGGGGTTTCACCATGTTGG	33821	A	A_
	CCA		TG CCAACATGGTGAAACCC	TCT		
			AC GGTGTGACCACTTTGGG	AGA		
			C	GC		
GAM2322	TU12B1-TY	3'	AGATGGGGTTTCACCATGTTGG	33826	A	_
	CCA		TG CCAACATGGTGAAACCC	ATCT		

			AC GGTGTACCACTTTGGG TAGA		
			C G		
GAM2322	TUCAN	3'	AGACAGGGTTTCACCATTTTGG 30963	A C	A_
	CCA		TG CCAA ATGGTGAAACCC TCT		
			AC GGTT TACCACTTTGGG AGA		
			C T AC		
GAM2322	UBF-fl	3'	GGGTTTCACCATGCTGGCCA 52628	A A	
			TG CCA CATGGTGAAACCC		
			AC GGT GTACCACTTTGGG		
			C C		
GAM2322	UBF-fl	3'	GGTTTCACCATGCTGGCCA 52629	A A	
			TG CCA CATGGTGAAACC		
			AC GGT GTACCACTTTGG		
			C C		
GAM2322	UBF-fl	3'	GGTTTTACCATGTTGGCCA 52630	A	
			TG CCAACATGGTGAAACC		
			AC GGTGTACCATTTTGG		
			C		
GAM2322	VDU1	3'	AGATGGGGTTTCACCATGTTGG 31117	A	—
	CCA		TG CCAACATGGTGAAACCC ATCT		
			AC GGTGTACCACTTTGGG TAGA		
			C G		
GAM2322	VPS33A	3'	ATGGTGTTTCACCATGTTGGCC 43609	A	—
	A		TG CCAACATGGTGAAAC CCAT		
			AC GGTGTACCACTTTG GGTA		
			C T		
GAM2322	WBSCR23	3'	AGACGGGGTTTCACCATGTTGG 47412	A	A_
	CCA		TG CCAACATGGTGAAACCC TCT		
			AC GGTGTACCACTTTGGG AGA		
			C GC		
GAM2322	ZNF17	3'	GGTCTTACCATGTTGGCCA 83274	A A	
			TG CCAACATGGTGA ACC		
			AC GGTGTACCAT TGG		
			C C		
GAM2322	LOC112817	3'	AGATGGGGTTTCACCGTGTGG 57315	A	—
	CCA		TG CCAACATGGTGAAACCC ATCT		
			AC GGTGTGCCACTTTGGG TAGA		
			C G		
GAM2322	LOC113523	5'	AGACAGGGTTTCACCATGTT 73408	A_	
			AACATGGTGAAACCC TCT		

		TTGTACCACTTTGGG AGA		
		AC		
GAM2322	LOC115098 5'	AGACGGACTCTTGCTATGTTGC 57393	AC	TG AAC_ A
	CCA	TG CAACATGG A CC TCT		
		AC GTTGTATC T GG AGA		
		CC GT CTCA C		
GAM2322	LOC115219 5'	AGACGGGGTTTCATCATGTTGG 73685	A	A_
	CCA	TG CCAACATGGTGAAACCC TCT		
		AC GGTGTACTACTTTGGG AGA		
		C GC		
GAM2322	LOC115648 3'	AGACGGGGTTTCACCATGTTGG 60016		A_
		CCAACATGGTGAAACCC TCT		
		GGTTGTACCACTTTGGG AGA		
		GC		
GAM2322	LOC119392 3'	AGACTGGGTTTCACCACGTTGG 59810	A A	_
	CCA	TG CCAAC TGGTGAAACCCA TCT		
		AC GGTG ACCACTTTGGGT AGA		
		C C C		
GAM2322	LOC120114 3'	AGATGGGGTTTCACCATGTTGG 76039	A	_
	CCA	TG CCAACATGGTGAAACCC ATCT		
		AC GGTGTACCACTTTGGG TAGA		
		C G		
GAM2322	LOC120224 5'	AGACAGGGTTTCACCATGTTTG 57881	C	A_
	TCA	TGAC AACATGGTGAAACCC TCT		
		ACTG TTGTACCACTTTGGG AGA		
		T AC		
GAM2322	LOC120939 3'	AGGGGGTTTCACCATGTTGGCC 76755	A	A
	A	TG CCAACATGGTGAAACCC TCT		
		AC GGTGTACCACTTTGGG GGA		
		C _		
GAM2322	LOC121504 3'	AGATACGGGGTTTCACCATGTT 74540	A	___
	GGCCA	TG CCAACATGGTGAAACCC ATCT		
		AC GGTGTACCACTTTGGG TAGA		
		C GCA		
GAM2322	LOC123628 5'	AGATGGACCTCTGTGGTTGGTC 76137	_	TGAAAC
	A	TGACCAAC ATGG CCATCT		
		ACTGGTTG TGTC GG TAGA		
		G TCCA_		
GAM2322	LOC124216 3'	AGATGGTTTCACCATGTTGGCC 74733	A	C
	A	TG CCAACATGGTGAAACC ATCT		

		AC GGTGTGACCACTTTGG TAGA		
		C _		
GAM2322	LOC124871 3'	AGACGGGTCTCACTATGTTGCC 74815	AC	A A
	CA	TG CAACATGGTGA ACCC TCT		
		AC GTTGTATCACT TGGG AGA		
		CC C C		
GAM2322	LOC125144 3'	AGACGGATTCTCTATGTTGCCC 74852	AC	T A CA
	A	TG CAACATGG GAA CC TCT		
		AC GTTGTATC CTT GG AGA		
		CC T A C_		
GAM2322	LOC126364 3'	AGATGGGGTTTCGCCATGTTGG 76182	A	_
	CCA	TG CCAACATGGTGAAACCC ATCT		
		AC GGTGTACCGCTTTGGG TAGA		
		C G		
GAM2322	LOC126661 3'	AGACAGGTTTTCCACCATGTTGC 75044	AC	_ CA
	CCA	TG CAACATGGTGAAA CC TCT		
		AC GTTGTACCACTTT GG AGA		
		CC T AC		
GAM2322	LOC126661 3'	AGATGGGGTTTCACCATGTTGG 75048	A	_
	CCA	TG CCAACATGGTGAAACCC ATCT		
		AC GGTGTACCACTTTGGG TAGA		
		C G		
GAM2322	LOC128077 3'	AGACAGGTTTCACCATGTTGG 75199	A	A_
	CCA	TG CCAACATGGTGAAACCC TCT		
		AC GGTGTACCACTTTGGG AGA		
		C AC		
GAM2322	LOC128077 3'	AGACGGGGTTTCACCATGTT 75200	A_	
		AACATGGTGAAACCC TCT		
		TTGTACCACTTTGGG AGA		
		GC		
GAM2322	LOC128989 3'	AGACGGGGTTTCACCATGTTGG 75309	A_	
	TCA	TGACCAACATGGTGAAACCC TCT		
		ACTGGTTGTACCACTTTGGG AGA		
		GC		
GAM2322	LOC130813 3'	AGATAGGGTCTCACTATGTTG 76262	A _	
		CAACATGGTGA ACCC ATCT		
		GTTGTATCACT TGGG TAGA		
		C A		
GAM2322	LOC130813 3'	AGATGGGGTTTCTCCATGTTGG 76264	T	_
	TCA	TGACCAACATGG GAAACCC ATCT		

		ACTGGTTGTACC CTTTGGG TAGA		
		T G		
GAM2322	LOC132241 5'	GTGGGTTTCACTATGTTGGCCA 75564	A	
		TG CCAACATGGTCAAACCCAT		
		AC GGTTGTATCACTTTGGGTG		
		C		
GAM2322	LOC132625 3'	AGATGGGGTTTCACCATGTTGG 76433	A	—
	CCA	TG CCAACATGGTCAAACCC ATCT		
		AC GGTTGTACCACTTTGGG TAGA		
		C G		
GAM2322	LOC135154 3'	AGACAAGGTTTCACCATGTT 75719	CA_	
		AACATGGTGAAACC TCT		
		TTGTACCACTTTGG AGA		
		AAC		
GAM2322	LOC135293 3'	AGACGGCATTTCACCATGTTGG 76676	A	C_ A
	CCA	TG CCAACATGGTGAAA CC TCT		
		AC GGTTGTACCACTTT GG AGA		
		C AC C		
GAM2322	LOC143187 3'	AGATGGAGTTTCACCATGTTGG 59754	A	—
	CCA	TG CCAACATGGTGAAAC CCATCT		
		AC GGTTGTACCACTTTG GG TAGA		
		C A		
GAM2322	LOC143916 3'	AGATGGGGTTTCACCTTGTGG 77136	A	T —
	CCA	TG CCAACA GGTGAAACCC ATCT		
		AC GGTTGT CCACTTTGGG TAGA		
		C T G		
GAM2322	LOC144742 5'	AGACAGGTTTTCACCATGTTGG 77453	A	_ CA
	CCA	TG CCAACATGGTGAAA CC TCT		
		AC GGTTGTACCACTTT GG AGA		
		C T AC		
GAM2322	LOC145268 5'	AGACAGAGTTTCACCATGTTGG 77570	A	CCA_
	CCA	TG CCAACATGGTGAAAC TCT		
		AC GGTTGTACCACTTTG AGA		
		C AGAC		
GAM2322	LOC145622 3'	AGGGGGTTTCACCACGTTGGCC 77801	A A A	
	A	TG CCAAC TGGTGAAACCC TCT		
		AC GGTTG ACCACTTTGGG GGA		
		C C —		
GAM2322	LOC145652 3'	TGGGTTATGTTGGCA 84407	A	GTGAA
		TG CCAACATG ACCCA		

AC GGTGTAT TGGGT

GAM2322 LOC146050 3' AGATGGGGTTTCACCATGTTGG 78100 A _
CCA TG CCAACATGGTGAAACCC ATCT
|| |||||
AC GGTGTACCACTTTGGG TAGA
C G

GAM2322 LOC146229 3' AGACGGGGTTTCACCATGTTGG 78253 A A_
CCA TG CCAACATGGTGAAACCC TCT
|| |||||
AC GGTGTACCACTTTGGG AGA
C GC

GAM2322 LOC146229 3' GGGTTTCACCATATTGGCCA 78298 A C
TG CCAA ATGGTGAAACCC
|| |||||
AC GGT TACCACTTTGGG
C A

GAM2322 LOC146229 3' GGTTCACCATGTTGGCCA 78301 A
TG CCAACATGGTGAAACC
|| |||||
AC GGTGTACCACTTTGG
C

GAM2322 LOC146346 5' AGACAGGATTTTCATCATGTTGG 78383 A _ CA
CCA TG CCAACATGGTGAAA CC TCT
|| ||||| || |||
AC GGTGTACTACTTT GG AGA
C A AC

GAM2322 LOC146429 5' AGACAGGGTTTCACCATG 84659 A_
CATGGTGAAACCC TCT
||||||| |||
GTACCACTTTGGG AGA
AC

GAM2322 LOC146603 5' AGACGGGGTTTCACCGTGTT 78587 A_
AACATGGTGAAACCC TCT
||||||| |||
TTGTGCCACTTTGGG AGA
GC

GAM2322 LOC146784 5' AGATGGGGTTTCACCATGTTGG 78705 A _
CCA TG CCAACATGGTGAAACCC ATCT
|| |||||
AC GGTGTACCACTTTGGG TAGA
C G

GAM2322 LOC146839 3' AGACGGGGTTTCACCGTGTT 84834 A_
AACATGGTGAAACCC TCT
||||||| |||
TTGTGCCACTTTGGG AGA
GC

GAM2322 LOC146894 3' AGATGGGGTTTCACCATGTTGG 59852 A _
CCA TG CCAACATGGTGAAACCC ATCT
|| |||||

		AC GGTGTGACCACTTTGGG TAGA		
		C G		
GAM2322	LOC146901 3'	AGACGGGGTTTCACCATGTTGG 84885	A	A_
	CCA	TG CCAACATGGTGAAACCC TCT		
		AC GGTGTGACCACTTTGGG AGA		
		C GC		
GAM2322	LOC146909 3'	AGATGGGGTTTCACCGTGTT 78758	—	
		AACATGGTGAAACCC ATCT		
		TTGTGCCACTTTGGG TAGA		
		G		
GAM2322	LOC146952 5'	AGACAGGGTTTCACCACATTGG 84922	A CA	A_
	CCA	TG CCAA TGGTGAAACCC TCT		
		AC GGTT ACCACTTTGGG AGA		
		C AC AC		
GAM2322	LOC147054 3'	GGTTTCTCCATGTTGGTCA 85008	T	
		TGACCAACATGG GAAACC		
		ACTGGTTGTACC CTTTGG		
		T		
GAM2322	LOC147071 5'	AGACGGAGTTTCACCATGTTGG 73348	— A	
	TTA	TGACCAACATGGTGAAAC CC TCT		
		ATTGGTTGTACCACTTTG GG AGA		
		A C		
GAM2322	LOC147080 5'	AGACAAGGTTTCACCATGTT 85023	CA_	
		AACATGGTGAAACC TCT		
		TTGTACCACTTTGG AGA		
		AAC		
GAM2322	LOC147166 3'	AGATGGGGTTTCACCATGTTGG 78881	A	—
	CCA	TG CCAACATGGTGAAACCC ATCT		
		AC GGTGTGACCACTTTGGG TAGA		
		C G		
GAM2322	LOC147276 3'	AGACGGGGCTTCTCCATGTTGG 78949	T A_ A	
	TCA	TGACCAACATGG GAA CCC TCT		
		ACTGGTTGTACC CTT GGG AGA		
		T CG C		
GAM2322	LOC147429 3'	AGATGGGGTTTCACCATGTAG 78990	C	—
	TCA	TGAC AACATGGTGAAACCC ATCT		
		ACTG TTGTACCACTTTGGG TAGA		
		A G		
GAM2322	LOC147694 3'	AGACGGGGTTTCACCGTGTT 79088	A_	
		AACATGGTGAAACCC TCT		

		TTGTGCCACTTTGGG AGA		
		GC		
GAM2322	LOC147817 3'	AGACAGGGGCTTCACCATGTTGG 79165	A	A A_
	CA	TG CCAACATGGTGAA CCC TCT		
		AC GGTTGTACCACTT GGG AGA		
		— C AC		
GAM2322	LOC147841 3'	AGATGGAGTTTCACCATGGTGG 79223	A	—
	TCA	TGACCA CATGGTGAAAC CCATCT		
		ACTGGT GTACCACTTTG GG TAGA		
		G A		
GAM2322	LOC147990 3'	AGACGGGGTTTCAGCATATTG 85210	C G	A_
		CAA ATG TGAAACCC TCT		
		GTT TAC ACTTTGGG AGA		
		A G GC		
GAM2322	LOC148147 3'	AGATGAGGTTTCACCTTGTTGG 79385	A T	—
	CCA	TG CCAACA GGTGAAACC CATCT		
		AC GGTTGT CCACTTTGG GTAG A		
		C T A		
GAM2322	LOC148189 5'	AGACGGGGTTTCACCATGTTG 79443		A_
		CAACATGGTGAAACCC TCT		
		GTTGTACCACTTTGGG AGA		
		GC		
GAM2322	LOC148195 3'	AGACAGGTTTCACCACATTGGT 85267	CA	CA
	CA	TGACCAA TGGTGAAACC TCT		
		ACTGGTT ACCACTTTGG AGA		
		AC AC		
GAM2322	LOC148443 3'	GGGTCTCACCATGTTGCCCA 79604	AC	A
		TG CAACATGGTGA ACCC		
		AC GTTGTACCACT TGGG		
		CC C		
GAM2322	LOC148709 3'	AGACAGGGTTTCTCCATGTTGG 79687	T	A_
	TCA	TGACCAACATGG GAAACCC TCT		
		ACTGGTTGTACC CTTTGGG AGA		
		T AC		
GAM2322	LOC148887 5'	AGACAGGGTTTCACCATGTTGG 85390		A_
	TCA	TGACCAACATGGTGAAACCC TCT		
		ACTGGTTGTACCACTTTGGG AGA		
		AC		
GAM2322	LOC149171 5'	AGATGGGGTTTCTCCATGTTGG 79962	T	—
	TCA	TGACCAACATGG GAAACCC ATCT		

		ACTGGTTGTACC CTTTGGG TAGA	
		T G	
GAM2322	LOC149478 3'	GGGTTTCACCATGTTGGCCA 80175 A	
		TG CCAACATGGTCAAACCC	
		AC GGTTGTACCACTTTGGG	
		C	
GAM2322	LOC149577 3'	AGACAGGCTTTGCTGTGTTGG 85664 A	_ CA
	CCA	TG CCAACATGGTGAAA CC TCT	
		AC GGTTGTGTCGCTTT GG AGA	
		C C AC	
GAM2322	LOC149692 3'	AGACAGGGTTTCACCATGTTGG 85724 A	A_
	CCA	TG CCAACATGGTCAAACCC TCT	
		AC GGTTGTACCACTTTGGG AGA	
		C AC	
GAM2322	LOC149711 3'	AGATGGGGTTTTACCATGTTGG 85837 A	_
	CCA	TG CCAACATGGTCAAACCC ATCT	
		AC GGTTGTACCATTTTGGG TAGA	
		C G	
GAM2322	LOC149821 5'	AGACGGAGTTTCACCGTGTT 85927	_ A
		AACATGGTGAAAC CC TCT	
		TTGTGCCACTTTG GG AGA	
		A C	
GAM2322	LOC150054 5'	GGTTTCCCATGTTGGCCA 85976 A	T
		TG CCAACATGG GAAACC	
		AC GGTTGTACC CTTTGG	
		C _	
GAM2322	LOC150166 5'	GGGTTTCACCATGTTGTCCA 86042 AC	
		TG CAACATGGTCAAACCC	
		AC GTTGTACCACTTTGGG	
		CT	
GAM2322	LOC150225 3'	AGACGGTTTCACCATGTGGGCC 86178 A A	CA
	A	TG CC ACATGGTCAAACC TCT	
		AC GG TGTACCACTTTGG AGA	
		C C C_	
GAM2322	LOC150282 5'	AGATGGCGTTTCACCATGTTGG 80535 A	_
	CCA	TG CCAACATGGTCAAAC CCATCT	
		AC GGTTGTACCACTTTG GG TAGA	
		C C	
GAM2322	LOC150397 3'	AGACGCAGTTTCACCGTGTTG 80649	CCA_
		CAACATGGTCAAAC TCT	

		GTTGTGCCACTTTG AGA		
		ACGC		
GAM2322	LOC150759 3'	AGATAGAATCTCACTATGTTG 80794	AACCC_	
		CAACATGGTGA ATCT		
		GTTGTATCACT TAGA		
		CTAAGA		
GAM2322	LOC151050 5'	AGACAGAGTTTCACCATGTTGG 80914 A	CCA_	
	CCA	TG CCAACATGGTGAAAC TCT		
		AC GGTGTACCACTTTG AGA		
		C AGAC		
GAM2322	LOC151057 3'	AGACGGGGTTTCACCATGTTGG 86382 A	A_	
	CCA	TG CCAACATGGTGAAACCC TCT		
		AC GGTGTACCACTTTGGG AGA		
		C GC		
GAM2322	LOC151201 3'	AGACGGGGTTTCACCATGTTGG 86464	A_	
		CCAACATGGTGAAACCC TCT		
		GGTGTACCACTTTGGG AGA		
		GC		
GAM2322	LOC151323 3'	AGATAGAATCTCACTATGTTG 81024	AACCC_	
		CAACATGGTGA ATCT		
		GTTGTATCACT TAGA		
		CTAAGA		
GAM2322	LOC151475 5'	AGACGAGGTTTCACCATGTTGG 86582 A	CA_	
	CCA	TG CCAACATGGTGAAACC TCT		
		AC GGTGTACCACTTTGG AGA		
		C AGC		
GAM2322	LOC151701 3'	AGACGGGGTTTCACCATGTTGG 86663 A	A_	
	CCA	TG CCAACATGGTGAAACCC TCT		
		AC GGTGTACCACTTTGGG AGA		
		C GC		
GAM2322	LOC152137 3'	GGGTTTCACCATGTTGGCCA 81321 A		
		TG CCAACATGGTGAAACCC		
		AC GGTGTACCACTTTGGG		
		C		
GAM2322	LOC152300 3'	AGACAGGGTTTCACCATATTGG 81379 A C	A_	
	CCA	TG CCAA ATGGTGAAACCC TCT		
		AC GGTT TACCACTTTGGG AGA		
		C A AC		
GAM2322	LOC152343 3'	AGGGGGTGTACCATGTTGGCC 81418 A	A A	
	A	TG CCAACATGGTGA ACCC TCT		

	AC GGTGTGACCACT TGGG GGA	
	C G _	
GAM2322 LOC152343 3'	GGTTTCACCATGTTGCCCA 81430 AC	
	TG CAACATGGTGAAACC	
	AC GTTGTACCACTTTGG	
	CC	
GAM2322 LOC152445 3'	AGACAGGGTTTCACCATGTT 86926	A_
	AACATGGTGAAACCC TCT	
	TTGTACCACTTTGGG AGA	
	AC	
GAM2322 LOC152719 5'	AGACGGGGTTTCACCATGTTGG 87014	A_
TCA	TGACCAACATGGTGAAACCC TCT	
	ACTGGTTGTACCACTTTGGG AGA	
	GC	
GAM2322 LOC152794 5'	AGATGGGGTTTCATCATGTTGG 81553 A	_
CCA	TG CCAACATGGTGAAACCC ATCT	
	AC GGTGTACTACTTTGGG TAGA	
	C G	
GAM2322 LOC152851 3'	AGACAGGATTTCACTATGTTGG 81588	_ CA
TCA	TGACCAACATGGTGAAA CC TCT	
	ACTGGTTGTATCACTTT GG AGA	
	A AC	
GAM2322 LOC153077 3'	AGATGGGGCTTCACCATGTTGG 87109 A	A_
CCA	TG CCAACATGGTGAA CCCATCT	
	AC GGTGTACCACTT GGGTAGA	
	C CG	
GAM2322 LOC153606 5'	AGATAGGGTTTCACCATGTTGG 87254 A	_
CCA	TG CCAACATGGTGAAACCC ATCT	
	AC GGTGTACCACTTTGGG TAGA	
	C A	
GAM2322 LOC153688 3'	AGACAGGGTTTCACCATGTTGG 87290 A	A_
CCG	TG CCAACATGGTGAAACCC TCT	
	GC GGTGTACCACTTTGGG AGA	
	C AC	
GAM2322 LOC153811 3'	GGTTTCACCACGTTGGCCA 81843 A A	
	TG CCAAC TGGTGAAACC	
	AC GGTG ACCACTTTGG	
	C C	
GAM2322 LOC154282 5'	AGATGGTGTTCACCATGTTGG 87398 A	_
CCA	TG CCAACATGGTGAAAC CCATCT	

		AC GGTGTACCACTTTG GGTAGA		
		C T		
GAM2322	LOC154877 3'	AGACAGGGTCTCACCATGTTGG 87522	A	A_
		CCAACATGGTGA ACCC TCT		
		GGTTGTACCACT TGGG AGA		
		C AC		
GAM2322	LOC154877 3'	GGTTTCACCATGTTGCCCA 87568 AC		
		TG CAACATGGTGAAACC		
		AC GTTGTACCACTTTGG		
		CC		
GAM2322	LOC155372 3'	AGACGGAATTTACCATGGTGG 82256	A A	C_ A
	CCA	TG CCA CATGGTGAAA CC TCT		
		AC GGT GTACCACTTT GG AGA		
		C G AA C		
GAM2322	LOC157506 3'	AGACGGGGTTTCACCATGTTGG 82360		A_
	TCA	TGACCAACATGGTGAAACCC TCT		
		ACTGGTTGTACCACTTTGGG AGA		
		GC		
GAM2322	LOC157623 3'	AGATGGAGTTTCACCATATTGC 82409	AC C	_
	CCA	TG CAA ATGGTGAAAC CCATCT		
		AC GTT TACCACTTTG GGTAGA		
		CC A A		
GAM2322	LOC157798 5'	AGACGGGGTTTCACCTTGTTGG 87851	A T	A_
	CCA	TG CCAACA GGTGAAACCC TCT		
		AC GGTTGT CCACTTTGGG AGA		
		C T GC		
GAM2322	LOC158014 5'	AGACGGAGTTTCACCATGTT 82550	_	A
		AACATGGTGAAAC CC TCT		
		TTGTACCACTTTG GG AGA		
		A C		
GAM2322	LOC158310 5'	AGACAGGGTTTCACAATGTTG 88072	G	A_
		CAACAT GTGAAACCC TCT		
		GTTGTA CACTTTGGG AGA		
		A AC		
GAM2322	LOC158402 5'	GGTTTCACCGTGTTGGCCA 88150	A	
		TG CCAACATGGTGAAACC		
		AC GGTTGTGCCACTTTGG		
		C		
GAM2322	LOC158476 3'	AGACAGGGTTTCACCATATTGG 88179	A C	A_
	CCA	TG CCAA ATGGTGAAACCC TCT		

		AC GGT TACCACTTTGGG AGA	
		C A AC	
GAM2322	LOC158476 3'	AGACAGGGTTTCACCATGTTGG 88182	A_
	TCA	TGACCAACATGGTGAAACCC TCT	
		ACTGGTTGTACCACTTTGGG AGA	
		AC	
GAM2322	LOC158549 5'	AGATAGGGGTTTCACCGTGTT 88214	—
		AACATGGTGAAACCC ATCT	
		TTGTGCCACTTTGGG TAGA	
		GA	
GAM2322	LOC158668 3'	GGTTTCACCATGCTGGTCA 69903 A	
		TGACCA CATGGTGAAACC	
		ACTGGT GTACCACTTTGG	
		C	
GAM2322	LOC158865 5'	AGATGGGGACTTCACCGTGTTG 88304 A	A_
	GCCA	TG CCAACATGGTGAA CCCATCT	
		AC GGTGTGCCACTT GGGTAGA	
		C CAG	
GAM2322	LOC160646 3'	AGATGGGGCTTCACCATGTTGG 83104 A	A_
	CCA	TG CCAACATGGTGAA CCCATCT	
		AC GGTGTACCACTT GGGTAGA	
		C CG	
GAM2322	LOC161829 3'	AGATGGGGTTTCACCATGTTGG 83182 A	—
	CCA	TG CCAACATGGTGAAACCC ATCT	
		AC GGTGTACCACTTTGGG TAGA	
		C G	
GAM2322	LOC162427 3'	GGGTTTCACCATGTTGGCCA 83227 A	
		TG CCAACATGGTGAAACCC	
		AC GGTGTACCACTTTGGG	
		C	
GAM2322	LOC169611 3'	AGACAGGATTTACCATGTTGG 83634 A	_ CA
	CCA	TG CCAACATGGTGAAA CC TCT	
		AC GGTGTACCACTTT GG AGA	
		C A AC	
GAM2322	LOC169611 3'	GGGTTTCACCACGTTGGCCA 83657 A A	
		TG CCAAC TGGTGAAACCC	
		AC GGTG ACCACTTTGGG	
		C C	
GAM2322	LOC170082 5'	AGATGGGGTTTCACCATGTT 83437	—
		AACATGGTGAAACCC ATCT	

TTGTACCACTTTGGG TAGA

G

GAM2322 LOC196047 5' GGGTTTCACCATGTCGGCCA 91160 A A

TG CC ACATGGTGAAACCC

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AC GG TGTACCACTTTGGG

C C

GAM2322 LOC196264 3' AGACGGGGTTTCACCATTTTGG 88979 A C A_

CCA TG CCAA ATGGTGAAACCC TCT

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AC GGTT TACCACTTTGGG AGA

C T GC

GAM2322 LOC196411 3' AGATGGGGTTTCACTATGTTGG 89039 A _

CCA TG CCAACATGGTGAAACCC ATCT

|| || || || || || || || || || ||

AC GGTTGTATCACTTTGGG TAGA

C G

GAM2322 LOC196529 3' AGACAGGGTTTCACTACGTTGG 89121 A A A_

CCA TG CCAAC TGGTGAAACCC TCT

|| || || || || || || || || || ||

AC GGTTG ATCACTTTGGG AGA

C C AC

GAM2322 LOC196529 3' AGATGGTGTTTCCCCACGTTGG 89122 A T _

TCA TGACCAAC TGG GAAAC CCATCT

||||| || || || || || || || || || || ||

ACTGGTTG ACC CTTTG GG TAGA

C C T

GAM2322 LOC197358 3' AGACGGGGTTTCATCATGTTGG 89412 A A_

CCA TG CCAACATGGTGAAACCC TCT

|| || || || || || || || || || ||

AC GGTTGTACTACTTTGGG AGA

C GC

GAM2322 LOC197358 3' AGATGGGGTTTCACCATGTTGA 89417 C _

TCA TGA CAACATGGTGAAACCC ATCT

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ACT GTTGTACCACTTTGGG TAGA

A G

GAM2322 LOC199699 3' AGACAGGGTTTCACCGTGTT 89665 A_

AACATGGTGAAACCC TCT

||||| || || || || || || || || || || ||

TTGTGCCACTTTGGG AGA

AC

GAM2322 LOC199725 5' AGACGGGATTTACCATGTTGG 91408 _ A

TCA TGACCAACATGGTGAAA CCC TCT

||||| || || || || || || || || || || ||

ACTGGTTGTACCACTTT GGG AGA

A C

GAM2322 LOC199786 3' AGATGGGGTTTCACCATGTTGG 89740 A _

CCA TG CCAACATGGTGAAACCC ATCT

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Accession	Gene	Position	Sequence	Length	GC Content	GC Skew	GC Bias	GC Bias2	GC Bias4	GC Bias8	GC Bias16	GC Bias32	GC Bias64	GC Bias128	GC Bias256	GC Bias512	GC Bias1024	GC Bias2048	GC Bias4096	GC Bias8192	GC Bias16384	GC Bias32768	GC Bias65536	GC Bias131072	GC Bias262144	GC Bias524288	GC Bias1048576	GC Bias2097152	GC Bias4194304	GC Bias8388608	GC Bias16777216	GC Bias33554432	GC Bias67108864	GC Bias134217728	GC Bias268435456	GC Bias536870912	GC Bias1073741824	GC Bias2147483648	GC Bias4294967296	GC Bias8589934592	GC Bias17179869184	GC Bias34359738368	GC Bias68719476736	GC Bias137438953472	GC Bias274877906944	GC Bias549755813888	GC Bias1099511627776	GC Bias2199023255552	GC Bias4398046511104	GC Bias8796093022208	GC Bias17592186044416	GC Bias35184372088832	GC Bias70368744177664	GC Bias140737488355328	GC Bias281474976710656	GC Bias562949953421312	GC Bias1125899906842624	GC Bias2251799813685248	GC Bias4503599627370496	GC Bias9007199254740992	GC Bias18014398509481984	GC Bias36028797018963968	GC Bias72057594037927936	GC Bias144115188075855872	GC Bias288230376151711744	GC Bias576460752303423488	GC Bias1152921504606846976	GC Bias2305843009213693952	GC Bias4611686018427387904	GC Bias9223372036854775808	GC Bias18446744073709551616	GC Bias36893488147419103232	GC Bias73786976294838206464	GC Bias147573952589676412928	GC Bias295147905179352825856	GC Bias590295810358705651712	GC Bias1180591620717411303424	GC Bias2361183241434822606848	GC Bias4722366482869645213696	GC Bias9444732965739290427392	GC Bias18889465931478580854784	GC Bias37778931862957161709568	GC Bias75557863725914323419136	GC Bias151115727451828646838272	GC Bias302231454903657293676544	GC Bias604462909807314587353088	GC Bias1208925819614629174706176	GC Bias2417851639229258349412352	GC Bias4835703278458516698824704	GC Bias9671406556917033397649408	GC Bias19342813113834066795298816	GC Bias38685626227668133590597632	GC Bias77371252455336267181195264	GC Bias154742504910672534362390528	GC Bias309485009821345068724781056	GC Bias618970019642690137449562112	GC Bias1237940039285380274899124224	GC Bias2475880078570760549798248448	GC Bias4951760157141521099596496896	GC Bias9903520314283042199192993792	GC Bias19807040628566084398385987584	GC Bias39614081257132168796771975168	GC Bias79228162514264337593543950336	GC Bias158456325028528675187087900672	GC Bias316912650057057350374175801344	GC Bias633825300114114700748351602688	GC Bias1267650600228229401496703205376	GC Bias2535301200456458802993406410752	GC Bias5070602400912917605986812821504	GC Bias10141204801825835211973625643008	GC Bias20282409603651670423947251286016	GC Bias40564819207303340847894502572032	GC Bias81129638414606681695789005144064	GC Bias162259276829213363391578010288128	GC Bias324518553658426726783156020576256	GC Bias649037107316853453566312041152512	GC Bias1298074214633706907132624082305024	GC Bias2596148429267413814265248164610048	GC Bias5192296858534827628530496329220096	GC Bias10384593717069655257060992658440192	GC Bias20769187434139310514121985316880384	GC Bias41538374868278621028243970633760768	GC Bias83076749736557242056487941267521536	GC Bias166153499473114484112975882535043072	GC Bias332306998946228968225951765070086144	GC Bias664613997892457936451903530140172288	GC Bias1329227995784915872903807060280344576	GC Bias2658455991569831745807614120560689152	GC Bias5316911983139663491615228241121378304	GC Bias10633823966279326983230456482242756608	GC Bias21267647932558653966460912964485513216	GC Bias42535295865117307932921825928971026432	GC Bias85070591730234615865843651857942052864	GC Bias170141183460469231731687303715884105728	GC Bias340282366920938463463374607431768211456	GC Bias680564733841876926926749214863536422912	GC Bias1361129467683753853853498429727072845824	GC Bias2722258935367507707706996859454145691648	GC Bias5444517870735015415413993718908291383296	GC Bias10889035741470030830827987437816582766592	GC Bias21778071482940061661655974875633165533184	GC Bias43556142965880123323311949751266331066368	GC Bias87112285931760246646623899502532662132736	GC Bias174224571863520493293247799005065324265472	GC Bias34844914
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		ATTGGTTGTACCACTTTGGG	AGA	
		AC		
GAM2322	LOC201173 5'	AGACGGAGTTTCACCATGTTGG	88667	_ A
	TCA	TGACCAACATGGTGAAAC	CC TCT	
		ACTGGTTGTACCACTTTG	GG AGA	
		A C		
GAM2322	LOC201220 5'	AGATGGAGTTTCACCATGTTGG	88703	_
	TCA	TGACCAACATGGTGAAAC	CCATCT	
		ACTGGTTGTACCACTTTG	GGTAGA	
		A		
GAM2322	LOC201294 3'	AGACGGGGTTTCACCATGTTGG	89572	A A_
	CCA	TG CCAACATGGTGAAACCC	TCT	
		AC GGTGTACCACTTTGGG	AGA	
		C GC		
GAM2322	LOC201411 3'	AGACAGGGTTTCACCATGTTGG	63634	A_
	TCA	TGACCAACATGGTGAAACCC	TCT	
		ACTGGTTGTACCACTTTGGG	AGA	
		AC		
GAM2322	LOC201626 3'	GGGTTTCGCCACGTTGGCCA	90436	A A
		TG CCAAC TGGTGAAACCC		
		AC GGTG ACCGCTTTGGG		
		C C		
GAM2322	LOC201627 3'	AGATGGGGTTTCTCCATGTTGG	90448	T _
	TCA	TGACCAACATGG GAAACCC	ATCT	
		ACTGGTTGTACC CTTTGGG	TAGA	
		T G		
GAM2322	LOC202460 5'	AGATGGGGTTTCACCATGTAGG	90663	A A _
	CCA	TG CC ACATGGTGAAACCC	ATCT	
		AC GG TGTACCACTTTGGG	TAGA	
		C A G		
GAM2322	LOC202934 3'	AGACAGGGTTTCACCACGTTGG	92025	A A A_
	CCA	TG CCAAC TGGTGAAACCC	TCT	
		AC GGTG ACCACTTTGGG	AGA	
		C C AC		
GAM2322	LOC203197 3'	AGATGGGGTTTCGCCATGTTGG	90804	A _
	CCA	TG CCAACATGGTGAAACCC	ATCT	
		AC GGTGTACCGCTTTGGG	TAGA	
		C G		
GAM2322	LOC203339 3'	AGATGGGGTTTCACCATGTT	92204	_
		AACATGGTGAAACCC	ATCT	

		TTGTACCACTTTGGG TAGA		
		G		
GAM2322	LOC203350 3'	AGACGGGGTTTCACCGTGTGG 92226	A	A_
	CCA	TG CCAACATGGTGAAACCC TCT		
		AC GGTTGTGCCACTTTGGG AGA		
		C GC		
GAM2322	LOC203378 3'	AGATGGGATTTTACCACATTGG 92271	CA	_
	TCA	TGACCAA TGGTGAAA CCCATCT		
		ACTGGTT ACCATTTT GGGTAGA		
		AC A		
GAM2322	LOC204804 3'	AGATGAGGTTTCACCTTGTGG 91033	A T	_
	CCA	TG CCAACA GGTGAAACC CATCT		
		AC GGTTGT CCACTTTGG GTAGA		
		C T A		
GAM2322	LOC219445 5'	AGACGGTGTTTCACCATATTGG 93195	A C	_ A
	CCA	TG CCAA ATGGTGAAAC CC TCT		
		AC GGTT TACCACTTTG GG AGA		
		C A T C		
GAM2322	LOC219673 5'	GGGTTTCACCATGTTGGCCA 94629	A	
		TG CCAACATGGTGAAACCC		
		AC GGTTGTACCACTTTGGG		
		C		
GAM2322	LOC219735 3'	AGACGGGGTTTCACCGTGTT 94722	A_	
		AACATGGTGAAACCC TCT		
		TTGTGCCACTTTGGG AGA		
		GC		
GAM2322	LOC219894 3'	AGATGGGGTTTCACCGTGTT 94896	_	
		AACATGGTGAAACCC ATCT		
		TTGTGCCACTTTGGG TAGA		
		G		
GAM2322	LOC220074 3'	AGACAAGGTTTCGCCATGTTGG 59954	A	CA_
	CCA	TG CCAACATGGTGAAACC TCT		
		AC GGTTGTACCGCTTTGG AGA		
		C AAC		
GAM2322	LOC220074 3'	AGACGGGGTTTCACCATGTT 59955	A_	
		AACATGGTGAAACCC TCT		
		TTGTACCACTTTGGG AGA		
		GC		
GAM2322	LOC220074 3'	AGATGGGGTTTCGCCATGTTGG 59961	A	_
	CCA	TG CCAACATGGTGAAACCC ATCT		

		AC GGTGTACCGCTTTGGG TAGA		
		C G		
GAM2322	LOC221060 3'	AGACGGTGTTTCACCATGTTAG 94828	C	_ A
	TCA	TGAC AACATGGTGAAAC CC TCT		
		ACTG TTGTACCACTTTG GG AGA		
		A T C		
GAM2322	LOC221296 3'	AGACGGGGTTCACCATGCTGG 93602	A A	A_
	CCA	TG CCA CATGGTGAAACCC TCT		
		AC GGT GTACCACTTTGGG AGA		
		C C GC		
GAM2322	LOC221692 3'	AGATGAAGGCTCCATGCTGTGT 93851	_ A	TGAAA _
	CA	TGAC CA CATGG CC CATCT		
		ACTG GT GTACC GG GTAGA		
		T C TC__ AA		
GAM2322	LOC222031 3'	AGACGAGGTTTCAACATGTTGG 95667	A	G CA_
	CCA	TG CCAACATG TGAAACC TCT		
		AC GGTGTAC ACTTTGG AGA		
		C A AGC		
GAM2322	LOC222068 3'	AGATGGGGTTTTACCATGTTGG 94268	A	_
	CCA	TG CCAACATGGTGAAACCC ATCT		
		AC GGTGTACCATTTTGGG TAGA		
		C G		
GAM2322	LOC222070 5'	AGACGGTGTTTCACCATGTTGG 95806	A	_ A
	CCA	TG CCAACATGGTGAAAC CC TCT		
		AC GGTGTACCACTTTG GG AGA		
		C T C		
GAM2322	LOC222224 5'	AGACAGGGTTCACCATGTTGG 95868	A	A_
	CCA	TG CCAACATGGTGAAACCC TCT		
		AC GGTGTACCACTTTGGG AGA		
		C AC		
GAM2322	LOC245771 5'	AGATGGGGTTTCATCATGTTGG 94466	A	_
	CCA	TG CCAACATGGTGAAACCC ATCT		
		AC GGTGTACTACTTTGGG TAGA		
		C G		
GAM2322	LOC253664 3'	AGATGGGGTTTCCCATGTTGG 96456	A	T _
	CCA	TG CCAACATGG GAAACCC ATCT		
		AC GGTGTACC CTTTGGG TAGA		
		C C G		
GAM2322	LOC253666 3'	AGACGGGGTTCACCATGTT 96757	A_	
		AACATGGTGAAACCC TCT		

		TTGTACCACTTTGGG AGA		
		GC		
GAM2322	LOC253805 3'	AGATAGGGTTTCACAATGTTGG 98166	A	G _
	CCA	TG CCAACAT GTGAAACCC ATCT		
		AC GGTGTGTA CACTTTGGG TAGA		
		C A A		
GAM2322	LOC254018 5'	AGATGGGGTTTCGCCATGTT 98736		_
		AACATGGTGAAACCC ATCT		
		TTGTACCGCTTTGGG TAGA		
		G		
GAM2322	LOC254219 3'	AGATGAACAGGGCTCCATGTTG 98318		TGAAA ____
		CAACATGG CC CATCT		
		GTTGTACC GG GTAGA		
		TCG__ ACAA		
GAM2322	LOC254268 3'	AGATGGGGTTTCACCATGTTGG 97137	A	_
	CCA	TG CCAACATGGTGAAACCC ATCT		
		AC GGTGTACCACTTTGGG TAGA		
		C G		
GAM2322	LOC254295 5'	AGACGGGGTTTCACCGTGTT 97886		A_
		AACATGGTGAAACCC TCT		
		TTGTGCCACTTTGGG AGA		
		GC		
GAM2322	LOC254655 3'	AGACGGGGTTTCACCATGTTGG 97213	A	A_
	CCA	TG CCAACATGGTGAAACCC TCT		
		AC GGTGTACCACTTTGGG AGA		
		C GC		
GAM2322	LOC254672 3'	GGTTTCACCATCTTGGTCA 96297	C	
		TGACCAA ATGGTGAAACC		
		ACTGGTT TACCACTTTGG		
		C		
GAM2322	LOC255465 3'	AGACGGGGTTTCACCATGTTGGC 99100	A	A
	CA	TG CCAACATGGTGAAACCC TCT		
		AC GGTGTACCACTTTGGG AGA		
		C C		
GAM2322	LOC255497 3'	AGACGGGGTTTCACCATGTTGG 98982	A	A_
	CCA	TG CCAACATGGTGAAACCC TCT		
		AC GGTGTACCACTTTGGG AGA		
		C GC		
GAM2322	LOC255645 3'	AGATGGGTGAGAGATGTGATCA 98471	CCA	GGTGAA
		TGA ACAT ACCCATCT		

		ACT TGTA TGGGTAGA		
		AG_ GAGAG_		
GAM2322	LOC255927 5'	AGACGGGGTTTCACCATCTTGG 97709	A C	A_
	CCA	TG CCAA ATGGTGAAACCC TCT		
		AC GGTT TACCACTTTGGG AGA		
		C C GC		
GAM2322	LOC256221 3'	AGACGGGGTTTCACCGTGTT 96905		A_
		AACATGGTGAAACCC TCT		
		TTGTGCCACTTTGGG AGA		
		GC		
GAM2322	LOC256267 3'	AGATGGGTTTTGCCATGTTGTC 98604	AC	TG
	CA	TG CAACATGG AAACCCATCT		
		AC GTTGTACC TTTGGGTAGA		
		CT GT		
GAM2322	LOC256306 3'	AGACGGGGTTTCACCATGTTGG 98503	A	A_
	CCA	TG CCAACATGGTGAAACCC TCT		
		AC GGTTGTACCACTTTGGG AGA		
		C GC		
GAM2322	LOC256364 5'	GATGGGTTGTACCTGGCCA 96445	A ACAT	A
		TG CCA GGTG AACCCATC		
		AC GGT CCAT TTGGGTAG		
		C _ G		
GAM2322	LOC257127 5'	AGACAGGTTTTTGCCATGTTGG 98494	A	TG _ CA
	CCA	TG CCAACATGG AAA CC TCT		
		AC GGTTGTACC TTT GG AGA		
		C GT T AC		
GAM2322	LOC257465 3'	AGATGGTGTTTCACCATGTTGG 82489	A	_
	CCA	TG CCAACATGGTGAAAC CCATCT		
		AC GGTTGTACCACTTTG GG TAGA		
		C T		
GAM2322	LOC257486 3'	AGACGGGGTTTCACCATGTTGG 69764	A	A_
	CCA	TG CCAACATGGTGAAACCC TCT		
		AC GGTTGTACCACTTTGGG AGA		
		C GC		
GAM2322	LOC51008 5'	AGATGGGGTTTCTCCATGTTGG 32527	T	_
	TCA	TGACCAACATGG GAAACCC ATCT		
		ACTGGTTGTACC CTTTGGG TAGA		
		T G		
GAM2322	LOC51159 5'	AGACGGGATTTCACCATGTTGG 33026	A	_ A
	CCA	TG CCAACATGGTGAAA CCC TCT		

		AC GGTGTGACCACTTT GGG AGA		
		C A C		
GAM2322	LOC51161	3' AGATGGGTCCCTGCACTTGG 33037	ACAT	AA___
		CCA GGTG ACCCATCT		
		GGT TCAC TGGGTAGA		
		_____ GTCCC		
GAM2322	LOC51193	5' AGACGGGGTTTCCCCATGTTGG 33357	T	A_
		TCA TGACCAACATGG GAAACCC TCT		
		ACTGGTTGTACC CTTTGGG AGA		
		C GC		
GAM2322	LOC51200	3' AGACAGGGTTTCTCCATGTTGG 33433	T	A_
		TCA TGACCAACATGG GAAACCC TCT		
		ACTGGTTGTACC CTTTGGG AGA		
		T AC		
GAM2322	LOC57107	3' AGATGGGGTTTCACTATGTTGG 40180		—
		TCA TGACCAACATGGTGAAACCC ATCT		
		ACTGGTTGTATCACTTTGGG TAGA		
		G		
GAM2322	LOC57146	3' AGATGGGGTTTCACCATGTTGG 40291		—
		TCA TGACCAACATGGTGAAACCC ATCT		
		ACTGGTTGTACCACTTTGGG TAGA		
		G		
GAM2322	LOC89932	3' AGACGGGGTTTCTCCATGTTGG 61440	T	A_
		TCA TGACCAACATGG GAAACCC TCT		
		ACTGGTTGTACC CTTTGGG AGA		
		T GC		
GAM2322	LOC89932	3' AGATGGGGTTTCACCATGTTGG 61444	A	—
		CCA TG CCAACATGGTGAAACCC ATCT		
		AC GGTGTGACCACTTTGGG TAGA		
		C G		
GAM2322	LOC90288	3' AGATGGGGTTTCACCATATTGG 62770	C	—
		TCA TGACCAA ATGGTGAAACCC ATCT		
		ACTGGTT TACCACTTTGGG TAGA		
		A G		
GAM2322	LOC90333	3' AGACTGGGTTTCACCGTGTT 62955		—
		AACATGGTGAAACCCA TCT		
		TTGTGCCACTTTGGGT AGA		
		C		
GAM2322	LOC90459	3' GGTTTCACCATGTTGGTCA 63559		
		TGACCAACATGGTGAAACC		

ACTGGTTGTACCACTTTGG

GAM2322 LOC90485 3' GGGTTTCACCATGTTGGCCA 63703 A
TG CCAACATGGTCAAACCC
|| |||||
AC GGTGTACCACTTTGGG
C

GAM2322 LOC90591 3' AGACGGGGCTTCACTATGTTGG 64141 A A_ A
CCA TG CCAACATGGTGAA CCC TCT
|| ||||| |||
AC GGTGTATCACTT GGG AGA
C CG C

GAM2322 LOC91250 5' AGATGGGGTTTCATCATGTTGG 65904 A _
CCA TG CCAACATGGTCAAACCC ATCT
|| ||||| |||||
AC GGTGTACTACTTTGGG TAGA
C G

GAM2322 LOC91561 5' AGACGGGGTTTCTCCATGTTGG 67039 T A_
TCA TGACCAACATGG GAAACCC TCT
||||||| ||||| |||
ACTGGTTGTACC CTTTGGG AGA
T GC

GAM2322 LOC91893 3' AGACGAGGTTTCACCGTGTT 68066 CA_
AACATGGTGAAACC TCT
||||||| |||
TTGTGCCACTTTGG AGA
AGC

GAM2322 LOC92148 5' AGACGGGGTTTCACCGTGTTAG 68870 C A_
TCA TGAC AACATGGTCAAACCC TCT
||| ||||| |||
ACTG TTGTGCCACTTTGGG AGA
A GC

GAM2322 LOC92267 3' AGATGGGGTTTCACCATATTGG 69162 A C _
CCA TG CCAA ATGGTCAAACCC ATCT
|| ||| ||||| |||||
AC GGT TACCACTTTGGG TAGA
C A G

GAM2322 LOC92303 3' AGATGGGTTTCACCATGTTGGC 69384 A
CA TG CCAACATGGTCAAACCCATCT
|| ||||| |||||
AC GGTGTACCACTTTGGGTAGA
C

GAM2322 LOC92466 3' AGATGGGTTTTGCCATGTTGTC 69960 AC TG
CA TG CAACATGG AAACCCATCT
|| ||||| |||||
AC GTTGTACC TTTGGGTAGA
CT GT

GAM2322 LOC92689 3' AGACAGGGTTTCACCATGTTGG 70769 A A_
CCA TG CCAACATGGTCAAACCC TCT
|| ||||| ||||| |||

			AC GGTGTGACCACTTTGGG AGA		
			C AC		
GAM2322	LOC92841	3'	AGACAGGGTTTCACCATGTTGG 71242	A	A_
		CCA	TG CCAACATGGTGAAACCC TCT		
			AC GGTGTGACCACTTTGGG AGA		
			C AC		
GAM2322	LOC92841	3'	AGACGGGGTTTCACCATGTT 71243	A_	
			AACATGGTGAAACCC TCT		
			TTGTACCACTTTGGG AGA		
			GC		
GAM2322	LOC93349	3'	AGACGGGGTTTCACTATGTTGG 57261	A	A_
		CCA	TG CCAACATGGTGAAACCC TCT		
			AC GGTGTATCACTTTGGG AGA		
			C GC		
GAM2323	A2M	5'	TCTGGTCTCCTCCAGCTCCT 5231	ACCA	A AC
			AGGA GGAG GA TCAGA		
			TCCT CCTC CT GGTCT		
			CGA_ _ CT		
GAM2323	ABCD1	3'	CTCTGAGTCCCGTGGGGCC 5260	AA _ A	GAA
			GG CCA GG GA CTCAGAG		
			CC GGT CC CT GAGTCTC		
			GG G _ _		
GAM2323	ADD2	3'	TTGGGCTCCCTCCTGCCTCCT 34374	AC	A A
			AGGA CAGGAG GA CTCAG		
			TCCT GTCCTC CT GGGTT		
			CC C C		
GAM2323	ADD2	3'	TTGGGCTCCCTCCTGCCTCCT 34375	AC	A A
			AGGA CAGGAG GA CTCAG		
			TCCT GTCCTC CT GGGTT		
			CC C C		
GAM2323	ADD2	3'	TTGGGCTCCCTCCTGCCTCCT 34376	AC	A A
			AGGA CAGGAG GA CTCAG		
			TCCT GTCCTC CT GGGTT		
			CC C C		
GAM2323	ADD2	3'	TTGGGCTCCCTCCTGCCTCCT 34384	AC	A A
			AGGA CAGGAG GA CTCAG		
			TCCT GTCCTC CT GGGTT		
			CC C C		
GAM2323	ALDH3A1	3'	CTCACTGGCTCTCCTGGCCCT 7307	AA	AACTCA
			AGG CCAGGAGAG GAG		

			TCC GGCCTCTC	CTC		
			C_	GGTCA_		
GAM2323	ALDH3B2	3'	CTCTGAGCCTCAGTTTCCT	7341	CCAG	AGAA
			AGGAA GAG CTCAGAG			
			TCCTT CTC GAGTCTC			
			TGA_ C__			
GAM2323	AOC3	3'	TCCTCCTCCTGTTTCCT	14961	C	A ACTCA
			AGGAAC AGGAG GA			GA
			TCCTTG TCCTC CT			CT
			- - C__			
GAM2323	AQP2	3'	AGTTCTCTTTTGTCTCCT	6667	AC	
			AGGA CAGGAGAGAACT			
			TCCT GTTTTCTCTTGA			
			-			
GAM2323	AQP6	5'	CTCCTTTTCTCTCCCGGTACCT	55001	A A	CTCA
			AGG ACC GGAGAGAA			GAG
			TCC TGG CCTCTCTT			CTC
			A C TTC_			
GAM2323	B3GAT1	3'	TCTGCTCCTCTCCTGGGCC	55058	AA	AACT
			GG CCAGGAGAG			CAGA
			CC GGTCTCTC			GTCT
			CG CTC_			
GAM2323	B3GAT1	3'	TCTGCTCCTCTCCTGGGCC	38455	AA	AACT
			GG CCAGGAGAG			CAGA
			CC GGTCTCTC			GTCT
			CG CTC_			
GAM2323	BTG2	3'	AGGCCTCTCCTGATTCCT	23141	C	AA
			AGGAA CAGGAGAG			CT
			TCCTT GTCCTCTC			GA
			A CG			
GAM2323	CACNG1	3'	TCTCTGAGTTCTCCTGGGCTGC	7412	AA_ A	A
	C		GG CC GGAG GAACTCAGAGA			
			CC GG TCTC CTTGAGTCTCT			
			GTC G _			
GAM2323	CD5L	3'	CTCTGCTTGTTCTCCTGAGCCC	20875	AAC	AACT
	T		AGG CAGGAGAG			CAGAG
			TCC GTCCTCTT			GTCTC
			CGA GTTC			
GAM2323	CSH2	3'	AGTGCCTCTCCTGGCCCT	40975	AA	A_
			AGG CCAGGAGAG			ACT

			TCC GGCCTCTC TGA		
			C_ CG		
GAM2323	CSH2	3'	AGTGCCTCTCCTGGCCCT 42942	AA	A_
			AGG CCAGGAGAG ACT		
			TCC GGCCTCTC TGA		
			C_ CG		
GAM2323	CSH2	3'	AGTGCCTCTCCTGGCCCT 42943	AA	A_
			AGG CCAGGAGAG ACT		
			TCC GGCCTCTC TGA		
			C_ CG		
GAM2323	CSH2	3'	AGTGCCTCTCCTGGCCCT 42944	AA	A_
			AGG CCAGGAGAG ACT		
			TCC GGCCTCTC TGA		
			C_ CG		
GAM2323	CSHL1	3'	AGTGCCTCTCCTGGCCCT 42933	AA	A_
			AGG CCAGGAGAG ACT		
			TCC GGCCTCTC TGA		
			C_ CG		
GAM2323	CSHL1	3'	AGTGCCTCTCCTGGCCCT 42939	AA	A_
			AGG CCAGGAGAG ACT		
			TCC GGCCTCTC TGA		
			C_ CG		
GAM2323	CSHL1	3'	AGTGCCTCTCCTGGCCCT 42940	AA	A_
			AGG CCAGGAGAG ACT		
			TCC GGCCTCTC TGA		
			C_ CG		
GAM2323	CSHL1	3'	AGTGCCTCTCCTGGCCCT 42941	AA	A_
			AGG CCAGGAGAG ACT		
			TCC GGCCTCTC TGA		
			C_ CG		
GAM2323	CSHL1	3'	AGTGCCTCTCCTGGCCCT 8983	AA	A_
			AGG CCAGGAGAG ACT		
			TCC GGCCTCTC TGA		
			C_ CG		
GAM2323	CXorf6	3'	CTGGGTTCTGTCCCAGCTCC 19704	ACCA	G
			GGA GGA AGAACTCAG		
			CCT CCT TCTTGGGTC		
			CGAC G		
GAM2323	CYP8B1	5'	TCTCTGAGCTTTCTCCTGGTTA 16542	_	A
	CC		GG AACCAGGAGAGA CTCAGAGA		

			CC TTGGTCCTCTTT GAGTCTCT		
			A C		
GAM2323	DGKG	5'	TTCTGTCTCTCGGTTCCCT 9045	AG	ACT
			AGGAACC GAGAGA CAGAG		
			TCCTTGG CTCTCT GTCTT		
			— —		
GAM2323	DOCK1	3'	CTCTGAGTGTGTCTGGCTCT 9105	A	AGAGA
			GGA CCAGG ACTCAGAG		
			TCT GGTCT TGAGTCTC		
			C GTG__		
GAM2323	DVL3	3'	CTCCTGAATTCCTCTCCTGGTT 16642	G	_ C _
	ACT		AG AACCAGGAGAG AA TCAG AG		
			TC TTGGTCCTCTC TT AGTC TC		
			A C A C		
GAM2323	DVL3	3'	CTCTGAGCCTCAGTTCC 16643	CAG	AGAA
			GGAAC GAG CTCAGAG		
			CCTTG CTC GAGTCTC		
			A__ C__		
GAM2323	EFNA3	3'	CCTGACTCCTGGTGCC 18251	A	AGAAC A
			GG ACCAGGAG TCAG G		
			CC TGGTCCTC AGTC C		
			G ____ C		
GAM2323	EIF2C1	3'	CTCCTTTTCTCCTTATTCCT 25189	CC	CTCA
			AGGAA AGGAGAGAA GAG		
			TCCTT TCCTCTTTT CTC		
			AT C__		
GAM2323	EN2	3'	CTCCTTCCTCCTGCTCCT 9256	AC	A CTCA
			AGGA CAGGAG GAA GAG		
			TCCT GTCCTC CTT CTC		
			C_ _ C__		
GAM2323	GH1	3'	AGTGCCTCTCCTGGCCCT 6706	AA	A_
			AGG CCAGGAGAG ACT		
			TCC GGTCTCTC TGA		
			C_ CG		
GAM2323	GH1	3'	AGTGCCTCTCCTGGCCCT 42889	AA	A_
			AGG CCAGGAGAG ACT		
			TCC GGTCTCTC TGA		
			C_ CG		
GAM2323	GH1	3'	AGTGCCTCTCCTGGCCCT 42892	AA	A_
			AGG CCAGGAGAG ACT		

			TCC GGCCTCTC TGA		
			C_ CG		
GAM2323	GH1	3'	AGTGCCTCTCCTGGCCCT 42894	AA	A_
			AGG CCAGGAGAG ACT		
			TCC GGCCTCTC TGA		
			C_ CG		
GAM2323	GH1	3'	AGTGCCTCTCCTGGCCCT 42896	AA	A_
			AGG CCAGGAGAG ACT		
			TCC GGCCTCTC TGA		
			C_ CG		
GAM2323	GPR56	3'	CTAAGAGGTTCTCTCCAAGCC 20271	AACCA	_ AG
			GG GGAGAGAAC TC AG		
			CC CCTCTCTTG AG TC		
			GAA_ G AA		
GAM2323	HDAC7A	3'	CTGGTTCTCTTCTAACCCCT 31833	AACC	T
			AGG AGGAGAGAAC CAG		
			TCC TCTTCTCTTG GTC		
			CCAA _		
GAM2323	HDAC7A	3'	CTGGTTCTCTTCTAACCCCT 33925	AACC	T
			AGG AGGAGAGAAC CAG		
			TCC TCTTCTCTTG GTC		
			CCAA _		
GAM2323	IFITM2	5'	CTCTGAGCCCTCAGCCCCT 22233	AACCA	A_ AA
			AGG GG GAG CTCAGAG		
			TCC CC CTC GAGTCTC		
			_ GA CC		
GAM2323	IMPG2	5'	TCTGTCCTCTCCTCATTCT 33190	CC	AACT
			AGGAA AGGAGAG CAGA		
			TCCTT TCCTCTC GTCT		
			AC CT_		
GAM2323	KRT6A	3'	CTGTCCTCTCCTGGCCTCC 19897	A_	AACT
			GGA CCAGGAGAG CAG		
			CCT GGCCTCTC GTC		
			CC CT_		
GAM2323	LAG3	5'	TCTCCAAGGCCCTCTCCTGGTC 11253	_	AA_ CA
	TCC		GGA ACCAGGAGAG CT GAGA		
			CCT TGGTCCTCTC GA CTCT		
			C CCG AC		
GAM2323	LALBA	3'	CTCTGAGCCTTGGGCCCT 11257	AA	AGAGAA
			AGG CCAGG CTCAGAG		

			TCC GGTTC GAGTCTC			
			CG C_____			
GAM2323	LDB1	5'	CTGCCTCTCCTGGTGCC 15310	A	AACT	
			GG ACCAGGAGAG CAG			
			CC TGGTCCTCTC GTC			
			G C____			
GAM2323	LFG	3'	TCCCTGAGCCGTTCTCCTGAGT 77242	AC	AA_ A	
	CC		GGA CAGGAGAG CTCAG GA			
			CCT GTCCTCTT GAGTC CT			
			GA GCC C			
GAM2323	MAP4	5'	TCCCGGCGCTCTCCTGGCTCC 48799	A	AA CA	
			GGA CCAGGAGAG CT GA			
			CCT GGTCTCTC GG CT			
			C GC CC			
GAM2323	MAP4	5'	TCCCGGCGCTCTCCTGGCTCC 11450	A	AA CA	
			GGA CCAGGAGAG CT GA			
			CCT GGTCTCTC GG CT			
			C GC CC			
GAM2323	MDFI	3'	TCTCTACCTCTCCCTGCTCCT 19982	AC	A ACTC	
			AGGA CAGG GAGA AGAGA			
			TCCT GTCC CTCT TCTCT			
			C_ _ CCA_			
GAM2323	MGAT3	3'	TCCCTGCCTCCTGCCGGCTCCT 11565	A A _ A	ACT A	
			AGGA CC GG AG GA CAG GA			
			TCCT GG CC TC CT GTC CT			
			C _ G _ CC_ C			
GAM2323	MIF	5'	CTCTGCGCGGGTCTCCTGGTCC 11582	A	GAACT_	
	T		AGGA CCAGGAGA CAGAG			
			TCCT GGTCTCT GTCTC			
			_ GGGCGC			
GAM2323	MPP2	3'	TCTCTGAGCAGCCTCCTACCTC 60522	ACC	AGAA	
	C		GGA AGGAG CTCAGAGA			
			CCT TCCTC GAGTCTCT			
			CCA CGAC			
GAM2323	NGFB	3'	TTCTACACTCTCCTGGGCCC 11785	AA	AACTC	
			GG CCAGGAGAG AGAG			
			CC GGTCTCTC TCTT			
			CG ACA_			
GAM2323	PEA15	3'	GGGATCCTTTCCTGGTCCCT 15012	A	AA_	
			AGG ACCAGGAGAG CTC			

TCC TGGTCCTTTC GGG
 C CTA
 GAM2323 PFKFB4 3' CTGAGTTCTTTTGGTCCC 17085 A GA
 GG ACCAG GAGAACTCAG
 || |||| |||||
 CC TGGTT TTCTTGAGTC
 C _
 GAM2323 PIK3C2B 3' CTCCATTCTCCTGGCCCT 12095 AA AACTCA
 AGG CCAGGAGAG GAG
 || ||||| ||
 TCC GGTCTCTT CTC
 C_ AC____
 GAM2323 POU2F2 3' TCTCCAGCAAGTCTCCTGGCCT 12216 AA GAACTCA
 AGG CCAGGAGA GAGA
 || ||||| ||
 TCC GGTCTCT CTCT
 _ GAACGAC
 GAM2323 PRSS16 3' TCTCTGTGTGTCTCCTAGTCAC 20784 GA C GA T
 T AG AC AGGAGA AC CAGAGA
 || || |||| || |||||
 TC TG TCCTCT TG GTCTCT
 AC A G_ T
 GAM2323 PTMA 5' TCCCTGAACTCTCGCTTTCTT 12560 CC _ AAC A
 AGGAA AG GAGAG TCAG GA
 |||| || |||| |||| ||
 TTCTT TC CTCTC AGTC CT
 _ G A_ C
 GAM2323 RAB36 3' CTCTGAGATCCCTAGGTCCT 18165 A _ A GAA
 AGGA CC AGG GA CTCAGAG
 |||| || || || |||||
 TCCT GG TCC CT GAGTCTC
 _ A _ A_
 GAM2323 RAD54L 5' TCCCTGAGTCTGATCCTGGTTT 14553 G_ A A
 C GGAACCAGGA AGA CTCAG GA
 ||||| || |||| ||
 CTTTGGTCCT TCT GAGTC CT
 AG _ C
 GAM2323 RBP5 3' CTCTGGGTCCCTCCTCACCCCT 49800 AACC A A
 AGG AGGAG GA CTCAGAG
 || |||| || |||||
 TCC TCCTC CT GGGTCTC
 CCAC C _
 GAM2323 SLA2 3' CTCCAGTGCTCCTACTGGTTCC 50888 GA_ A CA
 GGAACCAG GAG ACT GAG
 ||||| || || ||
 CCTTGGTC CTC TGA CTC
 ATC G C_
 GAM2323 SREBF2 3' CTGAGTTTCTCTCCTGAACC 17189 AAC _
 CT AGG CAGGAGAGA ACTCAG
 || ||||| |||||

			TCC GTCCTCTCT TGAGTC		
			CAA CTT		
GAM2323	SUFU	3'	TCCCTGAACTCTCTTTG 32941	AC	A
			CAGGAGAGA TCAG GA		
			GTTCTCTCT AGTC CT		
			CA C		
GAM2323	THY1	3'	TCTCTGAGTCAGCTGACCCCT 21900	AACCA	AGA A
			AGG GG GA CTCAGAGA		
			TCC TC CT GAGTCTCT		
			CCCAG GA _ _		
GAM2323	TLR9	5'	TCTCTGAGCCGCTGCTGCCCT 34310	AAC	G AGAA
			AGG CAG AG CTCAGAGA		
			TCC GTC TC GAGTCTCT		
			CC_ G GCC_		
GAM2323	TNS	3'	GAGGCTCTCTCCTGGTGCCT 42951	A	A_
			AGG ACCAGGAGAGA CTC		
			TCC TGGTCCTCTCT GAG		
			G CG		
GAM2323	TRAP100	3'	CTCCAGGATGTCTCCCGGTTTC 29723	A	GAA CA
	T		AGGAACC GGAGA CT GAG		
			TCTTTGG CCTCT GG CTC		
			C GTA AC		
GAM2323	UBE2G2	3'	TCTGGGTCCTTCCTGGTTCC 65497	A	A
			GGAACCAGGAG GA CTCAGA		
			CCTTGGTCCTT CT GGGTCT		
			C _		
GAM2323	VPREB3	3'	CTCTGAGCCTTGCTTCC 26310	C	AGAGAA
			GGAA CAGG CTCAGAG		
			CCTT GTTC GAGTCTC		
			C C _ _ _		
GAM2323	BHMT	3'	TCTCCAACTCTAGCCTGGTTT 9933	AG	ACTCA
	C		GGAACCAGG AGA GAGA		
			CTTTGGTCC TCT CTCT		
			GA CAAAC		
GAM2323	BLCAP	3'	GAGACTTTCTCCTGGCCCCT 22943	AA	A_
			AGG CCAGGAGAGA CTC		
			TCC GGTCCTCTTT GAG		
			CC CA		
GAM2323	C1orf34	3'	CTCTGAGTTCTGGGGCC 61305	AA	GGAGA
			GG CCA GAACTCAGAG		

CC GGT CTTGAGTCTC
 GG _____
 GAM2323 C5orf4 3' TCTCTGAGAGCATCCCAGACTC 51496 ACCA A GAA_
 C GGA GG GA CTCAGAGA
 ||| ||| |||||
 CCT CC CT GAGTCTCT
 CAGA _ ACGA
 GAM2323 CABP4 5' TCTCTGAGCCCTGTTATCC 59749 AC_ AGAGAA
 GGA CAGG CTCAGAGA
 ||| ||| |||||
 CCT GTCC GAGTCTCT
 ATT C_____
 GAM2323 CLDN4 3' CTCTGAGTCCTCTGCCCCTTCC 8954 CCA _ A
 GGAA GG AGAG ACTCAGAG
 ||| ||| |||||
 CCTT CC TCTC TGAGTCTC
 CC_ G C
 GAM2323 DKFZP434L1435 5' CCTGAGTTTCTGAGCCCT 93787 AAC GAGA A
 AGG CAGGA ACTCAG G
 ||| ||| |||||
 TCC GTCTT TGAGTC C
 CGA _____ C
 GAM2323 DKFZP434L1435 5' CTCTGGGCCCCCTGCCTCCT 93788 AC AGAGAA
 AGGA CAGG CTCAGAG
 ||| ||| |||||
 TCCT GTCC GGGTCTC
 CC CC_____
 GAM2323 DKFZP434L1435 5' CCTGAGTTTCTGAGCCCT 99584 AAC GAGA A
 AGG CAGGA ACTCAG G
 ||| ||| |||||
 TCC GTCTT TGAGTC C
 CGA _____ C
 GAM2323 DKFZP434L1435 5' CCTGAGTTTCTGAGCCCT 99684 AAC GAGA A
 AGG CAGGA ACTCAG G
 ||| ||| |||||
 TCC GTCTT TGAGTC C
 CGA _____ C
 GAM2323 DPCR1 3' TCTCTGAGTTCTCAGGACCCT 55999 AA AGGA
 AGG CC GAGAACTCAGAGA
 ||| ||| |||||
 TCC GG CTCTTGAGTCTCT
 CA A_____
 GAM2323 EPB41L1 3' TCTCTGAGCTCAGAAAGTGCC 71115 A CAGGA AA
 GG AC GAG CTCAGAGA
 ||| ||| |||||
 CC TG CTC GAGTCTCT
 G AAAGA ____
 GAM2323 FLJ13441 3' TCTCCAAGAAGCCCTGGTTTCT 43918 AGAGAA CA
 AGGAACCAGG CT GAGA
 ||||| |||

		TCTTTGGTCC	GA	CTCT		
		CGAA__	AC			
GAM2323	FLJ20079	3'	CTCCAAGTTCTGGTTCCT	34970	GGAGA	CA
			AGGAACCA	GA	ACT	GAG
			TCCTTGGT	CTTGA	CTC	
			_____	AC		
GAM2323	FLJ20694	3'	TCTCAACTCTTTCCTGATTCC	35980	C	ACTCA
			GGAA	CAGGAGAGA	GAGA	
			CCTT	GTCCTTTCT	CTCT	
			A	CAA__		
GAM2323	FLJ21438	3'	AGCCCTCTCCTGGTTTCT	62189	AA	
			AGGAACCAGGAGAG	CT		
			TCTTTGGT	CCTCTC	GA	
				CC		
GAM2323	FLJ22169	3'	CTCTGAGTGTTCCTGGCCCC	44232	AA	A A
			GG	CCAGG	GAG	ACTCAGAG
			CC	GGTCC	CTT	TGAGTCTC
			CC	_	G	
GAM2323	FLJ32926	3'	CTCACCTGTGTCTCCCGTTCC	58634	A	GA TCA_
	T		AGGAACC	GGAGA	AC	GAG
			TCCTTGG	CCTCT	TG	CTC
			C	G_	TCCA	
GAM2323	H-plk	5'	CTCCGGCCTCCTGGTTCC	32380	AGAAC	A
			GGAACCAGGAG	TC	GAG	
			CCTTGGT	CCTC	GG	CTC
			C_____	C		
GAM2323	KIAA0057	3'	CTCCAAGTCCTTTTGGTGCCT	25410	A	A A CA
			AGG	ACCAGGAG	GA	CT GAG
			TCC	TGGTTTTC	CT	GA CTC
			G	_ _	AC	
GAM2323	KIAA0275	3'	TTGGTTTCTACCCTGGCTCC	29336	A	AG CT
			GGA	CCAGG	AGAA	CAG
			CCT	GGTCC	TCTT	GTT
			C	CA	TG	
GAM2323	KIAA0769	5'	CTCCTCCTCCTGGTCCT	29756	A	A ACTCA
			AGGA	CCAGGAG	GA	GAG
			TCCT	GGTCCTC	CT	CTC
			_	_	C_____	
GAM2323	KIAA0892	3'	TCCCTGCTCAGCCTCTTGGTCC	71573	A	AGAACT A
	C		GG	ACCAGGAG	CAG	GA

			CC TGGTTCTC	GTC CT		
			C	CGACTC C		
GAM2323	KIAA0939	3'	CTCTGAGCCTCTTCTGCCCCCT	62712	AAC	AA
			AGG CAGGAGAG	CTCAGAG		
			TCC GTCTTCTC	GAGTCTC		
			CCC	C_		
GAM2323	KIAA1030	3'	CTTCAGTTCCTCTCCTGTTCCCT	94979	C	_ CA
			AGGAAC AGGAGAG	AACT GAG		
			TCCTTG TCCTCTC	TTGA TTC		
			_	C C_		
GAM2323	KIAA1034	3'	TCCCTGATCTCTCCTGTCC	63133	AC	AC A
			GGA CAGGAGAGA	TCAG GA		
			CCT GTCCTCTCT	AGTC CT		
			_	_ C		
GAM2323	KIAA1257	3'	TCTTGTGCGCCCTCTCCTGGCT	63420	GAA	AACTCA_
	ACT		AG CCAGGAGAG	GAGA		
			TC GGTCTCTC	TTCT		
			ATC	CCGCGTG		
GAM2323	KIAA1484	3'	TCCCTGTCTCTCCTGATTCT	70524	C	ACT A
			AGGAA CAGGAGAGA	CAG GA		
			TCTTT GTCCTCTCT	GTC CT		
			A	_ C		
GAM2323	KIAA1655	5'	TCTCCAAATCTCTTCTGTTCC	67204	C	ACTCA
			GGAAC AGGAGAGA	GAGA		
			CCTTG TCTTCTCT	CTCT		
			_	AAAC_		
GAM2323	KIAA1656	5'	GGGCTTCCTCCTGGTCCC	66380	A	A _
			GG ACCAGGAG	GAA CTC		
			CC TGGTCCTC	CTT GGG		
			C	_ C		
GAM2323	KIAA1673	3'	TCTCCTTTCCCCTTCTGGTCCC	71330	A	A_ CTCA
	T		AGG ACCAGGAG	GAA GAGA		
			TCC TGGTCTTC	CTT CTCT		
			C	CC TC_		
GAM2323	KIAA1727	3'	CTGTCCTCTCCTGCCTCCT	64759	AC	AACT
			AGGA CAGGAGAG	CAG		
			TCCT GTCCTCTC	GTC		
			CC	CT_		
GAM2323	KIAA1913	5'	CTCCCGTTCCCGGTCCCT	74317	A A	AGA TCA
			AGG ACC GG	GAAC GAG		

TCC TGG CC CTTG CTC
 C _ _ _ CC_
 GAM2323 KIAA1937 3' CTCTGACCCTGGTTCT 74070 AGAGAAC
 GGAACCAGG TCAGAG
 ||||| ||||
 TCTTGGTCC AGTCTC
 C _ _ _
 GAM2323 KIAA1949 5' TCTCCGGATCTCCCTCGGTCCC 99593 A _ A A CA
 T AGG ACC AGG GAGA CT GAGA
 ||| ||| ||| ||| || ||||
 TCC TGG TCC CTCT GG CTCT
 C C _ A C_
 GAM2323 KIAA1949 5' TCTCCGGATCTCCCTCGGTCCC 99702 A _ A A CA
 T AGG ACC AGG GAGA CT GAGA
 ||| ||| ||| ||| || ||||
 TCC TGG TCC CTCT GG CTCT
 C C _ A C_
 GAM2323 KIAA1949 5' TCTCCGGATCTCCCTCGGTCCC 93720 A _ A A CA
 T AGG ACC AGG GAGA CT GAGA
 ||| ||| ||| ||| || ||||
 TCC TGG TCC CTCT GG CTCT
 C C _ A C_
 GAM2323 LRG 3' TCTGGGTTCTCCAGCCCT 54827 AACCA A
 AGG GG GAGAACTCAGA
 ||| || ||||| |||||
 TCC CC CTCTTGGGTCT
 CCGA_ _
 GAM2323 MGC10765 3' TCTCTTTCCCTCTCCCTGTCCC 44568 A CA AACTC
 T AGG AC GGAGAG AGAGA
 ||| || ||||| |||||
 TCC TG CCTCTC TCTCT
 C TC CCTT_
 GAM2323 MGC14799 5' TCTCCCAGGTCCCCGAGTTCCT 51333 CA A GAA CA
 AGGAAC GG GA CT GAGA
 ||||| || || || |||||
 TCCTTG CC CT GA CTCT
 AG C G_ CC
 GAM2323 MGC34869 5' TCTCTGAGCCCGCAGTTCC 58719 CA_ AGAGAA
 GGAAC GG CTCAGAGA
 |||| || ||||| |||||
 CCTTG CC GAGTCTCT
 ACG C _ _ _
 GAM2323 MIDORI 3' CTGAGTCCTCTGCATGAGTTCT 74212 _ GG_ A
 GGAAC CA AGAG ACTCAG
 |||| || ||| |||||
 TCTTG GT TCTC TGAGTC
 A ACG C
 GAM2323 MSTP028 3' GGTCCACTCCTGGTTCCT 50066 AGA
 AGGAACCAGGAG ACT
 ||||| ||||| |||

			TCCTTGGTCCTC TGG		
			ACC		
GAM2323 NFAT5	5'	CTGAACCCCTCTCCTGGTCACC 57787	A_	AAC_	
		GG ACCAGGAGAG TCAG			
		CC TGGTCCTCTC AGTC			
		AC CCCA			
GAM2323 NFAT5	5'	CTGAACCCCTCTCCTGGTCACC 22746	A_	AAC_	
		GG ACCAGGAGAG TCAG			
		CC TGGTCCTCTC AGTC			
		AC CCCA			
GAM2323 NINJ2	3'	TCCCAGCTTCTCTCCTGGTTCC 33732		_ CA	
		GGAACCAGGAGAGAA CT GA			
		CCTTGGTCCTCTCTT GA CT			
		C CC			
GAM2323 NR6A1	3'	TCTCCAAGTTCTCCTTTTCT 54019	CC A	CA	
		GGAA AGG GAGAACT GAGA			
		TCTT TTC CTCTTGA CTCT			
		_ _ AC			
GAM2323 NR6A1	3'	TCTCCAAGTTCTCCTTTTCT 54025	CC A	CA	
		GGAA AGG GAGAACT GAGA			
		TCTT TTC CTCTTGA CTCT			
		_ _ AC			
GAM2323 NR6A1	3'	TCTCCAAGTTCTCCTTTTCT 9449	CC A	CA	
		GGAA AGG GAGAACT GAGA			
		TCTT TTC CTCTTGA CTCT			
		_ _ AC			
GAM2323 OSBPL7	5'	TCTCCTTCCTTCCTGGTTCCT 35306		A CTCA	
		AGGAACCAGGAG GAA GAGA			
		TCCTTGGTCCTT CTT CTCT			
		C C_			
GAM2323 PA26	3'	CTCTGCCTGCCTCCTGGTCCC 27829	A	AGAACT	
		GG ACCAGGAG CAGAG			
		CC TGGTCCTC GTCTC			
		C CGTCC_			
GAM2323 POLE3	3'	CTCTGTGCCTCCTGCTTCCT 34314	C	AGAACT	
		AGGAA CAGGAG CAGAG			
		TCCTT GTCCTC GTCTC			
		C CGT_			
GAM2323 PRDM7	3'	CTGTCTCCTCTCCTGATTTCC 54846	C_	AACT	
		GGAA CAGGAGAG CAG			

			CCTT GTCCTCTC GTC		
			TA CTCT		
GAM2323	PTGES2	3'	TCCCTGGGTTCCCTGGTTCC 47579	AGA	A
			GGAACCAGG GAACTCAG GA		
			CCTTGGTCC CTTGGGTC CT		
			C__ C		
GAM2323	RAB9B	5'	GGCCCTCTCCTGTTTCCT 33477	C	AA
			AGGAA CAGGAGAG CT		
			TCCTT GTCCTCTC GG		
			T CC		
GAM2323	RAI17	3'	TCTGTTTTTCTCCTAGTCCCT 92911	A C	CT
			AGG AC AGGAGAGAA CAGA		
			TCC TG TCCTCTTTT GTCT		
			C A T_		
GAM2323	RILP	3'	CTCTGAGTCTCAGTTTCC 49497	CCAG	GAA
			GGAA GAGA CTCAGAG		
			CCTT CTCT GAGTCTC		
			TGA_ _		
GAM2323	RNF36	5'	CTGCTTCTCTCCAGCTCCT 55799	ACCA	CT
			AGGA GGAGAGAA CAG		
			TCCT CCTCTCTT GTC		
			CGA_ C_		
GAM2323	TNFAIP3	3'	CTCTGAGTGTCTACCTCCT 21909	ACC	GAGA
			AGGA AGGA ACTCAGAG		
			TCCT TCCT TGAGTCTC		
			CCA G_		
GAM2323	TOLLIP	3'	CTCTGCTGCTCCTGCTCCT 39194	AC	AGAACT
			AGGA CAGGAG CAGAG		
			TCCT GTCCTC GTCTC		
			C_ GTC_		
GAM2323	WIT-1	5'	CTCTGAGCCTCAGTTTCCT 32397	CCAG	AGAA
			AGGAA GAG CTCAGAG		
			TCCTT CTC GAGTCTC		
			TGA_ C_		
GAM2323	LOC112476	3'	TCCCTGCATCTCTCCTGGCCTC 59788	A_	ACT A
			C GGA CCAGGAGAGA CAG GA		
			CCT GGTCTCTCT GTC CT		
			CC AC_ C		
GAM2323	LOC112724	3'	CTCTGAGCCTTGGTTTCT 57303	AGAGAA	
			AGGAACCAGG CTCAGAG		

		TCTTTGGTTC	GAGTCTC		
		C_____			
GAM2323	LOC123745 5'	CTCCGAGCTCTTCGGCTCC	76140	A A	AA A
		GGA CC GGAGAG CTC GAG			
		CCT GG CTTCTC GAG CTC			
		C _ _ C			
GAM2323	LOC126528 5'	TCTCTGAGTCTTCTCCAACCC	75031	AACCA	GA
		GG GGAGA ACTCAGAGA			
		CC CCTCT TGAGTCTCT			
		CAA_ TC			
GAM2323	LOC127281 3'	TCTCTGGGTCCCCCGGTGCC	75140	A A A	GAA
		GG ACC GG GA CTCAGAGA			
		CC TGG CC CT GGGTCTCT			
		G C C _			
GAM2323	LOC133121 3'	TCTCTGAGCAGGGACCTGCTCC	75590	AC	AGAGAA
	T	AGGA CAGG CTCAGAGA			
		TCCT GTCC GAGTCTCT			
		C_ AGGGAC			
GAM2323	LOC138389 5'	TCTCTCAATCTCCCTGGTTCCT	76745	A	ACTC
		AGGAACCAGG GAGA AGAGA			
		TCCTTGGTCC CTCT TCTCT			
		_ AAC_			
GAM2323	LOC143310 3'	CTCTGAGCCCAAGTATCCT	77046	_ CA	AGAGAA
		AGGA AC GG CTCAGAG			
		TCCT TG CC GAGTCTC			
		A AA C_____			
GAM2323	LOC144233 3'	TCTCTGAATCCTACCTGGTTTC	77248	_ A	AC
	T	AGGAACCAGG AG GA TCAGAGA			
		TCTTTGGTCC TC CT AGTCTCT			
		A _ A_			
GAM2323	LOC145123 5'	TCCCTGAACTCTCGCTTTCTT	68138	CC _	AAC A
		AGGAA AG GAGAG TCAG GA			
		TTCTT TC CTCTC AGTC CT			
		_ G A_ C			
GAM2323	LOC145739 3'	CTCTGAGTGACCCTGGTTTCT	77904	AGAGA	
		AGGAACCAGG ACTCAGAG			
		TCTTTGGTCC TGAGTCTC			
		CAG_			
GAM2323	LOC145919 3'	TCCCTGCCTCTCCTGCCTCC	78029	AC	AACT A
		GGA CAGGAGAG CAG GA			

	CCT GTCCTCTC GTC CT	
	CC C__ C	
GAM2323 LOC147160 5'	CTGAGTCCCACTGGTTCC 85073	GAGA A
	GGAACCAG GA CTCAG	
	CCTTGGTC CT GAGTC	
	ACC_ _	
GAM2323 LOC147645 3'	TCCCTGACCTCCCCTCCCAATT 79072	CCA A_ AC A
CTT	AGGAA GGAG GA TCAG GA	
	TTCTT CCTC CT AGTC CT	
	AAC CC CC C	
GAM2323 LOC147858 5'	TCTCCAGGGCTCCTGATTTCT 79270	C AGAA CA
	AGGAA CAGGAG CT GAGA	
	TCTTT GTCCTC GA CTCT	
	A GG_ C_	
GAM2323 LOC149837 5'	CTCTGAGTTTCTGCTGTATTCC 85896	C_ G A
T	AGGAA CAG AGAGA CTCAGAG	
	TCCTT GTC TCTTT GAGTCTC	
	AT G _	
GAM2323 LOC150273 3'	TCTCCATCTCTCCTGACCTCC 86214	AC_ ACTCA
	GGA CAGGAGAGA GAGA	
	CCT GTCCTCTCT CTCT	
	CCA AC__	
GAM2323 LOC150311 5'	TCTCTTTTCTCTCCCCACCCC 80569	AACCA CTC
	GG GGAGAGAA AGAGA	
	CC CCTCTCTT TCTCT	
	CCACC T__	
GAM2323 LOC150319 5'	CTCTGAGCCTCAGTTTCCT 80467	CCAG AGAA
	AGGAA GAG CTCAGAG	
	TCCTT CTC GAGTCTC	
	TGA_ C__	
GAM2323 LOC150481 3'	TCTAGACTCTCCCCTGGTTCTT 80715	A AC _
	AGGAACCAGG GAGA TC AGA	
	TTCTTGGTCC CTCT AG TCT	
	C C_ A	
GAM2323 LOC150630 3'	CTCTGAGCAGCTGTCCTAGTTC 86298	C G AA_
T	GGAAC AGGA AG CTCAGAG	
	TCTTG TCCT TC GAGTCTC	
	A G GAC	
GAM2323 LOC150928 5'	TCCCTGAACTCTCGCTTTCTT 74583	CC _ AAC A
	AGGAA AG GAGAG TCAG GA	

		TTCTT TC CTCTC AGTC CT		
		___ G A___ C		
GAM2323	LOC150998 3'	CTCTGAGCCTCAGTTCCT 86358	CAG	AGAA
		AGGAAC GAG CTCAGAG		
		TCCTTG CTC GAGTCTC		
		A___ C___		
GAM2323	LOC151979 3'	CTCAATTTCTTCCTGGTCCC 81248	A	G CTCA
		GG ACCAGGA AGAA GAG		
		CC TGGTCCT TCTT CTC		
		C _ TAA_		
GAM2323	LOC153232 5'	CTCCCATACTCCTGGTTCCT 87181		AGAACTCA
		AGGAACCAGGAG GAG		
		TCCTTGGTCCTC CTC		
		ATACC___		
GAM2323	LOC155038 3'	TCCCTGAGCTCTCCTGTCTCCT 82184	AC	AA A
		AGGA CAGGAGAG CTCAG GA		
		TCCT GTCCTCTC GAGTC CT		
		CT ___ C		
GAM2323	LOC158191 3'	TCCCTGAGTTCTGGCCGTTCT 82683	A AG	A
	T	AGGAACC GG AGAACTCAG GA		
		TTCTTGG CC TCTTGAGTC CT		
		_ GG C		
GAM2323	LOC158191 3'	TCTAGACTCTCCCCTGGTTCTT 82684	A	AC _
		AGGAACCAGG GAGA TC AGA		
		TTCTTGGTCC CTCT AG TCT		
		C C_ A		
GAM2323	LOC165741 3'	CTCTGAGCCCTGGCTCC 88606	A	AGAGAA
		GGA CCAGG CTCAGAG		
		CCT GGTCC GAGTCTC		
		C C___		
GAM2323	LOC201617 5'	GAGTTTCTCTCCAACCTCCT 91826	ACCA	_
		AGGA GGAGAGAA CTC		
		TCCT CCTCTCTT GAG		
		CAA_ T		
GAM2323	LOC219848 3'	CTCTGAGCCTTGGTTTCCT 93124	_	AGAGAA
		AGGAA CCAGG CTCAGAG		
		TCCTT GGTTT GAGTCTC		
		T C___		
GAM2323	LOC220522 3'	CTCTGAGTTCTTCGCTGCC 61138	AAC	GA
		GG CAG GAGAACTCAGAG		

	CC GTC TTCTTGAGTCTC		
	___ GC		
GAM2323 LOC221540 3'	TCCCTGAGTGCTCCCTGGTTTC 95480	A A A	
	GGAACCAGG GAG ACTCAG GA		
	CTTTGGTCC CTC TGAGTC CT		
	_ G C		
GAM2323 LOC253143 3'	CTCTGAGTTCCAGGTTTC 98729	A GAGA	
	GAACC GGA ACTCAGAG		
	CTTGG CCT TGAGTCTC		
	A ____		
GAM2323 LOC253573 3'	CTCTGAGTCACTGGTTTCT 98837	GAGAGA	
	AGGAACCAG ACTCAGAG		
	TCTTTGGTC TGAGTCTC		
	AC____		
GAM2323 LOC254016 3'	TCTCTGAGTCCTTGCTGGGTCC 98700	A GA A	
	GGA CCAG GAG ACTCAGAGA		
	CCT GGTC TTC TGAGTCTCT		
	G G_ C		
GAM2323 LOC254191 3'	TCTCTGGGAAGCTCTCAATCC 96414	ACCAG AA_	
	GGA GAGAG CTCAGAGA		
	CCT CTCTC GGGTCTCT		
	AA__ GAA		
GAM2323 LOC256830 5'	TGGGGCCCTCTCCTGGCTCC 96196	A AA_	
	GGA CCAGGAGAG CTCA		
	CCT GGTCCCTCTC GGGT		
	C CCG		
GAM2323 LOC257545 3'	TCCCTGAGTGCTCCCTGGTTTC 99644	A A A	
	GGAACCAGG GAG ACTCAG GA		
	CTTTGGTCC CTC TGAGTC CT		
	_ G C		
GAM2323 LOC257598 3'	TCCCTGAGTGCTCCCTGGTTTC 99752	A A A	
	GGAACCAGG GAG ACTCAG GA		
	CTTTGGTCC CTC TGAGTC CT		
	_ G C		
GAM2323 LOC56932 3'	TCCCTGAGTTTGGGCCACAGTC 70533	ACCA AGA A	
C	GGA GG GAACTCAG GA		
	CCT CC TTTGAGTC CT		
	GACA GGG C		
GAM2323 LOC81501 3'	CTCTTTTCTCCCTGCTCC 48632	AC A CTC	
	GGA CAGG GAGAA AGAG		

CCT GTCC CTCTT TCTC
 C_ _ T_
 GAM2323 LOC90139 3' CTGAGCCCTCTTCTCTCC 56267 ACC AA
 GGA AGGAGAG CTCAG
 ||| ||||| |||||
 CCT TCTTCTC GAGTC
 C_ _ CC
 GAM2323 LOC92249 5' TCTCAGATCTCTCCTGGTACC 69113 A A CA
 GG ACCAGGAGAGA CT GAGA
 || ||||| || |||||
 CC TGGTCCTCTCT GA CTCT
 A A _
 GAM2323 LOC92305 3' TCTTTGCCTCCCTCCTGCCCCCT 57238 AAC A ACT
 AGG CAGGAG GA CAGAGA
 ||| ||||| || |||||
 TCC GTCCTC CT GTTCT
 CC_ C CC_
 GAM2323 LOC93613 5' CTGAGTTCCTGGGACTT 73073 AA GAGA
 AGG CCAGGA ACTCAG
 ||| ||||| |||||
 TTC GGTCTT TGAGTC
 AG _
 GAM2324 ATP4A 3' CCAAGAGTCCCAGCCCCA 7372 CAGCCT _
 TGGGGCTG GGGC CTTGG
 ||||| ||| |||||
 ACCCCGAC CCTG GAACC
 _ A
 GAM2324 FCER2 3' ACCCTCTCCAGATGCAGCCCCA 10599 GC CCTT
 TGGGGCTGCA CTGGG GGT
 ||||| ||||| |||
 ACCCCGACGT GACCT CCA
 A_ CTC_
 GAM2324 FOXO1A 3' CCAATAACCCCAGCCCCA 10649 CAGCCT CC_
 TGGGGCTG GGG TTGG
 ||||| ||| |||||
 ACCCCGAC CCC AACC
 _ AAT
 GAM2324 INPPL1 3' ACCAAGGCCAGCTATGGCCCC 9602 GC C
 A TGGGGCT AGC TGGGCCTTGGT
 ||||| ||| |||||
 ACCCCGG TCG ACCCGGAACCA
 TA _
 GAM2324 LRP1 3' CCAAACCCCAGCCCCA 11358 CAGCCT CC
 TGGGGCTG GGG TTGG
 ||||| ||| |||||
 ACCCCGAC CCC AACC
 _ A_
 GAM2324 PIM1 5' GCCACAGCCACAGCCCCA 92686 CA C _
 TGGGGCTG GC TG GGC
 ||||| || |||

		ACCCCGAC CG AC CCG	
		AC _ A	
GAM2324 PRX2	3'	GTACCAGAGACTGCAGCCC 33308	C__ ____
		GGGCTGCAG CTGG GC	
		CCCGACGTC GACC TG	
		AGA A__	
GAM2324 RET	3'	GGCCAAGCCTCAGCCCCA 40549	C C G
		TGGGGCTG AG CT GGCC	
		ACCCCGAC TC GA CCGG	
		_ C A	
GAM2324 SLC5A2	3'	CTTGGTACCATAAGCCACAGCC 13180	CA C__ ____ CTTG
	TCA	TGGGGCTG GC TGG GC G	
		ACTCCGAC CG ACC TG C	
		AC AAT A__ GTTC	
GAM2324 ADAMTS10	5'	ACCAAGGCCCAGAGAGGGAGGC 48979	GCAGC__
	CC	GGGCT CTGGGCCTTGGT	
		CCCGG GACCCGGAACCA	
		AGGGAGA	
GAM2324 DC-TM4F2	3'	CCGTGCCTAGCCACAACCCCA 48898	C CA C CT
		TGGGG TG GC TGGGC TGG	
		ACCCC AC CG ATCCG GCC	
		A AC _ T_	
GAM2324 FBXO27	3'	ACCAAAACCCCTCCGATCCAGCC 74994	CAGCCT_ CC
	CCA	TGGGGCTG GGG TTGGT	
		ACCCCGAC CCC AACCA	
		CTAGCCT AA	
GAM2324 FLJ14249	3'	GTACCAGAAGCCCAGCCCCA 42644	CA __ ____
		TGGGGCTG GC CTGG GC	
		ACCCCGAC CG GACC TG	
		C_ AA A__	
GAM2324 GDF10	5'	CCCTGTCAGCTGCAGCCCCA 18298	CT__
		TGGGGCTGCAGC GGG	
		ACCCCGACGTCG CCC	
		ACTGT	
GAM2324 KIAA0140	3'	CTTGGTACCAGCAAGCCCAGCC 28514	CA __ ____ CTTG
	CCA	TGGGGCTG GC CTGG GC G	
		ACCCCGAC CG GACC TG C	
		C_ AAC A__ GTTC	
GAM2324 KIAA0444	3'	CCTTTCCCCAGGCACAGCCCCA 62998	CA CCTT
		TGGGGCTG GCCTGGG GG	

ACCCCGAC CGGACCC CC
 A_ CTTT
 GAM2324 KIAA0450 5' GCCCAGGCCGACCCCA 28357 C A
 TGGGG TGC GCCTGGGC
 ||||| ||| |||||
 ACCCC ACG CGGACCCG
 _ C
 GAM2324 KIAA1077 3' AGCCCCAGGCTGCAGCCC 73285 C
 GGGCTGCAGCCTGGG CT
 ||||| ||||| ||
 CCGACGTCGGACCC GA
 C
 GAM2324 MGC10986 3' GCCTTGGTACTCGCCAGGCTGC 48325 _____ CTTG
 AGCCTCA TGGGGCTGCAGCCTGG GC GT
 ||||| ||||| || ||
 ACTCCGACGTCGGACC TG CG
 GCTCA_ GTTC
 GAM2324 MGC11352 5' CCGTGCCTAGCCACAACCCCA 65430 C CA C CT
 TGGGG TG GC TGGGC TGG
 ||||| || || ||||| |||
 ACCCC AC CG ATCCG GCC
 A AC _ T_
 GAM2324 PPP1R16B 5' CCATGAGGCCCCAGCCCCA 62035 CAGCCT _
 TGGGGCTG GGGCCT TGG
 ||||| ||||| ||||| |||
 ACCCCGAC CCGGA ACC
 _____ GT
 GAM2324 TM4SF11 3' CTTGGTACTCCAGACCTGCAGC 32587 C_ _____ CTTG
 CCCA TGGGGCTGCAG CTGG GC G
 ||||| ||||| || || |
 ACCCCGACGTC GACC TG C
 CA TCA_ GTTC
 GAM2324 LOC154834 5' GTACACCAGGCTCAGCCCCA 87496 C _____
 TGGGGCTG AGCCTGG GC
 ||||| ||||| ||||| ||
 ACCCCGAC TCGGACC TG
 _ ACA_
 GAM2324 LOC200030 3' ACCAAGACCCATCATGCCCA 80124 TGCAGCC C
 TGGGGC TGGG CTTGGT
 ||||| ||||| ||||| |||||
 ACCCCG ACCC GAACCA
 TACT_ A
 GAM2324 LOC200030 3' ACCAAGACCCATCATGCCCA 80125 TGCAGCC C
 TGGGGC TGGG CTTGGT
 ||||| ||||| ||||| |||||
 ACCCCG ACCC GAACCA
 TACT_ A
 GAM2324 LOC200030 3' ACCAAGACCCATCATGCCCA 80126 TGCAGCC C
 TGGGGC TGGG CTTGGT
 ||||| ||||| ||||| |||||

		ACCCCG	ACCC GAACCA		
		TACT__	A		
GAM2324	LOC200030	3'	ACCAAGGCCCA	80127	TGCAGCC
			TGGGGC	TGGGCCTTGGT	
			ACCCCG	ACCCGGAACCA	
			TACC__		
GAM2324	LOC200030	3'	ACCAAGGCCCA	80128	TGCAGCC
			TGGGGC	TGGGCCTTGGT	
			ACCCCG	ACCCGGAACCA	
			TACC__		
GAM2324	LOC221431	3'	CCAAGACTCTGCAGCCC	93728	CCT GC
			GGGCTGCAG	GG CTTGG	
			CCCGACGTC	TC GAACC	
			__ A_		
GAM2325	LENG4	5'	GAACATCTCCCTAGCAACCGTG	44420	C GGAC
			CACGGT GT	GAGATGTTC	
			GTGCCA CG	CTCTACAAG	
			A ATCC		
GAM2325	ODF2	5'	GAACACCCCTGTCCACGTCC	11886	T AGA_
			GG CGTGGACG	TGTTC	
			CC GCACCTGT	ACAAG	
			T	CCCC	
GAM2325	FLJ10300	5'	AACATCTCTGGGCCATAC	36466	C A__
			GT GTGG C	GAGATGTT	
			CA TACC G	CTCTACAA	
			_ GG T		
GAM2325	KIAA0014	3'	AACATCTCGTGGCCGCGCT	28535	T _
			GG CGTGG	ACGAGATGTT	
			TC GCGCC	TGCTCTACAA	
			_ GG		
GAM2325	LOC158263	3'	GAACATCTCACCCAGCATCC	82728	TC_ AC
			GG G TGG	GAGATGTTC	
			CC C ACC	CTCTACAAG	
			TA G	CA	
GAM2326	CDH12	3'	CTTATCATTTAAAGTGGTGTA	15777	CCCAA GA
			TACACCACT	GAA ATAAG	
			ATGTGGTGA	TTT TATTC	
			AA__	AC	
GAM2326	GOCAP1	3'	ATTGTTCTTGGGAGCAGTGTA	43007	CA G
			TACAC	CTCCCAAGAA AAT	

		ATGTG GAGGGTTCTT TTA	
		AC G	
GAM2326	DKFZp434N2435 5'	CTTATTACTGTGGGGTGGT	98090 T AGAAG
		ACCAC CCCA AATAAG	
		TGGTG GGGT TTATTC	
		_ GTCA_	
GAM2326	DKFZP564I122 3'	CTTATTCTTCTCCCTCATGTGT	63877 CACTCCCA
	A	TACAC AGAAGAATAAG	
		ATGTG TCTTCTTATTC	
		TACTCCC_	
GAM2326	FLJ21791 3'	CTTATTTGCAGAAAGTGGTGTA	62126 CCCAAGAA
		TACACCACT GAATAAG	
		ATGTGGTGGA TTTATTC	
		AGACG__	
GAM2326	HMP19 3'	CTTATTCTTTGTTAGGAAAATG	88860 CCAC CAA_
	TA	TACA TCC GAAGAATAAG	
		ATGT AGG TTTCTTATTC	
		AAA_ ATTG	
GAM2326	KIAA1719 3'	TCTGTCTTGGGAGTGGTGTA	68742 _
		TACACCACTCCCAAGA AGA	
		ATGTGGTGAGGGTTCT TCT	
		G	
GAM2326	KIAA1853 3'	TTTTTCTTGGAAGCAGTG	69929 CA C
		CAC CT CCAAGAAGAA	
		GTG GA GGTTCCTTTT	
		AC A	
GAM2326	KIAA1877 3'	CTTATTCTTCTGCCATGAGT	66748 CCA__
		ACTC AGAAGAATAAG	
		TGAG TCTTCTTATTC	
		TACCG	
GAM2326	KIAA1906 3'	CTTATTCTTCTTGACTTTTGG	73571 CTCC_
		CCA CAAGAAGAATAAG	
		GGT GTTCTTCTTATTC	
		TTTCA	
GAM2326	OSBPL11 3'	CTTAATTTCCCAAGAGTGGTG	43206 CCAA AA
		CACCACTC GAAG TAAG	
		GTGGTGAG CTTT ATTC	
		AACC A_	
GAM2326	YME1L1 3'	TCATTCTTGATGTGGTGTA	58438 TCC _
		TACACCAC CAAGAA GA	

			ATGTGGTG GTTCTT CT		
			TA_ A		
GAM2326	ZNF262	3'	CTTATTTTGTGGGAGT 18723	A	
			ACTCCCAAG AGAATAAG		
			TGAGGGTTT TTTTATTC		
			G		
GAM2326	LOC91960	3'	TGTGGCTTGGAACGTGGTGTA 68294	TC_ AAGA	
			TACACCAC CCAAG ATA		
			ATGTGGTG GGTTT TGT		
			CAA GG_		
GAM2327	ARHGEF7	3'	GCACCCCCCATGTCGGTA 15322	_ _ CC	
			TGCC ATA GG GGGGTGC		
			ATGG TGT CC CCCCACG		
			C A _		
GAM2327	BACE	3'	TGGCACCTGTGGCCAGAGCA 58094	CATA _	
			TGC GGCCG GGGTGCCA		
			ACG CCGGT TCCACGGT		
			AGA_ G		
GAM2327	BIN3	3'	TGGTCCTCCAGCCCTGGCA 38582	TA C TG	
			TGCCA GGC GGGG CCA		
			ACGGT CCG CCTC GGT		
			C_ A CT		
GAM2327	BSN	3'	TGGCATGTTTGACCTGTGGCA 14393	C _	
			TGCCATAGG CGGG GTGCCA		
			ACGGTGTCC GTTT TACGGT		
			A G		
GAM2327	CRK	5'	GGCACCCCAGCGTTTAGGC 60545	A C_	
			GCC TAGGC GGGGTGCC		
			CGG ATTTG CCCCACGG		
			_ CGA		
GAM2327	CYB561	3'	TGGGCCCGGCCTTTGGCA 10353	T GTG	
			TGCCA AGGCCGGG CCA		
			ACGGT TCCGGCCC GGT		
			T G_		
GAM2327	DDOST	3'	TGGCATTTCCTATGTGCA 19068	_ CC	
			TGC CATAGG GGGGTGCCA		
			ACG GTATCC TTTTACGGT		
			T T_		
GAM2327	EGFL4	3'	TGGCACCCCTGCTGCTGACA 62477	C TA C	
			TG CA GGC GGGGTGCCA		

			AC GT TCG CCCCACGGT		
			A CG T		
GAM2327	HNF3B	3'	TGGCACCCCGGATCGAGG 41714	ATA _	
			CC GG CCGGGGTGCCA		
			GG CT GGCCCCACGGT		
			AG_ A		
GAM2327	LALBA	3'	TGGCACTTTCACTACAGCA 11258	CA GCC	
			TGC TAG GGGGTGCCA		
			ACG ATC TTTCACGGT		
			AC AC_		
GAM2327	MAPK8IP1	3'	GGCATGCTGGCCTGTGGCA 19581	G	
			TGCCATAGGCCGG GTGCC		
			ACGGTGTCCGGTC TACGG		
			G		
GAM2327	NHLH1	5'	TGGCACCTGACCATGG 20022	A C	
			CCAT GG CGGGGTGCCA		
			GGTA CC GTCCCACGGT		
			_ A		
GAM2327	NOTCH3	3'	TGGCCCAGCCTTATGGCA 6483	_ CGG T	
			TGCCATA GGC GG GCCA		
			ACGGTAT CCG CC CGGT		
			T A__ _		
GAM2327	NUDT2	3'	TGGTATTTGGCTCATGACA 8598	C AG G	
			TG CAT GCCGGG TGCCA		
			AC GTA CGGTTT ATGGT		
			A CT _		
GAM2327	PACSIN1	3'	TGGCACCCCGGGGACAGGCA 93887	ATAGG	
			TGCC CCGGGGTGCCA		
			ACGG GGCCCCACGGT		
			ACAGG		
GAM2327	PAM	3'	GCATTCTTAGCCTGTGGCA 57842	C_	
			TGCCATAGGC GGGGTGC		
			ACGGTGTCCG TCTTACG		
			AT		
GAM2327	SELENBP1	3'	TGGCACCCGACCCTTGGCA 15459	TA C G	
			TGCCA GG CGGG TGCCA		
			ACGGT CC GCCC ACGGT		
			TC A _		
GAM2327	SLC10A2	5'	TGGCATGGTTCCTATGGC 6595	_ GGG	
			GCCATAGG CC GTGCCA		

			CGGTATCC GG TACGGT		
			TT ____		
GAM2327	SNX9	3'	GCACCCCGGCGTCTCTGGC 33122	T ____	
			GCCA AG GCCGGGGTGC		
			CGGT TC CGGCCCCACG		
			C TG		
GAM2327	SYNGR1	3'	TGGCACCTCCTTTATGACA 17515	C CC	
			TG CATAGG GGGGTGCCA		
			AC GTATTT TCCCACGGT		
			A CC		
GAM2327	TAPBP	3'	TGGCACGATCTCGGCTCACGGC 13591	ATA ____	
	A		TGCC GGCCGGG GTGCCA		
			ACGG TCGGCTC CACGGT		
			CAC TAG		
GAM2327	UBE2B	3'	TGGCACTTCTGCCATGAGCA 13942	_ A C	
			TGC CAT GGC GGGGTGCCA		
			ACG GTA CCG CTTACGGT		
			A _ T		
GAM2327	UBE2L3	3'	TGGCACCCAGGGTTGGC 13966	TA G _	
			GCCA G CC GGGGTGCCA		
			CGGT T GG CCCCACGGT		
			_ G A		
GAM2327	ACTR1A	3'	GGCACCTCACCTGTGACA 63651	C CC	
			TG CATAGG GGGGTGCC		
			AC GTGTCC TCCCACGG		
			A AC		
GAM2327	ATP6V1B1	3'	TGGCACCCCAACACCGGCA 9882	ATA CC__	
			TGCC GG GGGGTGCCA		
			ACGG CC CCCCACGGT		
			_ ACAA		
GAM2327	C22orf2	3'	TGGCACCTTGGGTTGGCA 96089	TAG _	
			TGCCA GCC GGGGTGCCA		
			ACGGT TGG TCCCACGGT		
			_ GT		
GAM2327	CHSY1	3'	TGCTCCAGTCCTATGGCA 30575	_ C	
			TGCCATAGG C GGGGTG		
			ACGGTATCC G CCTCGT		
			T A		
GAM2327	CXYorf1	5'	TGGCACCAAGATCGGCCCTGGC 82923	TA ____	
	A		TGCCA GGCCGG GGTGCCA		

ACGGT CCGGCT CCACGGT
 C_ AGAA
 GAM2327 DKFZp547C176 3' TGGCATTTCATACCCATGGTA 67809 A CC_ GG
 TGCCAT GG G GTGCCA
 ||||| || | |||||
 ATGGTA CC C TACGGT
 C ATA TT
 GAM2327 DKFZP547L112 3' GGCACCCTGGATATAGCA 67131 C GG
 TGC ATA CCGGGGTGCC
 ||| ||| |||||
 ACG TAT GGTCCCACGG
 A A_
 GAM2327 FLJ10521 3' GCATCCTGGCCCCTGACA 36720 C TA
 TG CA GGCCGGGGTGC
 || || |||||
 AC GT CCGGTCCTACG
 A CC
 GAM2327 FLJ13952 3' TGGCACGATCTCGGCTCACGGC 46023 ATA ____
 A TGCC GGCCGGG GTGCCA
 |||| ||||| |||||
 ACGG TCGGCTC CACGGT
 CAC TAG
 GAM2327 FLJ20793 3' TGATATTCTGCCTATGGCA 93451 C C
 TGCCATAGGC GGGGTG CA
 ||||| ||||| ||
 ACGGTATCCG TCTTAT GT
 _ A
 GAM2327 FLJ21709 3' TGGCACGTGTTCTGTGGCA 78484 GC GG
 TGCCATAG CG GTGCCA
 ||||| || |||||
 ACGGTGTC GT CACGGT
 TT G_
 GAM2327 FLJ22318 3' TGGCACCTGGCTCCATGGCA 43145 A_ G
 TGCCAT GGCCGGG TGCCA
 ||||| ||||| |||||
 ACGGTA TCGGTCC ACGGT
 CC _
 GAM2327 GIT2 3' TGGACTTAAACCTTGGCA 29415 T CCG G
 TGCCA AGG GGGT CCA
 ||||| ||| |||||
 ACGGT TCC TTCA GGT
 _ AAA _
 GAM2327 ITGA8 5' TGGCACCTGCTATGTAGCA 94845 C _ CG
 TGC ATA GGC GGGTGCCA
 ||| ||| ||| |||||
 ACG TGT TCG TCCACGGT
 A A _
 GAM2327 KIAA0152 3' TGGCAGAGAGGGCCTTGGCA 28984 T GGGG_
 TGCCA AGGCC TGCCA
 ||||| ||||| |||||

		ACGGT TCCGG	ACGGT		
		—	GAGAG		
GAM2327	KIAA0173	5'	TGGCACCTTACCTCAGCA	28385	CAT CC
			TGC AGG GGGGTGCCA		
			ACG TCC TTCCACGGT		
			AC_ A_		
GAM2327	KIAA0295	3'	TGGCACTGGCCTGCAGCA	68676	CA GG
			TGC TAGGCC GGTGCCA		
			ACG GTCCGG TCACGGT		
			AC —		
GAM2327	KIAA0555	3'	TGGCACAATCTCGGCTCATGGC	60747	AG —
	A		TGCCAT GCCGGG GTGCCA		
			ACGGTA CGGCTC CACGGT		
			CT TAA		
GAM2327	KIAA0574	3'	TGGACCCCAACTCTATGGCA	69824	CC_ G
			TGCCATAGG GGGGT CCA		
			ACGGTATCT CCCCA GGT		
			CAA —		
GAM2327	KIAA0792	3'	TGGCCTGGGGCCTTGGCA	28770	T GG T
			TGCCA AGGCC GG GCCA		
			ACGGT TCCGG TC CGGT		
			— GG —		
GAM2327	KIAA1170	3'	TGGCATTGACCCATGGCA	70426	A C G
			TGCCAT GG CGGG TGCCA		
			ACGGTA CC GTTT ACGGT		
			C A —		
GAM2327	KIAA1317	3'	TGGCACTCATCCCATGGTA	87216	A CCG
			TGCCAT GG GGGTGCCA		
			ATGGTA CC CTCACGGT		
			C TA_		
GAM2327	KIAA1881	3'	GGTCTCCGGCCTTAGCA	97087	CAT T
			TGC AGGCCGGGG GCC		
			ACG TCCGGCCTC TGG		
			AT_ —		
GAM2327	LAMP3	3'	TGGCACGATCTCGGCTTATGGC	60213	—
	A		TGCCATAGGCCGGG GTGCCA		
			ACGGTATTCGGCTC CACGGT		
			TAG		
GAM2327	MGC19556	3'	TGGCACCCCTCCTGAATGG	54346	— CC
			CCAT AGG GGGGTGCCA		

GGTA TCC TCCCACGGT
AG _
GAM2327 MGC2574 3' TGGCACTCCAAACCCATGGC 44287 A CC_
GCCAT GG GGGGTGCCA
||||| || |||||
CGGTA CC CCTCACGGT
C AAA
GAM2327 MGC2647 3' GGCACCCCAGTGGTGGCA 74079 AG C
TGCCAT GC GGGGTGCC
||||| || |||||
ACGGTG TG CCCCACGG
G_ A
GAM2327 MIL1 3' GGTTTCTCAGCCTTGGCA 31727 T C T
TGCCA AGGC GGGG GCC
||||| ||||| |||||
ACGGT TCCG CTCT TGG
_ A T
GAM2327 NIP30 3' TGACACTCTGGTGCCATTGGC 46901 TA_ _ C
A TGCCA GGC CGGGGTG CA
||||| ||||| |||||
ACGGT CCG GTCTCAC GT
TAC TG A
GAM2327 NR4A3 3' GCACCCTGCTTCTACGCA 23720 CA C_
TGC TAGG CGGGGTGC
||| ||||| |||||
ACG ATCT GTCCCACG
C_ TC
GAM2327 PIB5PA 3' TGGCACCTCAACTGTGACA 66652 C GCC
TG CATAG GGGGTGCCA
|| ||||| |||||
AC GTGTC CTCCACGGT
A AA_
GAM2327 PIP5K1C 3' GGCACCCCGGTCGGCA 71305 ATA
TGCC GGCCGGGGTGCC
||||| |||||
ACGG CTGGCCCCACGG

GAM2327 PPAP2A 5' TGGCACACGAGCGCCTCGGCA 68443 AT _ GG
TGCC AGGC CG GTGCCA
||||| ||||| |||||
ACGG TCCG GC CACGGT
C_ CGA A_
GAM2327 RASSF2 3' TGGCATGCGGCCCTGGCA 29113 TA GG
TGCCA GGCCG GTGCCA
||||| ||||| |||||
ACGGT CCGGC TACGGT
CC G_
GAM2327 RCD-8 3' TGGCATCTGACCTTGGCA 27525 T C G
TGCCA AGG CGGG TGCCA
||||| ||||| |||||

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ACGGT TCC GTCT ACGGT
  _ A _
GAM2327 SARM 3' TGGCACCCAGTCCACTGGCA 31308 TA CCG
TGCCA GG GGGTGCCA
|||| || |||||||
ACGGT CC CCCACGGT
CA TGA
GAM2327 SIMRP7 5' GCACCCCGGCCGGGCA 93974 ATA
TGCC GGCCGGGGTGCC
|||| |||||||||
ACGG CCGGCCCCACG
G_
GAM2327 TREX1 5' TGGCACCCCCCTGCAGC 50619 CA CC
GC TAGG GGGGTGCCA
|| ||| |||||||
CG GTCC CCCCACGGT
AC _
GAM2327 TREX1 5' TGGCACCCCCCTGCAGC 50620 CA CC
GC TAGG GGGGTGCCA
|| ||| |||||||
CG GTCC CCCCACGGT
AC _
GAM2327 TSPEAR 3' TGGGCCCCAGCCTAGGGCA 59377 A CG G
TGCC TAGGC GGGT CCA
|||| |||| ||| |||
ACGG ATCCG CCCG GGT
G A_ _
GAM2327 ULK2 5' GGCACCCCTGGCCCGGCA 28688 ATA _
TGCC GGCC GGGGTGCC
|||| ||| |||||||
ACGG CCGG CCCCACGG
C_ T
GAM2327 LOC116028 3' TGGCATTTCCTAACGGCA 74099 A_ CCG
TGCC TAGG GGGTGCCA
|||| ||| |||||||
ACGG ATCC TTTACGGT
CA _
GAM2327 LOC126133 3' TGGCACAATCTCGGCCCACTGC 74916 CATA _
A TGC GGCCGGG GTGCCA
||| |||||| |||||
ACG CCGGCTC CACGGT
TCAC TAA
GAM2327 LOC139496 5' TGGCACCCCGGTGTGGC 76361 AG
GCCAT GCCGGGGTGCCA
|||| |||||||||
CGGTG TGGCCCCACGGT
_
GAM2327 LOC146445 3' TGGCACCCCTCCACTCGGCA 84686 AT GCC
TGCC AG GGGGTGCCA
|||| || |||||||

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ACGG TC TCCCACGGT
 C_ ACC
 GAM2327 LOC148089 3' TGGCACCTTCTGAGGCA 79335 A CC
 TGCC TAGG GGGGTGCCA
 |||| ||| |||||
 ACGG GTCT TCCCACGGT
 A _
 GAM2327 LOC151534 5' GGTCTCCGGCCTCGGCA 57487 AT T
 TGCC AGGCCGGGG GCC
 ||| ||||| |||
 ACGG TCCGGCCTC TGG
 C_ _
 GAM2327 LOC153769 3' TGGTCCTTCGGCCTCAGCA 81810 CAT TG
 TGC AGGCCGGGG CCA
 || ||||| |||
 ACG TCCGGCTTC GGT
 AC_ CT
 GAM2327 LOC158219 5' TGGCACCTTCCTCCAGCA 82693 CAT CC
 TGC AGG GGGGTGCCA
 || | |||||
 ACG TCC TCCCACGGT
 ACC T_
 GAM2327 LOC163994 5' TGGCACCTCTTTTCGGCA 88426 AT CC
 TGCC AGG GGGGTGCCA
 ||| || |||||
 ACGG TTT CTCCACGGT
 CT _
 GAM2327 LOC197342 3' TGGCGGGGGGCCTGTGGCA 89374 GGGG
 TGCCATAGGCC TGCCA
 ||||| |||
 ACGGTGTCCGG GCGGT
 GGG_
 GAM2327 LOC200093 5' TGGCACCAAGATCGGCCCTGGC 63779 TA _
 A TGCCA GGCCGG GGTGCCA
 |||| |||| |||||
 ACGGT CCGGCT CCACGGT
 C_ AGAA
 GAM2327 LOC219818 3' TGACACCCGCCTCACTGTGGCA 92540 _ CG C
 TGCCAT AGGC GGGTG CA
 |||| ||| |||| ||
 ACGGTG TCCG CCCAC GT
 TCAC _ A
 GAM2327 LOC255936 5' TGGCACTCCCCCATGCA 97964 C A CC
 TGC AT GG GGGGTGCCA
 || || || |||||
 ACG TA CC CCTCACGGT
 _ _ CC
 GAM2327 LOC256789 3' TGGCAAGTCGGACCTATGGC 99314 _ GG
 GCCATAGG CCGG TGCCA
 ||||| ||| ||||

		CGGTATCC GGCT ACGGT		
		A GA		
GAM2327	LOC257481 3'	TGGCGTCTTGGCCTTCGGCA 61766	AT	GT
		TGCC AGGCCGGG GCCA		
		ACGG TCCGGTTC CGGT		
		CT TG		
GAM2327	LOC51134 3'	TGACATTTTAACCTGTGGCA 32794	CC	C
		TGCCATAGG GGGGTG CA		
		ACGGTGTCC TTTTAC GT		
		AA A		
GAM2327	LOC90693 3'	TGGATTATATCCTATGGCA 57858	CCGG	G
		TGCCATAGG GGT CCA		
		ACGGTATCC TTA GGT		
		TATA _		
GAM2327	LOC91040 5'	TGGCACCAAGATCGGCCCTGGC 65354	TA	_____
	A	TGCCA GGCCGG GGTGCCA		
		ACGGT CCGGCT CCACGGT		
		C_ AGAA		
GAM2327	LOC91464 5'	TGGCACCTCCTTGGCCTA 66714	_____	
		TAGGCC GGGGTGCCA		
		ATCCGG TCCCACGGT		
		TTCC		
GAM2328	AQP6 5'	ATCCTTTCAGTGGCCTC 54983	A	CA
		GA GCCATTGAAA GAT		
		CT CGGTGACTTT CTA		
		C C_		
GAM2328	ATP11B 3'	GATCACCTGTTAATGGC 81126	AA	A_
		GCCATTG ACAG TGATC		
		CGGTAAT TGTC ACTAG		
		_ CC		
GAM2328	TRPC5 3'	ATCATCTGTTCTGGAActC 25924	AG_	TT A
		GA CCA GAA CAGATGAT		
		CT GGT CTT GTCTACTA		
		CAA _ _		
GAM2328	C1orf34 3'	CATGTGTCTTCATGGCTTC 61301	T _	G
		GAAGCCAT GAA ACA ATG		
		CTTCGGTA CTT TGT TAC		
		_ C G		
GAM2328	DKFZp761B1514 3'	ATCATCTGTTTGAActTC 51138	C	TTGA
		GAAG CA AACAGATGAT		

CTTC GT TTGTCTACTA
 A ____
 GAM2328 FLJ10346 5' GATCATCTGCCCTCCTCGGCCT 36525 A ATT AA_
 C GA GCC GA CAGATGATC
 || ||| || |||||
 CT CGG CT GTCTACTAG
 C CTC CCC
 GAM2328 FLJ12960 3' GATCATCTGTCCCAGGT 45300 AT AA
 GCC TG ACAGATGATC
 ||| || |||||
 TGG AC TGTCTACTAG
 ____ CC
 GAM2328 FLJ23563 3' CACCTGTAGGCCCTGGCTTTGT 68211 TTGAA_ A
 ACGAAGCCA ACAG TG
 ||||| ||| ||
 TGTTCGGT TGTC AC
 CCCGGA C
 GAM2328 MGC10911 5' TCCGTTTCAATGCCCGT 51182 AA C A
 ACG GC ATTGAAAC GA
 ||| || ||||| ||
 TGC CG TAACTTTG CT
 CC _ C
 GAM2328 LOC123095 5' TCTGTCTTTAATGGCTTC 76522 _
 GAAGCCATTGAA ACAGA
 ||||| ||||
 CTTCGGTAATTT TGTCT
 C
 GAM2328 LOC132617 5' CTGGGGCCCAATGGCTTCGT 76416 AAA_
 ACGAAGCCATTG CAG
 ||||| |||
 TGCTTCGGTAAC GTC
 CCGGG
 GAM2328 LOC135138 3' ATCATCTGTCTCTGTTGC 75710 C T A
 GC AT GA ACAGATGAT
 || ||| |||||
 CG TG CT TGTCTACTA
 T T C
 GAM2328 LOC196860 5' TCTGTCTTTAATGGCTTC 91217 _
 GAAGCCATTGAA ACAGA
 ||||| ||||
 CTTCGGTAATTT TGTCT
 C
 GAM2328 LOC221477 3' GATCATCTGGAGGCCGGCTTTG 93772 ATTGAAA
 T ACGAAGCC CAGATGATC
 ||||| |||||
 TGTTCGG GTCTACTAG
 CCGGAG_
 GAM2328 LOC56270 3' CGTTAGCTTCAGTGGCTCCG 39505 A ACA
 CG AGCCATTGAA GATG
 || ||||| |||

			GC TCGGTGACTT TTGC	
			C CGA	
GAM2329	CASP7	3'	ATCTGGAAGCCACCTCAC 54030	AACGAC
			GTGAGGTG TTCAGAT	
			CACTCCAC AGGTCTA	
			CGA__	
GAM2329	CASP7	3'	ATCTGGAAGCCACCTCAC 54031	AACGAC
			GTGAGGTG TTCAGAT	
			CACTCCAC AGGTCTA	
			CGA__	
GAM2329	NAT2	3'	TGTATCACCCAACTCACTAA 5232	_____ _
			TTAGTGA GGTGA ACG	
			AATCACT CCACT TGT	
			CAAC A	
GAM2329	TNFSF5	3'	ATCTGAAGCAGCAACCCCACTG 5366	A GAACGA
	A		TTAGTG GGT CTTCAGAT	
			AGTCAC CCA GAAGTCTA	
			C ACGAC_	
GAM2329	KIAA1879	5'	ATCTGAAGTGGGGTCCCCAAC 73928	GA T ACG_
			GT GG GA ACTTCAGAT	
			CA CC CT TGAAGTCTA	
			AC _ GGGG	
GAM2329	LOC124411	3'	ATCTGAAGCCATTTATCACA 74771	A CGA
			TG GGTGAA CTTCAGAT	
			AC CTATTT GAAGTCTA	
			A ACC	
GAM2329	LOC197416	3'	ATCTGAAGCCATTTATCACA 91321	A CGA
			TG GGTGAA CTTCAGAT	
			AC CTATTT GAAGTCTA	
			A ACC	
GAM2329	LOC220370	3'	AGTCACTCACCTCACTGA 94393	AC
			TTAGTGAGGTGA GACT	
			AGTCACTCCACT CTGA	
			CA	
GAM2330	CDH12	3'	CTTATCATTTAAAGTGGTGTA 15777	CCCAA GA
			TACACCACT GAA ATAAG	
			ATGTGGTGA TTT TATTC	
			AA__ AC	
GAM2330	GOCAP1	3'	ATTGTTCTTGAGCAGTGTA 43007	CA G
			TACAC CTCCCAAGAA AAT	

		ATGTG GAGGGTTCTT TTA	
		AC G	
GAM2330	DKFZp434N2435 5'	CTTATTACTGTGGGGTGGT	98090 T AGAAG
		ACCAC CCCA AATAAG	
		TGGTG GGGT TTATTC	
		_ GTCA_	
GAM2330	DKFZP564I122 3'	CTTATTCTTCTCCCTCATGTGT	63877 CACTCCCA
	A	TACAC AGAAGAATAAG	
		ATGTG TCTTCTTATTC	
		TACTCCC_	
GAM2330	FLJ21791 3'	CTTATTTGCAGAAAGTGGTGTA	62126 CCCAAGAA
		TACACCACT GAATAAG	
		ATGTGGTGGA TTTATTC	
		AGACG__	
GAM2330	HMP19 3'	CTTATTCTTTGTTAGGAAAATG	88860 CCAC CAA_
	TA	TACA TCC GAAGAATAAG	
		ATGT AGG TTTCTTATTC	
		AAA_ ATTG	
GAM2330	KIAA1719 3'	TCTGTCTTGGGAGTGGTGTA	68742 _
		TACACCACTCCCAAGA AGA	
		ATGTGGTGAGGGTTCT TCT	
		G	
GAM2330	KIAA1853 3'	TTTTTCTTGAAGCAGTG	69929 CA C
		CAC CT CCAAGAAGAA	
		GTG GA GGTTCCTTTT	
		AC A	
GAM2330	KIAA1877 3'	CTTATTCTTCTGCCATGAGT	66748 CCA__
		ACTC AGAAGAATAAG	
		TGAG TCTTCTTATTC	
		TACCG	
GAM2330	KIAA1906 3'	CTTATTCTTCTTGACTTTTGG	73571 CTCC_
		CCA CAAGAAGAATAAG	
		GGT GTTCTTCTTATTC	
		TTTCA	
GAM2330	OSBPL11 3'	CTTAATTTCCCAAGAGTGGTG	43206 CCAA AA
		CACCACTC GAAG TAAG	
		GTGGTGAG CTTT ATTC	
		AACC A_	
GAM2330	YME1L1 3'	TCATTCTTGATGTGGTGTA	58438 TCC _
		TACACCAC CAAGAA GA	

			ATGTGGTG GTTCTT CT		
			TA_ A		
GAM2330	ZNF262	3'	CTTATTTTGTGGGAGT 18723	A	
			ACTCCCAAG AGAATAAG		
			TGAGGGTTT TTTTATTC		
			G		
GAM2330	LOC91960	3'	TGTGGCTTGGAACGTGGTGTA 68294	TC_ AAGA	
			TACACCAC CCAAG ATA		
			ATGTGGTG GGTTT TGT		
			CAA GG_		
GAM2331	CDYL	3'	CTGAAACAAGCTCACCCGTAG 17887	_ A AA GC	
			CT CG GT AGCT TGTTTCAG		
			GA GC CA TCGA ACAAAGTC		
			T C C_ _		
GAM2331	CLCN6	3'	CTGGATAAAGCAGCTTCACTC 41696	A GT_	
			GAGT AAGCTGCT TTCAG		
			CTCA TTCGACGA AGGTC		
			C AAT		
GAM2331	CLCN6	3'	CTGGATAAAGCAGCTTCACTC 41703	A GT_	
			GAGT AAGCTGCT TTCAG		
			CTCA TTCGACGA AGGTC		
			C AAT		
GAM2331	CLCN6	3'	CTGGATAAAGCAGCTTCACTC 8904	A GT_	
			GAGT AAGCTGCT TTCAG		
			CTCA TTCGACGA AGGTC		
			C AAT		
GAM2331	IHPK1	3'	CTGAAACAGCCTCTCTC 97463	TAA CT	
			GAG AG GCTGTTTCAG		
			CTC TC CGACAAAGTC		
			_ TC		
GAM2331	KRT12	3'	ATAGAGCTTTACTCAAGT 5852	C G	
			ACT GAGTAAAGCT CTGT		
			TGA CTCATTTTCGA GATA		
			A _		
GAM2331	NFE2L1	3'	GGCTCAGCTCCACTCGGGT 13632	AA CT	
			ACTCGAGT AGCTG GTT		
			TGGGCTCA TCGAC CGG		
			CC T_		
GAM2331	PAX9	3'	CAGCAGCTTCACCCGGGT 21664	A A	
			ACTCG GT AAGCTGCTG		

			TGGGC CA TTCGACGAC		
			C C		
GAM2331	PRKCB1	3'	CTGAAACAACACAGTCACTCTA 71026	C	AAA C__
	G		CT GAGT GCTG TGTTCAG		
			GA CTCA TGAC ACAAAGTC		
			T C__ ACA		
GAM2331	TM4SF4	3'	AACCAGCTTTGCTCGAGT 17255		CT
			ACTCGAGTAAAGCTG GTT		
			TGAGCTCGTTTCGAC CAA		
			—		
GAM2331	ZNF205	3'	CTGGAACAGCCCCACTGGAGT 14370	G	AAAGCT
			ACTC AGT GCTGTTTCAG		
			TGAG TCA CGACAAGGTC		
			G CCC__		
GAM2331	FLJ20280	3'	CTGAAACAGGAGAATCACTTGA 35329		AAAG G
			TCGAGT CT CTGTTTCAG		
			AGTTCA GA GACAAAGTC		
			CTAA G		
GAM2331	KIAA1317	5'	CTGAAACAACAGCATCCGA 87211	AG	AAA C
			TCG T GCTG TGTTTCAG		
			AGC A CGAC ACAAAGTC		
			CT __ A		
GAM2331	MIC2L1	3'	CTGCCTCCAGCTTTACTGAG 49600	G	CTGTTT
			CTC AGTAAAGCTG CAG		
			GAG TCATTTTCGAC GTC		
			— CTCC__		
GAM2331	SEMA3E	5'	CTGAATGAACAGCTTTGCCCAA 25808	CGA	CTGT
	GT		ACT GTAAAGCTG TTCAG		
			TGA CGTTTCGAC AAGTC		
			ACC AAGT		
GAM2331	SEMA4G	5'	TGGCAGCTTCACTCAGAG 96334	_	A
			CTC GAGT AAGCTGCTG		
			GAG CTCA TTCGACGGT		
			A C		
GAM2331	LOC146953	3'	AAACATAGTTTTACTAAGT 78821	CG	C
			ACT AGTAAAGCTG TGTTT		
			TGA TCATTTTGAT ACAA		
			A_ _		
GAM2331	LOC200575	5'	AACCTGCAGCCCTACTTGAG 90251	AA	T_
			CTCGAGTA GCTGC GTT		

		GAGTTCAT CGACG CAA	
		CC TC	
GAM2331	LOC203427 5'	TGAAAGTCGCTACTCGAG 90923	AA T GT
		CTCGAGT AGC GCT TTCA	
		GAGCTCA TCG TGA AAGT	
		__ C __	
GAM2331	LOC257476 3'	CTGAAACAGCCTCTCTC 61922	TAA CT
		GAG AG GCTGTTTCAG	
		CTC TC CGACAAAGTC	
		__ TC	
GAM2331	LOC91049 5'	AAACGGCACCCCCCTCGAGT 65371	TAAAGC
		ACTCGAG TGCTGTTT	
		TGAGCTC ACGGCAAA	
		CCCC__	
GAM2332	CUL3 3'	CACATGAATAGTAATGTG 14570	C CG
		CACATTAC ATTC GTG	
		GTGTAATG TAAG CAC	
		A TA	
GAM2332	IL1F9 3'	TGTCCTAATTGTAATGTGTA 39514	C CC T
		TACACATTAC ATT GG GCA	
		ATGTGTAATG TAA CC TGT	
		T T_ _	
GAM2332	MGAT5 5'	TGCAGGGTTTATGGTAATG 11571	__ GG
		CATTACCAT TCC TGCA	
		GTAATGGTA GGG ACGT	
		TTT __	
GAM2332	NEU3 3'	TACTGGATAATAGTGCGTA 22834	A CCAT
		TAC CATT TCCGGTG	
		ATG GTGAT AGGTCAT	
		C AAT_	
GAM2332	ORC2L 5'	TGCAGCTGCAGAAATGTGTA 21663	ACCATTC _
		TACACATT CGG TGCA	
		ATGTGTAA GTC ACGT	
		GAC__ G	
GAM2332	SRGAP1 5'	TGCCAAATGGCAAATGTGTA 72724	A_ CC
		TACACATT CCATT GGTG	
		ATGTGTAA GGTA CCGT	
		AC A_	
GAM2332	B3GNT6 3'	TACCGATGACAATGTGTA 23452	AC TC
		TACACATT CAT CCGTG	

			ATGTGTAA GTA GCCAT		
			CA _		
GAM2332	ELOVL2	3'	TGCTGCTGGAATATGT 35439	TACC	_
			ACAT ATTCCGGT GCA		
			TGTA TAAGGTCG CGT		
			_____ T		
GAM2332	FLJ10719	3'	CACGAACGGTAATGTTA 63205	C	A CG
			A ACATTACC TTC GTG		
			A TGTAATGG AAG CAC		
			T C _		
GAM2332	FLJ12586	3'	CACTGGAATGAAATGTG 45207	AC	
			CACATT CATTCCGGTG		
			GTGTAA GTAAGGTCAC		
			A_		
GAM2332	FLJ20671	3'	TGCTGGCTCATGAAATGTGTA 35946	AC	T_
			TACACATT CAT CCGGTG		
			ATGTGTAA GTA GGTCGT		
			A_ CTC		
GAM2332	KIAA1466	5'	CACCAAATGACAAGTGTGTA 72408	AC_	CC
			TACACATT CATT GGTG		
			ATGTGTGA GTAA CCAC		
			ACA A_		
GAM2332	PREI3	3'	ACCAATGGTAATGGTA 66923	A	CC
			TAC CATTACCATT GGT		
			ATG GTAATGGTAA CCA		

GAM2332	PRO0618	3'	CATCTGTGGAAATGTGTA 27050	A	TCC
			TACACATT CCAT GGTG		
			ATGTGTAA GGTG CTAC		
			A T_		
GAM2332	ST7L	3'	GCAGGTTGGTAATGTG 35339	TT	GG
			CACATTACCA CC TGC		
			GTGTAATGGT GG ACG		
			T_ _		
GAM2332	ST7L	3'	GCAGGTTGGTAATGTG 57816	TT	GG
			CACATTACCA CC TGC		
			GTGTAATGGT GG ACG		
			T_ _		
GAM2332	ST7L	3'	GCAGGTTGGTAATGTG 58283	TT	GG
			CACATTACCA CC TGC		

		GTGTAATGGT GG ACG	
		T_ _	
GAM2332	TRAF4	3' TGCATTCTCAATGGCAATG 63321	A CC _
		CATT CCATT GG TGCA	
		GTAA GGTA CC ACGT	
		C CT TT	
GAM2332	ZNF347	3' CACACAAATGTAATGTGTA 51820	C CCG
		TACACATTAC ATT GTG	
		ATGTGTAATG TAA CAC	
		_ ACA	
GAM2332	LOC132720	3' TGCACCCTATGGTAATG 75577	TCC
		CATTACCAT GGTGCA	
		GTAATGGTA CCACGT	
		TC_	
GAM2332	LOC143879	3' CATCTCAGGTAATGTGTA 77158	ATTCC
		TACACATTACC GGTG	
		ATGTGTAATGG CTAC	
		ACT_	
GAM2332	LOC145786	5' CACAGGCTAATGCAATGTGTA 84490	AC _ G
		TACACATT CATT CC GTG	
		ATGTGTAA GTAA GG CAC	
		C_ TC A	
GAM2332	LOC158187	5' TGCACTGGGTGAACATGT 87999	TAC T
		ACAT CAT CCGGTGCA	
		TGTA GTG GGTCACGT	
		CAA _	
GAM2332	LOC162239	3' TGCATTCCAAATGAAATGTGTA 83211	AC CC_
		TACACATT CATT GGTGCA	
		ATGTGTAA GTAA TTACGT	
		A_ ACC	
GAM2332	LOC196527	3' CACTAATGAGAATGTGTA 89097	AC CC
		TACACATT CATT GGTG	
		ATGTGTAA GTAA TCAC	
		GA _	
GAM2332	LOC200609	5' TGCACTTGGGAAGAATGTGTA 91670	ACCA _
		TACACATT TTCCG GTGCA	
		ATGTGTAA AGGGT CACGT	
		GA_ T	
GAM2332	LOC221914	3' TGCAAATAAATGGTAATGT 95566	CCGG
		ACATTACCATT TGCA	

			TGTAATGGTAA ACGT		
			ATAA		
GAM2332	LOC254124	3'	TGCACCTGGATGGCAACGTG 98468	A A	C
			CAC TT CCATTC GGTGCA		
			GTG AA GGTAGG CCACGT		
			C C T		
GAM2333	BCL10	3'	TTTGAACAAGTGGGCCATT 15376	ATT	TC
			AGTGGCC CT TGTTCAAA		
			TTACCGG GA ACAAGTTT		
			GT_ _		
GAM2333	BLAME	3'	TGAACAGGGTCCATGGCCACT 39659	TC_	
			AGTGGCCAT TTCTGTTCA		
			TCACCGGTA GGGACAAGT		
			CCT		
GAM2333	BTG2	3'	ATTTGGCCAGGATGGCCAC 23142	CTT	TT
			GTGGCCATT CTG CAAAT		
			CACCGGTAG GAC GTTTA		
			_ CG		
GAM2333	F8	3'	GGCAAAGAATGGCTACTT 5528	C	
			AAGTGGCCATTCTT TGTT		
			TTCATCGGTAAGAA ACGG		
			A		
GAM2333	FXD6	3'	GCTTAAGAAAACCGGCCACTT 42094	A_	CT
			AAGTGGCC TTCTT GT		
			TTCACCGG AAGAA CG		
			CCAA TT		
GAM2333	NPTX2	3'	ACAGAAAAGAACAGCCATT 94083	CA	_
			AGTGGC TTCT TCTGT		
			TTACCG AAGA AGACA		
			AC AA		
GAM2333	CHODL	3'	ATTTGAACAAAAGAAGTGAC 46883	G CA	C
			GT GC TTCTT TGTTCAAAT		
			CA TG AAGAA ACAAGTTTA		
			G _ A		
GAM2333	HBOA	3'	AGCAAGGCAGAATGGCCAC 23929	_ _	
			GTGGCCATTCT TCT GTT		
			CACCGGTAAGA GGA CGA		
			C A		
GAM2333	HEMK	3'	TTGAGCAATGGCCACTT 32968	TCTTC	
			AAGTGGCCAT TGTTCAA		

TTCACCGGTA ACGAGTT

GAM2333 IMPACT 3' ATTTGAACTTAATCACCCTT 38003 CC CTTCT
AAGTGG ATT GTTCAAAT
||||| ||| |||||
TTCACC TAA CAAGTTTA
AC TT__

GAM2333 KIAA0293 3' ATTTGGATAGAACGGCCAC 61235 ATTC
GTGGCC TTCTGTTCAAAT
||||| |||||
CACCGG AAGATAGGTTTA
C__

GAM2333 KIAA0318 3' ATTTGAACAAAAGACTTACTT 69526 CCAT C
AAGTGG TCTT TGTTCAAAT
||||| ||| |||||
TTCATT AGAA ACAAGTTTA
C__ A

GAM2333 MGC10715 3' CAGTAAAGAATGGACACT 44497 G ____
AGTG CCATTCTT CTG
||| ||||| |||
TCAC GGTAAGAA GAC
A AAT

GAM2333 PRKCBP1 3' GGCAGGAGAACAGCCACTT 25751 CA
AAGTGGC TTCTTCTGTT
||||| |||||
TTCACCG AAGAGGACGG
AC

GAM2333 RNAC 3' GGACAGAATAGCCACTT 20494 CATT C
AAGTGGC TTCTGTTC
||||| |||||
TTCACCG AAGACAGG
AT__

GAM2333 XAP135 5' TTGATAGAGTACAAATGGCCAC 37486 C__ T
GTGGCCATT TTCTGT CAA
||||| ||||| |||
CACCGGTAA GAGATA GTT
ACAT _

GAM2333 XAP135 5' TTGATAGAGTACAAATGGCCAC 56657 C__ T
GTGGCCATT TTCTGT CAA
||||| ||||| |||
CACCGGTAA GAGATA GTT
ACAT _

GAM2333 LOC122970 3' ATGAAAGAATGGTCACTT 74637 CT
AAGTGGCCATTCTT GT
||||| |||
TTCAGTGGTAAGAA TA
AG

GAM2333 LOC145900 3' ATTTGAATGTTATAGCCACTT 78021 C TCTTCT
AAGTGGC AT GTTCAAAT
||||| ||| |||||

		TTCACCG TA TAAGTTTA	
		A TTG___	
GAM2333	LOC151959 5'	ATTTGAACAGGTAGACCCACTT 86711	CCAT _
		AAGTGG TCT TCTGTTCAAAT	
		TTCACC AGA GGACAAGTTTA	
		C___ T	
GAM2333	LOC220883 3'	AGCAAGGCAGAATGGCCAC 92889	_ _
		GTGGCCATTCT TCT GTT	
		CACCGGTAAGA GGA CGA	
		C A	
GAM2333	LOC221511 3'	TGAACAGAAGAGGACTT 92631	GG AT
		AAGT CC TCTTCTGTTCA	
		TTCA GG AGAAGACAAGT	
		— —	
GAM2333	LOC255995 3'	TGAACAGAAGTGCACAGGCTAC 98751	ATT___
	TT	AAGTGGCC CTTCTGTTCA	
		TTCATCGG GAAGACAAGT	
		ACACGT	
GAM2333	LOC257569 3'	TGAACAGAAGAGGACTT 99666	GG AT
		AAGT CC TCTTCTGTTCA	
		TTCA GG AGAAGACAAGT	
		— —	
GAM2333	LOC91380 5'	ATTTGAGCTTAAAAATGACACT 66436	GC C CT
		AGTG CATT TT GTTCAAAT	
		TCAC GTAA AA CGAGTTTA	
		A_ A TT	
GAM2334	AICDA 3'	CCCAGGAGGTGGAGGTTGCAGT 40692	G
	AA	TTACTGCAA CTCCGCCTCCTGGG	
		AATGACGTT GAGGTGGAGGACCC	
		G	
GAM2334	BHMT2 3'	CCCAGGAGGCGGAGCTTGCAGT 34730	
	GA	TTACTGCAAGCTCCGCCTCCTGGG	
		AGTGACGTTGAGGCGGAGGACCC	
GAM2334	BMP8 5'	CCCAGGAGGCGCTGGAGCAACA 9945	CAA _
	G	CTG GCTCC GCCTCCTGGG	
		GAC CGAGG CGGAGGACCC	
		AA_ TCG	
GAM2334	CA12 3'	CCCAGGAGGCGGAGGTTGCAGT 8687	G
	AA	TTACTGCAA CTCCGCCTCCTGGG	

			AATGACGTT GAGGCGGAGGACCC	
			G	
GAM2334	CUBN	3'	CCCAGGAGGCAGAGGTTGCAGT 8420	G C
	GA		TTACTGCAA CTC GCCTCCTGGG	
			AGTGACGTT GAG CGGAGGACCC	
			G A	
GAM2334	DDOST	3'	CCAGGAGGCAGAGCTTGCAGTG 19062	C
	A		TTACTGCAAGCTC GCCTCCTGG	
			AGTGACGTTTCGAG CGGAGGACC	
			A	
GAM2334	DFFA	3'	GAGGCAGAGCTTGCAGTGA 16594	C
			TTACTGCAAGCTC GCCTC	
			AGTGACGTTTCGAG CGGAG	
			A	
GAM2334	DGKI	5'	CCCAGGAGGCGGAGCTGGCAGT 17527	A
	GA		TTACTGC AGCTCCGCCTCCTGGG	
			AGTGACG TCGAGGCGGAGGACCC	
			G	
GAM2334	EGFL4	3'	CCCAGGAGGCGGAGGTTGCAGT 62461	G
	GA		TTACTGCAA CTCCGCCTCCTGGG	
			AGTGACGTT GAGGCGGAGGACCC	
			G	
GAM2334	ESR1	3'	CCCTCCCTGAACTTGCAGTAA 5511	C CGCCTCCT
			TTACTGCAAG TC GGG	
			AATGACG TTC AG CCC	
			A TCCCT__	
GAM2334	FCAR	3'	CCCAGGAGGCAGCTGTTGCAGT 56569	__ CC
	GA		TTACTGCA AGCT GCCTCCTGGG	
			AGTGACGT TCGA CGGAGGACCC	
			TG __	
GAM2334	FCAR	3'	CCCAGGAGGCAGCTGTTGCAGT 56570	__ CC
	GA		TTACTGCA AGCT GCCTCCTGGG	
			AGTGACGT TCGA CGGAGGACCC	
			TG __	
GAM2334	FGFR1	3'	CCCAGAAGGCAGAGGTTGCAGT 7020	G C C
	GA		TTACTGCAA CTC GCCT CTGGG	
			AGTGACGTT GAG CGGA GACCC	
			G A A	
GAM2334	GALNT7	3'	CCCAGGAGGCAGAGGTTGCAGT 55088	G C
	GA		TTACTGCAA CTC GCCTCCTGGG	

			AGTGACGTT GAG CGGAGGACCC	
			G A	
GAM2334	GPRK7	3'	CCCAGGAGGCGGAGGTTGTAG 58311	G
			CTGCAA CTCCGCCTCCTGGG	
			GATGTT GAGGCGGAGGACCC	
			G	
GAM2334	IAPP	3'	CCCAGGAGGCGGAGGTTGCAGT 6441	G
	GA		T TACTGCAA CTCCGCCTCCTGGG	
			AGTGACGTT GAGGCGGAGGACCC	
			G	
GAM2334	KCNA7	3'	GAGGCGGAGCTTGCAGTGA 49900	
			T TACTGCAAGCTCCGCCTC	
			AGTGACGTT CGAGGCGGAG	
GAM2334	KIF1B	3'	CCCAGGAGGCAGAGGTTGCAGT 31266	G C
	GA		T TACTGCAA CTC GCCTCCTGGG	
			AGTGACGTT GAG CGGAGGACCC	
			G A	
GAM2334	KNSL1	3'	CCCAGGAAGCGGGGTTGCAGTG 16943	G C
	A		T TACTGCAA CTCCGC TCCTGGG	
			AGTGACGTT GGGGCG AGGACCC	
			- A	
GAM2334	LAMC2	3'	CCCAGGAGGCGGAGGTTACAGT 19907	C G
	GA		T TACTG AA CTCCGCCTCCTGGG	
			AGTGAC TT GAGGCGGAGGACCC	
			A G	
GAM2334	LDLR	3'	CCCGGGAAGCGGAGCTTGCAGT 6732	C
	GA		T TACTGCAAGCTCCGC TCCTGGG	
			AGTGACGTT CGAGGCG AGGGCCC	
			A	
GAM2334	LRRC2	3'	CCCAGGAAGCAGAGGTTGCAGT 44742	G C C
	AA		T TACTGCAA CTC GC TCCTGGG	
			AATGACGTT GAG CG AGGACCC	
			G A A	
GAM2334	LUZP1	3'	CCCAGGAGGCGGAGGTTGCAGT 54399	G
	GA		T TACTGCAA CTCCGCCTCCTGGG	
			AGTGACGTT GAGGCGGAGGACCC	
			G	
GAM2334	MAFF	3'	CCCAGAAGGCAGAGGTTGTAG 25578	G C C
			CTGCAA CTC GCCT CTGGG	

		GATGTT GAG CGGA GACCC		
		G A A		
GAM2334	MOG	3'	CCCAGGAGGCAGAGGTTGCAGT 11670	G C
	GA		TTACTGCAA CTC GCCTCCTGGG	
			AGTGACGTT GAG CGGAGGACCC	
			G A	
GAM2334	MTMR8	3'	CCCGGGAGGCAGAGCTTGCAGT 31908	C
	GA		TTACTGCAAGCTC GCCTCCTGGG	
			AGTGACGTTGAG CGGAGGGCCC	
			A	
GAM2334	NFKBIL2	3'	CCCGGGAGGCGGAGCTTGCAGT 26449	
	GA		TTACTGCAAGCTCCGCCTCCTGGG	
			AGTGACGTTGAGGCGGAGGGCCC	
GAM2334	NPHS1	3'	CCCAGGAGGCGGAGGTTGCAGT 17369	G
	GA		TTACTGCAA CTCCGCCTCCTGGG	
			AGTGACGTT GAGGCGGAGGACCC	
			G	
GAM2334	NT5C2	3'	CCCAGGAGGCGGAGGTTGCAGT 25261	G
	GA		TTACTGCAA CTCCGCCTCCTGGG	
			AGTGACGTT GAGGCGGAGGACCC	
			G	
GAM2334	OGG1	5'	CCCGGGAGGCGGAGCTTGCAGT 34151	
	GA		TTACTGCAAGCTCCGCCTCCTGGG	
			AGTGACGTTGAGGCGGAGGGCCC	
GAM2334	PCDH11X	3'	CCCGGGAGGCGGAGCTTGCAGT 28009	
	GA		TTACTGCAAGCTCCGCCTCCTGGG	
			AGTGACGTTGAGGCGGAGGGCCC	
GAM2334	PCDH11Y	3'	CCCGGGAGGCGGAGCTTGCAGT 53158	
	GA		TTACTGCAAGCTCCGCCTCCTGGG	
			AGTGACGTTGAGGCGGAGGGCCC	
GAM2334	PPP1R12B	3'	CCCGGGAGGCGGAGCTTGCAGT 50351	
	GA		TTACTGCAAGCTCCGCCTCCTGGG	
			AGTGACGTTGAGGCGGAGGGCCC	
GAM2334	ROCK2	3'	CCCAGGAGACGGTGGTTGCAGT 66616	G _ C
	GA		TTACTGCAA CT CCG CTCCTGGG	

AGTGACGTT GG GGC GAGGACCC
 _ T A
 GAM2334 SLC26A4 3' CCCGGGAGGCGGAGCTTGCAGT 6525
 GA TTAAGCTCAAGCTCCGCCTCCTGGG
 |||||
 AGTGACGTTGAGGCGGAGGGCCC

GAM2334 SLC28A2 3' CCGGGAGGCGGAGCTTGCAG 16146
 CTGCAAGCTCCGCCTCCTGG
 |||||
 GACGTTGAGGCGGAGGGCC

GAM2334 SMG1 3' CCCAGGAGGCGGAGCTTGCAGT 31345
 GA TTAAGCTCAAGCTCCGCCTCCTGGG
 |||||
 AGTGACGTTGAGGCGGAGGACCC

GAM2334 TRADD 3' CCCAGAAGCGGGGCTTACAG 15037 C CTC
 CTG AAGCTCCGC CTGGG
 ||| ||||| ||||
 GAC TTCGGGGCG GACCC
 A AA_

GAM2334 TRIM14 3' CCCAGGAGGCGGAGATTGCAGT 29508 G
 GA TTAAGCTCAA CTCCGCCTCCTGGG
 ||||| |||||
 AGTGACGTT GAGGCGGAGGACCC
 A

GAM2334 UBE2G2 3' CCCAGGAGGCGGAGCTTGCAGT 65484
 GA TTAAGCTCAAGCTCCGCCTCCTGGG
 |||||
 AGTGACGTTGAGGCGGAGGACCC

GAM2334 VHL 3' CCCAGGAGGCGAAGATTGCAGT 6844 G C
 GA TTAAGCTCAA CT CGCCTCCTGGG
 ||||| || |||||
 AGTGACGTT GA GCGGAGGACCC
 A A

GAM2334 WIG1 3' CCCGGGAGGCGGAGCTTGCAGT 96098
 GA TTAAGCTCAAGCTCCGCCTCCTGGG
 |||||
 AGTGACGTTGAGGCGGAGGGCCC

GAM2334 ZNF36 3' CCCAGGAGGCAGAGGTTGCAGT 95580 G C
 GA TTAAGCTCAA CTC GCCTCCTGGG
 ||||| || |||||
 AGTGACGTT GAG CGGAGGACCC
 G A

GAM2334 ZNF91 3' CCCGGGAGGCGGAGCTTGCAGT 14279
 GA TTAAGCTCAAGCTCCGCCTCCTGGG
 |||||

AGTGACGTTTCGAGGCGGAGGGCCC

GAM2334	AGMAT	3'	CCCAGGAAGCGGAGGCTGCAGT 45739	AG	C
	GA		TTACTGCA CTCCTGGG		
			AGTGACGT GAGGCG AGGACCC		
			CG A		
GAM2334	AKR1B10	5'	CCCAGGAGACAGAGGTTGTAG 40079	G	CGC
			CTGCAA CTC CTCCTGGG		
			GATGTT GAG GAGGACCC		
			G ACA		
GAM2334	AP1GBP1	3'	CCCAGGAGGCGGAGGTTGCA 24344	G	
			TGCAA CTCCTGGG		
			ACGTT GAGGCGGAGGACCC		
			G		
GAM2334	ARNTL2	3'	CCCAGGAGGCAGAGATGGCAGT 39844	AAG	C
	GA		TTACTGC CTC GCCTCCTGGG		
			AGTGACG GAG CGGAGGACCC		
			GTA A		
GAM2334	BFAR	3'	CCCAGGAGGCGGAGGTTGCAG 61423	G	
			CTGCAA CTCCTGGG		
			GACGTT GAGGCGGAGGACCC		
			G		
GAM2334	BTN3A2	3'	CCCGGAAGGCAGAGCTTGCAGT 23874	C	C
	GA		TTACTGCAAGCTC GCCT CTGGG		
			AGTGACGTTTCGAG CGGA GGCCC		
			A A		
GAM2334	C20orf142	3'	CCCAGGAGGCAGAGGTTGCAGT 75279	G	C
	GA		TTACTGCAA CTC GCCTCCTGGG		
			AGTGACGTT GAG CGGAGGACCC		
			G A		
GAM2334	C6orf5	3'	CCCGGGAGGCGGAGCTTGCAGT 31983		
	GA		TTACTGCAAGCTCCGCCTCCTGGG		
			AGTGACGTTTCGAGGCGGAGGGCCC		
GAM2334	CBCIP2	3'	CCCGGGAGGCAGAGCTTGCAGT 52655	C	
	GA		TTACTGCAAGCTC GCCTCCTGGG		
			AGTGACGTTTCGAG CGGAGGGCCC		
			A		
GAM2334	CCR6	3'	CCCAGGAGGCAGAGGTTGCAGT 49399	G	C
	GA		TTACTGCAA CTC GCCTCCTGGG		

			AGTGACGTT GAG CGGAGGACCC	
			G A	
GAM2334	CDT1	3'	CCCAGGAGGCACAGCTTGCAGT 78159	CC
	GA		TTACTGCAAGCT GCCTCCTGGG	
			AGTGACGTT CGA CGGAGGACCC	
			CA	
GAM2334	CG012	3'	CCCAGGAGGCAGAGGCTACAGT 84153	CA _ C
	GA		TTACTG AGC TC GCCTCCTGGG	
			AGTGAC TCG AG CGGAGGACCC	
			A_ G A	
GAM2334	COE2	3'	CCCAGGAGGCACAGATTGCAGT 64908	G CC
	GA		TTACTGCAA CT GCCTCCTGGG	
			AGTGACGTT GA CGGAGGACCC	
			A CA	
GAM2334	CYorf14	3'	CCCAGGAGATGCAGGCTTGCAG 38203	CC _
	TGA		TTACTGCAAGCT GC CTCCTGGG	
			AGTGACGTT CGG CG GAGGACCC	
			A_ TA	
GAM2334	DDX34	3'	CCCGGGAGGCAGAGCTTGCAGT 28667	C
	GA		TTACTGCAAGCTC GCCTCCTGGG	
			AGTGACGTT CGAG CGGAGGGCCC	
			A	
GAM2334	dJ383J4.3	3'	CCCAGAAGACAGGCTGCAGTGA 67493	A CCGC C
			TTACTGCA GCT CT CTGGG	
			AGTGACGT CGG GA GACCC	
			_ ACA_ A	
GAM2334	DKFZP434B168	3'	GAGGCGGAGCTTGCAGTGA 31868	
			TTACTGCAAGCTCCGCCTC	
			AGTGACGTT CGAGGCGGAG	
GAM2334	DKFZP434C171	3'	CCCAGGAGGCGGAGCTTGCAGT 32188	
	GA		TTACTGCAAGCTCCGCCTCCTGGG	
			AGTGACGTT CGAGGCGGAGGACCC	
GAM2334	DKFZp434E169	3'	CCCGGGAGGCGGAGCTTGCAGT 51075	
	GA		TTACTGCAAGCTCCGCCTCCTGGG	
			AGTGACGTT CGAGGCGGAGGGCCC	
GAM2334	DKFZP434N1511	3'	CCCTGGAGGCAGAGCTTGCAGT 93056	C T
	GA		TTACTGCAAGCTC GCCTCC GGG	

			AGTGACGTTTCGAG CGGAGG CCC	
			A T	
GAM2334	DKFZP564I052	3'	CCCAGGAGGCAGAGGTTGCA 67282	G C
			TGCAA CTC GCCTCCTGGG	
			ACGTT GAG CGGAGGACCC	
			G A	
GAM2334	DKFZp566H0824	5'	CCCGGGAAGCGGAGCTTGCAGT 34482	C
	GA		TTACTGCAAGCTCCGC TCCTGGG	
			AGTGACGTTTCGAGGCG AGGGCCC	
			A	
GAM2334	DKFZP566J2046	3'	CCCGGGAGGCGGAGCTTACAGT 49136	C
	GA		TTACTG AAGCTCCGCCTCCTGGG	
			AGTGAC TTCGAGGCGGAGGGCCC	
			A	
GAM2334	DRF1	3'	CCCAGGAGGCAGAGGTTGCAGT 47745	G C
			ACTGCAA CTC GCCTCCTGGG	
			TGACGTT GAG CGGAGGACCC	
			G A	
GAM2334	FADS1	3'	CCCAGGAGGTCAAGCCTGCAG 26377	A CC
			CTGCA GCT GCCTCCTGGG	
			GACGT CGA TGGAGGACCC	
			C AC	
GAM2334	FBXO6	3'	CCCGGAAGGCAGAGCTTGCAGT 37990	C C
	GA		TTACTGCAAGCTC GCCT CTGGG	
			AGTGACGTTTCGAG CGGA GGCCC	
			A A	
GAM2334	FLJ00060	3'	CCCAGGAGGCAGAGCTTGCAGT 61743	C
	GA		TTACTGCAAGCTC GCCTCCTGGG	
			AGTGACGTTTCGAG CGGAGGACCC	
			A	
GAM2334	FLJ10008	3'	GAGGCAGAGCTTGCAGTGA 36188	C
			TTACTGCAAGCTC GCCTC	
			AGTGACGTTTCGAG CGGAG	
			A	
GAM2334	FLJ10460	3'	CCCAGGAGGCAGAGGTTGCAGT 36614	G C
	AA		TTACTGCAA CTC GCCTCCTGGG	
			AATGACGTT GAG CGGAGGACCC	
			G A	
GAM2334	FLJ10826	3'	CCCAGGAGGCGGAGGTTGCAGT 37246	G
	GA		TTACTGCAA CTCCGCCTCCTGGG	

			AGTGACGTT GAGGCGGAGGACCC	
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GAM2334	FLJ12298	3'	CCCAGGAGGCGGAAGTTGCAGT 50597	GC
		GA	TTACTGCAA TCCGCCTCCTGGG	
			AGTGACGTT AGGCGGAGGACCC	
			GA	
GAM2334	FLJ12671	3'	CCCAGGAGGCGGAGATTGCAGT 49106	G
		GA	TTACTGCAA CTCCGCCTCCTGGG	
			AGTGACGTT GAGGCGGAGGACCC	
			A	
GAM2334	FLJ12921	3'	AGGCGGAGCTTGCAGTGA 46391	
			TTACTGCAAGCTCCGCCT	
			AGTGACGTT CGAGGCGGA	
GAM2334	FLJ13117	3'	CCCAGGAGGCGGAGGCTGCAGT 43807	AG
		GA	TTACTGCA CTCCGCCTCCTGGG	
			AGTGACGT GAGGCGGAGGACCC	
			CG	
GAM2334	FLJ13621	3'	CCCGGGAGGCGGAGCTTGCAGT 47221	
		GA	TTACTGCAAGCTCCGCCTCCTGGG	
			AGTGACGTT CGAGGCGGAGGGCCC	
GAM2334	FLJ14397	3'	GAGGCGGAGCTTGCAGTGA 52326	
			TTACTGCAAGCTCCGCCTC	
			AGTGACGTT CGAGGCGGAG	
GAM2334	FLJ14466	3'	CCCAGGAGGCGGAGGTTGCAGT 52426	G
		GA	TTACTGCAA CTCCGCCTCCTGGG	
			AGTGACGTT GAGGCGGAGGACCC	
			G	
GAM2334	FLJ14490	3'	CCCAGGAGGCGGAGCTTGCAGT 52440	
		GA	TTACTGCAAGCTCCGCCTCCTGGG	
			AGTGACGTT CGAGGCGGAGGACCC	
GAM2334	FLJ20004	3'	CCCAGGAGGCAGAGGTTGCAGT 34754	G C
		GA	TTACTGCAA CTC GCCTCCTGGG	
			AGTGACGTT GAG CGGAGGACCC	
			G A	
GAM2334	FLJ20055	3'	CCCAGGAGGCAGAGGTTGCAG 34905	G C
			CTGCAA CTC GCCTCCTGGG	

			GACGTT GAG CGGAGGACCC	
			G A	
GAM2334	FLJ20069	3'	CCCAGGAGGCAGAGGTTGCAGT 34950	G C
	GA		TTACTGCAA CTC GCCTCCTGGG	
			AGTGACGTT GAG CGGAGGACCC	
			G A	
GAM2334	FLJ20211	3'	GAGGCAGAGGTTGCAGTAA 35261	G C
			TTACTGCAA CTC GCCTC	
			AATGACGTT GAG CGGAG	
			G A	
GAM2334	FLJ20241	3'	CCCAGGAGGCGGAGCTTGCAGT 35290	
	GA		TTACTGCAAGCTCCGCCTCCTGGG	
			AGTGACGTTGAGGCGGAGGACCC	
GAM2334	FLJ20694	3'	CCCAGGAGGCAGAGGTTGCAGT 35975	G C
	GA		TTACTGCAA CTC GCCTCCTGGG	
			AGTGACGTT GAG CGGAGGACCC	
			G A	
GAM2334	FLJ20783	3'	CCCAGGAGGCGGAGCTTGCAGT 36097	
	GA		TTACTGCAAGCTCCGCCTCCTGGG	
			AGTGACGTTGAGGCGGAGGACCC	
GAM2334	FLJ20972	3'	CCCAGGAGGCAGAGATTGCAGT 47385	G C
	GA		TTACTGCAA CTC GCCTCCTGGG	
			AGTGACGTT GAG CGGAGGACCC	
			A A	
GAM2334	FLJ21369	3'	CCCAGGAGGCAGAGGTTACAGT 46049	C G C
	AA		TTACTG AA CTC GCCTCCTGGG	
			AATGAC TT GAG CGGAGGACCC	
			A G A	
GAM2334	FLJ22313	3'	CCCAGGAGGCGGAGGTTGCAGT 42578	G
	GA		TTACTGCAA CTCCGCCTCCTGGG	
			AGTGACGTT GAGGCGGAGGACCC	
			G	
GAM2334	FLJ22692	3'	CCCAGGAGGCAGAGCTTGCAGT 47479	C
	GA		TTACTGCAAGCTC GCCTCCTGGG	
			AGTGACGTTGAG CGGAGGACCC	
			A	
GAM2334	FLJ22814	3'	CCCAGGAGGCGGAGCTTGCAGT 46722	
	GA		TTACTGCAAGCTCCGCCTCCTGGG	

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GAM2334 FLJ23040 3' GAGGCGGAGGTTGCAGTAA 47987 G
TTACTGCAA CTCCGCCTC
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AATGACGTT GAGGCGGAG
G

GAM2334 FLJ23499 3' CCCAGGAAGCAGAGGTTGCAGT 43131 G C C
GA TTACTGCAA CTC GC TCCTGGG
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AGTGACGTT GAG CG AGGACCC
G A A

GAM2334 FLJ23878 3' CCCGGAAGGCGGAGCTTGCAGT 59369 C
GA TTACTGCAAGCTCCGCCT CTGGG
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A

GAM2334 FLJ31737 3' CCCAGGAGGCCAAAGGCTGCAGT 59348 A CC_
GA TTACTGCA GCT GCCTCCTGGG
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AGTGACGT CGG CGGAGGACCC
_ AAA

GAM2334 GALNT6 3' CCCAGGAGGCAGAGGTTGCAGT 24245 G C
GA TTACTGCAA CTC GCCTCCTGGG
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AGTGACGTT GAG CGGAGGACCC
G A

GAM2334 GTPBP5 3' GAGGCGGAGCTTGCAGTGA 65975
TTACTGCAAGCTCCGCCTC
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AGTGACGTTTCGAGGCGGAG

GAM2334 HSA250303 3' CCCAGGAAGCAGAGGTTGCAGT 38020 G C C
GA TTACTGCAA CTC GC TCCTGGG
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AGTGACGTT GAG CG AGGACCC
G A A

GAM2334 KATII 3' CCCAGGAATTCAGGCTGCAGTA 33164 A CCGCC
A TTACTGCA GCT TCCTGGG
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AATGACGT CGG AGGACCC
_ ACTTA

GAM2334 KIAA0036 3' CCAGACAAGACCTGCAGTAA 28389 A C CGCCTC
TTACTGCA G TC CTGG
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AATGACGT C AG GACC
_ C AACA_

GAM2334 KIAA0184 3' GAGGCGGAGCTTGCAGTGA 65810
TTACTGCAAGCTCCGCCTC
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GAM2334	KIAA0408	3'	CCCGGGAGGCAGAGCTTGCAGT	28797	C
	GA		TTACTGCAAGCTC GCCTCCTGGG		
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			A		
GAM2334	KIAA0441	3'	CCCAGGAGGCGGAGGCTGCAGT	29629	AG
	GA		TTACTGCA CTCCGCCTCCTGGG		
			AGTGACGT GAGGCGGAGGACCC		
			CG		
GAM2334	KIAA0472	3'	CCCAGGAGACAGAGGCTGCA	72346	AG CGC
			TGCA CTC CTCCTGGG		
			ACGT GAG GAGGACCC		
			CG ACA		
GAM2334	KIAA0563	3'	GAGGCAGAGCTTGCAGTGA	29883	C
			TTACTGCAAGCTC GCCTC		
			AGTGACGTTTCGAG CGGAG		
			A		
GAM2334	KIAA0889	3'	CCCAGGAGGCGGAGGCTGCAGT	31769	AG
	GA		TTACTGCA CTCCGCCTCCTGGG		
			AGTGACGT GAGGCGGAGGACCC		
			CG		
GAM2334	KIAA0912	3'	CCCAGGAATTTGAGGTTGCAGT	65041	G CGCC
	AA		TTACTGCAA CTC TCCTGGG		
			AATGACGTT GAG AGGACCC		
			G TTTA		
GAM2334	KIAA0924	3'	CCCAGGAGGCGGAGCTTGCAGT	30357	
	GA		TTACTGCAAGCTCCGCCTCCTGGG		
			AGTGACGTTTCGAGGCGGAGGACCC		
GAM2334	KIAA1164	3'	CCCAGGAGGCAGTGATTGCAGT	70039	GCTCC
	GA		TTACTGCAA GCCTCCTGGG		
			AGTGACGTT CGGAGGACCC		
			AGTGA		
GAM2334	KIAA1228	3'	CCCAGGAGGCGGAGGTTGCAGT	65673	G
	GA		TTACTGCAA CTCCGCCTCCTGGG		
			AGTGACGTT GAGGCGGAGGACCC		
			G		
GAM2334	KIAA1244	3'	CCCAGGAGGCGGACGTTGCAGT	72443	GC
	GA		TTACTGCAA TCCGCCTCCTGGG		

			AGTGACGTT AGGCGGAGGACCC	
			GC	
GAM2334	KIAA1253	3'	CCCAGGAGGCAGAGGTTGCAGT 93549	G C
	GA		TTACTGCAA CTC GCCTCCTGGG	
			AGTGACGTT GAG CGGAGGACCC	
			G A	
GAM2334	KIAA1404	3'	CCCAGGAGGCGGAGGTTGCAGT 62686	G
	GA		TTACTGCAA CTCCGCCTCCTGGG	
			AGTGACGTT GAGGCGGAGGACCC	
			G	
GAM2334	KIAA1559	3'	CCCAAGAGGCAGAGTTTGCAGT 73453	C C
	GA		TTACTGCAAGCTC GCCTC TGGG	
			AGTGACGTTTGAG CGGAG ACCC	
			A A	
GAM2334	KIAA1594	3'	CCCAGGAGGCAGAGGTTGCAGT 72550	G C
	GA		TTACTGCAA CTC GCCTCCTGGG	
			AGTGACGTT GAG CGGAGGACCC	
			G A	
GAM2334	KIAA1644	3'	CCCAGAAGGCAGAGCTTGCAGT 86219	C C
	GA		TTACTGCAAGCTC GCCT CTGGG	
			AGTGACGTTTCGAG CGGA GACCC	
			A A	
GAM2334	KIAA1649	3'	CCCAGGAGGCAGAGGTCGCAGT 51227	AAG C
	GA		TTACTGC CTC GCCTCCTGGG	
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			CTG A	
GAM2334	KIAA1674	3'	CCCAGGAGACGGAGCTTGCAGT 69334	C
	GA		TTACTGCAAGCTCCG CTCCTGGG	
			AGTGACGTTTCGAGGC GAGGACCC	
			A	
GAM2334	KIAA1872	3'	CCCAGGAGGCAGAGATTGCAGT 63605	G C
			ACTGCAA CTC GCCTCCTGGG	
			TGACGTT GAG CGGAGGACCC	
			A A	
GAM2334	KIAA1872	3'	CCCAGGAGGCAGAGGTTGCAGT 63606	G C
	GA		TTACTGCAA CTC GCCTCCTGGG	
			AGTGACGTT GAG CGGAGGACCC	
			G A	
GAM2334	KIAA1879	3'	CCCGGGAGGCAGAACCTGCAGT 73935	AGC C
	GA		TTACTGCA TC GCCTCCTGGG	

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 CCA A
 GAM2334 KIAA1948 5' CCCAGGAGGCAGAGGCTGCAGT 83300 AG C
 GA TTA CTGCA CTC GCCTCCTGGG
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 CG A
 GAM2334 KIAA1948 3' CCCGGGAGGCGGAGCTTGCAGT 83301
 GA TTA CTGCAAGCTCCGCCTCCTGGG
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 GAM2334 KIAA1951 3' CCCGGGAGGCGGAGCTTGCAGT 74150
 GA TTA CTGCAAGCTCCGCCTCCTGGG
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 AGTGACGTT CGAGGCGGAGGGCCC

 GAM2334 LAP1B 3' CCCGGGAGGCGGAGGTTGCAGT 65190 G
 AA TTA CTGCAA CTCCGCCTCCTGGG
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 AATGACGTT GAGGCGGAGGGCCC
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 GAM2334 LGALS9 3' CCCAGGAGGCAGGCACAG 11298 CAA CC
 CTG GCT GCCTCCTGGG
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 A__ A_
 GAM2334 LIM 3' CCCAGGAGACGGAAGTTGCAGT 22321 GC C
 GA TTA CTGCAA TCCG CTCCTGGG
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 GA A
 GAM2334 LIMK2 3' CCCAGGAGGCAAGTGGGCGCAG 19921 AA C__
 CTGC GCTC GCCTCCTGGG
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 GACG CGGG CGGAGGACCC
 _ TGAA
 GAM2334 LSR68 3' CCCAAAAGGCGGAGGTTGCAGT 38553 G CC
 GA TTA CTGCAA CTCCGCCT TGGG
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 G AA
 GAM2334 MAWBP 3' CCCAGGAGGCAGAAGTTGCAGT 42381 GC C
 GA TTA CTGCAA TC GCCTCCTGGG
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 GA A
 GAM2334 MGC11352 3' CCCAGGAGGCGGAGCTTGCAGT 65429
 GA TTA CTGCAAGCTCCGCCTCCTGGG
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GAM2334	MGC12760	3'	CCCAGGAGGCGCTGGAGCAACA	52157	CAA	___
	G		CTG GCTCC GCCTCCTGGG			
			GAC CGAGG CGGAGGACCC			
			AA_ TCG			
GAM2334	MGC12945	3'	CCCAGGAAGCGGAGGTTGCAGT	51265	G	C
	GA		T TACTGCAA CTCCGC TCCTGGG			
			AGTGACGTT GAGGCG AGGACCC			
			G A			
GAM2334	MGC14407	3'	CCCAGGAGGCAGAGGTTGCAGT	52972	G	C
	GA		T TACTGCAA CTC GCCTCCTGGG			
			AGTGACGTT GAG CGGAGGACCC			
			G A			
GAM2334	MGC14436	3'	CCCGGGAGGCGGAGCTTACAGT	52925	C	
	GA		T TACTG AAGCTCCGCCTCCTGGG			
			AGTGAC TTCGAGGCGGAGGGCCC			
			A			
GAM2334	MGC16142	3'	CCCAGGAGGCAGAGATCGCAGT	52264	AAG	C
	GA		T TACTGC CTC GCCTCCTGGG			
			AGTGACG GAG CGGAGGACCC			
			CTA A			
GAM2334	MGC16175	3'	CCTGGGAGGCGGAGCTTGCAGT	52277		TG
	AA		T TACTGCAAGCTCCGCCTCC GG			
			AATGACGTTTCGAGGCGGAGG CC			
			GT			
GAM2334	MGC16703	3'	CCCGGGAGGCAGAGCTTGCAGT	73492	C	
	GA		T TACTGCAAGCTC GCCTCCTGGG			
			AGTGACGTTTCGAG CGGAGGGCCC			
			A			
GAM2334	MGC2562	3'	CCCAGGAGGCGGAGGTTGCAGT	51437	G	
	GA		T TACTGCAA CTCCGCCTCCTGGG			
			AGTGACGTT GAGGCGGAGGACCC			
			G			
GAM2334	MGC2663	3'	CCCAGGAAGCAGAGGTTGCAGT	44333	G	C C
	GA		T TACTGCAA CTC GC TCCTGGG			
			AGTGACGTT GAG CG AGGACCC			
			G A A			
GAM2334	MGC3207	3'	GAGGCAGAGCTTGCAGTGA	63239	C	
			T TACTGCAAGCTC GCCTC			

		AGTGACGTTTCGAG CGGAG		
		A		
GAM2334	MKRN4	3'	GAGGCGGAGCTTGCAATGA 48463	C
		TTA TGCAAGCTCCGCCTC		
		AGT ACGTTCGAGGCGGAG		
		A		
GAM2334	MRPL56	3'	CCCAGGAGGTGGAGTTGCAGTA 52755	G
	A		TTACTGCAA CTCCGCCTCCTGGG	
		AATGACGTT GAGGTGGAGGACCC		
		—		
GAM2334	MRPS18B	3'	CCCAGGAGGCGGAGGTTCAGT 26749	G
	GA		TTACTGCAA CTCCGCCTCCTGGG	
		AGTGACGTT GAGGCGGAGGACCC		
		G		
GAM2334	NMNAT	3'	GAGGCAGAGGTTGCAGTAA 43286	G C
		TTACTGCAA CTC GCCTC		
		AATGACGTT GAG CGGAG		
		G A		
GAM2334	PB1	3'	CCCAGGAGGCAGAGGTTGCAGT 36875	G C
	GA		TTACTGCAA CTC GCCTCCTGGG	
		AGTGACGTT GAG CGGAGGACCC		
		G A		
GAM2334	PDCD7	3'	CCCAGGAGGCAGAGCTTGCAGT 72601	C
	GA		TTACTGCAAGCTC GCCTCCTGGG	
		AGTGACGTTTCGAG CGGAGGACCC		
		A		
GAM2334	PPP1R3B	3'	GAGGCGGAGCTTACAGTGA 45142	C
		TTACTG AAGCTCCGCCTC		
		AGTGAC TTCGAGGCGGAG		
		A		
GAM2334	PRO1048	5'	CCCAGGAGGCAGAGCTTGCAGT 38107	C
	GA		TTACTGCAAGCTC GCCTCCTGGG	
		AGTGACGTTTCGAG CGGAGGACCC		
		A		
GAM2334	PRO2964	3'	CCCGGGAGGCGGAGCTTGCAGT 38257	
	GA		TTACTGCAAGCTCCGCCTCCTGGG	
		AGTGACGTTTCGAGGCGGAGGGCCC		
GAM2334	PSR	3'	CCCAGGAGGCAGAGGTTGCAGT 65783	G C
	GA		TTACTGCAA CTC GCCTCCTGGG	

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			G A	
GAM2334	RoXaN	3'	CCCAGGAGGCACAGTTTGCAGT 47282	CC
	GA		TTACTGCAAGCT GCCTCCTGGG	
			AGTGACGTTTGA CGGAGGACCC	
			CA	
GAM2334	RoXaN	3'	CCCAGGAGGCGGAGCTTACAGT 47283	C
	GA		TTACTG AAGCTCCGCCTCCTGGG	
			AGTGAC TTCGAGGCGGAGGACCC	
			A	
GAM2334	SC65	3'	CCCAGGAGGCGGAGCTTGCAGT 22292	
	GA		TTACTGCAAGCTCCGCCTCCTGGG	
			AGTGACGTTTCGAGGCGGAGGACCC	
GAM2334	SCYA5	3'	CCCGGGAGCGGAGCTTGCAGTG 12966	C
	A		TTACTGCAAGCTCCGC TCCTGGG	
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GAM2334	SEMA3E	3'	CCCGGGAAGCGGAGCTTGCAGT 25805	C
	GA		TTACTGCAAGCTCCGC TCCTGGG	
			AGTGACGTTTCGAGGCG AGGGCCC	
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GAM2334	SMAP-5	3'	CCCAGGAGGCGGAGCTTGCAGT 48658	
	GA		TTACTGCAAGCTCCGCCTCCTGGG	
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GAM2334	SPRY4	3'	CCCAGGAGGCGGAGGTTACAGT 49008	C G
			ACTG AA CTCCGCCTCCTGGG	
			TGAC TT GAGGCGGAGGACCC	
			A G	
GAM2334	SPTLC2	3'	CCCAGGAGGCGGAGGTTGCAGT 17988	G
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GAM2334	SSR3	3'	CCCAGGAGGCAGAGGTTGCAGT 24032	G C
	GA		TTACTGCAA CTC GCCTCCTGGG	
			AGTGACGTT GAG CGGAGGACCC	
			G A	
GAM2334	SYAP1	3'	CCCAGGAGGCAGAGGTTGCAG 52470	G C
			CTGCAA CTC GCCTCCTGGG	

			GACGTT GAG CGGAGGACCC	
			G A	
GAM2334	TACTILE	3'	CCCGGGAGGCAGAGCTTGCAGT 20584	C
	GA		TTACTGCAAGCTC GCCTCCTGGG	
			AGTGACGTTGAG CGGAGGGCCC	
			A	
GAM2334	THEA	3'	CCCAGGAGGCAGAGGTTACAGT 66883	C G C
	GA		TTACTG AA CTC GCCTCCTGGG	
			AGTGAC TT GAG CGGAGGACCC	
			A G A	
GAM2334	TMG4	3'	GAGGCAGAGGTTGCAGTAA 44214	G C
			TTACTGCAA CTC GCCTC	
			AATGACGTT GAG CGGAG	
			G A	
GAM2334	WSB1	3'	CCCAGGAGGTGGAGGTTGCAGT 56972	G
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GAM2334	WSB1	3'	CCCAGGAGGTGGAGGTTGCAGT 56973	G
	AA		TTACTGCAA CTCCGCCTCCTGGG	
			AATGACGTT GAGGTGGAGGACCC	
			G	
GAM2334	ZFP106	3'	CCCGGGAGGCAGAGATTGCAGT 42723	G C
	AA		TTACTGCAA CTC GCCTCCTGGG	
			AATGACGTT GAG CGGAGGGCCC	
			A A	
GAM2334	ZNF333	3'	CCCAGGAGGCAGAGGTTGCAGT 51591	G C
	GA		TTACTGCAA CTC GCCTCCTGGG	
			AGTGACGTT GAG CGGAGGACCC	
			G A	
GAM2334	ZNF347	3'	CCCAGGAGGCGGAGGTTGCAGT 51823	G
	GA		TTACTGCAA CTCCGCCTCCTGGG	
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GAM2334	LOC113523	3'	CCTGTGAGGCGGAGGTTGCAGT 73420	G C
	AA		TTACTGCAA CTCCGCCTC TGGG	
			AATGACGTT GAGGCGGAG GTCC	
			G T	
GAM2334	LOC115129	5'	CCCAGGAGACAGGTTGCAGTGA 73614	G CCGC
			TTACTGCAA CT CTCCTGGG	

		AGTGACGTT GA GAGGACCC	
		G CA__	
GAM2334	LOC116228 3'	AGGCGGAGGTTGCAGTAA 74225	G
		TTACTGCAA CTCCGCCT	
		AATGACGTT GAGGCGGA	
		G	
GAM2334	LOC116236 3'	CCCGGGAGGCGGAGCTTGCAGT 74241	
	GA	TTACTGCAAGCTCCGCCTCCTGGG	
		AGTGACGTTGAGGCGGAGGGCCC	
GAM2334	LOC116349 3'	CCCGGGAGGCGGAGCTTGCAGT 74273	
	GA	TTACTGCAAGCTCCGCCTCCTGGG	
		AGTGACGTTGAGGCGGAGGGCCC	
GAM2334	LOC119180 3'	CCAGGATGCTTTGCAG 74404	CTCC C
		CTGCAAG GC TCCTGG	
		GACGTTT CG AGGACC	
		___ T	
GAM2334	LOC127262 3'	CCCAGGAGGCGGAGGTTGCAGT 76595	G
	GA	TTACTGCAA CTCCGCCTCCTGGG	
		AGTGACGTT GAGGCGGAGGACCC	
		G	
GAM2334	LOC130026 3'	CCCGGGAGGCGGAGCTTGCAGT 57435	
	GA	TTACTGCAAGCTCCGCCTCCTGGG	
		AGTGACGTTGAGGCGGAGGGCCC	
GAM2334	LOC130535 3'	CCCAGGAGGCAGAAGTTGCAGT 76649	GC C
	GA	TTACTGCAA TC GCCTCCTGGG	
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		GA A	
GAM2334	LOC131965 3'	CCCAAGAGGCGGAGACTGCAGT 75521	AG C
	GA	TTACTGCA CTCCGCCTC TGGG	
		AGTGACGT GAGGCGGAG ACCC	
		CA A	
GAM2334	LOC133926 3'	CCCAGGAGGCAGAGTTGCAGT 75630	G C
	GA	TTACTGCAA CTC GCCTCCTGGG	
		AGTGACGTT GAG CGGAGGACCC	
		G A	
GAM2334	LOC139422 3'	CCCGGGAGGCGGAGCTTGCAGT 76345	
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GAM2334 LOC144465 3' GAGGCAGAGGTTGCAGTAA 77347 G C
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AATGACGTT GAG CGGAG
G A

GAM2334 LOC144817 3' CCCAGGAGGCAGAGGTTGCAAT 77512 C G C
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A G A

GAM2334 LOC145299 3' CCCGGGAAGCGGAGCTTGCAGT 84274 C
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GAM2334 LOC145333 3' GAGGCAGAGCTTGCAGTGA 84296 C
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GAM2334 LOC145438 3' CCCGGGAGGCGGAGCTTGCAGT 84311
GA TTACTGCAAGCTCCGCCTCCTGGG
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GAM2334 LOC145608 5' CCCGGGAGGCGGAGCTTGCAGT 84380
GA TTACTGCAAGCTCCGCCTCCTGGG
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GA TTACTGCAAGCTCCGCCTCCTGGG
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GAM2334 LOC145820 3' CCCGGGAGGCGGAGCTTGCAGT 77975
GA TTACTGCAAGCTCCGCCTCCTGGG
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G ACA

GAM2334 LOC146756 3' CCCGGGAGGCGGAGCTTGCAGT 84798
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GAM2334 LOC146901 3' CCCAGGAGACAGAGGTTGCAGT 84897 G CGC
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GAM2334 LOC146923 3' CCCAGGAGGCGGAGCTTGCAGT 78798
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GAM2334 LOC147071 3' GAGGCAGAGCTTGCAGTGA 73366 C
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GAM2334 LOC147599 3' CCCAGGAGGCAGAGGTTGCAGT 85161 G C
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GAM2334 LOC147649 3' CCCGGGAGGCGGAGCTTGCAGT 79058
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GAM2334 LOC149113 3' CCCAAAAGGCAGACATTGCAGT 79906 GC C CC
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GAM2334	LOC150185 3'	CCCAGGAGGCAGAGGTTGCAGT 86066	G C
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GAM2334	LOC153077 3'	GAGGCGGAGCTTGCAGTGA 87127	
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GAM2334	LOC154992 3'	CCCAAAGGCAGACATTGCAGT 82133	GC C CC
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		C G	
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GAM2334	LOC200014 3'	CCCAGGAAGCAGAGGTTGCAGT 89927	G C C
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GAM2334	LOC201220 3'	GAGGCAGAGCTTGCAGTGA 88721	C
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GAM2334	LOC201868 3'	CCCAAAAGGCAGACATTGCAGT 90519	GC C CC
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GAM2334	LOC201931 3'	CCCAGGAGGCGGAGCTTGCAGT 90563	
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GAM2334	LOC203246 3'	CCCGGAAGGCGGAGCTTGCAGT 90829	C
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GAM2334	LOC203276 3'	CCCAGGAGAGGAAGGTTGCAGT 92117	G _ GC
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GAM2334	LOC221288 3'	CCCGGGAGGCGGAGCTTGCAGT 95258	
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GAM2334	LOC221543 5'	GAGGCGGAGCTTGCAGTGA 95378	
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GAM2334	LOC221943 5'	CCCAGGAGGCGGAGGTTGCAGT 95620	G
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GAM2334	LOC257282 5'	CCCAGGAGGCAGAGGTTGCAAT 98134	C G C
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GAM2334	LOC257596 5'	GAGGCGGAGCTTGCAGTGA 99781	
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GAM2334	LOC51212 3'	CCCGGGAGGCAGAGCTTGCAGT 33500	C
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GAM2334	LOC85479	5' GAGGCGGAGCTTGCAGTGA 53567		
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GAM2334	LOC90038	3' CCCAGGAGAGGAAGGTTGCAGT 61799	G _	GC
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GAM2335 ST14 5' CCGGCAGGGACGACGCCT 42042 AC CAT
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GAM2335 HTGN29 5' GCCAACTGTGTGGCGGTCC 39885 _ TC T
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T TC C
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GAM2336 ARHA 3' CTCTGCACTCCACCTGA 71232 T_ A
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GAM2336 KPNB2 3' CTCTGCACCCAGGGAA 11226   G AGA
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GAM2336 MTMR1 5' CTGGACAGTCCCACAGGATC 70724   A _ G
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GAM2336 PKIG   3' CTCATGGAGCTCCACAGATC 23927   T AGTG _
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      C T A__
GAM2336 SHMT2 3' CTCCTTATTCCCTACAGAATC 19435   A CA
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GAM2336	TEM8	3'	CTCTAGCTTTCCACAAATC 50826	C	GC
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			T TTA		
GAM2336	ASB13	3'	CTGCGCTGTTCTACAGAA 45546		-
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GAM2336	CLIPR-59	3'	CTCTGCACCCTCAAGAA 32016	GTG	A
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GAM2336	Di-Ras2	3'	CTCTGGAGTCACAGAATC 34611		AGAGTG
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			CTA GAC CC CACGTCTC		
			TCC _ C_		
GAM2336	FLJ10432	3'	CTCTGCACTCCATGATGAA 39351	T_	GA
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GAM2336	KIAA1854	3'	CTCCGACCTCCCTACAGAATC	72205	A TGCA
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GAM2336	KIF13B	3'	CTTTCTCTCCACAAAGTC	31562	C TGC
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GAM2336	MAP	3'	CTCTTCAGGTTTCACAGAA	43367	GAG C
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GAM2336	PRKRI	5'	CTCTTCCCTCCACAGATC	21828	T AGTGC
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GAM2336	PRO0650	5'	CTGTGACGCTCCACAGAA	27071	A _
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			AAGACACCTC CA TGTC		
			G G		
GAM2336	RASSF2	3'	CTCCACCTTCTCTCCACAGAAT	29096	TGCA_
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GAM2336	TRIM26	3'	CTCTGCACTCTCTGGAAT	14347	GT
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GAM2336 LOC143326 3' CTCTGCCAACACAGGATC 77055 GAGAGT
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CTAGGACAC CGTCTC
AAC__

GAM2336 LOC144058 5' CTCTGAGGGCCACAGAATT 77181 AGAGTG
GATTCTGTGG CAGAG
||||||| |||||
TTAAGACACC GTCTC
GGGA__

GAM2336 LOC146443 3' CTCTTGACCCACAGAAT 78446 AGA G _
ATTCTGTGG GT CA GAG
||||||| |||||
TAAGACACC CA GT CTC
C_ G T

GAM2336 LOC146756 3' CTCTGAGAAGCCTCCACAGAAT 84801 A G__
C GATTCTGTGGAG GT CAGAG
||||||| |||||
CTAAGACACCTC CG GTCTC
_ AAGA

GAM2336 LOC165246 5' CTCCCACTGCCACAGAA 83365 AG CA
TTCTGTGG AGTG GAG
||||||| |||||
AAGACACC TCAC CTC
CG C_

GAM2336 LOC201304 3' CTCTGCACTCCAGAA 89604 TGGA
TTCTG GAGTGCAGAG
||||| |||||||
AAGAC CTCACGTCTC

GAM2336 LOC202052 3' CTCTGCAGGCATTCCACAGAGT 91898 A __
C GATTCTGTGGAG GT GCAGAG
||||||| |||||
CTGAGACACCTT CG CGTCTC
A GA

GAM2336 LOC206426 3' CTCCATCCTCTCCACAGCATC 91098 T TGCA
GAT CTGTGGAGAG GAG
||| ||||||| |||
CTA GACACCTCTC CTC
C CTAC

GAM2336 LOC219920 5' CTCCGCACTCTCCTGGGTC 94949 TGT A
GATTC GGAGAGTGC GAG
||||| ||||||| |||
CTGGG CCTCTCACG CTC
T_ C

GAM2336 LOC221354 3' CTCCAGAACCTCACACAGAATC 94012 _ A GCA_
GATTCTGTG GAG GT GAG
||||||| ||| |||

	CTAAGACAC CTC CA CTC	
	A _ AGAC	
GAM2336 LOC255423 5'	CTCTTACTGCCACAGAA 99439	AG C
	TTCTGTGG AGTG AGAG	
	AAGACACC TCAT TCTC	
	CG _	
GAM2336 LOC257354 3'	CTGCACTCTCTGGAATT 96789	GT
	GATTCT GGAGAGTGCAG	
	TTAAGG TCTCTCACGTC	
	—	
GAM2336 LOC257464 5'	CTCTTGCTTTCCCCAAAATC 91242	C T C
	GATT TG GGAGAGTG AGAG	
	CTAA AC CCTTTCGT TCTC	
	A C _	
GAM2336 LOC257494 3'	CTCTGCACTCTCTGGAAT 99632	GT
	ATTCT GGAGAGTGCAGAG	
	TAAGG TCTCTCACGTCTC	
	—	
GAM2336 LOC92840 3'	CTCCCAGGCCTCCACAGAGTC 57246	A GCA_
	GATTCTGTGGAG GT GAG	
	CTGAGACACCTC CG CTC	
	_ GACC	
GAM2337 CDH12 3'	CTTATCATTAAAGTGGTGTA 15777	CCCAA GA
	TACACCACT GAA ATAAG	
	ATGTGGTGA TTT TATTC	
	AA__ AC	
GAM2337 GOCAP1 3'	ATTGTTCTTGGGAGCAGTGTA 43007	CA G
	TACAC CTCCCAAGAA AAT	
	ATGTG GAGGGTTCTT TTA	
	AC G	
GAM2337 DKFZp434N2435 5'	CTTATTACTGTGGGGTGGT 98090	T AGAAG
	ACCAC CCCA AATAAG	
	TGGTG GGGT TTATTC	
	_ GTCA_	
GAM2337 DKFZP564I122 3'	CTTATTCTTCTCCCTCATGTGT 63877	CACTCCCA
A	TACAC AGAAGAATAAG	
	ATGTG TCTTCTTATTC	
	TACTCC_	
GAM2337 FLJ21791 3'	CTTATTTGCAGAAAGTGGTGTA 62126	CCCAAGAA
	TACACCACT GAATAAG	

		ATGTGGTGA	TTTATTC	
		AGACG__		
GAM2337	HMP19	3' CTTATTCTTTGTTAGGAAAATG 88860	CCAC CAA_	
	TA	TACA TCC GAAGAATAAG		
		ATGT AGG TTTCTTATTC		
		AAA_ ATTG		
GAM2337	KIAA1719	3' TCTGTCTTGGGAGTGGTGTA 68742	_	
		TACACCACTCCCAAGA AGA		
		ATGTGGTGAGGGTTCT TCT		
		G		
GAM2337	KIAA1853	3' TTTTCTTGGAAGCAGTG 69929	CA C	
		CAC CT CCAAGAAGAA		
		GTG GA GGTTCCTTTT		
		AC A		
GAM2337	KIAA1877	3' CTTATTCTTCTGCCATGAGT 66748	CCA_	
		ACTC AGAAGAATAAG		
		TGAG TCTTCTTATTC		
		TACCG		
GAM2337	KIAA1906	3' CTTATTCTTCTTGACTTTTGG 73571	CTCC_	
		CCA CAAGAAGAATAAG		
		GGT GTTCTTCTTATTC		
		TTTCA		
GAM2337	OSBPL11	3' CTTAATTTCCCAAGAGTGGTG 43206	CCAA AA	
		CACCACTC GAAG TAAG		
		GTGGTGAG CTTT ATTC		
		AACC A_		
GAM2337	YME1L1	3' TCATTCTTGATGTGGTGTA 58438	TCC _	
		TACACCAC CAAGAA GA		
		ATGTGGTG GTTCTT CT		
		TA_ A		
GAM2337	ZNF262	3' CTTATTTTGTGTTGGGAGT 18723	A	
		ACTCCCAAG AGAATAAG		
		TGAGGGTTT TTTTATTC		
		G		
GAM2337	LOC91960	3' TGTGGCTTGGAACGTGGTGTA 68294	TC_ AAGA	
		TACACCAC CCAAG ATA		
		ATGTGGTG GGTTT TGT		
		CAA GG_		
GAM2338	ABR	3' CCACCGTACACTTCCCACA 8452	T CGCTG A	
		TGT GGGAAGT GCG TGG		

ACA CCCTTCA TGC ACC
 _ CA_ C
 GAM2338 ABR 3' CCACCGTACACTTCCCACA 41996 T CGCTG A
 TGT GGGAAGT GCG TGG
 ||| ||||| ||| |||
 ACA CCCTTCA TGC ACC
 _ CA_ C
 GAM2338 B4GALT5 3' CCACCTTGACTTCCCAA 17684 CT CGA
 TTGGGAAGTCG GG TGG
 ||||| || |||
 AACCCTTCAGT CC ACC
 T_ _
 GAM2338 C21orf33 3' CCAAATGGCAACTTCCCACA 17380 T C GCGA
 TGT GGGAAGT GCTG TGG
 ||| ||||| ||| |||
 ACA CCCTTCA CGGT ACC
 _ A AAA_
 GAM2338 ETV3 3' CCATCACAGCTCCCCACA 19121 T AGTC GC
 TGT GGGA GCTG GATGG
 ||| ||| ||| |||||
 ACA CCCT CGAC CTACC
 C _ A_
 GAM2338 LHX5 3' CCACCGCCAGTACTCTCCCAGC 42559 _ C A
 A TGTGGGA AGT GCTGGCG TGG
 ||||| ||| ||||| |||
 ACGACCCT TCA TGACCGC ACC
 C _ C
 GAM2338 PIGN 3' CCAGTCGCACAACTTCCCACA 25601 T CGC _ _
 TGT GGGAAGT TG GCGA TGG
 ||| ||||| || ||| |||
 ACA CCCTTCA AC CGCT ACC
 _ _ A G
 GAM2338 C1orf24 3' CCACCTCGACTTCCCAA 54786 CT CGA
 TTGGGAAGTCG GG TGG
 ||||| || |||
 AACCCTTCAGC CC ACC
 T_ _
 GAM2338 cerk 3' CCATCGCCCCCCTCAACA 43163 AAGTCGCT
 TGTGTTGGG GGCGATGG
 ||||| |||||
 ACAACTC CCGCTACC
 CCCC_
 GAM2338 DKFZp434N074 5' TCCATCGCCAACAATACTC 63331 A CGC
 GGG AGT TGGCGATGGA
 ||| ||| |||||
 CTC TCA ACCGCTACCT
 A ACA
 GAM2338 KIAA0057 3' CCAAGGCATAACTTCCCAACA 25405 CGCTG GA
 TGTGTTGGGAAGT GC TGG
 ||||| || |||

		ACAACCCTTCA	CG	ACC		
		ATA__	GA			
GAM2338	LOC112687	3'	CCATCTCTGATTCCCAACA	73228	G	GCT C
			TGTTGGGAA TC	GG GATGG		
			ACAACCCTT AG	TC CTACC		
			_ __	T		
GAM2338	LOC158809	3'	TCAACAGAACCTCCCAACA	88259	A	CG GC
			TGTTGGGA GT	CTG GA		
			ACAACCCT CA	GAC CT		
			C A_	AA		
GAM2338	LOC219690	5'	TCCATCGCCTTCCCTCCCAGCA	94667	AGT	CGCT
			TGTTGGGA	GGCGATGGA		
			ACGACCCT	CCGCTACCT		
			CCCTT__			
GAM2339	ALS2	3'	TGGATTATCTACTACAGAGTGT	40884	AAC	C__
			ACACTCTGTA	AGA CCA		
			TGTGAGACAT	TCT GGT		
			CA_	ATTA		
GAM2339	COL18A1	3'	TGGGTCAGGCAGGGTGCAGTA	48343	CA	AAACA
			TAC CACTCTGT	GACCCA		
			ATG GTGGGACG	CTGGGT		
			AC	GA__		
GAM2339	COL18A1	3'	TGGGTCAGGCAGGGTGCAGTA	56163	CA	AAACA
			TAC CACTCTGT	GACCCA		
			ATG GTGGGACG	CTGGGT		
			AC	GA__		
GAM2339	COL18A1	3'	TGGGTCAGGCAGGGTGCAGTA	56165	CA	AAACA
			TAC CACTCTGT	GACCCA		
			ATG GTGGGACG	CTGGGT		
			AC	GA__		
GAM2339	ECT2	3'	TGGGTCTGTTTCACATGTG	36627	CTC	_
			CACA	TGT AAACAGACCCA		
			GTGT	ACA TTTGTCTGGGT		
			_	C		
GAM2339	GRAF	3'	TGGATCTGTTTGCATGCAGG	31254	A_	CTC C
			CC CA	TGTAACAGA CCA		
			GG GT	ACGTTTGTCT GGT		
			AC _	A		
GAM2339	SORCS1	3'	TTGTTCTCAAAGTGTGGTA	54685	C	TA
			TACCACACT	TG AACAG		

		ATGGTGTGA AC TTGTT		
		A TC		
GAM2339	TYK2	5' GGGTCTGTGCTGAATGTG 60565	C T AA	
		CACA TC GT ACAGACCC		
		GTGT AG CG TGTCTGGG		
		A T _		
GAM2339	UMOD	3' TCTCCTTAAAGAGTGTGG 14011	G AC	
		CCACACTCT TAA AGA		
		GGTGTGAGA ATT TCT		
		A CC		
GAM2339	WHSC1	3' TGGGCCTGTTTGCCGTCTGTG 30585	CTCT A	
		CACA GTAAACAG CCCA		
		GTGT CGTTTGTC GGGT		
		CTGC C		
GAM2339	WHSC1	3' TGGGCCTGTTTGCCGTCTGTG 56672	CTCT A	
		CACA GTAAACAG CCCA		
		GTGT CGTTTGTC GGGT		
		CTGC C		
GAM2339	WHSC1	3' TGGGCCTGTTTGCCGTCTGTG 56683	CTCT A	
		CACA GTAAACAG CCCA		
		GTGT CGTTTGTC GGGT		
		CTGC C		
GAM2339	ALDH9	3' TGGCCCTGTTTACAGAGGCAGT 7349	CACA AC	
	A	TAC CTCTGTAAACAG CCA		
		ATG GAGACATTGTC GGT		
		ACG_ CC		
GAM2339	DKFZp434N035	3' GGGCAGCTTCGCAGAGTGCAGT 51066	CA TA CAGA	
	A	TAC CACTCTG AA CCC		
		ATG GTGAGAC TT GGG		
		AC GC CGAC		
GAM2339	DKFZP434P0111	3' GGCCTGCCAGGGGTGTGGTG 67960	GTAAA A	
		TACCACACTCT CAG CC		
		GTGGTGTGGGG GTC GG		
		ACC_ C		
GAM2339	DKFZP586J1624	3' GGGTCTGTCTACACTGG 32047	CACTC A	
		CCA TGTA ACAGACCC		
		GGT ACAT TGTCTGGG		
		C_ C		
GAM2339	FLJ10803	3' TGGGTCTGTTTACAGCCTGGT 37213	CACT	
		ACCA CTGTAAACAGACCCA		

			TGGT GACATTTGTCTGGGT		
			CC__		
GAM2339	FLJ20507	5'	GGGTCTGTCCGGGCGTTGCGG 35746	A __	TAA
			CC CA C TCTG ACAGACCC		
			GG GT G GGGC TGTCTGGG		
			C T C C__		
GAM2339	FLJ20507	5'	GGGTCTGTCCGGGCGTTGCGG 60850	A __	TAA
			CC CA C TCTG ACAGACCC		
			GG GT G GGGC TGTCTGGG		
			C T C C__		
GAM2339	FLJ23132	3'	TGATTGCAAAGTGTGGTA 97842	C	A
			TACCACACT TGTA CA		
			ATGGTGTGA ACGTT GT		
			A A		
GAM2339	KIAA0326	3'	GGCCTGTTTCGGACTAGGGTG 64966	ACAC	T A
			TACC TCTG AAACAG CC		
			GTGG AGGC TTTGTC GG		
			GATC _ C		
GAM2339	KIAA1456	3'	TGGGTCTGTTTAAATCTATGTC 67572	C	CTCTG_
A			C ACA TAAACAGACCCA		
			A TGT ATTTGTCTGGGT		
			C ATCTAA		
GAM2339	KIAA1754	3'	GTCTTTTACAGAATGTGG 63933	C	C
			CCACA TCTGTAAA AGAC		
			GGTGT AGACATTT TCTG		
			A _		
GAM2339	MESDC2	3'	GTCCTTTGCAGAGTGTG 72921	CA	
			CACACTCTGTAAA GAC		
			GTGTGAGACGTTT CTG		
			C_		
GAM2339	MGC8407	3'	TGGGTCTGCTCTGGTGTGTG 44119	T	GTAAA
			CACAC CT CAGACCCA		
			GTGTG GG GTCTGGGT		
			T TCTC_		
GAM2339	OLFM3	3'	TGAGTCCATTTTCAAGTGTGGT 83027	C T	CA C
			ACCACACT TG AAA GAC CA		
			TGGTGTGA AC TTT CTG GT		
			_ T AC A		
GAM2339	PRO1331	5'	TCTCCCACCGAGTGTGGTA 48563	T	AAAC
			TACCACACTC GT AGA		

			ATGGTGTGAG CA TCT		
			C CCC_		
GAM2339	RCD-8	3'	GGTCTACAGCGTGTGGTA 27523	T	AAAC
			TACCACAC CTGT AGACC		
			ATGGTGTG GACA TCTGG		
			C ____		
GAM2339	LOC115207	3'	TGGATCTATTGGGGGAGTGTGG 57401	GTA C C	
			CCACACTCT AA AGA CCA		
			GGTGTGAGG TT TCT GGT		
			GGG A A		
GAM2339	LOC118978	5'	TGGGTCTGCCCACAGCTGTGGT 76506	CT	AAA
			ACCACA CTGT CAGACCCA		
			TGGTGT GACA GTCTGGGT		
			C_ CCC		
GAM2339	LOC146237	3'	TGGGCCTGTTTGTGCATGTG 84618	CTC _ A	
			CACA TGTA AACAG CCA		
			GTGT ACGT TTGTC GGGT		
			_ GT C		
GAM2339	LOC149371	3'	TGGGTCTGTTTATATGTGT 80095	TC	
			ACAC TGTAACAGACCCA		
			TGTG ATATTTGTCTGGGT		
			T_		
GAM2339	LOC152220	3'	GGTCGTCAGCAGTGTGGTA 86767	_	TAAACA
			TACCACACT CTG GACC		
			ATGGTGTGA GAC CTGG		
			C TG____		
GAM2339	LOC92771	3'	GGGCCCGGCTGAGTGTGGTG 54214	T	AAACAGA
			TACCACACTC GT CCC		
			GTGGTGTGAG CG GGG		
			T GCCC____		
GAM2340	CRTL1	5'	CCAACTTAAGCAGAACTTGAG 10303	CATT	G_
			CTCAAGTTT TGT AAGTTGG		
			GAGTTCAAG ACG TTCAACC		
			_ AA		
GAM2340	SLC4A4	3'	CCAACTAACAAGCAAAACCTG 14990	A CA	GAAG
	AG		CTCA GTTT TTTGT TTGG		
			GAGT CAAA GAACA AACC		
			C AC ATCA		
GAM2340	SNCG	3'	TTCCAAATAAACTTGAG 13287	C	T
			CTCAAGTTT ATTTG GAA		

GAGTTCAAA TAAAC CTT
 A _
 GAM2340 C20orf122 3' CCAACCCACCAAAGAAAACCT 55993 A CA _ AA
 GAG CTCA GTTT TTTG TG GTTGG
 |||| ||| ||| || ||||
 GAGT CAAA AAAC AC CAACC
 C AG C CC
 GAM2340 FLJ11142 3' CCAACCTCTGTTATGAAACTGA 37682 A TTGT A
 TCA GTTTCAT GA GTTGG
 ||| ||||| || |||||
 AGT CAAAGTA CT CAACC
 _ TTGT C
 GAM2340 FLJ20605 5' CCAACTTCTTGAAAACCTGA 35870 AG TTTGT
 TCA TTTCA GAAGTTGG
 ||| ||||| |||||
 AGT AAAGT CTTCAACC
 CA T____
 GAM2340 LOC254267 3' CCAACTTACAGTAAAACCT 96899 CAT A
 AAGTTT TTGTGA GTTGG
 ||||| ||||| |||||
 TTCAAA GACATT CAACC
 AT_ _
 GAM2340 LOC254419 5' CCAATGAAAATGAAACT 99373 GTGAA
 AGTTTCATTT GTTGG
 ||||| |||||
 TCAAAGTAAA TAACC
 AG____
 GAM2340 LOC256206 3' CCAACTTACAGTAAAACCT 96884 CAT A
 AAGTTT TTGTGA GTTGG
 ||||| ||||| |||||
 TTCAAA GACATT CAACC
 AT_ _
 GAM2341 p25 3' TCTGTGTGCCGCCTCCGAACA 23838 A G T CT
 TGTTCCGAG CGG CA CGC GA
 ||||| ||| || ||| ||
 ACAAGCCTC GCC GT GTG CT
 C _ _ T_
 GAM2342 AQP6 3' CCTCAGGGAGCCCCAGCTTCTT 9728 AGA _ GA T
 GAGAAGCT GC CT TG AGG
 ||||| || || || |||
 TTCTTCGA CG GG AC TCC
 CCC A G_ _
 GAM2342 AQP6 3' CCTCAGGGAGCCCCAGCTTCTT 54996 AGA _ GA T
 GAGAAGCT GC CT TG AGG
 ||||| || || || |||
 TTCTTCGA CG GG AC TCC
 CCC A G_ _
 GAM2342 BF 5' CCCCAGGCCAGCTTCTC 9921 AGA ATGTA
 GAGAAGCT GCCTG GG
 ||||| |||| ||

CTCTTCGA CGGAC CC
 CC_ C____
 GAM2342 C18orf1 3' CCCACAGCTCTAGCTCTC 60863 A CTGA A
 GAGA GCTAGAGC TGT GG
 |||| ||||| ||||
 CTCT CGATCTCG ACA CC
 _ ____ C
 GAM2342 CARD10 3' CCCTTGGCTCTGGCCTCTC 28036 A TGATGTA
 GAGA GCTAGAGCC GG
 |||| ||||| ||
 CTCT CGGTCTCGG CC
 C TTC____
 GAM2342 CHD4 3' GCCTTCTGGACCCTGGCTTCTC 8875 AG_ T TGT
 GAGAAGCTAG CC GA AGGC
 ||||| || || ||||
 CTCTTCGGTC GG CT TCCG
 CCA T ____
 GAM2342 HOXB9 3' CCACTTGACAGACTGTAGCTTC 43998 G C AT__ A
 TC GAGAAGCTA AG CTG GT GG
 ||||| || || || ||
 CTCTTCGAT TC GAC CA CC
 G A AGTT _
 GAM2342 LZTS1 3' ACGTCAGGCCCTGACTCCTC 41022 A C A
 GAG AG TAG GCCTGATGT
 ||| || |||||
 CTC TC GTC CGGACTGCA
 C A C
 GAM2342 MECP2 3' CCAACGGCCCCAGCTTCTC 18392 AGA TGAT A
 GAGAAGCT GCC GT GG
 ||||| || || ||
 CTCTTCGA CGG CA CC
 CCC ____ A
 GAM2342 PACSIN3 3' CCTGGTTCAGAGCCCAGCTTCT 33117 AGA _ TG
 C GAGAAGCT GC CTGA TAGG
 ||||| || || || ||||
 CTCTTCGA CG GACT GTCC
 CC_ A TG
 GAM2342 SORBS1 3' GCCTACATTCTCAGCT 31807 A CCT
 AGCT GAG GATGTAGGC
 |||| || |||||
 TCGA CTC TTACATCCG
 _ T__
 GAM2342 TAPBP 3' CTGCAAGCTCCGCCTCTC 13561 A TA CTGA
 GAGA GC GAGC TGTA
 |||| || || || ||||
 CTCT CG CTCG ACGTC
 C C_ A____
 GAM2342 UBE4A 5' ACTTCAGGCTCTGCCTCTC 17728 A T T
 GAGA GC AGAGCCTGA GT
 |||| || ||||| ||

			CTCT CG TCTCGGACT CA		
			C _ T		
GAM2342	DNAJA4	5'	GCTCAGGCAGCCCCAGCTTCTC 38361	AGA__	T
			GAGAAGCT GCCTGA GT		
			CTCTTCGA CGGACT CG		
			CCCCGA _		
GAM2342	HEMK	3'	GCCTACATCTCCCCTCAGCCTC 32959	A A	CCT_
	TC		GAGA GCT GAG GATGTAGGC		
			CTCT CGA CTC CTACATCCG		
			C _ CCCT		
GAM2342	HRH3	5'	GCTCAGGCTCCGGCTCCTC 24317	A TA	T
			GAG AGC GAGCCTGA GT		
			CTC TCG CTCGGACT CG		
			C GC _		
GAM2342	KIAA0296	3'	GCCTGCAGACCTCAGCTTCTC 28776	A	CCTGA
			GAGAAGCT GAG TGTAGGC		
			CTCTTCGA CTC ACGTCCG		
			_ CAG__		
GAM2342	KIAA0774	3'	GCCTGCGGGAGCTCCGGCTTCT 93406	TA _	GA
	C		GAGAAGC GAGC CT TGTAGGC		
			CTCTTCG CTCG GG GCGTCCG		
			GC A _		
GAM2342	KIAA0870	3'	GCCACGGAGCTCCAGCTTCTC 82382	A	CTGA A
			GAGAAGCT GAGC TGT GGC		
			CTCTTCGA CTCG GCA CCG		
			C AG__ _		
GAM2342	KIAA1257	3'	GCCTTGGAGACTCTAGCTTATC 63404	G	C GATGT
			GA AAGCTAGAG CT AGGC		
			CT TTCGATCTC GA TCCG		
			A A GGT__		
GAM2342	MGC4549	3'	GCCTTGGGGCTCTGGCT 51471		GATGT
			AGCTAGAGCCT AGGC		
			TCGGTCTCGGG TCCG		
			GT__		
GAM2342	RNO2	5'	CCTGTGGCCCCAGCTTCTC 53932	AGA	TGATG
			GAGAAGCT GCC TAGG		
			CTCTTCGA CGG GTCC		
			CCC T__		
GAM2342	WBSCR21	5'	GCCCCACGGCCCTAGCTTC 49303	A T A	TA
			GAAGCTAG GCC G TG GGC		

CTTCGATC CGG C AC CCG
C _ _ CC

GAM2342 LOC140219 5' CCTAGAGGGGAACCCTAGTTTC 76489 AG__ GATG
GAAGCTAG CCT TAGG
||||||| ||| ||||
CTTTGATC GGG ATCC
CCAA GAG_

GAM2342 LOC145719 5' CCTATGAAGCTCCAGCTTCTC 84461 A CTGA
GAGAAGCT GAGC TGTAGG
||||||| |||| |
CTCTTCGA CTCG GTATCC
C AA_

GAM2342 LOC145720 5' CCTATGAAGCTCCAGCTTCTC 84447 A CTGA
GAGAAGCT GAGC TGTAGG
||||||| |||| |
CTCTTCGA CTCG GTATCC
C AA_

GAM2342 LOC147080 5' CTGCAAGCTCCGCCTCTC 85035 A TA CTGA
GAGA GC GAGC TGTAG
|||| || |||| |
CTCT CG CTCG ACGTC
C C_ A_

GAM2342 LOC148195 3' CTGCAGGCTCTGCCTC 85281 AA T GAT
GAG GC AGAGCCT GTAG
||| || ||||| ||||
CTC CG TCTCGGA CGTC

GAM2342 LOC148946 3' GCCTAGCTCTGCTCTAGCCTC 85468 AA CT TG
GAG GCTAGAGC GA TAGGC
||| ||||| || ||||
CTC CGATCTCG CT ATCCG
_ T_ CG

GAM2342 LOC152300 3' CTGCAAGCTCTGCCTCTC 81383 A T CTGA
GAGA GC AGAGC TGTAG
|||| || |||| |
CTCT CG TCTCG ACGTC
C _ A_

GAM2342 LOC153243 5' GCCCACATCAGCTCCTCAAGCT 81663 A C__ A
TCTC GAGAAGCT GAG CTGATGT GGC
||||||| ||| ||||| |||
CTCTTCGA CTC GACTACA CCG
A CTC C

GAM2342 LOC157273 5' CCTTCAACTTAGCTTCTC 87719 A CC TGT
GAGAAGCT GAG TGA AGG
||||||| ||| ||| |||
CTCTTCGA TTC ACT TCC
_ A_ _

GAM2342 LOC165741 3' CCCTGGCTCCAGCTTTTC 88604 A TGATGTA
GAGAAGCT GAGCC GG
||||||| |||| |

CTTTTCGA CTCGG CC
 C TC____
 GAM2342 LOC196485 5' GCCTGTGAGGCTCTAATTC 89074 GC G GT
 GAA TAGAGCCT AT AGGC
 ||| ||||| || ||||
 CTT ATCTCGGA TG TCCG
 A_ G _
 GAM2342 LOC197114 5' CCTATGAAGCTCCGGCTTCTC 91267 TA CTGA
 GAGAAGC GAGC TGTAGG
 ||||| ||| |||||
 CTCTTCG CTCG GTATCC
 GC AA_
 GAM2342 LOC202500 5' CCTGGGGCCCTAGGCTTCTC 90687 _ A GATG
 GAGAAGC TAG GCCT TAGG
 ||||| ||| ||| |||
 CTCTTCG ATC CGGG GTCC
 G C ____
 GAM2342 LOC202986 5' GCCTGTGAGGCTCTAATTC 92068 GC G GT
 GAA TAGAGCCT AT AGGC
 ||| ||||| || ||||
 CTT ATCTCGGA TG TCCG
 A_ G _
 GAM2342 LOC221535 3' GCCCATCCCCAGGCTCTGGCC 95443 A ____ TA
 TCTC GAGA GCTAGAGCCT GATG GGC
 ||| ||||| ||| |||
 CTCT CGGTCTCGGA CTAC CCG
 C CCC C_
 GAM2342 LOC221832 3' GCCCTTCGACAGCTCTGGCCCC 94091 AA C A TA_
 TC GAG GCTAGAGC TG TG GGC
 ||| ||||| || || |||
 CTC CGGTCTCG AC GC CCG
 CC _ A TTC
 GAM2342 LOC253018 3' GCCCATCCCCAGGCTCTGGCC 97706 A ____ TA
 TCTC GAGA GCTAGAGCCT GATG GGC
 ||| ||||| ||| |||
 CTCT CGGTCTCGGA CTAC CCG
 C CCC C_
 GAM2342 LOC254111 5' GCCCACATCAGCTCCTTGAGCT 97983 A____ C A
 TCTC GAGAAGCT GAGC TGATGT GGC
 ||||| ||| ||||| |||
 CTCTTCGA CTCG ACTACA CCG
 GTTC _ C
 GAM2342 LOC256895 3' GTCAGACTCTAGCTCTC 98655 A C
 GAGA GCTAGAG CTGAT
 ||| ||||| |||||
 CTCT CGATCTC GACTG
 _ A
 GAM2342 LOC257548 3' GCCCATCCCCAGGCTCTGGCC 99582 A ____ TA
 TCTC GAGA GCTAGAGCCT GATG GGC
 ||| ||||| ||| |||

CTCT CGGTCTCGGA CTAC CCG
 C CCC C_
 GAM2342 LOC257549 3' GCCCCATCCCCAGGCTCTGGCC 99589 A ____ TA
 TCTC GAGA GCTAGAGCCT GATG GGC
 |||| ||||| ||| |||
 CTCT CGGTCTCGGA CTAC CCG
 C CCC C_
 GAM2342 LOC257610 3' GCCCCATCCCCAGGCTCTGGCC 99682 A ____ TA
 TCTC GAGA GCTAGAGCCT GATG GGC
 |||| ||||| ||| |||
 CTCT CGGTCTCGGA CTAC CCG
 C CCC C_
 GAM2342 LOC257611 3' GCCCCATCCCCAGGCTCTGGCC 99691 A ____ TA
 TCTC GAGA GCTAGAGCCT GATG GGC
 |||| ||||| ||| |||
 CTCT CGGTCTCGGA CTAC CCG
 C CCC C_
 GAM2342 LOC51020 3' CCTACTAATAGGCTCTGCCCCT 32676 AA T AT_
 C GAG GC AGAGCCTG GTAGG
 ||| || ||||| |||||
 CTC CG TCTCGGAT CATCC
 CC _ AAT
 GAM2342 LOC81691 3' GTCAGGCTGTAGCCTC 48919 AA G
 GAG GCTA AGCCTGAT
 ||| ||| |||||
 CTC CGAT TCGGACTG
 _ G
 GAM2343 ALDH3A2 3' CAGTGGTCTTCATTCTTCCTC 69798 A _TG
 GA GAAGAATGAAG T CTG
 || ||||| |||
 CT CTTCTTACTTC G GAC
 C TGT
 GAM2343 EGLN2 5' CATGGCCCAATTCTTCTCCCA 54913 A GAA C
 TGG AGAAGAAT GTTG TG
 ||| ||||| ||| |||
 ACC TCTTCTTA CGGT AC
 C ACC _
 GAM2343 EGR2 5' CAGCAACTCCTGGCTTCCCA 6374 AA AATGA
 TGG GAAG AGTTGCTG
 ||| ||| |||||
 ACC CTTC TCAACGAC
 _ GGTCC
 GAM2343 PCDH11X 3' CAACTTAATTTTCTTCCA 28006 ATG
 TGGAAGAAGA AAGTTG
 ||||| |||||
 ACCTTCTTTT TTCAAC
 AA_
 GAM2343 PCDH11Y 3' CAACTTGATTTTCTTCCA 53154 A G
 TGGAAGAAGA T AAGTTG
 ||||| |||||

ACCTTCTTTT A TTCAAC
 _ G
 GAM2343 PCMT1 3' ATCTTCTGCTCTTTCTTCTTCC 19405 T A TGCT
 A TGGAAGAAGAA GA GT GAT
 ||||| || || ||
 ACCTTCTTCTT CT CG CTA
 T _ TCTT
 GAM2343 POU4F1 3' ATCTGCAACTTCATTTTCCCCC 21760 AA A T
 A TGG GAAGA TGAAGTTGC GAT
 || |||| ||||| ||
 ACC CTTTT ACTTCAACG CTA
 CC _ T
 GAM2343 SP100 3' CAGGTCAGTCTTCTTCCA 13337 A AG
 TGGAAGAAGA TGA TTG
 ||||| || ||
 ACCTTCTTCT ACT GAC
 G G_
 GAM2343 C17orf31 3' TAGCCCCTCACCTTCTTCC 34543 AA A TT
 GGAAGAAG TGA G GCTG
 ||||| || | ||
 CCTTCTTC ACT C CGAT
 CC _ CC
 GAM2343 C20orf29 3' AGCTCACCCCGCTCTTCTTCCA 37706 A AA T_
 TGGAAGAAGA TG GT GCT
 ||||| || || ||
 ACCTTCTTCT GC CA CGA
 C CC CT
 GAM2343 DKFZP586M1120 3' ATCCCCAACACCATTTCTTCCCC 49276 AA AA CT
 CA TGG GAAGAATG GTTG GAT
 || ||||| || || ||
 ACC CTTCTTAC CAAC CTA
 CC CA CC
 GAM2343 FLJ12671 5' AGCTTACCTCATTTTCTCCCA 49101 A A T_
 TGG AGAAGAATGA GT GCT
 || ||||| || || ||
 ACC TCTTTTACT CA CGA
 C C TT
 GAM2343 FLJ21162 3' GCTCCCATTTCTTCTTCCA 46373 A_
 TGGAAGAAGAATG AGT
 ||||| || ||
 ACCTTCTTCTTAC TCG
 CC
 GAM2343 FLJ23467 3' TCAGGCTTCATTCCTTCC 45014 AA TG
 GGAAG GAATGAAGT CTGA
 |||| ||||| || ||
 CCTTC CTTACTTCG GACT
 _ _
 GAM2343 ING4 3' TCAACACTTTTCTTCTTCCA 60431 A AT T C
 TGGA GAAGA GAAGT G TGA
 |||| |||| |||| | ||

ACCT CTTCT TTTCA C ACT
 _ _ _ A
 GAM2343 KIAA0016 3' TCAGCAGTTTTTTCTCCCA 29312 A TGAAG
 TGG AGAAGAA TTGCTGA
 ||| ||||| |||||
 ACC TCTTTTT GACGACT
 C T____
 GAM2343 KIAA0420 3' GCTGACCTCATTCTTTCTTCCA 64091 _ A _
 TGGAAGAA GAATGA GTT GC
 ||||| ||||| ||| ||
 ACCTTCTT CTTACT CAG CG
 T C T
 GAM2343 KIAA1157 3' ATCTGTTTTTTATTCCCCTTCC 72696 AA TT T
 A TGGAAG GAATGAAG GC GAT
 ||||| ||||| || |||
 ACCTTC CTTATTTT TG CTA
 CC T_ T
 GAM2343 MGC5590 3' ATCAGCTCCCATCTCTCTCCCA 44148 A _ A AAGTT
 TGG AGA AGA TG GCTGAT
 ||| ||| ||| || |||||
 ACC TCT TCT AC CGACTA
 C C _ CCT__
 GAM2343 NKG7 5' ATCAGCAGCCTCTTCCTCCTCC 20023 A A T A
 A TGGA GA GAA GA GTTGCTGAT
 |||| || ||| || |||||
 ACCT CT CTT CT CGACGACTA
 C C _ C
 GAM2343 PRO1617 5' ATCAATGATTTACCATTTCTTC 38337 GAA GC
 CA TGGAAGAA TGAAGTT TGAT
 ||||| ||||| |||||
 ACCTTCTT ACTTTAG ACTA
 ACC TA
 GAM2343 RHO6 3' CAGCTTCATGCCTCTTCCA 27873 AGA
 TGGAAGA ATGAAGTTG
 ||||| |||||
 ACCTTCT TACTTCGAC
 CCG
 GAM2343 UBE3B 3' AACTTCATTTCTCTTCCA 77439 AG
 TGGAAGA AATGAAGTT
 ||||| |||||
 ACCTTCT TTAATTCAA
 CT
 GAM2343 LOC121219 3' CAGCTTCTGGTCCTCTTCTTCC 74483 ATGA_ TT
 A TGGAAGAAGA AG GCTG
 ||||| || |||
 ACCTTCTTCT TC CGAC
 CCTGG TT
 GAM2343 LOC153387 5' CAGCAGATTTTTTCTTCCA 87224 TGAAG
 TGGAAGAAGAA TTGCTG
 ||||| |||||

ACCTTCTTTT GACGAC
 TA____
 GAM2343 LOC257354 3' GCTGACCTCATTCTTTCTTCCA 96793 _ A _
 TGGAAGAA GAATGA GTT GC
 ||||| ||||| ||
 ACCTTCTT CTTACT CAG CG
 T C T
 GAM2344 COL5A3 3' CTCCCCACCCCTTGAACCC 32317 A AA
 GGGTTCAAGGG TGG AG
 ||||| ||
 CCCAAGTTCCC ACC TC
 C CC
 GAM2344 NOTCH2 3' GTGACTCTCTGCCCTTGGACCC 44579 A A
 A TGGGTTCAAGGG TGG A AGTCAC
 ||||| ||
 ACCCAGGTTCCC GTCT TCAGTG
 _ C
 GAM2344 ZNF179 3' ACTTCTACCCTTAAAC 24087 C A A
 GTT AAGGG TGGAA GT
 || ||||| ||
 CAA TTCCC ATCTT CA
 A _ _
 GAM2344 FLJ10803 3' TGACTTTCAGTTAAAGCC 37210 CAAGG G
 GGTT GAT GAAAGTCA
 ||| || |||||
 CCGA TTG CTTTCAGT
 AA__ A
 GAM2344 FLJ13089 5' TGGCAGCCCTTGAACCCA 71429 ATGGAAA
 TGGGTTCAAGGG GTCA
 ||||| ||
 ACCCAAGTTCCC CGGT
 GA____
 GAM2344 KIAA1210 3' TTCCATCCCCCAAACCCA 98086 CAA
 TGGGTT GGGATGGAA
 ||||| |||||
 ACCCAA CCCTACCTT
 ACC
 GAM2344 KIAA1594 3' TGAGAGAATCACTTGAACCCA 72554 G GGAAAG
 TGGGTTCAAG GAT TCA
 ||||| || ||
 ACCCAAGTTC CTA AGT
 A AGAG__
 GAM2344 KIAA1958 5' GTGACTTTGAACCCCAAACCCA 82789 CAA ATGG
 TGGGTT GGG AAAGTCAC
 ||||| || |||||
 ACCCAA CCC TTTCAGTG
 A__ CAAG
 GAM2344 LCE 3' ACTTTCCAAATGAAACCC 44255 _ AGGGA
 GGGTT CA TGGAAAGT
 ||||| || |||||

CCCAA GT ACCTTTCA
 A AA____
 GAM2344 MARCKS 3' ACTTTCCACCCTGCCCA 11411 TCA A
 TGGGT AGGG TGGAAAGT
 |||| ||| |||||
 ACCCG TCCC ACCTTTCA

 GAM2344 SIRPB1 3' TCCTATCCCTCAAACCCA 21369 CA _
 TGGGTT AGGGAT GGA
 ||||| ||||| ||
 ACCCAA TCCCTA CCT
 AC T
 GAM2344 TUB 5' GTGGGACCATCCCTTAAACCCA 13900 C AAAG
 TGGGTT AAGGGATGG TCAC
 ||||| ||||| |||
 ACCCAA TTCCCTACC GGTG
 A AG____
 GAM2344 LOC158263 3' GTGACTCCTGGGGCCCTGAGCC 82731 A AT____ AA
 CA TGGGTTCA GGG GGA GTCAC
 ||||| || ||| |||||
 ACCCGAGT CCC CCT CAGTG
 _ GGGGT _
 GAM2344 LOC256073 5' ACCTTCCATCCCCCATCCA 98483 TCAA A
 TGGGT GGGATGGAA GT
 |||| ||||| ||
 ACCTA CCCTACCTT CA
 CCC_ C
 GAM2344 LOC257486 3' TTCCATCCCCCAAACCCA 69785 CAA
 TGGGTT GGGATGGAA
 ||||| |||||
 ACCCAA CCCTACCTT
 ACC
 GAM2344 LOC80298 3' ACTTTTACCTTGAACC 48061 GATG
 GGTTC AAGG GAAAGT
 ||||| |||||
 CCAAGTTCC TTTTCA
 A____
 GAM2344 LOC90620 3' ACTTCCCATTCTGAACCC 64325 A GG A
 GGGTTCA G ATGG AAGT
 ||||| | ||| ||||
 CCCAAGT C TACC TTCA
 _TT C
 GAM2344 LOC92912 3' ACTTTCCTATATTGAGCCCA 71404 GGGAT
 TGGGTTCAA GGAAAGT
 ||||| |||||
 ACCCGAGTT CCTTTCA
 ATAT_
 GAM2345 ALDH1B1 3' TTGTTTTTGGGAGGTTTTG 7333 TT TT
 CA G TCTCAGAAAGCAA
 || | ||||| |||||

			GT T AGGGTTTTTGT		
			TT GG		
GAM2345	ARNT2	3'	TTGCTTCTGGGGAAATGGCAGG 30093	_	ATTG
	TG		TACC GC TTTCTCAGAAGCAA		
			GTGG CG AAGGGGTCTTCGTT		
			A GTA_		
GAM2345	BCL11B	3'	TTGTTTTTGGGGTGGGGGGTGT 57581	G	_
	GG		CCGCATT TT TCTCAGAAGCAA		
			GGTGTGG GG GGGGTTTTTGT		
			G GT		
GAM2345	BCL7A	3'	TTGTTTTTGGGGGCTAATTGGT 40998	C	T
	G		TACCG ATTG TTCTCAGAAGCAA		
			GTGGT TAAT GGGGGTTTTTGT		
			_ C		
GAM2345	C18orf1	3'	TTGTTTTTGTGTAATGCGG 60876	TTTCT	
			CCGCATTG CAGAAGCAA		
			GGCGTAAT GTTTTTGT		
			GT__		
GAM2345	CHD2	3'	TTGTTTTTGAAGATCTGGTA 8872	CATTG	T
			TACCG TTTC CAGAAGCAA		
			ATGGT GAAG GTTTTTGT		
			CTA__ _		
GAM2345	CYP19	3'	TTGAGGGAGAAATAGTCGGTG 49168	C	AGAAG
			TACCG ATTGTTTCTC CAA		
			GTGGC TGATAAAGAG GTT		
			_ GGA__		
GAM2345	DAAM2	3'	TTGAGGGGGCGGGCGGTG 93907	A	TT_
			TACCGC TTGT C TCAG		
			GTGGCG GGCG G AGTT		
			_ GG G		
GAM2345	DGKI	3'	TCTGAGGAATGGTGAGGTG 17530	G	TG
			TACC CAT TTTCTCAGA		
			GTGG GTG AAGGAGTCT		
			A GT		
GAM2345	DLST	3'	TTGCTTCTCCCTAGTGCTGGTA 10418	_	TTTCTC
			TACC GCATTG AGAAGCAA		
			ATGG CGTGAT TCTTCGTT		
			T CCC__		
GAM2345	DSCR1	3'	TGTTTCTTTTATGTGGTG 16623	TGTTTCTC	
			TACCGCAT AGAAGCA		

			GTGGTGTA	TCTTTGT		
			TTT_____			
GAM2345	DTNA	3'	TTGCTTCTTTTTCAATGTAGTG	53279	CG	TTTCTC
			TAC CATTG	AGAAGCAA		
			GTG GTAAC	TCTTCGTT		
			AT TTTT__			
GAM2345	DTNA	3'	TTGCTTCTTTTTCAATGTAGTG	9145	CG	TTTCTC
			TAC CATTG	AGAAGCAA		
			GTG GTAAC	TCTTCGTT		
			AT TTTT__			
GAM2345	EGFL4	3'	GGCAGTGAGGGACGATGGGGTG	62469	G	TT GAA AA
			TACC CATTGT	CTCA GC		
			GTGG GTAGCA	GAGT CG		
			G GG GA_ GT			
GAM2345	EGR1	3'	TTGCCCATGGGATATGTGGTG	10494	TGTT	GAA
			TACCGCAT	TCTCA GCAA		
			GTGGTGTA	AGGGT CGTT		
			T___ ACC			
GAM2345	ELK3	5'	CTGGGGAATAATGCAGTA	19092	C	
			TAC GCATTGTTTCTCAG			
			ATG CGTAATAAGGGGTC			
			A			
GAM2345	FANCE	3'	TGTTTTTGAGAGAAGGTA	41904	GCATTG	
			TACC TTTCTCAGAAGCA			
			ATGG AGAGAGTTTTTGT			
			A_____			
GAM2345	FGF12	3'	TGCTTGTTGCAATGTGGTA	41063	TTCT	GA
			TACCGCATTGT	CA AGCA		
			ATGGTGTAACG	GT TCGT		
			TT__ __			
GAM2345	GCNT2	5'	TTGTTTTGAAAAACAGTGGGGT	9458	G	C G
	G		TACC CATTGTTT	TCAGAA CAA		
			GTGG GTGACAAA	AGTTTT GTT		
			G A _			
GAM2345	HAO1	3'	TTGCTTTTGACTTTTCAATGGG	34512	G	TTTC_
	TG		TACC CATTG	TCAGAAGCAA		
			GTGG GTAAC	AGTTTTTCGTT		
			_ TTTTC			
GAM2345	HGF	3'	TTGCAATATAGAGATCATGTGG	95894	T	CAGAA
	TA		TACCGCAT	GTTTCT GCAA		

		ATGGTGTA TAGAGA CGTT	
		C TATAA	
GAM2345 KCNK7	3'	TTGAGAAGGGGGTGAGTGGTG 54060	A___ G
		TACCGC TT TTTCTCAG	
		GTGGTG GG GAAGAGTT	
		AGTG G	
GAM2345 MAP3K7IP1	3'	TTGCTTCTTCCTTCTGGTGCTG 21494	C GTTTCTC
	TG	TAC GCATT AGAAGCAA	
		GTG CGTGG TCTTCGTT	
		T TCTTCCT	
GAM2345 MEN1	3'	TTGTTTTTTAATAATGTGGTA 95016	TCTC
		TACCGCATTGTT AGAAGCAA	
		ATGGTGTAATAA TTTTGTT	
		T___	
GAM2345 MLLT7	3'	TTGTGCCTGGGAGTGTGTGGTG 21044	TGT AA
		TACCGCAT TTCTCAG GCAA	
		GTGGTGTG GAGGGTC TGTT	
		T___ CG	
GAM2345 NRCAM	3'	TTGTTTTTAGGCATAAACAATG 18458	___ TC
	TG	CGCATTGTTT C AGAAGCAA	
		GTGTAACAAA G TTTTGTT	
		TAC GA	
GAM2345 OSR1	3'	TTGTGGAGATGGTCTGGTG 18841	C TG T G
		TACCG AT TTTC CA AA	
		GTGGT TG AGAG GT TT	
		C GT _ G	
GAM2345 PCLO	3'	TGCTTCTGAAATATGGTA 95891	C GTTTC
		TACCG ATT TCAGAAGCA	
		ATGGT TAA AGTCTTCGT	
		A _____	
GAM2345 PCSK2	3'	TTGTTTCTGAGAAAAGAACG 12001	CATTG
		CG TTTCTCAGAAGCAA	
		GC AAAGAGTCTTTGTT	
		AAGA_	
GAM2345 PIGA	3'	TTGCTTTTGGGGGGTTTTTGT 12078	TT_ TT
		GCA G TCTCAGAAGCAA	
		TGT T GGGGTTTTCGTT	
		TTT GG	
GAM2345 PIGA	3'	TTGCTTTTGGGGGGTTTTTGT 12079	TT_ TT
		GCA G TCTCAGAAGCAA	

		TGT T GGGGTTTTTCGTT		
		TTT GG		
GAM2345	PIGA	3' TTGCTTTTGGGGGGTTTTTGT 12080	TT_ TT	
		GCA G TCTCAGAAGCAA		
		TGT T GGGGTTTTTCGTT		
		TTT GG		
GAM2345	PKP4	5' TTGTTTTTGAGGGGCGGGC 14637	A TT	
		GC TTGT CTCAGAAGCAA		
		CG GGCG GAGTTTTTGT		
		_ GG		
GAM2345	PPP1R2	3' TTGTTTTTGGGGGGTTTTTGT 21788	TT_ TT	
		GCA G TCTCAGAAGCAA		
		TGT T GGGGTTTTTGT		
		TTT GG		
GAM2345	PTP4A2	3' TTGCTTGTGAAGCGGTGTAGTA 14446	CG TC G	
		TAC CATTGTT TCA AAGCAA		
		ATG GTGGCGA AGT TTCGTT		
		AT _ G		
GAM2345	RPE	5' TTGCTTTTGGGAGCCAGCGGTA 62879	AT T	
		TACCGC TG TTCTCAGAAGCAA		
		ATGGCG AC GAGGGTTTTTCGTT		
		_ C		
GAM2345	RTKN	5' CTGTGGGACAGTGTGGTA 53502	TT T	
		TACCGCATTGT C CAG		
		ATGGTGTGACA G GTC		
		GG T		
GAM2345	SH2D2A	3' TCTGAGGAATGGTTTGGTG 15608	C TG	
		TACCG AT TTTCTCAGA		
		GTGGT TG AAGGAGTCT		
		T GT		
GAM2345	SLC19A1	3' TTGCTGGAAGAGGTGGGTGGTG 13223	A TG CAGA	
		TACCGC T TTTCT AGCAA		
		GTGGTG G GGAGA TCGTT		
		_ GT AGG_		
GAM2345	SMARCA2	3' TTGTTTTTTTACACTGTGGTA 13244	T TTCTC	
		TACCGCA TGT AGAAGCAA		
		ATGGTGT ACA TTTTGT		
		C TT__		
GAM2345	SNAP25	3' TGCTGTGAAACAGTGTGG 56425	TCAGA	
		CCGCATTGTTTC AGCA		

GGTGTGACAAAG TCGT
TG____

GAM2345 TARDBP 5' TTGTGGGAGCGAAGCGGTG 24793 A T G
TACCGC TTGTTTC CA AA
||||| ||||| || ||
GTGGCG AGCGAGG GT TT
A _ G

GAM2345 TDG 5' TTGCTTCTGGCTGGGTGCGGTG 13649 GTTTC
TACCGCATT TCAGAAGCAA
||||||| |||||
GTGGCGTGG GGTCTTCGTT
GTC__

GAM2345 TPST1 3' TTGTTTCTGAGAAGTTGGG 14583 G TTG
CC CA TTTCTCAGAAGCAA
|| || |||||
GG GT GAAGAGTCTTTGTT
_ T__

GAM2345 WHSC1 3' CTGGGAGGGGGTGTGGTG 24670 G
TACCGCATT TTTCTCAG
||||| |||||
GTGGTGTGG GGAGGGTC
G

GAM2345 ZNF289 3' TTGTATTGAAACAAAGTGGTG 65934 A TCAGAA
TACCGC TTGTTTC GCAA
||||| ||||| |||
GTGGTG AACAAAG TGTT
A TTA__

GAM2345 APOL2 3' GAACCCTGAGAGGCAGGTGGTA 48788 A AAGCAA
TACCGC TTGTTTCTCAG
||||| |||||
ATGGTG GACGGAGAGTC
_ CCAAGT

GAM2345 ARHGDIG 3' GGGCAGGCAGGAGCAGTGTGGT 8625 CAGAA AA
A TACCGCATTGTTTCT GC
||||| ||||| ||
ATGGTGTGACGAGGA CG
CGGA_ GGG

GAM2345 ARPC4 3' TGCGGGAGGTGGGTGGTG 20361 A TG AGAA
TACCGC T TTTCTC GCA
||||| ||||| |||
GTGGTG G GGAGGG CGT
_ GT _

GAM2345 AUTL1 3' TTGTTTTTATATAAAGCAGTG 52728 CG CTC__
TAGTG TAC CATTGTTT AGAAGCAA
|| ||||| |||||
GTG GTGACGAA TTTTGT
AT ATATAT

GAM2345 BLP2 3' TTGTCCGTAGGAGTTGATGTGG 55299 GT CAGAA
TG TACCGCATT TTCT GCAA
||||| ||| |||

			GTGGTGTAG GAGG TGTT		
			TT ATGCC		
GAM2345	BRD4	3'	GTGCAAAGGGAATAGTGCCGT 55254	C	CAGAA A
	G		TAC GCATTGTTTCT GCA		
			GTG CGTGATAAGGG CGT		
			C AAAA_ GT		
GAM2345	C1orf34	3'	CTGGGAGCTGATGTGGTG 61308	GT	
			TACCGCATT TTCTCAG		
			GTGGTGTAG GAGGGTC		
			TC		
GAM2345	C20orf30	3'	TTGTAGCAAATGGAACAATGTG 27111		TCAGAA_
	GTA		TACCGCATTGTTTC GCAA		
			ATGGTGTAACAAGG TGTT		
			TAAACGA		
GAM2345	C20orf80	3'	TGTTTATACAATGTGGTA 65884		TTCTCAG
			TACCGCATTGT AAGCA		
			ATGGTGTAACA TTTGT		
			TA_____		
GAM2345	C20orf82	3'	TGCCCCTGGGGAGCGATGTGG 85876		AA
			CCGCATTGTTTCTCAG GCA		
			GGTGTAGCGAGGGGTC CGT		
			CC		
GAM2345	C9orf9	3'	TTGCCCAAACAGGATGGTGTGG 39040	TG	CTCAGAA
	TA		TACCGCAT TTT GCAA		
			ATGGTGTG AGG CGTT		
			GT ACAAACC		
GAM2345	CLDN1	3'	TTGCTTCATCTGTAAGCGGTG 41191	A	TTTCTCA
			TACCGC TTG GAAGCAA		
			GTGGCG AAT CTTCGTT		
			_ GTCTA__		
GAM2345	COQ3	3'	TTGTTTCTGAGAACTATAGT 70737	__	
			ATTGT TTCTCAGAAGCAA		
			TGATA AAGAGTCTTTGTT		
			TC		
GAM2345	COVA1	3'	TTGCTTCTGTTGTCAGTGTG 73645		TTTCT
			CGCATTG CAGAAGCAA		
			GTGTGAC GTCTTCGTT		
			TGTT_		
GAM2345	DCAMKL1	3'	TTGTTTTTGGGGGGGAGGTGG 17605	A	G TT
			CCGC TT T CTCAGAAGCAA		

GGTG GA G GGGTTTTTGT
_ G GG
GAM2345 DKFZP586H2123 3' TGCCTGAAGCAGTGTGG 62613 TCAGAA
CCGCATTGTTTC GCA
||||||| |||
GGTGTGACGAAG CGT
TG____
GAM2345 DOC2A 5' TGGAGCTGAGGGGCAGTGCGG 14564 TT AAG
CCGCATTGT CTCAG CA
||||||| |||| ||
GGCGTGACG GAGTC GT
GG GAG
GAM2345 EAF1 5' TTGCTTCTGGACCCGGGTGG 53526 A TT T
CCGC TTG TC CAGAAGCAA
||| ||| || |||||
GGTG GGC AG GTCTTCGTT
_ CC _
GAM2345 ESDN 3' TTGGGGAAAATGTGGTG 56067 G
TACCGCATT TTTCTCAG
||||||| |||||
GTGGTGTA AAGGGGT

GAM2345 FLJ10407 3' TTGCTTTTTGTGTGTGTGGTA 36581 TGTTTCTC
TACCGCAT AGAAGCAA
||||||| |||||
ATGGTGTG TTTTCGTT
TGTGT____
GAM2345 FLJ10921 3' TTGCTTCTGAGGAAGCAATG 37395 _
CATTGTTTC TCAGAAGCAA
||||||| |||||
GTAACGAAG AGTCTTCGTT
G
GAM2345 FLJ11149 3' TTGCTTTTGAGAATCAGATAGT 37690 _____
GTG CGCATTGTT TCTCAGAAGCAA
||||||| |||||
GTGTGATAG AGAGTTTTCGTT
ACTA
GAM2345 FLJ11301 3' TGCTTCAAAGTGTGTGGTG 37812 TGTT CA
TACCGCAT CT GAAGCA
||||||| || |||||
GTGGTGTG GA CTTCGT
T____ AA
GAM2345 FLJ12788 3' TTGGTGGGGGACATAGTGTGGT 42851 _ TT GAAGCAA
G TACCGCAT TGT CTCA
||||||| ||| |||
GTGGTGTG ACA GGGT
AT GG GGTT
GAM2345 FLJ14442 3' TTGTTGAAGGGAGGATGTGGTA 52393 G TT CAGA
TACCGCATT T CT AGCAA
||||||| | || |||||

ATGGTGTAG A GA TTGTT
 G GG AG__
 GAM2345 FLJ20793 3' TTGCTTTTGCAGAATTTGGTG 93453 CATTGT _
 TACCG TTCT CAGAAGCAA
 |||| ||| |||||
 GTGGT AAGA GTTTTCGTT
 TT__ C
 GAM2345 FLJ22405 3' TGTTCCTGGGGAGGAGGG 42815 GCA G
 CC TT TTTCTCAGAAGCA
 || || |||||
 GG GA GAGGGGTCTTTGT
 __ G
 GAM2345 FLJ22693 3' TTGCTTTTAAATAATGTG 43050 TCTC
 CGCATTGTT AGAAGCAA
 ||||| |||||
 GTGTAATAA TTTTCGTT
 T__
 GAM2345 FLJ31121 3' TGCAGAGGTAATGCTGTG 59210 C TT CAGAA
 TAC GCATTG TCT GCA
 ||| ||||| ||| |||
 GTG CGTAAT AGA CGT
 T GG ____
 GAM2345 GRM5 3' TTGCTCTAGGGAAGCAGTGCG 63245 _ A
 CGCATTGTTTCTC AGA GCAA
 ||||| ||| |||
 GCGTGACGAAGGG TCT CGTT
 A _
 GAM2345 KALI 3' TTGACTTATTGAGAAATAATGC 54700 C _ _
 AGTG TAC GCATTGTTTCTCAG AAG CAA
 ||| ||||| ||| |||
 GTG CGTAATAAAGAGTT TTC GTT
 A A A
 GAM2345 KIAA0376 5' TTGCGAGGGAGCGATGCGGTG 66219 CAGAA
 TACCGCATTGTTTCT GCAA
 ||||| ||| |||
 GTGGCGTAGCGAGGG CGTT
 AG__
 GAM2345 KIAA0515 3' CTGGGAAGCGATGGGGTG 64548 G
 TACC CATTGTTTCTCAG
 |||| |||||
 GTGG GTAGCGAAGGGTC
 G
 GAM2345 KIAA0552 5' CTGAGGGGCAGAGCGGTG 28991 A TT
 TACCGC TTGT CTCAG
 |||| ||| |||
 GTGGCG GACG GAGTC
 A GG
 GAM2345 KIAA0720 3' CTGGGAAGTAATGGGGTG 62983 G
 TACC CATTGTTTCTCAG
 |||| |||||

	GTGG GTAATGAAGGGTC	
	G	
GAM2345 KIAA0914	5' TTGTTTCTCCAGCCGTGCGGTG 30298	T TCTC
	TACCGCAT GTT AGAAGCAA	
	GTGGCGTG CGA TCTTTGTT	
	C CC__	
GAM2345 KIAA0978	3' CAAGTTGGGAATGATGTGGTG 70990	TG T AAGCAA
	TACCGCAT TTTC CAG	
	GTGGTGTA AAGG GTT	
	GT _ GAACA	
GAM2345 KIAA1023	3' TTGCTTCTGAGAACAGCAGGGT 34684	GCA T
G	TACC TTGTT CTCAGAAGCAA	
	GTGG GACAA GAGTCTTCGTT	
	GAC _	
GAM2345 KIAA1068	3' TTGTTTCTGGTTTACAGTGGTG 31690	AT TTC
	TACCGC TGT TCAGAAGCAA	
	GTGGTG ACA GGTCTTTGTT	
	_ TTT	
GAM2345 KIAA1183	3' TTGTCCCTGGGGCAATGTG 63201	TT AA
	CGCATTGT CTCAG GCAA	
	GTGTAACG GGGTC TGTT	
	_ CC	
GAM2345 KIAA1196	3' TTGTTTCTGGTTGTGTGGT 62157	TGTTT T
	ACCGCAT C CAGAAGCAA	
	TGGTGTG G GTCTTTGTT	
	TT__ _	
GAM2345 KIAA1393	3' TTGTTTTTGGGGGAAGGGGTA 72578	GCATTG TT
	TACC T CTCAGAAGCAA	
	ATGG A GGGTTTTTGTT	
	GGA__ GG	
GAM2345 KIAA1494	3' TTGTGAGATAGTGGTGGTA 68985	_ T
	TACCGC ATTGTTTC CAG	
	ATGGTG TGATAGAG GTT	
	G T	
GAM2345 KIAA1789	5' GCTAGAGAAGCAGTGTGGTG 67703	AGA AA
	TACCGCATTGTTTCTC AGC	
	GTGGTGTGACGAAGAG TCG	
	A_ A	
GAM2345 KIAA1814	3' TTGCTTAGCTAGCAGTGCG 70882	TCTCAG
	CGCATTGTT AAGCAA	

GCGTGACGA TTCGTT
 TCGA__
 GAM2345 MGC1127 3' GCACTTGGGGGGTGGGTGGTG 54332 A TG TT AA AA
 TACCGC T T CTCAG GC
 ||||| | | |||| |
 GTGGTG G G GGGTT CG
 _GT GG CA A
 GAM2345 MGC11349 3' TTCGGGGGAGGATGATGTGGTG 47792 TG _ A_
 TACCGCAT TT TCTC GAA
 ||||| || ||| ||
 GTGGTGTA AG AGGG CTT
 GT G GG
 GAM2345 MGC15606 3' TTGTTTCTGAGCCTAATGAGGT 59528 G TTT
 A TACC CATTG CTCAGAAGCAA
 ||| |||| |||||
 ATGG GTAAT GAGTCTTTGTT
 A CC_
 GAM2345 MGC23280 3' TTGAAGGAATAATGGGTG 59056 G _
 TACC CATTGTTTCT CAG
 ||| ||||| |||
 GTGG GTAATAAGGA GTT
 _ A
 GAM2345 MGC4737 3' GGCAGGAGAGATGGTGCCGTA 49645 C TG AGAA AA
 TAC GCAT TTTCTC GC
 ||| ||| |||| |
 ATG CGTG AGAGAG CG
 C GT GA__ GT
 GAM2345 NDST4 5' TTGTTTTGAAAAGGACAATGTG 42919 CTCA_
 CGCATTGTTT GAAGCAA
 ||||| |||||
 GTGTAACAGG TTTTGTT
 AAAAG
 GAM2345 NMT1 3' TTGCTCTAGAGAGAAGCAAGTG 41153 A _ A
 GTG TACCGC TTGTTTCTC AGA GCAA
 ||||| ||||| ||| ||||
 GTGGTG AACGAAGAG TCT CGTT
 _ AGA _
 GAM2345 NY-REN-25 3' TTGTTTCAAATATGCAGTGTGG 61267 TTCTCA
 TA TACCGCATTGT GAAGCAA
 ||||| |||||
 ATGGTGTGACG CTTTGTT
 TATAAA
 GAM2345 p25 3' TTGCTTTCCTGAGAAGATGCGG 23841 GT _
 TG TACCGCATT TTCTCAG AAGCAA
 ||||| ||||| |||||
 GTGGCGTAG AAGAGTC TTCGTT
 _ CT
 GAM2345 PABPC5 3' TTGTTTTTGAGAAGTCAGT 55937 _
 ATTG TTTCTCAGAAGCAA
 ||| |||||

		TGAC GAAGAGTTTTTGTT	
		T	
GAM2345	PRO0365	5' TGCTGGAGAGATAATGTGGTG 26999	AGA
		TACCGCATTGTTTCTC AGCA	
		GTGGTGTAATAGAGAG TCGT	
		G__	
GAM2345	PTD015	5' TTTGAGGAGACAGTGCGGTG 93313	_
		TACCGCATTGTTTC TCAGA	
		GTGGCGTGACAGAG AGTTT	
		G	
GAM2345	RNAHP	3' TTGGGGAGCAATTTGGTA 24779	C
		TACCG ATTGTTTCTCAG	
		ATGGT TAACGAGGGGTT	
		T	
GAM2345	RYK	3' TCAGTTTGGTGGATGGTGTGGT 83511	TG TC AGCAA
	G	TACCGCAT TT TCAGA	
		GTGGTGTG AG GGTTT	
		GT GT GACT	
GAM2345	SCYD1	3' TTGCATGAGGCTAGTGTGGTG 92562	TT GAA
		TACCGCATTG TCTCA GCAA	
		GTGGTGTGAT GGAGT CGTT	
		C_ A__	
GAM2345	SLC38A5	5' TTGTTTCTGAGTCTGCCTGTGT 54314	T_ TT_
	G	CGCAT GT CTCAGAAGCAA	
		GTGTG CG GAGTCTTTGTT	
		TC TCT	
GAM2345	STAM2	3' TTGTTTTTCTTCCTGCAATGTG 20710	TTCTC_
	GTG	TACCGCATTGT AGAAGCAA	
		GTGGTGTAACG TTTTGT	
		TCCTTC	
GAM2345	TUSP	5' TTGTTGACTAGTGGTGTGGTG 40037	TG TC AGAA
		TACCGCAT TT TC GCAA	
		GTGGTGTG GA AG TGTT	
		GT TC GT__	
GAM2345	UHRF2	3' TTGCTGCATTAGTGTAAATGTGG 73833	TTT CAGA_
	TG	TACCGCATTG CT AGCAA	
		GTGGTGTAAT GA TCGTT	
		GT_ TTACG	
GAM2345	USP20	3' TTGTAGAAGCAGGTGGTG 22904	A _
		TACCGC TTGTTTCT CAG	

		GTGGTG GACGAAGA GTT		
		— T		
GAM2345 VI	3'	TTGCACACTGGGGTGATGGGTG 26490	G TG TT	AA_
		TACC CAT T CTCAG GCAA		
		GTGG GTA G GGGTC CGTT		
		— GT — ACA		
GAM2345 LOC115131	3'	CTCAGGAATGGTGTGGTG 59804	TG C	
		TACCGCAT TTTCT AG		
		GTGGTGTG AAGGA TC		
		GT C		
GAM2345 LOC120114	3'	TTGTTTTTGAGAGGTGACTGGT 76057	CA TG	
A		TACCG T TTTCTCAGAAGCAA		
		ATGGT A GGAGAGTTTTTGTT		
		C_ GT		
GAM2345 LOC120856	3'	TTGTTTCTGAAGAAATGTG 74477	GTT _	
		CGCATT TCT CAGAAGCAA		
		GTGTAA AGA GTCTTTGTT		
		— A		
GAM2345 LOC126964	3'	TTGTTTAAAGGGAAGAGTGTGG 75120	G CAG	
TG		TACCGCATT TTTCT AAGCAA		
		GTGGTGTGA AAGGG TTTGTT		
		G AAA		
GAM2345 LOC128954	5'	TTGCTTCTGAGGGCAGCTGTG 76309	_ T	
		CGCA TTGTT CTCAGAAGCAA		
		GTGT GACGG GAGTCTTCGTT		
		C _		
GAM2345 LOC129676	5'	CTTCTGAGAGGCAGGCGGTG 76233	A	
		TACCGC TTGTTTCTCAGAAG		
		GTGGCG GACGGAGAGTCTTC		
		—		
GAM2345 LOC144348	3'	TTGTTTCTGAGGAGGCATATGT 77303	_ _	
G		CGCAT TGTTTC TCAGAAGCAA		
		GTGTA ACGGAG AGTCTTTGTT		
		T G		
GAM2345 LOC144603	3'	TGTTTCTGGGGAGGAGGG 61012	GCA G	
		CC TT TTTCTCAGAAGCA		
		GG GA GAGGGGTCTTTGT		
		— G		
GAM2345 LOC146176	5'	TTGCTAGCAAAACACTGTGGTG 78194	T CTCAGA	
		TACCGCA TGTTT AGCAA		

		GTGGTGT ACAAA	TCGTT		
		C ACGA__			
GAM2345	LOC149684 3'	TTGTGATGGGAGAGGTGGTGCG	85769	TG	AGAA_
	G	CCGCAT TTTCTC	GCAA		
		GGCGTG GGAGAG	TGTT		
		GT GGTAG			
GAM2345	LOC149706 5'	CTGGGGAGTAGGTGGTG	85803	A	
		TACCGC TTGTTTCTCAG			
		GTGGTG GATGAGGGGTC			
		—			
GAM2345	LOC149722 5'	CTGGGGAACAAAGTGGTG	85752	A	
		TACCGC TTGTTTCTCAG			
		GTGGTG AACAAGGGGTC			
		A			
GAM2345	LOC150372 3'	CTGGGAGGCAGTGGGTG	80610	G	
		TACC CATTGTTTCTCAG			
		GTGG GTGACGGAGGGTC			
		—			
GAM2345	LOC152925 3'	TTGCTTTAAAAGAAGCAATGCA	81622	C	CA_
	GTA	TAC GCATTGTTTCT	GAAGCAA		
		ATG CGTAACGAAGA	TTTCGTT		
		A AAA			
GAM2345	LOC155179 3'	TTGCTTCTGAGAACAGCAGGGT	82234	GCA	T
	G	TACC TTGTT CTCAGAAGCAA			
		GTGG GACAA GAGTCTTCGTT			
		GAC			
		—			
GAM2345	LOC163861 5'	TTGTCATGGAAACAGTGTGG	88418	T	GAA
		CCGCATTGTTTC CA	GCAA		
		GGTGTGACAAAG GT	TGTT		
		_ AC_			
GAM2345	LOC168283 5'	TTGCTTGCAAGGAAGCAGTGCG	83576	CAG_	
		CGCATTGTTTCT	AAGCAA		
		GCGTGACGAAGG	TTTCGTT		
		AACG			
GAM2345	LOC196418 3'	TTGTTTCTGAGGAGGCATATGT	89054	—	—
	G	CGCAT TGTTTC TCAGAAGCAA			
		GTGTA ACGGAG AGTCTTTGTT			
		T G			
GAM2345	LOC197414 3'	TGTGTGGAGGATGTGGTG	89460	GTTT	AGAA
		TACCGCATT CTC	GCA		

	GTGGTGTAG GAG TGT	
	____ GTG_	
GAM2345 LOC199708 3'	TGCTTCTGAGAAATTGT 79306 TT	
	GCA GTTTCTCAGAAGCA	
	TGT TAAAGAGTCTTCGT	

GAM2345 LOC203414 3'	TTGTCAACTGGGGGTGATGTGG 90915	TG TT T AA_
	CCGCAT T C CAG GCAA	
	GGTGTA G G GTC TGTT	
	GT GG_ AAC	
GAM2345 LOC221271 3'	TTGTTTTTTGAGAAGGGGGGTA 93537	GCA G
	TACC TT TTTCTCAGAAGCAA	
	ATGG GG GAAGAGTTTTTGT	
	____ G	
GAM2345 LOC222104 3'	TTGCTAGTTGAATTATGTGGTG 94287	TGT TCAGA
	TACCGCAT TTC AGCAA	
	GTGGTGTA AAG TCGTT	
	TT_ TTGA_	
GAM2345 LOC253115 3'	TTGTTCCGGGATGGTGTGGTG 96126	TG TT TCA G
	TACCGCAT T C GAA CAA	
	GTGGTGTA A G CTT GTT	
	GT GG C__ _	
GAM2345 LOC253348 5'	TTGAGGGAGCAGTCGGTG 98109	C _
	TACCG ATTGTTTC TCAG	
	GTGGC TGACGAGG AGTT	
	_____ G	
GAM2345 LOC257556 3'	TTGTTCCGGGATGGTGTGGTG 99554	TG TT TCA G
	TACCGCAT T C GAA CAA	
	GTGGTGTA A G CTT GTT	
	GT GG C__ _	
GAM2345 LOC257617 3'	TTGTTCCGGGATGGTGTGGTG 99648	TG TT TCA G
	TACCGCAT T C GAA CAA	
	GTGGTGTA A G CTT GTT	
	GT GG C__ _	
GAM2345 LOC93349 3'	CTGAGGAACAGTTGGTA 57267	C
	TACCG ATTGTTTCTCAG	
	ATGGT TGACAAGGAGTC	

GAM2346 ACVRL1 3'	TCTGGGTAGAGGTAGTGTGA 5239	C ____ A
	TCACAC ACT CCCA GA	

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AGTGTG TGG GGGT CT
A AGAT _
GAM2346 EYA4 5' CTACTTGGGAGTGGCAGGA 15884 ACA A
TC CCACTCCCAAG AG
|| ||||| ||
AG GGTGAGGGTTC TC
GAC A
GAM2346 GOCAP1 3' ATTGTTCTTGGGAGCAGTGT 43006 CA G
ACAC CTCCCAAGAA AAT
|||| ||||| |||
TGTG GAGGGTTCTT TTA
AC G
GAM2346 HPSE 3' TATTCTTCTTTATGGCTG 22862 _ CTCCC
CA CCA AAGAAGAATA
|| ||| |||||
GT GGT TTCTTCTTAT
C AT__
GAM2346 MAPRE2 3' TCTTTTATCCTGGTGTGA 27335 CTCCC
TCACACCA AAGAAGA
||||| |||||
AGTGTGGT TTTTCT
CCTA_
GAM2346 PEX3 3' TTATTCTTATGGAAATGGTG 14638 CTC AG
CACCA CCA AAGAATAA
|||| ||| |||||
GTGGT GGT TTCTTATT
AAA A_
GAM2346 STAC 3' ATTCTTCTTTAGGGCAGT 13423 _ _
ACT CCC AAGAAGAAT
||| ||| |||||
TGA GGG TTCTTCTTA
C AT
GAM2346 KIAA1906 3' TTATTCTTCTTGACTTTTGG 73577 CTCC_
CCA CAAGAAGAATAA
||| |||||
GGT GTTCTTCTTATT
TTTCA
GAM2346 MMD 3' TTATGGCACTTGGGAGTGGGGT 60513 A AAGA
GA TCAC CCACTCCCAAG ATAA
||||| |||||
AGTG GGTGAGGGTTC TATT
G ACGG
GAM2346 SLC11A2 3' TTGTTCTTCTTAAATGTGACAT 7053 CAC TCCC
GA TCA CAC AAGAAGAATAA
||| ||| |||||
AGT GTG TTCTTCTTGTT
ACA TAAA
GAM2346 SR-BP1 3' ATTCTTCCTTTGGGGGTATG 20787 CC _
CA ACTCCCAA GAAGAAT
|| ||||| |||||

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		GT TGGGGGTT CTTCTTA	
		A_ TC	
GAM2346	TU12B1-TY 3'	ATTCTGGAGTGCAGTGGTGTGA 33829	CC AGA_
		TCACACCACT CA AGAAT	
		AGTGTGGTGA GT TCTTA	
		C_ GAGG	
GAM2346	LOC143146 3'	TTTTGTTGGAGGTGGTGT 60768	TC G
		ACACCAC CCAA AAGA	
		TGTGGTG GGTT TTTT	
		GA G	
GAM2346	LOC170261 3'	TTATTCTTTGTGAAAGTGGT 83471	CC A
		ACCACT CA GAAGAATAA	
		TGGTGA GT TTTCTTATT	
		AA G	
GAM2346	LOC257051 3'	TTATTCTTTGTGAAAGTGGT 98053	CC A
		ACCACT CA GAAGAATAA	
		TGGTGA GT TTTCTTATT	
		AA G	
GAM2347	A1BG 3'	AACTCCTGAGCTCAGGTGATCC 56274	G
	A	TGGATCACCTGAG TCAGGAGTT	
		ACCTAGTGGACTC AGTCCTCAA	
		G	
GAM2347	A1BG 3'	GAACTCTTGGGCTCAAGTGATC 56290	C G
	C	GGATCAC TGAG TCAGGAGTTC	
		CCTAGTG ACTC GGTTCTCAAG	
		A G	
GAM2347	ADAMTS4 3'	GAACTCCTGACCTCAGGTAATC 18758	C
		GAT ACCTGAGGTCAGGAGTTC	
		CTA TGGACTCCAGTCCTCAAG	
		A	
GAM2347	ADAMTS4 3'	GAACTCCTGACCTTAGGTGATC 18759	
	CA	TGGATCACCTGAGGTCAGGAGTTC	
		ACCTAGTGGATTCCAGTCCTCAAG	
GAM2347	AGL 5'	GAACTCCTGGACTCAAGCAACC 7213	ATCACC GT
	C	GG TGAG CAGGAGTTC	
		CC ACTC GTCCTCAAG	
		CAACGA AG	
GAM2347	ALDH1B1 3'	GAACTCCTGACCTCAGGTGATC 7324	
	CA	TGGATCACCTGAGGTCAGGAGTTC	

ACCTAGTGGACTCCAGTCCTCAAG

GAM2347	APAF1	3'	GA	ACTCTTGGCCTCAAGTAATC	25972	C	C
	C			GGAT AC TGAGGTCAGGAGTTC			
				CCTA TG ACTCCGGTTCTCAAG			
				A A			
GAM2347	APM1	3'	AA	CTCCTGACTTTGTGATCCA	17749	CT	
				TGGATCAC GAGGTCAGGAGTT			
				ACCTAGTG TTTCAGTCCTCAA			
				—			
GAM2347	APM1	3'	GA	ACTCCTGGCCTAGGTGATCC	17781	G	
	A			TGGATCACCT AGGTCAGGAGTTC			
				ACCTAGTGGA TCCGGTCCTCAAG			
				—			
GAM2347	AQP6	3'	TC	CTGACCCCAGATGCCCA	55016	AT	C A
				TGG CA CTG GGTCAGGA			
				ACC GT GAC CCAGTCCT			
				C_ A C			
GAM2347	AQP6	3'	TC	CTGACCCCAGATGCCCA	55017	AT	C A
				TGG CA CTG GGTCAGGA			
				ACC GT GAC CCAGTCCT			
				C_ A C			
GAM2347	ARCN1	3'	GA	ACTCCTGAGCTCAGGCAATC	9752	CA	G
	C			GGAT CCTGAG TCAGGAGTTC			
				CCTA GGA CTC AGTCCTCAAG			
				AC G			
GAM2347	ARSF	5'	GA	ACTCCCGACCTCAAGTGATC	65208	C	A
	C			GGATCAC TGAGGTC GGAGTTC			
				CCTAGTG ACTCCAG CCTCAAG			
				A C			
GAM2347	ATP1B2	3'	GA	ACTCCCGACCTCAGGTGATC	9834		A
	CA			TGGATCACCTGAGGTC GGAGTTC			
				ACCTAGTGGACTCCAG CCTCAAG			
				C			
GAM2347	ATP6V1A1	3'	GA	ACTCCAGACCTCAGGTGATC	9868		A
	C			GGATCACCTGAGGTC GGAGTTC			
				CCTAGTGGACTCCAG CCTCAAG			
				A			
GAM2347	ATP7A	3'	AA	CTCCTAACCTCAGGTGATCC	5307		C
	A			TGGATCACCTGAGGT AGGAGTT			

			ACCTAGTGGACTCCA TCCTCAA		
			A		
GAM2347	AXL	3'	AACTCCTGACCTCAAGTGATCT 41868	C	
			GGATCAC TGAGGTCAGGAGTT		
			TCTAGTG ACTCCAGTCCTCAA		
			A		
GAM2347	B4GALT5	3'	GAACTCCTGGACTCAAGCAATC 17687	CACC	GT
	C		GGAT TGAG CAGGAGTTC		
			CCTA ACTC GTCCTCAAG		
			ACGA AG		
GAM2347	C7	3'	AACTCCTGACCTCAGGTAATCC 6973	C	
			GGAT ACCTGAGGTCAGGAGTT		
			CCTA TGGACTCCAGTCCTCAA		
			A		
GAM2347	CASP10	3'	AACTCCTGGGCTCAAGCGATCC 53233	ACC	G
			GGATC TGAG TCAGGAGTT		
			CCTAG ACTC GGTCTCAA		
			CGA G		
GAM2347	CASP10	3'	AACTCCTGGGCTCAAGCGATCC 53234	ACC	G
			GGATC TGAG TCAGGAGTT		
			CCTAG ACTC GGTCTCAA		
			CGA G		
GAM2347	CBFA2T2	3'	AACCCCGGACCTCAGGTGATCC 18696	A	A
			GGATCACCTGAGGTC GG GTT		
			CCTAGTGGACTCCAG CC CAA		
			G C		
GAM2347	CBFB	3'	GAACTCCTGGCATCAAGCGATC 43439	ACC	G
	C		GGATC TGA GTCAGGAGTTC		
			CCTAG ACT CGGTCCTCAAG		
			CGA A		
GAM2347	CBFB	3'	GAACTCCTGGCATCAAGCGATC 43440	ACC	G
	C		GGATC TGA GTCAGGAGTTC		
			CCTAG ACT CGGTCCTCAAG		
			CGA A		
GAM2347	CCNF	3'	GAACTCATGACCTCAAGTGATC 10074	C	G
	C		GGATCAC TGAGGTCA GAGTTC		
			CCTAGTG ACTCCAGT CTCAAG		
			A A		
GAM2347	CDH1	3'	AACTCCTGGCCTCAAGCAATCC 16395	CACC	
			GGAT TGAGGTCAGGAGTT		

			CCTA ACTCCGGTCCTCAA		
			ACGA		
GAM2347	CDH1	3'	AACTCCTGGGCTCAAGTGATCC 16396	C	G
			GGATCAC TGAG TCAGGAGTT		
			CCTAGTG ACTC GGTCCTCAA		
			A G		
GAM2347	CHRN4	3'	GAACTCCTGACCTCAGATGACC 7449	A	C
	CA		TGG TCA CTGAGGTCAGGAGTTC		
			ACC AGT GACTCCAGTCCTCAAG		
			C A		
GAM2347	CLECSF12	3'	GAACTCCTGACCTCAAGTGATC 77211	C	
	T		GGATCAC TGAGGTCAGGAGTTC		
			TCTAGTG ACTCCAGTCCTCAAG		
			A		
GAM2347	CNP	3'	GAACTCCTGGGCTCAAGCAATC 53621	CACC	G
	C		GGAT TGAG TCAGGAGTTC		
			CCTA ACTC GGTCCTCAAG		
			ACGA G		
GAM2347	COX15	3'	GAACTCCTGACCTCAGGTAATC 16490	C	
	C		GGAT ACCTGAGGTCAGGAGTTC		
			CCTA TGGACTCCAGTCCTCAAG		
			A		
GAM2347	CRTAP	3'	GAACTCTTGACTTCAGATGATC 22078	C	
	CA		TGGATCA CTGAGGTCAGGAGTTC		
			ACCTAGT GACTTCAGTTCTCAAG		
			A		
GAM2347	CXCL16	3'	GAACTCCTGAGTCAAGTGATCC 42167	C	GG
			GGATCAC TGA TCAGGAGTTC		
			CCTAGTG ACT AGTCCTCAAG		
			A G_		
GAM2347	CYP1A2	3'	AACTCCTGACCTCAAGTGATCT 7492	C	
			GGATCAC TGAGGTCAGGAGTT		
			TCTAGTG ACTCCAGTCCTCAA		
			A		
GAM2347	CYP1A2	3'	GAACTCCTGACCCCAAGTTATC 7514	C	C A
	CA		TGGAT AC TG GGTCAGGAGTTC		
			ACCTA TG AC CCAGTCCTCAAG		
			T A C		
GAM2347	CYP2B6	3'	CCTGGCCTCAGGTGATCCA 7558		
			TGGATCACCTGAGGTCAGG		

ACCTAGTGGACTCCGGTCC

GAM2347 CYP2B6 3' GAACTCCTGAACTCAAGTGATT 7561 C G
CA TGGATCAC TGAG TCAGGAGTTC

||||| ||| |||||
ACTTAGTG ACTC AGTCCTCAAG
A A

GAM2347 CYP4F3 3' GAACTCCTAACCTCAGGTGATC 8007 C
CA TGGATCACCTGAGGT AGGAGTTC

||||||| |||||
ACCTAGTGGACTCCA TCCTCAAG
A

GAM2347 DFFB 3' AACTCCTGACCTCAGGTGATCC 88746
GGATCACCTGAGGTCAGGAGTT

|||||||
CCTAGTGGACTCCAGTCCTCAA

GAM2347 DFFB 3' GAACTCCTGACCTCAGGTGATC 88770
T GGATCACCTGAGGTCAGGAGTTC

|||||||
TCTAGTGGACTCCAGTCCTCAAG

GAM2347 DIAPH2 3' GAACTCCTAGCCTCAAGCAATC 24592 CACC TC
CA TGGAT TGAGG AGGAGTTC

|||| ||| |||||
ACCTA ACTCC TCCTCAAG
ACGA GA

GAM2347 DISC1 3' AACTCCTGACCTCAGGCGATCC 38494 A
A TGGATC CCTGAGGTCAGGAGTT

|||| |||||
ACCTAG GGA CTCCAGTCCTCAA
C

GAM2347 DSCR3 3' GAACTCCTAGACTCAAGTGATC 21312 C G _
C GGATCAC TGAG TC AGGAGTTC

||||| ||| || |||||
CCTAGTG ACTC AG TCCTCAAG
A _ A

GAM2347 DSCR3 3' GAACTCCTGACCTCGTGACCCA 21313 A CT
TGG TCAC GAGGTCAGGAGTTC

||| ||| |||||
ACC AGTG CTCCAGTCCTCAAG
C _

GAM2347 EPB72 3' GAACTCCTAACCTCAGGTGATC 15873 C
CA TGGATCACCTGAGGT AGGAGTTC

||||||| |||||
ACCTAGTGGACTCCA TCCTCAAG
A

GAM2347 F2RL2 3' GAACTCCTGACCTCAAGTGATC 15896 C
T GGATCAC TGAGGTCAGGAGTTC

||||| |||||

			TCTAGTG ACTCCAGTCCTCAAG		
			A		
GAM2347	F3	3'	GAATTCCTGACCTCAGTTGATC 67677	C	
	CA		TGGATCA CTGAGGTCAGGAGTTC		
			ACCTAGT GACTCCAGTCCTTAAG		
			T		
GAM2347	FABP2	3'	GAACCCCTGGCCTCAAGCAATC 5535	CACC	A
	C		GGAT TGAGGTCAGG GTTC		
			CCTA ACTCCGGTCC CAAG		
			ACGA C		
GAM2347	FCAR	3'	GAACTCCCGACCTCAGGTGATC 56571		A
	CA		TGGATCACCTGAGGTC GGAGTTC		
			ACCTAGTGGACTCCAG CCTCAAG		
			C		
GAM2347	FCAR	3'	GAACTCCTGACCTCAGGTGATC 56572		
	CA		TGGATCACCTGAGGTCAGGAGTTC		
			ACCTAGTGGACTCCAGTCCTCAAG		
GAM2347	G6PC	3'	GAACTCCTGACCTCAAGTGATC 5660	C	
	CA		TGGATCAC TGAGGTCAGGAGTTC		
			ACCTAGTG ACTCCAGTCCTCAAG		
			A		
GAM2347	GNE	3'	GAACTCCTGACCTCAGGTGATC 19669		
	C		GGATCACCTGAGGTCAGGAGTTC		
			CCTAGTGGACTCCAGTCCTCAAG		
GAM2347	GPR81	3'	CCTGACCTCAGGTGATCC 51745		
			GGATCACCTGAGGTCAGG		
			CCTAGTGGACTCCAGTCC		
GAM2347	GRAF	3'	GAACTCCTGACCTCAAGTGATC 31236	C	
	T		GGATCAC TGAGGTCAGGAGTTC		
			TCTAGTG ACTCCAGTCCTCAAG		
			A		
GAM2347	HCS	3'	AACTCCTGAGCTCAAGCAATCC 38956	CACC	G
			GGAT TGAG TCAGGAGTT		
			CCTA ACTC AGTCCTCAA		
			ACGA G		
GAM2347	HLCS	5'	GAACTCCTGACCTCGTGATCCA 6412	CT	
			TGGATCAC GAGGTCAGGAGTTC		

ACCTAGTG CTCCAGTCCTCAAG

GAM2347 IFNAR2 3' GAACTCCTGACCTCAAGTGATC 7900 C
T GGATCAC TGAGGTCAGGAGTTC
||||| |||||||||
TCTAGTG ACTCCAGTCCTCAAG
A

GAM2347 IL11 3' GAACTCCTGACCTCAGGTGATC 7183
C GGATCACCTGAGGTCAGGAGTTC
||||| |||||||||
CCTAGTGGACTCCAGTCCTCAAG

GAM2347 JAK3 3' GAACTCCTAACCTCAAGTGATC 5830 C C
C GGATCAC TGAGGT AGGAGTTC
||||| ||||| |||||
CCTAGTG ACTCCA TCCTCAAG
A A

GAM2347 JRK 3' GAACTCTTGGCCTCAAGCGATC 87826 ACC
C GGATC TGAGGTCAGGAGTTC
|||| |||||||||
CCTAG ACTCCGGTTCTCAAG
CGA

GAM2347 LNK 3' GAATGTCTGACCTCAGGTGATC 19644 GA
CA TGGATCACCTGAGGTCAG GTTC
||||| ||||| |||
ACCTAGTGGACTCCAGTC TAAG
TG

GAM2347 LZTS1 3' AACTTGTGGCCTCAAGCAATCC 41019 CACC G
A TGGAT TGAGGTCA GAGTT
|||| ||||| |||||
ACCTA ACTCCGGT TTCAA
ACGA G

GAM2347 MAK 3' AACTCCTGACCTCAGGTGATCC 20933
A TGGATCACCTGAGGTCAGGAGTT
||||| |||||||||
ACCTAGTGGACTCCAGTCCTCAA

GAM2347 MEFV 3' AACTCCTGACCTCAGGTGATGC 5917 G
A TG ATCACCTGAGGTCAGGAGTT
|| |||||||||
AC TAGTGGACTCCAGTCCTCAA
G

GAM2347 MEFV 3' GAACTCCTGACCTCAGGTGATC 5937
CA TGGATCACCTGAGGTCAGGAGTTC
||||| |||||||||
ACCTAGTGGACTCCAGTCCTCAAG

GAM2347 MHC2TA 3' GAACTCTTGACCTCGGGTGATC 5983
CA TGGATCACCTGAGGTCAGGAGTTC
||||| |||||||||

ACCTAGTGGGCTCCAGTTCTCAAG

GAM2347 MICB 3' AACTCCTGACCTCAGGTGATCT 21016
GGATCACCTGAGGTCAGGAGTT
|||||
TCTAGTGGACTCCAGTCCTCAA

GAM2347 MLANA 3' AACTCCTGACCTCAGGTGATCT 19752
GGATCACCTGAGGTCAGGAGTT
|||||
TCTAGTGGACTCCAGTCCTCAA

GAM2347 MPL 3' GAACTCCTAACCTCGGGTGATC 19354 C
CA TGGATCACCTGAGGT AGGAGTTC
|||||
ACCTAGTGGGCTCCA TCCTCAAG
A

GAM2347 MRPL49 3' AACTCCTGACTCGAAGTGATCC 70154 CTGA
GGATCAC GGTCAGGAGTT
|||||
CCTAGTG TCAGTCCTCAA
AAGC

GAM2347 MYCL2 3' CCTGACCTAGGTGATCCA 19373 G
TGGATCACCT AGGTCAGG
|||||
ACCTAGTGGA TCCAGTCC

GAM2347 NCOA6 5' AACTCCTGACCTCAAGTGATCC 26816 C
A TGGATCAC TGAGGTCAGGAGTT
|||||
ACCTAGTG ACTCCAGTCCTCAA
A

GAM2347 NCOA6 5' GAACTCCTGAGCTCAAGCAGTC 26835 CACC G
CA TGGAT TGAG TCAGGAGTTC
|||||
ACCTG ACTC AGTCCTCAAG
ACGA G

GAM2347 NDRG3 3' AACTCCTGACCTCAGGTGATCC 42759
A TGGATCACCTGAGGTCAGGAGTT
|||||
ACCTAGTGGACTCCAGTCCTCAA

GAM2347 NQO1 3' AACTCCTGACCTCAGGTGATCC 8037
GGATCACCTGAGGTCAGGAGTT
|||||
CCTAGTGGACTCCAGTCCTCAA

GAM2347 NT5C2 5' CCTGACGTCAAGTGATCCA 25262 C G
TGGATCAC TGA GTCAGG
|||||

		ACCTAGTG ACT CAGTCC	
		A G	
GAM2347 PDE6B	3'	GAACCTCCTGACCTCAGGTGATC 6076	
		GATCACCTGAGGTCAGGAGTTC	
		CTAGTGGACTCCAGTCCTCAAG	
GAM2347 PER2	3'	GAACCTCCTGACCTCAAGCGATC 43351	ACC
CA		TGGATC TGAGGTCAGGAGTTC	
		ACCTAG ACTCCAGTCCTCAAG	
		CGA	
GAM2347 PIK3CD	3'	GAACCTCCTGACCTCAGGTGATC 18491	
CA		TGGATCACCTGAGGTCAGGAGTTC	
		ACCTAGTGGACTCCAGTCCTCAAG	
GAM2347 PMCHL1	3'	GAACCTCCTGACCTCGTGATCCA 49916	CT
		TGGATCAC GAGGTCAGGAGTTC	
		ACCTAGTG CTCCAGTCCTCAAG	
GAM2347 PPEF2	3'	GAACCTCCCAACCTCAGGTGATC 21775	CA
CA		TGGATCACCTGAGGT GGAGTTC	
		ACCTAGTGGACTCCA CCTCAAG	
		AC	
GAM2347 PPID	3'	GAACCTCCTGACCTTGTGATCCA 88825	CT
		TGGATCAC GAGGTCAGGAGTTC	
		ACCTAGTG TTCCAGTCCTCAAG	
GAM2347 PRKR	3'	AACTCCTGACCTCAAGTAATCC 12334	C C
A		TGGAT AC TGAGGTCAGGAGTT	
		ACCTA TG ACTCCAGTCCTCAA	
		A A	
GAM2347 PRKWNK3	3'	AACTCCTAACCTTGTGATCC 62221	CT C
		GGATCAC GAGGT AGGAGTT	
		CCTAGTG TTCCA TCCTCAA	
		A	
GAM2347 PTGES	3'	GAACCTCCTGGCCTCAAGTGATC 18060	C
CA		TGGATCAC TGAGGTCAGGAGTTC	
		ACCTAGTG ACTCCGGTCCTCAAG	
		A	
GAM2347 RBBP9	3'	GAACCTCCTGGCCTCAAGTGATC 70690	C
CA		TGGATCAC TGAGGTCAGGAGTTC	

			ACCTAGTG ACTCCGGTCCTCAAG	
			A	
GAM2347	RGS9	5'	AACTCCTGGGCTCAAGCGATCC 15166	ACC G
			GGATC TGAG TCAGGAGTT	
			CCTAG ACTC GGTCTCAA	
			CGA G	
GAM2347	RHD	3'	AACTCCTGACCTCAAGTGATCT 32797	C
			GGATCAC TGAGGTCAGGAGTT	
			TCTAGTG ACTCCAGTCCTCAA	
			A	
GAM2347	RHD	3'	AACTCCTGACCTCAAGTGATCT 32798	C
			GGATCAC TGAGGTCAGGAGTT	
			TCTAGTG ACTCCAGTCCTCAA	
			A	
GAM2347	RP2	3'	GAATCCTGACCTCAGGTGATC 23602	
	C		GGATCACCTGAGGTCAGGAGTTC	
			CCTAGTGGACTCCAGTCCTCAAG	
GAM2347	RPH3AL	3'	GAATCCTGGTCTCAAGTGATC 23733	C GT
	C		GGATCAC TGAG CAGGAGTTC	
			CCTAGTG ACTC GTCCTCAAG	
			A TG	
GAM2347	SAS	3'	GAATCCTGACCTCAGGTGATC 21100	
	CA		TGGATCACCTGAGGTCAGGAGTTC	
			ACCTAGTGGACTCCAGTCCTCAAG	
GAM2347	SCML2	3'	AACTCCTGACCTCAGGTGATCC 21417	
			GGATCACCTGAGGTCAGGAGTT	
			CCTAGTGGACTCCAGTCCTCAA	
GAM2347	SEDL	3'	AACTCCTGACCTCAGTTGATCC 28064	C
	A		TGGATCA CTGAGGTCAGGAGTT	
			ACCTAGT GACTCCAGTCCTCAA	
			T	
GAM2347	SEDL	3'	GAATCCTGACCTCGTGATCCA 28098	CT
			TGGATCAC GAGGTCAGGAGTTC	
			ACCTAGTG CTCCAGTCCTCAAG	
			—	
GAM2347	SEPN1	3'	GAATTCTGACCTCAGGTGATC 66971	
	CA		TGGATCACCTGAGGTCAGGAGTTC	

ACCTAGTGGACTCCAGTCTTCAAG

GAM2347 SERPINB9 3' GAACTCCTGGCCTCAAGCAATC 16020 CACC
C GGAT TGAGGTCAGGAGTTC

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CCTA ACTCCGGTCCTCAAG
ACGA

GAM2347 SH3BP2 3' GAACTCCTGACCTCAACTGATC 13071 CC
C GGATCA TGAGGTCAGGAGTTC

||||| |||||||||
CCTAGT ACTCCAGTCCTCAAG
CA

GAM2347 SH3BP2 3' GAACTCCTGACCTCAGGTGATC 13072
T GGATCACCTGAGGTCAGGAGTTC

||||| |||||||||
TCTAGTGGACTCCAGTCCTCAAG

GAM2347 SHOX 3' AACTCCTGGGCTCAAGCAATCC 6556 CACC G
GGAT TGAG TCAGGAGTT

||||| ||| |||||||
CCTA ACTC GGTCTCAA
ACGA G

GAM2347 SHOX 3' GAACTCCTGACCTCAGGTGATC 6573
CA TGGATCACCTGAGGTCAGGAGTTC

||||| |||||||||
ACCTAGTGGACTCCAGTCCTCAAG

GAM2347 SHOX 3' GAACTCCTGACCTCAGGTGATC 6574
T GGATCACCTGAGGTCAGGAGTTC

||||| |||||||||
TCTAGTGGACTCCAGTCCTCAAG

GAM2347 SIL 3' AACTCCCGACCTCAGGTGATCC 13147 A
GGATCACCTGAGGTC GGAGTT

||||| |||||
CCTAGTGGACTCCAG CCTCAA
C

GAM2347 SIL 5' TCCTGACTTCAGGTGATCCA 13164
TGGATCACCTGAGGTCAGGA

||||| |||||||||
ACCTAGTGGACTTCAGTCCT

GAM2347 SLA2 3' GAACTCCTGACCTCAGGTGATC 50889
CA TGGATCACCTGAGGTCAGGAGTTC

||||| |||||||||
ACCTAGTGGACTCCAGTCCTCAAG

GAM2347 SLC14A2 5' GAACTTCTGACGTCAAGTGATC 24117 C G
CA TGGATCAC TGA GTCAGGAGTTC

||||| ||| |||||||||

			ACCTAGTG ACT CAGTCTTCAAG	
			A G	
GAM2347	SLC17A5	3'	GAACTCCTGGCTTCAAGCGATC 25831	ACC
	C		GGATC TGAGGTCAGGAGTTC	
			CCTAG ACTTCGGTCCTCAAG	
			CGA	
GAM2347	SLC3A2	5'	GAACTCTTGGCCTCAGGTGATC 11520	
	C		GGATCACCTGAGGTCAGGAGTTC	
			CCTAGTGGACTCCGGTTCTCAAG	
GAM2347	SMAC	5'	GAACTCCTGGGCTCAAGTGATC 57999	C G
	C		GGATCAC TGAG TCAGGAGTTC	
			CCTAGTG ACTC GGTCCTCAAG	
			A G	
GAM2347	SMAC	5'	GAATTCCTGACCTCAAGTGATC 58000	C
	CA		TGGATCAC TGAGGTCAGGAGTTC	
			ACCTAGTG ACTCCAGTCCTTAAG	
			A	
GAM2347	SNX15	3'	GAACTCCTGACCTCAAGTGATC 74119	C
	CA		TGGATCAC TGAGGTCAGGAGTTC	
			ACCTAGTG ACTCCAGTCCTCAAG	
			A	
GAM2347	SPN	3'	AACTCCTGACCTCAGGTGATCT 13361	
	A		TGGATCACCTGAGGTCAGGAGTT	
			ATCTAGTGGACTCCAGTCCTCAA	
GAM2347	SULT2B1	5'	AACTCCTGACCTCAGGTGATCC 17218	
	A		TGGATCACCTGAGGTCAGGAGTT	
			ACCTAGTGGACTCCAGTCCTCAA	
GAM2347	TAF11	3'	GAACTCCTGGGCTTAAGTGACC 20120	A C G
	C		GG TCAC TGAG TCAGGAGTTC	
			CC AGTG ATTC GGTCCTCAAG	
			C A G	
GAM2347	TAT	3'	AACTCCTGACCTCAGGCAATCT 6243	CA
			GGAT CCTGAGGTCAGGAGTT	
			TCTA GGACTCCAGTCCTCAA	
			AC	
GAM2347	TBXA2R	3'	GAACTCCTGACCTCAGGTGATT 8357	
	CA		TGGATCACCTGAGGTCAGGAGTTC	

ACTTAGTGGACTCCAGTCCTCAAG

GAM2347 TES 3' AACTCCTGACCTCAGATGATCC 72454 C
GGATCA CTGAGGTCAGGAGTT
||||| |||||||||
CCTAGT GACTCCAGTCCTCAA
A

GAM2347 TMPRSS3 3' AACCCCTGACCTCAAATGAT 44008 CC A
ATCA TGAGGTCAGG GTT
||| ||||||| ||
TAGT ACTCCAGTCC CAA
AA C

GAM2347 TNFRSF10B 3' CCTGACCTCAGGTGATCCA 15222
TGGATCACCTGAGGTCAGG
|||||||||||
ACCTAGTGGACTCCAGTCC

GAM2347 TNFRSF10B 3' GAACTCCTGACCTCAGGTGATC 15226
CA TGGATCACCTGAGGTCAGGAGTTC
|||||||||||
ACCTAGTGGACTCCAGTCCTCAAG

GAM2347 TNFSF9 3' GAACTCCTGGACTTAGACGATC 15097 AC GT
C GGATC CTGAG CAGGAGTTC
|||| ||| |||||
CCTAG GATTC GTCCTCAAG
CA AG

GAM2347 TP53 3' AACTCCTGGGCTCAGGCGATCC 6789 A G
A TGGATC CCTGAG TCAGGAGTT
|||| |||| |||||
ACCTAG GGA CTC GGT CCTCAA
C G

GAM2347 TPMT 3' GAGCTCCTGACCTCAGGTGATC 6312
TA TGGATCACCTGAGGTCAGGAGTTC
|||||||||||
ATCTAGTGGACTCCAGTCCTCGAG

GAM2347 TRAF5 3' AACTCCTGACCTCAAGTGATCT 17262 C
GGATCAC TGAGGTCAGGAGTT
||||| |||||||||
TCTAGTG ACTCCAGTCCTCAA
A

GAM2347 TRPM6 3' AACTCCTGACCTCAGATGATCC 35017 C
A TGGATCA CTGAGGTCAGGAGTT
||||| |||||||||
ACCTAGT GACTCCAGTCCTCAA
A

GAM2347 TRPV1 3' GAACTCCTGACCTCAGGTGATC 55672
C GGATCACCTGAGGTCAGGAGTTC
|||||||||||

CCTAGTGGACTCCAGTCCTCAAG

GAM2347 TUFT1 3' GAATTCCTGACCTCAGGTGATC 39674
CA TGGATCACCTGAGGTCAGGAGTTC
|||||
ACCTAGTGGACTCCAGTCCTTAAG

GAM2347 VENTX2 3' AACTCCTGACCCTGTGATCC 27849 CTGA
GGATCAC GGTCAGGAGTT
||||| |||||
CCTAGTG CCAGTCCTCAA
TC__

GAM2347 VHL 3' AACTCCTGACCTCAGGTGATCC 6812
GGATCACCTGAGGTCAGGAGTT
|||||
CCTAGTGGACTCCAGTCCTCAA

GAM2347 WHSC1 3' GAACTCCTGACCTCGTGATCCA 56695 CT
TGGATCAC GAGGTCAGGAGTTC
||||| |||||
ACCTAGTG CTCCAGTCCTCAAG

GAM2347 XRCC2 3' GAACTCCTGACCTCAAGTGATC 19500 C
CA TGGATCAC TGAGGTCAGGAGTTC
||||| |||||
ACCTAGTG ACTCCAGTCCTCAAG
A

GAM2347 ZNF133 5' GAACTGCTGACCTCAGGTGATC 14296 G
CA TGGATCACCTGAGGTCAG AGTTC
||||| |||||
ACCTAGTGGACTCCAGTC TCAAG
G

GAM2347 ZNF157 3' AACTCCTGACCTCAGGTGATCC 14318
A TGGATCACCTGAGGTCAGGAGTT
|||||
ACCTAGTGGACTCCAGTCCTCAA

GAM2347 ZNF264 3' AACTCCTGACCTTGTGATCC 14177 CT
GGATCAC GAGGTCAGGAGTT
||||| |||||
CCTAGTG TTCCAGTCCTCAA

GAM2347 AAK1 3' GAACTCCTGACCTCAGGTGATC 30522
C GGATCACCTGAGGTCAGGAGTTC
|||||
CCTAGTGGACTCCAGTCCTCAAG

GAM2347 AP3S2 3' GAACTCCTGGACCTCAAGTGAT 20651 C _
CTA TGGATCAC TGAGGTC AGGAGTTC
||||| ||||| |||||

			ATCTAGTG ACTCCAG TCCTCAAG	
			A G	
GAM2347	ARHF	3'	GAACTCCTGACCTCGTGATCCA 39268	CT
			TGGATCAC GAGGTCAGGAGTTC	
			ACCTAGTG CTCCAGTCCTCAAG	
			—	
GAM2347	ARHGAP5	5'	GAACTCCCAACCTCAGGTGATC 77601	CA
	C		GGATCACCTGAGGT GGAGTTC	
			CCTAGTGGACTCCA CCTCAAG	
			AC	
GAM2347	ASB16	3'	CTGACCTCAGGTGATCCA 55982	
			TGGATCACCTGAGGTCAG	
			ACCTAGTGGACTCCAGTC	
			—	
GAM2347	ASE-1	3'	GAACTCCTGACCTCGTGATCCA 24979	CT
			TGGATCAC GAGGTCAGGAGTTC	
			ACCTAGTG CTCCAGTCCTCAAG	
			—	
GAM2347	ATP1B4	3'	GAACTCCTGACCTCAAGTGATC 24843	C
	C		GGATCAC TGAGGTCAGGAGTTC	
			CCTAGTG ACTCCAGTCCTCAAG	
			A	
GAM2347	BA108L7.2	3'	GAACTCCTGACCTCAGGTGATC 49074	
	CA		TGGATCACCTGAGGTCAGGAGTTC	
			ACCTAGTGGACTCCAGTCCTCAAG	
			—	
GAM2347	C13orf1	3'	AACTCCTGACCTCATGATCCA 40343	CC
			TGGATCA TGAGGTCAGGAGTT	
			ACCTAGT ACTCCAGTCCTCAA	
			—	
GAM2347	C1QTNF6	3'	GAACTCCTGACTTCAGGTGACC 49992	A
	CA		TGG TCACCTGAGGTCAGGAGTTC	
			ACC AGTGGACTTCAGTCCTCAAG	
			C	
GAM2347	C20orf142	3'	AACTCCTGACCGCAGGTGATCC 75266	A
	A		TGGATCACCTG GGTCAGGAGTT	
			ACCTAGTGGAC CCAGTCCTCAA	
			G	
GAM2347	C21orf25	3'	GAACTCCTGACCTCAGGTGATC 64293	
	CA		TGGATCACCTGAGGTCAGGAGTTC	

ACCTAGTGGACTCCAGTCCTCAAG

GAM2347 C3F 3' GAACTCCTGACCGCAAGTGATC 20476 C A
CA TGGATCAC TG GGTCAGGAGTTC
||||| || |||||
ACCTAGTG AC CCAGTCCTCAAG
A G

GAM2347 C6orf33 3' GAACTCCTGAACTCAAGTGATC 56715 C G
C GGATCAC TGAG TCAGGAGTTC
||||| ||| |||||
CCTAGTG ACTC AGTCCTCAAG
A A

GAM2347 C9orf14 5' GAACTCCTGACCTGAAGTGATG 87957 G CTG
CA TG ATCAC AGGTCAGGAGTTC
|| ||| |||||
AC TAGTG TCCAGTCCTCAAG
G AAG

GAM2347 C9orf9 3' GAACTCCTGACCTCAACTGGTC 39019 CC
CA TGGATCA TGAGGTCAGGAGTTC
||||| |||||
ACCTGGT ACTCCAGTCCTCAAG
CA

GAM2347 CARD6 3' GAACTCCCGACCTCAGGTGATC 51841 A
C GGATCACCTGAGGTC GGAGTTC
||||||| |||||
CCTAGTGGACTCCAG CCTCAAG
C

GAM2347 CDC14B 3' GAACTCCTGACCTCAAGTGATC 14776 C
T GGATCAC TGAGGTCAGGAGTTC
||||| |||||
TCTAGTG ACTCCAGTCCTCAAG
A

GAM2347 CENPH 3' GAACTCCTGAGCTCAGGCAGTC 43565 CA G
CA TGGAT CCTGAG TCAGGAGTTC
|||| |||| |||||
ACCTG GGA CTC AGTCCTCAAG
AC G

GAM2347 CIP29 3' GAACTCCTGAGCTCAGGTGATC 51376 G
CA TGGATCACCTGAG TCAGGAGTTC
||||||| |||||
ACCTAGTGGACTC AGTCCTCAAG
G

GAM2347 COLEC12 3' GAACTCCTGGCCTCAAGCAACC 56102 ATCACC
C GG TGAGGTCAGGAGTTC
|| |||||
CC ACTCCGGTCCTCAAG
CAACGA

GAM2347 COLEC12 3' AACTTCTGGCCTCAAGTGATCC 48603 C
A TGGATCAC TGAGGTCAGGAGTT
||||| |||||

			ACCTAGTG ACTCCGGTCTTCAA	
			A	
GAM2347	CPSF2	3'	AACTCCCGACCTCAGGTGATCC 62252	A
			GGATCACCTGAGGTC GGAGTT	
			CCTAGTGGACTCCAG CCTCAA	
			C	
GAM2347	CPSF2	3'	AACTCCTGACCTCAAGCGATCC 62253	ACC
	A		TGGATC TGAGGTCAGGAGTT	
			ACCTAG ACTCCAGTCCTCAA	
			CGA	
GAM2347	DBR1	3'	AACTCCTGACCTCAGGCGATCC 33054	A
	A		TGGATC CCTGAGGTCAGGAGTT	
			ACCTAG GGAAGTCCAGTCCTCAA	
			C	
GAM2347	DCOIM	3'	AACTCCTGGCCTCAAGTGATCC 50503	C
			GGATCAC TGAGGTCAGGAGTT	
			CCTAGTG ACTCCGGTCCTCAA	
			A	
GAM2347	DKFZp434A2417	3'	AACTCCCAACCTCAGGTGATCT 66671	CA
			GGATCACCTGAGGT GGAGTT	
			TCTAGTGGACTCCA CCTCAA	
			AC	
GAM2347	DKFZP434B044	3'	GAATCCTTACCTCAGGTGATC 49717	C
	CA		TGGATCACCTGAGGT AGGAGTTC	
			ACCTAGTGGACTCCA TCCTCAAG	
			T	
GAM2347	DKFZP434D146	3'	AACTCCTGCCCTCAAGTGATCC 32128	C T
	A		TGGATCAC TGAGG CAGGAGTT	
			ACCTAGTG ACTCC GTCCTCAA	
			A C	
GAM2347	DKFZP434J037	3'	AACTCCCGACCTCAGGTGATCC 48933	A
	A		TGGATCACCTGAGGTC GGAGTT	
			ACCTAGTGGACTCCAG CCTCAA	
			C	
GAM2347	DKFZp547H025	3'	AACTCTTGACTTCAAGTGATCC 39762	C
	A		TGGATCAC TGAGGTCAGGAGTT	
			ACCTAGTG ACTTCAGTTCTCAA	
			A	
GAM2347	DKFZP564G092	5'	GAATCCTGACCTCAAGTAATC 32159	C C
	T		GGAT AC TGAGGTCAGGAGTTC	

		TCTA TG ACTCCAGTCCTCAAG		
		A A		
GAM2347	DKFZP564K0322 3'	AACTTCTGGCCTCAAGTGATCC 50183	C	
		GGATCAC TGAGGTCAGGAGTT		
		CCTAGTG ACTCCGGTCTTCAA		
		A		
GAM2347	DKFZP564O0423 3'	AACTCCTGGCCTCAGGCGATCC 93335	A	
	A	TGGATC CCTGAGGTCAGGAGTT		
		ACCTAG GGA CTCCGGTCCTCAA		
		C		
GAM2347	DKFZP564O0523 3'	GAACCTCCTGACCTTGTGATACA 50420	G	CT
		TG ATCAC GAGGTCAGGAGTTC		
		AC TAGTG TTCCAGTCCTCAAG		
		A _		
GAM2347	DKFZP566I1024 3'	GAACCTCCTGGCCTCAAGCGATC 70649	ACC	
	C	GGATC TGAGGTCAGGAGTTC		
		CCTAG ACTCCGGTCCTCAAG		
		CGA		
GAM2347	DKFZp761O0113 5'	GAACCTCCCGGACTCGGGTGATC 37892		GT A
	CA	TGGATCACCTGAG C GGAGTTC		
		ACCTAGTGGGCTC G CCTCAAG		
		AG C		
GAM2347	DKFZp762P2111 3'	GAACCTCCTGATGTTAGGTGACC 87634	A	G
	C	GG TCACCTGA GTCAGGAGTTC		
		CC AGTGGATT TAGTCCTCAAG		
		C G		
GAM2347	DSCR6 3'	GAACCTCCTGACCTCAGGTGATC 39067		
	CA	TGGATCACCTGAGGTCAGGAGTTC		
		ACCTAGTGGACTCCAGTCCTCAAG		
GAM2347	EVI5 3'	AACTTCTGACCTCAGGTGATCC 20187		
	A	TGGATCACCTGAGGTCAGGAGTT		
		ACCTAGTGGACTCCAGTCTTCAA		
GAM2347	EVI5 3'	GAACCTCCTAACCTCAAGTGATC 20207	C	C
	CA	TGGATCAC TGAGGT AGGAGTTC		
		ACCTAGTG ACTCCA TCCTCAAG		
		A A		
GAM2347	FBP17 3'	AACTCCTGACCTCAGGTGATCC 73137		
		GGATCACCTGAGGTCAGGAGTT		

CCTAGTGGACTCCAGTCCTCAA

GAM2347 FER1L4 3' GAACCCCTGACCTCAAGTGATC 48121 C A
CA TGGATCAC TGAGGTCAGG GTTC

||||| ||||||| |||
ACCTAGTG ACTCCAGTCC CAAG
A C

GAM2347 FLB6421 3' GAACTCCTGAGCTCAAGTGATC 39644 C G
C GGATCAC TGAG TCAGGAGTTC

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CCTAGTG ACTC AGTCCTCAAG
A G

GAM2347 FLJ10232 3' GAACTCCTGACCTCAGGTGATC 36379
CA TGGATCACCTGAGGTCAGGAGTTC

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ACCTAGTGGACTCCAGTCCTCAAG

GAM2347 FLJ10298 3' AACTCCTGACCTAGTGATCCA 36448 CTG
TGGATCAC AGGTCAGGAGTT

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ACCTAGTG TCCAGTCCTCAA
A__

GAM2347 FLJ10607 3' AACTCCTGAGCTCAAGTGATCC 77618 C G
GGATCAC TGAG TCAGGAGTT

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CCTAGTG ACTC AGTCCTCAA
A G

GAM2347 FLJ10713 3' AACTCCTGGACTCAAGTGATC 36992 C GT
GATCAC TGAG CAGGAGTT

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CTAGTG ACTC GTCCTCAA
A AG

GAM2347 FLJ10901 3' GAACTCCTGACCTCAAGTGATC 37360 C
CA TGGATCAC TGAGGTCAGGAGTTC

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ACCTAGTG ACTCCAGTCCTCAAG
A

GAM2347 FLJ11186 3' GAACTCCTGGCTACAAGTGATC 37725 C A
C GGATCAC TG GGTCAGGAGTTC

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CCTAGTG AC TCGGTCCTCAAG
A A

GAM2347 FLJ11193 3' AACTCCTGGGCACAAGCAATCC 37742 CAC GAG _
A TGGAT CT GTC AGGAGTT

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ACCTA GA CGG TCCTCAA
AC_ ACA G

GAM2347 FLJ12363 3' AACTCCTGACCTCAGGTGATCT 50623
GGATCACCTGAGGTCAGGAGTT

|||||||

TCTAGTGGACTCCAGTCCTCAA

GAM2347 FLJ12668 3' AACTCCTGACCTCAGGGGATCC 47151 A
A TGGATC CCTGAGGTCAGGAGTT

||||| |||||||||
ACCTAG GGACTCCAGTCCTCAA
G

GAM2347 FLJ12687 3' AACTCCTGACCTCAAGTGATCC 46737 C
A TGGATCAC TGAGGTCAGGAGTT

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ACCTAGTG ACTCCAGTCCTCAA
A

GAM2347 FLJ12747 3' GATTCCCGACCTCAGGTGATCC 50666 A
GGATCACCTGAGGTC GGAGTT

||||||| |||||
CCTAGTGGACTCCAG CCTTAG
C

GAM2347 FLJ12787 3' AACTCCTGACCTCAAGTGATCT 50685 C
A TGGATCAC TGAGGTCAGGAGTT

||||| |||||||||
ATCTAGTG ACTCCAGTCCTCAA
A

GAM2347 FLJ12903 3' GAACTCCTGACCTCAGGTGATC 43070
T GGATCACCTGAGGTCAGGAGTTC

||||||| |||||||||
TCTAGTGGACTCCAGTCCTCAAG

GAM2347 FLJ12975 3' GAACTCCTGACCTCATGATCC 70194 CC
GGATCA TGAGGTCAGGAGTTC

||||| |||||||||
CCTAGT ACTCCAGTCCTCAAG

GAM2347 FLJ13072 5' GAACTCCTGACCTCAGGTAATC 91390 C
C GGAT ACCTGAGGTCAGGAGTTC

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CCTA TGGACTCCAGTCCTCAAG
A

GAM2347 FLJ13102 3' GAACTCCTGACCTCAGGTGATT 46532
C GGATCACCTGAGGTCAGGAGTTC

||||||| |||||||||
CTTAGTGGACTCCAGTCCTCAAG

GAM2347 FLJ13197 3' GAACTCCTGACCTCAAGTGATC 45179 C
CA TGGATCAC TGAGGTCAGGAGTTC

||||| |||||||||
ACCTAGTG ACTCCAGTCCTCAAG
A

GAM2347 FLJ13305 5' GATTCCTGACCTCAAGTGACCC 91712 A C
A TGG TCAC TGAGGTCAGGAGTT

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		ACC AGTG ACTCCAGTCCTTAG	
		C A	
GAM2347	FLJ13590	5' GAACTCCTGACCTCAAGTGATC 46206	C
		C GGATCAC TGAGGTCAGGAGTTC	
		CCTAGTG ACTCCAGTCCTCAAG	
		A	
GAM2347	FLJ13952	3' CCTGACGTCAGGTGATCCA 46011	G
		TGGATCACCTGA GTCAGG	
		ACCTAGTGGACT CAGTCC	
		G	
GAM2347	FLJ14351	3' GAACTCCTGAGCTCAAGCAATC 45648	CACC G
		C GGAT TGAG TCAGGAGTTC	
		CCTA ACTC AGTCCTCAAG	
		ACGA G	
GAM2347	FLJ14950	3' GAACTCCTGACCGCAGGTAATC 52788	C A
		CA TGGAT ACCTG GGTCAGGAGTTC	
		ACCTA TGGAC CCAGTCCTCAAG	
		A G	
GAM2347	FLJ14957	3' GAACTCCTGACCTCAGGTGATC 52818	
		CA TGGATCACCTGAGGTCAGGAGTTC	
		ACCTAGTGGACTCCAGTCCTCAAG	
GAM2347	FLJ20034	3' AACTCCCGACCTCAGGTGATCC 34827	A
		GGATCACCTGAGGTC GGAGTT	
		CCTAGTGGACTCCAG CCTCAA	
		C	
GAM2347	FLJ20045	3' GAACTCCTGACCTCGTGATCCA 34884	CT
		TGGATCAC GAGGTCAGGAGTTC	
		ACCTAGTG CTCCAGTCCTCAAG	
GAM2347	FLJ20344	3' GAACTCCTGACCTCAAGTGATC 35481	C
		C GGATCAC TGAGGTCAGGAGTTC	
		CCTAGTG ACTCCAGTCCTCAAG	
		A	
GAM2347	FLJ20452	3' GAACTCCTGACCTCAGGTGATC 35648	
		CA TGGATCACCTGAGGTCAGGAGTTC	
		ACCTAGTGGACTCCAGTCCTCAAG	
GAM2347	FLJ20507	3' GAACTCCTAACCTCAGGTTATC 60844	C C
		CA TGGAT ACCTGAGGT AGGAGTTC	

			ACCTA TGGACTCCA TCCTCAAG		
			T A		
GAM2347	FLJ20671	3'	GAAGTGGCTGGCCTCAAGCGATC 35938	ACC	G
		CA	TGGATC TGAGGTCAG AGTTC		
			ACCTAG ACTCCGGTC TCAAG		
			CGA G		
GAM2347	FLJ20813	3'	AACTCCTGACCTCATGATCCA 36123	CC	
			TGGATCA TGAGGTCAGGAGTT		
			ACCTAGT ACTCCAGTCCTCAA		
			—		
GAM2347	FLJ21324	5'	AACTCCTGACCTCAAGTGATCT 92837	C	
			GGATCAC TGAGGTCAGGAGTT		
			TCTAGTG ACTCCAGTCCTCAA		
			A		
GAM2347	FLJ21459	3'	GAAGTGGCTGGCCTCAAGCGATC 44804		
		C	GGATCACCTGAGGTCAGGAGTTC		
			CCTAGTGGACTCCAGTCCTCAAG		
GAM2347	FLJ22002	3'	GAACCTCTGACCTCAGGTGATC 96360	GA	
		CA	TGGATCACCTGAGGTCAG GTTC		
			ACCTAGTGGACTCCAGTC CAAG		
			TC		
GAM2347	FLJ22329	3'	GAAGTGGCTGGCCTCAAGTGATC 45400	C	
		T	GGATCAC TGAGGTCAGGAGTTC		
			TCTAGTG ACTCCAGTCCTCAAG		
			A		
GAM2347	FLJ22529	3'	GAAGTGGCTGGCCTCAAGTGATC 45943	C	
		T	GGATCAC TGAGGTCAGGAGTTC		
			TCTAGTG ACTCCAGTCCTCAAG		
			A		
GAM2347	FLJ22625	3'	AACTGCTGACTTCAGGTGATCC 45584	G	
		A	TGGATCACCTGAGGTCAG AGTT		
			ACCTAGTGGACTTCAGTC TCAA		
			G		
GAM2347	FLJ22684	3'	AACTCCTGACCTCAGGTGATCC 47459		
			GGATCACCTGAGGTCAGGAGTT		
			CCTAGTGGACTCCAGTCCTCAA		
GAM2347	FLJ22794	3'	GAAGTGGCTGGCCTCGTGATCCA 93246	CT	
			TGGATCAC GAGGTCAGGAGTTC		

ACCTAGTG CTCCAGTCCTCAAG

GAM2347 FLJ23416 3' GAACTCCTGAGCTCAAGCAATC 50932 CACC G
C GGAT TGAG TCAGGAGTTC

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CCTA ACTC AGTCCTCAAG
ACGA G

GAM2347 FLJ23556 3' GAACTCCTGACCTCAGGTGA 46440
TCACCTGAGGTCAGGAGTTC
|||||||
AGTGGA CTCCAGTCCTCAAG

GAM2347 FLJ23563 3' CCTGACCTCAGGTGATCC 68214
GGATCACCTGAGGTCAGG
|||||||
CCTAGTGGACTCCAGTCC

GAM2347 FLJ30532 3' AGCTCCTGACCTCAGATGATCT 59215 C
A TGGATCA CTGAGGTCAGGAGTT
||||| |||||
ATCTAGT GACTCCAGTCCTCGA
A

GAM2347 FLJ31101 3' GAACTCCTGACCTCATGATCCA 36161 CC
TGGATCA TGAGGTCAGGAGTTC
||||| |||||
ACCTAGT ACTCCAGTCCTCAAG

GAM2347 FLJ31153 3' GAACTCCTGACCTCAGGTGATC 58747
T GGATCACCTGAGGTCAGGAGTTC
|||||||
TCTAGTGGACTCCAGTCCTCAAG

GAM2347 FLJ32865 3' AACCCCTGACCTCAGGCAATCT 58792 CA A
GGAT CCTGAGGTCAGG GTT
||| ||||| |||
TCTA GGA CTCCAGTCC CAA
AC C

GAM2347 FLJ32894 3' GAACTCCTGACCTCGGGATCCA 58997 A T
TGGATC CC GAGGTCAGGAGTTC
|||| || |||||
ACCTAG GG CTCCAGTCCTCAAG

GAM2347 GAL3ST-4 3' GAACTCCTCACCTCAGGTGATC 45279 C
CA TGGATCACCTGAGGT AGGAGTTC
||||||| |||||
ACCTAGTGGACTCCA TCCTCAAG
C

GAM2347 GGA2 3' GAACTCCTGACCTCAGGTGATC 57667
C GGATCACCTGAGGTCAGGAGTTC
|||||||

CCTAGTGGACTCCAGTCCTCAAG

GAM2347	GGA2	3'	GA	ACTCCTGACCTCAGGTGATC	57668	
	C			GGATCACCTGAGGTCAGGAGTTC		
				CCTAGTGGACTCCAGTCCTCAAG		
GAM2347	GMPPB	5'	GA	ATTCCTGACCTCAGGTGATC	26219	
	CA			TGGATCACCTGAGGTCAGGAGTTC		
				ACCTAGTGGACTCCAGTCCTTAAG		
GAM2347	GNG4	3'	AA	CTCCTGACCTCGTGATCCA	16833	CT
				TGGATCAC	GAGGTCAGGAGTT	
				ACCTAGTG	CTCCAGTCCTCAA	
GAM2347	H2AV	3'	AA	CTCCTGACCTCAGGCGATCC	25753	A
				GGATC	CCTGAGGTCAGGAGTT	
				CCTAG	GGACTCCAGTCCTCAA	
				C		
GAM2347	HRH4	3'	AA	CTCCTGGGCTGAAACAATCC	41518	CACCTG G
				GGAT	AG TCAGGAGTT	
				CCTA	TC GGTCCTCAA	
				ACAAAG	G	
GAM2347	HRH4	3'	GA	ACTCCTTGGCTCAAGCAATC	41538	CAC GA _
	C			GGAT	CT GGTCAGGAGTTC	
				CCTA	GA TCGGT CCTCAAG	
				AC_	AC T	
GAM2347	HSMPP8	3'	GA	ACTCCTGACCTCAGGTGATC	95133	
	C			GGATCACCTGAGGTCAGGAGTTC		
				CCTAGTGGACTCCAGTCCTCAAG		
GAM2347	HSPC065	3'	GA	ACTCCTGACCTCATGATCCA	27151	CC
				TGGATCA	TGAGGTCAGGAGTTC	
				ACCTAGT	ACTCCAGTCCTCAAG	
GAM2347	JAM1	3'	AA	CTCCTGACCTCTTGATCC	34205	CCT
				GGATCA	GAGGTCAGGAGTT	
				CCTAGT	CTCCAGTCCTCAA	
				T_		
GAM2347	JAM1	3'	AA	CTCCTGACCTCTTGATCC	34206	CCT
				GGATCA	GAGGTCAGGAGTT	

			CCTAGT CTCCAGTCCTCAA		
			T__		
GAM2347	KIAA0022	3'	AACTCCTGACCTCAAGTGATCC 30273	C	
	A		TGGATCAC TGAGGTCAGGAGTT		
			ACCTAGTG ACTCCAGTCCTCAA		
			A		
GAM2347	KIAA0063	3'	AACTCCCGACCTCAAGTGATCT 30245	C	A
			GGATCAC TGAGGTC GGAGTT		
			TCTAGTG ACTCCAG CCTCAA		
			A C		
GAM2347	KIAA0161	3'	AACTCCTGACCTCAGGTGATCT 29183		
			GGATCACCTGAGGTCAGGAGTT		
			TCTAGTGGACTCCAGTCCTCAA		
GAM2347	KIAA0186	3'	AACTCCTGACCTCAAGTGACCC 41089	A	C
	A		TGG TCAC TGAGGTCAGGAGTT		
			ACC AGTG ACTCCAGTCCTCAA		
			C A		
GAM2347	KIAA0186	3'	CCTGACCTCAAGTGACCCA 41104	A	C
			TGG TCAC TGAGGTCAGG		
			ACC AGTG ACTCCAGTCC		
			C A		
GAM2347	KIAA0205	3'	GAACCTCCTGACCTCAGGTGATC 30213		
	T		GGATCACCTGAGGTCAGGAGTTC		
			TCTAGTGGACTCCAGTCCTCAAG		
GAM2347	KIAA0210	5'	GAACCTGCTGACCTCAAGTAATC 29158	C	C G
	C		GGAT AC TGAGGTCAG AGTTC		
			CCTA TG ACTCCAGTC TCAAG		
			A A G		
GAM2347	KIAA0391	3'	AACTCCTGACCTCAGGTGATCC 28594		
	A		TGGATCACCTGAGGTCAGGAGTT		
			ACCTAGTGGACTCCAGTCCTCAA		
GAM2347	KIAA0447	3'	GAACCTCCTCGGCTCAAGCAATC 72122	CAC	GA _
	C		GGAT CT GGTC AGGAGTTC		
			CCTA GA TCGG TCCTCAAG		
			AC_ AC C		
GAM2347	KIAA0472	5'	GAACCTCCTGACCTCAAACGATC 72351	ACC	
	T		GGATC TGAGGTCAGGAGTTC		

			TCTAG ACTCCAGTCCTCAAG	
			CAA	
GAM2347	KIAA0475	3'	GACTCCTGACCCAGGTGATCC 30117	A
	A		TGGATCACCTG GGTCAGGAGTT	
			ACCTAGTGGAC CCAGTCCTCAG	
			C	
GAM2347	KIAA0513	5'	GAATCCTGACCTCAGGTGAGC 29029	A
	CA		TGG TCACCTGAGGTCAGGAGTTC	
			ACC AGTGGACTCCAGTCCTCAAG	
			G	
GAM2347	KIAA0513	3'	GAATCCTGACCTCAGGTGATC 29030	
	C		GGATCACCTGAGGTCAGGAGTTC	
			CCTAGTGGACTCCAGTCCTCAAG	
GAM2347	KIAA0527	3'	GAATCCTGACCTCAAGTGATC 97497	C
	T		GGATCAC TGAGGTCAGGAGTTC	
			TCTAGTG ACTCCAGTCCTCAAG	
			A	
GAM2347	KIAA0555	3'	GAATCCTGACCTCAAGTGATC 60741	C
	T		GGATCAC TGAGGTCAGGAGTTC	
			TCTAGTG ACTCCAGTCCTCAAG	
			A	
GAM2347	KIAA0557	3'	GAATCCCGACCTTGTGATCCA 78561	CT A
			TGGATCAC GAGGTC GGAGTTC	
			ACCTAGTG TTCCAG CCTCAAG	
			— C	
GAM2347	KIAA0562	3'	AACTCCTGACCTTGTGATCCA 28810	CT
			TGGATCAC GAGGTCAGGAGTT	
			ACCTAGTG TTCCAGTCCTCAA	
			—	
GAM2347	KIAA0594	3'	GAATCCTGACCTTGTGATCCA 65512	CT
			TGGATCAC GAGGTCAGGAGTTC	
			ACCTAGTG TTCCAGTCCTCAAG	
			—	
GAM2347	KIAA0599	3'	GAATTCTGACCTCAGGTGATC 77692	
	CA		TGGATCACCTGAGGTCAGGAGTTC	
			ACCTAGTGGACTCCAGTCTTCAAG	
GAM2347	KIAA0682	3'	GAATCCCAACCTCAAGTGATC 30021	C CA
	CA		TGGATCAC TGAGGT GGAGTTC	

ACCTAGTG ACTCCA CCTCAAG
 A AC
 GAM2347 KIAA0682 3' GAATTCCTGACCTCAAGTGATC 30022 C
 CA TGGATCAC TGAGGTCAGGAGTTC
 ||||| |||||
 ACCTAGTG ACTCCAGTCCTTAAG
 A
 GAM2347 KIAA0720 3' GAACTCCTGACCCCAAGTGTTT 62984 T C A
 C GGA CAC TG GGTCAGGAGTTC
 ||| ||| || |||||
 CCT GTG AC CCAGTCCTCAAG
 T A C
 GAM2347 KIAA0737 3' GAACTCCTGACCTCATGATCC 29808 CC
 GGATCA TGAGGTCAGGAGTTC
 ||||| |||||
 CCTAGT ACTCCAGTCCTCAAG
 —
 GAM2347 KIAA0828 3' AACTCCTGGGCTCAAGCAATCC 82106 CACC G
 GGAT TGAG TCAGGAGTT
 ||| ||| |||||
 CCTA ACTC GGCCTCAA
 ACGA G
 GAM2347 KIAA0841 3' GAACTCCTGACCTCAAGTGATC 71895 C
 T GGATCAC TGAGGTCAGGAGTTC
 ||||| |||||
 TCTAGTG ACTCCAGTCCTCAAG
 A
 GAM2347 KIAA0889 3' GAACTCCCGACCTCAAGTGATC 31776 C A
 C GGATCAC TGAGGTC GGAGTTC
 ||||| ||||| |||||
 CCTAGTG ACTCCAG CCTCAAG
 A C
 GAM2347 KIAA0924 3' AACTCCTGACCTTGTGATCC 30345 CT
 GGATCAC GAGGTCAGGAGTT
 ||||| |||||
 CCTAGTG TTCCAGTCCTCAA
 —
 GAM2347 KIAA0931 3' GAACTCTTGACCTCAGGTGATC 68011
 CA TGGATCACCTGAGGTCAGGAGTTC
 |||||
 ACCTAGTG GACTCCAGTTCTCAAG
 —
 GAM2347 KIAA0961 3' AACTCCTGACCTCAGGTGATCC 30381
 A TGGATCACCTGAGGTCAGGAGTT
 |||||
 ACCTAGTG GACTCCAGTCCTCAA
 —
 GAM2347 KIAA1040 3' GAACTCCTGACCTCAGGTGATC 72686
 T GGATCACCTGAGGTCAGGAGTTC
 |||||

TCTAGTGGACTCCAGTCCTCAAG

GAM2347 KIAA1054 3' GAACTCCTGACCTCAAGTGATC 68964 C
GATCAC TGAGGTCAGGAGTTC
||||| |||||||||
CTAGTG ACTCCAGTCCTCAAG
A

GAM2347 KIAA1128 3' GAACTCCTGACCTCAAGTGATC 69005 C
CA TGGATCAC TGAGGTCAGGAGTTC
||||| |||||||||
ACCTAGTG ACTCCAGTCCTCAAG
A

GAM2347 KIAA1161 5' AACTCCTGACCTAGTGATGCA 82634 G CTG
TG ATCAC AGGTCAGGAGTT
|| ||| |||||||||
AC TAGTG TCCAGTCCTCAA
G A__

GAM2347 KIAA1170 3' AACTCCTGACCTCAGGTGATCC 70402
GGATCACCTGAGGTCAGGAGTT
||||| |||||||||
CCTAGTGGACTCCAGTCCTCAA

GAM2347 KIAA1198 3' AACTCCTGACCTCAGGTGATCT 63970
GGATCACCTGAGGTCAGGAGTT
||||| |||||||||
TCTAGTGGACTCCAGTCCTCAA

GAM2347 KIAA1198 3' AACTCTTGACCTCAAATGATCC 63971 CC
A TGGATCA TGAGGTCAGGAGTT
||||| |||||||||
ACCTAGT ACTCCAGTTCTCAA
AA

GAM2347 KIAA1198 3' GAACTCCTGACCTCAGGTAATC 64035 C
CA TGGAT ACCTGAGGTCAGGAGTTC
||||| |||||||||
ACCTA TGGACTCCAGTCCTCAAG
A

GAM2347 KIAA1200 3' GAACTCCTGACCTCAGGTGATC 63037
T GGATCACCTGAGGTCAGGAGTTC
||||| |||||||||
TCTAGTGGACTCCAGTCCTCAAG

GAM2347 KIAA1243 3' CTTGACCTCAAGTAACCA 74025 ATC C
TGG AC TGAGGTCAGG
||| || |||||||||
ACC TG ACTCCAGTTC
AA_ A

GAM2347 KIAA1254 3' TCCTGACCTCAAGTGATCCA 70567 C
TGGATCAC TGAGGTCAGGA
||||| |||||||||

ACCTAGTG ACTCCAGTCCT
 A
 GAM2347 KIAA1257 3' AACTCCCGACTTCAGGTGATCC 63382 A
 GGATCACCTGAGGTC GGAGTT
 |||||
 CCTAGTGGACTTCAG CCTCAA
 C
 GAM2347 KIAA1257 3' AACTCCTGGTCACAAGTAATCC 63383 C C A GT
 GGAT AC TG G CAGGAGTT
 ||| || | |||||
 CCTA TG AC C GTCCTCAA
 A A A TG
 GAM2347 KIAA1320 5' GAATTCCTGACCTCAAGTGATC 69840 C
 TA TGGATCAC TGAGGTCAGGAGTTC
 ||||| |||||
 ATCTAGTG ACTCCAGTCCTTAAG
 A
 GAM2347 KIAA1396 3' AACTCCTGTGCTCAAGTGACCC 63666 A C GT
 GG TCAC TGAG CAGGAGTT
 || ||| ||| |||||
 CC AGTG ACTC GTCCTCAA
 C A GT
 GAM2347 KIAA1465 3' GATCTCTTGACCTCAGGTGATC 61498 T
 CA TGGATCACCTGAGGTCAGGAG TC
 ||||| ||||| ||
 ACCTAGTGGACTCCAGTTCTC AG
 T
 GAM2347 KIAA1467 3' GAACTCCTGACCTCAGATAATC 72067 CAC
 CA TGGAT CTGAGGTCAGGAGTTC
 |||| |||||
 ACCTA GACTCCAGTCCTCAAG
 ATA
 GAM2347 KIAA1493 3' AACTCCTGACCTCAGGTGATCC 64827
 A TGGATCACCTGAGGTCAGGAGTT
 ||||| |||||
 ACCTAGTGGACTCCAGTCCTCAA

 GAM2347 KIAA1508 3' GAACTCCTGACCTCAGGTAATC 62550 C
 CA TGGAT ACCTGAGGTCAGGAGTTC
 |||| |||||
 ACCTA TGGACTCCAGTCCTCAAG
 A
 GAM2347 KIAA1530 3' GAACTCCTAGCCTCAAGCGATC 68560 ACC TC
 C GGATC TGAGG AGGAGTTC
 |||| ||| |||||
 CCTAG ACTCC TCCTCAAG
 CGA GA
 GAM2347 KIAA1571 3' AACTCCTGACCTTGTGGTCCA 61609 CT
 TGGATCAC GAGGTCAGGAGTT
 ||||| |||||

ACCTGGTG TTCCAGTCCTCAA

GAM2347 KIAA1615 3' AACTCCCCGACCTCAGGTGATCC 69261 A
A TGGATCACCTGAGGTC GGAGTT

|||||
ACCTAGTGGACTCCAG CCTCAA
C

GAM2347 KIAA1617 3' GAACTCCCAACCTCAAGTGATC 93077 C CA
T GGATCAC TGAGGT GGAGTTC

|||||
TCTAGTG ACTCCA CCTCAAG
A AC

GAM2347 KIAA1649 3' GAACTCCTGGGCACAAGTGATC 51236 C AG _
C GGATCAC TG GTC AGGAGTTC

|||||
CCTAGTG AC CGG TCCTCAAG
A A_ G

GAM2347 KIAA1655 3' AACTCCTGACCTCCAGTGATCC 67167 CT
A TGGATCAC GAGGTCAGGAGTT

|||||
ACCTAGTG CTCCAGTCCTCAA
AC

GAM2347 KIAA1712 3' AACTCCTGACCTCAGGTGATCT 68142
GGATCACCTGAGGTCAGGAGTT

|||||
TCTAGTGGACTCCAGTCCTCAA

GAM2347 KIAA1737 3' GAACTCCTGACCTCAGTTGATC 67941 C
C GGATCA CTGAGGTCAGGAGTTC

|||||
CCTAGT GACTCCAGTCCTCAAG
T

GAM2347 KIAA1755 3' AACTCCTGGGCTCAAGTGATCC 62002 C G
GGATCAC TGAG TCAGGAGTT

|||||
CCTAGTG ACTC GGTCCTCAA
A G

GAM2347 KIAA1829 3' GAACTCCTGACTTTAGGTGATC 62643
CA TGGATCACCTGAGGTCAGGAGTTC

|||||
ACCTAGTGGATTTCAGTCCTCAAG

GAM2347 KIAA1922 5' GAACTCCTGACCTCAGGTGATC 73993
C GGATCACCTGAGGTCAGGAGTTC

|||||
CCTAGTGGACTCCAGTCCTCAAG

GAM2347 KIAA1962 3' GAACTCCTGGGCTCAAGTGATC 82801 C G
C GGATCAC TGAG TCAGGAGTTC

|||||

			CCTAGTG ACTC GGCCTCAAG		
			A G		
GAM2347	KIAA1971	3'	GAACCTCCTGACCTCGTGATCCA 74679	CT	
			TGGATCAC GAGGTCAGGAGTTC		
			ACCTAGTG CTCCAGTCCTCAAG		
			—		
GAM2347	KIAA1987	5'	GAACCTTCTGACCTCAGGTGATC 89383		
	CA		TGGATCACCTGAGGTCAGGAGTTC		
			ACCTAGTGGACTCCAGTCTTCAAG		
GAM2347	KLK7	3'	GAACGCCTGACCTCAGATGATC 58389	C	A
	CA		TGGATCA CTGAGGTCAGG GTTC		
			ACCTAGT GACTCCAGTCC CAAG		
			A G		
GAM2347	LAMP3	3'	GAACCTTTGACCTCAGGTGATC 60203		
	CA		TGGATCACCTGAGGTCAGGAGTTC		
			ACCTAGTGGACTCCAGTTCTCAAG		
GAM2347	LIECG3	3'	GAACCTCCTGGGCTCAAGCGGTC 88798	ACC	G
	CA		TGGATC TGAG TCAGGAGTTC		
			ACCTGG ACTC GGCCTCAAG		
			CGA G		
GAM2347	LNIR	3'	GAACCTCCTGGGCTCAAGCAATC 48871	CACC	G
	C		GGAT TGAG TCAGGAGTTC		
			CCTA ACTC GGCCTCAAG		
			ACGA G		
GAM2347	MAP-1	3'	GAACCTCCTGACCTCAAGTGATC 42440	C	
	CA		TGGATCAC TGAGGTCAGGAGTTC		
			ACCTAGTG ACTCCAGTCCTCAAG		
			A		
GAM2347	MCLC	3'	GAACCTCCTGACCTCAAGTGACC 31381	A	C
	C		GG TCAC TGAGGTCAGGAGTTC		
			CC AGTG ACTCCAGTCCTCAAG		
			C A		
GAM2347	MCM10	3'	AACTCCTGAGCACTAGCAATCC 38171	CAC	AG_
	A		TGGAT CTG G TCAGGAGTT		
			ACCTA GAT C AGTCCTCAA		
			AC_ CA G		
GAM2347	MEF-2	3'	AACTCCTGACCTCGTGATCCA 65012	CT	
			TGGATCAC GAGGTCAGGAGTT		

ACCTAGTG CTCCAGTCCTCAA

GAM2347 MGC10200 3' GAGCTCCTGAGCTCAAACAATC 59645 CACC G
CA TGGAT TGAG TCAGGAGTTC

||||| ||||| |||||
ACCTA ACTC AGTCCTCGAG
ACAA G

GAM2347 MGC11386 3' AACTCCTGGGCTCAAGCAATCC 53049 CACC G
GGAT TGAG TCAGGAGTT

||||| ||||| |||||
CCTA ACTC GGTCTCAA
ACGA G

GAM2347 MGC13159 3' GAACTCCTGGGATCAAGTGATC 53037 C GG
C GGATCAC TGA TCAGGAGTTC

||||| ||||| |||||
CCTAGTG ACT GGTCTCAAG
A AG

GAM2347 MGC1842 3' GAACCCCTGAGCTCAGGTGATC 66255 G A
CA TGGATCACCTGAG TCAGG GTTC

||||| ||||| |||||
ACCTAGTGGACTC AGTCC CAAG
G C

GAM2347 MGC20235 3' GAACTCCTGGGCTCAAGCGATC 59553 ACC G
C GGATC TGAG TCAGGAGTTC

||||| ||||| |||||
CCTAG ACTC GGTCTCAAG
CGA G

GAM2347 MGC21675 3' GAACTCCTGACCTCAGGTGATC 54591
CA TGGATCACCTGAGGTCAGGAGTTC

||||| ||||| |||||
ACCTAGTGGACTCCAGTCCTCAAG

GAM2347 MGC21738 3' GAACTCCTGACCTCAAGTGATC 59576 C
C GGATCAC TGAGGTCAGGAGTTC

||||| ||||| |||||
CCTAGTG ACTCCAGTCCTCAAG
A

GAM2347 MGC2474 3' GAACTCCTGCCCTCAGGTGATC 43957 T
CA TGGATCACCTGAGG CAGGAGTTC

||||| ||||| |||||
ACCTAGTGGACTCC GTCCTCAAG
C

GAM2347 MKRN4 3' GAACTCCTGACCTCAGGTGATC 48462
CA TGGATCACCTGAGGTCAGGAGTTC

||||| ||||| |||||
ACCTAGTGGACTCCAGTCCTCAAG

GAM2347 MLZE 5' GAACTCCTGACCTCGGGATCCA 49451 A T
TGGATC CC GAGGTCAGGAGTTC

||||| ||||| |||||

ACCTAG GG CTCCAGTCCTCAAG

GAM2347 MMPL1 3' GAACTCTTGGGCTCAAGCGATC 15964 ACC G
C GGATC TGAG TCAGGAGTTC
||||| ||||| |||||
CCTAG ACTC GGTTCTCAAG
CGA G

GAM2347 moblak 3' AACTCCTGACTTCAGGTGATCC 56377
GGATCACCTGAGGTCAGGAGTT
|||||
CCTAGTGGACTTCAGTCCTCAA

GAM2347 MRPL44 3' GAACTCCTGACCTCAGGTGATC 43597
CA TGGATCACCTGAGGTCAGGAGTTC
|||||
ACCTAGTGGACTCCAGTCCTCAAG

GAM2347 NFAT5 3' GAACTCCTAACCTCCAGTGATC 57769 CT C
CA TGGATCAC GAGGT AGGAGTTC
||||| ||||| |||||
ACCTAGTG CTCCA TCCTCAAG
AC A

GAM2347 NINJ2 3' GAACTCCTGACCTCAGGTGATC 33724
T GGATCACCTGAGGTCAGGAGTTC
|||||
TCTAGTGGACTCCAGTCCTCAAG

GAM2347 Nup43 3' GAACTCCTGACCACAGGTAATC 45346 C A
GAT ACCTG GGTCAGGAGTTC
||| ||||| |||||
CTA TGGAC CCAGTCCTCAAG
A A

GAM2347 NXN 3' GAACTCCTGACCTCAGGTGATC 42674
CA TGGATCACCTGAGGTCAGGAGTTC
|||||
ACCTAGTGGACTCCAGTCCTCAAG

GAM2347 OCT11 3' GAACTCCTGACCTCCTGATCCA 27589 CCT
TGGATCA GAGGTCAGGAGTTC
||||| |||||
ACCTAGT CTCCAGTCCTCAAG
C__

GAM2347 PELI1 5' AACTCCCAACCTCAAGTGATCC 40614 C CA
GGATCAC TGAGGT GGAGTT
||||| ||||| |||||
CCTAGTG ACTCCA CCTCAA
A AC

GAM2347 PELI1 5' GAACTCCTGACCTCAAGTGATC 40639 C
T GGATCAC TGAGGTCAGGAGTTC
||||| |||||

			TCTAGTG ACTCCAGTCCTCAAG		
			A		
GAM2347	PIG7	3'	GAATCCTGGGCTCAAGCGATC 17969	ACC	G
	C		GGATC TGAG TCAGGAGTTC		
			CCTAG ACTC GGTCTCAAG		
			CGA G		
GAM2347	PIP3-E	3'	AACTCCTGACCTCAGGTGATCT 67339		
			GGATCACCTGAGGTCAGGAGTT		
			TCTAGTGGACTCCAGTCCTCAA		
GAM2347	POLR2D	3'	AACTCCTGGGCTCAAGTGATCC 17837	C	G
			GGATCAC TGAG TCAGGAGTT		
			CCTAGTG ACTC GGTCTCAA		
			A G		
GAM2347	PRO0899	5'	GAATCCTGGGCCCAAGCAATC 38310	CAC	GA _
	C		GGAT CT GGTC AGGAGTTC		
			CCTA GA CCGG TCCTCAAG		
			AC_ AC G		
GAM2347	PRO1992	3'	GAATCAACCTCAGGTGATCC 26904		CAG
			GGATCACCTGAGGT GAGTTC		
			CCTAGTGGACTCCA CTCAAG		
			A_		
GAM2347	PRO2955	3'	AACTCCTGACCTCAGGTGATCC 38228		
	A		TGGATCACCTGAGGTCAGGAGTT		
			ACCTAGTGGACTCCAGTCCTCAA		
GAM2347	PSTPIP2	3'	AACTCCTGACCTCAGGTGATCC 44644		
	A		TGGATCACCTGAGGTCAGGAGTT		
			ACCTAGTGGACTCCAGTCCTCAA		
GAM2347	RASSF2	3'	GAATCCTGACCTCGTGATCCA 29098	CT	
			TGGATCAC GAGGTCAGGAGTTC		
			ACCTAGTG CTCCAGTCCTCAAG		
GAM2347	RES4-25	3'	GAATCCCGACCTCAGGTAATC 65266	C	A
	CA		TGGAT ACCTGAGGTC GGAGTTC		
			ACCTA TGGACTCCAG CCTTAAG		
			A C		
GAM2347	RNF8	3'	AATTCCTGACCTTAAGTGATCC 15552	C	
	A		TGGATCAC TGAGGTCAGGAGTT		

			ACCTAGTG ATTCCAGTCCTTAA		
			A		
GAM2347	Rpo1-2	3'	GACCCTGACCTCAAGTGATCCA 39220	C	A
			TGGATCAC TGAGGTCAGG GTT		
			ACCTAGTG ACTCCAGTCC CAG		
			A		
GAM2347	Rpo1-2	3'	GACCCTGACCTCAAGTGATCCA 39221	C	A
			TGGATCAC TGAGGTCAGG GTT		
			ACCTAGTG ACTCCAGTCC CAG		
			A		
GAM2347	SARM	3'	GAACCTCCTGGGCTCAAGTGATC 31290	C	G
	C		GGATCAC TGAG TCAGGAGTTC		
			CCTAGTG ACTC GGTCCTCAAG		
			A G		
GAM2347	SCAMP-4	3'	GAACCTCCTGACCTCAAGTGATC 55347	C	
	CA		TGGATCAC TGAGGTCAGGAGTTC		
			ACCTAGTG ACTCCAGTCCTCAAG		
			A		
GAM2347	SCYA22	3'	AACTCCTGGGCTCAAGCGATCC 92565	ACC	G
			GGATC TGAG TCAGGAGTT		
			CCTAG ACTC GGTCCTCAA		
			CGA G		
GAM2347	SCYA22	3'	GAACCTCCTGACCTCAAGTGATC 92593	C	
	CA		TGGATCAC TGAGGTCAGGAGTTC		
			ACCTAGTG ACTCCAGTCCTCAAG		
			A		
GAM2347	SCYA22	3'	GAACCTCCTGTCCTCAGGTAATC 92594	C	T
	C		GGAT ACCTGAGG CAGGAGTTC		
			CCTA TGGACTCC GTCCTCAAG		
			A T		
GAM2347	SCYA28	3'	GAACCTTCTGATCTCAAGTGATC 39542	C	
	CA		TGGATCAC TGAGGTCAGGAGTTC		
			ACCTAGTG ACTCTAGTCTTCAAG		
			A		
GAM2347	SFXN2	3'	GAACCTCCTGACCTCAGGTGATC 74375		
	C		GGATCACCTGAGGTCAGGAGTTC		
			CCTAGTGGACTCCAGTCCTCAAG		
GAM2347	SIRPB1	3'	GAACCTCCCGACCTCAGGTGATC 21366		A
	CA		TGGATCACCTGAGGTC GGAGTTC		

			ACCTAGTGGACTCCAG CCTCAAG		
			C		
GAM2347	SLC12A8	3'	GAACTCCTGACCTCGTGATCCA 45236	CT	
			TGGATCAC GAGGTCAGGAGTTC		
			ACCTAGTG CTCCAGTCCTCAAG		
			—		
GAM2347	SLC2A10	3'	GAACTCCTGAGCTCAAGTGATC 48551	C	G
	CA		TGGATCAC TGAG TCAGGAGTTC		
			ACCTAGTG ACTC AGTCCTCAAG		
			A G		
GAM2347	SLC6A14	3'	GAACTCCCGACCTCAAGTGATC 24308	C	A
	T		GGATCAC TGAGGTC GGAGTTC		
			TCTAGTG ACTCCAG CCTCAAG		
			A C		
GAM2347	STAF65(gamma)	3'	AACTCCTGACCTCAAGTGATCT 30056	C	
			GGATCAC TGAGGTCAGGAGTT		
			TCTAGTG ACTCCAGTCCTCAA		
			A		
GAM2347	STRBP	5'	GAACTCCTGAACGCAAGTGATC 37818	C	AGG
	C		GGATCAC TG TCAGGAGTTC		
			CCTAGTG AC AGTCCTCAAG		
			A GCA		
GAM2347	TBCC	3'	GAACTCCTGACCTCAGGTGATC 13603		
	CA		TGGATCACCTGAGGTCAGGAGTTC		
			ACCTAGTGGACTCCAGTCCTCAAG		
GAM2347	TCL6	3'	AACTCCTGAGCTCAAGCGATCC 40453	ACC	G
			GGATC TGAG TCAGGAGTT		
			CCTAG ACTC AGTCCTCAA		
			CGA G		
GAM2347	TCL6	5'	GAACTCCTGACCAAGTGATCCA 40473	CTGA	
			TGGATCAC GGTGAGGAGTTC		
			ACCTAGTG CCAGTCCTCAAG		
			AA__		
GAM2347	TGIF2	3'	GAACTCCTGACCTCGTGAGCCA 41750	A	CT
			TGG TCAC GAGGTCAGGAGTTC		
			ACC AGTG CTCCAGTCCTCAAG		
			G __		
GAM2347	TRIM16	3'	AACTCCTGACCTCGTGATGCA 22359	G	CT
			TG ATCAC GAGGTCAGGAGTT		

			AC TAGTG CTCCAGTCCTCAA	
			G _	
GAM2347	TRIM5	3'	GAACCTCTGACCTCAGGTGATC 53468	GA
	CA		TGGATCACCTGAGGTCAG GTTC	
			ACCTAGTGGACTCCAGTC CAAG	
			TC	
GAM2347	TRIM5	3'	GAACCTCTGACCTCAGGTGATC 53469	GA
	CA		TGGATCACCTGAGGTCAG GTTC	
			ACCTAGTGGACTCCAGTC CAAG	
			TC	
GAM2347	TRIM6	3'	GAACCTCTGACCTCAGGTGATC 55179	C A
	CA		TGGATCAC TG GGTCAGGAGTTC	
			ACCTAGTG AC CCAGTCCTCAAG	
			A G	
GAM2347	TU12B1-TY	3'	GAACCTCTGACCTCAGATAATC 33847	CAC
	T		GGAT CTGAGGTCAGGAGTTC	
			TCTA GACTCCAGTCCTCAAG	
			ATA	
GAM2347	TU12B1-TY	3'	GAACCTCTGACCTTGGGTAATC 33848	C TG
	CA		TGGAT ACC AGGTCAGGAGTTC	
			ACCTA TGG TCCAGTCCTCAAG	
			A GT	
GAM2347	TUCAN	3'	GAACCTCTGGCCTCAAGTGATC 30976	C
	CA		TGGATCAC TGAGGTCAGGAGTTC	
			ACCTAGTG ACTCCGGTCCTCAAG	
			A	
GAM2347	TUSP	3'	GAACCTCTGACCTCAGGTGATC 40025	
	C		GGATCACCTGAGGTCAGGAGTTC	
			CCTAGTGGACTCCAGTCCTCAAG	
GAM2347	UBF-fl	3'	AACTCCTGACCTCAAGTGATCC 52613	C
	A		TGGATCAC TGAGGTCAGGAGTT	
			ACCTAGTG ACTCCAGTCCTCAA	
			A	
GAM2347	VDU1	3'	AACTCCTGACCTCAGGTGATCC 31111	
	A		TGGATCACCTGAGGTCAGGAGTT	
			ACCTAGTGGACTCCAGTCCTCAA	
GAM2347	VMP	3'	GAACCTCTGGGCTCAAGCGATC 55762	ACC G
	C		GGATC TGAG TCAGGAGTTC	

			CCTAG ACTC GGTCTCAAG	
			CGA G	
GAM2347	VPS33A	3'	AACTCCTGACCTCAGGTGATCC 43604	
	A		TGGATCACCTGAGGTCAGGAGTT	
			ACCTAGTGGACTCCAGTCCTCAA	
GAM2347	WBSCR23	3'	AACTCCTGACCTCAGGTGATCC 47405	
	A		TGGATCACCTGAGGTCAGGAGTT	
			ACCTAGTGGACTCCAGTCCTCAA	
GAM2347	WIT-1	3'	GAACCTCTGACCCAGATTCA 32398	ACC A
			TGGATC TG GGTCTCAGGAGTTC	
			ACTTAG AC CCAGTCCTCAAG	
			— C	
GAM2347	ZNF177	5'	AACTCCTGCTCTCAAGTGATCC 14355	C GT
			GGATCAC TGAG CAGGAGTT	
			CCTAGTG ACTC GTCCTCAA	
			A TC	
GAM2347	ZNF338	3'	GAACCTCTGACCTCAAGTGATC 42255	C
	T		GGATCAC TGAGGTCAGGAGTTC	
			TCTAGTG ACTCCAGTCCTCAAG	
			A	
GAM2347	ZTL1	3'	GAACCTCTGACCTCAGGTGATC 43519	
	T		GGATCACCTGAGGTCAGGAGTTC	
			TCTAGTGGACTCCAGTCCTCAAG	
GAM2347	LOC112687	3'	AACTCCTGACCTCATGTAATCC 73214	C C
	A		TGGAT AC TGAGGTCAGGAGTT	
			ACCTA TG ACTCCAGTCCTCAA	
			A T	
GAM2347	LOC112817	3'	GAACCTCTGACCTCAGGTGATC 57325	
	CA		TGGATCACCTGAGGTCAGGAGTTC	
			ACCTAGTGGACTCCAGTCCTCAAG	
GAM2347	LOC113026	3'	CCTGACCTCAAGTGATCC 56727	C
			GGATCAC TGAGGTCAGG	
			CCTAGTG ACTCCAGTCC	
			A	
GAM2347	LOC113523	3'	GAACCTCTGACCTCACACAATC 73422	CACC
	C		GGAT TGAGGTCAGGAGTTC	

		CCTA ACTCCAGTCCTCAAG	
		ACAC	
GAM2347	LOC115098 5'	GAACCTCCTGGCCTCAAGCAATC 57394	CACC
	C	GGAT TGAGGTCAGGAGTTC	
		CCTA ACTCCGGTCCTCAAG	
		ACGA	
GAM2347	LOC115219 5'	AACTCCTGACGTCGTGATCC 73680	CT G
		GGATCAC GA GTCAGGAGTT	
		CCTAGTG CT CAGTCCTCAA	
		— G	
GAM2347	LOC115648 3'	GAACCTCCTGACCTCAGGTGATC 60021	
	CA	TGGATCACCTGAGGTCAGGAGTTC	
		ACCTAGTGGACTCCAGTCCTCAAG	
GAM2347	LOC119392 3'	GAACCTCCTGACCTCAGGTGATC 59813	
	CA	TGGATCACCTGAGGTCAGGAGTTC	
		ACCTAGTGGACTCCAGTCCTCAAG	
GAM2347	LOC120114 3'	AACTCCTGACCTCGTAATCCA 76031	C CT
		TGGAT AC GAGGTCAGGAGTT	
		ACCTA TG CTCCAGTCCTCAA	
		A —	
GAM2347	LOC120224 5'	GAACCTCCTGACCTCAGGTGATC 57887	
	T	GGATCACCTGAGGTCAGGAGTTC	
		TCTAGTGGACTCCAGTCCTCAAG	
GAM2347	LOC120939 3'	GAACCTCCTGACGTCAGGTGATC 76761	G
	C	GGATCACCTGA GTCAGGAGTTC	
		CCTAGTGGACT CAGTCCTCAAG	
		G	
GAM2347	LOC121504 3'	GAACCTCCTGGCCTCAAGTGATT 74545	C
	CA	TGGATCAC TGAGGTCAGGAGTTC	
		ACTTAGTG ACTCCGGTCCTCAAG	
		A	
GAM2347	LOC124216 3'	AACTCCTGACCTCGTGATCC 74730	CT
		GGATCAC GAGGTCAGGAGTT	
		CCTAGTG CTCCAGTCCTCAA	
		—	
GAM2347	LOC125194 5'	AACTCCTGGCTTCAAGTGATCC 74859	C
		GGATCAC TGAGGTCAGGAGTT	

		CCTAGTG ACTTCGGTCCTCAA	
		A	
GAM2347	LOC126364 3'	GAACCTCCTGACCTCAAGCGATC 76191	ACC
	T	GGATC TGAGGTCAGGAGTTC	
		TCTAG ACTCCAGTCCTCAAG	
		CGA	
GAM2347	LOC126661 3'	GAACCTCCTGGGCTCAACTGATC 75056	CC G
	CA	TGGATCA TGAG TCAGGAGTTC	
		ACCTAGT ACTC GGTCTCAAG	
		CA G	
GAM2347	LOC126669 3'	AACTCCTGACCTCAAATGATCC 75916	CC
	A	TGGATCA TGAGGTCAGGAGTT	
		ACCTAGT ACTCCAGTCCTCAA	
		AA	
GAM2347	LOC128077 3'	GAACCTCCTGACATAAGGTAATC 75214	C GAG
	CA	TGGAT ACCT GTCAGGAGTTC	
		ACCTA TGGA CAGTCCTCAAG	
		A ATA	
GAM2347	LOC128989 3'	GAACCTCCTGACGTGGTGATCCA 75315	TGAG
		TGGATCACC GTCAGGAGTTC	
		ACCTAGTGG CAGTCCTCAAG	
		TG__	
GAM2347	LOC130639 5'	GAACCTCCTGACCTCAAGTGATC 75479	C
	C	GGATCAC TGAGGTCAGGAGTTC	
		CCTAGTG ACTCCAGTCCTCAAG	
		A	
GAM2347	LOC130813 3'	AACTCCCAACTTCAGGTGATCC 76257	CA
		GGATCACCTGAGGT GGAGTT	
		CCTAGTGGACTTCA CCTCAA	
		AC	
GAM2347	LOC132241 5'	GAACGCCTGACCTCAAGTGATC 75561	C A
	C	GGATCAC TGAGGTCAGG GTTC	
		CCTAGTG ACTCCAGTCC CAAG	
		A G	
GAM2347	LOC135154 3'	GAACCTCCTGACCTCAGTTGATC 75730	C
	CA	TGGATCA CTGAGGTCAGGAGTTC	
		ACCTAGT GACTCCAGTCCTCAAG	
		T	
GAM2347	LOC135293 3'	AACTCCTGGGCTCAAGCAATCC 76673	CACC G
		GGAT TGAG TCAGGAGTT	

		CCTA ACTC GGCCTCAA	
		ACGA G	
GAM2347	LOC135293 3'	GAACCTCCTGACCTCAGGTGATG 76684	G
	CA	TG ATCACCTGAGGTCAGGAGTTC	
		AC TAGTGGACTCCAGTCCTCAAG	
		G	
GAM2347	LOC135818 3'	GAACCTCCTGACCTCAGGTGATC 75747	
	T	GGATCACCTGAGGTCAGGAGTTC	
		TCTAGTGGACTCCAGTCCTCAAG	
GAM2347	LOC139422 5'	GAACCTCCTGAGCTCAAGCAATC 76350	CACC G
	C	GGAT TGAG TCAGGAGTTC	
		CCTA ACTC AGTCCTCAAG	
		ACGA G	
GAM2347	LOC142927 5'	AACTCCTGGCCTCAAGTGATCC 76937	C
		GGATCAC TGAGGTCAGGAGTT	
		CCTAGTG ACTCCGGTCCTCAA	
		A	
GAM2347	LOC143916 3'	AACTTCTGACCTCAGGTGATCC 77131	
	A	TGGATCACCTGAGGTCAGGAGTT	
		ACCTAGTGGACTCCAGTCTTCAA	
GAM2347	LOC144305 3'	AACTCCTGGACCCAAGCGATCC 83965	AC GA _
		GGATC CT GGTC AGGAGTT	
		CCTAG GA CCAG TCCTCAA	
		C_ AC G	
GAM2347	LOC144317 5'	GAACCTCCTGACCTCAGGTGATC 77294	
	CA	TGGATCACCTGAGGTCAGGAGTTC	
		ACCTAGTGGACTCCAGTCCTCAAG	
GAM2347	LOC144519 3'	GAACCTCCTGACCTGAAGCGATC 77372	AC G_
	C	GGATC CT AGGTCAGGAGTTC	
		CCTAG GA TCCAGTCCTCAAG	
		C_ AG	
GAM2347	LOC144519 5'	GAACCTCCTGGGCTCAAGTGGTC 77373	C G
	CA	TGGATCAC TGAG TCAGGAGTTC	
		ACCTGGTG ACTC GGCCTCAAG	
		A G	
GAM2347	LOC144524 5'	AACTCCTGAACCTCAGGTGATCC 84044	G
		GGATCACCTGAG TCAGGAGTT	

		CCTAGTGGACTC AGTCCTCAA		
		A		
GAM2347	LOC144742 5'	GAAC	TCATGGCCTCAAATGATC 77459	CC G
	CA		TGGATCA TGAGGTCA GAGTTC	
			ACCTAGT ACTCCGGT CTCAAG	
			AA A	
GAM2347	LOC145009 3'	GAAC	TCCTGACCTCGTGATCCA 60974	CT
			TGGATCAC GAGGTCAGGAGTTC	
			ACCTAGTG CTCCAGTCCTCAAG	
			—	
GAM2347	LOC145082 5'	CCTAAC	CCTAAGGTGATCCA 84185	G C
			TGGATCACCT AGGT AGG	
			ACCTAGTGGA TCCA TCC	
			A A	
GAM2347	LOC145268 5'	GAAC	TCCTAACCTCGGGTGATC 77578	C
	CA		TGGATCACCTGAGGT AGGAGTTC	
			ACCTAGTGGGCTCCA TCCTCAAG	
			A	
GAM2347	LOC145453 5'	AACTC	CTGACCTCAAGGATCT 77649	ACC
			GGATC TGAGGTCAGGAGTT	
			TCTAG ACTCCAGTCCTCAA	
			GA_	
GAM2347	LOC145725 3'	GAAC	TCCTGGGCTCAAGTGATC 77882	C G
	C		GGATCAC TGAG TCAGGAGTTC	
			CCTAGTG ACTC GGTCCTCAAG	
			A G	
GAM2347	LOC145732 3'	GAAC	TCCTGGGCTCAAGTGATC 77894	C G
	C		GGATCAC TGAG TCAGGAGTTC	
			CCTAGTG ACTC GGTCCTCAAG	
			A G	
GAM2347	LOC145813 5'	GAAC	TCCTGGGCTCAAGCGATC 84508	ACC G
	C		GGATC TGAG TCAGGAGTTC	
			CCTAG ACTC GGTCCTCAAG	
			CGA G	
GAM2347	LOC145873 5'	GAAC	TCCTGAACTCAAGTAATC 78011	C C G
	CA		TGGAT AC TGAG TCAGGAGTTC	
			ACCTA TG ACTC AGTCCTCAAG	
			A A A	
GAM2347	LOC146050 3'	AACTC	CCCGACCTCAGGTGATCT 78094	A
			GGATCACCTGAGGTC GGAGTT	

		TCTAGTGGACTCCAG CCTCAA	
		C	
GAM2347	LOC146108 3'	AACTCCTGGCTTCAAGCAATCC 78145	CACC
		GGAT TGAGGTCAGGAGTT	
		CCTA ACTTCGGTCCTCAA	
		ACGA	
GAM2347	LOC146229 3'	AACTCCTGACCTCAAGTGATCC 78237	C
	A	TGGATCAC TGAGGTCAGGAGTT	
		ACCTAGTG ACTCCAGTCCTCAA	
		A	
GAM2347	LOC146229 3'	AACTCCTGACCTCAGGTGATCC 78238	
	A	TGGATCACCTGAGGTCAGGAGTT	
		ACCTAGTGGACTCCAGTCCTCAA	
GAM2347	LOC146229 3'	AACTCCTGACTTCAAATGATCC 78239	CC
	A	TGGATCA TGAGGTCAGGAGTT	
		ACCTAGT ACTTCAGTCCTCAA	
		AA	
GAM2347	LOC146336 3'	GAACTCTTGGGCTCAAGTGATC 78372	C G
	C	GGATCAC TGAG TCAGGAGTTC	
		CCTAGTG ACTC GGTTCCTCAAG	
		A G	
GAM2347	LOC146346 5'	GAACTCCTGACCACATGTGGTC 78396	C A
	CA	TGGATCAC TG GGTCAGGAGTTC	
		ACCTGGTG AC CCAGTCCTCAAG	
		T A	
GAM2347	LOC146894 3'	GAACTCCTGACCTCAAATGAGC 59861	A CC
	C	GG TCA TGAGGTCAGGAGTTC	
		CC AGT ACTCCAGTCCTCAAG	
		G AA	
GAM2347	LOC146901 3'	GAACTCCTGACCTCAGGTGATC 84900	
	CA	TGGATCACCTGAGGTCAGGAGTTC	
		ACCTAGTGGACTCCAGTCCTCAAG	
GAM2347	LOC146909 3'	GAACTCCTGACCTCAGGTGATC 78771	
	C	GGATCACCTGAGGTCAGGAGTTC	
		CCTAGTGGACTCCAGTCCTCAAG	
GAM2347	LOC146952 5'	AACTCCTGACCTCAGATGATCT 84918	C
	A	TGGATCA CTGAGGTCAGGAGTT	

		ATCTAGT GACTCCAGTCCTCAA		
		A		
GAM2347	LOC147054 3'	GAACTCCCGATCTCAGGTGATC 85006		A
	C	GGATCACCTGAGGTC GGAGTTC		
		CCTAGTGGACTCTAG CCTCAAG		
		C		
GAM2347	LOC147276 3'	GAACTCCTGACCTCAAGTGATC 78961		C
	CA	TGGATCAC TGAGGTCAGGAGTTC		
		ACCTAGTG ACTCCAGTCCTCAAG		
		A		
GAM2347	LOC147817 3'	AACTCCTGACCTTATAATCC 79161		CACC
		GGAT TGAGGTCAGGAGTT		
		CCTA ATTCCAGTCCTCAA		
		AT__		
GAM2347	LOC147817 3'	AACTCCTGGCTTCAAGTGATCC 79162		C
		GGATCAC TGAGGTCAGGAGTT		
		CCTAGTG ACTTCGGTCCTCAA		
		A		
GAM2347	LOC147841 3'	GAACTCCTGACCTCAGGTGATC 79227		
	CA	TGGATCACCTGAGGTCAGGAGTTC		
		ACCTAGTGGACTCCAGTCCTCAAG		
GAM2347	LOC147935 3'	AACTCCTGGGCTCAAGTGATCC 85202		C G
		GGATCAC TGAG TCAGGAGTT		
		CCTAGTG ACTC GGTCCTCAA		
		A G		
GAM2347	LOC147990 3'	GAACTCCTGGGCTCAAGCGATC 85222		ACC G
	C	GGATC TGAG TCAGGAGTTC		
		CCTAG ACTC GGTCCTCAAG		
		CGA G		
GAM2347	LOC148195 3'	GAACTCCTGACCTCAGGTGAGC 85282		A
	C	GG TCACCTGAGGTCAGGAGTTC		
		CC AGTGGACTCCAGTCCTCAAG		
		G		
GAM2347	LOC148645 5'	GAACTCCTGGGCCCAAGTGATC 85334		C A _
	C	GGATCAC TG GGTC AGGAGTTC		
		CCTAGTG AC CCGG TCCTCAAG		
		A _ G		
GAM2347	LOC148709 3'	AACTCCCGACCTTAGGTGATGC 79685		G A
	A	TG ATCACCTGAGGTC GGAGTT		

		AC TAGTGGATTCCAG CCTCAA	
		G C	
GAM2347	LOC148918 5'	GAACCTCCTGACCTCAGGTGATC 79827	
	CA	TGGATCACCTGAGGTCAGGAGTTC	
		ACCTAGTGGACTCCAGTCCTCAAG	
GAM2347	LOC149478 3'	GAACCTCCTGACTTCATGTGATC 80169	C
	C	GGATCAC TGAGGTCAGGAGTTC	
		CCTAGTG ACTTCAGTCCTCAAG	
		T	
GAM2347	LOC149577 3'	ACTCCTGACCTCAAGTGATCCA 85663	C
		TGGATCAC TGAGGTCAGGAGT	
		ACCTAGTG ACTCCAGTCCTCA	
		A	
GAM2347	LOC149577 3'	GAACCTCCTGACCTCAAGTGATC 85675	C
	CA	TGGATCAC TGAGGTCAGGAGTTC	
		ACCTAGTG ACTCCAGTCCTCAAG	
		A	
GAM2347	LOC149692 3'	GAACCTCCTGACCTCAGGTGATC 85734	
	CA	TGGATCACCTGAGGTCAGGAGTTC	
		ACCTAGTGGACTCCAGTCCTCAAG	
GAM2347	LOC149711 3'	AACTCCTGACCTCAGGTGATCC 85829	
	A	TGGATCACCTGAGGTCAGGAGTT	
		ACCTAGTGGACTCCAGTCCTCAA	
GAM2347	LOC150054 5'	GAACCTATGACCTCAGGTGATC 85972	G
	C	GGATCACCTGAGGTCA GAGTTC	
		CCTAGTGGACTCCAGT TTCAAG	
		A	
GAM2347	LOC150225 3'	AACTCCTGACCTCAGATGATTC 86174	C
	A	TGGATCA CTGAGGTCAGGAGTT	
		ACTTAGT GACTCCAGTCCTCAA	
		A	
GAM2347	LOC150282 5'	GAACCTCCTGACCTCAGGTGATC 80543	
	CA	TGGATCACCTGAGGTCAGGAGTTC	
		ACCTAGTGGACTCCAGTCCTCAAG	
GAM2347	LOC150290 3'	AACTCCTGGCCTCAAGCAATCC 80581	CACC
		GGAT TGAGGTCAGGAGTT	

		CCTA ACTCCGGTCCTCAA	
		ACGA	
GAM2347	LOC150397 3'	GAACCCCTGACCTCAGGTGATC 80662	A
	C	GGATCACCTGAGGTCAGG GTTC	
		CCTAGTGGACTCCAGTCC CAAG	
		C	
GAM2347	LOC150407 3'	AACTCCTGGGCTCAAGTAATCC 80634	C C G
		GGAT AC TGAG TCAGGAGTT	
		CCTA TG ACTC GGTCTCAA	
		A A G	
GAM2347	LOC150587 3'	AACTCCTGGGCTCAAGCAATCC 86238	CACC G
		GGAT TGAG TCAGGAGTT	
		CCTA ACTC GGTCTCAA	
		ACGA G	
GAM2347	LOC150587 3'	AACTCCTGGGCTCAAGCGATCC 86239	ACC G
		GGATC TGAG TCAGGAGTT	
		CCTAG ACTC GGTCTCAA	
		CGA G	
GAM2347	LOC150960 3'	AATTCCTGACCTCAGGTGATCC 80859	
	A	TGGATCACCTGAGGTCAGGAGTT	
		ACCTAGTGGACTCCAGTCCTTAA	
GAM2347	LOC151201 3'	GAACTCCTGGTTTCAAGCGATC 86476	ACC GT
	C	GGATC TGAG CAGGAGTTC	
		CCTAG ACTT GTCCTCAAG	
		CGA TG	
GAM2347	LOC151701 3'	GAACTCCTGACCTCAGATGATC 86671	C
	T	GGATCA CTGAGGTCAGGAGTTC	
		TCTAGT GACTCCAGTCCTCAAG	
		A	
GAM2347	LOC151826 3'	GAACTCCTGACATCAGGTGATC 81181	G
	CA	TGGATCACCTGA GTCAGGAGTTC	
		ACCTAGTGGACT CAGTCCTCAAG	
		A	
GAM2347	LOC152137 3'	GAACCCCTGACCTCAAGTGATC 81316	C A
	CA	TGGATCAC TGAGGTCAGG GTTC	
		ACCTAGTG ACTCCAGTCC CAAG	
		A C	
GAM2347	LOC152343 3'	GAACTCCTGTGCTCAAGTGATC 81426	C GT
	C	GGATCAC TGAG CAGGAGTTC	

		CCTAGTG ACTC GTCCTCAAG	
		A GT	
GAM2347	LOC152794 5'	GAACCTCCTGACCTCAGGTGATC 81558	
	C	GGATCACCTGAGGTCAGGAGTTC	
		CCTAGTGGACTCCAGTCCTCAAG	
GAM2347	LOC153077 3'	GAACCTCCTGACCTCAGGTGATC 87125	
	CA	TGGATCACCTGAGGTCAGGAGTTC	
		ACCTAGTGGACTCCAGTCCTCAAG	
GAM2347	LOC153443 3'	AACTCCTGGGCTCAAGTGATCC 81686	C G
		GGATCAC TGAG TCAGGAGTT	
		CCTAGTG ACTC GGCCTCAA	
		A G	
GAM2347	LOC153606 5'	GAACCTCCTGACTGCAGGTGATC 87256	A
	C	GGATCACCTG GGCAGGAGTTC	
		CCTAGTGGAC TCAGTCCTCAAG	
		G	
GAM2347	LOC153688 3'	GAACCTCCCAACCTCAGGTGATC 87311	CA
	C	GGATCACCTGAGGT GGAGTTC	
		CCTAGTGGACTCCA CCTCAAG	
		AC	
GAM2347	LOC153688 3'	GAACCTCCTGGGCTCAAGCGATC 87312	ACC G
	CA	TGGATC TGAG TCAGGAGTTC	
		ACCTAG ACTC GGCCTCAAG	
		CGA G	
GAM2347	LOC153811 3'	AACTCCTGACCTCAAATGATCC 81816	CC
	A	TGGATCA TGAGGTCAGGAGTT	
		ACCTAGT ACTCCAGTCCTCAA	
		AA	
GAM2347	LOC153883 5'	GAACCTCCTGACCTCAAGTGATC 81894	C
	CA	TGGATCAC TGAGGTCAGGAGTTC	
		ACCTAGTG ACTCCAGTCCTCAAG	
		A	
GAM2347	LOC154007 3'	GAACCTCCTGGGCTCAGATGATC 81927	C G
	C	GGATCA CTGAG TCAGGAGTTC	
		CCTAGT GACTC GGCCTCAAG	
		A G	
GAM2347	LOC154726 3'	AACTCCTGGGCTCAGATGATCC 82003	C G
	A	TGGATCA CTGAG TCAGGAGTT	

	ACCTAGT GACTC GGCCTCAA	
	A G	
GAM2347 LOC154877 3'	AACTCCTGGGCTCAAGTGATCC 87512	C G
	GGATCAC TGAG TCAGGAGTT	
	CCTAGTG ACTC GGCCTCAA	
	A G	
GAM2347 LOC154877 3'	GAAC TCCCGACCTCAGGTGATC 87547	A
TA	TGGATCACCTGAGGTC GGAGTTC	
	ATCTAGTGGACTCCAG CCTCAAG	
	C	
GAM2347 LOC154877 5'	GAAC TCTAGGCTCAAGTGATC 87548	C G _
C	GGATCAC TGAG TC AGGAGTTC	
	CCTAGTG ACTC GG TCCTCAAG	
	A _ A	
GAM2347 LOC154877 3'	GAAC TCTGACCTTACGTGATC 87549	C
CA	TGGATCAC TGAGGTCAGGAGTTC	
	ACCTAGTG ATTCCAGTCCTCAAG	
	C	
GAM2347 LOC154930 3'	GAAC TCTGACTTGAAATGATC 82090	CCTG
CA	TGGATCA AGGTCAGGAGTTC	
	ACCTAGT TTCAGTCCTCAAG	
	AAAG	
GAM2347 LOC157247 5'	GAAC TCTGACCTCAGGTGATC 82296	
CA	TGGATCACCTGAGGTCAGGAGTTC	
	ACCTAGTGGACTCCAGTCCTCAAG	
GAM2347 LOC157623 3'	AACTCCTGGGCTCAAGTGATCC 82405	C G
	GGATCAC TGAG TCAGGAGTT	
	CCTAGTG ACTC GGCCTCAA	
	A G	
GAM2347 LOC157867 5'	AACTCCTGGCTTCAAGCAATCC 87871	CACC
	GGAT TGAGGTCAGGAGTT	
	CCTA ACTTCGGTCCTCAA	
	ACGA	
GAM2347 LOC158310 5'	GAAC TCTGACCTTAAGTGATC 88081	C
CA	TGGATCAC TGAGGTCAGGAGTTC	
	ACCTAGTG ATTCCAGTCCTCAAG	
	A	
GAM2347 LOC158476 3'	GAAC TCTGACCCCAGGTGATC 88193	A
C	GGATCACCTG GGCAGGAGTTC	

		CCTAGTGGAC CCAGTCCTCAAG	
		C	
GAM2347	LOC158865 5'	GAACCTCCTGACCTCAAGTGAT 88307	C
		ATCAC TGAGGTCAGGAGTTC	
		TAGTG ACTCCAGTCCTCAAG	
		A	
GAM2347	LOC160646 3'	GAACCTCCTGACCTTCAGGTGAT 83111	—
	CCA	TGGATCACCTGA GGTCAGGAGTTC	
		ACCTAGTGGACT CCAGTCCTCAAG	
		T	
GAM2347	LOC162427 3'	AACTCCTGACCTCAAGTGAGCT 83217	A C
		GG TCAC TGAGGTCAGGAGTT	
		TC AGTG ACTCCAGTCCTCAA	
		G A	
GAM2347	LOC162461 5'	GAACCTCCTAGGCTCAAGTGATC 83238	C G _
	C	GGATCAC TGAG TC AGGAGTTC	
		CCTAGTG ACTC GG TCCTCAAG	
		A _ A	
GAM2347	LOC169611 3'	AACTCCTGACCTCAGGTGATCC 83627	
	A	TGGATCACCTGAGGTCAGGAGTT	
		ACCTAGTGGACTCCAGTCCTCAA	
GAM2347	LOC169611 3'	GAACCTCCTGACCTTAGGTGATC 83648	
	C	GGATCACCTGAGGTCAGGAGTTC	
		CCTAGTGGATTCCAGTCCTCAAG	
GAM2347	LOC196047 5'	AACTCCTGACCTCAGGTGATCC 91133	
	A	TGGATCACCTGAGGTCAGGAGTT	
		ACCTAGTGGACTCCAGTCCTCAA	
GAM2347	LOC196529 3'	GAACCTCCTGATCTCAGGCAATC 89132	CA
	CA	TGGAT CCTGAGGTCAGGAGTTC	
		ACCTA GGACTCTAGTCCTCAAG	
		AC	
GAM2347	LOC196957 3'	GAACCTCCTGGGCTCAAGTGATC 89187	C G
	C	GGATCAC TGAG TCAGGAGTTC	
		CCTAGTG ACTC GGTCCTCAAG	
		A G	
GAM2347	LOC196961 3'	GAACCTCCTGGGCTCAAGTGATC 89201	C G
	C	GGATCAC TGAG TCAGGAGTTC	

		CCTAGTG ACTC GGCCTCAAG	
		A G	
GAM2347	LOC197138 3'	GAACCTCCTGGGCTCAAGTGATC 89250	C G
	C	GGATCAC TGAG TCAGGAGTTC	
		CCTAGTG ACTC GGCCTCAAG	
		A G	
GAM2347	LOC197358 3'	AACTCCTGACCTCAAGTGATCC 89403	C
	A	TGGATCAC TGAGGTCAGGAGTT	
		ACCTAGTG ACTCCAGTCCTCAA	
		A	
GAM2347	LOC197358 3'	GAACCTCCTGACCTCAGGTGATC 89431	
	CA	TGGATCACCTGAGGTCAGGAGTTC	
		ACCTAGTGGACTCCAGTCCTCAAG	
GAM2347	LOC199725 5'	GAACCTCCTGACCTCGTGATC 91418	CT
		GATCAC GAGGTCAGGAGTTC	
		CTAGTG CTCCAGTCCTCAAG	
GAM2347	LOC199786 3'	AACTCCTGGACTCAAGCAATCC 89729	CACC GT
		GGAT TGAG CAGGAGTT	
		CCTA ACTC GTCCTCAA	
		ACGA AG	
GAM2347	LOC199786 3'	GAACCTCCTGACCTCATGATCC 89752	CC
		GGATCA TGAGGTCAGGAGTTC	
		CCTAGT ACTCCAGTCCTCAAG	
GAM2347	LOC199906 3'	AACTCCTGACCTCAGGCGATCC 89838	A
		GGATC CCTGAGGTCAGGAGTT	
		CCTAG GGACTCCAGTCCTCAA	
		C	
GAM2347	LOC200014 3'	GAACCTCCTGACCTCATGATCCA 89934	CC
		TGGATCA TGAGGTCAGGAGTTC	
		ACCTAGT ACTCCAGTCCTCAAG	
GAM2347	LOC200314 3'	GAACCTCCTGACCTCAGGTGATC 91599	
	CA	TGGATCACCTGAGGTCAGGAGTTC	
		ACCTAGTGGACTCCAGTCCTCAAG	
GAM2347	LOC200316 3'	GAACCTCCTGACCTCAGGTGATC 90180	
	T	GGATCACCTGAGGTCAGGAGTTC	

TCTAGTGGACTCCAGTCCTCAAG

GAM2347 LOC200339 3' GAACTCCTGGCCTCAAGCGATC 91615 ACC
CA TGGATC TGAGGTCAGGAGTTC

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ACCTAG ACTCCGGTCCTCAAG
CGA

GAM2347 LOC200407 3' AACTCCTGACCTCAGGTGATCC 91621
A TGGATCACCTGAGGTCAGGAGTT

|||||||||||
ACCTAGTGGACTCCAGTCCTCAA

GAM2347 LOC201164 3' AACTCCTGACCTCAAGTGATCC 89480 C
A TGGATCAC TGAGGTCAGGAGTT

||||| |||||||||
ACCTAGTG ACTCCAGTCCTCAA
A

GAM2347 LOC201411 3' GAACTCCAGACCTCAGGTGATC 63641 A
TA TGGATCACCTGAGGTC GGAGTTC

||||||||||| |||||
ATCTAGTGGACTCCAG CCTCAAG
A

GAM2347 LOC201510 3' AACTCCTGGTCTCAAGTGATCC 89627 C GT
GGATCAC TGAG CAGGAGTT

||||| ||| |||||
CCTAGTG ACTC GTCCTCAA
A TG

GAM2347 LOC201626 3' GAACTCCTGACCTCAGGTGATC 90432
CA TGGATCACCTGAGGTCAGGAGTTC

|||||||||||
ACCTAGTGGACTCCAGTCCTCAAG

GAM2347 LOC201627 3' AACTCCCGACCTCAGGTGATCC 90442 A
GGATCACCTGAGGTC GGAGTT

||||||||||| |||||
CCTAGTGGACTCCAG CCTCAA
C

GAM2347 LOC203197 3' ACTCCTGACCTCAGGTGATCCA 90799
TGGATCACCTGAGGTCAGGAGT

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ACCTAGTGGACTCCAGTCCTCA

GAM2347 LOC203197 3' GAACTCCTGACCTCAGGTGATC 90811
CA TGGATCACCTGAGGTCAGGAGTTC

|||||||||||
ACCTAGTGGACTCCAGTCCTCAAG

GAM2347 LOC203378 3' AACTCCTCCACTCAGGTGATCC 92267 GTC
A TGGATCACCTGAG AGGAGTT

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	ACCTAGTGGACTC TCCTCAA		
	ACC		
GAM2347 LOC204804 3'	GAACCTCCTGGCCTCAGGTGATC 91042		
CA	TGGATCACCTGAGGTCAGGAGTTC		
	ACCTAGTGGACTCCGGTCCTCAAG		
GAM2347 LOC219529 5'	AACTCCTGAGCCCAGGTGATCC 94560	A	_
	GGATCACCTG GG TCAGGAGTT		
	CCTAGTGGAC CC AGTCCTCAA		
	_ G		
GAM2347 LOC219673 5'	AACGCCTGACCTCAAGTAATCC 94603	C	C A
A	TGGAT AC TGAGGTCAGG GTT		
	ACCTA TG ACTCCAGTCC CAA		
	A A G		
GAM2347 LOC219673 5'	GAACCTCCTGGGCTCAAGTGATC 94624	C	G
C	GGATCAC TGAG TCAGGAGTTC		
	CCTAGTG ACTC GGTCCTCAAG		
	A G		
GAM2347 LOC220074 3'	AACTCCTGACCTCAGGTGATCT 59949		
	GGATCACCTGAGGTCAGGAGTT		
	TCTAGTGGACTCCAGTCCTCAA		
GAM2347 LOC220074 3'	GAACCTCCTGACCTCAGGTGATC 59977		
C	GGATCACCTGAGGTCAGGAGTTC		
	CCTAGTGGACTCCAGTCCTCAAG		
GAM2347 LOC220662 3'	GAACCTCCTGGACTCAAGCAATC 92818	CACC	GT
C	GGAT TGAG CAGGAGTTC		
	CCTA ACTC GTCCTCAAG		
	ACGA AG		
GAM2347 LOC221060 3'	GAACCTCCTGACCTCAGGTGATC 94831		
C	GGATCACCTGAGGTCAGGAGTTC		
	CCTAGTGGACTCCAGTCCTCAAG		
GAM2347 LOC221964 3'	GAACCTCCTGACCTCAGGTGATC 95605		
CA	TGGATCACCTGAGGTCAGGAGTTC		
	ACCTAGTGGACTCCAGTCCTCAAG		
GAM2347 LOC222031 3'	GAACCTCCTGACCTCAGGTGATC 95680		
CA	TGGATCACCTGAGGTCAGGAGTTC		

ACCTAGTGGACTCCAGTCCTCAAG

GAM2347 LOC222068 3' GACTCCTGACCTCAGTTGATCC 94275 C
A TGGATCA CTGAGGTCAGGAGTT
||||| |||||||||
ACCTAGT GACTCCAGTCCTCAG
T

GAM2347 LOC222070 5' GAACTCCTGGCCTCAAGTGACC 95814 A C
C GG TCAC TGAGGTCAGGAGTTC
|| ||| |||||||||
CC AGTG ACTCCGGTCCTCAAG
C A

GAM2347 LOC245771 5' GAACTCCTGACCTCAAGTGATC 94473 C
CA TGGATCAC TGAGGTCAGGAGTTC
||||| |||||||||
ACCTAGTG ACTCCAGTCCTCAAG
A

GAM2347 LOC253805 3' GAACTCCTGACCTCAGATGATT 98174 C
CA TGGATCA CTGAGGTCAGGAGTTC
||||| |||||||||
ACTTAGT GACTCCAGTCCTCAAG
A

GAM2347 LOC253981 3' GAACTCCTGACCTCAGGCGATC 97536 A
TA TGGATC CCTGAGGTCAGGAGTTC
||||| |||||||||
ATCTAG GGA CTCCAGTCCTCAAG
C

GAM2347 LOC254268 3' AACTCCTGACCTCAAGTGATCC 97133 C
GGATCAC TGAGGTCAGGAGTT
||||| |||||||||
CCTAGTG ACTCCAGTCCTCAA
A

GAM2347 LOC254351 5' AGCTCCTGACCTCGGGTGATCC 96681
A TGGATCACCTGAGGTCAGGAGTT
||||| |||||||||
ACCTAGTGGGCTCCAGTCCTCGA

GAM2347 LOC254532 5' AACTCCTGACCTCAAGTGATCC 98441 C
A TGGATCAC TGAGGTCAGGAGTT
||||| |||||||||
ACCTAGTG ACTCCAGTCCTCAA
A

GAM2347 LOC254655 3' GAACTCCTGACCTCAGGTGATC 97219
CA TGGATCACCTGAGGTCAGGAGTTC
||||| |||||||||
ACCTAGTGGACTCCAGTCCTCAAG

GAM2347 LOC254672 3' GAACTCCTGACCCTGTGATCCA 96294 CTGA
TGGATCAC GGT CAGGAGTTC
||||| |||||||||

		ACCTAGTG CCAGTCCTCAAG		
		TC__		
GAM2347	LOC254778 3'	AACTCCTGGGTTCAAGAGATCC 97825	ACC	G
	A	TGGATC TGAG TCAGGAGTT		
		ACCTAG ACTT GGTCTCAA		
		AGA G		
GAM2347	LOC255065 5'	AACTCCTGACCTCAAGTAATCC 98367	C	C
	A	TGGAT AC TGAGGTCAGGAGTT		
		ACCTA TG ACTCCAGTCCTCAA		
		A A		
GAM2347	LOC255065 5'	CCTGACCTCAAGTAATCCA 98370	C	C
		TGGAT AC TGAGGTCAGG		
		ACCTA TG ACTCCAGTCC		
		A A		
GAM2347	LOC255458 5'	AACTCCTGGGCTCAAGCGATCC 98930	ACC	G
		GGATC TGAG TCAGGAGTT		
		CCTAG ACTC GGTCTCAA		
		CGA G		
GAM2347	LOC255497 3'	AACTCCTGACCTCAGGTG 98978		
		CACCTGAGGTCAGGAGTT		
		GTGGACTCCAGTCCTCAA		
GAM2347	LOC255707 3'	TCTTGAAGTCAAGTGATCCA 98733	C	G
		TGGATCAC TGAG TCAGGA		
		ACCTAGTG ACTC AGTTCT		
		A A		
GAM2347	LOC256306 3'	GAACACCTGACCTCAAATGATC 98514	CC	A
	C	GGATCA TGAGGTCAGG GTTC		
		CCTAGT ACTCCAGTCC CAAG		
		AA A		
GAM2347	LOC256364 5'	AACTCCTGGCCTCAGGTGACCC 96440	A	
		GG TCACCTGAGGTCAGGAGTT		
		CC AGTGGACTCCGGTCCTCAA		
		C		
GAM2347	LOC257127 5'	GAACCTGACCTCAGGTGATC 98496		
	C	GGATCACCTGAGGTCAGGAGTTC		
		CCTAGTGGACTCCAGTCCTCAAG		
GAM2347	LOC257465 3'	GAACCTGACCTTGGTGATCC 82495	T	
	A	TGGATCAC GAGGTCAGGAGTTC		

ACCTAGTGG TTCCAGTCCTCAAG

GAM2347 LOC51008 5' GAACTCCCGACCTCAGGTGATC 32532 A
CA TGGATCACCTGAGGTC GGAGTTC

|||||
ACCTAGTGGACTCCAG CCTCAAG
C

GAM2347 LOC51193 3' AACTCCTGGACTCAAGCAATCC 33352 CACC GT
GGAT TGAG CAGGAGTT

|||| |||
CCTA ACTC GTCCTCAA
ACGA AG

GAM2347 LOC51200 3' AACTCCCAACCTCAGGTGATCT 33430 CA
GGATCACCTGAGGT GGAGTT

|||||
TCTAGTGGACTCCA CCTCAA
AC

GAM2347 LOC51219 5' GAACTCCCGACCTCAGGTGATC 33544 A
T GGATCACCTGAGGTC GGAGTTC

|||||
TCTAGTGGACTCCAG CCTCAAG
C

GAM2347 LOC57107 3' GAACTCCTGACCTCAGGTGATC 40187
C GGATCACCTGAGGTCAGGAGTTC

|||||
CCTAGTGGACTCCAGTCCTCAAG

GAM2347 LOC57146 3' AACTCCTGACCTCAGGTGCTCC 40285 T
A TGGA CACCTGAGGTCAGGAGTT

||||
ACCT GTGGACTCCAGTCCTCAA
C

GAM2347 LOC89231 3' GAACTCCTGGACTCAAGCAATC 94298 CACC GT
C GGAT TGAG CAGGAGTTC

|||| |||
CCTA ACTC GTCCTCAAG
ACGA AG

GAM2347 LOC89932 3' GAACTCCCGACCTCAGGTAATC 61459 C A
C GGAT ACCTGAGGTC GGAGTTC

||||
CCTA TGGACTCCAG CCTCAAG
A C

GAM2347 LOC90072 3' GAACTCCCGACCTCAAGTGATC 61958 C A
C GGATCAC TGAGGTC GGAGTTC

||||
CCTAGTG ACTCCAG CCTCAAG
A C

GAM2347 LOC90110 5' GAACTTCTGACCTCAAGTGGTC 62178 C
CA TGGATCAC TGAGGTCAGGAGTTC

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		ACCTGGTG ACTCCAGTCTTCAAG		
		A		
GAM2347	LOC90288 3'	GAACTACTGACCTCAGCTGATC 62788	C	G
	CA	TGGATCA CTGAGGTCAG AGTTC		
		ACCTAGT GACTCCAGTC TCAAG		
		C A		
GAM2347	LOC90408 5'	GAACTCCTGACTTCAAGTGATC 63344	C	
	CA	TGGATCAC TGAGGTCAGGAGTTC		
		ACCTAGTG ACTTCAGTCCTCAAG		
		A		
GAM2347	LOC90459 3'	GAACTCCTGACCTCAAGTGATT 63555	C	
	T	GGATCAC TGAGGTCAGGAGTTC		
		TTTAGTG ACTCCAGTCCTCAAG		
		A		
GAM2347	LOC90591 3'	GAACTCCTGACCTCAGGTGATC 64166		
	CA	TGGATCACCTGAGGTCAGGAGTTC		
		ACCTAGTGGACTCCAGTCCTCAAG		
GAM2347	LOC90591 3'	GAACTCCTGACCTGAAGTGATC 64167	CTG	
	CA	TGGATCAC AGGTCAGGAGTTC		
		ACCTAGTG TCCAGTCCTCAAG		
		AAG		
GAM2347	LOC91115 3'	AACTCCTGACCTCAGATGGTCC 65532	C	
	A	TGGATCA CTGAGGTCAGGAGTT		
		ACCTGGT GACTCCAGTCCTCAA		
		A		
GAM2347	LOC91547 3'	GAACTCCTGGGCTCAAGTGATC 67002	C G	
	C	GGATCAC TGAG TCAGGAGTTC		
		CCTAGTG ACTC GGTCCTCAAG		
		A G		
GAM2347	LOC91561 5'	GAACTCCTGACCTCAGGTGATC 67043		
	T	GGATCACCTGAGGTCAGGAGTTC		
		TCTAGTGGACTCCAGTCCTCAAG		
GAM2347	LOC92267 3'	AACTCCTGACCTCAAGTGATCC 69159	C	
		GGATCAC TGAGGTCAGGAGTT		
		CCTAGTG ACTCCAGTCCTCAA		
		A		
GAM2347	LOC92303 3'	GAATTCCAGACCTCAGGTGATC 69391	A	
	CA	TGGATCACCTGAGGTC GGAGTTC		

		ACCTAGTGGACTCCAG CCTTAAG	
		A	
GAM2347	LOC92697 5'	GAAGTCCCAACCTCAGGTGATC 70810	CA
	C	GGATCACCTGAGGT GGAGTTC	
		CCTAGTGGACTCCA CCTCAAG	
		AC	
GAM2347	LOC92841 3'	GAAGTCCCTGACCTCAAGTGATC 71252	C
	C	GGATCAC TGAGGTCAGGAGTTC	
		CCTAGTG ACTCCAGTCCTCAAG	
		A	
GAM2347	LOC92876 5'	GACTCCTGACCTCAGGTGATCC 71349	
	A	TGGATCACCTGAGGTCAGGAGTT	
		ACCTAGTGGACTCCAGTCCTCAG	
GAM2347	LOC93408 5'	AACTCCTGGCCTCAAGTGATCC 57281	C
		GGATCAC TGAGGTCAGGAGTT	
		CCTAGTG ACTCCGGTCCTCAA	
		A	
GAM2348	AP1G1 3'	AACCTCCCTTTTTATTTCTTGA 8518	TGTCACAAA
	G	TTCAAGAAAT AGGTT	
		GAGTTCTTTA TCCAA	
		TTTTTCCC_	
GAM2348	EFNA3 3'	AACCCCTGACCTTTCTTGA 18248	TT CAAAA
		TCAAGAAA GTCA GGTT	
		AGTTCTTT CAGT CCAA	
		C_ CCC_	
GAM2348	IL13RA1 3'	TTGTGACAACCTTCCTGAG 9577	A A
		TTCA GAA TTGTCACAA	
		GAGT CTT AACAGTGTT	
		C C	
GAM2348	RAB18 3'	AACCTTTTTCTAGTTCTTGAA 41449	ATTGTCAC
		TTCAAGAA AAAAGGTT	
		AAGTTCTT TTTTCCAA	
		GATCT__	
GAM2348	FLJ22357 3'	AACCTTCTAACTTGTTTCTTGA 42619	TGTCACAA
		TCAAGAAAT AAGGTT	
		AGTTCTTTG TTCCAA	
		TTCAATC_	
GAM2348	HSPC019 3'	AACCTCCCTGACAATTTT 26714	CAAA
		AGAAATTGTCA AGGTT	

TTTTAAACAGT TCCAA
 CCC_
 GAM2348 KIAA0826 3' AACCTTTCAAATGTTACCTTCT 83523 ATT C ____
 TGAA TTCAAGAA GT ACA AAAGGTT
 ||||| || ||| |||||
 AAGTTCTT CA TGT TTTCCAA
 C__ T AAAC
 GAM2348 NYD-SP11 3' ACCTCCTACAGTTTCTGAA 50053 A CACAAA
 TTCA GAAATTGT AGGT
 ||| ||||| |||
 AAGT CTTTGACA TCCA
 _ TCC__
 GAM2348 LOC134265 3' AACCTTTTACAAACACTTGA 75649 AAA CAC
 TCAAG TTGT AAAAGGTT
 |||| ||| |||||
 AGTTC AACA TTTTCCAA
 ACA ____
 GAM2348 LOC143524 3' AACCTTTTGTGAGGAGCTGAA 77092 AGAAA G
 TTCA TT TCACAAAAGGTT
 ||| || |||||
 AAGT AG AGTGTTTCCAA
 CG__ G
 GAM2348 LOC219940 3' AACCTCGTTTCCATTTCTTGAA 94998 TGTC AAA
 TTCAAGAAAT AC AGGTT
 ||||| || |||||
 AAGTTCTTTA TG TCCAA
 CCTT C__
 GAM2348 LOC257457 3' AACCTTTTGACTGTTTTTT 63314 T CA
 AAGAAAT GTCA AAAGGTT
 ||||| ||| |||||
 TTTTTTG CAGT TTTCCAA
 T ____
 GAM2349 HRH1 3' CTCAAACATGTTTAGAGTGGA 7819 A TGG
 TCCA TCTGA GCATGTTTGAG
 ||| |||| |||||
 AGGT AGATT TGTACAACTC
 G ____
 GAM2349 TRIM37 3' CTCAAATTTGTCATCAG 31625 G T
 CTGATGG CA GTTTGAG
 ||||| || |||||
 GACTACT GT TAAACTC
 _ T
 GAM2349 HTMP10 3' CTCAAAAAAGCCATCAGATCTG 53758 CA G ATG
 A TC ATCTGATGG C TTTGAG
 || ||||| | |||||
 AG TAGACTACC G AA ACTC
 TC _ AAA
 GAM2349 PAK2 5' CTCAAATATCACCAAACTAGA 67140 A__ GC
 TCTG TGG ATGTTTGAG
 ||| || |||||

		AGAT ACC TATAAACTC		
		CAA AC		
GAM2349	SEMA6A	3' CTCGAGTACCCACCAGA	40818	A CA
		TCTG TGGG TGTTTGAG		
		AGAC ACCC ATGAGCTC		
		C _		
GAM2349	TTY7	3' TCAAACATGCAGGCTGGA	50019	AT GATGG
		TCCA CT GCATGTTTGA		
		AGGT GA CGTACAACT		
		CG _		
GAM2349	LOC144766	3' CTCAAACATGAGAAGACTGGG	77481	A GATGGG
		TCCA TCT CATGTTTGAG		
		GGGT AGA GTACAAACTC		
		C AGA_		
GAM2349	LOC201685	5' TAAACACCCATCAGATGGA	91845	A CA
		TCCA TCTGATGGG TGTTTG		
		AGGT AGACTACCC ACAAAT		
		_ _		
GAM2349	LOC221596	5' CTCAAACAAAACTCAGATT	93623	TG GCA
		AATCTGA G TGTTTGAG		
		TTAGACT C ACAAACCTC		
		_ AAA		
GAM2349	LOC93622	3' CTCTGCAGACCATCAGAT	57729	GCA TT
		ATCTGATGG TGT GAG		
		TAGACTACC ACG CTC		
		AG_ T_		
GAM2350	CCND2	3' CATGCGGGTCCATAACAGCCAA	10046	AGCCAT_ TT
		TTGGC GATCT GCATG		
		AACCG CTGGG CGTAC		
		ACAATAC _		
GAM2350	FGFR1	3' CATGCAGTGCCGGCTGCCAA	7019	ATGATCT
		TTGGCAGCC TTGCATG		
		AACCGTCGG GACGTAC		
		CCGT_		
GAM2350	FUT3	3' GCTGGGCTTACGGCTGCCAG	5624	A T_ TT
		TTGGCAGCC TGA CT GC		
		GACCGTCGG ACT GG CG		
		C TC GT		
GAM2350	PLN	5' TGTGATGATCACAGCTGCCAA	12174	CA TTG
		TTGGCAGC TGATC T CA		

		AACCGTCG ACTAG A GT	
		AC T GT	
GAM2350 PVR	3'	CATGCAAGAAGTACTGCCAA 22490	CC GA T
		TTGGCAG AT TCTT GCATG	
		AACCGTC TG AGAA CGTAC	
		A_ A_ _	
GAM2350 CTAGE-1	3'	CATGCAAGCTGGGCCACCAA 42960	CA ATGATC
		TTGG GCC TTTGCATG	
		AACC CGG GAACGTAC	
		AC GTC__	
GAM2350 FLJ12488	3'	TATGCAGACCTGACTGCCAA 49159	C TGATC
		TTGGCAG CA TTTGCATG	
		AACCGTC GT AGACGTAT	
		A CC__	
GAM2350 HN1L	3'	TGGAGATCACGGCTGCTAA 58622	A TT
		TTGGCAGCC TGATCT G	
		AATCGTCGG ACTAGA T	
		C GG	
GAM2350 KIAA1643	3'	TGTTTGAGGTCATGGCCACCAA 65159	CA T_
		TTGG GCCATGATCTT GCA	
		AACC CGGTACTGGAG TGT	
		AC TT	
GAM2350 MGC13071	3'	GAAGAAAACATGGCTGCCAA 52065	A__
		TTGGCAGCCATG TCTTT	
		AACCGTCGGTAC AGAAG	
		AAA	
GAM2350 SLC26A9	3'	TATGCCATCTGGCTGCCAA 54720	T CTTT
		TTGGCAGCCA GAT GCATG	
		AACCGTCGGT CTA CGTAT	
		_ C__	
GAM2350 SLC26A9	3'	TATGCCATCTGGCTGCCAA 54721	T CTTT
		TTGGCAGCCA GAT GCATG	
		AACCGTCGGT CTA CGTAT	
		_ C__	
GAM2350 TADA3L	5'	CGGAGATCTCGGCCGCCAA 22038	A AT
		TTGGC GCC GATCTTTG	
		AACCG CGG CTAGAGGC	
		C CT	
GAM2350 LOC221416	3'	AGGACCACTGGCTGCCAA 95403	_ A
		TTGGCAGCCA TG TCTT	

		AACCGTCGGT AC AGGA	
		C C	
GAM2351 AGL	5'	AAAGACCCTCTTCAGACTTGA 7210	CG A_
		TCAAGTCT GGAG TCTTT	
		AGTTCAGA TCTC AGAAA	
		CT CC	
GAM2351 PDYN	3'	AAAGATCTCCTGTGCACCTGA 44580	A CT_
		TCA GT CGGGAGATCTTT	
		AGT CA GTCCTCTAGAAA	
		C CGT	
GAM2351 PRKCQ	3'	GAAAGGTTTCAAGACTTGATA 21817	CGG
		TATCAAGTCT GAGATCTTTC	
		ATAGTTCAGA CTTTGAAAG	
		A_	
GAM2351 DNAJA2	3'	GAAAGGTTTCTGAAACTCGATA 60488	A C G
		TATC AGT TCGG AGATCTTTC	
		ATAG TCA AGTC TTTGAAAG	
		C A _	
GAM2351 FLJ14124	5'	GAAAGATTCTTAAAACT 46356	CTC
		AGT GGGAGATCTTTC	
		TCA TTCTTTAGAAAG	
		AAA	
GAM2351 MGC15606	3'	AAAGATCTGGACTTAATA 59515	C CGGG
		TAT AAGTCT AGATCTTT	
		ATA TTCAGG TCTAGAAA	
		A _	
GAM2351 TNKS2	3'	GAAAGATCTTTACTCACTT 48219	CTCG
		AAGT GGAGATCTTTC	
		TTCA TTTCTAGAAAG	
		CTCA	
GAM2351 LOC151826	3'	AAAGATCTCATAACTTTATA 81170	C CTCGG
		TAT AAGT GAGATCTTT	
		ATA TTCA CTCTAGAAA	
		T ATA_	
GAM2351 LOC157567	3'	AAAGAATATGAAGGCTTGATA 82389	_ GGAGA
		TATCAAGTCT CG TCTTT	
		ATAGTTCGGA GT AGAAA	
		A ATA_	
GAM2351 LOC90190	3'	GAAAGAGGGAAGACTTGAT 62423	CGGGAGA
		ATCAAGTCT TCTTTC	

			TAGTTCAGA	AGAAAG	
			AGGG__		
GAM2351	LOC90643	3'	AAAGATCCTAATGCACTTGATG	64436	CTCG_ A
			TATCAAGT	GG GATCTTT	
			GTAGTTCA	TC CTAGAAA	
			CGTAA _		
GAM2352	ARL4	3'	TTCTCTGGTCTGATTTTG	20415	AATAT
			TAAAATCA	CCAGAGAA	
			GTTTTAGT	GGTCTCTT	
			CT__		
GAM2352	CYP3A4	3'	TTCTCTGGAGTATTCTATAA	34368	A CAAATA
			TTATA AAT	TCCAGAGAA	
			AATAT TTA	AGGTCTCTT	
			C TG__		
GAM2352	PRKWNK3	3'	TCTTTGATACTTGATTTTTTAA	62240	T A C
			TTA AAAATCAA	TATC AGAGA	
			AAT TTTTAGTT	ATAG TTTCT	
			T C _		
GAM2352	TEM7	3'	CTCTGAACTGGATTTTATAG	40257	AAATATC
			TTATAAAATC	CAGAG	
			GATATTTTAG	GTCTC	
			GTCAA__		
GAM2352	ENDO180	3'	TTCTCTGTAGTTGATTTTTTAA	21270	T ATATC
			TTA AAAATCAA	CAGAGAA	
			AAT TTTTAGTT	GTCTCTT	
			T GAT__		
GAM2352	FLJ12331	3'	TCTCTGGATGGCTTTTA	47115	TCAAA
			TAAAA	TATCCAGAGA	
			ATTTT	GTAGGTCTCT	
			CG__		
GAM2352	FLJ13110	3'	CTCTGAAGGTGATTTTGTA	43586	AATATC
			TTATAAAATCA	CAGAG	
			AATGTTTTAGT	GTCTC	
			GGAA__		
GAM2352	FLJ32332	3'	TTCTCTGGCAGAGTGACTTTA	58947	A AATAT
			TAAA TCA	CCAGAGAA	
			ATTT AGT	GGTCTCTT	
			C GAGAC		
GAM2352	KIAA0861	3'	TTCTGGTTATTTAATTTTATAG	90361	C T
			TTATAAAAT	AAATA CCAGAG	

		GATATTTTA TTTAT GGTCTT		
		A T		
GAM2352	KIAA1615	3' TCCGGTTATTTGATTTTATAA 69288	_	T A
		TTATAAAA TCAAATA CC GA		
		AATATTTT AGTTTAT GG CT		
		T T C		
GAM2352	KIAA1829	3' GGATATTTATTTTATAA 62649	TC	
		TTATAAAA AAATATCC		
		AATATTTT TTTATAGG		
		TA		
GAM2352	MGC19556	3' TCCTGGTGATTGATTTTA 54344	A T	A
		TAAAATCAA TA CCAG GA		
		ATTTTAGTT GT GGTC CT		
		A _ _		
GAM2352	TPD52	3' CTCTGTATATTTGATTCTTA 18670	_	C
		TAA AATCAAATAT CAGAG		
		ATT TTAGTTTATA GTCTC		
		C T		
GAM2352	LOC149332	3' TTGGGTGATCCTGATTTTATAA 85551	AA__	
		TTATAAAATCA TATCCAG		
		AATATTTTAGT GTGGGT		
		CCTA		
GAM2352	LOC149837	5' TCTCTGGAAGGATTTTATGA 85907	AAATA	
		TTATAAAATC TCCAGAGA		
		AGTATTTTAG AGGTCTCT		
		GA__		
GAM2352	LOC158337	3' TCTCTGGATCTTTTATGA 88113	TCAAAT	
		TTATAAAA ATCCAGAGA		
		AGTATTTT TAGGTCTCT		
		C__		
GAM2353	EAT2	3' TAAATGATTTTGTGAGCTA 80055	A	C
		TAGCT ATAAAATCA TTA		
		ATCGA TGTTTTAGT AAT		
		C A		
GAM2353	KIAA0534	3' AATCAAGTAATTTTATTAGCT 71927	C	A
		AGCTAATAAAAT ACTT ATT		
		TCGATTATTTTA TGAA TAA		
		A C		
GAM2353	KIAA1524	3' TGATTGATTTTATTGCTA 73840	T	C
		TAGC AATAAAATCA TTA		

ATCG TTATTTTAGT AGT
 _ T
 GAM2353 YAP1 3' TGAATTAAAGTGGCACCAGCTA 21466 AATAAAA _
 TAGCT TCACTT AATTCA
 |||| |||| ||||
 ATCGA GGTGAA TTAAGT
 CCAC__ A
 GAM2353 LOC155038 3' TGAATGATTTTATTGCTA 82185 T C
 TAGC AATAAAATCA TTA
 ||| ||||| |||
 ATCG TTATTTTAGT AGT
 _ A
 GAM2353 LOC257319 3' TGAATTAAGTGATGCTTTAACT 97475 C TAAA
 AG TAA ATCACTTAATTCA
 || ||| |||||
 TC ATT TAGTGAATTAAGT
 A TCG_
 GAM2354 CAPN2 3' CCCATGCAATCACACCATGC 10011 GA GG C A
 GCA GTGTGA GCA TG GG
 ||| ||||| ||| ||
 CGT CACACT CGT AC CC
 AC AA _ _
 GAM2354 FZD1 3' CCTCTTGCCCTCACACTCTGGT 14498 G CT
 A TA CAGAGTGTGAGGGCA GAGG
 || ||||| ||||
 AT GTCTCACACTCCCGT CTCC
 G T_
 GAM2354 IRS2 3' CCCAGTGCCTATCTTCTCTG 60439 TGT _ A
 CAGAG GA GGGCACTG GG
 |||| || ||||| ||
 GTCTC CT TCCGTGAC CC
 TT_ A _
 GAM2354 LDB1 5' CCGTCAGCCCTCACCCCTGC 15309 AGT AC _
 GCAG GTGAGGGC TGA GG
 |||| ||||| ||| ||
 CGTC CACTCCCG ACT CC
 CC_ _ G
 GAM2354 LRP4 3' CCCAGTACCCTCAGTGCCTGCT 65061 A _ C A
 AGCAG GTG TGAGGG ACTG GG
 |||| ||| ||||| ||| ||
 TCGTC CGT ACTCCC TGAC CC
 _ G A _
 GAM2354 PTMS 3' CTCCACCCTCACTCTGC 12563 GT CACT
 GCAGAGT GAGGG GAG
 ||||| |||| |||
 CGTCTCA CTCCC CTC
 _ AC_
 GAM2354 SLC14A2 5' GTGCCACCACACCCTGCTA 24125 A AG
 TAGCAG GTGTG GGCAC
 ||||| |||| ||||

ATCGTC CACAC CCGTG
 C CA
 GAM2354 TEAD3 3' CCCAGCACACACACTCCCTGC 13668 AGG AC A
 GCA GAGTGTG GC TG GG
 ||| ||||| || ||
 CGT CTCACAC CG AC CC
 CC ACA _ _
 GAM2354 C17orf31 3' CCTGGGTCCCTCACACTTCGC 34537 AG C G
 GC AGTGTGAGGG ACT AGG
 || ||||| || ||
 CG TCACACTCCC TGG TCC
 CT _ G
 GAM2354 DDX33 3' CCTCAGTGCGTGACCCTGT 39785 A GTGAGG
 GCAG GT GCACTGAGG
 ||| || |||||
 TGTC CA CGTGA CTCC
 C GTG _
 GAM2354 DKFZP434J037 3' CCACAACCCCCACACTCCACT 48942 CA A CAC A
 AG GAGTGTG GGG TG GG
 || ||||| || ||
 TC CTCACAC CCC AC CC
 AC _ CCA A
 GAM2354 DNAJC5 3' CCCAGCACCCCTGCCTGCT 62134 AGT GA CA A
 AGCAG GT GGG CTG GG
 |||| || || ||
 TCGTC CG CCC GAC CC
 _ TC AC _
 GAM2354 FLJ12891 3' CCCAGAAGGTCATACTCTGC 46922 GGGCA A
 GCAGAGTGTGA CTG GG
 ||||| || ||
 CGTCTCATACT GAC CC
 GGAA _ _
 GAM2354 FLJ13187 3' CCCACTCCTCACACTCTTCTA 45163 C CAC A
 TAG AGAGTGTGAGGG TG GG
 ||| ||||| || ||
 ATC TCTCACACTCCT AC CC
 T C _ _
 GAM2354 FLJ22029 3' CTCAGTGCGAGCTCTGC 46908 GTGAGG
 GCAGAGT GCACTGAG
 ||||| |||||
 CGTCTCG CGTGA CTCC
 A _
 GAM2354 H-L(3)MBT 3' CCAGCGTCACTTCTGCTA 50401 T AGG A A
 TAGCAGAG GTG GC CTG G
 ||||| || || ||
 ATCGTCTT CAC TG GAC C
 _ _ C _
 GAM2354 KIAA0607 3' CCCAGTGATTACACTCCACTG 72953 CA GGG A
 TAG GAGTGTGA CACTG GG
 ||| ||||| || ||

GTC CTCACATT GTGAC CC
 AC A__ _
 GAM2354 KIAA1297 5' CTCAGTGCCCCGCCCCACTG 72638 AGT A
 CAG GTG GGGCACTGAG
 ||| ||| |||||
 GTC CGC CCCGTGACTC
 ACC _
 GAM2354 MGC3035 5' CCCAGAGGAGCCACACTCTG 44396 GAG A__ A
 CAGAGTGT GGC CTG GG
 ||||| ||| |||
 GTCTCACA CCG GAC CC
 _ AGGA _
 GAM2354 MRPL37 3' CCTCAGTGCCCGTTTGGCCTGC 66841 A GTGA_
 TG TAGCAG GT GGGCACTGAGG
 ||||| ||| |||||
 GTCGTC CG CCCGTGACTCC
 _ GTTTG
 GAM2354 NDRG4 3' CCTTCCAGCCCACACTCTGC 40378 GA ACT
 GCAGAGTGT GGGC GAGG
 ||||| ||| |||
 CGTCTCACA CCG TTCC
 _ ACC
 GAM2354 NDRG4 3' CCTTCCAGCCCACACTCTGC 43577 GA ACT
 GCAGAGTGT GGGC GAGG
 ||||| ||| |||
 CGTCTCACA CCG TTCC
 _ ACC
 GAM2354 PP591 5' CCCAGTGCCCTGTAGACCTGGC 48146 _ A G _ A
 GC AG GT TG AGGGCACTG GG
 || ||| ||| ||||| ||
 CG TC CA AT TCCCGTGAC CC
 G _ G G _
 GAM2354 PPI5PIV 3' CCCAACACCCCGTGCTCTGC 39583 TG A CAC A
 GCAGAG TG GGG TG GG
 ||||| ||| |||
 CGTCTC GC CCC AC CC
 GT C ACA _
 GAM2354 SDC3 3' CCCAAATACACCCACACTCTGG 28464 _ A GCAC__ A
 C GC AGAGTGTG GG TG GG
 || ||||| || |||
 CG TCTCACAC CC AC CC
 G _ ACATAA _
 GAM2354 LOC129195 5' CCCAATGCCCTCACCTGC 76316 AGT C A
 GCAG GTGAGGGCA TG GG
 ||| ||||| ||| |||
 CGTC CACTCCCGT AC CC
 _ A _
 GAM2354 LOC129195 5' CCCAATGCCCTCACCTGC 76317 AGT C A
 GCAG GTGAGGGCA TG GG
 ||| ||||| ||| |||

		CGTC CACTCCCGT AC CC		
		_____ A _		
GAM2354	LOC129195 5'	CCCAATGCCCTCACCTGC 76318	AGT	C A
		GCAG GTGAGGGCA TG GG		
		CGTC CACTCCCGT AC CC		
		_____ A _		
GAM2354	LOC153205 3'	CCCACCCCTTCTCACACTCTGC 87154		CAC A
		GCAGAGTGTGAGGG TG GG		
		CGTCTCACACTCTT AC CC		
		CCC _		
GAM2354	LOC153328 3'	CCAATGCCCACTCTGCTA 81676	GTGA	C A
		TAGCAGAGT GGGCA TG G		
		ATCGTCTCA CCCGT AC C		
		_____ A _		
GAM2354	LOC204845 5'	CCTCAGTGCCAGTGTCTCTGC 91063	TG AG	
		GCAGAG TG GGCAGT GAGG		
		CGTCTC GT CCGT GACTCC		
		CT GA		
GAM2354	LOC222031 3'	CTCAGCACTCACACTGC 95678	GA	GGCA
		GCA GTGTGAG CTGAG		
		CGT CAACTC GACTC		
		_____ AC _		
GAM2354	LOC257357 5'	CCTCTCCAACCTCACATCCTAC 97340	C AG	GCACT
	TA	TAG AG TGTGAGG GAGG		
		ATC TC ACACTCC CTCC		
		A CT AACCT		
GAM2355	ACATN 5'	GACTGGCTCCCGGCTTCAG 17596	AGTG	CA A
		TTGAAGCC GGG CCA TC		
		GACTTCGG CCC GGT AG		
		_____ TC C		
GAM2355	B3GALT2 3'	GTGTCTCAGGCTCAA 15032	A AG	
		TTGA GCC TGGGGCAC		
		AACT CGG ACTCTGTG		

GAM2355	CD164 3'	GGACTAGTGCAGAGGCTTTAA 21197	AGTGGG	CAA
		TTGAAGCC GCAC TCC		
		AATTTCGG CGTG AGG		
		AGA _ ATC		
GAM2355	DRG2 3'	TGGTTAGTGGCTTCAA 9131	G	GGGC
		TTGAAGCCA TG ACCA		

AACTTCGGT AT TGGT
 G ____
 GAM2355 HPS4 3' ATTGGTGCCACAAGCTTC 42226 CAG G
 GAAGC TG GGCACCAAT
 |||| | |||||
 CTTCG AC CCGTGGTTA
 A__ A
 GAM2355 SDPR 5' GACTGGTGCCCTGAGCTCCAA 17400 A CAG A
 TTG AGC TGGGGCACCA TC
 ||| ||| ||||| ||
 AAC TCG GTCCCGTGGT AG
 C A__ C
 GAM2355 C5orf6 3' GATTGGCTGTGCCAGCTTC 33954 CAG G _
 GAAGC TGG GCA CCAATC
 |||| ||| ||| |||||
 CTTCG ACC TGT GGTTAG
 ____ G C
 GAM2355 C8orf17 3' GGACCACACTGGCTGCAA 39998 A G CA
 TTG AGCCAGTG GG CC
 ||| ||||| || ||
 AAC TCGGTCAC CC GG
 G A A_
 GAM2355 CABP5 5' GACTGGTGCCCTGCGAGCTCCA 39562 A CA TG A
 TG AGC G GGGCACCA TC
 || ||| | ||||| ||
 AC TCG C CCCGTGGT AG
 C AG GT C
 GAM2355 FLJ13940 3' GGAAGTGGTGCCCCACAGGCTTT 47309 A A
 AA TTGAAGCC GTGGGGCACCA TCC
 ||||| ||||| |||
 AATTCGG CACCCCGTGGT AGG
 A C
 GAM2355 KCNMB2 3' ATTGGTGGACTGGTTTCAA 20684 GGGG
 TTGAAGCCAGT CACCAAT
 ||||| |||||
 AACTTTGGTCA GTGGTTA
 G_
 GAM2355 KIAA0530 3' GATTGGTGTATAGCTTTAA 71431 CAGTGGG
 TTGAAGC GCACCAATC
 ||||| |||||
 AATTCG TGTGGTTAG
 ATA____
 GAM2355 KIAA1522 3' GGATTGGCCTTCCTGTGCCTCA 65607 A _ TG AC
 A TTGA GC CAG GGGC CAATCC
 ||| ||| ||| |||||
 AACT CG GTC TCCG GTTAGG
 C T CT _
 GAM2355 KIAA1853 3' GGATGCCCCACTAGTCCAA 69924 AA C _
 TTG GC AGTGGGGCA CC
 ||| || ||||| ||

AAC TG TCACCCCGT GG
 C_ A A
 GAM2355 LOXL4 3' GATTGGTCTAAACTTCAA 50859 CCAG GGC
 TTGAAG TGG ACCAATC
 ||||| || |||||
 AACTTC ATC TGGTTAG
 AA__ __
 GAM2355 LSR7 5' GGACCGGCCCTGCCCCGGCTT 38280 AGT __ AA
 CAA TTGAAGCC GGGGCA CC TCC
 ||||| ||||| || |||
 AACTTCGG CCCCCT GG AGG
 C__ CCC CC
 GAM2355 PLK 3' GGA CTGGTGCCCTCCTCACT 18525 CC TG A
 AG AG GGGCACCA TCC
 || || ||||| |||
 TC TC CCCGTGGT AGG
 AC CT C
 GAM2355 STK22D 3' GGTCCCCACTGGCCGCAA 50145 AA C
 TTG GCCAGTGGGG ACC
 || ||||| |||
 AAC CGGTCACCCC TGG
 GC _
 GAM2355 LOC124871 3' TGCTGCCCCACCAGCTTCAG 74818 CA C
 TTGAAGC GTGGGGCA CA
 ||||| ||||| ||
 GACTTCG CACCCCGT GT
 AC C
 GAM2355 LOC157349 3' GACTGGCTGCTGGCTCCGA 82341 A TG GGCA A
 TTG AGCCAG G CCA TC
 || ||||| | ||| ||
 AGC TCGGTC C GGT AG
 C GT__ C
 GAM2355 LOC222550 5' GGATCAATATCGTGCTGGCTT 96018 G CACCA
 AAGCCAGTG GG ATCC
 ||||| || |||
 TTCGGTCGT CT TAGG
 G ATAAC
 GAM2356 SLC20A2 3' CACCCCCAGGCTCTACTC 23115 _ A A
 GA TAGAGCCT GG GTG
 || ||||| || |||
 CT ATCTCGGA CC CAC
 C C C
 GAM2356 ARP5 5' CACTCCCAGGCTCTGGGGGCTG 72031 GA A
 G TCAGTCT TAGAGCCT GGAGTG
 ||||| ||||| |||||
 GGTCGGG GTCTCGGA CCTCAC
 G_ C
 GAM2356 DKFZP434O125 3' CACCCTAAACATCAGACT 65583 AGAGCC A
 AGTCTGAT TAGG GTG
 ||||| |||| |||

TCAGACTA ATCC CAC
 CAAA__ C
 GAM2356 KIAA1023 3' CACTCCCAAGCTCCATGGCTGG 34674 TGATA CTA
 TCAGTC GAGC GGAGTG
 ||||| ||| |||||
 GGTCGG CTCG CCTCAC
 TAC__ AAC
 GAM2356 LOC135932 3' CACTCCTAAGCTCTGACCGCT 76696 CTGA C
 AGT TAGAGC TAGGAGTG
 || ||||| |||||
 TCG GTCTCG ATCCTCAC
 CCA_ A
 GAM2356 LOC150225 3' CACCCCTAGGCTGTGGAAGC 86181 T GA G A
 G CT TA AGCCTAGG GTG
 | || ||||| |||
 C GA GT TCGGATCC CAC
 _ AG G C
 GAM2356 LOC152573 5' CACTCCGCAGCTATCAGAC 81495 AGCCTA
 GTCTGATAG GGAGTG
 ||||| |||||
 CAGACTATC CCTCAC
 GACG__
 GAM2356 LOC155179 3' CACTCCCAAGCTCCATGGCTGG 82222 TGATA CTA
 TCAGTC GAGC GGAGTG
 ||||| ||| |||||
 GGTCGG CTCG CCTCAC
 TAC__ AAC
 GAM2356 LOC256980 3' CACTCCTCAAGCCTCCCAAAC 96926 C AT A CT_
 GT TG AG GC AGGAGTG
 || || || |||||
 CA AC TC CG TCCTCAC
 A CC _ AAC
 GAM2356 LOC90371 5' CACTCCGTCTCCTCCAGACTGA 63157 ATA CCTA
 TCAGTCTG GAG GGAGTG
 ||||| || |||||
 AGTCAGAC CTC CCTCAC
 CTC TG_
 GAM2357 CDH12 3' CTTATCATTTAAAGTGGTGTA 15777 CCCAA GA
 TACACCACT GAA ATAAG
 ||||| || |||||
 ATGTGGTGA TTT TATTC
 AA__ AC
 GAM2357 GOCAP1 3' ATTGTTCTTGGGAGCAGTGTA 43007 CA G
 TACAC CTCCCAAGAA AAT
 |||| ||||| |||
 ATGTG GAGGGTTCTT TTA
 AC G
 GAM2357 DKFZp434N2435 5' CTTATTACTGTGGGGTGGT 98090 T AGAAG
 ACCAC CCCA AATAAG
 |||| ||| |||||

		TGGTG GGGT TTATTC	
		_ GTCA_	
GAM2357	DKFZP564I122	3' CTTATTCTTCTCCCTCATGTGT 63877	CACTCCCA
	A	TACAC AGAAGAATAAG	
		ATGTG TCTTCTTATTC	
		TACTCCC_	
GAM2357	FLJ21791	3' CTTATTTGCAGAAAGTGGTGTA 62126	CCCAAGAA
		TACACCACT GAATAAG	
		ATGTGGTGA TTTATTC	
		AGACG__	
GAM2357	HMP19	3' CTTATTCTTTGTTAGGAAAATG 88860	CCAC CAA_
	TA	TACA TCC GAAGAATAAG	
		ATGT AGG TTTCTTATTC	
		AAA_ ATTG	
GAM2357	KIAA1719	3' TCTGTCTTGGGAGTGGTGTA 68742	_
		TACACCACTCCCAAGA AGA	
		ATGTGGTGAGGGTTCT TCT	
		G	
GAM2357	KIAA1853	3' TTTTCTTGAAGCAGTG 69929	CA C
		CAC CT CCAAGAAGAA	
		GTG GA GGTTCTTTTT	
		AC A	
GAM2357	KIAA1877	3' CTTATTCTTCTGCCATGAGT 66748	CCA__
		ACTC AGAAGAATAAG	
		TGAG TCTTCTTATTC	
		TACCG	
GAM2357	KIAA1906	3' CTTATTCTTCTTGACTTTTGG 73571	CTCC_
		CCA CAAGAAGAATAAG	
		GGT GTTCTTCTTATTC	
		TTTCA	
GAM2357	OSBPL11	3' CTTAATTTCCCAAGAGTGGTG 43206	CCAA AA
		CACCACTC GAAG TAAG	
		GTGGTGAG CTTT ATTC	
		AACC A_	
GAM2357	YME1L1	3' TCATTCTTGATGTGGTGTA 58438	TCC _
		TACACCAC CAAGAA GA	
		ATGTGGTG GTTCTT CT	
		TA_ A	
GAM2357	ZNF262	3' CTTATTTTGTGGGAGT 18723	A
		ACTCCCAAG AGAATAAG	

			TGAGGGTTT TTTTATTC		
			G		
GAM2357	LOC91960	3'	TGTGGCTTGGAACGTGGTGTA 68294	TC_	AAGA
			TACACCAC CCAAG ATA		
			ATGTGGTG GGTTC TGT		
			CAA GG_		
GAM2358	LAMC1	3'	TTGCAAAGTTTTCACGTCA 11275	C CC_	
			TGACGTGGA AT GCAA		
			ACTGCACTT TG CGTT		
			T AAA		
GAM2358	OPA1	3'	TTGCGGGTGGAACAGTCA 56430	G GA_	
			TGAC TG CATCCGCAA		
			ACTG AC GTGGGCGTT		
			_ AAG		
GAM2358	PITX2	5'	TTGCGGAGGGTGCGCTCA 6161	C G A_	
			TGA GTG AC TCCGCAA		
			ACT CGC TG AGGCGTT		
			_ G GG		
GAM2358	KIAA1962	5'	TTGCGGATGCTGATGCA 82803	A _ A	
			TG CGT GG CATCCGCAA		
			AC GTA TC GTAGGCGTT		
			_ G _		
GAM2358	LOC144848	3'	TGGAGGATGTCCACATCA 73961	C	G_
			TGA GTGGACATCC CA		
			ACT CACCTGTAGG GT		
			A AG		
GAM2358	LOC221495	5'	TTGCAGGGGCATCACGTTA 95498	ACA _	
			TGACGTGG TCC GCAA		
			ATTGCACT GGG CGTT		
			ACG A		
GAM2358	LOC256520	3'	GCAGATTTTGTCTACGTCA 97667	_ _ _ C	
			TGACGTGGA CA TC GC		
			ACTGCATCT GT AG CG		
			T TTT A		
GAM2359	CSNK1G2	3'	CAACCAAATGCTGCACCAAAG 8987	TC	ACTACC
			CTTTGGTG TGGTTG		
			GAAACCACG ACCAAC		
			TCGTAAA_		
GAM2359	LMO2	5'	AACCAGGCCACCAAGAGG 19933	_	CTCACTA
			CCTTT GGTG CCTGGTT		

		GGAGA CCAC	GGACCAA	
		A C_____		
GAM2359	MIPOL1	3' CAACACTGTGTAAACACCAAAG	77588	CT__ TACCTG
		CTTTGGTG CAC GTTG		
		GAAACCAC GTG CAAC		
		AAAT TCA_____		
GAM2359	TNFAIP2	3' AACCAGGCAACACCAAGG	21913	CTCACTA
		CTTTGGTG CCTGGTT		
		GGAACCAC GGACCAA		
		AAC_____		
GAM2359	C21orf100	3' AGCCAAGGAACACCAAAG	59504	C A ACC
		CTTTGGTG TC CT TGGTT		
		GAAACCAC AG GA ACCGA		
		A _ _____		
GAM2359	GPR9	5' AACCACAAGCACCAAAG	9484	CACTACC
		CTTTGGTGCT TGGTT		
		GAAACCACGA ACCAA		
		AC_____		
GAM2359	KIAA1466	3' CAACATTTATATAGAGCACCAA	72407	ACTACCTG_
		AGG CCTTTGGTGCTC GTTG		
		GGAAACCACGAG CAAC		
		ATATATTTA		
GAM2359	MGC2491	3' CAACCAGGTAGTGAGCACCAAA	44094	
		GG CCTTTGGTGCTCACTACCTGGTTG		
		GGAAACCACGAGTGATGGACCAAC		
GAM2359	PRO2015	3' GCCAATGAGACCAAAGG	38162	G CTACC
		CCTTTGGT CTCA TGGT		
		GGAAACCA GAGT ACCG		
		_ A_____		
GAM2359	LOC158293	3' ACCAGCAGAACACCAAAGG	82744	C ACTAC
		CCTTTGGTG TC CTGGT		
		GGAAACCAC AG GACCA		
		A AC_____		
GAM2359	LOC219347	3' AACTAACAAGCACCAAGG	94569	CACTACC
		CTTTGGTGCT TGGTT		
		GGAACCACGA ATCAA		
		ACA_____		
GAM2359	LOC256130	3' ATGAGGCAATGAGACACCAAAG	97755	_ CTA G
		G CCTTTGGTG CTCA CCT GT		

GGAAACCAC GAGT GGA TA
 A AAC G
 GAM2359 LOC92231 3' CAACCAGGTAACAAACTAAAG 69089 GCTCAC
 CTTTGGT TACCTGGTTG
 ||||| |||||
 GAAATCA ATGGACCAAC
 AAACA_

GAM2360 AAT1 3' TGTGTTTCATGCAACAGCCA 81334 ATC AGA
 TGGC GT GTGAACACA
 ||| || |||||
 ACCG CA TACTTGTGT
 A__ ACG

GAM2360 ACCN1 3' TGTGTTCACCCATGGTGCC 8462 AGA
 GGCATCGT GTGAACACA
 ||||| |||||
 CCGTGGTA CACTTGTGT
 CC_

GAM2360 BSN 3' TGTTCACTGGGGTGGCA 14396 G G AG
 TG CATC T AGTGAACA
 || ||| | |||||
 AC GTGG G TCACTTGT
 G G__

GAM2360 CDKN2B 3' TCGTTCACTCCAATGTC 55314 CGTA A
 GGCAT GAGTGAAC CA
 |||| ||||| ||
 CTGTA CTCACTTG GT
 AC__ C

GAM2360 CLASP1 5' TGTATTCTGACGATGATGCCA 65897 AGAGT C
 TGGCATCGT GAA ACA
 ||||| ||| |||
 ACCGTAGTA CTT TGT
 GCAGT A

GAM2360 DDEF2 3' TGTCTCTAATGCCA 15291 CG GT
 TGGCAT TAGA GAACA
 |||| ||| ||||
 ACCGTA ATCT CTTGT

GAM2360 EPB41L2 3' TGTATAGTTACGATGCCA 9294 AG A
 TGGCATCGTAG TG ACA
 ||||| || |||
 ACCGTAGCATT AT TGT
 G_ A

GAM2360 ETV5 3' GTGTTCACTAACATGCC 16729 C AG
 GGCAT GT AGTGAACAC
 |||| || |||||
 CCGTA CA TCACTTGTG
 _ A_

GAM2360 FBXL7 3' TGTTCACTCAACAATGCCA 25500 C A
 TGGCAT GT GAGTGAACA
 |||| || |||||

		ACCGTA CA CTC	ACTTGT	
		A A		
GAM2360	GNRHR	5'	TGTGTTCACTTTTATCACCA 6391	CATCGT
			TGG AGAGTGAACACA	
			ACC TTCACTTGTGT	
			ACTATT	
GAM2360	IFNAR2	3'	TGTGGAGCTCCCCACGATGCCA 7907	A__ GAA
			TGGCATCGT GAGT CACA	
			ACCGTAGCA CTCG GTGT	
			CCC AG_	
GAM2360	NPR2L	3'	TGTGTTCACTGTGCTGCCA 22603	T TAG
			TGGCA CG AGTGAACACA	
			ACCGT GC TCACTTGTGT	
			C TG_	
GAM2360	POP2	3'	TGTGTTACAGAATGGCCA 42409	AT AGA
			TGGC CGT GTGAACACA	
			ACCG GTA CACTTGTGT	
			_ AGA	
GAM2360	PTGIS	3'	GTGTCCATTGATGTCA 8223	TAGA A
			TGGCATCG GTG ACAC	
			ACTGTAGT TAC TGTG	
			_ C	
GAM2360	STARD5	3'	TGTGTTCACTCTTTGGAACA 48319	GCA T
			TG TCG AGAGTGAACACA	
			AC GGT TCTCACTTGTGT	
			AA_ T	
GAM2360	TNFRSF6B	3'	GTGTCCACCTGGTGCC 53098	GT A A
			GGCATC AG GTG ACAC	
			CCGTGG TC CAC TGTG	
			_ _ C	
GAM2360	XK	3'	TGTGTTCAATTGACACCA 41156	CA TAGA
			TGG TCG GTGAACACA	
			ACC AGT TACTTGTGT	
			AC _	
GAM2360	ZNFN1A3	3'	TGTGTTACAGGGGTAGCCA 60859	_ GTAGA
			TGGC ATC GTGAACACA	
			ACCG TGG CACTTGTGT	
			A GGA_	
GAM2360	EDG2	5'	GTGTTACACCTACAACCA 9178	CATC A_
			TGG GTAG GTGAACAC	

ACC CATC CACTTGTG
 AA__ CAC
 GAM2360 EDG2 5' GTGTTACACCTACAACCA 55134 CATC A__
 TGG GTAG GTGAACAC
 ||| ||| |||||
 ACC CATC CACTTGTG
 AA__ CAC
 GAM2360 FLJ21324 5' TGTGTGGCCCCCGATGCCA 92863 TAGA GA
 TGGCATCG GT ACACA
 ||||| || |||||
 ACCGTAGC CG TGTGT
 CCCC G_
 GAM2360 FLJ30681 3' TGTGTTACACAATAGACCA 93442 CA G GA
 TGG TC TA GTGAACACA
 ||| ||| |||||
 ACC AG AT CACTTGTGT
 __ _ AA
 GAM2360 FUT10 5' TGCTTCCTCTCGATGCCA 51993 T T _
 TGGCATCG AGAG GAA CA
 ||||| ||| ||| ||
 ACCGTAGC TCTC CTT GT
 __ _ C
 GAM2360 GFR 3' GTGTTCAAGGAAGTGATGTCA 25450 TAGAG
 TGGCATCG TGAACAC
 ||||| |||||
 ACTGTAGT ACTTGTG
 GAAGG
 GAM2360 HN1L 3' TGTACTCACATCACAATGTCA 58623 C A _ AC
 TGGCAT GT GA GTGA ACA
 ||||| ||| ||| |||
 ACTGTA CA CT CACT TGT
 A _ A CA
 GAM2360 KIAA0008 3' TGTGTTCACTTCTATAGC 29240 ATC _
 GC GTAGA GTGAACACA
 || ||||| |||||
 CG TATCT CACTTGTGT
 A__ T
 GAM2360 KIAA0141 3' TGTGCTCACTTTGGCC 29396 ATCG A
 GGC TAGAGTGA CACA
 ||| ||||| |||
 CCG GTTTCAC TGT
 __ _ C
 GAM2360 KIAA0298 3' TGTGTTCAAAGTGAAGCCA 77081 ATCG AG
 TGGC TAG TGAACACA
 ||| ||| |||||
 ACCG GTC ACTTGTGT
 AA__ AA
 GAM2360 KIAA0447 3' TGTGCTCACTGCGCTGC 72135 T AG A
 GCA CGT AGTGA CACA
 ||| ||| ||||| |||

		CGT GCG TCACT GTGT		
		C _ C		
GAM2360 KIAA0876	3'	TGTGCCCACTCTGTGCC	65321	CGT AA
		GGCAT AGAGTG CACA		
		CCGTG TCTCAC GTGT		
		_ CC		
GAM2360 KIAA0972	3'	TGTGTTCAAACCTCAGTGCCA	30683	CGT AG
		TGGCAT AG TGAACACA		
		ACCGTG TC ACTTGTGT		
		AC_ AA		
GAM2360 KIAA0981	3'	GTGTTCAACCACTGTATGCCA	62092	C A_
		TGGCAT GTAG GTGAACAC		
		ACCGTA TGTC CACTTGTG		
		_ AC		
GAM2360 KIAA1280	5'	TTCACTCCCTTGATGTCA	70295	TA_
		TGGCATCG GAGTGAA		
		ACTGTAGT CTCACCT		
		TCC		
GAM2360 KIAA1384	3'	TGTGTTCAAGAATGATTCCA	65181	C AGAG
		TGG ATCGT TGAACACA		
		ACC TAGTA ACTTGTGT		
		T AGA_		
GAM2360 KIAA1635	5'	TGTGTTCACTAAACTCCA	68462	CATC AG
		TGG GT AGTGAACACA		
		ACC CA TCACTTGTGT		
		T_ AA		
GAM2360 KIAA1813	3'	GTGTTCACTGTTACCCA	70832	CATC _
		TGG GTAG AGTGAACAC		
		ACC CATT TCACTTGTG		
		_ G		
GAM2360 MCAM	3'	GTGTTCACTTGCTCCCA	22464	CATC G
		TGG GTA AGTGAACAC		
		ACC CGT TCACTTGTG		
		CT_ _		
GAM2360 MGC27171	3'	GTGTTCAATTGGATCCA	58702	C GTAG
		TGG ATC AGTGAACAC		
		ACC TAG TTA CTTGTG		
		_ G_		
GAM2360 MGC4415	3'	TGTGCTCACTCTGTCTGCCA	49767	TCG A
		TGGCA TAGAGTGA CACA		

		ACCGT GTCTCACT GTGT	
		CT_ C	
GAM2360	NY-REN-25	3' TGTGTTCACTCTAAAAATGC 61266	CG_
		GCAT TAGAGTGAACACA	
		CGTA ATCTCACTTGTGT	
		AAA	
GAM2360	PC326	5' GTGTCCATTGATGCCA 38027	TAGA A
		TGGCATCG GTG ACAC	
		ACCGTAGT TAC TGTG	
		_____ C	
GAM2360	PCDH10	5' TGTTTAACGGTGCCA 40823	AGAG
		TGGCATCGT TGAACA	
		ACCGTGGCA ATTTGT	

GAM2360	PCDH10	5' TGTTTAACGGTGCCA 53105	AGAG
		TGGCATCGT TGAACA	
		ACCGTGGCA ATTTGT	

GAM2360	PEX16	3' CGCTCTCCTGTGACGATGCCA 55157	_____
		TGGCATCGT AGAGTG	
		ACCGTAGCA TCTCGC	
		GTGTCC	
GAM2360	SARM	3' TGTGTTTCAGAGGTGACTGCCA 31309	_ AGAG
		TGGCA TCGT TGAACACA	
		ACCGT AGTG ACTTGTGT	
		C GAG_	
GAM2360	STK29	3' TGTCACCTCCACGAGGCCA 88967	A A _ A
		TGGC TCGT GAG TGA CA	
		ACCG AGCA CTC ACT GT	
		G C C _	
GAM2360	TRAF3	3' TGTGTCCCTTCGATGCCA 60457	TA T A
		TGGCATCG GAG GA CACA	
		ACCGTAGC TTC CT GTGT	
		_____ C _	
GAM2360	LOC126206	3' TGTGTTCACTCTACGTTG 76176	T
		CA CGTAGAGTGAACACA	
		GT GCATCTCACTTGTGT	
		T	
GAM2360	LOC143720	3' TGTGTTTCACCTCTGACCA 61066	CA T A
		TGG TCG AG GTGAACACA	

		ACC AGT TC CACTTGTGT		
		__ C __		
GAM2360	LOC153769 3'	GTGCCCAC TTTATGCCCA	81809	CAT AA
		TGG CGTAGAGTG CAC		
		ACC GTATTTAC GTG		
		CC_ CC		
GAM2360	LOC256158 5'	TGTGTTCA CACCCTGCC	99520	TC AGA
		GGCA GT GTGAACACA		
		CCGT CA CACTTGTGT		
		CC C__		
GAM2360	LOC91960 3'	TGTGTCCCCACGGTGCCA	68295	AGAGT A
		TGGCATCGT GA CACA		
		ACCGTGGCA CT GTGT		
		CCC__ _		
GAM2361	BRCA1 3'	GTGACTCTTCTGCCCTTGAG	24572	A _
		TTCAAGGG TGGAA AGTCAC		
		GAGTTCCC GTCTT TCAGTG		
		_ C		
GAM2361	CA12 3'	TGACCCAATCTGCCTTTGAA	8692	A AA__
		TTCAAGGG TGA GTCA		
		AAGTTTCC GTCT CAGT		
		_ AACC		
GAM2361	CHRM1 5'	TGACTTTCCCCTGAG	96436	A ATG
		TTCA GGG GAAAGTCA		
		GAGT CCC CTTTCAGT		
		- -		
GAM2361	DLG5 3'	GGTGACTTTGGCATTCTT	83820	G_
		AGGGATG AAAGTCACC		
		TTCTTAC TTTCAGTGG		
		GG		
GAM2361	FOXE1 3'	ACTCTCCCCCTTTCCCTTGAG	16775	T__ A
		TTCAAGGGA GGA AGT		
		GAGTTCCCT CCT TCA		
		TTCCC C		
GAM2361	FTH1 3'	GGTGACTTCCCTGGTCACC	68714	_ _ A
		GG GAT GG AAGTCACC		
		CC CTG CC TTCAGTGG		
		A GT C		
GAM2361	GFAP 3'	GTGACTCATCCTCTTGAA	10783	_ GAA
		TTCAAG GGATG AGTCAC		

			AAGTTC CCTAC TCAGTG		
			T ____		
GAM2361	GRINL1A	3'	GGTGACTTTCATGTGCTTGAA 70064	GGATG	
			TTCAAG GAAAGTCACC		
			AAGTTC CTTTCAGTGG		
			GTGTA		
GAM2361	JDP1	3'	GATTCCTCCATCCTTGAA 41724	G A_	
			TTCAAGG ATGGA AGTC		
			AAGTTCC TACCT TTAG		
			_ CC		
GAM2361	KCND2	3'	GTGACTTTCCTACTTTTG 25385	AT	
			CAAGGG GGAAAGTCAC		
			GTTTTC CCTTTCAGTG		
			AT		
GAM2361	LECT2	5'	GACTTGCTCCATCCTCTT 11296	_ _	
			AAG GGATGGA AAGTC		
			TTC CCTACCT TTCAG		
			T CG		
GAM2361	MASP1	3'	GGTGACTTCATCTCTTCGAA 10297	_ AA	
			TTC AAGGGATGG AGTCACC		
			AAG TTCTCTACT TCAGTGG		
			C _		
GAM2361	NOTCH2	3'	GGTGACTCTCTGCCCTTGGA 44577	A A	
			TTCAAGGG TGGA AGTCACC		
			AGGTTCCC GTCT TCAGTGG		
			_ C		
GAM2361	Nrap	3'	TGACCTCCACCCTCCTTGGA 43623	A_ AA	
			TTCAAGGG TGGA GTCA		
			AGGTTCCT ACCT CAGT		
			CCC C_		
GAM2361	Nrap	3'	TGACCTCCACCCTCCTTGGA 58322	A_ AA	
			TTCAAGGG TGGA GTCA		
			AGGTTCCT ACCT CAGT		
			CCC C_		
GAM2361	NT5C3	3'	GGTATCACCATCTCTTGAA 33660	AAA C	
			TTCAAGGGATGG GT ACC		
			AAGTTCTCTACC TA TGG		
			AC_ _		
GAM2361	PITX2	3'	GGCAACTCCGCCCTTGAA 6157	A AA_	
			TTCAAGGG TGGA GTC		

			AAGTTCCC GCCT CGG		
			_ CAA		
GAM2361	PML	3'	GTGACCCTTCTGTCCCTAGA 53812	A	A_
			TC AGGGATGGAA GTCAC		
			AG TCCCTGTCTT CAGTG		
			A CC		
GAM2361	PML	3'	GTGACCCTTCTGTCCCTAGA 53818	A	A_
			TC AGGGATGGAA GTCAC		
			AG TCCCTGTCTT CAGTG		
			A CC		
GAM2361	PTGIS	3'	GTGCACCACCCTTTGAA 8222	A	AAA T
			TTCAAGGG TGG G CAC		
			AAGTTCC ACC C GTG		
			C A__		
GAM2361	RAB36	3'	GGTAACTCACTCTGCAGCCCTT 18173	AT__	A__ C
	GAA		TTCAAGGG GGA AGT ACC		
			AAGTTCCC TCT TCA TGG		
			GACG CAC A		
GAM2361	TIMP4	3'	GTGACCATCACATCCCTT 13757	_	AA
			AAGGGATG GA GTCAC		
			TTCCCTAC CT CAGTG		
			A AC		
GAM2361	ZK1	3'	GTACAGTCATCCCTTGA 20575	AAA	C
			TCAAGGGATGG GT AC		
			AGTCCCTACT CA TG		
			GA_ _		
GAM2361	AFAP	3'	GATGTCCATCCTTGAA 41607	G	AA
			TTCAAGG ATGGA GTC		
			AAGTTCC TACCT TAG		
			_ G_		
GAM2361	AKL3L	3'	TGACTTGTTTCCTTTGAA 33271		TGGA
			TTCAAGGGA AAGTCA		
			AAGTTTCCT TTCAGT		
			TTG_		
GAM2361	ATP10D	3'	GGCATTCAATCCCTGAA 73527	A	AA
			TTCA GGGATGGA GTC		
			AAGT CCTTACTT CGG		
			C A_		
GAM2361	C20orf72	3'	GGTGACTCTTGTAATCCCTTGA 54607	_	G _
	G		TTCAAGGGA TG AA AGTCACC		

			GAGTTCCT AT TT TCAGTGG	
			C G C	
GAM2361	EFA6R	3'	GTGAGTCATCCCTTGA 31639	AAAG
			TCAAGGGATGG TCAC	
			AGTTCCTACT AGTG	
			G__	
GAM2361	EPB41L1	3'	TGACTCTCCTTTGAA 71118	T GAA
			TTCAAGGGA G AGTCA	
			AAGTTTCCT C TCAGT	
			— — —	
GAM2361	FLJ10008	3'	GGCAACCTGTCCCTTGAG 36190	AAA
			TTCAAGGGATGG GTC	
			GAGTTCCTGTC CGG	
			CAA	
GAM2361	FLJ11726	3'	GTGACCCAGGCTCTTTGAA 47027	_ A_ AAA
			TTCAAGG G TGG GTCAC	
			AAGTTTC C ACC CAGTG	
			T GG _	
GAM2361	FLJ12847	3'	GGTGACTTTCTGATGACTGAA 45078	A GG _
			TTCA G AT GGAAAGTCACC	
			AAGT C TA TCTTTCAGTGG	
			_ AG G	
GAM2361	FLJ12891	3'	GGTGACCGCAGCCCCTTGGA 46929	A_ GAAA
			TTCAAGGG TG GTCACC	
			AGGTTCCC AC CAGTGG	
			CG GC__	
GAM2361	FLJ12891	3'	GGTGACTTCTCAGAGCCTGAA 46930	A GA_ GA
			TTCA GG TG AAGTCACC	
			AAGT CC AC TTCAGTGG	
			_ GAG TC	
GAM2361	FLJ20498	3'	TGACCCTCCACTCCTTGAA 39282	GA AA
			TTCAAGG TGGA GTCA	
			AAGTTCC ACCT CAGT	
			TC CC	
GAM2361	GFR	3'	TGACTTCTTATCCCTGGA 25451	A GA
			TTCA GGGATG AAGTCA	
			AGGT CCCTAT TTCAGT	
			_ TC	
GAM2361	GREB1	5'	GACTCCATCCTCTTGAA 72839	_ AA
			TTCAAG GGATGGA GTC	

			AAGTTC CCTACCT CAG		
			T _		
GAM2361	HSNOV1	3'	GGTGGGTCAGCCCTTGAA 34439	ATG AAG	
			TTCAAGGG GA TCACC		
			AAGTTCCC CT GGTGG		
			GA_ G_		
GAM2361	KIAA0731	3'	GACCTTTCCATCCTTGAA 67479	G _	
			TTCAAGG ATGGAAAG TC		
			AAGTTCC TACCTTTC AG		
			_ C		
GAM2361	KIAA1046	3'	GGTGACTTTCTTTTTTTG 30662	T	
			CAAGGGA GGAAAGTCACC		
			GTTTTTT TCTTTCAGTGG		
			_		
GAM2361	KIAA1084	3'	GGTGACTTTCCCTTTT 30502	AT	
			AAGGG GGAAAGTCACC		
			TTTTC CCTTTCAGTGG		
			_		
GAM2361	KIAA1276	5'	GGTGATTTATGCCCTGAA 67032	A ATGGA	
			TTCA GGG AAGTCACC		
			AAGT CCC TTTAGTGG		
			_ GTA_		
GAM2361	KIAA1495	5'	GGTTATTTGCACCCCTTGAA 73566	A G GTC	
			TTCAAGGG TG AAA ACC		
			AAGTTCCC AC TTT TGG		
			C G AT_		
GAM2361	KIAA1755	5'	GGTACCCTCCATCCCTCGA 62018	A AA C	
			TC AGGGATGGA GT ACC		
			AG TCCCTACCT CA TGG		
			C CC _		
GAM2361	KIAA1798	3'	TGACTTTTCTTTGAA 61249	TGGA	
			TTCAAGGGA AAGTCA		
			AAGTTTCTT TTCAGT		
			_		
GAM2361	KIAA1940	3'	GACCTTCCATCCCTGAA 80782	A A	
			TTCA GGGATGGAA GTC		
			AAGT CCCTACCTT CAG		
			_ C		
GAM2361	MGC4737	5'	TGACTTTCTGTGGCTTGGA 49652	GG	
			TTCAAG ATGGAAAGTCA		

AGGTTC TGTCTTTCAGT
 GG
 GAM2361 NTT73 3' GTGACTTTTAACTTG 36495 GGA
 CAAG TGGAAAGTCAC
 ||| |||||
 GTTC ATTTTTCAGTG
 A__
 GAM2361 P2RXL1 3' CGGTGACCCCCAGCCCAACCC 19559 A_____ AAA ____
 CTTGGA TTCAAGGG TGG GTCACC G
 ||||| || ||||| |
 AGGTTCAC ACC CAGTGG C
 CAACCCG CCC ____
 GAM2361 PRO1600 5' GGCAACCCTATCTCTTGAG 26877 AAA_
 TTCAAGGGATGG GTC
 ||||| |||
 GAGTTCTCTATC CGG
 CCAA
 GAM2361 RBM5 3' GTGGTCCATCTCCCGAA 20507 AA AAG
 TTC GGGATGGA TCAC
 || ||||| |||
 AAG CTCTACCT GGTG
 CC ____
 GAM2361 SLC5A7 3' ACTTCAGTCACTCCCTTGAA 41802 _ A__
 TTCAAGGGA TGG AAGT
 ||||| || |||
 AAGTCCCT ACT TTCA
 C GAC
 GAM2361 SRPK2 3' GGTGACTCTCATTCTTT 13412 AA
 AAGGGATGG AGTCACC
 ||||| |||||
 TTTCTTACT TCAGTGG
 C_
 GAM2361 ZNF297B 3' GTGACTTTCTAAATATGAA 26670 AGGGA
 TTCA TGGAAAGTCAC
 ||| |||||
 AAGT ATCTTTCAGTG
 ATAA_
 GAM2361 ZNF297B 3' GTGACTTTCTAAATATGAA 82705 AGGGA
 TTCA TGGAAAGTCAC
 ||| |||||
 AAGT ATCTTTCAGTG
 ATAA_
 GAM2361 LOC116113 3' GTGCCTCCATCCCCAGAA 93841 AA AA T
 TTC GGGATGGA G CAC
 || ||||| |||
 AAG CCCTACCT C GTG
 AC C__
 GAM2361 LOC122792 3' GTGACTTTCCTTTTGT 59827 AT
 CAAGGG GGAAAGTCAC
 ||||| |||||

GTTTTT CCTTTCAGTG

GAM2361 LOC138855 3' GGTGACTTCCCTGGTCACC 75893 _ _ A
GG GAT GG AAGTCACC
|| ||| || |||||
CC CTG CC TTCAGTGG
A GT C

GAM2361 LOC143943 3' GGCTACCCCCACCCCTTGGA 83919 A AA_
TTCAAGGG TGG AGTC
||||| ||| |||
AGGTTCCC ACC TCGG
C CCCA

GAM2361 LOC145231 3' GGCTTGTCATCCCTTGA 84253 _
TCAAGGGATGGA AAGTC
||||||| |||
AGTTCCTACCT TTCGG
G

GAM2361 LOC146337 5' GGCAACTCTAGCCTTTGAA 84643 A AA_
TTCAAGGG TGGA GTC
||||| ||| |||
AAGTTTCC ATCT CGG
G CAA

GAM2361 LOC146499 5' GGTGACTTTGAAGACTTGGA 71367 GGATGG
TTCAAG AAAGTCACC
||||| |||||
AGGTTC TTTCAGTGG
AGAAG_

GAM2361 LOC147176 5' GGTGACTTTGAAGACTTGGA 61147 GGATGG
TTCAAG AAAGTCACC
||||| |||||
AGGTTC TTTCAGTGG
AGAAG_

GAM2361 LOC147463 3' TGACTTTGAGGTCCTTGGA 79005 ATGG
TTCAAGGG AAAGTCA
||||| |||||
AGGTTCCCT TTTCAGT
GGAG

GAM2361 LOC151057 3' GGTGACCCTACCCTTGAG 86393 A AAA
TTCAAGGG TGG GTCACC
||||| ||| |||||
GAGTTCCC ATC CAGTGG
_ C_

GAM2361 LOC152018 3' GACCTCCACCCCTTGAA 86728 A_ AA
TTCAAGGG TGGA GTC
||||| ||| |||
AAGTTCCC ACCT CAG
CC C_

GAM2361 LOC152179 5' GGTGACTTGAAACCCTGAG 86743 A ATGGA
TTCA GGG AAGTCACC
||| ||| |||||

		GAGT CCC TTCAGTGG	
		_ AAAG_	
GAM2361	LOC153565 3'	GGTGACTTCCCTGGTCACC 81758	_ _ A
		GG GAT GG AAGTCACC	
		CC CTG CC TTCAGTGG	
		A GT C	
GAM2361	LOC155435 3'	GGTGACTTTGGTAGCCCTTGAG 82270	ATGG_
		TTCAAGGG AAAGTCACC	
		GAGTTCCC TTTCAGTGG	
		GATGG	
GAM2361	LOC253336 3'	GTAACCTTCTTCATCCCTTGAA 99181	_ C
		TTCAAGGGATG GAAAGT AC	
		AAGTCCCTAC CTTTCA TG	
		TT A	
GAM2361	LOC256714 3'	TGACCTTTTCTTCTTTGAA 98046	T _
		TTCAAGGGA GGAAAG TCA	
		AAGTTTCTT CTTTTC AGT	
		_ C	
GAM2361	LOC256815 3'	GATTCCCCTCCCTTGAA 96362	T AA
		TTCAAGGGA GG AGTC	
		AAGTCCCT CC TTAG	
		_ CC	
GAM2361	LOC51696 3'	TGGCTTTCTACCCCCTGAA 33093	A A
		TTCA GGG TGGAAAGTCA	
		AAGT CCC ATCTTTCGGT	
		C C	
GAM2361	LOC90576 3'	GTACAGTCATCCCTTGA 64078	AAA C
		TCAAGGGATGG GT AC	
		AGTCCCTACT CA TG	
		GA_ _	
GAM2361	LOC96610 5'	GGTGACTTTGAAGACTTGGA 56054	GGATGG
		TTCAAG AAAGTCACC	
		AGGTTC TTTCAGTGG	
		AGAAG_	
GAM2362	TERF1 3'	CCCAAATCCTGTTCCAATGA 34391	C TA C
		TCATTGGA ACG GATT GGG	
		AGTAACCT TGT CTAA CCC	
		_ C_ A	
GAM2362	FLJ10159 3'	CCATGTCACGCCATCCAATGAC 36334	CA_ A TC
		GTCATTGGA CGT GAT GG	

		CAGTAACCT GCA CTG CC		
		ACC _ TA		
GAM2362	FLJ14213 3'	CCGATGCTCCCAATGACG 46216	ACAC	GAT
		CGTCATTGG GTA TCGG		
		GCAGTAACC CGT AGCC		
		CT_ _		
GAM2362	MGC10715 3'	ATTTACCAGACATCCAATGAC 44495	CAC_	
		GTCATTGGA GTAGAT		
		CAGTAACCT CATTTA		
		ACAGAC		
GAM2362	MOST2 5'	CCAGGACTGCCCAATGAC 40059	ACAC	A _
		GTCATTGG GTAG TTC GG		
		CAGTAACC CGTC AGG CC		
		_ _ A		
GAM2362	LOC150370 3'	CCGGGTCTACGTGCCCATGAC 86123	T	A
		GTCAT GG CACGTAGATTTCGG		
		CAGTA CC GTGCATCTGGGCC		
		C _		
GAM2362	LOC152620 3'	CCCAAATCCTGTTCCAATGA 60707	C	TA C
		TCATTGGA ACG GATT GGG		
		AGTAACCT TGT CTAA CCC		
		_ C_ A		
GAM2362	LOC158668 3'	CCCAAATCCTGTTCCAATGA 69896	C	TA C
		TCATTGGA ACG GATT GGG		
		AGTAACCT TGT CTAA CCC		
		_ C_ A		
GAM2363	DLG5 5'	GTGAGCTCCATCCTGCGGAA 83821	A	AAAG
		TTCC CGGGATGGG TCAC		
		AAGG GTCCTACCT AGTG		
		C CG_		
GAM2363	FLRT1 3'	GTGACTTTCCTCCGCAGAA 60366	CA	GAT
		TTC CGG GGGAAAGTCAC		
		AAG GCC TCCTTTCAGTG		
		AC _		
GAM2363	GNAS 3'	TGGTGCCCCCGTGGAG 6714	AT	AAAG
		TTCCACGGG GGG TCA		
		GAGGTGCCC CCC GGT		
		_ GT_		
GAM2363	LIMK1 3'	CTTCTCCCACCCGTGGA 11331	A	_
		TCCACGGG TGGGA AAG		

		AGGTGCCC ACCCT TTC		
		C C		
GAM2363	LIMK1	3' CTTCTCCCACCCCGTGGG 11332	A	_
		TCCACGGG TGGGA AAG		
		AGGTGCCC ACCCT TTC		
		C C		
GAM2363	SOX11	3' GTGACTTTTGCCCAAGGAA 13322	AC	ATGG
		TTCC GGG GAAAGTCAC		
		AAGG CCC TTTTCAGTG		
		AA G__		
GAM2363	ZNF83	5' TGA CTCTCAGTGTCTGTGGAA 37537	ATGG	A
		TTCCACGGG GA AGTCA		
		AAGGTGTCT CT TCAGT		
		GTGA C		
GAM2363	AP3M2	3' ACCTTCCCGTTGGTCGGAA 23298	_ G G	A
		TTCC AC G ATGGGAA GT		
		AAGG TG T TGCCCTT CA		
		C G_ C		
GAM2363	ASAH	3' GTGAACTCCACCTCCGTGGAA 16304	ATG	AAG
		TTCCACGGG GGA TCAC		
		AAGGTGCCT CCT AGTG		
		CCA CA_		
GAM2363	FLJ10508	3' GTGACTTTGTAATCCCAGGAA 36684	AC	GGG
		TTCC GGGAT AAAGTCAC		
		AAGG CCCTA TTTTCAGTG		
		A_ ATG		
GAM2363	FLJ22301	5' GTGACCTCCCCATCCCGAGG 46181	A	AAA
		CC CGGGATGGG GTCAC		
		GG GCCCTACCC CAGTG		
		A CTC		
GAM2363	HSP105B	3' ACTTTCAGATTCCTGTGGAA 22807	TGG_	
		TTCCACGGGA GAAAGT		
		AAGGTGTCCT CTTTCA		
		TAGA		
GAM2363	KIAA0293	3' GACCCCATTTCCCGTGTGAA 61238	_	___ AAA
		TTC CACGGGA TGGG GTC		
		AAG GTGCCCT ACCC CAG		
		T TT _		
GAM2363	KIAA0295	3' GTGACCTCCCTTTCCCTCCGTGG 68672	AT_	AA
	AA	TTCCACGGG GGGA GTCAC		

AAGGTGCCT CCCT CAGTG
 CCTTT C_
 GAM2363 KIAA0427 3' ACTTTCCTCTGCGCGGAA 29370 A _ TG
 TTCC CG GGA GGAAAGT
 ||| || ||| |||||
 AAGG GC TCT CCTTTCA
 C G _
 GAM2363 MGC33317 3' GTGACTTTTGATTCCCATGGAG 59499 C TGGG
 TTCCA GGGA AAAGTCAC
 |||| ||| |||||
 GAGGT CCCT TTTCAGTG
 A TAG_
 GAM2363 PROZ 3' GTGACCTTTTCTTCCCTGGAA 15307 C T A
 TTCCA GGGA GGGAA GTCAC
 |||| ||| |||| |||||
 AAGGT CCCT TCTTT CAGTG
 _ T C
 GAM2363 LOC144559 3' GTGACTTTTTCACGTAGAA 77385 C GGA GG
 TTC ACG TG AAAGTCAC
 ||| ||| || |||||
 AAG TGC AC TTTCAGTG
 A _ TT
 GAM2363 LOC165127 5' GTGACTTTACTGGGCCACGGAA 83353 ACG A_ G
 TTCC GG TGG AAAGTCAC
 ||| || ||| |||||
 AAGG CC GTC TTTCAGTG
 CA_ GG A
 GAM2363 LOC201522 3' GTGACCCTGGTGCTGTGGAA 89638 G G AAA
 TTCCACGG AT GG GTCAC
 ||||| || ||| |||||
 AAGGTGTC TG TC CAGTG
 G G C_
 GAM2363 LOC219899 3' TGACTTTCCACCTGTG 93135 A
 CACGGG TGGGAAAGTCA
 ||||| |||||
 GTGTCC ACCCTTTCAGT
 _
 GAM2363 LOC219938 5' TGACCTTCCTGTCCCATAGGA 93181 AC_ A
 TCC GGGATGGGAA GTCA
 ||| ||||| |||
 AGG CCCTGTCCTT CAGT
 ATA C
 GAM2363 LOC255515 3' TGACTTTTTTCACGTAGAA 97813 C GGA GG
 TTC ACG TG AAAGTCA
 ||| ||| || |||||
 AAG TGC AC TTTCAGT
 A _ TT
 GAM2364 TERF1 3' CCCAAATCCTGTTCCAATGA 34391 C TA C
 TCATTGGA ACG GATT GGG
 ||||| ||| ||| |||

		AGTAACCT TGT CTAA CCC	
		_ C_ A	
GAM2364	FLJ10159 3'	CCATGTCACGCCATCCAATGAC 36334	CA_ A TC
		GTCATTGGA CGT GAT GG	
		CAGTAACCT GCA CTG CC	
		ACC _ TA	
GAM2364	FLJ14213 3'	CCGATGCTCCCAATGACG 46216	ACAC GAT
		CGTCATTGG GTA TCGG	
		GCAGTAACC CGT AGCC	
		CT__ _	
GAM2364	MGC10715 3'	ATTTACCAGACATCCAATGAC 44495	CAC__
		GTCATTGGA GTAGAT	
		CAGTAACCT CATTTA	
		ACAGAC	
GAM2364	MOST2 5'	CCAGGACTGCCCAATGAC 40059	ACAC A _
		GTCATTGG GTAG TTC GG	
		CAGTAACC CGTC AGG CC	
		_ _ _ A	
GAM2364	LOC150370 3'	CCGGGTCTACGTGCCCATGAC 86123	T A
		GTCAT GG CACGTAGATTCCG	
		CAGTA CC GTGCATCTGGGCC	
		C _	
GAM2364	LOC152620 3'	CCCAAATCCTGTTCCAATGA 60707	C TA C
		TCATTGGA ACG GATT GGG	
		AGTAACCT TGT CTAA CCC	
		_ C_ A	
GAM2364	LOC158668 3'	CCCAAATCCTGTTCCAATGA 69896	C TA C
		TCATTGGA ACG GATT GGG	
		AGTAACCT TGT CTAA CCC	
		_ C_ A	
GAM2365	FMR2 3'	GAAAGCACCTGGTTTGCACCAT 10693	_ _ C
	T	GATGGT CAG CCAGGTGC TTC	
		TTACCA GTT GGTCCACG AAG	
		C T A	
GAM2365	ARHGEF4 5'	AAGTGAACCGACCATCAA 53368	AGCCA GC_
		TTGATGGTC GGT CTT	
		AACTACCAG CCA GAA	
		_ _ _ AGT	
GAM2365	CABP4 3'	AAACACCTGGCCTCAAT 59748	T GTCA CC
		ATTGA G GCCAGGTG TT	

			TAAC T C	CGGTCCAC	AA		
			— — — —	AA			
GAM2365	CDV-1	5'	ACTGTGGCTGACACCAAT	49688	ATG	—	
			ATTG GTCAGCCA GGT				
			TAAC CAGTCGGT TCA				
			CA_ G				
GAM2365	FLJ23598	3'	AAGACACCCCCCTGGACCCATC	96501	—	CCA	C
			AAT ATTGATGG TCAG GGTG CTT				
			TAACTACC GGTC CCAC GAA				
			CA CCC A				
GAM2365	PTPRR	3'	GAAGACTTGTGACACCATCAAT	56450	AGC	GC	
			ATTGATGGTC CAGGT CTTC				
			TAACTACCAG GTTCA GAAG				
			ACT —				
GAM2365	RHOBTB1	3'	GCACAAGCTCACCATCAAT	93093	C	CAG	
			ATTGATGGT AGC GTGC				
			TAACTACCA TCG CACG				
			C AA_				
GAM2365	LOC146181	3'	TACTCTGGCTGACCATCA	69151	—		
			TGATGGTCAGCCAG GTG				
			ACTACCAGTCGGTC CAT				
			T				
GAM2365	LOC255452	3'	AAGTGAACCGACCATCAA	99383	AGCCA	GC_	
			TTGATGGTC GGT CTT				
			AACTACCAG CCA GAA				
			— — — — AGT				
GAM2365	LOC51026	3'	GCATTCTTGACCATGAAT	32686	G	CCA	
			ATT ATGGTCAG GGTGC				
			TAA TACCAGTT TTACG				
			G C_				
GAM2365	LOC85479	5'	AAGGCACCTGGCTCCTCAG	53555	T	TC	
			TTGA GG AGCCAGGTGCCTT				
			GACT CC TCGGTCCACGGAA				
			— —				
GAM2366	DFFB	3'	CAACTTCCAGAGGACAGCT	88761	C	CCA	
			AGCTG CCTT GAGGTTG				
			TCGAC GGAG CTTCAAC				
			A AC_				
GAM2366	DLEU2	5'	CAATTCTGGAGAACAGC	21207	CCC	G	
			GCTG TTCCAGAG TTG				

			CGAC GAGGTCTT AAC	
			AA_ _	
GAM2366	ESR1	3'	ATTTCTAAAATGGCAGCTT 5510	C CC
			AAGCTGCC TT AGAGGT	
			TTCGACGG AA TCTTTA	
			T AA	
GAM2366	GABRE	5'	CAGCCTCTGAAAAATCAGCT 42056	CCC
			AGCTG TTCCAGAGGTTG	
			TCGAC AAGGTCTCCGAC	
			TAA	
GAM2366	GABRE	5'	CAGCCTCTGAAAAATCAGCT 42060	CCC
			AGCTG TTCCAGAGGTTG	
			TCGAC AAGGTCTCCGAC	
			TAA	
GAM2366	GABRE	5'	CAGCCTCTGAAAAATCAGCT 42070	CCC
			AGCTG TTCCAGAGGTTG	
			TCGAC AAGGTCTCCGAC	
			TAA	
GAM2366	GCDH	3'	CATTTACCCTGAAATAGCAGCT 26531	CC C A TG
	T		AAGCTGC TT CAG GGT GTG	
			TTCGACG AA GTC CCA TAC	
			AT A _ TT	
GAM2366	GCDH	3'	CATTTACCCTGAAATAGCAGCT 5673	CC C A TG
	T		AAGCTGC TT CAG GGT GTG	
			TTCGACG AA GTC CCA TAC	
			AT A _ TT	
GAM2366	GPC1	3'	ATCTCTGGAAGGGGCAGC 10856	_
			GCTGCCC TTCCAGAGGT	
			CGACGGG AAGGTCTCTA	
			G	
GAM2366	IL2RB	3'	CACTGGCCTCCAGAAGGGCAGC 7932	CA TG
	T		AGCTGCCCTTC GAGGT GTG	
			TCGACGGAAG CTCCG CAC	
			AC GT	
GAM2366	LDOC1	3'	CACCAACCCCTGAAGGGGCCGT 25546	T C A
			GC GCCCTT CAG GGTG	
			TG CGGGGA GTC CCAACCAC	
			C A C	
GAM2366	MMP19	5'	CACCTGGTTGGAAGGACAAC 43301	C C AGGTT
			AG TG CCTTCCAG GGTG	

		TC AC GGAAGGTT CCAC	
		A A GGT__	
GAM2366 PBX3	3'	ACCAATCAAACACAGCTT 21667	CCC CCAGA
		AAGCTG TT GGTGGT	
		TTCGAC AA CTAACCA	
		ACA A__	
GAM2366 PEX14	3'	CTGGCCCTGGGAGGGCAGCTT 64401	A TG
		AAGCTGCCCTTCCAG GGT G	
		TTCGACGGGAGGGTC CCG C	
		_ GT	
GAM2366 RBM3	5'	ACCAACCCAGAGCATGCTT 71001	_ C TCCAGA
		AAGC TGC CT GGTGGT	
		TTCG ACG GA CCAACCA	
		T A C__	
GAM2366 SYT1	3'	ATTTCGTGGAAGGGCAGC 20112	_
		GCTGCCCTTCCA GAGGT	
		CGACGGGAAGGT CTTTA	
		G	
GAM2366 BAT8	3'	CCCTGGGAGGGCAACTT 22964	C A
		AAG TGCCCTTCCAG GG	
		TTC ACGGAGGGTC CC	
		A _	
GAM2366 C1orf33	3'	CCTCTGGAGAGAGCAGCTT 32982	C _
		AAGCTGC CT TCCAGAGG	
		TTCGACG GA AGGTCTCC	
		A G	
GAM2366 CCR6	3'	CACCAATTGGATAAAGCAGCT 49397	CCT_ GAG
		AGCTGC TCCA GTTGGTG	
		TCGACG AGGT TAACCAC	
		AAAT _	
GAM2366 CCR6	3'	CACCAATTGGATAAAGCAGCT 16438	CCT_ GAG
		AGCTGC TCCA GTTGGTG	
		TCGACG AGGT TAACCAC	
		AAAT _	
GAM2366 FAM3D	3'	CACATCCTACCCGGAAGACCAG 57945	CC AG_ TTG
C		GCTG CTTCC AGG GTG	
		CGAC GAAGG TCC CAC	
		CA CCCA TA_	
GAM2366 FLJ11267	3'	CAGTTTCCTGAAAGGGAGC 39496	G C _ GG
		GCT CCCTT CAG A TTG	

		CGA GGGAA GTC T GAC	
		_ A C TT	
GAM2366	FLJ20716	3' CAGCACAGAAGGGCAGCT 36038	CAGAG
		AGCTGCCCTTC GTTG	
		TCGACGGGAAG CGAC	
		ACA__	
GAM2366	FLJ21432	3' CACCAACAGAAGTAGCAGC 44940	C_ CAGAG
		GCTGC CTTC GTTGGTG	
		CGACG GAAG CAACCAC	
		AT A__	
GAM2366	GTPBP1	3' ACCAACCCAAAGACAGCT 16261	CC CCAGA
		AGCTG CTT GGTTGGT	
		TCGAC GAA CCAACCA	
		A_ AC__	
GAM2366	HTEX4	5' CTTTCCCTGAAGGGGCAGCTT 93723	C A TT
		AAGCTGCCCTT CAG GG GG	
		TTCGACGGGGA GTC CC TC	
		A _ TT	
GAM2366	HTEX4	5' CTTTCCCTGAAGGGGCAGCTT 99564	C A TT
		AAGCTGCCCTT CAG GG GG	
		TTCGACGGGGA GTC CC TC	
		A _ TT	
GAM2366	HTEX4	5' CTTTCCCTGAAGGGGCAGCTT 99720	C A TT
		AAGCTGCCCTT CAG GG GG	
		TTCGACGGGGA GTC CC TC	
		A _ TT	
GAM2366	KIAA0125	3' CAACCTCCTAGAAGGACACTT 29560	C C CA_
		AAG TG CCTTC GAGGTTG	
		TTC AC GGAAG CTCCAAC	
		_ A ATC	
GAM2366	KIAA0494	5' CAACCCTGGAAGGCAGCT 29399	C A
		AGCTGCC TTCCAG GGTTG	
		TCGACGG AAGGTC CCAAC	
		- -	
GAM2366	KIAA0515	3' CAGCCTCCGGGAGGGCAGCTT 64544	A
		AAGCTGCCCTTCC GAGGTTG	
		TTCGACGGGAGGG CTCCGAC	
		C	
GAM2366	KIAA0914	3' CAGCTCTGGAAGGCAGC 30293	C G
		GCTGCC TTCCAGAG TTG	

CGACGG AAGGTCTC GAC

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      - -
GAM2366 KPNA6  3' CACCAGCCAGCGGAAGAGCAGC 25539  C  AGA
                  GCTGC CTTCC  GGTGGGTG
                  ||||| |||||  |||||
                  CGACG GAAGG  CCGACCAC
                  A  CGA
GAM2366 MGC3123 3' GGCTGCCTGCAAGGGCAGCT 44347  C  A_
                  AGCTGCCCTT CAG  GGTT
                  ||||| |||||  |||||
                  TCGACGGGAA GTC  TCGG
                  C  CG
GAM2366 SS18L1 3' CAGCCCCTGGAGGGCAGC 65949  T  A
                  GCTGCCCT CCAG  GGTTG
                  ||||| |||||  |||||
                  CGACGGGA GGTC  CCGAC
                  -  C
GAM2366 TFIP11 3' ACCTTCAAAAGGGTAACTT 25118  C  CCA
                  AAG TGCCCTT  GAGGT
                  ||| |||||  |||||
                  TTC ATGGGAA  TTCCA
                  A  AAC
GAM2366 TGIF2  3' CCTCCAGAGAGGCAGCTT 41746  C  CA
                  AAGCTGCC TTC  GAGG
                  ||||| |||  |||||
                  TTCGACGG GAG  CTCC
                  A  AC
GAM2366 WBSCR22 3' CACGCGGTTCTGGAAAGGCACT 34466  C  C  G TT _
      T          AAG TGCC TTCCAGA G  G GTG
                  ||| ||||| ||||| | | |||
                  TTC ACGG AAGGTCT T  C CAC
                  -  A  _GG G
GAM2366 WNT8A  3' GACTTCTGAAGAGCAGC 50033  C  C
                  GCTGC CTTC AGAGGTT
                  ||||| |||||  |||||
                  CGACG GAAG TCTTCAG
                  A  _
GAM2366 WNT8A  3' GACTTCTGAAGAGCAGC 55257  C  C
                  GCTGC CTTC AGAGGTT
                  ||||| |||||  |||||
                  CGACG GAAG TCTTCAG
                  A  _
GAM2366 LOC144563 5' CACCAACCTGTGCAGGCAGC 77391  CTTC G
                  GCTGCC  CA AGGTTGGTG
                  ||||| ||  |||||
                  CGACGG  GT TCCAACCAC
                  AC_  G
GAM2366 LOC150271 3' CTGGCTCTGGAGGACAGCT 86136  C  T  G TG
                  AGCTG CCT CCAGAG T  G
                  ||||| ||| ||||| | |
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	TCGAC GGA GGTCTC G C	
	A _ _ GT	
GAM2366 LOC152271 3'	CACCAACCTGCGCAGGCAGC 81352	CTTCCAG
	GCTGCC AGGTTGGTG	
	CGACGG TCCAACCAC	
	ACGCG_	
GAM2366 LOC154092 3'	CTGACTCTGGTAAGGGCAGC 87368	_ G TG
	GCTGCCCTT CCAGAG T G	
	CGACGGGAA GGTCTC A C	
	T _ GT	
GAM2366 LOC155060 3'	CATTACCTGGGAAAGGCAGCTT 87603	C AG T
	AAGCTGCC TTCC AGGT GGTG	
	TTCGACGG AAGG TCCA TTAC	
	A G_ _	
GAM2366 LOC159121 5'	CAATTCTGAGAGGGCAGC 88384	TC G
	GCTGCCCT CAGAG TTG	
	CGACGGGA GTCTT AAC	
	GA _	
GAM2366 LOC169026 5'	CAAGTCTCCCTAGAAAAGCAGT 83599	CC CA_ _
TT	AAGCTGC TTC GAGG TTG	
	TTTGACG AAG CTCT AAC	
	AA ATCC G	
GAM2366 LOC200311 3'	CTGGCTCTGGAGGACAGCT 91575	C T G TG
	AGCTG CCT CCAGAG T G	
	TCGAC GGA GGTCTC G C	
	A _ _ GT	
GAM2366 LOC202347 5'	ACCTGCCTGGGAAAACAGCTT 91943	CCC AG T
	AAGCTG TTCC AGGT GGT	
	TTCGAC AAGG TCCG CCA	
	AA_ G_ T	
GAM2366 LOC203025 5'	CAAGCTAGAGGGCAGCTT 90743	CCAG G
	AAGCTGCCCTT AG TTG	
	TTCGACGGGAG TC AAC	
	A_ G	
GAM2366 LOC221540 5'	CAGGCTCTGGAACAGCAGCT 95476	CC G
	AGCTGC TTCCAGAG TTG	
	TCGACG AAGGTCTC GAC	
	AC G	
GAM2366 LOC257545 5'	CAGGCTCTGGAACAGCAGCT 99640	CC G
	AGCTGC TTCCAGAG TTG	

	TCGACG AAGGTCTC GAC		
	AC G		
GAM2366 LOC257598 5'	CAGGCTCTGGAACAGCAGCT 99748	CC	G
	AGCTGC TTCCAGAG TTG		
	TCGACG AAGGTCTC GAC		
	AC G		
GAM2366 LOC57862 3'	CTGACTCCTGGAAGAGCAACT 41322	C C	AG TG
	AG TGC CTTCCAG GT G		
	TC ACG GAAGGTC CA C		
	A A CT GT		
GAM2366 LOC91974 5'	GACCCAGGAAGGGCAGCT 68363	AGA	
	AGCTGCCCTTCC GGTT		
	TCGACGGAAGG CCAG		
	AC_		
GAM2367 TERF1 3'	CCCAAATCCTGTTCCAATGA 34391	C TA	C
	TCATTGGA ACG GATT GGG		
	AGTAACCT TGT CTAA CCC		
	_ C_ A		
GAM2367 FLJ10159 3'	CCATGTCACGCCATCCAATGAC 36334	CA_ A	TC
	GTCATTGGA CGT GAT GG		
	CAGTAACCT GCA CTG CC		
	ACC _ TA		
GAM2367 FLJ14213 3'	CCGATGCTCCCAATGACG 46216	ACAC	GAT
	CGTCATTGG GTA TCGG		
	GCAGTAACC CGT AGCC		
	CT_ _		
GAM2367 MGC10715 3'	ATTTACCAGACATCCAATGAC 44495	CAC_	
	GTCATTGGA GTAGAT		
	CAGTAACCT CATTTA		
	ACAGAC		
GAM2367 MOST2 5'	CCAGGACTGCCCAATGAC 40059	ACAC A	_
	GTCATTGG GTAG TTC GG		
	CAGTAACC CGTC AGG CC		
	_ _ A		
GAM2367 LOC150370 3'	CCGGGTCTACGTGCCCATGAC 86123	T A	
	GTCAT GG CACGTAGATTCCG		
	CAGTA CC GTGCATCTGGGCC		
	C _		
GAM2367 LOC152620 3'	CCCAAATCCTGTTCCAATGA 60707	C TA	C
	TCATTGGA ACG GATT GGG		

			AGTAACCT TGT CTAA CCC		
			_ C_ A		
GAM2367	LOC158668	3'	CCCAAATCCTGTTCCAATGA 69896	C TA C	
			TCATTGGA ACG GATT GGG		
			AGTAACCT TGT CTAA CCC		
			_ C_ A		
GAM2368	ACHE	3'	CTCGACGAGGCGGAGCGCCAGT 32332	A__ AGAACAC	
			GGA TCCATTGGC CCG CGAG		
			AGGTGACCG GGC GCTC		
			CGA GGAGCA_		
GAM2368	FUT5	3'	CTCGGTGTGAGCGCCAGCGGA 10727	A ACC AGA	
			TCC TTGGC G ACACCGAG		
			AGG GACCG C TGTGGCTC		
			C __ GAG		
GAM2368	FLJ20626	3'	CTCGGTGTTCTCGGGGCCTGGA 35901	TT A	
			TCCA GGC CCGAGAACACCGAG		
			AGGT CCG GGCTCTTGTGGCTC		
			_ G		
GAM2368	LOC158401	5'	TCAGTCTTGACCAATGGA 82805	CA ACACC	
			TCCATTGG CCGAGA GA		
			AGGTAACC GGTTCT CT		
			A_ GA__		
GAM2368	LOC219920	5'	TCGGCCTGGTGCCAAGGA 94963	A G AACA	
			TCC TTGGCACC AG CCGA		
			AGG AACCGTGG TC GGCT		
			_ _ C__		
GAM2368	LOC221463	3'	TGGTCCTCAGTAACCAATGGA 93711	C_ C AAC	
			TCCATTGG AC GAG ACCG		
			AGGTAACC TG CTC TGGT		
			AA A C__		
GAM2368	LOC91355	5'	CGGTAGACGGACCAATGGA 66306	CA AGAAC	
			TCCATTGG CCG ACCG		
			AGGTAACC GGC TGGC		
			A_ AGA__		
GAM2369	ELF3	3'	TGACCTTGACCTTGACCAA 16685	T GAT AAA	
			TTGGT CAAGG GG GTCA		
			AACCA GTTCC TC CAGT		
			_ AGT _		
GAM2369	JAK2	3'	TGACCTTCATTCTGAGACCAA 18318	CAA AA	
			TTGGTT GGGATGGA GTCA		

			AACCAG TCTTACTT CAGT		
			AG_ C_		
GAM2369	SLC10A2	5'	ACTCTCTGTCTTGACCAA 6590	CAA	A
			TTGGTT GGGATGGA AGT		
			AACCAG TTCTGTCT TCA		
			_____ C		
GAM2369	FLJ10803	3'	GTGACTTTTCAGTTAAAGCCAA 37205	CAAGG	G
			TTGGTT GAT GAAAGTCAC		
			AACCGA TTG CTTTCAGTG		
			AA_____ A		
GAM2369	KIAA1958	5'	GTGACTTTGAACCCCAAACC 82788	CAA	ATGG
			GGTT GGG AAAGTCAC		
			CCAA CCC TTTTCAGTG		
			A_ CAAG		
GAM2369	MARCKS	3'	ACTTTCCACCCTGCCCA 11411	TTCA	A
			TGG AGGG TGGAAAGT		
			ACC TCCC ACCTTTCA		
			CG_____		
GAM2369	TUB	5'	GTGGGACCATCCCTTAAACC 13898	C	AAAG
			GGTT AAGGGATGG TCAC		
			CCAA TTCCCTACC GGTG		
			A AG_____		
GAM2369	LOC80298	3'	ACTTTTACCTTGAACCA 48062	GATG	
			TGGTTCAAGG GAAAGT		
			ACCAAGTTCC TTTTCA		
			A_____		
GAM2370	CDC25C	3'	TCCTCATGTCTTCTCACA 10135	A	GA
			TGTGA GAAGACATG GA		
			ACACT CTTCTGTAC CT		
			_____ TC		
GAM2370	CDC25C	3'	TCCTCATGTCTTCTCACA 43333	A	GA
			TGTGA GAAGACATG GA		
			ACACT CTTCTGTAC CT		
			_____ TC		
GAM2370	ERBB3	3'	CCATTCCTCAGCTTCTCACA 10536	ACA	GA
			TGTGAAGAAG TG GAATGG		
			ACACTTCTTC AC CTTACC		
			G_ TC		
GAM2370	MUC4	5'	CCATTCCCCCATGTCTCCTCCC 37873	T A A	A_
	A		TG GA GA GACATGG GAATGG		

				AC CT CT CTGTACC CTTACC			
				C C _ CC			
GAM2370	MUC4	5'	CCATTCCCCCATGTCTCCTCCC	57155	T A A	A_	
	A		TG GA GA GACATGG GAATGG				
			AC CT CT CTGTACC CTTACC				
			C C _ CC				
GAM2370	PPP2R1A	3'	TCCACCTCCCGTCCTCCCCAT	27249	AA A	AT	AA
			GTG GA GAC GGAG TGGG				
			TAC CT CTG CCTC ACCT				
			CC C C_ C_				
GAM2370	SACM2L	3'	CCATTCCATACCCTTCTTCAC	42883	AC_	GA	
			GTGAAGAAG ATGGA ATGG				
			CACTTCTTC TACCT TACC				
			CCA _				
GAM2370	SACM2L	3'	CCATTCCATACCCTTCTTCAC	55455	AC_	GA	
			GTGAAGAAG ATGGA ATGG				
			CACTTCTTC TACCT TACC				
			CCA _				
GAM2370	SLC21A9	3'	TCCATTCTGGCTCCTCCAC	24383	A A	ACATGG	
			GTG AG AG AGAATGGA				
			CAC TC TC TCTTACCT				
			C C GG_				
GAM2370	SNAP25	3'	CCACCCGTGTTCTCCTCCA	13268	T A AG	AGAA	
			TG GA GA ACATGG TGG				
			AC CT CT TGTGCC ACC				
			_ C CT C_				
GAM2370	SNAP25	3'	CCACCCGTGTTCTCCTCCA	56422	T A AG	AGAA	
			TG GA GA ACATGG TGG				
			AC CT CT TGTGCC ACC				
			_ C CT C_				
GAM2370	TCF7	3'	CCATTCACAGAGCCTTTTTCAC	13617	ACA_	GA	
	A		TGTGAAGAAG TG GAATGG				
			ACACTTTTTC AC CTTACC				
			CGAG A_				
GAM2370	BC002942	3'	TTCCACGTCATCTTCACA	66072	A A		
			TGTGAAGA GAC TGGAG				
			ACACTTCT CTG ACCTT				
			A C				
GAM2370	C20orf111	5'	TCCACTCCAATCAGTCTATCTT	33630	_ A_	AA	
	CACA		TGTGAAGA AGAC TGGAG TGGG				

A C A C T T C T T C T G A C C T C A C C T
 A A C T A _
 GAM2370 DKFZp434D0513 5' CCAATTGATATTTTCTTCACA 62519 C G GAA
 TGTGAAGAAGA AT GA TGG
 ||||||| || || |||
 A C A C T T C T T T T T A T T A C C
 A G A _
 GAM2370 FLJ23153 3' CTTTCATGTCCTCTACACA 45269 A A
 TGTG AGA GACATGGAG
 |||| ||| |||||
 A C A C T C T C T G T A C T T C
 A C
 GAM2370 KIAA0053 3' CCATTCTCCAGGACTTCTCCA 30289 A ACA
 T G A G A A G T G G A G A A T G G
 || |||| |||||
 A C T C T T C A C C T C T T A C C
 C A G G
 GAM2370 KIAA0143 3' TTCCTCATCTTCTTCACA 65411 CAT
 TGTGAAGAAGA GGAG
 ||||||| |||
 A C A C T T C T T C T C C T T
 A C T
 GAM2370 KIAA0239 5' CCATCGATGGCACCTTCTTCA 31616 A _ _ G GAA
 T G A A G A A G C A T G A T G G
 |||||| ||| || |||
 A C T T C T T C G T A C T A C C
 C A C G G _
 GAM2370 KIAA0335 3' CCATTCCCTCTCTTCTTCCA 29670 T CAT A
 T G G A A G A A G G G G A A T G G
 || ||||| || |||||
 A C C T T C T T C T C C C T T A C C
 _ C T _ _
 GAM2370 KIAA1076 3' CCATTCTGTCCCCTTCCCA 66120 T AA TGGA
 T G G A A G G A C A G A A T G G
 || |||| ||| |||||
 A C C T T C C T G T C T T A C C
 C C C _ _
 GAM2370 KIAA1271 3' TCCATTCTCTTCAGCTCCCTAC 70147 AA A ACAT
 A T G T G G A G G G A G A A T G G A
 |||| || | |||||
 A C A T C T C T C T C T T A C C T
 C C _ G A C T
 GAM2370 MYH10 5' CCATGTTGCTTCTTCACA 69671 _
 TGTGAAGAAG ACATGG
 ||||||| |||||
 A C A C T T C T T C T G T A C C
 G T
 GAM2370 PMF1 3' CCTTTACCATGTTCTCTCCACA 24285 A AG A T
 TGTG AGA ACATGG GAA GG
 |||| ||| ||||| ||| ||

			ACAC TCT TGTACC TTT CC		
			C CT A _		
GAM2370	PMX2B	5'	CCACTCCAGCCACCTTCTCCAT 15382	A	ACA__ AA
	A		TGTG AGAAG TGGAG TGG		
			ATAC TCTTC ACCTC ACC		
			C CACCG _		
GAM2370	ZNF262	3'	TCCATTCTCAGTTTCTTCCCCA 18726	AA	C G
	CA		TGTG GAAGA AT GAGAATGGA		
			ACAC CTTCT TG CTCTTACCT		
			CC T A		
GAM2370	ZNF317	3'	CCACTCTCATCTTCTTCCA 72474	T	CATG A
			TG GAAGAAGA GAGA TGG		
			AC CTTCTTCT CTCT ACC		
			_ A__ C		
GAM2370	LOC115817	5'	CCACTCAGCCCCTTCTTCAC 57411		ACATG AA
			GTGAAGAAG GAG TGG		
			CACTTCTTC CTC ACC		
			CCCGA _		
GAM2370	LOC120114	3'	TCCACTAGAACTTCTTCACA 76053		ACA_ AGAA
			TGTGAAGAAG TGG TGGA		
			ACACTTCTTC ATC ACCT		
			AAAG _		
GAM2370	LOC125268	3'	CCAGACTCCCTCTTCACA 76573	A	ACAT AA
			TGTGAAGA G GGAG TGG		
			ACACTTCT C CCTC ACC		
			_ _ _ AG		
GAM2370	LOC136345	3'	CCATTCTTTGTCCTTCCCCATA 76711	AA	AC TG
			TGTG GAAG A GAGAATGG		
			ATAC CTTC T TTCTTACC		
			CC C_ GT		
GAM2370	LOC144512	3'	TCCATTCTCTCCATCCCTTC 84041	AC	_
			GAAG ATGGAGA ATGGA		
			CTTC TACCTCT TACCT		
			CC CT		
GAM2370	LOC146894	3'	TCCACTCTTTTCTTCTTCACA 59865	CAT	A
			TGTGAAGAAGA GGAGA TGGA		
			ACACTTCTTCT TTTCT ACCT		
			_ C		
GAM2370	LOC200609	5'	TCCATTCTCTTATCCCCTCA 91668	A	AA CAT
			TGA G GA GGAGAATGGA		

ACT C CT TCTCTTACCT
 _ CC AT_
 GAM2370 LOC221140 3' CCATTCTCCCCTGCTCACA 95145 AGA ACAT
 TGTGA AG GGAGAATGG
 |||| || |||||
 ACACT TC CCTCTTACC
 CG_ AC_
 GAM2370 LOC254143 3' TCCATTCTCTCCATCCCTTC 98255 AC _
 GAAG ATGGAGA ATGGA
 ||| ||||| ||||
 CTTT TACCTCT TACCT
 CC CT
 GAM2370 LOC257109 3' TCCATTCTCCATGATCCCTCAC 97308 AGAA _
 GTGA GA CATGGAGAATGGA
 ||| || |||||
 CACT CT GTACCTCTTACCT
 CC_ A
 GAM2370 LOC55833 3' CCATCTGCCTTCAGGTCTTCTT 65528 A A_
 CACA TGTGAAGAAGAC TGGAG ATGG
 ||||| |||| ||||
 ACACTTCTTCTG ACTTC TACC
 G CGTC
 GAM2371 BRCA1 3' TTGTTACTGAGCCACAG 24582 G ACC
 CTGTGGCT CAG AACAA
 ||||| || ||||
 GACACCGA GTC TTGTT
 _ A_
 GAM2371 CMAR 3' TTGCTGGTCTAGTCACGCAT 19039 T GC A
 ATGC GTGGCT AGACCA CAA
 ||| ||||| ||||| |||
 TACG CACTGA TCTGGT GTT
 _ _ C
 GAM2371 DAZL 3' TTTGTTGGTCTGAATACA 68701 GCTG
 TGTG CAGACCAACAAA
 ||| |||||
 ACAT GTCTGGTTGTTT
 AA_
 GAM2371 ELF3 5' TGCCGGCCTGCCTGCCACAGC 16686 T_ A AA
 GCTGTGGC GCAG CC CA
 ||||| |||| || ||
 CGACACCG CGTC GG GT
 TC C CC
 GAM2371 FBXL7 3' TTGTCAACTCAATACCATAGCA 25503 C_ C ACCA
 TGCTGTGG TG AG ACAA
 ||||| || || ||||
 ACGATACC AC TC TGTT
 ATA _ AAC_
 GAM2371 ITGA4 5' TGTTGGGGTCAGCCACAGC 7959 CAGA
 GCTGTGGCTG CCAACA
 ||||| |||||

		CGACACCGAC GGTTGT	
		TGG_	
GAM2371 KCNK3	3'	TGTCAGTCTGCAGAAATGGTCG 11179	T GG CA
		A GCTGT CTGCAGAC ACA	
		G TGGTA GACGTCTG TGT	
		C A_ AC	
GAM2371 MCP	3'	TTGGACCAGTCAGCACAGCAT 11486	G _ AGA_
		ATGCTGTG CTG C CCAA	
		TACGACAC GAC G GGTT	
		_ T ACCA	
GAM2371 MS4A7	5'	TGATCCCCAGCCACAGCA 41355	CA C
		TGCTGTGGCTG GA CA	
		ACGACACCGAC CT GT	
		CC A	
GAM2371 NT5M	3'	TTGGTCTCAGCCACAGCA 39894	C
		TGCTGTGGCTG AGACCAA	
		ACGACACCGAC TCTGGTT	
		_	
GAM2371 PSAP	3'	TCTTGGCAGAAACCACAGCAT 69888	___ _
		ATGCTGTGG CTGC AGA	
		TACGACACC GACG TCT	
		AAA GT	
GAM2371 PTP4A2	5'	GGCTCAGCACAGCAT 55370	G C A
		ATGCTGTG CTG AG CC	
		TACGACAC GAC TC GG	
		_ _ _	
GAM2371 PTP4A2	5'	GGCTCAGCACAGCAT 14441	G C A
		ATGCTGTG CTG AG CC	
		TACGACAC GAC TC GG	
		_ _ _	
GAM2371 PTPRF	3'	TTTGTTAAGAAAACTACAGCA 56142	CTGCAGACC
T		ATGCTGTGG AACAAA	
		TACGACATC TTGTTT	
		AAAAAGAA_	
GAM2371 PTPRF	3'	TTTGTTAAGAAAACTACAGCA 12610	CTGCAGACC
T		ATGCTGTGG AACAAA	
		TACGACATC TTGTTT	
		AAAAAGAA_	
GAM2371 RAB5C	3'	CTGCTGGGAAACCACAGCAT 60526	___ _
		ATGCTGTGG CT GCAG	

TACGACACC GG CGTC
 AAAG T
 GAM2371 SPG7 3' TTGCTGGTCTAGTCACGCAT 13349 T GC A
 ATGC GTGGCT AGACCA CAA
 |||| |||| |||| ||
 TACG CACTGA TCTGGT GTT
 _ _ C
 GAM2371 TRIM9 3' TTGAGTTGCAGTCCACAGCAT 31465 _ AC
 ATGCTGTGG CTGCAG CAA
 |||| |||| ||
 TACGACACC GACGTT GTT
 T GA
 GAM2371 AF9Q34 5' TGCCGGTCTGCAGCTGAGC 51724 G AA
 GCT TGGCTGCAGACC CA
 || |||| |||| ||
 CGA GTCGACGTCTGG GT
 _ CC
 GAM2371 C11orf11 3' GGCTGCAGCCACACCAT 94879 C A
 ATG TGTGGCTGCAG CC
 || |||| |||| ||
 TAC ACACCGACGTC GG
 C _
 GAM2371 FGD3 3' TGCTGGTCTGCAGCGTGGTCC 73283 T TG G A
 A GC TG CTGCAGACCA CA
 | || || |||| ||
 C TG GC GACGTCTGGT GT
 C GT _ C
 GAM2371 FLJ10898 5' GGTCAGTGCAACTACAGCA 60138 C _
 TGCTGTGG TGCA GACC
 |||| |||| ||
 ACGACATC ACGT CTGG
 A GA
 GAM2371 FLJ11850 3' TTGATCTGCAGCAACTCGT 43026 CT G C
 ATG GT GCTGCAGA CAA
 || || |||| ||
 TGC CA CGACGTCT GTT
 T_ A A
 GAM2371 FLJ13110 3' TGTAATGCAAACACAGCAT 43587 GC GACCA
 ATGCTGTG TGCA ACA
 |||| |||| ||
 TACGACAC ACGT TGT
 AA AAA_
 GAM2371 FLJ21313 3' TGTTGGCCTAGTGGACAGC 43935 GG TG _ A
 GCTGT C C AG CCAACA
 |||| | || ||||
 CGACA G G TC GGTGT
 _ GT A C
 GAM2371 GP 5' TGCTGACCTGCAGCCTGTGGC 37977 TG _ AC A
 GC T GGCTGCAG CA CA
 || |||| || ||

		CG G CCGACGTC GT GT	
		GT T CA C	
GAM2371 IL18BP	3'	TGCCCTCCAGCCACAGCA 20315	C AC
		TGCTGTGGCTG AG CA	
		ACGACACCGAC TC GT	
		C CC	
GAM2371 KIAA0625	3'	TGGGCCAGCAGCCACAGCAT 31179	AGA_
		ATGCTGTGGCTGC CCA	
		TACGACACCGACG GGT	
		ACCG	
GAM2371 KIAA0766	3'	TGTTAGCTCACCATAGCA 29677	C C ACC
		TGCTGTGG TG AG AACA	
		ACGATACC AC TC TTGT	
		_ _ GA_	
GAM2371 LEPROTL1	3'	TTGTTGGCCATTACGCA 31704	T GC CAGA
		TGC GTG TG CCAACAA	
		ACG CAC AC GGTGTT	
		_ TT C__	
GAM2371 MGC27434	3'	TTGTTGTGTT CAGCCACA 59595	CA _
		TGTGGCTG GAC CAACAA	
		ACACCGAC TTG GTTGTT	
		_ T	
GAM2371 TRAF4	3'	TGGGCTGGCTAAACCACAGCA 63322	CT__ _ A
		TGCTGTGG GC AG CCA	
		ACGACACC CG TC GGT	
		AAAT G G	
GAM2371 WDR9	3'	TTGCTGGTCTTTGTAGCAGCAT 54458	G TGC A
		ATGCTGT GC AGACCA CAA	
		TACGACG TG TCTGGT GTT	
		A TT_ C	
GAM2371 ZNF384	3'	TGTCCTCTAGCCACAGCAT 56798	C AC
		ATGCTGTGGCTG AG CA	
		TACGACACCGAT TC GT	
		C CT	
GAM2371 LOC129073	5'	TGCTGGTCTGCAGGACACA 76313	G_ A
		TGTG CTGCAGACCA CA	
		ACAC GACGTCTGGT GT	
		AG C	
GAM2371 LOC143437	5'	TGGATTCCACAGCCACACA 83860	C CA _
		TG TGTGGCTG GA CCA	

	AC ACACCGAC CT GGT		
	— AC TA		
GAM2371 LOC145725 5'	TTGCTGGTCACACAGTCAC 77890	CA_	A
	GTGGCTG GACCA CAA		
	CACTGAC CTGGT GTT		
	ACA C		
GAM2371 LOC145732 5'	TTGCTGGTCACACAGTCAC 77902	CA_	A
	GTGGCTG GACCA CAA		
	CACTGAC CTGGT GTT		
	ACA C		
GAM2371 LOC146669 3'	CTGTAGCCACCACAGCAT 78661	—	
	ATGCTGT GGCTGCAG		
	TACGACA CCGATGTC		
	CCA		
GAM2371 LOC150271 3'	TTGGGCTGCCACAGCA 86151	T AGA	
	TGCTGTGGC GC CCAA		
	ACGACACCG CG GGTT		
	T —		
GAM2371 LOC150368 3'	TGGAAGCCCCGCAGCCACTGCA 80519	T AGA—	
T	ATGC GTGGCTGC CCA		
	TACG CACCGACG GGT		
	T CCCCAGAA		
GAM2371 LOC151446 3'	TTTGTCAAGGTGCCACAGCA 86577	TGCAG A_	
	TGCTGTGGC ACC ACAA		
	ACGACACCG TGG TGTTT		
	— AAC		
GAM2371 LOC157740 3'	GTTAATCTGCAGCAGAGC 82467	G G CC	
	GCT TG CTGCAGA AAC		
	CGA AC GACGTCT TTG		
	G _ AA		
GAM2371 LOC163231 5'	TTGTTAAGTCTCAGCCACACAT 83341	C _ ACC	
	ATG TGTGGCTG CAG AACAA		
	TAC ACACCGAC GTC TTGTT		
	_ T AA_		
GAM2371 LOC196812 3'	TTTGTCAAGTCTAAGTTACAG 91130	GC CA	
	CTGTGGCT AGAC ACAA		
	GACATTGA TCTG TGTTT		
	A_ AC		
GAM2371 LOC196957 5'	TTGCTGGTCACACAGTCAC 89196	CA_	A
	GTGGCTG GACCA CAA		

	CACTGAC CTGGT GTT		
	ACA C		
GAM2371 LOC196961 5'	TTGCTGGTCACACAGTCAC 89209	CA_	A
	GTGGCTG GACCA CAA		
	CACTGAC CTGGT GTT		
	ACA C		
GAM2371 LOC197138 5'	TTGCTGGTCACACAGTCAC 89258	CA_	A
	GTGGCTG GACCA CAA		
	CACTGAC CTGGT GTT		
	ACA C		
GAM2371 LOC200314 3'	TTTGTAAATGTGCACCCACAGCA 91609	C	GACCA
	TGCTGTGG TGCA AAAAA		
	ACGACACC ACGT TGTTT		
	C GTAA_		
GAM2371 LOC200781 5'	GGTGTCTGCAGGCACAGCAT 91724	G	___
	ATGCTGTG CTGCAG ACC		
	TACGACAC GACGTC TGG		
	G CTG		
GAM2371 LOC201305 3'	GTTGGTCCCCACAGCA 89608	CTGCA	
	TGCTGTGG GACCAAC		
	ACGACACC CTGGTTG		
	C___		
GAM2371 LOC221178 3'	TGCAGGTCCAAACACAGCAT 95178	GC CA	AA
	ATGCTGTG TG GACC CA		
	TACGACAC AC CTGG GT		
	AA _ AC		
GAM2371 LOC222493 5'	TGTCAGTCTGTGGCACAGCA 96013	G TG	CA
	TGCTGTG C CAGAC ACA		
	ACGACAC G GTCTG TGT		
	_GT AC		
GAM2371 LOC253152 3'	TCTGTTTACCAGTCACAGCA 97169	_____	
	TGCTGTGGCTG CAGA		
	ACGACACTGAC GTCT		
	CATT		
GAM2371 LOC253531 5'	TGGATTCCACAGCCACACA 98226	C	CA _
	TG TGTGGCTG GA CCA		
	AC ACACCGAC CT GGT		
	_ AC TA		
GAM2371 LOC256267 5'	TTGTTGGTCTGGCTTCA 98620	T TG	
	TG GGC CAGACCAACAA		

AC TCG GTCTGGTTGTT
 T _
 GAM2371 LOC257017 5' TGTTGATCTACCGTAGTAT 99223 CTGC C
 ATGCTGTGG AGA CAACA
 ||||| |||||
 TATGATGCC TCT GTTGT
 A_ A
 GAM2371 LOC92466 5' TTGTTGGTCTGGCTTCA 69976 T TG
 TG GGC CAGACCAACAA
 || ||| |||||
 AC TCG GTCTGGTTGTT
 T _
 GAM2372 SRGAP1 3' GGAAGACACCATCTCCAA 72716 A C CA
 TTG AGGTGG GTCT TCT
 ||| ||||| ||| |||
 AAC TCTACC CAGA AGG
 C A _
 GAM2372 CL24751 5' AGACCAGACGCCACTCCAA 65322 AA CA
 TTG GGTGGCGTCT TCT
 ||| ||||| ||| |||
 AAC TCACCGCAGA AGA
 C_ CC
 GAM2372 FLJ22672 3' AGACTTTGGGAAGCCACCTTCA 46595 G TCT
 A TTGAAGGTGGC TCTCA GTCT
 ||||| ||||| ||| |||
 AACTTCCACCG AGGGT CAGA
 A TT_
 GAM2372 KIAA1017 3' AGGAAAGACACCACCCCAA 24267 AA C CA
 TTG GGTGG GTCT TCT
 ||| ||||| ||| |||
 AAC CCACC CAGA GGA
 CC A AA
 GAM2372 KIAA1303 3' AGAAGGAGACGCCCTCCAA 66599 A T A_
 TTG AGG GGCGTCTC TCT
 ||| ||| ||||| ||| |||
 AAC TCC CCGCAGAG AGA
 C _ GA
 GAM2372 LOC127428 3' ACAGAAACATCACCTTCAA 75150 GC CTCA
 TTGAAGGTG GT TCTGT
 ||||| || |||||
 AACTTCCAC CA AGACA
 TA A_
 GAM2373 GPD1 3' TCATGCCACCACATTTG 60398 C C
 TAAATG GGTGGCAT GA
 ||||| ||||| || |||
 GTTTAC CCACCGTA CT
 A _
 GAM2373 IL5RA 5' TCGCATGGCCACCGCATTT 6906 AT_
 AAATGCGGTGGC CGA
 ||||| ||| |||

		TTTACGCCACCG GCT		
		GTAC		
GAM2373	MYO1C	3' TGCCGATGCCAAATATTTG 61873	CGG	A
		TAAATG TGGCATCG CA		
		GTTTAT ACCGTAGC GT		
		AA_ C		
GAM2373	C6orf37	3' TGTCACACTGCATTTA 68097	GCATC	
		TAAATGCGGTG GACA		
		ATTTACGTCAC CTGT		
		A_____		
GAM2373	DNAJC6	3' TTGCAGAACCACCGCATT 29498	CA GA	
		AATGCGGTGG TC CAA		
		TTACGCCACC AG GTT		
		A_ AC		
GAM2373	FLJ11210	3' GTCGATGTGCATGCTTTTA 60319	T GTG	
		TAAA GCG GCATCGAC		
		ATTT CGT TG TAGCTG		
		T ACG		
GAM2373	FLJ12476	3' TCGATCTTCTGCATTTA 43270	T C	
		TAAATGCGG GG ATCGA		
		ATTTACGTC TC TAGCT		
		T _		
GAM2373	KIAA1034	3' TCGATGGCATCCGCATTTG 63134	_ G	
		TAAATGCGG TG CATCGA		
		GTTTACGCC AC GTAGCT		
		T G		
GAM2373	KIAA1987	3' TCATGTAAGTGCATTTA 89391	G C	
		TAAATGCGGT GCAT GA		
		ATTTACGTCA TGTA CT		
		A _		
GAM2373	MGC16063	3' TGTCCTGGCCACTGCATT 54929	ATC	
		AATGCGGTGGC GACA		
		TTACGTCACCG CTGT		
		GTC		
GAM2373	LOC147949	3' TGTCAGATGTCCACATTGCA 79279	_ _ _	
		TGCG GTGG CATC GACA		
		ACGT CACC GTAG CTGT		
		TA T A		
GAM2373	LOC150577	3' GTCCTCACCGCATTTG 86258	CATC	
		TAAATGCGGTGG GAC		

		GTTTACGCCACT	CTG		
		C___			
GAM2373	LOC158219	3'	TGTGTGTCACCACATTT	82694	C CG
			AAATG GGTGGCAT ACA		
			TTTAC CCACTGTG TGT		
			A _		
GAM2373	LOC202020	3'	TGTCTCACCACATTTA	90605	C CATC
			TAAATG GGTGG GACA		
			ATTTAC CCACT CTGT		
			A _		
GAM2373	LOC90826	5'	TGTCGATGCAGGTTTATTTG	64788	CGGTG
			TAAATG GCATCGACA		
			GTTTAT CGTAGCTGT		
			TTGGA		
GAM2373	LOC93587	3'	TTGTCTTTACCTGCATTTA	73042	_ CATC
			TAAATGC GGTGG GACAA		
			ATTTACG CCATT CTGTT		
			T T__		
GAM2374	ANKT	3'	TCTCTATAGAATATAGTA	33460	CGAA
			TATTATG TCTATAGAGA		
			ATGATAT AGATATCTCT		
			A__		
GAM2374	FLJ12892	3'	TATTCTCTATTTTATAAATAAT	68458	GCGAATCT
			A TATTAT ATAGAGAATA		
			ATAATA TATCTCTTAT		
			AATATTT_		
GAM2374	FLJ22009	3'	TCCTGTATTTGCATAATA	60922	TC A
			TATTATGCGAA TATAG GA		
			ATAATACGTTT ATGTC CT		
			_ _		
GAM2374	RPH3A	3'	ATTCTCTACAGAAGCAT	30930	GAA A
			ATGC TCT TAGAGAAT		
			TACG AGA ATCTCTTA		
			A_ C		
GAM2374	LOC257465	3'	TATTCTCTATAAATCATAA	82501	CGA C
			TTATG AT TATAGAGAATA		
			AATAC TA ATATCTCTTAT		
			_ A		
GAM2375	ATF7	3'	TCCCAGCCCCGGAGCCTCATA	23404	_ TAGA CC
			TATGAGGC CC GCT GGGA		

		ATACTCCG GG CGA CCCT		
		A CCC_ _		
GAM2375 CREBBP	5'	CCCGCCGGTCCCGGGCCCCA	16495	A TA G C_
		TG GGCCG GA CT CGGG		
		AC CCGGG CT GG GCCC		
		C CC _ CC		
GAM2375 EGLN2	5'	TTGGGGCTCCAGAACCTC	34522	CC A
		GAGG CT GAGCTCCGG		
		CTCC GA CTCGGGGTT		
		AA C		
GAM2375 GNA11	5'	CCCAGTGACTCTGGGCCTCA	76586	T C C_
		TGAGGCC AGAG TC GGG		
		ACTCCGGG TCTC AG CCC		
		_ _ TGA		
GAM2375 LATS2	3'	GTCCCGGAGCCGGTGCCCTCA	28135	_ _ TAGA
		TGAGG C CC GCTCCGGGAC		
		ACTCC G GG CGAGGCCCTG		
		C T C_		
GAM2375 NLGN3	3'	GTCTCTCTGGCTCTAGGACC	39121	C CC_
		GG CCTAGAGCT GGGAC		
		CC GGATCTCGG CTCTG		
		A TCT		
GAM2375 NOTCH1	5'	GTCCCGGAGCCCCAAGTGCTT	92138	C AGA_
		AGGC CT GCTCCGGGAC		
		TTCG GA CGAGGCCCTG		
		T ACCC		
GAM2375 PCDH1	3'	CCCATTCCAGGGCCTCA	51575	A CTCC
		TGAGGCCCT GAG GGG		
		ACTCCGGGA CTT CCC		
		C A_		
GAM2375 PML	3'	TCCCAGAGGGGCCTCAT	53805	TAGAG C
		ATGAGGCC CTC GGGA		
		TACTCCGGG GAG CCCT		
		_ _ _ A		
GAM2375 RBBP9	3'	TCCGGAGTCTAGAGCCCCA	70699	A C G
		TG GGC CTAGA CTCCGGG		
		AC CCG GATCT GAGGCCT		
		C A _		
GAM2375 UBQLN1	5'	CCGAGCTCCGGGGCCCCA	26473	A TA C
		TG GGCCG GAGCTC GG		

AC CCGGG CTCGAG CC
 C GC _
 GAM2375 ARTN 5' CCCGGGCCTGGAGCCCCA 55114 A C A T
 TG GGC CTAG GC CCGGG
 || ||| ||| ||| |||
 AC CCG GGTC CG GGCCC
 C A _ _
 GAM2375 CNTNAP1 3' CCCAAAGGAGAAGCCTCATG 14641 CCTAGAG _
 TATGAGGC CTCC GGG
 ||||| ||| |||
 GTACTCCG GAGG CCC
 AA _ AAA
 GAM2375 FLJ10898 5' CCCCAAGCCAGGCACAGCCTCA 60130 _ AGA CC
 TA TATGAGGC CCT GCT GGG
 ||||| ||| ||| |||
 ATACTCCG GGA CGA CCC
 ACAC C _ AC
 GAM2375 KIAA1977 5' CGAAGGCTCAGGGCCTCA 74765 A C _
 TGAGGCCCT GAGCT CG
 ||||| ||| ||| |||
 ACTCCGGGA CTCGG GC
 _ AA
 GAM2375 P24B 3' TCCTGCTCTAGGGCCCCTCA 24774 _ TCC
 TGA GGCCCTAGAGC GGGA
 || ||||| ||| |||
 ACT CCGGATCTCG TCCT
 CC _
 GAM2375 LOC146669 3' GTCTTTCTCCAGGGGCCTCA 78664 A _ CTCC
 TGAGGCCCT GAG GGGAC
 ||||| ||| ||| |||
 ACTCCGGGG CTC TTCTG
 AC T _
 GAM2375 LOC170127 5' CCCGGAGCCCCAGGGGCCCA 83456 A AGA _
 TG GGCCCT GCTCCGGG
 || ||||| |||||
 AC CCGGGG CGAGGCC
 _ ACCC
 GAM2375 LOC256812 5' CCCGGAGCCCCCTGGGCCCA 99406 A TAGA _
 TG GGCC GCTCCGGG
 || ||||| |||||
 AC CCGGG CGAGGCC
 C TCCCC
 GAM2375 LOC90408 5' CCCCTCTCCGAGGCCTCATA 63342 CTA CTCC
 TATGAGGCC GAG GGG
 ||||| ||| |||
 ATACTCCGG CTC CCC
 AGC TC _
 GAM2376 PACE4 3' GGCCATCCTCACATGTGACA 11951 CA AC TT
 TGTTACATG AG TG GCC
 ||||| ||| ||| |||

		ACAGTGTAC TC AC CGG	
		AC CT _	
GAM2376 PACE4	3'	GGCCATCCTCACATGTGACA 57163	CA AC TT
		TGTTACATG AG TG GCC	
		ACAGTGTAC TC AC CGG	
		AC CT _	
GAM2376 PHKA2	3'	TTGGCATGGCTGCCTTGATGTA 6090	G ACT _
ACA		TGTTACAT CAAG GT TGCCAA	
		ACAATGTA GTTC CG ACGGTT	
		_ CGT GT	
GAM2376 SH3GL2	3'	TTGGCAATGCTGCTTATAACA 13099	CAT AGAC
		TGTTA GCA TGTTGCCAA	
		ACAAT CGT GTAACGGTT	
		ATT C_	
GAM2376 SLC1A1	3'	GCATAGTTCTGCAATAACA 16056	CA AG T
		TGTTA TGCA ACTGT GC	
		ACAAT ACGT TGATA CG	
		A_ CT _	
GAM2376 FLJ10352	3'	TGACAGTTACATGGTAACA 50473	_ CAA
		TGTTAC ATG GACTGTTG	
		ACAATG TAC TTGACAGT	
		G A_	
GAM2376 FLJ20093	3'	TGGAGGTTTTACCACATGTAAC 35040	C_ GTTG
A		TGTTACATG AAGACT CCA	
		ACAATGTAC TTTTGG GGT	
		ACCA A_	
GAM2376 FLJ32861	5'	GCAACAGTAACATAAGCA 59381	AC CAAG
		TGTT ATG ACTGTTGC	
		ACGA TAC TGACAACG	
		A_ AA_	
GAM2376 GOLPH3	3'	TAGCAGATGTTGCATGTAA 42394	GA_
		TTACATGCAA CTGTTG	
		AATGTACGTT GACGAT	
		GTA	
GAM2376 KIAA0903	3'	CGGTCCTGCCACATGTAACA 71910	_ A
		TGTTACAT GCA GACTG	
		ACAATGTA CGT CTGGC	
		CAC C	
GAM2376 KIAA0993	3'	TAGCTTATCTTGCATAGAACA 64823	AC CT_
		TGTT ATGCAAGA GTTG	

		ACAA TACGTTCT CGAT	
		GA ATT	
GAM2376 KIAA1500	3'	CAACAGTGCCTTGCATGTAACA 64806	___
		TGTTACATGCAAG ACTGTTG	
		ACAATGTACGTTT TGACAAC	
		CG	
GAM2376 KIAA1576	3'	AGCATGTCCCAACATGTAACA 66488	CAA_ _
		TGTTACATG GAC TGTT	
		ACAATGTAC CTG ACGA	
		AACC T	
GAM2376 KIAA1679	3'	TTGGCAACTGGTCTGCATGTAA 70720	A _
		TTACATGCA GACT GTTGCCAA	
		AATGTACGT CTGG CAACGGTT	
		_ T	
GAM2376 MGC14425	3'	TAGCAGTCCCGCAGTAACA 52950	A AA
		TGTTAC TGC GACTGTTG	
		ACAATG ACG CTGACGAT	
		_ CC	
GAM2376 MRPL35	3'	TAGCAGGTTTGCATGCAGCA 34024	A A
		TGTT CATGCAAG CTGTTG	
		ACGA GTACGTTT GACGAT	
		C G	
GAM2376 NDST3	5'	TTGGCGACGGGTCTTGCATGTG 17722	_
ACA		TGTTACATGCAAGACT GTTGCCAA	
		ACAGTGACGTTCTGG CAGCGGTT	
		G	
GAM2376 TSCOT	3'	CAACAGTTTTGCACGAACA 53511	ACA
		TGTT TGCAAGACTGTTG	
		ACAA ACGTTTTGACAAC	
		GC_	
GAM2376 LOC149734	3'	GACATCTTGCATATAACA 85795	C C
		TGTTA ATGCAAGA TGTT	
		ACAAT TACGTTCT ACAG	
		A _	
GAM2376 LOC161003	3'	CAACACTGTTTCATGTAACA 59912	CA_ AC
		TGTTACATG AG TGTTG	
		ACAATGTAC TC ACAAC	
		TTG _	
GAM2376 LOC201780	3'	TGGTTCACATCATACATGTAAC 90485	CAA C T_
A		TGTTACATG GA TGT GCCA	

		ACAATGTAC CT ACA TGGT	
		ATA _ CT	
GAM2376	LOC256160 3'	TGGTTCACATCATACATGTAAC 97565	CAA C T_
	A	TGTTACATG GA TGT GCCA	
		ACAATGTAC CT ACA TGGT	
		ATA _ CT	
GAM2377	ALPP 3'	CGAGGTCATGCCACTGCACTG 69416	AAA _
		CAGTGCAG CAT ACTTTG	
		GTCACGTC GTA TGGAGC	
		ACC C	
GAM2377	ARHGDIA 3'	TCGTTGCTGCTTCTGCCTGT 16298	T A TACTT
		ACAG GCAGAA CA TGA	
		TGTC CGTCTT GT GCT	
		_ C CGTT_	
GAM2377	ASTN 3'	TCAAATCCCTTGTGCACTGT 69873	G ACATAC
		ACAGTGCA AA TTTGA	
		TGTCACGT TT AAACT	
		G CCCT__	
GAM2377	BTAF1 3'	TCAAATATTTGCACTGT 72872	AACA C
		ACAGTGCAGA TA TTTGA	
		TGTCACGTTT AT AAACT	

GAM2377	NFYA 3'	TCAAGGTCATGTTTCTCACTGT 41659	C _
		ACAGTG AGAAACAT ACTTTGA	
		TGTCAC TCTTTGTA TGGAAC	
		_ C	
GAM2377	NFYA 3'	TCAAGGTCATGTTTCTCACTGT 11784	C _
		ACAGTG AGAAACAT ACTTTGA	
		TGTCAC TCTTTGTA TGGAAC	
		_ C	
GAM2377	PRSS7 3'	CAAAGTATGTCACTGT 12419	CAGAA
		ACAGTG ACATACTTTG	
		TGTCAC TGTATGAAAC	

GAM2377	RAG1 3'	TTTAGAGCTTCTGCAT 6548	ACATA
		GTGCAGAA CTTTGAA	
		TACGTCTT GAGATTT	
		C_____	
GAM2377	SNX6 5'	TTCAAAGTGATGCTGCTCTG 41444	T AAACA
		CAG GCAG TACTTTGAA	

			GTC CGTC GTGAAACTT		
			T GTA__		
GAM2377	SUDD	3'	TCAATTATGTTTCCAGACTGT 15160	GCA	CT
			ACAGT GAAACATA TTGA		
			TGTCA CTTTGTAT AACT		
			GAC T_		
GAM2377	UTY	3'	TTCAGGAAATTTCTGCAC 24064	CATAC	
			GTGCAGAAA TTTGAA		
			CACGTCTTT GGACTT		
			AAA__		
GAM2377	ZNF217	3'	TTCAAAATATGTTTTTGTGT 22549	TG	C
			G CAGAAACATA TTTGAA		
			T GTTTTTGTAT AAAC TT		
			GT A		
GAM2377	ZNF217	3'	TTTCAAAAATAAATTTGCACTG 22552		AACATAC
	T		ACAGTGCAGA TTTGAAA		
			TGTCACGTTT AAAC TT		
			AAATAA_		
GAM2377	CNNM1	3'	TTTCAGCCCAGCGTTTCTGCAA 40127	G	ATACT_
	TG		CA TGCAGAAAC TTTGAAA		
			GT ACGTCTTTG GACTTT		
			A CGACCC		
GAM2377	DSCR6	3'	TTTCAAAGCTCCTTCTGCATTG 39081		ACATA
	T		ACAGTGCAGAA CTTTGAAA		
			TGTTACGTCTT GAAAC TT		
			CCTC_		
GAM2377	FLJ13105	3'	TCAAAGTAGATGCAATGT 47177	G	GAAACA
			ACA TGCA TACTTTGA		
			TGT ACGT ATGAAACT		
			A AG__		
GAM2377	FLJ20312	3'	TTTCAAAATACATTTTTGTATT 35412		CA C
			AGTGCAGAAA TA TTTGAAA		
			TTATGTTTTT AT AAAC TT		
			AC A		
GAM2377	FLJ20419	3'	TTCAGTGCCCTGTACTG 35610	AAA	ACTT
			CAGTGCAG CAT TGAA		
			GTCATGTC GTG ACTT		
			CCC ____		
GAM2377	FLJ22031	3'	TTCAAAGTATGTTAATACTTGT 47590	_	CAGA
			ACA GTG AACATACTTTGAA		

		TGT CAT TTGTATGAACTT	
		T AA__	
GAM2377	FLJ22283	5' GAGTGCATTTCCCTGCACTGT 50901	__ CA
		ACAGTGC A GAAA TACTT	
		TGTCACGT CTTT GTGAG	
		CC AC	
GAM2377	FLJ22746	3' TCATTTGTTTCTGCACT 45921	TACTT
		AGTGCAGAAACA TGA	
		TCACGTCTTTGT ACT	
		TT__	
GAM2377	KIAA0237	3' TTCACATGGCTTCTGCAT 29234	A_ ACTT
		GTGCAGAA CAT TGAA	
		TACGTCTT GTA ACTT	
		CG C__	
GAM2377	KIAA0483	3' AAGCATGTCTTGCACTGT 31472	AA A
		ACAGTGCAG ACAT CTT	
		TGTCACGTT TGTA GAA	
		C_ C	
GAM2377	KIAA0603	3' TTTCAAAGTACATTTGCA 29838	AACA
		TGCAGA TACTTTGAAA	
		ACGTTT ATGAACTTT	
		AC__	
GAM2377	KIAA0923	3' TTCAAAGTATATTGCCT 26709	T AAAC
		AG GCAG ATACTTTGAA	
		TC CGTT TATGAACTT	
		_ A__	
GAM2377	KIAA1042	3' GAAGTGCCCCTGCACTGT 31048	AAACA
		ACAGTGCAG TACTTT	
		TGTCACGTC GTGAAG	
		CCC__	
GAM2377	KIAA1393	3' TTTCAAAGTATGTGGCACTCG 72580	C AGAA
		A AGTGC ACATACTTTGAAA	
		G TCACG TGTATGAACTTT	
		C G__	
GAM2377	KIAA1468	3' CAAAGATATTTGCACTG 93424	AAC A
		CAGTGCAGA AT CTTTG	
		GTCACGTTT TA GAAAC	
		A__ _	
GAM2377	LY75	3' TCAAAGTAAAAATTGAACTGT 11400	G AAACA
		ACAGT CAG TACTTTGA	

		TGTCA GTT ATGAAACT		
		A AAAA_		
GAM2377	ZNFN1A2	3' AGTATGTTTTACTGT	33217	CA
		ACAGTG GAAACATACT		
		TGTCAC TTTTGTATGA		
		A_		
GAM2377	LOC132948	3' CAAAGTATTTCTATACTG	59845	C A C
		CAGTG AG AA ATACTTTG		
		GTCAT TC TT TATGAAAC		
		A C _		
GAM2377	LOC133482	3' TTCAAAAATTTTGCAGTGT	75597	ACATAC
		ACAGTGCAGAA TTTGAA		
		TGTCACGTTTT AACTT		
		AA_____		
GAM2377	LOC143154	3' TTCAAAGTTATCTATACTG	76996	C__ AACAT
		CAGTG AGA ACTTTGAA		
		GTCAC TCT TGAAACTT		
		ATA AT_____		
GAM2377	LOC152503	3' TCAGATATGTTTTTGCAGT	86980	C
		AGTGCAGAAACATA TTTGA		
		TCACGTTTTTGTAT AGACT		

GAM2377	LOC219294	3' TTCAAAGTTATCTATACTG	94601	C__ AACAT
		CAGTG AGA ACTTTGAA		
		GTCAC TCT TGAAACTT		
		ATA AT_____		
GAM2377	LOC221271	3' TTCACTATGTTTCCACAC	93536	CA CTT
		GTG GAAACATA TGAA		
		CAC CTTTGTAT ACTT		
		AC C__		
GAM2377	LOC255057	3' TCACGTCTGTGCACTGT	97097	AGAA T TT
		ACAGTGC ACA AC TGA		
		TGTCACG TGT TG ACT		
		_____ C C_		
GAM2378	GPD1	3' TCATGCCACCACATTTG	60398	C C
		TAAATG GGTGGCAT GA		
		GTTTAC CCACCGTA CT		
		A _		
GAM2378	IL5RA	5' TCGCATGGCCACCGCATTT	6906	AT__
		AAATGCGGTGGC CGA		

		TTTACGCCACCG GCT		
		GTAC		
GAM2378	MYO1C	3' TGCCGATGCCAAATATTTG 61873	CGG	A
		TAAATG TGGCATCG CA		
		GTTTAT ACCGTAGC GT		
		AA_ C		
GAM2378	C6orf37	3' TGTCACACTGCATTTA 68097	GCATC	
		TAAATGCGGTG GACA		
		ATTTACGTCAC CTGT		
		A_____		
GAM2378	DNAJC6	3' TTGCAGAACCACCGCATT 29498	CA GA	
		AATGCGGTGG TC CAA		
		TTACGCCACC AG GTT		
		A_ AC		
GAM2378	FLJ11210	3' GTCGATGTGCATGCTTTTA 60319	T GTG	
		TAAA GCG GCATCGAC		
		ATTT CGT TG TAGCTG		
		T ACG		
GAM2378	FLJ12476	3' TCGATCTTCTGCATTTA 43270	T C	
		TAAATGCGG GG ATCGA		
		ATTTACGTC TC TAGCT		
		T _		
GAM2378	KIAA1034	3' TCGATGGCATCCGCATTTG 63134	_ G	
		TAAATGCGG TG CATCGA		
		GTTTACGCC AC GTAGCT		
		T G		
GAM2378	KIAA1987	3' TCATGTAAGTGCATTTA 89391	G C	
		TAAATGCGGT GCAT GA		
		ATTTACGTCA TGTA CT		
		A _		
GAM2378	MGC16063	3' TGTCCTGGCCACTGCATT 54929	ATC	
		AATGCGGTGGC GACA		
		TTACGTCACCG CTGT		
		GTC		
GAM2378	LOC147949	3' TGTCAGATGTCCACATTGCA 79279	_ _ _	
		TGCG GTGG CATC GACA		
		ACGT CACC GTAG CTGT		
		TA T A		
GAM2378	LOC150577	3' GTCCTCACCGCATTTG 86258	CATC	
		TAAATGCGGTGG GAC		

GTTTACGCCACT CTG
 C____
 GAM2378 LOC158219 3' TGTGTGTCACCACATTT 82694 C CG
 AAATG GGTGGCAT ACA
 ||||| ||||| ||
 TTTAC CCACTGTG TGT
 A ____
 GAM2378 LOC202020 3' TGTCTCACCACATTTA 90605 C CATC
 TAAATG GGTGG GACA
 ||||| ||||| ||||
 ATTTAC CCACT CTGT
 A ____
 GAM2378 LOC90826 5' TGTCGATGCAGGTTTATTTG 64788 CGGTG
 TAAATG GCATCGACA
 ||||| ||||| |||||
 GTTTAT CGTAGCTGT
 TTGGA
 GAM2378 LOC93587 3' TTGTCTTTACCTGCATTTA 73042 _ CATC
 TAAATGC GGTGG GACAA
 ||||| ||||| |||||
 ATTTACG CCATT CTGTT
 T T____
 GAM2379 ATF7 3' TCCCAGCCCCGGAGCCTCATA 23404 _ TAGA CC
 TATGAGGC CC GCT GGGA
 ||||| || || ||||
 ATACTCCG GG CGA CCCT
 A CCC_ ____
 GAM2379 CREBBP 5' CCCGCCGGTCCCGGGCCCCA 16495 A TA G C_
 TG GGCCC GA CT CGGG
 || ||||| || || ||||
 AC CCGGG CT GG GCCC
 C CC _ CC
 GAM2379 EGLN2 5' TTGGGGCTCCAGAACCTC 54926 CC A
 GAGG CT GAGCTCCGG
 |||| || ||||| ||||
 CTCC GA CTCGGGGTT
 AA C
 GAM2379 GNA11 5' CCCAGTGA CTCTGGGCCTCA 10810 T C C_
 TGAGGCC AGAG TC GGG
 ||||| |||| || ||||
 ACTCCGGG TCTC AG CCC
 _ _ TGA
 GAM2379 LATS2 3' GTCCCGGAGCCGGTGCCCTCA 28135 __ TAGA
 TGAGG C CC GCTCCGGGAC
 ||||| || ||||| |||||
 ACTCC G GG CGAGGCCCTG
 C T C____
 GAM2379 NLGN3 3' GTCTCTCTGGCTCTAGGACC 39121 C CC_
 GG CCTAGAGCT GGGAC
 || ||||| |||||

CC GGATCTCGG CTCTG
 A TCT
 GAM2379 NOTCH1 5' GTCCCGGAGCCCCAAGTGCTT 92138 C AGA_
 AGGC CT GCTCCGGGAC
 ||||| || |||||
 TTCG GA CGAGGCCCTG
 T ACCC
 GAM2379 RBBP9 3' TCCGGAGTCTAGAGCCCCA 70699 A C G
 TG GGC CTAGA CTCCGGG
 || ||| ||||| |||||
 AC CCG GATCT GAGGCCT
 C A _
 GAM2379 UBQLN1 5' CCGAGCTCCGGGGCCCCA 26473 A TA C
 TG GGCCC GAGCTC GG
 || ||||| ||||| ||
 AC CCGGG CTCGAG CC
 C GC _
 GAM2379 ARTN 5' CCCGGGCCTGGAGCCCCA 15612 A C A T
 TG GGC CTAG GC CCGGG
 || ||| ||||| || |||||
 AC CCG GGTC CG GGCCC
 C A _ _
 GAM2379 CNTNAP1 3' CCCAAAGGAGAAGCCTCATG 14641 CCTAGAG ____
 TATGAGGC CTCC GGG
 ||||| ||| |||
 GTACTCCG GAGG CCC
 AA_____ AAA
 GAM2379 FLJ10898 5' CCCCAAGCCAGGCACAGCCTCA 60130 ____ AGA CC
 TA TATGAGGC CCT GCT GGG
 ||||| ||| ||| |||
 ATACTCCG GGA CGA CCC
 ACAC C_ AC
 GAM2379 KIAA1977 5' CGAAGGCTCAGGGCCTCA 74765 A C_
 TGAGGCCCT GAGCT CG
 ||||| ||||| ||
 ACTCCGGGA CTCGG GC
 _ AA
 GAM2379 P24B 3' TCCTGCTCTAGGGCCCCTCA 24774 ____ TCC
 TGA GGCCCTAGAGC GGGA
 ||| ||||| ||||| |||||
 ACT CCGGGATCTCG TCCT
 CC ____
 GAM2379 LOC146669 3' GTCTTTCTCCAGGGGCCTCA 78664 A_ CTCC
 TGAGGCCCT GAG GGGAC
 ||||| ||| |||||
 ACTCCGGGG CTC TTCTG
 AC T____
 GAM2379 LOC170127 5' CCCGGAGCCCCAGGGGCCCA 83456 A AGA_
 TG GGCCCT GCTCCGGG
 || ||||| |||||

		AC CCGGGG CGAGGCCC	
		— ACCC	
GAM2379	LOC256812 5'	CCCGGAGCCCCCTGGGCCCCA 99406	A TAGA_
		TG GGCCG GCTCCGGG	
		AC CCGGG CGAGGCCC	
		C TCCCC	
GAM2379	LOC90408 5'	CCCCTCTCCGAGGCCTCATA 63342	CTA CTCC
		TATGAGGCC GAG GGG	
		ATACTCCGG CTC CCC	
		AGC TC__	
GAM2380	ALDH1A1 3'	GTGACTCTTGAAGTACTTA 7306	C GA G
		TAAGTGCT CAAG GGT GC	
		ATTCATGA GTTC TCA TG	
		A _ G	
GAM2380	ARHGAP6 3'	TGGCCACTGGCACACTTA 8612	CT AGGAG
		TAAGTG CCA GTGGCCA	
		ATTCAC GGT CACCGGT	
		AC _____	
GAM2380	ARHGAP6 3'	TGGCCACTGGCACACTTA 26433	CT AGGAG
		TAAGTG CCA GTGGCCA	
		ATTCAC GGT CACCGGT	
		AC _____	
GAM2380	ASH1 5'	GGCCACCCCTCTTCCCCACTT 38089	CTCCA_ A
		AAGTG AGG GGTGGCC	
		TTTAC TCC CCACCGG	
		CCCTTC C	
GAM2380	ENG 3'	GCCACTGGCTTGGAACAC 5498	C GA
		GTG TCCAAG GGTGGC	
		CAC AGGTTT TCACCG	
		A GG	
GAM2380	GALNT3 3'	CACTCCACTTGAAGCACTTA 16825	C GA_
		TAAGTGCT CAAG G GTG	
		ATTCACGA GTTC C CAC	
		A AC T	
GAM2380	HDAC4 3'	GTGGGGCTCTTTGGAGCAC 21249	GA GG
		GTGCTCCAAG GGT CCAC	
		CACGAGGTTT TCG GGTG	
		TC G_	
GAM2380	MASP1 3'	GTGATCCCTTGGAGCAC 58217	A G
		GTGCTCCAAGG GGT GC	

CACGAGGTTCC CTA TG
_ G
GAM2380 ROCK2 3' GTGGCCTCAAAGGCACTTA 66623 CCAAG G
TAAGTGCT GAGGT GC
||||| |||||
ATTCACGG CTCCG TG
AAA_ G
GAM2380 SNCAIP 3' GCCACCTATAAGCTTGGGGCAC 97609 G____
GTGCTCCAAG AGGTGGC
||||||| |||||
CACGGGGTTC TCCACCG
GAATA
GAM2380 C14orf4 3' GCCACCTCCTTTGCCCT 67918 T TCC
AG GC AAGGAGGTGGC
|| || |||||
TC CG TTCCTCCACCG
C T_
GAM2380 CLIPR-59 3' TGGTCACCCTGAAGCCCTTA 32022 T CCAA A
TAAG GCT GG GGTGGCCA
||| || |||||
ATTC CGA TC CCACTGGT
C AG_ _
GAM2380 FLJ10620 3' GTGGCCCGTGCCAAAGCACTTA 36865 CCAA AGGT
TAAGTGCT GG GGCCAC
||||| || |||||
ATTCACGA CC CCGGTG
AA_ GTGC
GAM2380 FLJ12838 3' GTTACCTAAAGCACTTA 45315 CCAAGG
TAAGTGCT AGGTGGC
||||| |||||
ATTCACGA TCCATTG
AA_
GAM2380 FLJ14681 3' GTGGCTCCCCAGAGCACTT 52597 CAA A TG
AAGTGCTC GG GG GCCAC
||||| || |||||
TTCACGAG CC CC CGGTG
A_ _ CT
GAM2380 FLJ23360 3' GCCACCTCCTGCTGGGCAC 43831 CA_
GTGCTC AGGAGGTGGC
||||| |||||
CACGGG TCCTCCACCG
TCG
GAM2380 FLJ23375 5' GTGGCCATGCTCTTGGAGCACT 46953 AG
AGTGCTCCAAGG GTGGCCAC
||||||| |||||
TCACGAGGTTCT TACCGGTG
CG
GAM2380 KIAA0232 3' GTAGCATGCCTGGAGCATCA 73123 A A AG_ G
A GTGCTCCA GG GT GC
| ||||| || |||

		A TACGAGGT CC CG TG		
		C _ GTA A		
GAM2380 KIAA0295	3'	GCAGCCCCTGGGAGCAC 68665	A A G	
		GTGCTCC AGG GGT GC		
		CACGAGG TCC CCG CG		
		G _ A		
GAM2380 KIAA1389	3'	GTTACCTTAGAGACTTA 70319	G CAAG	
		TAAGT CTC GAGGTGGC		
		ATTCA GAG TTCCATTG		
		_ A _		
GAM2380 KIAA1878	3'	GCAGCCCCTGGAGCAC 93367	A A G	
		GTGCTCCA GG GGT GC		
		CACGAGGT CC CCG CG		
		_ _ A		
GAM2380 KLHL8	3'	GTTAACCCTGTAGCACTTA 63517	CCA AGG	
		TAAGTGCT AGG TGGC		
		ATTCACGA TCC ATTG		
		TG_ CA_		
GAM2380 KLHL8	3'	TGACCACCTTTCAACACTT 63519	CTCCAA C	
		AAGTG GGAGGTGG CA		
		TTCAC TTTCCACC GT		
		AAC_ A		
GAM2380 MGC13090	3'	GTGGCCACTTGGCCAAAGCGC 52122	CCAA _	
		GTGCT GG AGGTGGCCAC		
		CGCGA CC TTCACCGGTG		
		AA_ GG		
GAM2380 MGC33177	3'	ATTTACCTTAGAGCATTTA 58626	C _	
		TAAGTGCTC AAGG AGGT		
		ATTTACGAG TTCC TTTA		
		A A		
GAM2380 PPP1R13B	3'	CCATCACCTTGAGCACT 31656	A	
		AGTGCTCCAAGG GGTGG		
		TCACGAGGTTCC CTACC		
		A		
GAM2380 SHANK3	3'	GTGACCACCTCCTTCGCAGC 66110	CC_ C	
		GCT AAGGAGGTGG CAC		
		CGA TTCCTCCACC GTG		
		CGC A		
GAM2380 SIAT8C	5'	GCCACCTCCTCGCCGGCAC 32447	CCA_	
		GTGCT AGGAGGTGGC		

		CACGG TCCTCCACCG CCGC	
GAM2380	SNX11	3' GTAGCCCTAGAGCACTT 26173	CAA A G
		AAGTGCTC GG GGT GC TTCACGAG TC CCG TG A__ _ A	
GAM2380	WAC	5' GCAGCCTTACCAGGCACTTA 56070	CCAAG G
		TAAGTGCT GAGGT GC ATTCACGG TTCCG CG ACCA_ A	
GAM2380	YAP	5' GGCCACCCCCTCTTCCTCACTT 58206	CTCCA_ A
		AAGTG AGG GGTGGCC TTCAC TCC CCACCGG TCCTTC C	
GAM2380	YAP	5' GGCCACCCCCTCTTCCTCACTT 37332	CTCCA_ A
		AAGTG AGG GGTGGCC TTCAC TCC CCACCGG TCCTTC C	
GAM2380	LOC140275	3' ATCTCCCTTAAAGTACTTA 75295	CC _
		TAAGTGCT AAGG AGGT ATTCATGA TTCC TCTA AA C	
GAM2380	LOC146488	5' GTGGCCACACCTGGAACACT 71361	C A AG
		AGTG TCCA GG GTGGCCAC TCAC AGGT CC CACCGGTG A _ A_	
GAM2380	LOC146713	3' GGTACCTCGGAGCCACT 84738	_ AAG
		AGTG CTCC GAGGTGGCC TCAC GAGG CTCCACTGG C _	
GAM2380	LOC147958	5' GGCCACAGGGCACTTA 88526	CAAGGAG
		TAAGTGCTC GTGGCC ATTCACGGG CACCGG A_____	
GAM2380	LOC148137	3' CCTCCCTCCTTGAAGCACTT 59094	C T_
		AAGTGCT CAAGGAGG GG TTCACGA GTTCCTCC CC A CT	
GAM2380	LOC150203	3' GTGACCATTGTTGGAGCAC 61136	G _ G
		GTGCTCCAA GA GGT GC 	

CACGAGGTT TT CCA TG
G A G
GAM2380 LOC151521 3' GTGGCCACACTTGAAACAC 86624 CTC GAG
GTG CAAG GTGGCCAC
||| ||| |||||
CAC GTTC CACCGGTG
AAA A__
GAM2380 LOC151996 5' GTAGCCATGACATTGGAGCAC 86722 GGAG C
GTGCTCAA GTGGC AC
||||||| |||||
CACGAGGTT TACCG TG
ACAG A
GAM2380 LOC152790 5' GCACGCTTCTTAAAGCACT 87060 CCA _
AGTGCT AGGAGGTG GC
||||| ||||| ||
TCACGA TTCTTCGC CG
AA_ A
GAM2380 LOC153688 3' GTGGCCACTTGATTAGAGACCT 87330 TG C GG
AG CTC AA AGGTGGCCAC
|| ||| || |||||
TC GAG TT TTCACCGGTG
CA A AG
GAM2380 LOC154860 3' GCGGCCTCTGGAGCCTTA 87505 T AG G
TAAG GCTCCA GAGGT GC
|||| ||||| |||||
ATTG CGAGGT CTCCG CG
_ _ G
GAM2380 LOC164714 5' GGCTGGCGTCCTTGGAGC 88587 G _
GCTCCAAGGA GT GGCC
||||||| || |||
CGAGGTTCTT CG TCGG
G G
GAM2380 LOC196374 3' GCCACCTCCTTCCTGAACAC 89029 C C__
GTG TC AAGGAGGTGGC
||| || |||||
CAC AG TTCCTCCACCG
A TCC
GAM2380 LOC196955 3' GCAGGCCTTGGAGCCTTA 77868 T AGGTG
TAAG GCTCCAAGG GC
|||| ||||| ||
ATTG CGAGGTTCC CG
_ GGA__
GAM2380 LOC199720 3' TGGCCAAGCTGGAGCACT 89706 AG AGG
AGTGCTCCA G TGGCCA
||||||| | |||||
TCACGAGGT C ACCGGT
_ GA_
GAM2380 LOC200138 5' GTGGCCACCTCCTTGGAGCACT 91543
TA TAAGTGCTCCAAGGAGGTGGCCAC
||||||| |||||

ATTCACGAGGTTCTCCACCGGTG

GAM2380 LOC203378 5' TGGTCAACCTTGAACATT 92309 C AGG
AGTG TCCAAGG TGGCCA
||||| |||||
TTAC AGGTTCC ACTGGT
A A__

GAM2380 LOC205258 5' CACTGCTCCTCAGAGCACTTG 92361 CA _
TAAGTGCTC AGGAG GTG
||||| |||||
GTTACAGAG TCCTC CAC
AC GT

GAM2380 LOC219654 3' TACCCTCTGAGCACTTA 92940 CA GA
TAAGTGCTC AG GGTG
||||| || ||||
ATTCACGAG TC CCAT
_ TC

GAM2380 LOC220827 3' TGGCTACCTTAGAGCAC 92885 CAAG
GTGCTC GAGGTGGCCA
||||| |||||||
CACGAG TTCCATCGGT
A__

GAM2380 LOC222160 3' TGGCTCTCACTTTGGAGCACTT 95795 A GT
A TAAGTGCTCCAAGG G GGCCA
||||||| |||||
ATTCACGAGGTTTC C TCGGT
A TC

GAM2381 ELF3 3' TGACCTTGACCTTGACCAA 16685 T GAT AAA
TTGGT CAAGG GG GTCA
||||| || ||||
AACCA GTTCC TC CAGT
_ AGT _

GAM2381 JAK2 3' TGACCTTCATTCTGAGACCAA 18318 CAA AA
TTGGTT GGGATGGA GTCA
||||| ||||||| ||||
AACCAG TCTTACTT CAGT
AG_ C_

GAM2381 SLC10A2 5' ACTCTCTGTCTTGACCAA 6590 CAA A
TTGGTT GGGATGGA AGT
||||| ||||||| ||||
AACCAG TTCTGTCT TCA
_ C

GAM2381 FLJ10803 3' GTGACTTTCAGTTAAAGCCAA 37205 CAAGG G
TTGGTT GAT GAAAGTCAC
||||| || |||||||
AACCGA TTG CTTTCAGTG
AA_ A

GAM2381 KIAA1958 5' GTGACTTTGAACCCCAAACC 82788 CAA ATGG
GGTT GGG AAAGTCAC
||||| || |||||||

CCAA CCC TTTCAGTG
 A__ CAAG
 GAM2381 MARCKS 3' ACTTTCCACCCTGCCCA 11411 TTCA A
 TGG AGGG TGGAAAGT
 ||| |||| |||||
 ACC TCCC ACCTTTCA
 CG__ _
 GAM2381 TUB 5' GTGGGACCATCCCTTAAACC 13898 C AAAG
 GGTT AAGGGATGG TCAC
 |||| ||||| ||||
 CCAA TTCCCTACC GGTG
 A AG__
 GAM2381 LOC80298 3' ACTTTTACCTTGAACCA 48062 GATG
 TGGTTCAAGG GAAAGT
 ||||| |||||
 ACCAAGTTCC TTTTCA
 A__
 GAM2382 TIM3 3' ACTTCTGTATTCGTGGACCAA 52346 T _ A
 TTGGT CCACGGG ATGGAA GT
 |||| ||||| ||||| ||
 AACCA GGTGCTT TGTCTT CA
 _ A _
 GAM2382 FLJ23142 5' ACTTTCCATAACAACCAA 45025 CCACGGG
 TTGGTT ATGGAAAGT
 ||||| |||||
 AACCAA TACCTTTCA
 CAA____
 GAM2382 KIAA0793 3' TGACCTTCCATCTGGTGAACCA 29696 C G A
 A TTGGTTC AC GGATGGAA GTCA
 ||||| || ||||| ||||
 AACCAAG TG TCTACCTT CAGT
 _ G C
 GAM2382 KIAA1878 3' TGACTTTCATTTCTGAGACC 93372 TC C GG
 GGT CA G ATGGAAAGTCA
 ||| ||| |||||
 CCA GT C TACCTTTCAGT
 GA _ TT
 GAM2383 GNA11 5' CTCTGGGCCTCACAGAGCCCC 10812 A AC C TG
 GG GCTCT GAG GTC GAG
 || |||| ||| ||| |||
 CC CGAGA CTC CGG CTC
 C CA _ GT
 GAM2383 HSD3B2 3' CTCTTTTGACTAATAGAGCTCC 5774 CG _ TCT
 AT ATGGAGCTCTA AG CG GGAG
 ||||| || ||| ||||
 TACCTCGAGAT TC GT TCTC
 AA A TT_
 GAM2383 PODXL 3' CTCCAGCAGCACACAGAGCTC 19415 ACGA_ GT
 CA TGGAGCTCT GC CTGGAG
 ||||| || |||||

		ACCTCGAGA CG GACCTC		
		CACCA AC		
GAM2383	PRM1	5' TCAGCTGCCCACAGAGTTCCA 12394	ACGA T	
		TGGAGCTCT GCG CTGG		
		ACCTTGAGA CGT GACT		
		CACC C		
GAM2383	FLJ10539	3' TCCAGAATGTAGAGCCCAT 36763	A	AGCG
		ATGG GCTCTACG TCTGGA		
		TACC CGAGATGT AGACCT		
		— A —		
GAM2383	FLJ12770	3' CTCCAGACTTGGCCAGAACTCC 50678	C	ACGAGC
	A	TGGAG TCT GTCTGGAG		
		ACCTC AGA CAGACCTC		
		A CCGTT		
GAM2383	FLJ20040	3' CTCGACCTCGCAGAGCTCC 39158	A C T	
		GGAGCTCT CGAG GTC GG		
		CCTCGAGA GCTC CAG TC		
		C _ C		
GAM2383	FLJ32356	3' CTCCAGACACTCCTTGACTGCA 59020	G C TAC C	
	T	ATG AG TC GAG GTCTGGAG		
		TAC TC AG CTC CAGACCTC		
		G _ TTC A		
GAM2383	HML2	5' CTCCAGACCTCCCACAGCTCCA 22022	CTAC C	
		TGGAGCT GAG GTCTGGAG		
		ACCTCGA CTC CAGACCTC		
		CACC _		
GAM2383	KIAA0545	3' CTCCAGACGCTCGGCTCCA 63842	TCTA _	
		TGGAGC CGAG CGTCTGGAG		
		ACCTCG GCTC GCAGACCTC		
		— C		
GAM2383	MYO3B	3' CCAGAGTCAGGGCTCCAT 58108	ACGA G	
		ATGGAGCTCT GC TCTGG		
		TACCTCGGGA TG AGACC		
		C _ _		
GAM2383	LOC122614	3' CTCCAGACACATGTGAGCCCAT 76100	A T AGC	
		ATGG GCTC ACG GTCTGGAG		
		TACC CGAG TGT CAGACCTC		
		_ _ ACA		
GAM2383	LOC124895	5' CCAGACGCCCTGGACTCC 74819	C CGA	
		GGAG TCTA GCGTCTGG		

CCTC AGGT CGCAGACC
 _ CC_
 GAM2383 LOC136442 3' CCAGACGCTGGCGCTCCA 55260 T ACG
 TGGAGC CT AGCGTCTGG
 ||||| || |||||
 ACCTCG GG TCGCAGACC
 C ____
 GAM2383 LOC145951 3' CCAAAGTTCGACTTGTAGAGCC 78034 A _ TC____
 CCAT ATGG GCTCTACGAG CG TGG
 ||| ||||| || |||
 TACC CGAGATGTTC GC ACC
 C A TTGAA
 GAM2383 LOC146820 3' CCAGGTGTAGAACTTCAT 78737 C AGCG
 ATGGAG TCTACG TCTGG
 ||||| ||||| |||||
 TACTTC AGATGT GGACC
 A ____
 GAM2383 LOC199714 5' CTCCAGGCACCCGTGAAGCCCC 89700 A C AGC
 A TGG GCT TACG GTCTGGAG
 ||| ||| ||| |||||
 ACC CGA GTGC CGGACCTC
 C A CCA
 GAM2383 LOC254219 3' CTCCAGATGAACAGGGCTCCAT 98321 ACGAG
 ATGGAGCTCT CGTCTGGAG
 ||||| ||||| |||||
 TACCTCGGGA GTAGACCTC
 CAA____
 GAM2383 LOC92078 3' CCGGCTCACAAGGCTCCAT 68598 CTAC GTC
 ATGGAGCT GAGC TGG
 ||||| ||| |||
 TACCTCGG CTCG GCC
 AACA ____
 GAM2384 ACT 5' CCACAATCCAGGGGGGCCAT 40420 CCG AAC
 ATGGCCCCT GGA TGTGG
 ||||| ||| |||||
 TACCGGGGG CCT ACACC
 A__ A__
 GAM2384 ADAM11 3' GCCACAGCTCAACTCGGGGGC 41490 TC AAA____
 GCCCC CGGG CTGTGGC
 |||| ||| |||||
 CGGGG GCTC GACACCG
 _ AACTC
 GAM2384 ADAM11 3' GCCACAGCTCAACTCGGGGGC 11487 TC AAA____
 GCCCC CGGG CTGTGGC
 |||| ||| |||||
 CGGGG GCTC GACACCG
 _ AACTC
 GAM2384 CDC34 3' GCCGCACCCCGGAGGAGCCA 16390 C AAAC
 TGGC CCTCCGGG TGTGGC
 ||| ||||| |||||

ACCG GGAGGCC ACGCCG
 A C____
 GAM2384 CRI1 3' GCCACAGTTATCAAAGGCTA 27537 CCTCCG A
 TGGCC GG AACTGTGGC
 ||||| || |||||
 ATCGG CT TTGACACCG
 AAA__ A
 GAM2384 FLII 3' GCCACAGTCCCCAGTAGCC 10656 CC CC AA
 GGC CT GGG ACTGTGGC
 ||| || ||| |||||
 CCG GA CCC TGACACCG
 AT __ C_
 GAM2384 FZD10 3' GCCACACCCCAAGGAAGGCCA 24214 CC _ AAAC T
 TGGCC TCC GGG TG GGC
 ||||| ||| ||| |||||
 ACCGG AGG CCC AC CCG
 A_ A CC__ _
 GAM2384 GNA11 5' CCACAGCCCCGGGGGCCG 76585 TC AAA
 TGGCCCC CGGG CTGTGG
 ||||| ||| |||||
 GCCGGGG GCC GACACC
 __ C_
 GAM2384 IGHMBP2 3' GCCACAGAGGAGCGGAGGGGCC 10984 GGAAA
 GGCCCCCTCCG CTGTGGC
 ||||| |||||
 CCGGGGAGGC GACACCG
 GAGGA
 GAM2384 MAGEA3 5' CCAGAGGCCCCCGGAGGAGC 19315 C AAA G
 GC CCTCCGGG CT TGG
 || ||||| |||||
 CG GGAGGCC GA ACC
 A CCG G
 GAM2384 PYGB 3' CCAGGGGTCCCGGAGGAACC 12687 CC AA G
 GG CCTCCGGA CT TGG
 || ||||| |||||
 CC GGAGGCCCT GG ACC
 AA G_ G
 GAM2384 PYGB 3' CCATGTTTCCAGGAGGGGCCAT 12689 G T
 ATGGCCCCTCC GGAAAC GTGG
 ||||| ||||| |||||
 TACCGGGGAGG CCTTTG TACC
 A _
 GAM2384 SLC6A6 3' GCCACAGTCCTTCCTGGGGC 13183 TCC _
 GCCCC GGGAA ACTGTGGC
 ||||| ||||| |||||
 CGGGG TCCTT TGACACCG
 __ CC
 GAM2384 UBTF 3' CCATTCCTTCCCAGAGGGGCC 27252 C ACT
 GGCCCCCTC GGGAA GTGG
 ||||| ||||| |||||

CCGGGGAG CCCTT TACC
A CCT
GAM2384 CBCIP2 3' GCCACACGGA CTGAGGGGCC 52658 C AAAC
A TGGCCCCTC GGG TGTGGC
||||||| ||| |||||
ACCGGGGAG CTC ACACCG
A AGGC
GAM2384 FEM-2 3' GCCACAGTCCCATGAGGGCC 28316 C C_ AA
GGCCC TC GGGA CTGTGGC
||||| || ||| |||||
CCGGG AG CCCT GACACCG
_ TA _
GAM2384 FLJ10199 3' GCCACAGTTGAGAAGCGGAGGG 71755 GGA____
GCCA TGGCCCCTCCG AACTGTGGC
||||||| |||||
ACCGGGGAGGC TTGACACCG
GAAGAG
GAM2384 FLJ11715 3' ACAGTGTCCCCAGGAGGCCAT 44972 _ CC A
ATGGCC CCT GGGA ACTGT
||||| ||| ||| |||||
TACCGG GGA CCCT TGACA
A C_ G
GAM2384 FLJ12505 5' CCCGGTCCCGGAGCAGCCA 45713 CC AA T
TGGC CTCCGGGA CTG GG
||| ||||| ||| ||
ACCG GAGGCCCT GGC CC
AC _ _
GAM2384 KIAA0828 3' GTTTCCCAGGAAGGCCAT 82119 CC _
ATGGCC TCC GGGAAC
||||| ||| |||||
TACCGG AGG CCCTTTG
A_ A
GAM2384 KIAA1190 3' CCACAGTTCTGGGAGCC 71643 CCC G A
GGC TCC GGAA CTGTGG
||| ||| ||| |||||
CCG AGG TCTT GACACC
_ G _
GAM2384 KIAA1297 5' CCATGCCCAAGAAGGCCA 72634 CC C AAAC
TGGCC TC GGG TGTGG
||||| ||| ||| |||||
ACCGG AG CCC GTACC
A_ A _
GAM2384 PASK 5' GCCACAGAGTTGGGGGGCCAT 31415 T GAAA
ATGGCCCC CCGG CTGTGGC
||||||| ||| |||||
TACCGGGG GGTT GACACCG
_ GA_
GAM2384 PCDH17 3' GCCACAGTTCCTGCAGCCA 27836 CCCTC A
TGGC CGGG AACTGTGGC
||| ||| |||||

		ACCG GTCC TTGACACCG	
		AC__ C	
GAM2384	RIL	3' CCATGCTGCCCTGAAGGGGCCA 14885	C A AACT
		TGGCCCT CGGG GTGG	
		ACCGGGGA GTCC TACC	
		A CGTCG	
GAM2384	SREC	3' GCAGTGCTCCCGAGGGGCC 14905	A_
		GGCCCTCCGGGA ACTGT	
		CCGGGAGGCCCT TGACG	
		CG	
GAM2384	TRAF2	3' GCCGGCTCACGAGGGGCCA 41236	G AACTG
		TGGCCCTCCG GA TGGC	
		ACCGGGAGGC CT GCCG	
		A CG__	
GAM2384	LOC123242	5' CCACAGCCACCTGGAGGCCA 76111	CC AAA_
		TGGCC TCCGGG CTGTGG	
		ACCG AGGTCC GACACC	
		_ ACCC	
GAM2384	LOC124460	5' CCAAGAGCTCGAAGGGGCCAT 76559	C AAA G
		ATGGCCCT CGGG CT TGG	
		TACCGGGA GCTC GA ACC	
		A GA_ _	
GAM2384	LOC132166	3' GCCAGCGCCGAGGGGGCCA 75537	TC A AACTG
		TGGCCC CGGG TGGC	
		ACCGGG GCCC ACCG	
		GA GCG__	
GAM2384	LOC146958	5' GCCACAGTCTCAAGTGGACAT 84944	G C CC AA
		ATG CC CT GGGA CTGTGGC	
		TAC GG GA CTCT GACACCG	
		A T A_ _	
GAM2384	LOC149420	3' GCCACAGTTTCCTAAGCGC 80155	CC CC
		GC CT GGGAACTGTGGC	
		CG GA TCCTTTGACACCG	
		C_ A_	
GAM2384	LOC152317	3' GCCACAGTCTGGGAGAGCCA 86831	CC G AA
		TGGC CTCC GGA CTGTGGC	
		ACCG GAGG TCT GACACCG	
		A_ G _	
GAM2384	LOC157450	3' CCACAGCTCCCGGGTCAT 71531	CTCC A
		ATGGCCC GGGAA CTGTGG	

		TACTGGG CCCTT GACACC	
		_____ C	
GAM2384	LOC157807 5'	GCCACAGTTTCAGCAGACCAT 82513	CCC CCGG
		ATGG CT GAAACTGTGGC	
		TACC GA CTTTGACACCG	
		A__ CGA_	
GAM2384	LOC157923 5'	GCCACAGTCCAGAGAAGGCCA 82526	C_ C GAA
		TGGCC CTC GG ACTGTGGC	
		ACCGG GAG CC TGACACCG	
		AA A ____	
GAM2384	LOC158510 5'	CCAGAGGCCCGGAGGAGC 82833	C AAA G
		GC CCTCCGGG CT TGG	
		CG GGAGGCCG GA ACC	
		A CCG G	
GAM2384	LOC196860 3'	CCACAGTTCCCCGGAAAGTGCT 91214	CCC_ A
		GGC TCCGGG AACTGTGG	
		TCG AGGCCC TTGACACC	
		TGAA C	
GAM2384	LOC203235 5'	GCCAGGGCCCCCAGAGGGGCC 92099	C AAA G
		GGCCCCTC GGG CT TGGC	
		CCGGGGAG CCC GG ACCG	
		A CC_ G	
GAM2384	LOC220739 3'	GCCACAGTAGGAGGGGCCA 94521	GGGAA
		TGGCCCCTCC ACTGTGGC	
		ACCGGGGAGG TGACACCG	
		A____	
GAM2384	LOC222166 5'	CCCGGCCCGGAGGAGCC 95733	C AAA T
		GGC CCTCCGGG CTG GG	
		CCG GGAGGCCG GGC CC	
		A C_ _	
GAM2384	LOC253001 5'	CCACAGCCCACCTGGAGGCCA 97990	CC AAA_
		TGGCC TCCGGG CTGTGG	
		ACCGG AGGTCC GACACC	
		_ ACCC	
GAM2384	LOC254057 3'	GCCCCTATCCCAGAGGGGCC 98782	C AACTGT
		GGCCCCTC GGGA GGC	
		CCGGGGAG CCCT CCG	
		A ATCC_	
GAM2384	LOC92558 3'	GCCACCTCCCAGAGGGGCC 70312	C AACT
		GGCCCCTC GGGA GTGGC	

		CCGGGGAG CCCT CACCG	
		A C__	
GAM2384	LOC93626	5' CCACAGCCCCGGGGGCGG	73128 TC AAA
		TGGCCCC CGGG CTGTGG	
		GCCGGGG GCCC GACACC	
		__ C__	
GAM2385	BBS2	3' CCCTGGTGAACCCCGGGTG	49880 AC CA T
		CATCCGGG TC CGG GG	
		GTGGGCCC AG GTC CC	
		CA TG _	
GAM2385	BMP1	3' GCCACCGTGGGGAGCCGATG	21532 C GA
		CATC GG CTCCACGGTGGC	
		GTAG CC GGGGTGCCACCG	
		_ GA	
GAM2385	CHRNA4	3' GCTGGGAAGGTCCCGAATG	7438 C _ A
		CAT CGGGAC TCC CGGT	
		GTA GCCCTG AGG GTCG	
		A GA _	
GAM2385	CMRF35	3' ACCTCTGAGTGCCCGGATG	22905 _ CAC
		CATCCGGG ACTC GGT	
		GTAGGCCC TGAG CCA	
		G TCT	
GAM2385	GPR30	3' GCCACCGTGGGGGAACTG	9493 GA_
		CGG CTCCACGGTGGC	
		GTC GGGGTGCCACCG	
		AAG	
GAM2385	MAL	3' GCCACCGTGACCTGAGA	11433 _ ACTC
		TC CGGG CACGGTGGC	
		AG GTCC GTGCCACCG	
		A A__	
GAM2385	NTRK2	5' GCCCCAGAGAGTCCCGGA	21635 CAC T
		TCCGGGACTC GG GGC	
		AGGCCCTGAG CC CCG	
		AGA _	
GAM2385	PPT2	5' GCCACCGTGGGTTCCAGA	18949 C T
		TC GGGAC CCACGGTGGC	
		AG CCTTG GGTGCCACCG	
		A _	
GAM2385	ROCK2	5' GCCCGGGTGGAGTCCCGG	66619 GGT
		CCGGGACTCCAC GGC	

			GGCCCTGAGGTG CCG		
			GGC		
GAM2385 SEZ6L	5'	GCCCTCAGGAGCCCCGGA	41205	A AC T	
		TCCGGG CTCC GG GGC			
		AGGCCG GAGG TC CCG			
		C AC _			
GAM2385 SHOX	3'	GCCACCGTGCTCCGGG	6577	ACTC	
		TCCGGG CACGGTGGC			
		GGGCCT GTGCCACCG			
		C__			
GAM2385 SYNGR3	3'	GCCACCGTGCCCCACAAGATG	16119	C__ ACTC	
		CATC GGG CACGGTGGC			
		GTAG CCC GTGCCACCG			
		AACA C__			
GAM2385 TRPV3	3'	GCCTCCTGAAGTCCCGGGTG	96815	C C T	
		CATCCGGGACT CA GG GGC			
		GTGGGCCCTGA GT CC CCG			
		A _ T			
GAM2385 ANXA13	3'	CCCTTAAGAGTCCCGGAT	16291	CAC T	
		ATCCGGGACTC GG GG			
		TAGGCCCTGAG TC CC			
		AAT _			
GAM2385 C20orf18	5'	GCAGTGGAGGTCCCGGATG	49179	_ G	
		CATCCGGGAC TCCAC GT			
		GTAGGCCCTG AGGTG CG			
		G A			
GAM2385 C20orf21	3'	GCCTGAATGGAGTCCTGGA	35570	CGGT	
		TCCGGGACTCCA GGC			
		AGGTCCTGAGGT CCG			
		AAGT			
GAM2385 DDX31	3'	ACCTGGAAGCCCCGGGTG	57611	A _ C	
		CATCCGGG CT CCA GGT			
		GTGGGCCC GA GGT CCA			
		C A _			
GAM2385 EZFIT	3'	CATCCTGGAGTCCAGATG	41377	CG C	
		CATC GGA CTCCA GGTG			
		GTAG CCTGAGGT CTAC			
		A_ C			
GAM2385 FLJ22969	5'	GCCACCGTGGTCAGGAT	69206	GG CT	
		ATCC GA CCACGGTGGC			

			TAGG CT GGTGCCACCG		
		A_ _			
GAM2385	FLJ23375	3'	GCTCGTTTGGAGTCCTGGA 46949	CGGT	
			TCCGGGACTCCA GGC		
			AGGTCCTGAGGT TCG		
			TTGC		
GAM2385	HSU24186	5'	GCCGTCCGTGGAGCCCCAGA 26239	C A _	
			TC GGG CTCCACGG TGGC		
			AG CCC GAGGTGCC GCCG		
			A C T		
GAM2385	KIAA0095	5'	GCCATCGAAGAGTCCCGGA 92558	CA	
			TCCGGGACTC CGGTGGC		
			AGGCCCTGAG GCTACCG		
			AA		
GAM2385	KIAA0700	3'	GCCACCTGGGCCCGGGTG 72522	A T C	
			CATCCGGG C CCA GGTGGC		
			GTGGGCC C G GT CCACCG		
			C _ _		
GAM2385	KIAA1956	3'	GCCACCGTGGAAGTCATGG 79079	G _	
			CCG GACT CCACGGTGGC		
			GGT CTGA GGTGCCACCG		
			A A		
GAM2385	MGC19595	5'	CCACCGTGAGCGTCCCGGA 54182	TC_	
			TCCGGGAC CACGGTGG		
			AGGCCCTG GTGCCACC		
			CGA		
GAM2385	MMP28	3'	GCCACCGAGCTGCCCTGGATG 44445	ACTCCA	
			CATCCGGG CGGTGGC		
			GTAGGTCC GCCACCG		
			CGTCGA		
GAM2385	MVD	3'	CCACCAAGTGCCTCGGATG 11716	ACTC _	
			CATCCGGG CAC GGTGG		
			GTAGGCTC GTG CCACC		
			C__ AA		
GAM2385	SAMHD1	3'	GCCACCGTGTAGCCAGAT 61989	CG A C	
			ATC GG CT CACGGTGGC		
			TAG CC GA GTGCCACCG		
			A_ _ T		
GAM2385	SLC25A18	3'	CCCTTTCGAATCCCTGGATG 49751	_ C CAC T	
			CATCC GGGA TC GG GG		

		GTAGG CCCT AG TC CC	
		T A CTT _	
GAM2385 STK36	5'	GCTGGGGGCGTCCCAGATG 72584	C T A_
		CATC GGGAC CC CGGT	
		GTAG CCCTG GG GTCG	
		A C GG	
GAM2385 WFDC3	5'	GTCTCTGGAATCCTGGAT 98704	C C T
		ATCCGGGA TCCA GG GGC	
		TAGGTCCT AGGT CT CTG	
		A _ _	
GAM2385 LOC124602	3'	GCCTTCGAGGAGTCCCGGA 74786	A T
		TCCGGGACTCC CGG GGC	
		AGGCCCTGAGG GCT CCG	
		A T	
GAM2385 LOC147976	5'	ACCGTGGAAGTCCCAGAT 79284	C _
		ATC GGGACT CCACGGT	
		TAG CCCTGA GGTGCCA	
		A A	
GAM2385 LOC150946	3'	GCTTTGGAGTCCGAGATG 86348	CG C
		CATC GGA CTCCA GGT	
		GTAG CCTGAGGT TCG	
		AG T	
GAM2385 LOC152200	3'	ACTGTGGTATCCCGGATG 86752	CT
		CATCCGGGA CCACGGT	
		GTAGGCCCT GGTGTCA	
		AT	
GAM2385 LOC170127	5'	GCCACTCGCTGTCCCGGA 83458	TCCA _
		TCCGGGAC CG GTGGC	
		AGGCCCTG GC CACCG	
		TC_ T	
GAM2385 LOC197342	3'	GCTCCTTGGTGCCCCGGATG 89370	ACT C T
		CATCCGGG CCA GG GGC	
		GTAGGCCG GGT CC TCG	
		CGT T _	
GAM2385 LOC203397	3'	GCCTTCGAGGAGTCCCGGA 90899	A T
		TCCGGGACTCC CGG GGC	
		AGGCCCTGAGG GCT CCG	
		A T	
GAM2385 LOC255146	3'	GCTGATGGAACCCGGATG 97346	AC _
		CATCCGGG TCCA CGGT	

			GTAGGCCC AGGT GTCG		
			A_ A		
GAM2385	LOC92841	3'	GCCACCGTGCCTCACCAGA 71255	C _ CTC	
			TC GG GA CACGGTGGC		
			AG CC CT GTGCCACCG		
			A A CC_		
GAM2386	BAZ2A	3'	ACACGAGAGGAAAGCTGCT 26502	_ GA	
			AGCAGCTTTT TC CGTGT		
			TCGTCGAAAG AG GCACA		
			G A_		
GAM2386	FMR1	3'	ACACATCATCTGTAAGCTGTTT 10677	TTTC_ C	
			AAGCAGCTT GA GTGT		
			TTTGTCGAA CT CACA		
			TGTCTA A		
GAM2386	GEMIN5	5'	ACACACCGAAAGGGTCTCT 90638	CA AC	
			AG GCTTTTTTCG GTGT		
			TC TGGGAAAGC CACA		
			TC CA		
GAM2386	GEMIN5	3'	ACACCTTGAAGAACTGC 90639	C C	
			GCAG TTTTTCGA GTGT		
			CGTC AAGAAGTT CACA		
			A C		
GAM2386	JAM3	3'	ACACATCAGACCATAGTTGCTT 52485	TTT_ _ C	
			AAGCAGCT TC GA GTGT		
			TTCGTTGA AG CT CACA		
			TACC A A		
GAM2386	MTA1L1	3'	ACAAATAAAAAGCTGTTT 17631	CGACG	
			AAGCAGCTTTTT TGT		
			TTTGTCGAAAAA ACA		
			TAA_		
GAM2386	OTOF	3'	ACATGGTCAAAAAGCTCCTT 17827	C C _	
			AAG AGCTTTTT GAC GTGT		
			TTC TCGAAAAA CTG TACA		
			C _ G		
GAM2386	SFTPC	3'	ACGGGCAAGAAGCTGCTT 88877	CGA	
			AAGCAGCTTTTT CGT		
			TTCGTCGAAGAA GCA		
			CGG		
GAM2386	SLC20A1	5'	ACACATCTTGAAAGGCGCT 60095	A C_ C	
			AGC GCTTTTT GA GTGT		

			TCG CGGAAAG CT CACA		
			— TT A		
GAM2386	AFAP	3'	ACACGAATTGGAAGCTGCTT 41601	TCGA	
			AAGCAGCTTTT CGTGT		
			TTCGTCGAAGG GCACA		
			TTAA		
GAM2386	C1orf22	3'	ACACATTGGAAGCCAGCT 48038	A_ C	
			AGC GCTTTTTCGA GTGT		
			TCG CGAAAAGGTT CACA		
			AC A		
GAM2386	CUL4A	5'	ACACGTGGCGGAAGCTGC 14568	TCG	
			GCAGCTTTT ACGTGT		
			CGTCGAAGG TGCACA		
			CGG		
GAM2386	DNAJC5	3'	ACACGCATGGAAGCTGCTT 62131	TCGA	
			AAGCAGCTTTT CGTGT		
			TTCGTCGAAGG GCACA		
			TAC_		
GAM2386	DUSP9	3'	ACACATCTGGTGGGCTGTTT 9156	TT TC C	
			AAGCAGCT T GA GTGT		
			TTTGTCCG G CT CACA		
			GT GT A		
GAM2386	FLJ12547	3'	ACACATCAAAAAGTTGACT 47124	_ C C	
			AG CAGCTTTTT GA GTGT		
			TC GTTGAAAAA CT CACA		
			A _ A		
GAM2386	FLJ14624	3'	ACACATCTGTGTAAGCTGCTT 71842	TTT _ C	
			AAGCAGCTT C GA GTGT		
			TTCGTCGAA G CT CACA		
			TGT T A		
GAM2386	FLJ20040	3'	ACACAGTCTGGAAGCAGC 39156	A _ _	
			GC GCTTTTTC GAC GTGT		
			CG CGAAAAGG CTG CACA		
			A T A		
GAM2386	KIAA1061	3'	ACACAGTTGGAAGCCACT 71713	CA T _	
			AG GCTTTT CGAC GTGT		
			TC CGAAAG GTTG CACA		
			AC _ A		
GAM2386	KIAA1819	5'	ACAGTTGAAAAGCTGT 70248	T G	
			GCAGCTTTT CGAC TGT		

TGTCGAAAA GTTG ACA

GAM2386 MGC10924 3' ATGTTTGAAAAAGCTCTT 48309 C _
AAG AGCTTTTTCGA CGT
||| ||||| |||
TTC TCGAAAAAGTT GTA
_ T
GAM2386 MGC26768 5' ACACGTCGAAGCTGCTGC 58909 TT
GCAGC TTTCGACGTGT
|||| |||||
CGTCG GAAGCTGCACA
TC
GAM2386 P5-1 3' ACATGCCAAAAGTTGCTT 22888 TCGA
AAGCAGCTTTT CGTGT
||||| |||
TTCGTTGAAAA GTACA
CC_
GAM2386 RASAL2 3' ACACAGACAAAAGCTGTT 17909 _ GAC
AGCAGCTTTT TC GTGT
||||| || |||
TTGTCGAAAA AG CACA
C A_
GAM2386 RNB6 3' ACACACCGCAGAGCTGTCC 33399 A TT AC
A GCAGCTTT CG GTGT
| ||||| || |||
C TGTCGAGA GC CACA
C C_ CA
GAM2386 STIM2 3' ACACAGGGTTGAAAGCTGTT 40857 TT _
AGCAGCTT TCGAC GTGT
||||| ||| |||
TTGTCGAA AGTTG CACA
_ GGA
GAM2386 YR-29 3' ACACCAATTGAAGAACTGC 30299 C C_
GCAG TTTTTCGA GTGT
||| ||||| |||
CGTC AAGAAGTT CACA
A AAC
GAM2386 ZNF297B 3' ACATTATAGATAAAGCTGCTT 26634 T GAC_
AAGCAGCTTT TC GTGT
||||| || |||
TTCGTCGAAA AG TACA
T ATAT
GAM2386 LOC133362 5' ACACAGGAGCAAGAGCTGC 76454 _ GAC
GCAGCTTTT TC GTGT
||||| || |||
CGTCGAGAA AG CACA
CG GA_
GAM2386 LOC151556 3' ACACATAGGAAGCTGACT 81072 _ CGAC
AG CAGCTTTT GTGT
|| ||||| |||

		TC GTCGAAGGA CACA	
		A TA__	
GAM2386	LOC196759 3'	ACACAGTGGAAGCTGTTT 88906	TTT G _
		AAGCAGCT TC AC GTGT	
		TTTGTCTGA AG TG CACA	
		__ G A	
GAM2386	LOC219541 3'	ACCTGCTGATAAAAGCTGC 93192	_ A T
		GCAGCTTTT TCG CG GT	
		CGTCGAAAA AGT GT CA	
		T C C	
GAM2386	LOC221687 3'	ACACAAGAGGAAAGTTGCT 93866	_ GAC
		AGCAGCTTTT TC GTGT	
		TCGTTGAAAG AG CACA	
		G AA_	
GAM2386	LOC56891 5'	ACACAATTCCGAAGAGCTGC 39687	C C__
		GCAGCTTTTT GA GTGT	
		CGTCGAGAAG CT CACA	
		C TAA	
GAM2386	LOC91344 3'	ACACCAATTGGAAAACTGC 66230	C C__
		GCAG TTTTTCGA GTGT	
		CGTC AAAAGGTT CACA	
		A AAC	
GAM2387	HLCS 3'	AATGCCCAAGCCTTCTTT 6401	A__
		AAAGAAGGCT GCATT	
		TTTCTTCCGA CGTAA	
		ACC	
GAM2387	MN1 3'	CAAACAATGAATGCCCTCTT 11649	A_ TAG
		AAGA GGC CATTGTTTG	
		TTCT CCG GTAACAAAC	
		CC TAA	
GAM2387	SIRT1 3'	CAAGACTAACTTTCTTTTAA 25288	C CA
		TTAAAAGAAGG TAG TTG	
		AATTTTCTTTC ATC AAC	
		A AG	
GAM2387	KIAA0594 3'	CAAACAAATTATCTTCTTTTAA 65506	C CA
		TTAAAAGAAGG TAG TTGTTTG	
		AATTTTCTTCT ATT AACAAAC	
		_ A_	
GAM2387	LOC203636 3'	CAAACAATGGGGTGCTTC 90974	_ AG
		GAAG GCT CATTGTTTG	

		CTTC TGG GTAACAAAC	
		G G_	
GAM2387	LOC219392 5'	CAAATGGAGTGCTAGCTTCCCT 92766	A_ _
	T	AAG AGGCTAGCATT GTTTG	
		TTC TTCGATCGTGA TAAAC	
		CC GG	
GAM2388	TERF1 3'	CCCAAATCCTGTTCCAATGA 34391	C TA C
		TCATTGGA ACG GATT GGG	
		AGTAACCT TGT CTAA CCC	
		_ C_ A	
GAM2388	FLJ10159 3'	CCATGTCACGCCATCCAATGAC 36334	CA_ A TC
		GTCATTGGA CGT GAT GG	
		CAGTAACCT GCA CTG CC	
		ACC _ TA	
GAM2388	FLJ14213 3'	CCGATGCTCCCAATGACG 46216	ACAC GAT
		CGTCATTGG GTA TCGG	
		GCAGTAACC CGT AGCC	
		CT_ _	
GAM2388	MGC10715 3'	ATTACCAGACATCCAATGAC 44495	CAC_
		GTCATTGGA GTAGAT	
		CAGTAACCT CATTTA	
		ACAGAC	
GAM2388	MOST2 5'	CCAGGACTGCCCAATGAC 40059	ACAC A _
		GTCATTGG GTAG TTC GG	
		CAGTAACC CGTC AGG CC	
		_ _ A	
GAM2388	LOC150370 3'	CCGGGTCTACGTGCCCATGAC 86123	T A
		GTCAT GG CACGTAGATTTCGG	
		CAGTA CC GTGCATCTGGGCC	
		C _	
GAM2388	LOC152620 3'	CCCAAATCCTGTTCCAATGA 60707	C TA C
		TCATTGGA ACG GATT GGG	
		AGTAACCT TGT CTAA CCC	
		_ C_ A	
GAM2388	LOC158668 3'	CCCAAATCCTGTTCCAATGA 69896	C TA C
		TCATTGGA ACG GATT GGG	
		AGTAACCT TGT CTAA CCC	
		_ C_ A	
GAM2389	ANK1 3'	CGGTGGCTGACCCAGGATTGCA 40407	AT_ A_
		TGCAGTCCTGG GG GCCG	

		ACGTTAGGACC TC TGGC		
		CAG GG		
GAM2389	ANK1	3' CGGTGGCTGACCCAGGATTGCA 40408	AT_ A_	
		TGCAGTCCTGG GG GCCG		
		ACGTTAGGACC TC TGGC		
		CAG GG		
GAM2389	EPHA8	3' TCGCCCCATCCAGGTGCCGC 40439	A _ A C	
		GC GT CCTGGATGG GC GA		
		CG CG GGACCTACC CG CT		
		C T C A		
GAM2389	GATA6	3' TCGTTTGCAAGACTGCATTG 19146	C GATG C	
		CAATGCAGTC TG GAGC GA		
		GTTACGTCAG AC TTTG CT		
		A G_ A		
GAM2389	MEN1	3' GCTCCATCCAAAATTGCTGCA 56352	CC_	
		TGCAGT TGGATGGAGC		
		ACGTCG ACCTACCTCG		
		TTAAA		
GAM2389	NFYB	5' CCAACCAGGGCTGCATTG 21609	A	
		CAATGCAGTCCTGG TGG		
		GTTACGTCGGGACC ACC		
		A		
GAM2389	NQO1	5' TCGCGCCCCGGA CTGCA 8057	T AT A C	
		TGCAGTCC GG GG GC GA		
		ACGTCAGG CC CC CG CT		
		_ _ G A		
GAM2389	PPP1R2	3' TCAGTCCAAA ACTGCATT 21787	CC G	
		AATGCAGT TGGAT GA		
		TTACGTCA ACCTG CT		
		AA A		
GAM2389	TAC3	3' CGGACTCCTGGACTGCATT 26037	TGGAT _	
		AATGCAGTCC GGAG CCG		
		TTACGTCAGG CCTC GGC		
		T_ A		
GAM2389	TGM2	3' GCTCCCTAGACTGCATCC 17245	A C AT	
		C ATGCAGTC TGG GGAGC		
		C TACGTCAG ATC CCTCG		
		C _ _		
GAM2389	ZNF255	5' GCTCCATCCAAGTTGCTGCA 20497	CC_	
		TGCAGT TGGATGGAGC		

ACGTCG ACCTACCTCG
 TTGA
 GAM2389 BDG-29 5' TCGACTCCATCATCCACAAC 72807 CC ____ C
 AGT TGA TGGAG CGA
 ||| ||| ||||| |||
 TCA ACCT ACCTC GCT
 AC ACT A
 GAM2389 C6orf29 3' CGGCCCTGATCCAGGACTGCA 52457 ____ A
 TGCAGTCCTGGAT GG GCCG
 ||||| ||| |||
 ACGTCAGGACCTA CC CGGC
 GT _
 GAM2389 FLJ12691 3' CTAGGCCAGGACTACATTG 45000 C A_
 CAATG AGTCCTGG TGG
 ||||| ||||| |||
 GTTAC TCAGGACC ATC
 A GG
 GAM2389 FLJ12787 3' TCGGCTCTGAAGAACTGACA 50697 _ C GGAT
 TG CAGT CT GGAGCCGA
 || ||||| |||
 AC GTCA GA TCTCGGCT
 A A AG_
 GAM2389 FLJ14596 5' CGGAACCCAGAGACTGCATCA 52515 A _ ATGGAG
 C ATGCAGTC CTGG CCG
 | ||||| ||| |||
 A TACGTCAG GACC GGC
 C A CAA_
 GAM2389 KIAA0478 5' CGGCTCCATCCAGGAGTA 30177 AG
 TGC TCCTGGATGGAGCCG
 ||| ||||| |||||
 ATG AGGACCTACCTCGGC
 _
 GAM2389 KIAA1193 3' CGGCTGAGGTCTGCATTG 68266 T GGATGG
 CAATGCAG CCT AGCCG
 ||||| ||| |||||
 GTTACGTC GGA TCGGC
 T G_
 GAM2389 KIAA1813 5' TCAGCCCTGTTTCAGACCAGCAT 70833 A_ C A C
 TG CAATGC GTC TGGATGG GC GA
 ||||| ||| ||||| |||
 GTTACG CAG ACTTGTC CG CT
 AC _ C A
 GAM2389 MGC23937 3' CCATTTCCTCCAACTGCATTG 59601 CC ____
 CAATGCAGT TGG ATGG
 ||||| ||| |||
 GTTACGTCA ACC TACC
 A_ CTT
 GAM2389 PIGQ 3' TCGCAGCACCAGGACTGC 16106 A GA C
 GCAGTCCTGG TG GC GA
 ||||| ||| |||

CGTCAGGACC AC CG CT
 _ GA A

GAM2389 SSB-3 5' GCCCCTGCTGGGACTGCACTG 55959 A TG AT A
 CA TGCAGTCC G GG GC
 || ||||| | ||
 GT ACGTCAGG C CC CG
 C GT GT C

GAM2389 LOC120856 3' TCAGCCCCATGGGCTCTAATTG 74474 GC_ TGG A C
 CAAT AGTCC ATGG GC GA
 ||| |||| ||| ||
 GTTA TCGGG TACC CG CT
 ATC _ C A

GAM2389 LOC153743 3' TCAGTCCAAAACACTGCATT 61132 CC G
 AATGCAGT TGGAT GA
 ||||| |||||
 TTACGTCA ACCTG CT
 AA A

GAM2389 LOC200339 3' CTCTTTAAGGACTGTATTG 91614 GGAT
 CAATGCAGTCCT GGAG
 ||||| |||||
 GTTATGTCAGGA TCTC
 ATT_

GAM2389 LOC221964 3' TCAGTGTAGTCCAGGATCACA 95612 CA GGA C
 TG GTCCTGGAT GC GA
 || ||||| ||
 AC TAGGACCTG TG CT
 AC ATG A

GAM2389 LOC257426 3' CGGCTCCATGCCCACTGC 67216 CCT _
 GCAGT GG ATGGAGCCG
 |||| || |||||
 CGTCA CC TACCTCGGC
 CC_ G

GAM2389 LOC51024 3' TCAGCCCCATCATGTGCTTTG 32682 T GTCCTG A C
 CAA GCA GATGG GC GA
 ||| || ||||| ||
 GTT CGT CTACC CG CT
 T GTA_ C A

GAM2389 LOC91522 3' GCTCCATCCTGGCTGCTTG 66917 T CT
 CAA GCAGTC GGATGGAGC
 || ||||| |||||
 GTT CGTCGG CCTACCTCG
 _ T_

GAM2390 BCL7A 3' CCTCCAGAAAGGAGAGACGCA 40981 CAG C
 TGTGTCTC TCCT TCTGGAGG
 ||||| ||| |||||
 ACGCAGAG AGGA AGACCTCC
 _ A

GAM2390 ELMO1 3' AGAGAGGAATGAAAACACA 56153 CTC G
 TGTGT CA TCCTCTCT
 |||| || |||||

			ACACA GT AGGAGAGA		
			AAA A		
GAM2390	F2RL3	3'	GGAGAGGACACAGAGACACA 15520	CA_	
			TGTGTCTC GTCCTCTCT		
			ACACAGAG CAGGAGAGG		
			ACA		
GAM2390	FBLN2	3'	CCTGAGGACCAGAGACAC 10574	CA	TCT
			GTGTCTC GTCCTC GG		
			CACAGAG CAGGAG CC		
			AC T__		
GAM2390	GRIK3	3'	CCGTGAGGCCAGAGACACA 7718	CA T	TC
			TGTGTCTC G CCTC TGG		
			ACACAGAG C GGAG GCC		
			AC _ T_		
GAM2390	ZNF278	3'	CCTCCAGAGAAGACTGGCACA 50267	TCT	C
			TGTG CCAGTC TCTCTGGAGG		
			ACAC GGTCAG AGAGACCTCC		
			__ A		
GAM2390	ABCA9	5'	CCTCCAGAACATGCAGAGACCC 55364	T	CA CCTC
	A		TG GTCTC GT TCTGGAGG		
			AC CAGAG CG AGACCTCC		
			C A_ TACA		
GAM2390	DKFZP566M1046	5'	CCGGATGAAGCAGACTGGAGAC 50446	C__ _	
	ACA		TGTGTCTCCAGTC TC TCTGG		
			ACACAGAGGTCAG AG AGGCC		
			ACGA T		
GAM2390	FLJ13902	3'	CCACGGGGACTGAAGACACA 45379	C	TC
			TGTGTCT CAGTCCTC TGG		
			ACACAGA GTCAGGGG ACC		
			A C_		
GAM2390	FLJ22501	5'	CCAGAAGAACTGAGACACA 45703	C	C C
			TGTGTCTC AGT CT TCTGG		
			ACACAGAG TCA GA AGACC		
			_ A _		
GAM2390	FLJ22615	3'	CCTCCAGCTCACTGGAGACA 69038	CCTCT	
			TGTCTCCAGT CTGGAGG		
			ACAGAGGTCA GACCTCC		
			CTC__		
GAM2390	KIAA0574	3'	CTTTAGAGAGCTGAAAACACA 69813	CTC	TC
			TGTGT CAG CTCTCTGGAG		

ACACA GTC GAGAGATTTTC
 AAA _
 GAM2390 MGC3771 5' GGAGAGGACACAGAGACACA 49056 CA_
 TGTGTCTC GTCCTCTCT
 ||||| |||||
 ACACAGAG CAGGAGAGG
 ACA
 GAM2390 PRO1386 3' CCTCCAGAAAGGACTGGGCAT 49215 CT C
 GTGT CCAGTCCT TCTGGAGG
 ||| ||||| |||||
 TACG GGTGAGGA AGACCTCC
 _ A
 GAM2390 PTPNS1 3' CCTCCCAAAGGACTGGAGACA 55838 CTCT
 TGTCTCCAGTCCT GGAGG
 ||||| |||||
 ACAGAGGTCAGGA CCTCC
 AAC_
 GAM2390 SEMA3C 5' CGGGAAAAGGACTGGAGACACA 22105 C__ TG
 TGTGTCTCCAGTCCT TC G
 ||||| |||
 ACACAGAGGTCAGGA GG C
 AAA GT
 GAM2390 SMARCF1 3' CCTCCAGAAAAACGGATCACA 21184 TC A CCTC
 TGTG TCC GT TCTGGAGG
 ||| ||| |||||
 ACAC AGG CA AGACCTCC
 T_ _ AAA_
 GAM2390 UBF-fl 3' CCTCCAGAGTAGCTGGAAATAC 52622 C CCT
 A
 TGTGT TCCAGT CTCTGGAGG
 ||||| |||||
 ACATA AGGTCG GAGACCTCC
 A AT_
 GAM2390 LOC143692 5' CCCCAGAGAGACAAAAGATACA 77101 CCA C A
 TGTGTCT GTC TCTCTGG GG
 ||||| ||| ||||| ||
 ACATAGA CAG AGAGACC CC
 AAA _ _
 GAM2391 SNAI2 3' CTCAGGTGCCTTAAAAAGT 13240 C C AC
 AC TTTTG GGC ACCTGAG
 || ||||| ||| |||||
 TG AAAAT CCG TGGACTC
 A T _
 GAM2391 BRPF3 3' CAGATGGCAAGAGGTC 93926 GGCA C
 GACCTTTTGC CA CTG
 ||||| ||| |||
 CTGGAGAACG GT GAC
 _ A
 GAM2391 CSMD1 3' TCAAATGTGTGTCAGGGTCTT 53787 TTGC CC
 AAGACCTT GGCACA TGA
 ||||| ||||| |||

TTCTGGGA CTGTGT ACT
 _____ AA
 GAM2391 FLJ10204 3' CTCAAATGCCCATAAAAGGT 36356 C_ CACC
 ACCTTTTG GGCA TGAG
 ||||| ||| |||
 TGGAAAAT CCGT ACTC
 AC AA__
 GAM2391 FLJ10874 5' TCAGGTGTGCCGAAGCTCT 37328 C TTG
 AGA CTT CGGCACACCTGA
 ||| ||| |||||
 TCT GAA GCCGTGTGGACT
 C ____
 GAM2391 FLJ12800 5' CAAGTGTCTGACTCGCAAAGGC 43525 AC C____ C
 CCT AG CTTTTGCGG ACAC TG
 || ||||| ||| ||
 TC GGAAACGCT TGTG AC
 CC CAGTC A
 GAM2391 KIAA0939 3' CAAGTGAGCTGCAAGAGG 62709 A C
 CCTTTTGCGGC CAC TG
 ||||| ||| ||
 GGAGAACGTCTG GTG AC
 A A
 GAM2391 MVD 3' CAGGTGTCAGGAGAGGTC 11715 GCGGC
 GACCTTTT ACACCTG
 ||||| |||||
 CTGGAGAG TGTGGAC
 GAC__
 GAM2391 SRPK1 3' CTCAGGTGTTCTATAAACAGTC 13405 CT CG C
 GAC TTTG G ACACCTGAG
 ||| ||| | |||||
 CTG AAAT C TGTGGACTC
 AC AT T
 GAM2391 UPK1A 3' CTCAGGTGTGCCCTGAAA 23785 C
 TTTTG GGCACACCTGAG
 |||| |||||
 AAAGT CCGTGTGGACTC
 C
 GAM2391 VEGFC 3' TCATCTGCAAAGGCCT 19475 A CACACC
 AG CCTTTTGCGG TGA
 || ||||| |||
 TC GGAAAACGTC ACT
 C T____
 GAM2391 LOC136319 5' GGTGGCCGCAAAAGAACTT 75772 AC A
 AAG CTTTTGCGGC CACC
 ||| ||||| |||
 TTC GAAAACGCCG GTGG
 AA _
 GAM2391 LOC143677 3' CAGGGGCAAAAGGCTCT 83894 _ GGCACA
 AGA CCTTTTGC CCTG
 ||| ||||| |||

		TCT GGAAAACG	GGAC		
		C	G_____		
GAM2391	LOC146330	5'	CAGGTGTGCAAGGCCT	78377	A TTGCG
			AG CCTT GCACACCTG		
			TC GGAA CGTGTGGAC		
			C _____		
GAM2391	LOC150406	3'	CTCAGGTGTGCCCCGCGGGA	80672	_
			TTTTGCGG CACACCTGAG		
			AGGGCGCC GTGTGGACTC		
			C		
GAM2391	LOC151361	3'	CTCACACCCACAGAAGGTCTT	86503	C CACACC
			AAGACCTTTTG GG TGAG		
			TTCTGGAAGAC CC ACTC		
			A CAC_____		
GAM2391	LOC201771	5'	TCAATCCGTAAAAAGTCTT	70519	C CACACC
			AAGAC TTTTGCGG TGA		
			TTCTG AAAATGCC ACT		
			A TA_____		
GAM2391	LOC204970	3'	TCAGGTGCGCCAGACCGT	90969	CT C A
			AC TTTG GGC CACCTGA		
			TG AGAC CCG GTGGACT		
			CC _ C		
GAM2391	LOC221191	3'	CAGGTGTGGGAAGGTC	95219	GCGG
			GACCTTTT CACACCTG		
			CTGGAAGG GTGTGGAC		

GAM2391	LOC256158	5'	CAGGTATCGGATAAAGGTTT	99483	TG_ CAC
			AGACCTTT CGG ACCTG		
			TTTGAAA GCT TGGAC		
			TAG A_____		
GAM2392	ABCC1	5'	TGCGCCGCCGCCGCCGCC	39607	A_ C
			GGCGGCGGCGGCG GGC CA		
			CCGCCGCCGCCGC CCG GT		
			CG C		
GAM2392	ABCC1	5'	TGCGCCGCCGCCGCCGCC	18436	A_ C
			GGCGGCGGCGGCG GGC CA		
			CCGCCGCCGCCGC CCG GT		
			CG C		
GAM2392	ABCC1	5'	TGCGCCGCCGCCGCCGCC	39600	A_ C
			GGCGGCGGCGGCG GGC CA		

CCGCCGCCGCCGC CCG GT
 CG C
 GAM2392 ACCN1 3' CTTGGGCCCCGCCGTGCGTCCC 8460 C _ A
 T AGG GGCG GCGGCG GGCCCAAG
 ||| ||| ||||| |||||
 TCC CTGC TGCCGC CCGGGTTC
 _ G C
 GAM2392 ACCN2 5' GGACCCGCCGCCGGCT 39629 GG A C
 GGC CGGCGGCG GG CC
 ||| ||||| || ||
 TCG GCCGCCGC CC GG
 _ _ A
 GAM2392 ACTN2 5' GCCCGCCGCCCGCCGCCT 8471 _ A
 AGGCGGCGG CGGCG GGC
 ||||| |||| |||
 TCCGCCGC GCCGC CCG
 C _
 GAM2392 ADD1 3' TCCTGAGCCTCACCTTTCCTGC 27202 C__ C C A
 CGTC GGCGGCGG GG GAGGC CA GA
 ||||| || |||| || ||
 CTGCCGTC CC CTCCG GT CT
 CTTT A A C
 GAM2392 ADD1 3' TCCTGAGCCTCACCTTTCCTGC 27212 C__ C C A
 CGTC GGCGGCGG GG GAGGC CA GA
 ||||| || |||| || ||
 CTGCCGTC CC CTCCG GT CT
 CTTT A A C
 GAM2392 AP2B1 5' TCTCCGCTCCCGCCGCCACC 8895 C C G CA
 GG GGCGGCGG GAG CC AGA
 || ||||| || || |||
 CC CCGCCGCC CTC GG TCT
 A _ _ CC
 GAM2392 ARHC 5' GGACCTGCCCAACGCCGCCT 18973 GC_ G C
 AGGCGGCG GGC AGG CC
 ||||| || || || ||
 TCCGCCGC CCG TCC GG
 AAC _ A
 GAM2392 ARHG 5' GGAGCCGCTGCCGCCGCC 9793 GA _
 GGCGGCGGCGGC GGC CC
 ||||| || || || ||
 CCGCCGCCGTCG CCG GG
 _ A
 GAM2392 ARNTL 5' GGA CTCACCGCCGCCGCC 8626 C GC
 GGCGGCGGCGG GAG CC
 ||||| || || || || ||
 CCGCCGCCGCC CTC GG
 A A_
 GAM2392 BARX2 3' CTTGGGCCTGTACCTCC 14716 C C G
 GG GG GGC AGGCCCAAG
 || || || |||||

			CC CC CTG TCCGGGTTC		
			T A _		
GAM2392	BCL11A	5'	GCCGCCGCCGCCGCCGCC 43466	A_	
			GGCGGCGGCGGCG GGC		
			CCGCCGCCGCCGC CCG		
			CG		
GAM2392	BCL11A	5'	GCCGCCGCCGCCGCCGCC 57502	A_	
			GGCGGCGGCGGCG GGC		
			CCGCCGCCGCCGC CCG		
			CG		
GAM2392	BCL11A	5'	GCCGCCGCCGCCGCCGCC 36338	A_	
			GGCGGCGGCGGCG GGC		
			CCGCCGCCGCCGC CCG		
			CG		
GAM2392	BIN3	3'	CCTAGGCAGGCCGCCGTCT 38575	G_ G_	
			AGGCGGCGGC GC AGG		
			TCTGCCGCCG CG TCC		
			GA GA		
GAM2392	BMP3	5'	CCTCGGCTCCGCCGCCGGCT 8657	G	___
			AG CGGCGGCGG CGAGG		
			TC GCCGCCGCC GCTCC		
			G TCG		
GAM2392	BMP8	5'	GCCCCGCCGCCGCCGCC 9947	_	A
			GGCGGCGG CGGCG GGC		
			CCGCCGCC GCCGC CCG		
			C C		
GAM2392	BTAF1	5'	TCTTGACCCCTGCTTACCGGC 72873	_ C_	CGA C
	C		GGC GG GCGG GG CCAAGA		
			CCG CC TCGTC CC GGTCT		
			G AT C_ A		
GAM2392	C1orf6	5'	GGCCCACCGCCGCCGCC 39696	CGA	
			GGCGGCGGCGG GGCC		
			CCGCCGCCGCC CCGG		
			AC_		
GAM2392	CACNA1A	3'	GGGCCTCGGGCCCGGCCT 5359	GGC	GG
			AGGC GGC CGAGGCC		
			TCCG CCG GCTCCGGG		
			GC_ G_		
GAM2392	CACNA2D2	5'	GCCGCCGCCGCCGCCGCC 21224	A_	
			GGCGGCGGCGGCG GGC		

		CCGCCGCCGCCGC CCG		
		CG		
GAM2392	CAPON	5' GGCCCCGCCACGCGTCGCCGC 64662	_____	A
		GCGGCGGC GGCG GGCC		
		CGCCGCTG CCGC CCGG		
		CGCA C		
GAM2392	CDA	3' CTTGGGACTTAGAACACCGCCG 10128	CGGCG_ _	
	CC	GGCGGCGG AGG CCCAAG		
		CCGCCGCC TTC GGGTTC		
		ACAAGA A		
GAM2392	CDC34	5' GGGCCCCTCCGCCGCCGCC 16391	CGA	
		GGCGGCGGCGG GGCCC		
		CCGCCGCCGCC CCGGG		
		TCC		
GAM2392	CDH2	5' CCGCCGCCGCCGCCGCCT 10144	A_	
		AGGCGGCGGCGGCG GG		
		TCCGCCGCCGCCGC CC		
		CG		
GAM2392	CDH2	5' GCCGCCGCCGCCGCCGCC 10145	A_	
		GGCGGCGGCGGCG GGC		
		CCGCCGCCGCCGC CCG		
		CG		
GAM2392	CDK2AP1	5' GGCCTCGCCGCCGCCGCC 17353		
		GGCGGCGGCGGCGAGGCC		
		CCGCCGCCGCCGCTCCGG		
GAM2392	CHIC2	5' CCTCAGCCTCCGCCGCCT 25047	C _	
		AGGCGGCGG GGC GAGG		
		TCCGCCGCC CCG CTCC		
		T A		
GAM2392	CLASP1	3' CTTGCCTTGCCGCCGCCTCC 65892	C	CC
		GG GGCGGCGGCGAGGC AAG		
		CC CCGCCGCCGTTCCG TTC		
		T _		
GAM2392	CLTCL1	5' CTGCCGCTGCCGCCGCCGCC 64420	A_	CCA
	C	GGCGGCGGCGGCG GGC AG		
		CCGCCGCCGCCGC TCG TC		
		CG CCG		
GAM2392	CNTNAP2	5' CTTGAGCGCCGCCGCCGCC 27092	GG	AGGC
		GGC CGGCGGCG CCAAG		

		CCG GCCGCCGC GGTTC		
		GA		
GAM2392	CSDA	5' CCTCGGCCGCCGCCCT 14688		—
		AGGCGGCGGCGGCG GAGG		
		TCCGCCGCCGCCG CTCC		
		G		
GAM2392	CUL3	5' GGTCGCCGCCGCCGCC 14573	AG	
		GGCGGCGGCGGCG GCG		
		CCGCCGCCGCCGC TGG		
GAM2392	CYP26A1	5' CCTCCCCACCGCCGCT 55122	C C_	
		AGGCGGCGG GG GAGG		
		TCCGCCGCC CC CTCC		
		A CC		
GAM2392	DLX2	3' GGCCCGCTGCCGCCACC 16606	C A	
		GG GGCGGCGGCG GGCC		
		CC CCGCCGTCGC CCGG		
		A		
GAM2392	E2F1	5' GCGCCGCCGCCGCCCT 85949	AG	
		AGGCGGCGGCGGCG GC		
		TCCGCCGCCGCCGC CG		
		CG		
GAM2392	ELAVL1	5' GCCGCGCCGCCGCCCT 9223	A	
		AGGCGGCGGCGGCG GGC		
		TCCGCCGCCGCCGC CCG		
		G		
GAM2392	EXT1	5' CCGCCGCCGCCGCCCT 5521	A_	
		AGGCGGCGGCGGCG GG		
		TCCGCCGCCGCCGC CC		
		CG		
GAM2392	FMNL	5' CCGCCGCCGCCGCCCT 20867	A_	
		AGGCGGCGGCGGCG GG		
		TCCGCCGCCGCCGC CC		
		CG		
GAM2392	FMNL	5' GCCGCCGCCGCCGCCGCC 20871	A_	
		GGCGGCGGCGGCG GGC		
		CCGCCGCCGCCGC CCG		
		CG		
GAM2392	FMNL	5' GCCTGCGCCGCCGCTGCC 20872	—	
		GGCGGCGGCGGCG AGGC		

		CCGTCGCCGCCGC TCCG	
		G	
GAM2392	FMNL	5' GGAGCAGCGCCACCGCCGCC 20873	C AG _
		GGCGGCGG GGCG GC CC	
		CCGCCGCC CCGC CG GG	
		A GA A	
GAM2392	FMR2	5' GCCCGCCGCCGCCGCCT 10694	A
		AGGCGGCGGCGGCG GGC	
		TCCGCCGCCGCCGC CCG	
GAM2392	FOXG1B	5' GGTCGCCGCGCCGCC 19134	G AG
		GGCGGCG CGGCG GCC	
		CCGCCGC GCCGC TGG	
GAM2392	FTH1	5' CCGCCGCCGCCGCCGCCT 68712	A_
		AGGCGGCGGCGGCG GG	
		TCCGCCGCCGCCGC CC	
		CG	
GAM2392	G6PT1	5' CTTCGCCGCCGCCGCCT 9403	_
		AGGCGGCGG CGGCGAGG	
		TCCGCCGCC GCCGCTTC	
		C	
GAM2392	GABPB1	5' CTCGGGTCCCCGCACCACT 19138	C CG CGA A
		AGG GG GCGG GGCCC AG	
		TCC CC CGCC CTGGG TC	
		A A_ C_ C	
GAM2392	GARS	5' COTTGCCCGCCGCCGCCT 10757	_
		AGGCGGCGGCGG CGAGG	
		TCCGCCGCCGCC GTTCC	
		C	
GAM2392	GAS1	5' GGCGGCCGCCGCTGCC 10761	GAG
		GGCGGCGGCGGC GCC	
		CCGTCGCCGCCG CGG	
		G_	
GAM2392	GCLM	5' TCTCGGGCCTCGGGCACCGC 10791	CG GG A
		GCGG GC CGAGGCC AGA	
		CGCC CG GCTCCGGG TCT	
		A_ G_ C	
GAM2392	GNA11	5' GGGCCGGCCCGCCCGCCT 10815	C CGA
		AGGCGG GGCGG GGCCC	

			TCCGCC CCGCC CCGGG		
			— CGG		
GAM2392	GNAQ	5'	GGCCTGGCCGCGCCCC 10825	C	G
			GG GCGGCGGC AGGCC		
			CC CCGCCGCCG TCCGG		
			— G		
GAM2392	GNAS	5'	GCCGCCGCGCCGCCGCC 6712		A_
			GGCGGCGGCGGCG GGC		
			CCGCCGCCGCCG CCG		
			CG		
GAM2392	GNAS	5'	GCCGCCGCGCCGCCGCC 55388		A_
			GGCGGCGGCGGCG GGC		
			CCGCCGCCGCCG CCG		
			CG		
GAM2392	GNB2	5'	CCGCCGCCGCCGCCCT 19171		A_
			AGGCGGCGGCGGCG GG		
			TCCGCCGCCGCCG CC		
			CG		
GAM2392	GPC1	5'	CCTCGGCCGCCGCCCT 10858		—
			AGGCGGCGGCGGC GAGG		
			TCCGCCGCCGCCG CTCC		
			G		
GAM2392	GRM7	5'	CCTCCAGCGCCGCCGCC 7783		—
			GGCGGCGGCGGC GAGG		
			CCGCCGCCGCCG CTCC		
			CGAC		
GAM2392	GUCY1A2	5'	GGTCCCGCCACCGCCGCCT 7804	C	A
			AGGCGGCGG GGCG GGCC		
			TCCGCCGCC CCGC CTGG		
			A C		
GAM2392	HAGH	5'	TCTCGGGCCGCCGCCGCCG 19224		A_ A
	CT		GGCGGCGGCGGCG GGCCC AGA		
			TGCGCGCCGCCG CCGGG TCT		
			CG C		
GAM2392	HDAC5	5'	GCTGCTGCCGCCGCCGCC 19621		A_
			GGCGGCGGCGGCG GGC		
			CCGCCGCCGCCGT TCG		
			CG		
GAM2392	HDAC5	5'	GCTGCTGCCGCCGCCGCC 58299		A_
			GGCGGCGGCGGCG GGC		

		CCGCCGCCGCCGT TCG		
		CG		
GAM2392	HIC1	5' GGGCCTCCGCCGCCGCCT 88660	CG	
		AGGCGGCGGCGG AGGCC		
		TCCGCCGCCGCC TCCGGG		
		—		
GAM2392	HIVEP1	5' GGCGCCGCCGCCGCC 10922	AG	
		GGCGGCGGCGGCG GCC		
		CCGCCGCCGCCGC CGG		
		CG		
GAM2392	HLX1	5' CCTCGGCTGCCGCCGCCT 41983	—	
		AGGCGGCGGCGGC GAGG		
		TCCGCCGCCGTCG CTCC		
		G		
GAM2392	HMG2	5' GCTGCCGTCGCCGCCGCC 19808	A_	
		GGCGGCGGCGGCG GGC		
		CCGCCGCCGCTGC TCG		
		CG		
GAM2392	HMOX1	5' CCTCAGCGCAGCCGCCGCC 10942	G ____	
		GGCGGCGGC GC GAGG		
		CCGCCGCCG CG CTCC		
		A CGA		
GAM2392	HR	5' CCTAGAGCGCCCCGCCGCC 18915	C ____	
		GGCGGCGG GCG AGG		
		CCGCCGCC CCGC TCC		
		C GAGA		
GAM2392	IGFBP1	5' TCTGCCGCCGCCGCCGCCAC 6996	C	A CCA
	C	GG GGCGGCGGCG GGC AGA		
		CC CGGCCGCC CCG TCT		
		A G CCG		
GAM2392	JAG2	5' CCGCCGCCGCCGCCGCCT 11094	A_	
		AGGCGGCGGCGGCG GG		
		TCCGCCGCCGCCGC CC		
		CG		
GAM2392	JAG2	5' GCCCGCGCCGCCGCCGCC 11095	A_	
		GGCGGCGGCGGCG GGC		
		CCGCCGCCGCCGC CCG		
		GC		
GAM2392	KCNJ5	5' TGAGCCCCCTGCACCGCCGCT 7980	CG A__ C	
		GGCGGCGG GCG GGC CA		

		TCGCCGCC CGT CCG GT		
		A_ CCCC A		
GAM2392	KCNQ3	5' GGGCTTGCAGCCGCCGCCG 16928		_____
	CCT	AGGCGCGGCGGCG AGGCCC		
		TCCGCCGCCGCCG TCGGG		
		CGACG		
GAM2392	KIF3B	5' GCCGCCGCCGCCGCC 17805	A_	
		GGCGGCGGCGGCG GGC		
		CCGCCGCCGCCG CCG		
		CG		
GAM2392	KPNB1	5' TCTTAGGAGGAGTCGCCGCCG 11220	GG C_	
	CGCC	GGCGGCGGCGGCGA CC AAGA		
		CCGCCGCCGCCGCT GG TTCT		
		GA AGGA		
GAM2392	LASS1	3' GGCCCAGCCGCCGCCCT 41476	C	GA
		GG GGCGGCGGC GGCC		
		TC CCGCCGCCG CCGG		
		— AC		
GAM2392	LMO2	5' CCTAGGCCGCGCCCCCT 19937	C	G_
		AGG GGCGGCGGC AGG		
		TCC CCGCCGCCG TCC		
		C GA		
GAM2392	LMO4	5' CCGCCGCCGCCGCCCT 23180	A_	
		AGGCGGCGGCGGCG GG		
		TCCGCCGCCGCCG CC		
		CG		
GAM2392	MADH7	5' CCTCGGGCCGCCGCCGCT 20924		_____
		GGCGGCGGCGGC GAGG		
		TCGCCGCCGCCG CTCC		
		GG		
GAM2392	NFATC3	5' GCTGCCGCCGCCGCCCT 17050	A_	
		AGGCGGCGGCGGCG GGC		
		TCCGCCGCCGCCG TCG		
		CG		
GAM2392	NRXN2	5' GGCGCCGCCGCCGCCCT 31312	AG	
		AGGCGGCGGCGGCG GCC		
		TCCGCCGCCGCCG CGG		
		CG		
GAM2392	NRXN2	5' GGCGCCGCCGCCGCCCT 57822	AG	
		AGGCGGCGGCGGCG GCC		

		TCCGCCGCCGCCGC CGG		
		CG		
GAM2392	NSEP1	5' CCACCGCCGCCGCCGCCT 75235	—	A_
		AGGC GGC GGC GGC GGC GG		
		TCCG CCGCCGCCGC CC		
		G CA		
GAM2392	ODC1	5' CTGTAGCCGCCGCCGCCGCC 11884	GA	CCA
		GGCGGCGGCGGC GGC AG		
		CCGCCGCCGCCG CCG TC		
		— ATG		
GAM2392	PCTK1	5' GCCACCGCCGCCGCCGCC 53424	A_	
		GGCGGCGGCGGC GGC		
		CCGCCGCCGCCGC CCG		
		CA		
GAM2392	PCTK1	5' GCCACCGCCGCCGCCGCC 21678	A_	
		GGCGGCGGCGGC GGC		
		CCGCCGCCGCCGC CCG		
		CA		
GAM2392	PK428	5' CCTGCGCCGCCGCCGCCT 14601	G	—
		AGGCGGC GCGGCG AGG		
		TCCGCCG CGCCGC TCC		
		G G		
GAM2392	PLCG1	5' GGCCTGTGCCGCCGCCGCC 12160	—	
		GGCGGCGGCGGC AGGCC		
		CCGCCGCCGCCGT TCCGG		
		G		
GAM2392	PPARG	5' CCGAGCCGCAGCCGCCGCCT 57759	—	GA
		AGGCGGCGGC GGC GG		
		TCCGCCGCCG CCG CC		
		ACG AG		
GAM2392	PPARG	5' CCGAGCCGCAGCCGCCGCCT 18529	—	GA
		AGGCGGCGGC GGC GG		
		TCCGCCGCCG CCG CC		
		ACG AG		
GAM2392	PPP2R5C	3' CCTCGCAGTGTGCGCCGCC 12249	—	
		GGCGGCGGCG GCGAGG		
		CCGCCGCTGT CGCTCC		
		GA		
GAM2392	PPP2R5E	5' GTCGTGCGCCGCCGCCGCC 21806	—	
		GGCGGCGGCGGCGA GGC		

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          CCGCCGCCGCCGCT CTG
              G
GAM2392 PRKAR1A 5' CCTCGCGCCCGCCGCC 12282  ____
          GGCGGCGGCG GCGAGG
          ||||| ||||
          CCGCCGCCGC CGCTCC
              CCG
GAM2392 PTMA 5' CTTGCTCGCCGAGCCGCCT 12559 G GCC
          AGGCGGC GCGGCGAG CAAG
          ||||| ||||| |||
          TCCGCCG CGCCGCTC GTTC
              A ____
GAM2392 PTPRG 5' GGCTGCTCGCCGCCGCCGCC 12615 ____
          GGCGGCGGCGGCGAG GCC
          ||||| ||||| |||
          CCGCCGCCGCCGCTC CGG
              GT
GAM2392 PTPRS 3' CCTGGCACGGCCGCCGCCT 12630 __ G
          AGGCGGCGGC G GC AGG
          ||||| | |||
          TCCGCCGCCG C CG TCC
              G A G
GAM2392 PTPRS 3' CCTGGCACGGCCGCCGCCT 56467 __ G
          AGGCGGCGGC G GC AGG
          ||||| | |||
          TCCGCCGCCG C CG TCC
              G A G
GAM2392 PTPRS 3' CCTGGCACGGCCGCCGCCT 56468 __ G
          AGGCGGCGGC G GC AGG
          ||||| | |||
          TCCGCCGCCG C CG TCC
              G A G
GAM2392 PTPRS 3' CCTGGCACGGCCGCCGCCT 56469 __ G
          AGGCGGCGGC G GC AGG
          ||||| | |||
          TCCGCCGCCG C CG TCC
              G A G
GAM2392 PYGM 3' TCTTGGGCCAGCCCCAGCACCT 20037 CG _ C GA
          AGG GC GG GGC GGCCCAAGA
          || || || || |||||
          TCC CG CC CCG CCGGGTTCT
              A_ A _ A_
GAM2392 RAP1GA1 3' TGGGCCTCCATCACCCCT 12776 C C GC CG
          AGG GG G GG AGGCCCA
          ||| || || |||||
          TCC CC C CC TCCGGGT
              _ A TA _
GAM2392 RHEB2 5' GCCCGCCGCCGCCCT 20047 C A
          AGG GGCGGCGGCG GGC
          || ||||| |||

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TCC CCGCCGCCGC CCG

GAM2392	RNPEPL1	5'	GGGCCCGCGCCGCCGCC	37217	G	A
			GGCGGCGGCG CG GGCCC			
			CCGCCGCCGC GC CCGGG			
GAM2392	ROR1	5'	CCGCCGCCGCCGCCCT	18459	A	_
			AGGCGGCGGCGGCG GG			
			TCCGCCGCCGCCGC CC			
			CG			
GAM2392	RREB1	5'	GTCCGAGCGCCGCCGCCGCC	12911	A	__
			GGCGGCGGCGGCG GGC			
			CCGCCGCCGCCGC CTG			
			GAGC			
GAM2392	SCN8A	5'	GGGCCCGCGTTAGGGCCGCCG	27216	G	_____ A
	CT		GGCGGCGGC GCG GGCCC			
			TCGCCCGC CGC CCGGG			
			GGATTG C			
GAM2392	SH3BP4	5'	GCCACTACGCGCCGCCGCCGCC	28002	A	_____
			GGCGGCGGCGGCG GGC			
			CCGCCGCCGCCGC CCG			
			CATCA			
GAM2392	SLC6A8	5'	GGAGCCGCCGCCGCCGCCGCC	20072	A	_ _
			GGCGGCGGCGGCG GGC CC			
			CCGCCGCCGCCGC CCG GG			
			CG A			
GAM2392	SLC7A1	5'	GGAGCCCGCGCCGCCCGGCT	13198	G	A _
			AG CGGCGGCGGCG GGC CC			
			TC GCCGCCGCCGC CCG GG			
			G C A			
GAM2392	SLC9A3	3'	GCCCACCGCCGCCGCCGC	16066	A	_____
			GCGGCGGCGGCG GGC			
			CGCCGCCGCCGC CCG			
			CAC			
GAM2392	SLC9A3R2	3'	CTTGGGCTCAGCCTGCC	62101	_	_
			GGC GGC GAGGCCCAAG			
			CCG CCG CTCCGGGTTC			
			T A			
GAM2392	SMG1	5'	CCTCCGCCGCCGCCTCCT	31346	C	_
			AGG GGCGGCGGCG AGG			

			TCC CCGCCGCCGC TCC		
			T C		
GAM2392	SMG1	5'	GCCCTCCGCCGCCGCT 31349	CGA	
			AGGCGGCGGCGG GGC		
			TCCGCCGCCGCC CCG		
			TC_		
GAM2392	TACSTD1	5'	GGCCTCGCGCTGCCCGGCC 11408	___ G	
			GGC GGCGGCG CGAGGCC		
			CCG CCGTCGC GCTCCGG		
			GC _		
GAM2392	TAF15	5'	GGCCGCCGCGCCGCCT 14470	G GA	
			AGGCGGCG CGGC GGCC		
			TCCGCCGC GCCG CCGG		
			_ _		
GAM2392	TAF15	5'	GGCCGCCGCGCCGCCT 58319	G GA	
			AGGCGGCG CGGC GGCC		
			TCCGCCGC GCCG CCGG		
			_ _		
GAM2392	TBL1X	5'	GCCGCCGCCGCCGCCGCC 20136	A_	
			GGCGGCGGCGGCG GGC		
			CCGCCGCCGCCGC CCG		
			CG		
GAM2392	TBX6	3'	CTTGGGCCTGCCACCCACC 17232	C C_ G	
			GG GG GGC AGGCCCAAG		
			CC CC CCG TCCGGGTTC		
			A CAC _		
GAM2392	TM4SF2	5'	GCCGCCGCCGCCGCCGCC 17252	A_	
			GGCGGCGGCGGCG GGC		
			CCGCCGCCGCCGC CCG		
			CG		
GAM2392	TMEFF2	5'	GCCACCGCCGCCGCCT 32998	CGA	
			AGGCGGCGGCGG GGC		
			TCCGCCGCCGCC CCG		
			A_		
GAM2392	TOP1	5'	TCTCGGGCCCACAGTCACCGCC 13826	C GA_ A	
	GCTT		AGGCGGCGG GGC GGCCC AGA		
			TTCGCCGCC CTG CCGGG TCT		
			A ACAC C		
GAM2392	TP53BP2	5'	GCTGCCGCCGCCGCCGCCT 19464	A_	
			AGGCGGCGGCGGCG GGC		

		TCCGCCGCCGCCGC TCG	
		CG	
GAM2392	UBQLN1	5' TGAGTCACCGCCGCCGCCGC 26478	A_ C
		GCGGCGGCGGCG GGC CA	
		CGCCGCCGCCGC CTG GT	
		CA A	
GAM2392	USP7	5' GCCGCCGCCGCCGCCGCC 14418	A_
		GGCGGCGGCGGCG GGC	
		CCGCCGCCGCCGC CCG	
		CG	
GAM2392	VIPR2	3' CCTCAGGAGGTCACCTGCCGCC 14061	_ C ____
		GGCGGC GG GGC GAGG	
		CCGCCG CC CTG CTCC	
		T A GAGGA	
GAM2392	ZFP103	5' CTCGGGCCCCGGCCTGCCGCC 20227	_ GG A A
		GGCGGC GGC CG GGCCC AG	
		CCGCCG CCG GC CCGGG TC	
		T _ C C	
GAM2392	ZNF219	5' GCCGCCGCCGCCGCCGCC 33556	A_
		GGCGGCGGCGGCG GGC	
		CCGCCGCCGCCGC CCG	
		CG	
GAM2392	ZNF278	5' GCCCCGCCGCCGCCGCCT 27499	A
		AGGCGGCGGCGGCG GGC	
		TCCGCCGCCGCCGC CCG	
		C	
GAM2392	ZNF278	5' GCCGCCGCCGCCGCCGCC 27500	_ A_
		GGCGG CGGCGGCG GGC	
		CCGCC GCCGCCGC CCG	
		C CG	
GAM2392	ZNF278	5' GGCCCGCGCCACCGCC 27501	C G A
		GGCGG GGCG CG GGCC	
		CCGCC CCGC GC CCGG	
		A _ _	
GAM2392	ZNF278	5' TCTTGGCTGCGCGCCGGCGCCG 27503	G AG _
	CCT	AGGCGGCG CGGCG GC CCAAGA	
		TCCGCCGC GCCGC CG GGTCT	
		G G_ TC	
GAM2392	ZNF278	5' GCCCCGCCGCCGCCGCCT 50268	A
		AGGCGGCGGCGGCG GGC	

			TCCGCCGCCGCCGC CCG		
			C		
GAM2392	ZNF278	5'	GCCGCCGCCGCCGCCGCC 50269	_	A_
			GGCGG CGGCGGCG GGC		
			CCGCC GCCGCCGC CCG		
			C CG		
GAM2392	ZNF278	5'	GGCCCGCGCCACCGCC 50274	C	G A
			GGCGG GGCG CG GGCC		
			CCGCC CCGC GC CCGG		
			A _ _		
GAM2392	ZNF278	5'	TCTTGGCTGCGCGCCGGCGCCG 50277	G	AG _
	CCT		AGGCGGCG CGGCG GC CCAAGA		
			TCCGCCGC GCCGC CG GGTTCT		
			G G_ TC		
GAM2392	ZNF278	5'	GCCCCGCCGCCGCCGCCT 50281	A	
			AGGCGGCGGCGGCG GGC		
			TCCGCCGCCGCCGC CCG		
			C		
GAM2392	ZNF278	5'	GCCGCCGCCGCCGCCGCC 50282	_	A_
			GGCGG CGGCGGCG GGC		
			CCGCC GCCGCCGC CCG		
			C CG		
GAM2392	ZNF278	5'	GGCCCGCGCCACCGCC 50283	C	G A
			GGCGG GGCG CG GGCC		
			CCGCC CCGC GC CCGG		
			A _ _		
GAM2392	ZNF278	5'	TCTTGGCTGCGCGCCGGCGCCG 50284	G	AG _
	CCT		AGGCGGCG CGGCG GC CCAAGA		
			TCCGCCGC GCCGC CG GGTTCT		
			G G_ TC		
GAM2392	ZNF278	5'	GCCCCGCCGCCGCCGCCT 50286	A	
			AGGCGGCGGCGGCG GGC		
			TCCGCCGCCGCCGC CCG		
			C		
GAM2392	ZNF278	5'	GCCGCCGCCGCCGCCGCC 50287	_	A_
			GGCGG CGGCGGCG GGC		
			CCGCC GCCGCCGC CCG		
			C CG		
GAM2392	ZNF278	5'	GGCCCGCGCCACCGCC 50288	C	G A
			GGCGG GGCG CG GGCC		

			CCGCC CCGC GC CCGG		
			A _ _		
GAM2392	ZNF278	5'	TCTTGGCTGCGCGCCGGCGCCG 50289	G	AG _
	CCT		AGGCGGCG CGGCG GC CCAAGA		
			TCCGCCGC GCCGC CG GGTTC		
			G G_ TC		
GAM2392	AP1S2	5'	CTTCGCCGCCGCCGCCGCCGCC 15347	A_	CC
			GGCGGCGGCGGCG GGC AAG		
			CCGCCGCCGCCGC CCG TTC		
			CG C_		
GAM2392	ARTN	5'	CTCGGGCCCCAGCCCTCGCTGC 55116	C	GA_ A
	C		GGCGGCGG GGC GGCCC AG		
			CCGTCGCT CCG CCGGG TC		
			C ACC C		
GAM2392	ATP6V0A1	3'	CTTGGGTCTCCACCACCCCT 18986	C C C C	
			AGG GG GG GG GAGGCCCAAG		
			TCC CC CC CC CTCTGGGTTC		
			_ A A _		
GAM2392	BTBD3	3'	GGCTTCCCCGCCGCCACC 31029	C	C
			GG GGCGGCGG GAGGCC		
			CC CGCGGCC CTTCGG		
			A C		
GAM2392	C14orf4	5'	GGGCCGCCGCCGCCGC 67919	GA	
			GCGGCGGCGGC GGCCC		
			CGCCGCCGCCG CCGGG		
			—		
GAM2392	C1orf17	5'	GGCAGCCGCCGCCGCC 68766	GAG	
			GGCGGCGGCGGC GCC		
			CCGCCGCCGCCG CGG		
			A_		
GAM2392	C1orf2	5'	TGGGCTCCAGGCCGCCGCCCCC 96269	C	GA_
	T		AGG GGCGGCGGC GGCCCA		
			TCC CGCGCGCCG TCGGGT		
			C GACC		
GAM2392	C1orf2	5'	TGGGCTCCAGGCCGCCGCCCCC 22730	C	GA_
	T		AGG GGCGGCGGC GGCCCA		
			TCC CGCGCGCCG TCGGGT		
			C GACC		
GAM2392	C20orf27	5'	CCTGCAGCCGCCGCCGCT 35823	G_	
			GGCGGCGGCGGC AGG		

		TCGCCGCCGCCG TCC		
		ACG		
GAM2392	CAMTA2	3' CCTCGGTTCCCACTGCCT 61883	C C	_____
		AGGCGG GG GG CGAGG		
		TCCGTC CC CC GCTCC		
		A A CTTG		
GAM2392	CCNE1	5' GCCGTCGCCGCCGCCCT 8791		—
		AGGCGGCGGCGGCGA GGC		
		TCCGCCGCCGCCGCT CCG		
		G		
GAM2392	CENTA2	3' TGGGCCTTCCCCGCAACC 37869	CG C C	
		GG GCGG GG GAGGCCCA		
		CC CGCC CC TTCCGGGT		
		AA — —		
GAM2392	CUL2	5' CCGCCGCCGCCGCCCT 14577	A_	
		AGGCGGCGGCGGCG GG		
		TCCGCCGCCGCCGC CC		
		CG		
GAM2392	DCAMKL1	5' GGCCCCGCCGCCGCC 17601	C A	
		GG GGCGGCGGCG GGCC		
		CC CGCCGCCGC CCGG		
		— C		
GAM2392	DKFZP434A0131	3' TGGGCCTTCCTCGCGGCC 39155	G C C	
		GGC GCGG GG GAGGCCCA		
		CCG CGCT CC TTCCGGGT		
		G — —		
GAM2392	DKFZp547E052	3' CTTGGGCCCCGCCACGTT 51091	GC CGA	
		GGCG GGCGG GGCCCAAG		
		TTGC CCGCC CCGGGTTC		
		A_ —		
GAM2392	DKFZp761A052	5' CCGCCGCCGCCGCCCT 73376	A_	
		AGGCGGCGGCGGCG GG		
		TCCGCCGCCGCCGC CC		
		CG		
GAM2392	DKFZP761F241	5' GGGCTCCCCGCCGCCGCC 49584	C G	
		GGCGGCGGCGG GAG CCC		
		CCGCCGCCGCC CTC GGG		
		C —		
GAM2392	DXS9928E	5' GCCGCCGCCGCCGCCGCC 17474	A_	
		GGCGGCGGCGGCG GGC		

CCGCCGCCGCCGC CCG
 CG
 GAM2392 DZIP1 5' CTTAGGCCGCCGCCGCCGC 30702 GA C
 GCGGCCGCCGCC GC CC AAG
 ||||| ||| |||
 CGCCGCCGCCGCC CCGG TTC
 — A
 GAM2392 EPB41L1 3' TCTTGGGCCTCAGTTTCCCGAC 71117 G C C _
 T AG CGG GG GGC GAGGCCCAAGA
 || ||| ||| |||||
 TC GCC CT TTG CTCCGGGTTCT
 A _ _ A
 GAM2392 FASTK 5' TCTGTGCCGCCGCCGCCCT 47689 _
 AGCGGCCGCCGCCG AGG
 ||||| |||
 TCCGCCGCCGCCGT TCT
 G
 GAM2392 FER1L4 3' GTTTCGCTGCCGCCGCCCT 48135
 AGCGGCCGCCGCCGAGGC
 |||||
 TCCGCCGCCGTCGCTTTG
 GAM2392 FLJ10276 3' TCTTGGGCCTCTGCTCACACCT 36427 CGGC GC
 AGG GGCG GAGGCCCAAGA
 || ||| |||||
 TCC TCGT CTCCGGGTTCT
 ACAC _
 GAM2392 FLJ12761 5' GGGCGCCGCCGCCGCC 44923 GAG
 GCGGCCGCCGCC GCCC
 ||||| |||
 CGCCGCCGCCGCC CGGG
 —
 GAM2392 FLJ13187 5' CTTCGCTGTCGCCGCCGCCGCC 45164 _ CC
 GGCGGCCGCCGCCGA GGC AAG
 ||||| ||| |||
 CCGCCGCCGCCGCCCT TCG TTC
 G C_
 GAM2392 FLJ13220 5' CCTGACGCCTCCGCCGCC 41921 C _
 GGCGGCCGCCGCC AGG
 ||||| ||| |||
 CCGCCGCCGCCGCC TCC
 T AG
 GAM2392 FLJ13456 5' GGCCCGCCGCCGCCGCC 66553 CG A
 GG GCGGCCGCCGCC GGCC
 || ||||| |||
 CC CGCCGCCGCCGCC CCGG
 CA _
 GAM2392 FLJ14466 5' GGGCCCCGCCACCGGCCGCC 52430 C A
 GGCGGCCGCCGCC GGCC
 ||||| ||| |||||

		CCGCCGCC CCGC CCGGG	
		A C	
GAM2392	FLJ20257	5' GGCCCCGCCGCCGCCGCT 39489	A
		GGCGGCGGCGGCG GGCC	
		TCGCCGCCGCCGC CCGG	
		C	
GAM2392	FLJ20506	5' GCTGCCGCCGCCGCCGCC 35723	A_
		GGCGGCGGCGGCG GGC	
		CCGCCGCCGCCGC TCG	
		CG	
GAM2392	FLJ20557	5' CCTCGGCCACGCCGCCT 62570	GC _
		AGGCGGCG GGC GAGG	
		TCCGCCGC CCG CTCC	
		AC G	
GAM2392	FLJ22390	5' GGCCTTGCCGCCGCCACCT 43032	C
		AGG GGCGGCGGCGAGGCC	
		TCC CCGCCGCCGTTCCGG	
		A	
GAM2392	FLJ22408	5' CCTGAGCCCTGACACCGCTT 45985	___ C G_
		AGGCGG CGG GGC AGG	
		TTCGCC GTC CCG TCC	
		ACA _ AG	
GAM2392	FLJ31762	5' CCTACCGCCGCCGCCGCC 58765	___
		GGCGGCGGCGGCG AGG	
		CCGCCGCCGCCGC TCC	
		CA	
GAM2392	GABPB2	5' CTCGGGTCCCCGCACACCT 10751	C CG CGA A
		AGG GG GCGG GGCCC AG	
		TCC CC CGCC CTGGG TC	
		A A_ C_ C	
GAM2392	GC20	5' GGCTTCCGCCGCCGCC 69474	CG
		GGCGGCGGCGG AGGCC	
		CCGCCGCCGCC TTCGG	
		—	
GAM2392	GGA2	3' TCTCAAGCTGCCACCTCCT 57685	C C _
		AGG GG GGCGGC GAGG	
		TCC CC CCGTCG CTCT	
		T A AA	
GAM2392	GGA2	3' TCTCAAGCTGCCACCTCCT 31174	C C _
		AGG GG GGCGGC GAGG	

			TCC CC CCGTCG CTCT		
			T A AA		
GAM2392	GIT2	5'	CCGCCGCCACCGCCGCCT 55149	C	A_
			AGGCGGCGG GGCG GG		
			TCCGCCGCC CCGC CC		
			A CG		
GAM2392	GIT2	5'	CCGCCGCCACCGCCGCCT 55152	C	A_
			AGGCGGCGG GGCG GG		
			TCCGCCGCC CCGC CC		
			A CG		
GAM2392	GIT2	5'	CCGCCGCCACCGCCGCCT 58287	C	A_
			AGGCGGCGG GGCG GG		
			TCCGCCGCC CCGC CC		
			A CG		
GAM2392	GIT2	5'	CCGCCGCCACCGCCGCCT 29409	C	A_
			AGGCGGCGG GGCG GG		
			TCCGCCGCC CCGC CC		
			A CG		
GAM2392	GPT2	3'	CTCGGGCCTCGCAGAGGCCGCT 56769	GGCG	A
			GGCGGC GCGAGGCC AG		
			TCGCCG CGCTCCGGG TC		
			GAGA C		
GAM2392	H2AFY	5'	CTTGCACTGCCGCCGCCGCC 57595	GA	C_
			GGCGGCGGCGGC GGC CAAG		
			CCGCCGCCGCCG TCG GTTC		
			— AC		
GAM2392	H2AFY	5'	CTTGCACTGCCGCCGCCGCC 57596	GA	C_
			GGCGGCGGCGGC GGC CAAG		
			CCGCCGCCGCCG TCG GTTC		
			— AC		
GAM2392	HELO1	5'	CCTCCGCCGCCGCCGCCT 41796	—	
			AGGCGGCGGCGGCG AGG		
			TCCGCCGCCGCCGC TCC		
			C		
GAM2392	HSPC063	5'	GGGCCCGGCGCCGCCGCC 27122	G	A
			GGCGGCGGCG CG GGCCC		
			CCGCCGCCGC GC CCGGG		
			G _		
GAM2392	HUMAGCB	5'	GGCCTTGCCGCCGCGACC 26132	CG	
			GG GCGGCGGCGAGGCC		

		CC CGCCGCCGTTCCGG		
		AG		
GAM2392	KHDRBS3	5' GTGCCGCCGCCGCCCT	22658	AG
		AGGCGGCGGCGGCG GC		
		TCCGCCGCCGCCGC TG		
		CG		
GAM2392	KHSRP	5' CCGCCGCCGCCGCCCT	14880	A_
		AGGCGGCGGCGGCG GG		
		TCCGCCGCCGCCGC CC		
		CG		
GAM2392	KIAA0211	5' GCAGTCGCCGCCGCCGCC	28286	G_
		GGCGGCGGCGGCGA GC		
		CCGCCGCCGCCGCT CG		
		GA		
GAM2392	KIAA0444	3' GGCCTCGCCAGGGCTCCCT	63003	C GGC
		AGG GGC GGCGAGGCC		
		TCC TCG CCGCTCCGG		
		C GGA		
GAM2392	KIAA0445	5' CTGGGCCTCCTACCGTC	28637	CG C A
		GGCGG G GAGGCCCA G		
		CTGCC C CTCCGGGT C		
		AT_ C		
GAM2392	KIAA0537	5' GGCCGCCGCCGCCGCCGCC	29929	A_
		GGCGGCGGCGGCG GGCC		
		CCGCCGCCGCCGC CCGG		
		CG		
GAM2392	KIAA0544	3' GGCCTCGCCACCACCAGCC	71470	_ C C
		GGC GG GG GGCGAGGCC		
		CCG CC CC CCGCTCCGG		
		A A A		
GAM2392	KIAA0963	5' CTGGAGTCCCGCCGCC	31032	CGA _ A
		GGCGGCGG GGC CCA G		
		CCGCCGCC CTG GGT C		
		_ A C		
GAM2392	KIAA0995	5' GCCCGGCCGCTCGCCGCCT	73252	_ A
		AGGCGGCG GCGGCG GGC		
		TCCGCCGC CGCCGC CCG		
		T C		
GAM2392	KIAA1393	3' GCCGCCGCCGCCGCCGCC	72572	A_
		GGCGGCGGCGGCG GGC		

		CCGCCGCCGCCGC CCG	
		CG	
GAM2392 KIAA1511	5'	CCGAGCAGCCGCCGCCCT 70726	GA__
		AGGCGGCGGCGGC GG	
		TCCGCCGCCGCCG CC	
		ACGAG	
GAM2392 KIAA1940	5'	CTCGGCGTGCTCGACGCCGCCG 80781	G _ _ A
	CCT	AGGCGGCGGCG CGAG GC CC AG	
		TCCGCCGCCGC GCTC TG GG TC	
		A G C C	
GAM2392 KRTHB5	5'	TCCTGAGCCTCGCACTCTGCCG 11248	CG_ C A
	CC	GGCGGCGG GCGAGGC CA GA	
		CCGCCGTC CGCTCCG GT CT	
		TCA A C	
GAM2392 LBP-32	5'	GCAGCCGCCGCCGCCCT 28041	AG_
		AGGCGGCGGCGGCG GC	
		TCCGCCGCCGCCG CG	
		CGA	
GAM2392 LCP	5'	GGGCCCGCGCCGCCGCCGCC 27478	A_
		GGCGGCGGCGGCG GGCCC	
		CCGCCGCCGCCGC CCGGG	
		GC	
GAM2392 LEPROTL1	5'	GCTGCTGCCGCCGCCCT 31703	A_
		AGGCGGCGGCGGCG GGC	
		TCCGCCGCCGCCGT TCG	
		CG	
GAM2392 LRN	3'	TGAAACTGCTGCCGCCGCC 11355	G GCC
		GGCGGCGGCGGC AG CA	
		CCGCCGCCGTCTG TC GT	
		_ AAA	
GAM2392 MAD3	5'	GGCCGGCCCGCCGCCAGCT 49340	_ CGA
		GGC GGCGGCGG GGCC	
		TCG CCGCCGCC CCGG	
		A CGG	
GAM2392 Magmas	3'	CCCGCCCACCCGCCGCCCT 32683	C__ A
		AGGCGGCGG GGCG GG	
		TCCGCCGCC CCGC CC	
		CCAC _	
GAM2392 MAP	5'	GTCGTCGCCGCCGCCGCC 43369	_
		GGCGGCGGCGGCGA GGC	

		CCGCCGCCGCCGCT CTG		
		G		
GAM2392	MAP2K3	5' GCCGCAGTCGCCGCCGCC 59687		_____
		GGCGGCGGCGGCGA GGC		
		CCGCCGCCGCCGCT CCG		
		GACG		
GAM2392	MAP3K3	5' CTTAGCCACCGCCGCC 11540	CGA	CC
		GGCGGCGGCGG GGC AAG		
		CCGCCGCCGCC CCG TTC		
		A__ A_		
GAM2392	MAPK8IP2	3' TCCTGGGCCCCCAATACCCCT 58209	C	CGGC CGA A
		AGG GG GG GGCCCA GA		
		TCC CC CC CCGGGT CT		
		_ ATAA C__ C		
GAM2392	MAPK8IP2	3' TCCTGGGCCCCCAATACCCCT 25590	C	CGGC CGA A
		AGG GG GG GGCCCA GA		
		TCC CC CC CCGGGT CT		
		_ ATAA C__ C		
GAM2392	MAPK8IP2	3' TCCTGGGCCCCCAATACCCCT 33576	C	CGGC CGA A
		AGG GG GG GGCCCA GA		
		TCC CC CC CCGGGT CT		
		_ ATAA C__ C		
GAM2392	MAPKAPK2	5' GGCCGGGCCCCCGCCGCC 53099	C	GA
		GGCGGCGG GGC GGCC		
		CCGCCGCC CCG CCGG		
		C GG		
GAM2392	MAPKAPK2	5' GGCCGGGCCCCCGCCGCC 17663	C	GA
		GGCGGCGG GGC GGCC		
		CCGCCGCC CCG CCGG		
		C GG		
GAM2392	MESDC1	5' CTCGGGCCACCCCGCGCCGCC 42899	G	CGA_ A
		GGCGGCG CGG GGCCC AG		
		CCGCCGC GCC CCGGG TC		
		_ CCAC C		
GAM2392	MGC10772	5' GGGCCGCCGCCGCTCC 48295	C	GA
		GG GGCGGCGGC GGCCC		
		CC CCGCCGCCG CCGGG		
		T _____		
GAM2392	MGC15437	5' CCTCCGCTGCCGCCGCT 52844		_____
		AGGCGGCGGCGGCG AGG		

		TCCGCCGCCGTCGC TCC	
		C	
GAM2392	MGC20255	3' GGCCCCAGCGCAGCTGCCT 54541	G G GA_
		AGGCGGC GCG C GGCC	
		TCCGTCG CGC G CCGG	
		A _ ACC	
GAM2392	MGC20460	5' CCTCCACCGCCTCCGCCGCCT 54902	C ____
		AGGCGGCGG GGC GAGG	
		TCCGCCGCC CCG CTCC	
		T CCAC	
GAM2392	MGC2601	5' GGCTGCTCCCGCCGCCGCC 44096	C _
		GGCGGCGGCGG GAG GCC	
		CCGCCGCCGCC CTC CGG	
		_ GT	
GAM2392	MGC2817	5' CCTCAGTCGCCGCCGCCT 70738	_
		AGGCGGCGGCGGC GAGG	
		TCCGCCGCCGCTG CTCC	
		A	
GAM2392	MGC4415	3' CCTTCCCCCGCCGCCGCC 49759	C__
		GGCGGCGGCGG GAGG	
		CCGCCGCCGCC TTCC	
		CCC	
GAM2392	MISS	5' CCTCGGACCCATCGCCGCTT 58639	GC ____
		AGGCGGCG GG CGAGG	
		TTCGCCGC CC GCTCC	
		TA CAG	
GAM2392	MRPL20	3' GCGTCGCCAGCCACCGCC 36205	C _ G
		GGCGG GGC GGCGA GC	
		CCGCC CCG CCGCT CG	
		A A G	
GAM2392	NFAT5	5' CTCAGGCTCGCCGCCACC 57786	C G CA
		GG GGCGGCGAG CC AG	
		CC CCGCCGCTC GG TC	
		A _ AC	
GAM2392	NPTXR	5' CTCGGGCGCCCCCGCCGCC 55209	C GAG A
		GGCGGCGG GGC GCCC AG	
		CCGCCGCC CCG CGGG TC	
		C _ C	
GAM2392	NPTXR	5' CTCGGGCGCCCCCGCCGCC 27432	C GAG A
		GGCGGCGG GGC GCCC AG	

		CCGCCGCC CCG CGGG TC	
		C _ C	
GAM2392 NTN4	5'	GGGGCTCCCGCCGCCCC 63582	C C G
		GG GCGGCGG GAG CCC	
		CC CGCGCC CTC GGG	
		_ _ G	
GAM2392 PARVA	5'	CCTCAGTCCCGCCGCCGCC 37181	C_
		GGCGGCGGCGG GAGG	
		CCGCCGCCGCC CTCC	
		CTGA	
GAM2392 PCDH17	5'	CCGCCGCCGCCGCTGCCT 27834	A_
		AGGCGGCGGCGGCG GG	
		TCCGTCGCCGCCGC CC	
		CG	
GAM2392 PDE4DIP	5'	CCGCCGCCGCCGCCGCT 28406	A_
		AGGCGGCGGCGGCG GG	
		TCCGCCGCCGCCGC CC	
		CG	
GAM2392 PEAS	3'	TCCTGGGCCTCAGCTCTGCC 55140	C _ A
		GGCGG GGC GAGGCCCA GA	
		CCGTC TCG CTCCGGGT CT	
		_ A C	
GAM2392 PEG10	3'	CCGCCGCCACAGCCGCCGCT 31202	_ A_
		AGGCGGCGGC GGCG GG	
		TCCGCCGCCG CCGC CC	
		ACA CG	
GAM2392 PIP5K1C	5'	CTCGGGCGCCCCCGCCGCCGTC 71298	CGAG A
		GGCGGCGGCGG GCCC AG	
		CTGCCGCCGCC CGGG TC	
		CCCG C	
GAM2392 PIP5K2B	5'	TCTTTCGCCGCCGCCGCCGCC 57701	GA CC
		GGCGGCGGCGGC GGC AAGA	
		CCGCCGCCGCCG CCG TTCT	
		_ CT	
GAM2392 PIP5K2B	5'	TCTTTCGCCGCCGCCGCCGCC 14530	GA CC
		GGCGGCGGCGGC GGC AAGA	
		CCGCCGCCGCCG CCG TTCT	
		_ CT	
GAM2392 PORIMIN	5'	GCTCTCGCCGCCGCCACCT 54704	C _
		AGG GGCGGCGGCGAG GC	

			TCC CCGCCGCCGCTC CG		
			A T		
GAM2392	PPM1A	5'	GGCTGCCGCCGCCGCCGCT 41010	A_	
			AGGCGGCGGCGGCG GGCC		
			TCCGCCGCCGCCGC TCGG		
			CG		
GAM2392	PTDSS1	5'	TCTCGGGCTGGGGCCGCCCA 29254	C	GA_ A
	CC		GG GGCGGCGGC GGCCC AGA		
			CC CCGCCGCC TCGGG TCT		
			A GGG C		
GAM2392	PTP4A1	5'	CTGCAGCCACCGCCACGCGCT 14405	C	CGA CCA
			AGGCGG GGCGG GGC AG		
			TCCGCC CCGCC CCG TC		
			A A_ ACG		
GAM2392	PTP4A1	5'	GCCACGACCACGCCGCGCT 14408	C _ A	
			AGGCGGCGG GG CG GGC		
			TCCGCCGCC CC GC CCG		
			A A A		
GAM2392	R32184_3	3'	TGGGCCCGTCTCGCCT 54201	C	CGA
			AGGCGG GGCGG GGCCCA		
			TCCGCT CTGCC CCGGGT		
			— —		
GAM2392	Rab11-FIP3	5'	GGCCGCCCGCCGCC 28786	C	GA
			GGCGGCGG GGC GGCC		
			CCGCCGCC CCG CCGG		
			— —		
GAM2392	RICH1	5'	GGGCCGCCGCCGCCACC 36482	C	GA
			GG GGCGGCGGC GGCCC		
			CC CCGCCGCC CCGGG		
			A —		
GAM2392	RPS6KC1	5'	CTTGAGCCACCGCCCC 25779	C	CGA _
			GG GGCGG GGC CCAAG		
			CC CCGCC CCG GGTTC		
			— A_ A		
GAM2392	SAST	5'	GCCGCCGCCGCCGCCGCT 63661	A_	
			AGGCGGCGGCGGCG GGC		
			TCCGCCGCCGCCGC CCG		
			CG		
GAM2392	SCAP	5'	GCCGCCGCCGCCGCCGCC 64472	A_	
			GGCGGCGGCGGCG GGC		

			CCGCCGCCGCCGC CCG		
			CG		
GAM2392	SCOP	5'	GGGCCAGCCCCGCGTC 93427	C	GA
			GGCGGCGG GGC GGCCC		
			CTGCCGCC CCG CCGGG		
			— A —		
GAM2392	SFRS4	5'	GCTTTGCCCGCCGCGCCT 20060	—	
			AGGCGGCGGCGG CGAGGC		
			TCCGCCGCCGCC GTTTCG		
			C		
GAM2392	SLK	5'	GGGTCGCCGCCCGCCT 28891	C	AG
			AGGCGG GGCGGCG GCCC		
			TCCGCC CCGCCGC TGGG		
			— —		
GAM2392	SMARCF1	5'	CCTCCGCCGCCGCCAGCC 21185	—	—
			GGC GGCGGCGGCG AGG		
			CCG CCGCCGCCGC TCC		
			A C		
GAM2392	SMARCF1	5'	GGCCGCCGCCGCCGCCT 21191		GA
			AGGCGGCGGCGGC GGCC		
			TCCGCCGCCGCCG CCGG		
			—		
GAM2392	SMARCF1	5'	CCTCCGCCGCCGCCAGCC 58224	—	—
			GGC GGCGGCGGCG AGG		
			CCG CCGCCGCCGC TCC		
			A C		
GAM2392	SMARCF1	5'	GGCCGCCGCCGCCGCCT 58225		GA
			AGGCGGCGGCGGC GGCC		
			TCCGCCGCCGCCG CCGG		
			—		
GAM2392	SMARCF1	5'	CCTCCGCCGCCGCCAGCC 38041	—	—
			GGC GGCGGCGGCG AGG		
			CCG CCGCCGCCGC TCC		
			A C		
GAM2392	SMARCF1	5'	GGCCGCCGCCGCCGCCT 38043		GA
			AGGCGGCGGCGGC GGCC		
			TCCGCCGCCGCCG CCGG		
			—		
GAM2392	SMT3H2	5'	CCTCGTCCACCGCTGCCGCCT 23658	—	
			AGGCGGCGGCGG CGAGG		

			TCCGCCGTCGCC	GCTCC		
			ACCT			
GAM2392	SPS	5'	GGGCCCCGCCGCCGCC	25310	CGA	
			GGCGGCGGCGG	GGCCC		
			CCGCCGCCGCC	CCGGG		
GAM2392	STK29	3'	GCCTCGCCGCCGCCGCC	88965	—	
			GGCGGCGG	CGGCGAGGC		
			CCGCCGCC	GCCGCTCCG		
			C			
GAM2392	STRIN	5'	GGGCCGCCACCGTCACCT	33231	C	C GA
			AGG	GGCGG GGC		GGCCC
			TCC	CTGCC CCG		CCGGG
			A	A		—
GAM2392	SUI1	5'	GCCACCGCCGCCGCCGCCCT	20538		A_
			AGGCGGCGGCGGCG	GGC		
			TCCGCCGCCGCCGC	CCG		
			CA			
GAM2392	TAF6L	5'	TGGGCGCCGCCGCCACCGCC	22387	C	AG
			GGCGG	GGCGGCG		GCCCA
			CCGCC	CCGCCGC		CGGGT
			A	CG		
GAM2392	TIP120A	5'	CTTCTGTACGCCCGCCGCCGCC	38036	C	AG CC
			GGCGGCGG	GGCG GC		AAG
			CCGCCGCC	CCGC TG		TTC
			—	A_ TC		
GAM2392	TRIP-Br2	5'	GCCTGCCGCCGCCGCCCT	29267		G
			AGGCGGCGGCGGC	AGGC		
			TCCGCCGCCGCCG	TCCG		
GAM2392	VEGFC	5'	GGACCCGCTCCCGCCGCCT	19474	C	A C
			AGGCGGCGG	GGCG GG		CC
			TCCGCCGCC	TCGC CC		GG
			C	— A		
GAM2392	XPO5	5'	GCTTCCCACCCCGCCGCC	92876	C	C_
			GGCGGCGG	GG		GAGGC
			CCGCCGCC	CC		CTTCG
			C	ACC		
GAM2392	ZFP91	5'	CCTCCGCCTCCGCCGCCT	54872	C	—
			AGGCGGCGG	GGCG		AGG

TCCGCCGCC CCGC TCC
 T C
 GAM2392 ZNF333 3' CTTGGGCCCCACCTCATCCT 51592 CGGC C CGA
 AGG GG GG GGCCCAAG
 ||| ||| |||||
 TCC CC CC CCGGGTTC
 TACT A ____
 GAM2392 LOC122792 5' CTGTCTTCGCCGCCGCGCT 59823 CCGA
 GGCGGCGGCGGCGAGG AG
 ||||| ||||| ||
 TCGCCGCCGCCGCTTC TC
 TG____
 GAM2392 LOC126410 3' CTTGGGCTCAGGCCCGCC 74993 C GA_
 GGCGG GGC GGCCCAAG
 ||||| ||| |||||
 CCGCC CCG TCGGGTTC
 _ GAC
 GAM2392 LOC128499 5' GGACCTTGCCGCGGCCGCCT 75264 G C
 AGGCGGC GCGGCGAGG CC
 ||||| ||||| ||
 TCCGCCG CGCCGTTCC GG
 G A
 GAM2392 LOC132422 5' CTGGGGGCCCGCCGCCCGCC 76402 C CGA A_
 GG GGCGGCGG GGCCC AG
 || ||||| |||| ||
 CC CCGCCGCC CCGGG TC
 _ _ GG
 GAM2392 LOC133728 5' CCTCGTGGGACTGCCGCCACCT 76458 C ____
 AGG GGCGGCGG CGAGG
 ||| ||||| ||||
 TCC CCGCCGTC GCTCC
 A AGGGT
 GAM2392 LOC134147 5' GCCCGGCGCCACGCCGCCT 57961 _ G A
 AGGCGGC GGCG CG GGC
 ||||| ||| ||| ||
 TCCGCCG CCGC GC CCG
 CA G _
 GAM2392 LOC134353 5' CTCGGGCAGGACTCGTCGCCGC 75662 ____ A
 C GGCGGCGGCGAG GCCC AG
 ||||| ||||| |||| ||
 CCGCCGCTGCTC CGGG TC
 AGGA C
 GAM2392 LOC138428 5' GGA CTGGCCACCGCCT 75859 C GG GC
 AGGCGG GGC CGAG CC
 ||||| ||| |||| ||
 TCCGCC CCG GCTC GG
 A _ A_
 GAM2392 LOC144017 5' CCTCGGTCCGCCACGGCCT 83929 _ GC _
 AGGC G GGCGG CGAGG
 |||| | |||| ||||

		TCCG C CCGCC GCTCC		
		G A_ TG		
GAM2392	LOC145123 5'	CTTGCTCGCCGAGCCGCCT 68137	G	GCC
		AGGCGGC GCGGCGAG CAAG		
		TCCGCCG CGCCGCTC GTTC		
		A ____		
GAM2392	LOC147341 5'	GCCACCGCCGCCGCCGCC 85119	A_	
		GGCGGCGGCGGCG GGC		
		CCGCCGCCGCCGC CCG		
		CA		
GAM2392	LOC148014 3'	CTTAGGCCTGGTTCCCTGCCGC 79309	_ CG G C	
	CT	AGGCGGC GG GC AGGCC AAG		
		TCCGCCG CC TG TCCGG TTC		
		T CT G A		
GAM2392	LOC148479 5'	GCTCACCGCCGCCGCCGCC 79614	A__	
		GGCGGCGGCGGCG GGC		
		CCGCCGCCGCCGC TCG		
		CAC		
GAM2392	LOC148534 5'	GGCTCGGCGCAGCCGCCGCC 79638	G A__	
		GGCGGCGGC GCG G GCC		
		CCGCCGCCG CGC C CGG		
		A GG T		
GAM2392	LOC149579 5'	CTGGGCCTCCTACCGTC 71691	CG C A	
		GGCGG G GAGGCCCA G		
		CTGCC C CTCCGGGT C		
		AT_ C		
GAM2392	LOC150067 5'	CTGGGCCGCCGCCCTCC 60960	C GA A	
		GG GGCGGC GGCCCA G		
		CC CCGCCG CCGGGT C		
		T _ C		
GAM2392	LOC150067 5'	GCCGCCGCCGCCGCCCCT 60961	A_	
		AGGCGGCGGCGGCG GGC		
		TCCGCCGCCGCCGC CCG		
		CG		
GAM2392	LOC150928 5'	CTTGCTCGCCGAGCCGCCT 74582	G GCC	
		AGGCGGC GCGGCGAG CAAG		
		TCCGCCG CGCCGCTC GTTC		
		A ____		
GAM2392	LOC151588 5'	TGAGCTTCGCCCACCACCT 60634	C C CG C	
		AGG GG GG GCGAGGC CA		

	TCC CC CC CGCTTCG GT		
	A A _ A		
GAM2392 LOC152328 3'	TCCTGGGCCTCAAGTGCCCTCC 81369	C C GC_ A	
C	GG GG GGCG GAGGCCCA GA		
	CC TC CCGT CTCCGGGT CT		
	C _ GAA C		
GAM2392 LOC153474 5'	CCTCGCGCGCGCCGCGCC 81701	__	
	GGCGGCGGCG GCGAGG		
	CCGCCGCCGC CGCTCC		
	GCG		
GAM2392 LOC153546 5'	GCTGCGGCGCGCCGCGCC 81744	G A_	
	GGCGGCGGCG CG GGC		
	CCGCCGCCGC GC TCG		
	G CG		
GAM2392 LOC153546 5'	GGGCCCGCGCGCCGCGCC 81745	G A	
	GGCGGCGGCG CG GGCCC		
	CCGCCGCCGC GC CCGGG		
	_ C		
GAM2392 LOC157848 3'	CTTGGGCCCAAGCCAGCT 82518	_ GGC CGA	
	GGC GGC GG GGCCAAG		
	TCG CCG CC CCGGGTTC		
	A AA_ __		
GAM2392 LOC158056 5'	TCCTGGGCCCGGGCCCCAGCC 82595	_ C GG A A	
	GGC GG GGC CG GGCCCA GA		
	CCG CC CCG GC CCGGGT CT		
	A _ G_ C C		
GAM2392 LOC158293 5'	CTCAGGCCGGTCGGCCGCGCT 82745	_ GA CA	
	GGCGGCGGC GGC GGCC AG		
	TCGCCGCCG CTG CCGG TC		
	G G_ AC		
GAM2392 LOC196500 5'	TCTCCACCGCCGCGCC 89088	C_	
	GGCGGCGGCGG GAGG		
	CCGCCGCCGC CTCT		
	ACC		
GAM2392 LOC197423 5'	CCCCGCCGCGCGCCCT 78422	_ A	
	AGGCGGCGGCGG CG GG		
	TCCGCCGCCGCC GC CC		
	C C		
GAM2392 LOC197423 5'	GCCCGCCGCGCCTCCT 78426	C A	
	AGG GGCGGCGGCG GGC		

		TCC CCGCCGCCGC CCG			
		T _			
GAM2392	LOC200220 5'	GCGCTCCCCGCCGCCACC	90038	C	C _
		GG GCGGCGG GAG GC			
		CC CCGCCGCC CTC CG			
		A C G			
GAM2392	LOC201203 5'	GCAGCCGCCGCCGCC	89516		AG_
		GGCGGCGGCGGCG GC			
		CCGCCGCCGCCG CG			
		CGA			
GAM2392	LOC201915 5'	CCTCAGCCGCCGCCGCC	90554	_	_
		GGCGGCGG CGGC GAGG			
		CCGCCGCC GCCG CTCC			
		C A			
GAM2392	LOC220110 5'	GCCCCGCCGCGCCGCCT	95115	G	A
		AGGCGGCG CGGCG GGC			
		TCCGCCG GCGC CCG			
		_ C			
GAM2392	LOC220558 5'	CCTCTGCCGCCGCCGCCT	92772		_
		AGGCGGCGGCGGC GAGG			
		TCCGCCGCCGCCG CTCC			
		T			
GAM2392	LOC220565 5'	CCTCCGCCGCCGCCTCCT	92440	C	_
		AGG GGCGGCGGCG AGG			
		TCC CCGCCGCCG TCC			
		T C			
GAM2392	LOC220565 5'	GCCCTCCGCCGCCGCCT	92445		CGA
		AGGCGGCGGCGG GGC			
		TCCGCCGCCGCC CCG			
		TC_			
GAM2392	LOC220932 3'	CTTGCGTGCGCGCGCC	94755	G	AGGC
		GGCGGCGGC GCG CCAAG			
		CCGCCGCCG TGC GGTTC			
		G _			
GAM2392	LOC221250 5'	CCTCCACGCCGCCGCCGCC	93477		_
		GGCGGCGGCGGC GAGG			
		CCGCCGCCGCCG CTCC			
		CCAC			
GAM2392	LOC221424 5'	CCTCCGCCACAGCCGCCGCCT	95269	_	_
		AGGCGGCGGC GGCG AGG			

		TCCGCCGCCG CCGC TCC		
		ACA C		
GAM2392	LOC221687 5'	GGGCCCTGGGCCGCCGCC 93870	GG	A
		GGCGGCGGC CG GGCCC		
		CCGCCGCCG GT CCGGG		
		G_ C		
GAM2392	LOC221687 5'	TGGGCCGCCGCCGCC 93875	GG	GA
		GGC CGGCGGC GGCCCA		
		CCG GCCGCCG CCGGGT		
		— —		
GAM2392	LOC221773 5'	TCTTGGGACCCACCGCTGCC 92699	C	CGAGG
		GGCGGCGG GG CCAAGA		
		CCGTCGCC CC GGGTTCT		
		A CA—		
GAM2392	LOC245771 5'	GCTACTGCTGCCGCCT 94479	CGA	
		AGGCGGCGGCGG GGC		
		TCCGCCGTCGTC TCG		
		A—		
GAM2392	LOC253152 5'	TGGGCCCGCCGCCCTCC 97170	C	A
		GG GGCGGCGGCG GGCCCA		
		CC CCGCCGCCG CCGGGT		
		T C		
GAM2392	LOC254102 3'	GGCGTCCGCCGCCGCC 96391	C	A _
		GG GGCGGCGGCG GGC CC		
		CC CCGCCGCCG CTG GG		
		— — C		
GAM2392	LOC254381 5'	GGGCCCGCCGCCCTCC 99331	C C	A
		GG GG GGCGGCG GGCCC		
		CC TC CCGCCGC CCGGG		
		— — C		
GAM2392	LOC255313 5'	CCTCAGCCCGCTCGCCACC 97941	C	_ _ _
		GG GGCG GCGG C GAGG		
		CC CCGC CGCC G CTCC		
		A T C A		
GAM2392	LOC255328 5'	GCTGCACCTGCCGCCCT 98341	CGA_	
		AGGCGGCGGCGG GGC		
		TCCGCCGCCGTC TCG		
		CACG		
GAM2392	LOC256586 5'	GGCTTCCCGTCCGCCGCC 96619	_	C
		GGCGGCGG CGG GAGGCC		

CCGCCGCC GCC CTTCGG
 T _
 GAM2392 LOC257481 3' GGCTCCGTCGCCGCC 61765 CGA
 GGCGGCGGCGG GGCC
 ||||| |||
 CCGCCGCTGCC TCGG

—
 GAM2392 LOC51072 5' CTGGGCCGCCGCCTCC 32545 C GA A
 GG GGCGGC GGCCA G
 || |||| |||| |
 CC CCGCCG CCGGGT C
 T _ C

GAM2392 LOC51072 5' GCCGCCGCCGCCGCCGCT 32546 A_
 AGGCGGCGGCGGCG GGC
 ||||| |||
 TCCGCCGCCGCCGC CCG
 CG

GAM2392 LOC51092 5' GTCGCCGCCGCCGCCGCC 32592 A_
 GGCGGCGGCGGCG GGC
 ||||| |||
 CCGCCGCCGCCGC CTG
 CG

GAM2392 LOC51104 5' TGGGGCGCCGCCGTCT 32603 C AGG
 GG GGCGGCGGCG CCGA
 || ||||| |||
 TC CTGCCGCCGC GGGT
 _ G_

GAM2392 LOC51133 5' CCTCCGGCCGCCGCCGCC 32787 _
 GGCGGCGGCGGC GAGG
 ||||| |||
 CCGCCGCCGCCG CTCC
 GC

GAM2392 LOC55901 5' TGAGCCTTCCCGTCCGCCT 38545 CG C C
 AGGCGG GCGG GAGGC CA
 |||| ||| |||| ||
 TCCGCC TGCC TTCCG GT
 _ C A

GAM2392 LOC91170 3' CTCGGCAGCCACCGCCACCACC 65733 C C A_ _ A
 GCC GGCGG GG GGCG GGC CC AG
 |||| || ||| || ||
 CCGCC CC CCGC CCG GG TC
 A A CA AC C

GAM2392 LOC91252 5' GGATCGCCGCCGCCGCC 65938 GG
 GGCGGCGGCGGCGA CC
 ||||| |||
 CCGCCGCCGCCGCT GG
 A_

GAM2392 LOC91272 5' CCTCCGCCGCTGCCGCCT 66032 _
 AGGCGGCGGCGGCG AGG
 ||||| |||

TCCGCCGTCGCCGC TCC
 C
 GAM2392 LOC91408 5' GCCGCCGCCGCCGCCGCC 66518 A_
 GGCGGCGGCGGCG GGC
 ||||| ||
 CCGCCGCCGCCGC CCG
 CG
 GAM2392 LOC91408 5' TCTGCTCCCGCCGCCGCCGCC 66520 A CCCA
 GGCGGCGGCGGCG GG AGA
 ||||| || ||
 CCGCCGCCGCCGC CC TCT
 _ TCG_
 GAM2392 LOC92710 3' TCTCAGGCCTCACCTGAAGCT 70869 GG _ C CA
 GGC C GG GAGGCC AGA
 || | || || ||
 TCG G CC CTCCGG TCT
 AA T A AC
 GAM2392 LOC93129 5' CTGGGCGCCCGCCGCCT 71956 CG GAG A
 AGGCGGCGG GC GCCCA G
 || || || || ||
 TCCGCCGCC CG CGGGT C
 _ _ C
 GAM2393 ETV5 3' TGATGACAATTTCCATTTT 16730 CG C
 GAA GGAAG TTGTCATCA
 || || || || || || || ||
 CTT CCTTT AACAGTAGT
 TA _
 GAM2393 HTRA3 3' TGAGCCGGCTTCCCCTTCCCA 90585 A C T CA
 TG GAA GGGAAGCT GT TCA
 || || || || || || || ||
 AC CTT CCCTTCGG CG AGT
 C C C _
 GAM2393 KCNK5 3' TTGATGGCCTCTTCCCCCCTCA 14973 AAC CTT
 TGAG GGGAAG GTCATCAA
 || || || || || || || ||
 ACTC CCCTTC CGGTAGTT
 CC_ TC_
 GAM2393 MTM1 3' TGGTGTTGGCTTCCCCTC 6007 AAC TGT
 GAG GGGAAGCT CATCA
 || || || || || || || ||
 CTC CCCTTCGG GTGGT
 _ TT_
 GAM2393 NFRKB 5' TGGTCCAGCTTCCCTTCCTCA 21608 AAC T TC
 TGAG GGGAAGCT G ATCA
 || || || || || || || ||
 ACTC CCCTTCGA C TGGT
 CTT _ C_
 GAM2393 STX1A 3' GGCCTCAGCTTCCCTTCCCA 17213 A C T_
 TG GAA GGGAAGCT GTC
 || || || || || || || ||

AC CTT CCCTTCGA CGG
 C _ CTC
 GAM2393 B3GNT7 3' TTGGTGTGAAACTTCCTGTTCC 71684 A C GT
 CA TG GAACGGGAAG TT CATCAA
 || ||||| || |||||
 AC CTTGTCCTTC AA GTGGTT
 C A GT
 GAM2393 BA108L7.2 3' TGACATCTGGCTTCCCTTCTCA 49082 C ____
 TGAGAA GGGAAGCT TGTCA
 ||||| ||||| |||||
 ACTCTT CCCTTCGG ACAGT
 _ TCT
 GAM2393 BRPF3 3' GGCAGCTTCCCCCTCTCA 93932 AC T
 TGAGA GGGAAGCT GTC
 ||||| ||||| |||||
 ACTCT CCCTTCGA CGG
 CC _
 GAM2393 C3orf4 3' TGATATTTTCCCCACCTCTCA 39597 AC__ CT
 TGAGA GGGAAG TGTCA
 ||||| ||||| |||||
 ACTCT CCCTTT ATAGT
 CCAC T_
 GAM2393 EPB41L4 3' ACAAGCTTCCCGCCTCA 42422 AA
 TGAG CGGGAAGCTTGT
 ||||| ||||| |||||
 ACTC GCCCTTCGAACA
 C_
 GAM2393 FLJ14457 5' GAGCCGGGGCTTCCCCTTCTCA 52407 C GTCA
 TGAGAA GGGAAGCTT TC
 ||||| ||||| |||||
 ACTCTT CCCTTCGGG AG
 C GCCG
 GAM2393 FLJ20254 3' GCAGCCTCCTGTTCCCA 35297 A A T
 TG GAACGGGA GCT GT
 || ||||| |||||
 AC CTTGTCCT CGA CG
 C C _
 GAM2393 HLA-DOA 3' ACTAGCTTCCCTTCCCA 10929 A C T
 TG GAA GGGAAGCT GT
 || ||||| |||||
 AC CTT CCCTTCGA CA
 C _ T
 GAM2393 MGC29654 5' TGACCCTCCTGTTCCCA 67210 A A CTT
 TG GAACGGGA G GTCA
 || ||||| |||||
 AC CTTGTCCT C CAGT
 C _ C_
 GAM2393 RAB35 3' TTGATGACTGCTCCCCG 23421 A TT
 CGGG AGC GTCATCAA
 ||||| ||||| |||||

GCCC TCG CAGTAGTT
 C T_
 GAM2393 LOC149386 5' ATGACAAGCTTCCCGTTTTCA 85554
 TGAGAACGGGAAGCTTGTCAT
 |||||
 ACTTTTGCCCTTCGAACAGTA

GAM2393 LOC253974 3' TTGATGACAAATTTCCCGTTCT 99285 C
 CA TGAGAACGGGAAG TTGTCATCAA
 |||||
 ACTCTTGCCCTTT AACAGTAGTT
 A

GAM2394 ACT 5' CCACAATCCAGGGGGCCAT 40420 CCG AAC
 ATGGCCCCT GGA TGTGG
 ||||| ||| ||||
 TACCGGGGG CCT ACACC
 A_ A_

GAM2394 ADAM11 3' GCCACAGCTCAACTCGGGGGC 41490 TC AAA_
 GCCCC CGGG CTGTGGC
 |||| ||| |||||
 CGGGG GCTC GACACCG
 _ AACTC

GAM2394 ADAM11 3' GCCACAGCTCAACTCGGGGGC 11487 TC AAA_
 GCCCC CGGG CTGTGGC
 |||| ||| |||||
 CGGGG GCTC GACACCG
 _ AACTC

GAM2394 CDC34 3' GCCGCACCCCGGAGGAGCCA 16390 C AAAC
 TGGC CCTCCGGG TGTGGC
 |||| ||||| |||||
 ACCG GGAGGCCC ACGCCG
 A C_

GAM2394 CRI1 3' GCCACAGTTATCAAAGGCTA 27537 CCTCCG A
 TGGCC GG AACTGTGGC
 |||| || |||||
 ATCGG CT TTGACACCG
 AAA_ A

GAM2394 FLII 3' GCCACAGTCCCCAGTAGCC 10656 CC CC AA
 GGC CT GGG ACTGTGGC
 ||| || ||| |||||
 CCG GA CCC TGACACCG
 AT _ C_

GAM2394 FZD10 3' GCCCACCCTCCAGGAAGGCCA 24214 CC _ AAAC T
 TGGCC TCC GGG TG GGC
 |||| ||| ||| |||
 ACCGG AGG CCC AC CCG
 A_ A CC_ _

GAM2394 GNA11 5' CCACAGCCCCGGGGGCCG 76585 TC AAA
 TGGCCCC CGGG CTGTGG
 ||||| ||| |||||

GCCGGGG GCCC GACACC
 — C—
 GAM2394 IGHMBP2 3' GCCACAGAGGAGCGGAGGGGCC 10984 GGAAA
 GGCCCCTCCG CTGTGGC
 ||||| |||||
 CCGGGGAGGC GACACCG
 GAGGA
 GAM2394 MAGEA3 5' CCAGAGGCCCGGAGGAGC 19315 C AAA G
 GC CCTCCGGG CT TGG
 || ||||| |||||
 CG GGAGGCCC GA ACC
 A CCG G
 GAM2394 PYGB 3' CCAGGGGTCCCGGAGGAACC 12687 CC AA G
 GG CCTCCGGGA CT TGG
 || ||||| |||||
 CC GGAGGCCCT GG ACC
 AA G_ G
 GAM2394 PYGB 3' CCATGTTTCCAGAGGGGCCAT 12689 G T
 ATGGCCCCTCC GGAAAC GTGG
 ||||| ||||| |||||
 TACCGGGGAGG CCTTTG TACC
 A —
 GAM2394 SLC6A6 3' GCCACAGTCCTTCCTGGGGC 13183 TCC —
 GCCCC GGGAA ACTGTGGC
 |||| |||| |||||
 CGGGG TCCTT TGACACCG
 — CC
 GAM2394 UBTF 3' CCATTCTTCCCAGAGGGGCC 27252 C ACT
 GGCCCCTC GGGAA GTGG
 ||||| ||||| |||||
 CCGGGGAG CCCTT TACC
 A CCT
 GAM2394 CBCIP2 3' GCCACACGGA CTGAGGGGCC 52658 C AAAC
 A TGGCCCCTC GGG TGTGGC
 ||||| ||||| |||||
 ACCGGGGAG CTC ACACCG
 A AGGC
 GAM2394 FEM-2 3' GCCACAGTCCCATGAGGGCC 28316 C C_ AA
 GGCCC TC GGGA CTGTGGC
 |||| || |||| |||||
 CCGGG AG CCCT GACACCG
 — TA —
 GAM2394 FLJ10199 3' GCCACAGTTGAGAAGCGGAGGG 71755 GGA—
 GCCA TGGCCCCTCCG AACTGTGGC
 ||||| ||||| |||||
 ACCGGGGAGGC TTGACACCG
 GAAGAG
 GAM2394 FLJ11715 3' ACAGTGTCCCAGGAGGCCAT 44972 — CC A
 ATGGCC CCT GGGA ACTGT
 ||||| ||||| ||||| |||||

TACCGG GGA CCCT TGACA
 A C_ G
 GAM2394 FLJ12505 5' CCCGGTCCCGGAGCAGCCA 45713 CC AA T
 TGGC CTCCGGGA CTG GG
 |||| ||||| ||| ||
 ACCG GAGGCCCT GGC CC
 AC _ _
 GAM2394 KIAA0828 3' GTTTCCAGGAAGGCCAT 82119 CC _
 ATGGCC TCC GGGAAAC
 ||||| ||| |||||
 TACCGG AGG CCCTTTG
 A_ A
 GAM2394 KIAA1190 3' CCACAGTTCTGGGAGCC 71643 CCC G A
 GGC TCC GGAA CTGTGG
 ||| ||| ||| |||||
 CCG AGG TCTT GACACC
 _ G _
 GAM2394 KIAA1297 5' CCATGCCCAGAAGGCCA 72634 CC C AAAC
 TGGCC TC GGG TGTGG
 |||| ||| ||||
 ACCGG AG CCC GTACC
 A_ A _
 GAM2394 PASK 5' GCCACAGAGTTGGGGGGCCAT 31415 T GAAA
 ATGGCCCC CCGG CTGTGGC
 ||||| ||| |||||
 TACCGGGG GGTT GACACCG
 _ GA_
 GAM2394 PCDH17 3' GCCACAGTTCCTGCAGCCA 27836 CCCTC A
 TGGC CGGG AACTGTGGC
 ||| ||| |||||
 ACCG GTCC TTGACACCG
 AC_ C
 GAM2394 RIL 3' CCATGCTGCCCTGAAGGGGCCA 14885 C AAAC
 TGGCCCCT CGGG GTGG
 ||||| ||| |||
 ACCGGGGA GTCC TACC
 A CGTCG
 GAM2394 SREC 3' GCAGTGCTCCCGGAGGGGCC 14905 A_
 GGCCCCTCCGGGA ACTGT
 ||||| |||||
 CCGGGGAGGCCCT TGACG
 CG
 GAM2394 TRAF2 3' GCCGGCTCACGGAGGGGCCA 41236 G AACTG
 TGGCCCCTCCG GA TGGC
 ||||| ||| |||
 ACCGGGGAGGC CT GCCG
 A CG_
 GAM2394 LOC123242 5' CCACAGCCCACCTGGAGGCCA 76111 CC AAA_
 TGGCC TCCGGG CTGTGG
 |||| ||||| |||||

	ACCGG AGGTCC GACACC	
	___ ACCC	
GAM2394 LOC124460 5'	CCAAGAGCTCGAAGGGGCCAT 76559	C AAA G
	ATGGCCCCT CGGG CT TGG	
	TACCGGGGA GCTC GA ACC	
	A GA_ _	
GAM2394 LOC132166 3'	GCCAGCGCCCGAGGGGGCCA 75537	TC AA ACTG
	TGGCCCC CGGG TGGC	
	ACCGGGG GCCC ACCG	
	GA GCG_ _	
GAM2394 LOC146958 5'	GCCACAGTCTCAAGTGGACAT 84944	G C CC AA
	ATG CC CT GGGA CTGTGGC	
	TAC GG GA CTCT GACACCG	
	A T A_ _	
GAM2394 LOC149420 3'	GCCACAGTTTCCTAAGCGC 80155	CC CC
	GC CT GGGAACTGTGGC	
	CG GA TCCTTTGACACCG	
	C_ A_	
GAM2394 LOC152317 3'	GCCACAGTCTGGGAGAGCCA 86831	CC G AA
	TGGC CTCC GGA CTGTGGC	
	ACCG GAGG TCT GACACCG	
	A_ G _	
GAM2394 LOC157450 3'	CCACAGCTTCCCGGGTCAT 71531	CTCC A
	ATGGCCC GGGAA CTGTGG	
	TACTGGG CCCTT GACACC	
	___ C	
GAM2394 LOC157807 5'	GCCACAGTTTCAGCAGACCAT 82513	CCC CCGG
	ATGG CT GAACTGTGGC	
	TACC GA CTTTGACACCG	
	A_ CGA_	
GAM2394 LOC157923 5'	GCCACAGTCCAGAGAAGGCCA 82526	C_ C GAA
	TGGCC CTC GG ACTGTGGC	
	ACCGG GAG CC TGACACCG	
	AA A _	
GAM2394 LOC158510 5'	CCAGAGGCCCCCGGAGGAGC 82833	C AAA G
	GC CCTCCGGG CT TGG	
	CG GGAGGCCC GA ACC	
	A CCG G	
GAM2394 LOC196860 3'	CCACAGTTCCCGGAAAGTGCT 91214	CCC_ A
	GGC TCCGGG AACTGTGG	

		TCG AGGCCC TTGACACC		
		TGAA C		
GAM2394	LOC203235 5'	GCCAGGGCCCCCAGAGGGGCC 92099	C	AAA G
		GGCCCCTC GGG CT TGGC		
		CCGGGGAG CCC GG ACCG		
		A CC_ G		
GAM2394	LOC220739 3'	GCCACAGTAGGAGGGGCCA 94521	GGGAA	
		TGGCCCCTCC ACTGTGGC		
		ACCGGGGAGG TGACACCG		
		A ____		
GAM2394	LOC222166 5'	CCCGGCCCCGAGGAGCC 95733	C	AAA T
		GGC CCTCCGGG CTG GG		
		CCG GGAGGCCC GGC CC		
		A C_ _		
GAM2394	LOC253001 5'	CCACAGCCCACCTGGAGGCCA 97990	CC	AAA_
		TGGCC TCCGGG CTGTGG		
		ACCGG AGGTCC GACACC		
		_ ACCC		
GAM2394	LOC254057 3'	GCCCCTATCCCAGAGGGGCC 98782	C	AACTGT
		GGCCCCTC GGGA GGC		
		CCGGGGAG CCCT CCG		
		A ATCC_		
GAM2394	LOC92558 3'	GCCACCTCCCAGAGGGGCC 70312	C	AACT
		GGCCCCTC GGGA GTGGC		
		CCGGGGAG CCCT CACCG		
		A C_		
GAM2394	LOC93626 5'	CCACAGCCCCGGGGGCCG 73128	TC	AAA
		TGGCCCC CGGG CTGTGG		
		GCCGGGG GCCC GACACC		
		_ C_		
GAM2395	ETV5 3'	TGATGACAAATTTCCATTC 16730	CG	C
		GAA GGAAG TTGTCATCA		
		CTT CCTTT AACAGTAGT		
		TA _		
GAM2395	HTRA3 3'	TGAGCCGGCTTCCCCTTCCCA 90585	A C	T CA
		TG GAA GGGAAGCT GT TCA		
		AC CTT CCCTTCGG CG AGT		
		C C C _		
GAM2395	KCNK5 3'	TTGATGGCCTCTTCCCCCTCA 14973	AAC	CTT
		TGAG GGGAAG GTCATCAA		

			ACTC CCCTTC CGGTAGTT			
			CC_ TC_			
GAM2395	MTM1	3'	TGGTGTGGCTTCCCCTC 6007 AAC TGT			
			GAG GGGAAGCT CATCA			
			CTC CCCTTCGG GTGGT			
			____ TT_			
GAM2395	NFRKB	5'	TGGTCCAGCTTCCCTTCCTCA 21608 AAC TTC			
			TGAG GGGAAGCT G ATCA			
			ACTC CCCTTCGA C TGGT			
			CTT _C_			
GAM2395	STX1A	3'	GGCCTCAGCTTCCCTTCCCA 17213 A C T__			
			TG GAA GGGAAGCT GTC			
			AC CTT CCCTTCGA CGG			
			C _ CTC			
GAM2395	B3GNT7	3'	TTGGTGTGAACTTCCTGTTCC 71684 A C GT			
	CA		TG GAACGGGAAG TT CATCAA			
			AC CTTGTCCTTC AA GTGGTT			
			C A GT			
GAM2395	BA108L7.2	3'	TGACATCTGGCTTCCCTTCTCA 49082 C ____			
			TGAGAA GGGAAGCT TGTCA			
			ACTCTT CCCTTCGG ACAGT			
			_ TCT			
GAM2395	BRPF3	3'	GGCAGCTTCCCCCTCTCA 93932 AC T			
			TGAGA GGGAAGCT GTC			
			ACTCT CCCTTCGA CGG			
			CC _			
GAM2395	C3orf4	3'	TGATATTTTCCCCACCTCTCA 39597 AC__ CT			
			TGAGA GGGAAG TGTCA			
			ACTCT CCCTTT ATAGT			
			CCAC T_			
GAM2395	EPB41L4	3'	ACAAGCTTCCCGCCTCA 42422 AA			
			TGAG CGGGAAGCTTGT			
			ACTC GCCCTTCGAACA			
			C_			
GAM2395	FLJ14457	5'	GAGCCGGGGCTTCCCCTTCTCA 52407 C GTCA			
			TGAGAA GGGAAGCTT TC			
			ACTCTT CCCTTCGGG AG			
			C GCCG			
GAM2395	FLJ20254	3'	GCAGCCTCCTGTTCCCA 35297 A A T			
			TG GAACGGGA GCT GT			

AC CTTGTCCT CGA CG
 C C _
 GAM2395 HLA-DOA 3' ACTAGCTTCCCTTCCCA 10929 A C T
 TG GAA GGGAAGCT GT
 || ||| ||||| ||
 AC CTT CCCTTCGA CA
 C _ T
 GAM2395 MGC29654 5' TGACCCTCCTGTTCCCA 67210 A A CTT
 TG GAACGGGA G GTCA
 || ||||| | |||
 AC CTTGTCCT C CAGT
 C _ C_
 GAM2395 LOC149386 5' ATGACAAGCTTCCCGTTTTCA 85554
 TGAGAACGGGAAGCTTGTCAT
 |||||
 ACTTTTGCCCTTCGAACAGTA

 GAM2395 LOC253974 3' TTGATGACAAATTTCCCGTTCT 99285 C
 CA TGAGAACGGGAAG TTGTCATCAA
 ||||| |||||
 ACTCTTGCCCTTT AACAGTAGTT
 A
 GAM2396 C6orf28 3' AACCCCAAGTCCCAGCCC 41290 A_ T A
 GG TG GGAATTGG GTT
 || || ||||| |||
 CC AC CCTGAACC CAA
 CG _ C
 GAM2396 DREV1 3' AACTGCATTCCACATCCT 32616 ACT G
 AGGATGTGG TG AGTT
 ||||| || |||
 TCCTACACC AC TCAA
 CTT G
 GAM2396 GMPPB 5' AACCCCAAGTCCTGTATTCTAG 97425 CA GT_ A
 TA TGC AGGAT GGAATTGG GTT
 || |||| ||||| |||
 ATG TCTTA CCTGAACC CAA
 A_ TGT C
 GAM2396 LOC148758 3' AACATAGAGATCACACATCCT 79716 _ _ GGA
 AGGATGTG GA CTT GTT
 ||||| || ||| |||
 TCCTACAC CT GAG CAA
 A A ATA
 GAM2396 LOC157931 5' AACCCCAAATCCATAGCTCTGG 87935 AG A C A
 CCA G TGTGGA TTGG GTT
 || | |||| |||| |||
 GGT C ATACCT AACC CAA
 CT G A C
 GAM2396 LOC200473 5' CCTGTTCCACACCTTGGCA 91645 A CTT
 TGCCAAGG TGTGGA GG
 ||||| ||||| ||

ACGGTTCC ACACCT CC
 _ TGT
 GAM2396 LOC200734 3' AACTCCAAACCCAGACTCGC 90270 CA GA T AC
 GC AG TG GG TTGGAGTT
 || || || || |||||
 CG TC AC CC AACCTCAA
 C_ AG _ A_

GAM2396 LOC202134 5' AACTCCAGTATGTCCCCCAGC 91911 CAA ATGT ____
 A TGC GG GGAC TTGGAGTT
 ||| || ||| |||||
 ACG CC CCTG GACCTCAA
 AC_ C____ TAT

GAM2396 LOC220954 5' ACTCCAAGTCCCTCTGCA 94756 CAA TGT
 TGC GGA GGAATTGGAGT
 ||| ||| |||||
 ACG TCT CCTGAACCTCA
 ____ C____

GAM2396 LOC255452 5' AGCTCCCCACATCCCCTGCA 99386 CAA ACTT
 TGC GGATGTGG GGAGTT
 ||| ||||| |||||
 ACG CCTACACC CCTCGA
 TCC ____

GAM2397 ADAMTS3 3' AGGTGTCCTTTGTTTTGTGT 27271 GC TCC
 GCGCAAG CA GAGGGCACCT
 ||||| || |||||
 TGTGTTT GT TTCCTGTGGA
 TT ____

GAM2397 ALDH1B1 3' AGGTGCTTTTCCTTGTCTGTGT 7315 _ CATCC
 GC GCGCA AGGC GAGGGCACCT
 ||||| ||| |||||
 CGTGT TCTG TTTTCGTGGA
 G TTCC_

GAM2397 ARNT2 3' GGTGTCCCTGGCTTTTGT 30089 C TCCGA
 GCG AAGGCCA GGGCACC
 ||| ||||| |||||
 TGT TTTCGGT CCTGTGG
 _ C____

GAM2397 ATM 3' AGGTGGGAGGATGGCTTGCGC 5287 G GAGGG
 GCGCAAG CCATCC CACCT
 ||||| ||||| |||||
 CGCGTTC GGTAGG GTGGA
 _ AGG__

GAM2397 BACH2 3' AGGTGTTTTTTGTTTTGT 41774 GC TCC
 GCAAG CA GAGGGCACCT
 ||||| || |||||
 TGTTT GT TTTTGTGGA
 TT ____

GAM2397 CBFA2T3 3' TTTTGGGGGGTTTGTGT 19022 AT
 GCGCAAGGCC CCGAGG
 ||||| |||||

		TGTGTTTTGG GGTTTT	
		GG	
GAM2397 CDC5L	5'	GTTTGATGGTTTTGTGT 8812	CGA
		GCGCAAGGCCATC GGGC	
		TGTGTTTTGGTAG TTTG	
		—	
GAM2397 CELSR1	3'	GGTGGGGATGGCTTTGT 27275	GAGGG
		GCAAGGCCATCC CACC	
		TGTTTCGGTAGG GTGG	
		G—	
GAM2397 DFFB	3'	AGGTGCCTTTTTTTGTTTTTTTG 88759	C GC TCC
T		GCG AAG CA GAGGGCACCT	
		TGT TTT GT TTTCCGTGGA	
		T TT TT_	
GAM2397 EMS1	3'	GTTCTTGGGTGGTTTTGGGT 19095	G
		GC CAAGGCCATCCGAGGGC	
		TG GTTTTGGTGGGTTCTTG	
		G	
GAM2397 FE65L2	3'	GGGTGTCTTCTCTTTTCTTGAT 21294	_ CCATCC
GC		GCG CAAGG GAGGGCACCT	
		CGT GTTCT CTTCTGTGGG	
		A TTTCT_	
GAM2397 FE65L2	3'	GGGTGTCTTCTCTTTTCTTGAT 21295	_ CCATCC
GC		GCG CAAGG GAGGGCACCT	
		CGT GTTCT CTTCTGTGGG	
		A TTTCT_	
GAM2397 FLT1	3'	GGGTGTATGTGTGTTTTGTGC 10660	_ CCGAGG
		GCGCAAGGC CAT GCACCT	
		CGTGTTTTG GTG TGTGGG	
		T TA—	
GAM2397 GPT	5'	GGGTGCTCTCTTGCCCTGGCGT 19188	A CATCC
		GCGC AGGC GAGGGCACCT	
		TGCG TCCG CTCTCGTGGG	
		G TT—	
GAM2397 HGF	3'	GGGTGTTTTCTGTTGTTTTGT 95892	C CC
		GCAAGGC AT GAGGGCACCT	
		TGTTTTG TG CTTTTGTGGG	
		T T_	
GAM2397 JUP	3'	GGGTGCTTAGTTGGCTTTGC 11112	TCCGA
		GCAAGGCCA GGGCACCT	

			CGTTTCGGT	TTCGTGGG		
			TGA__			
GAM2397	LEP	3'	GGTGTCTTAAGCCTTTTGC	5867	C	CATCCG
			GCG AAGGC	AGGGCACCT		
			CGT TTCCG	TTCTGTGG		
			T AA__			
GAM2397	LFNG	3'	GGGTGTTCTTGT TTTTGC	94213		CCATC
			GCAAGG	CGAGGGCACCT		
			CGTTTT	GTTCTTGTGGG		
			TT__			
GAM2397	LIF	3'	GGGTGCCTTTCTGTCTTGC	11305		CATCC
			GCAAGG	GAGGGCACCT		
			CGTTCTG	TTCCGTGGG		
			TC__			
GAM2397	MGAT1	3'	AGGTGCAGGGAGGAAGGCCTTG	11551		A GAGG_
	TGC		GCGCAAGGCC TCC	GCACCT		
			CGTGTTCCGG AGG	CGTGGA		
			A AGGGA			
GAM2397	MORC	5'	AGGTGTCCTTGTCCCCTTGAGT	27794	G	CCATC
			GC CAAGG	CGAGGGCACCT		
			TG GTTCC	GTTCTGTGGA		
			A CCT__			
GAM2397	MPZ	3'	AGGTGCTTTCCTCTTTGC	6748		CCATCC
			GCAAGG	GAGGGCACCT		
			CGTTTC	CTTTCGTGGA		
			TCC__			
GAM2397	NRG1	3'	AGGTGTTTTTTGTTTTGT	16901		GC TCC
			GCAAG CA	GAGGGCACCT		
			TGTTT GT	TTTTTGTGGA		
			TT__			
GAM2397	NUFIP1	3'	GGGTGCTTTGCCTGTTTTGGGT	25637	G	CATCCG
			GC CAAGGC	AGGGCACCT		
			TG GTTTTG	TTTCGTGGG		
			G TCCG__			
GAM2397	PCOLCE2	3'	AGGTGTTACAATCTTGTCTTGC	26275		CATCCGAG
	GT		GCGCAAGGC	GGCACCT		
			TGCGTTCTG	TTGTGGA		
			TTCTAACA			
GAM2397	RABL2A	3'	AGGTGTTTTTTGGTGT TTTTGT	26405		GC C
			GCAAG CATC	GAGGGCACCT		

		TGTTT GTGG TTTTGTGGA	
		TT T	
GAM2397	RABL2B	3' AGGTGTTTTTTGGTGTGTGT 23973	GC C
		GCAAG CATC GAGGGCACCT	
		TGTTT GTGG TTTTGTGGA	
		TT T	
GAM2397	RAD17	5' AGGTGTTTATAGGCTATGTGT 12734	A ATCCGA
		GCGCA GGCC GGGCACCT	
		TGTGT TCGG TTTGTGGA	
		A ATA__	
GAM2397	RENT1	3' AGGTGCTTTTGGCCCCATTGCG 12808	_ CCAT
		CGCAA GG CCGAGGGCACCT	
		GCGTT CC GGTTCGTGGA	
		A CC__	
GAM2397	SLC2A8	3' AGGTGCTTTTGGAGGTTGGGT 28148	AA A
		GC GGCC TCCGAGGGCACCT	
		TG TTGG AGGTTTCGTGGA	
		GG _	
GAM2397	SMARCC1	3' GGGTGTTTTGGTAGAGCTTGG 13253	A CAT_
	T	GC AGGC CCGAGGGCACCT	
		TG TTCG GGTTTTGTGGG	
		G AGAT	
GAM2397	SOX13	3' GGTGTCTCAGGTTCTGTGT 20284	AG ATCC G
		GCGCA GCC GAGG CACC	
		TGTGT TGG CTCT GTGG	
		CT A__ _	
GAM2397	SPF30	3' AGGTGTTTTTGTGTGTGT 20793	CCATC
		GCAAGG CGAGGGCACCT	
		TGTTT GTTTTGTGGA	
		TT__	
GAM2397	STXBP1	3' GGGTGTTTTAAAACCTTGT 13479	CCATCC
		GCAAGG GAGGGCACCT	
		TGTTCC TTTTGTGGG	
		AAAA__	
GAM2397	SULT1C1	3' AGGTGTTCTTTCCCTTGC 8317	CCATCC
		GCAAGG GAGGGCACCT	
		CGTTCC TTCTTGTTGGA	
		CTT__	
GAM2397	SUPT6H	3' GGGTGACAGGCTGGATGGCCTT 61032	AGGG__
	GTG	CGCAAGGCCATCCG CACCT	

			GTGTTCCGGTAGGT	GTGGG	
			CGGACA		
GAM2397	TDG	3'	GGGTGCTTTGAAGTGCCTTGC	13648	C CCG
			GCAAGGC AT AGGGCACCT		
			CGTTCCG TG TTTCGTGGG		
			_ AAG		
GAM2397	TM6SF2	3'	GGTGTCTTTAGTCTTGGC	72817	G CATCC
			GC CAAGGC GAGGGCACC		
			CG GTTCTG TTTCTGTGG		
			_ A _		
GAM2397	TRIM39	3'	GGTTTCTAGGATGGTTTTGTGT	41451	G C
			GCGCAAGGCCATCC AGGG ACC		
			TGTGTTTTGGTAGG TCTT TGG		
			A _		
GAM2397	TRPM8	3'	GGTGCTATGTCCTTGTGT	44207	C CCGAG
			GCGCAAGG CAT GGCACC		
			TGTGTTCC GTA TCGTGG		
			T _		
GAM2397	VAT1	3'	AGGTGCCCTCATCGTGGTCTGT	22089	A CC_
	GC		GCGCA GGCCAT GAGGGCACCT		
			CGTGT CTGGTG CTCCCGTGGA		
			_ CTA		
GAM2397	VIPR2	3'	AGGTGTCTTTAACTGTCATTGT	14058	_ CATCC
	GT		GCGCAA GGC GAGGGCACCT		
			TGTGTT CTG TTTCTGTGGA		
			A TCAA_		
GAM2397	ZNF264	3'	GGGTGCTTTTTTTGTTTGTGT	14220	GC TCC
			GCGCAAG CA GAGGGCACCT		
			TGTGTTT GT TTTTCGTGGG		
			_ T _		
GAM2397	ABLIM	3'	GGTGTCTCATCCTTGC	22984	CCATCC
			GCAAGG GAGGGCACC		
			CGTTCC CTCCTGTGG		
			TA _		
GAM2397	C1QR1	3'	AGGAAAGATGGAGGTTTTGTGC	24866	A AGGGCA
			GCGCAAGGCC TCCG CCT		
			CGTGTTTTGG AGGT GGA		
			_ AGAAA_		
GAM2397	C20orf110	3'	GGGTGTCTTTCCAGCCTTTGC	80365	C CATCC
			GCG AAGGC GAGGGCACCT		

CGT TTCCG TTTCTGTGGG
 _ ACC_
 GAM2397 CENTG1 3' GGGTGCTCTCGGGTTGTGTCTG 29357 A _ _
 T GCA GGC CA TCCGAGGGCACCT
 ||| ||| || |||||
 TGT CTG GT GGGCTCTCGTGGG
 _ T T
 GAM2397 CPSF2 3' GGGTGTTTTTTTTTGT TTTTGT 62275 CATCC
 GCAAGGC GAGGGCACCT
 ||||| |||||
 TGTTTTG TTTTGTGGG
 TTTT_
 GAM2397 D21S2056E 3' GCTGTGGCTGGCCTTGTGC 14867 T AG
 GCGCAAGGCCA CCG GGC
 ||||| ||| |||
 CGTGTTCCGGT GGT TCG
 C G_
 GAM2397 DKFZP434B103 5' AGGTGTGTCTAGGGCCTTGTGC 32223 ATCC GG
 GCGCAAGGCC GA GCACCT
 ||||| || |||||
 CGTGTTCCGG CT TGTGGA
 GA_ G_
 GAM2397 DKFZP434C1715 3' GGTGTTTTCTTCTTTGT 87356 CCATCC
 GCAAGG GAGGGCACC
 ||||| |||||
 TGTTTC CTTTTGTGG
 TT____
 GAM2397 DKFZp434I1117 3' GTGCCTTGGGGGCCTTGTGT 62847 AT G
 GCGCAAGGCC CC AGGGCAC
 ||||| || |||||
 TGTGTTCCGG GG TTCCGTG
 _ G
 GAM2397 DKFZP564I0422 3' AGGTGTTTTTTGTTTTTGT 49509 GC TCC
 GCAAG CA GAGGGCACCT
 |||| || |||||
 TGTTT GT TTTTTGTGGA
 TT ____
 GAM2397 DPYSL4 3' AGGTGCTTGGCGGTCTTGC 22225 AT AG
 GCAAGGCC CCG GGCACCT
 ||||| ||| |||||
 CGTTCTGG GGT TCGTGGA
 C_ _
 GAM2397 ELL2 3' GGGTGTTTTTTTGT TTTTGT 24897 CC CC
 GCAAGG AT GAGGGCACCT
 |||| || |||||
 TGTTTT TG TTTTGTGGG
 TT TT
 GAM2397 FLJ10204 3' TTTTGGATGTTTTGTGT 36358 C
 GCGCAAGGC ATCCGAGG
 ||||| |||||

TGTGTTTTG TAGGTTTT

GAM2397 FLJ10297 3' AGGTGCCCTGCCTGAGTTGTGT 36436 AG _ TC G
GC GCGCA GC CA C AGGGCACCT
|||| ||| | |||||
CGTGT TG GT G TCCCGTGGA
GT A CC_
GAM2397 FLJ10661 3' GGGTGTTCCTTTTCAGCCTTGC 36917 CATCC
GCAAGGC GAGGGCACCT
||||| |||||
CGTTCCG TTCTTGTGGG
ACTT_
GAM2397 FLJ12838 3' AGGTGTTTTGACATGTTTAGTG 45314 A CATCCG
T GCGC AGGC AGGGCACCT
||| ||| |||||
TGTG TTTG TTTTGTGGA
A TACAG_
GAM2397 FLJ13449 3' AGGTGTCATTTGTGGTTTTGT 44927 CCGAG
GCAAGGCCAT GGCACCT
||||||| |||||
TGTTTTGGTG CTGTGGA
TTTA_
GAM2397 FLJ14775 3' GGGACTGGATGGTTTTTGC 52681 C G GGCA
GCG AAGGCCATCC AG CC
|| ||||| || ||
CGT TTTGGTAGG TC GG
_ _ AG_
GAM2397 FLJ20421 3' GGGAAAATGGGTTGCTTTGTGT 35614 C AGGGCA
GCGCAAGGC ATCCG CC
||||||| ||||| ||
TGTGTTTCG TGGGT GG
T AAAAG_
GAM2397 FLJ20452 3' GGTGTTCCAGGCCTGTGT 35650 A ATCCGA
GCGCA GGCC GGGCACC
|||| ||| |||||
TGTGT CCGG CTTGTGG
_ AC____
GAM2397 FLJ21596 3' GGTGTCCAGGGTCTTGC 46121 ATCCGA
GCAAGGCC GGGCACC
||||||| |||||
CGTTCTGG CCTGTGG
GA____
GAM2397 FLJ32762 5' GGTGCCCCGGCGGTCTTTGC 59485 CCAT A_
GCAAGG CCG GGGCACC
||||| ||| |||||
CGTTTC GGC CCCGTGG
T__ GG
GAM2397 FSD1 3' GGGTGTTTTTTGGGGGAGTCGC 44541 CAAGG A
GCG CC TCCGAGGGCACCT
||| || |||||

CGC GG GGGTTTTTGTGGG
TGA__ _

GAM2397 FYCO1 3' AGGAGAGCTGGATGTTTTGCGT 44766 C GAG A__
GCGCAAGGC ATCC GGC CCT
||||||| ||| ||| |||
TGC GTTTT TAGG TCG GGA
_ _ _ AGA

GAM2397 gm117 3' GGGTGCTTTTCAACAGTCTTTG 79590 C CATCC
T GCG AAGGC GAGGGCACCT
||| ||||| |||||
TGT TTCTG TTTTCGTGGG
_ ACAAC

GAM2397 GPR88 5' GGTGCTCTCCTCTTGAGC 42138 G CCATCC
GC CAAGG GAGGGCACC
|| ||||| |||||
CG GTTCT CTCTCGTGG
A C__

GAM2397 HERC3 3' GGTGTTTTTGT TTTTGT 28236 CCATC
GCAAGG CGAGGGCACC
||||| |||||
TGTTTT GTTTTTGTGG
T__

GAM2397 KBRAS2 3' GGTGTCCAGGTATTGTGT 34627 G ATCCGA
GCGCAA GCC GGGCACC
||||| ||| |||||
TGTGTT TGG CCTGTGG
A A__

GAM2397 KIAA0057 3' GGGTGCTTTTTTGCTTTTG 25422 C CATCC
CG AAGGC GAGGGCACCT
|| ||||| |||||
GT TTTCG TTTCTGTGGG
_ TT__

GAM2397 KIAA0062 3' GGGTGTTTTCCCTTTTTGTGC 70787 CCATCC
GCGCAAGG GAGGGCACCT
||||||| |||||
CGTGT TTT CTTTTGTGGG
TCC__

GAM2397 KIAA0125 3' GGTGCTCAGGCTTTGC 29575 ATCCGA
GCAAGGCC GGGCACC
||||||| |||||
CGTTTCGG CTCGTGG
A__

GAM2397 KIAA0218 3' GGGTGCCCCCTTGCTTTGC 29295 TCCGA
GCAAGGCCA GGGCACCT
||||||| |||||
CGTTTCGGT CCCGTGGG
TCC__

GAM2397 KIAA0775 3' AGGTGCCCTGGAGCCCTTGTGT 28949 CCA G
GCGCAAGG TCC AGGGCACCT
||||||| ||| |||||

TGTGTTCC AGG TCCCGTGGA
 CG_ _
 GAM2397 KIAA0998 5' GGGAAGTTGGGTGGTTCTGTGC 31257 AG GGGCA
 GCGCA GCCATCCGA CC
 |||| ||||| ||
 CGTGT TGGTGGGTT GG
 CT GAAG_
 GAM2397 KIAA1169 3' GGGTGCCTTTTAGCTTTTGTGT 35883 _ CATCC
 GCGCAAG GC GAGGGCACCT
 ||||| || |||||
 TGTGTTT CG TTTCCGTGGG
 T AT__
 GAM2397 KIAA1265 3' GGGTGTTCCTTTCTGTTTTGT 71338 CATCC
 GCAAGGC GAGGGCACCT
 ||||| |||||
 TGTTTTG TTCTTGTGGG
 TCT__
 GAM2397 LASP1 3' AGGTGTCTCTGGGCCTGTGTGT 21574 _ ATC AG
 GCGCA AGGCC CG GGCACCT
 |||| ||| || |||||
 TGTGT TCCGG GT CTGTGGA
 G _ CT
 GAM2397 LAT1-3TM 5' GGGTGAGGGGGATGGTTGTGTG 49146 AG GAGGG
 T
 GCGCA GCCATCC CACCT
 |||| ||||| ||||
 TGTGT TGGTAGG GTGGG
 GT GGGA_
 GAM2397 LGALS8 3' GGTGTTCTCAGTCCTTGC 22449 CCATCC
 GCAAGG GAGGGCACC
 ||||| |||||
 CGTTCC CTCTTGTGG
 TGA__
 GAM2397 LYPLA2 3' GGTGTTTTTCTTGTGTGT 24387 GGC TCC
 GCGCAA CA GAGGGCACC
 |||| || |||||
 TGTGTT GT TTTTGTGG
 _ TC_
 GAM2397 MARCO 3' AGGTGTCCTCGGGCT 23189 ATC
 GGCC CGAGGGCACCT
 ||| |||||
 TCGG GCTCCTGTGGA
 _
 GAM2397 MGC11324 3' AGGTGCCCTTTTGGCTTTTGT 52147 C TCC
 GCG AAGGCCA GAGGGCACCT
 || ||||| |||||
 TGT TTTCGGT TTCCCGTGGA
 _ TT_
 GAM2397 MGC13102 3' GGTGTGTGTGTCTTTGTGC 51293 C TC GAGG
 GCGCAAGG CA C GCACC
 ||||| || | ||||

		CGTGTTTC GT G TGTGG	
		T GT ____	
GAM2397	MGC16279	3' GGGTGTTCCTTTTCAGCCTTGC 52989	CATCC
		GCAAGGC GAGGGCACCT	
		CGTTCCG TTCTTGTGGG	
		ACTT_	
GAM2397	MGC16491	5' AGGTGTTCCCTGGCTTTGT 54736	TCCGA
		GCAAGGCCA GGGCACCT	
		TGTTTCGGT CTTGTGGA	
		CC__	
GAM2397	MGC2655	5' AGGTGTTCCAGGCCTTGCAGC 44548	_ ATCCGA
		GC GCAAGGCC GGGCACCT	
		CG CGTTCCGG CTTGTGGA	
		A AC__	
GAM2397	MGC3067	5' GGGAGTCGGGCGGTCTTGTGC 44409	AT GGGCA
		GCGCAAGGCC CCGA CC	
		CGTGTTCTGG GGCT GG	
		CG GAG__	
GAM2397	MGC9753	3' GGGACTCGGGTGGCCTGCGC 54196	A GGCA
		GCGCA GGCCATCCGAG CC	
		CGCGT CCGGTGGGCTC GG	
		_ AG__	
GAM2397	P24B	3' GGGTGCCCTTGGTGAGCTGTGT 24773	AG _ T
		GCGCA GC CA CCGAGGGCACCT	
		TGTGT CG GT GGTCCCGTGGG	
		_ A _	
GAM2397	PRKAG3	3' GGGCACCTGGGATGGATGGCCT 34291	G_____ GCA
	TGT	GCAAGGCCATCC AGG CC	
		TGTTCCGGTAGG TCC GG	
		TAGGG ACG	
GAM2397	PTPRT	3' AGGTGTTCTTTGCTTTTTTGTG 56486	CCATCC
	T	GCGCAAGG GAGGGCACCT	
		TGTGTTTT TTCTTGTGGA	
		TTCGT_	
GAM2397	RNF24	3' GGTGTCTGGGTCTTGTG 24282	ATCCGA
		CGCAAGGCC GGGCACC	
		GTGTTCTGG TCTGTGG	
		G_____	
GAM2397	SLC2A12	3' GGGTGTCTTTGGACCAATGC 59739	A_ CCA
		GCA GG TCCGAGGGCACCT	

CGT CC AGGTTTCTGTGGG
AA ____

GAM2397 SLK 3' AGGTGTTTTCTTTTTGT 28888 CCATCC
GCAAGG GAGGGCACCT
||||| |||||||
TGTTTT CTTTTGTGGA
TTC____

GAM2397 TLK2 3' AGGTGCTTTTATTTTCTTGC 78806 CCATCC
GCAAGG GAGGGCACCT
||||| |||||||
CGTTCT TTTTCGTGGA
TTTA____

GAM2397 TRAF2 3' GCACCTAGTGGATGGCCTTGTG 41235 G_____ GCA
T GCGCAAGGCCATCC AGG C
||||||||| ||| |
TGTGTTCCGGTAGG TCC G
TGA ACG

GAM2397 LOC120114 3' TCTTGTATGGCTTTGTGC 76054 C
GCGCAAGGCCAT CGAGG
||||||||| |||||
CGTGTTTCGGTA GTTCT
T

GAM2397 LOC143666 3' GGTGTCCTCCCCGTGTGC 83887 A CCATCC
GCGCA GG GAGGGCACC
||||| || |||||||
CGTGT CC CTCCTGTGG
G C_____

GAM2397 LOC145601 3' AGGTGTCTATAGGTTTCTGT 84348 C ATCCGA
GCG AAGGCC GGGCACCT
||| ||||| |||||||
TGT TTTTGG TCTGTGGA
C ATA____

GAM2397 LOC145781 3' GGTGCTCTTTCCTCTTGGT 77958 G CCATCC
GC CAAGG GAGGGCACC
|| ||||| |||||||
TG GTTCT TTCTCGTGG
_ CCT____

GAM2397 LOC149175 3' AGGTGTTTTTCTTTTTGC 79947 CCATCC
GCAAGG GAGGGCACCT
||||| |||||||
CGTTTT TTTTGTGGA
TC____

GAM2397 LOC150819 5' GGTGCTCTTCTCTGTGC 86312 AG CCATCC
GCGCA G GAGGGCACC
||||| | |||||||
CGTGT C TTCTCGTGG
CT T_____

GAM2397 LOC157663 3' AGGTGTTTTTGTGTTTTATTTGT 82449 GCCATC
GT GCGCAAG CGAGGGCACCT
||||| |||||||

		TGTGTTT	GTTTTTGTGGA		
		ATTTTT			
GAM2397	LOC157697 5'	AGGTGCCCTCGGGTTCAGCAGT	82462	AG C__	
	G	CA GC ATCCGAGGGCACCT			
		GT CG TGGGCTCCCGTGGA			
		GA ACT			
GAM2397	LOC158046 5'	AGGTGTCCTCGGGTCTCAGGTG	59901	AAGGCC	
		CGC ATCCGAGGGCACCT			
		GTG TGGGCTCCTGTGGA			
		GACTC_			
GAM2397	LOC159199 5'	AGGAGCTGGATGAGCCTTGTGC	83057	_ GAG A	
		GCGCAAGGC CATCC GGC CCT			
		CGTGTTCCG GTAGG TCG GGA			
		A _ A			
GAM2397	LOC199907 3'	GCCTTTGGGTGGCCTTTGT	89829	C	
		GCG AAGGCCATCCGAGGGC			
		TGT TTCCGGTGGGTTTCCG			
		-			
GAM2397	LOC200958 3'	AGGTGTCCTTGGACTCACCTTG	66505	G CCA_	
	GC	GC CAAGG TCCGAGGGCACCT			
		CG GTTCC AGGTTCTGTGGA			
		_ ACTC			
GAM2397	LOC220073 5'	GGGTGTTCTTTTCAGCCTTGC	95074	CATCC	
		GCAAGGC GAGGGCACCT			
		CGTTCCG TTCTTGTGGG			
		ACTT_			
GAM2397	LOC220662 3'	GGTGGTGGTAGTTTTGTGT	92828	CAT AGGG	
		GCGCAAGGC CCG CACC			
		TGTGTTTTG GGT GTGG			
		AT_ G__			
GAM2397	LOC221683 5'	GCCTGGAGGTTTTGCGC	95329	A GA	
		GCGCAAGGCC TCC GGGC			
		CGCGTTTTGG AGG TCCG			
		- -			
GAM2397	LOC221833 3'	GGTGCTTTTTTCTTATGC	94115	C CCATCC	
		GCG AAGG GAGGGCACC			
		CGT TTCT TTTTCGTGG			
		A T__			
GAM2397	LOC253258 3'	GGTGTCTCTCCCGTGTGC	98231	A CCATCC	
		GCGCA GG GAGGGCACC			

CGTGT CC CTCCTGTGG
 G C____
 GAM2397 LOC255739 3' AGGTGCTCTTTTCTGTTTTGC 97904 GC TCC
 GCAAG CA GAGGGCACCT
 |||| || ||||||||
 CGTTT GT TTCTCGTGGA
 TT CTT
 GAM2397 LOC255809 3' GGGTGCCCTTGGGTGTGTTGTG 98583 G C
 T GCGCAA GC ATCCGAGGGCACCT
 |||| || ||||||||
 TGTGTT TG TGGGTTCCCGTGGG
 G _
 GAM2397 LOC51291 3' GGGTGCTTTTGCTACTTTGGT 33811 G CCATC
 GC CAAGG CGAGGGCACCT
 || |||| ||||||||
 TG GTTTC GTTTTCGTGGG
 _ ATC_
 GAM2397 LOC90297 5' GGTGCCCTCATCCTTGGC 62853 G CCATCC
 GC CAAGG GAGGGCACC
 || |||| ||||||||
 CG GTTCC CTCCCGTGG
 _ TA____
 GAM2397 LOC91064 5' GGTGTCCTCTGCCTGTGT 65389 A CATCC
 GCGCA GGC GAGGGCACC
 |||| || ||||||||
 TGTGT CCG CTCCTGTGG
 _ T____
 GAM2397 LOC91069 3' GGGTGTTCTTTTCAGCCTTGC 65403 CATCC
 GCAAGGC GAGGGCACCT
 |||| || ||||||||
 CGTTCCG TTCTTGTGGG
 ACTT_
 GAM2397 LOC93613 3' GGGTGTTTTTGCCAGGTTGC 73078 AG AT_
 GCA GCC CCGAGGGCACCT
 || || ||||||||
 CGT TGG GGTTTTGTGGG
 _ ACC
 GAM2398 ANXA1 5' CTTCAGAGAAGAATTTCT 7351 CC
 AGGAA CTTCTCTGAAG
 |||| ||||||||
 TCTTT GAAGAGACTTC
 AA
 GAM2398 BSN 3' CTTCAGAGAGGGCTCCT 14383 A T
 AGGA CCCT CTCTGAAG
 |||| || ||||||||
 TCCT GGGA GAGACTTC
 C _
 GAM2398 CCR9 3' TGCCTCTGGAGGAGCCCT 22798 AACC _ A
 AGG CTTCTCT GA GCA
 || |||| || ||||

			TCC GAGGAGG CT CGT			
			C___ T C			
GAM2398	CCR9	3'	TGCCTCTGGAGGAGCCCT 49126	AACC		_ A
			AGG CTTCTCT GA GCA			
			TCC GAGGAGG CT CGT			
			C___ T C			
GAM2398	CHP	5'	TGCTCCCGGAGGAGCTCC 24323	ACC		A_
			GGA CTTCTCTG AGCA			
			CCT GAGGAGGC TCGT			
			C___ CC			
GAM2398	DLG5	5'	CTGCCGCTAAAGAAGGGTCCCT 83814	A		CTGA AA
			AGG ACCCTTCT AGC CAG			
			TCC TGGGAAGA TCG GTC			
			C AA___ CC			
GAM2398	EPHA8	3'	TGCTTCAACAGGAAAACAGGGT 40440			___ C___
	TCC		GGAACCCT TCT TGAAGCA			
			CCTTGGGA AGG ACTTCGT			
			CAAA ACA			
GAM2398	NDRG3	3'	CTGTTACATAGAGAGGCTCCT 42765	ACC		AAGC
			AGGA CTTCTCTG AACAG			
			TCCT GGAGAGAT TTGTC			
			C___ ACA_			
GAM2398	NDRG3	3'	CTGTTACATAGAGAGGCTCCT 50120	ACC		AAGC
			AGGA CTTCTCTG AACAG			
			TCCT GGAGAGAT TTGTC			
			C___ ACA_			
GAM2398	PCDH8	5'	CTGGAACCAGAGAAGACTTCC 11995	CC		AAGCAA
	T		AGGAA CTTCTCTG CAG			
			TCCTT GAAGAGAC GTC			
			CA CAAAG_			
GAM2398	PK428	5'	TTGAATTCAGAGAAGCACCCC 14604	AACC		G_
			GG CTTCTCTGAA CAA			
			CC GAAGAGACTT GTT			
			CCAC AA			
GAM2398	RAB7L1	3'	CTGGGTGACAGAGAAGGACTCC 15404	AC		AA AA
			GGA CTTCTCTG GC CAG			
			CCT GGAAGAGAC TG GTC			
			CA AG G_			
GAM2398	SURF5	3'	CTGGGTTTCAGAGCAGAGCTCC 23126	ACC T		AA
	T		AGGA CTCTCTGAAGC CAG			

			TCCT GA GAGACTTTG GTC		
			CGA C G_		
GAM2398	TCF8	3'	CTGTTGTTAAGAAGCGTCCCT 48428	A C	CTGA
			AGG AC CTTCT AGCAACAG		
			TCC TG GAAGA TTGTTGTC		
			C C A__		
GAM2398	XPR1	3'	GTGCTTTAGAGTCCT 17623	ACCCTT	A
			AGGA CTCTGAAGCA C		
			TCCT GAGATTTCGT G		
			_____ C		
GAM2398	BLR1	5'	TGCCACAGAGGGGCCCT 53120	AA	C AA
			AGG CCCTTCT TG GCA		
			TCC GGGGAGA AC CGT		
			CC C _		
GAM2398	BMF	3'	TGCTAAGAAGACGGGTTCT 54289	T _	GA
			AGGAACCC TCT CT AGCA		
			TCCTTGGG AGA GA TCGT		
			C A A_		
GAM2398	C20orf124	5'	TTGGGGGCCAGAGAAGGTTCC 45844	C	AA AA_
			GGAACC TTCTCTG GC CAG		
			CCTTGG AAGAGAC CG GTT		
			_ _ GGG		
GAM2398	DKFZP586I2223	3'	CTGCTGCTTTGGGAGGATTCT 31876	C	CT A
			AGGAA CCTTCT GAAGCA CAG		
			TCTTT GGAGGG TTTCGT GTC		
			A _ C		
GAM2398	FAF1	3'	TGCGTCAGGAGAAGGGCTCCT 23899	A	_ A
			AGGA CCCTTCTC TGA GCA		
			TCCT GGGAAGAG ACT CGT		
			C G G		
GAM2398	FBP17	3'	CTGCTGCCCCAGCCGGGCTTCT 73149	A	TTCT AA A
			AGGA CCC CTG GCA CAG		
			TCTT GGG GAC CGT GTC		
			C CC_ CC C		
GAM2398	FLJ12425	3'	TGTTTGTCAGAGAAAAATCC 87096	ACCC	AGC
			GGA TTCTCTGA AACA		
			CCT AAGAGACT TTGT		
			AAA_ GT_		
GAM2398	FLJ14326	5'	GCTCAGAGAAGAGCTTCC 50775	CC_	A
			GGAA CTTCTCTGA GC		

CCTT GAAGAGACT CG
 CGA _
 GAM2398 FLJ22301 5' TGCCCCTTAGAGAAGAACCCT 46183 AACC A__
 AGG CTTCTCTGA GCA
 ||| ||||| |||
 TCC GAAGAGATT CGT
 CAA_ CCC
 GAM2398 GABARAPL1 3' TGCTAATGAAAAGGGTTCTT 49426 C TGA
 AGGAACCCTT TC AGCA
 ||||| || |||
 TTCTTGGGAA AG TCGT
 A TAA
 GAM2398 GGA2 3' CTGTTGCTTCAGTCTCAGTTAC 31166 G CTTCT
 T AG AAC CTGAAGCAACAG
 || ||| |||||
 TC TTG GACTTCGTTGTC
 A ACTCT_
 GAM2398 GGA2 3' CTGTTGCTTCAGTCTCAGTTAC 57666 G CTTCT
 T AG AAC CTGAAGCAACAG
 || ||| |||||
 TC TTG GACTTCGTTGTC
 A ACTCT_
 GAM2398 KIAA0447 3' TGTTTAGAGGAAGGCCCC 72137 AA C G
 GG CC TTCTCTGAA CA
 || || ||||| ||
 CC GG AGGAGATTT GT
 CC A _
 GAM2398 KIAA0963 3' TGCTCAGAGGAGCCCT 31035 AACC A
 AGG CTTCTCTGA GCA
 ||| ||||| |||
 TCC GAGGAGACT CGT
 C__ _
 GAM2398 KIAA1449 3' CTGCAGAGACAGGGTTCC 40837 _ A
 GGAACCCT TCTCTG AG
 ||||| ||||| ||
 CCTTGGGA AGAGAC TC
 C G
 GAM2398 KIAA1755 3' CTGTTGCCTCAGAGAGGGCC 62014 AAC A
 GG CCTTCTCTGA GCAACAG
 || ||||| |||||
 CC GGGAGAGACT CGTTGTC
 _ C
 GAM2398 KIAA1798 3' GTTTTGGAAGGATTCCT 61248 C CT
 AGGAA CCTTCT GAAGC
 |||| |||| ||||
 TCCTT GGAAGG TTTTG
 A _
 GAM2398 KIAA1879 5' CTGCCGTGTCAGAGAAAATCC 73939 ACCC A AA
 GGA TTCTCTGA GC CAG
 ||| ||||| || |||

CCT AAGAGACT TG GTC
 AA__ G CC
 GAM2398 MGC26655 3' TTGCTTGGAGAGAATCC 57125 ACCC G
 GGA TTCTCT AAGCAA
 ||| ||||| |||||
 CCT GAGAGG TTCGTT
 AA__ _
 GAM2398 PRO1331 5' TGCCCCCAAAGAAGAGTCCT 48564 A C C AA_
 AGGA C CTTCT TG GCA
 ||||| ||||| || |||
 TCCT G GAAGA AC CGT
 _A A CCC
 GAM2398 PRSS25 5' TGCTGCTTCAGGAGCGCC 26032 AACCC T A
 GG TTC CTGAAGCA CA
 || ||| ||||| ||
 CC GAG GACTTCGT GT
 GC__ _ C
 GAM2398 PRSS25 5' TGCTGCTTCAGGAGCGCC 59676 AACCC T A
 GG TTC CTGAAGCA CA
 || ||| ||||| ||
 CC GAG GACTTCGT GT
 GC__ _ C
 GAM2398 SAMHD1 3' CTGCCAGCCTGGAGAAGGCCT 61983 AC GAA AA_
 CC GGA CTTCTCT GC CAG
 ||| ||||| || |||
 CCT GGAAGAGG CG GTC
 CC TC_ ACCC
 GAM2398 SCHIP1 3' CTGTTGGATTGAGGGTTCCT 28141 TTC G_
 AGGAACCC TCTGAA CAACAG
 ||||| ||||| |||||
 TCCTTGGG AGACTT GTTGTC
 _ AG
 GAM2398 SPAF 5' TGCTTCGGCTAGGGTACCT 83522 A TCT
 AGG ACCCT CTGAAGCA
 ||| ||||| |||||
 TCC TGGGA GGCTTCGT
 A TC_
 GAM2398 STK36 3' CTGTTGGTGCCAGAGAAGAGTC 72582 A C AA _
 CT AGGA C CTTCTCTG GC AACAG
 ||||| ||||| || |||||
 TCCT G GAAGAGAC TG TTGTC
 _A CG G
 GAM2398 LOC126528 3' TGCCAGAGGAGGGCTCC 75032 A AA
 GGA CCCTTCTCTG GCA
 ||| ||||| ||||| |||
 CCT GGGAGGAGAC CGT
 C _
 GAM2398 LOC128344 3' TGAAGTCAGAGGAGGACTCC 75248 AC AG_
 GGA CTTCTCTGA CA
 ||| ||||| ||||| ||

	CCT GGAGGAGACT GT	
	CA GAA	
GAM2398 LOC144524 5'	CTGTTGCTCCAAAGATGACCT 84054	AACCCT C A
	AGG TCT TG AGCAACAG	
	TCC AGA AC TCGTTGTC	
	AGT__ A C	
GAM2398 LOC146237 3'	CTGCTGCCTCTCTGGGGTTCT 84609	TCTCT A A
	GGAACCCT GA GCA CAG	
	TCTTGGGG CT CGT GTC	
	TCT__ C C	
GAM2398 LOC147077 3'	CTGCTGCCCTCTTTCAGGGGTC 78849	A CTCT A_ A
CT	AGGA CCCTT GA GCA CAG	
	TCCT GGGGA CT CGT GTC	
	_ CTTT CC C	
GAM2398 LOC148181 5'	CTGTTGCTTCACTGCGGCCTCC 79433	AC TTCTC
	GGA CC TGAAGCAACAG	
	CCT GG ACTTCGTTGTC	
	CC CGTC_	
GAM2398 LOC150035 5'	GCAAATAGAGAAGGGTTCCT 85957	AA_
	AGGAACCCTTCTCTG GC	
	TCCTTGGGAAGAGAT CG	
	AAA	
GAM2398 LOC150577 3'	CTGCTGCCCCCGCACAGGGTTT 86255	TCTCTGAA A
CT	AGGAACCCT GCA CAG	
	TCTTTGGGA CGT GTC	
	CACGCCCC C	
GAM2398 LOC154990 5'	CTGTTGCTTCACTGCGGCCTCC 82149	AC TTCTC
	GGA CC TGAAGCAACAG	
	CCT GG ACTTCGTTGTC	
	CC CGTC_	
GAM2398 LOC201191 3'	CTGCTGCTTCCTCAGAGGGCAC 91344	AA CTCT A
CT	AGG CCCTT GAAGCA CAG	
	TCC GGGAG CTTCGT GTC	
	AC ACTC C	
GAM2398 LOC220002 3'	CTGCCACCTTCAGAGGGGTTCC 93272	TT CAA_
T	AGGAACCC CTCTGAAG CAG	
	TCCTTGGG GAGACTTC GTC	
	_ CACC	
GAM2398 LOC255057 3'	CTGGGGCAGAGCAGGGTTCCT 97094	T GAA AA
	AGGAACCCT CTCT GC CAG	

TCCTTGGGA GAGA CG GTC
 C ____ GG
 GAM2398 LOC255217 5' TGCTGGGATGGGAGAGGGGTCC 98790 A GA____
 C GG ACCCTTCTCT AGCA
 || ||||| ||||
 CC TGGGGAGAGG TCGT
 C GTAGGG
 GAM2398 LOC255535 5' GCCCAGAGAGGGGCTCC 97418 A AA
 GGA CCCTTCTCTG GC
 ||| ||||| ||
 CCT GGGGAGAGAC CG
 C C_
 GAM2398 LOC90410 5' CTGTCACTCCTTCAGAGCAGAA 63353 ACC T CA____
 CTCCT AGGA CT CTCTGAAG ACAG
 ||| || ||||| ||||
 TCCT GA GAGACTTC TGTC
 CAA C CTCAC
 GAM2399 DLEC1 3' ATGTGGAACAACAGCAAGTCA 24715 GC__ G
 TGACTTGCTGT CTG AT
 ||||| ||| ||
 ACTGAACGACA GGT TA
 ACAA G
 GAM2399 DLEC1 3' ATGTGGAACAACAGCAAGTCA 24727 GC__ G
 TGACTTGCTGT CTG AT
 ||||| ||| ||
 ACTGAACGACA GGT TA
 ACAA G
 GAM2399 FST 3' GCATCTCACTGCAAGTCA 22026 T CCT
 TGACTTGC GTG GGATGC
 ||||| ||| |||||
 ACTGAACG CAC TCTACG
 T ____
 GAM2399 GABRA3 3' GAAGCATCCAGGCACCCAA 7692 CT C
 TTG GTGCCTGGATGC TC
 ||| ||||| ||| ||
 AAC CACGGACCTACG AG
 C_ A
 GAM2399 HCFC1 3' AGGCTTGCCAGCAAGTCA 71545 T CTGGAT
 TGACTTGCTG GC GCCT
 ||||| || |||||
 ACTGAACGAC CG CGGA
 _ TT____
 GAM2399 IRTA2 3' AGTAACCCAGCAAGTCA 49229 TGCCT A C
 TGACTTGCTG GG TGC T
 ||||| || ||| |
 ACTGAACGAC CC ATG A
 ____ A A
 GAM2399 C3AR1 5' GAGACATCCAGGTGCTGAAGC 15765 ____ TG C
 GCT G CCTGGATG CTC
 ||| | ||||| |||

			CGA C GGACCTAC GAG			
			AGT GT A			
GAM2399	CBARA1	3'	GAAGCATCCAGTTCTCAAATC	21394	C	CTGTGC C
			GA TTG CTGGATGC TC			
			CT AAC GACCTACG AG			
			A TCTT__ A			
GAM2399	EPB41L1	3'	CACTTGACAGCAAAGCA	71102	AC	CT A
			TG TTGCTGTGC GG TG			
			AC AACGACACG TC AC			
			GA T_ _			
GAM2399	FLJ32884	5'	GCAGGAGGACAGCAAGTCA	59136	G	GGA
			TGACTTGCTGT CCT TGC			
			ACTGAACGACA GGA ACG			
			_ GG_			
GAM2399	LOC201799	3'	AGACACCAAACACAGCAAGT	90488	CC	A C
			ACTTGCTGTG TGG TG CT			
			TGAACGACAC ACC AC GA			
			AA _ A			
GAM2399	LOC219392	5'	GAGGCATCCAGACTGTTGATCA	92767	CTT	T GC
			TGA GC GT CTGGATGCCTC			
			ACT TG CA GACCTACGGAG			
			AGT T _			
GAM2399	LOC222028	3'	TTAGAAATCACAGCAAGTCA	95707	C_	
			TGACTTGCTGTG CTGG			
			ACTGAACGACAC GATT			
			TAAA			
GAM2400	TADA2L	3'	ACAGGAGGCAGAGGTTGCA	9437	G	A GAA
			TGCAA CCTCTG CT TGT			
			ACGTT GGAGAC GG ACA			
			_ _ AGG			
GAM2400	BRPF3	3'	ACAACCTTCAGAGGCTTCA	93922	C	CTGAA
			TG AAGCCTCTGA TGT			
			AC TTCGGAGACT ACA			
			_ TTCA_			
GAM2400	FLJ10244	3'	ACAGGAGGCAGAGGTTGCA	36394	G	A GAA
			TGCAA CCTCTG CT TGT			
			ACGTT GGAGAC GG ACA			
			_ _ AGG			
GAM2400	FLJ10290	3'	GATGTGAGCAGTCAGAGACTGA	36430	CA C	AA GT
	CA		TG AG CTCTGACTG T ATC			

AC TC GAGACTGAC G TAG
 AG A GA TG
 GAM2400 FLJ11011 3' ATACATTTTTGACAGAGGCTT 37536 ACT_
 AAGCCTCTG GAATGTAT
 ||||| |||||
 TTCGGAGAC TTTACATA
 AGTT
 GAM2400 FLJ14775 3' ACTTGGTCAGTCAGCAGCTTAC 52678 C CT AT_
 A TG AAGC CTGACTGA GT
 || ||| ||||| ||
 AC TTCG GACTGACT CA
 A AC GGTT
 GAM2400 JIK 3' ATACACTTAGGGGCTCACA 33262 CA CTGAA
 TG AGCCTCTGA TGTAT
 || ||||| ||||
 AC TCGGGGATT ACATA
 AC C____
 GAM2400 KLF12 3' GATGCACATTCAGAAGCTCACA 24363 CA C C AA
 TG AGC TCTGA TG TGTATC
 || ||| ||||| || |||||
 AC TCG AGACT AC ACGTAG
 AC A T ____
 GAM2400 SPINLW1 3' GATACATGTGCAGGACCTGCA 40231 A CC ACTGA
 TGCA G TCTG ATGTATC
 |||| | ||| |||||
 ACGT C GGAC TACATAG
 _CA GTG____
 GAM2400 ZNF294 3' ATACATTTCTTTAAGACTTGTA 71382 C C CT
 TGCAAG CT TGA GAATGTAT
 ||||| || ||| |||||
 ATGTTC GA ATT TTTACATA
 A _ TC
 GAM2400 LOC254041 5' ACAGAGGGCCTGAGGCTTGCA 96548 TGA_ GAA
 TGCAAGCCTC CT TGT
 ||||| || |||
 ACGTTCGGAG GG ACA
 TCCG AG_
 GAM2400 LOC92499 5' ACAGAGGGCCTGAGGCTTGCA 70099 TGA_ GAA
 TGCAAGCCTC CT TGT
 ||||| || |||
 ACGTTCGGAG GG ACA
 TCCG AG_
 GAM2401 ATRN 3' ATCTTTTAAAGGCAGTAATGGA 58444 CG_ GG
 TCCATT GCT TAAAAGAT
 |||| | ||| |||||
 AGGTAA CGG AATTTTCTA
 TGA A_
 GAM2401 CHC1 3' ATCTTTTAAACATTTTGAAT 8858 CTG
 ATTCGG GTTAAAAGAT
 |||| | |||||

			TAAGTT CAATTTTCTA		
			TTA		
GAM2401	GM2A	3'	ATCTGCCACAGCAGAATGGAG 68374	G	GTAAAA
			CTCCATTC GCTG AGAT		
			GAGGTAAG CGAC TCTA		
			A ACCG__		
GAM2401	LDOC1	5'	TTGGCCGAGCCGAACCGAG 25549	CA	_
			CTC TTCGGCT GGTAA		
			GAG AAGCCGA CCGGTT		
			CC G		
GAM2401	NEDD4	3'	TCCTTTAACCAAACCTGAA 70546	C_	A
			TTCGG TGGTTAAA GA		
			AAGTC ACCAATTT CT		
			AA C		
GAM2401	RCN1	3'	TTGGGAAGCCAAACGGAGT 60375	A C	GG
			ACTCC TT GGCT TTAA		
			TGAGG AA CCGA GGTT		
			C A AG		
GAM2401	FLJ11068	3'	CTTGGAACCAATGGAGT 37587	TCGGC	AA
			ACTCCAT TGGTT AAG		
			TGAGGTA ACCAA TTC		
			_____ GG		
GAM2401	FLJ21596	3'	CTTTTAAAAACAAAATGGAGT 46115	CGGCTGG	
			ACTCCATT TTAAAAG		
			TGAGGTAA AATTTTC		
			AACAAA_		
GAM2401	G2	3'	CTTTTAAAAAGCGTATGGAGT 67241	TCG	GG
			ACTCCAT GCT TTAAAAG		
			TGAGGTA CGA AATTTTC		
			TG_ AA		
GAM2401	KIAA1198	3'	TTAACACTGAATGGAG 64073	CTG	
			CTCCATTCGG GTTAA		
			GAGGTAAGTC CAATT		
			A_		
GAM2401	LOC253003	3'	ATCTTTTAACATTTTGAAT 98673	CTG	
			ATTCGG GTTAAAAGAT		
			TAAGTT CAATTTTCTA		
			TTA		
GAM2402	CENTD2	5'	CCGGAGATACCTCCAAAGCCGG 58271	A	CAGA
			TC GCTTTGGAGG TCTGG		

			GG CGAAACCTCC AGGCC		
			C ATAG		
GAM2402	IGFBP4	3'	TCCAGACCCACTCCCAAAGCT 9554	AG CAGA	
			AGCTTTGG G TCTGGA		
			TCGAAACC C AGACCT		
			CT ACCC		
GAM2402	MGST2	5'	CCAGACCTGCCTGCCTTCCTGA 11578	CTTT _ A	
			TCAG GG AGGCAG TCTGG		
			AGTC CC TCCGTC AGACC		
			CTT_ G C		
GAM2402	NUCB1	3'	CCAGAAGGGTCCCAGAGCTGA 21638	A AGA	
			TCAGCTTTGG GGC TCTGG		
			AGTCGAGACC CTG AGACC		
			_ GGA		
GAM2402	P53AIP1	3'	CCAAATCTGAAATAAAAGCTGG 42335	GGAGG C	
			TCAGCTTT CAGAT TGG		
			GGTCGAAA GTCTA ACC		
			ATAAA A		
GAM2402	RELN	5'	CCGGCGTCTCCAAACTGA 95955	C AGAT	
			TCAG TTTGGAGGC CTGG		
			AGTC AAACCTCTG GGCC		
			A C__		
GAM2402	S100A1	3'	CCAGACCTGCCTCTTCCCCCTG 21846	CTTT_ A	
			CAG GGAGGCAG TCTGG		
			GTC TCTCCGTC AGACC		
			CCCCT C		
GAM2402	WHSC1	3'	CCAGATCTACACAGCGGA 30580	A T GAGGC	
			TC GCT TG AGATCTGG		
			AG CGA AC TCTAGACC		
			G C A__		
GAM2402	WHSC1	3'	CCAGATCTACACAGCGGA 56667	A T GAGGC	
			TC GCT TG AGATCTGG		
			AG CGA AC TCTAGACC		
			G C A__		
GAM2402	WHSC1	3'	CCAGATCTACACAGCGGA 56678	A T GAGGC	
			TC GCT TG AGATCTGG		
			AG CGA AC TCTAGACC		
			G C A__		
GAM2402	AP1GBP1	3'	CCAAATTTCCAAAGATGA 24343	G GGCA C	
			TCA CTTTGGG GAT TGG		

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AGT GAAACCT TTA ACC
A ____ A
GAM2402 AP1GBP1 3' CCAAATTTCCAAAGATGA 55436 G GGCA C
TCA CTTTGGG GAT TGG
||| ||||| ||| |||
AGT GAAACCT TTA ACC
A ____ A
GAM2402 BHLHB2 3' CCAAAGTGCACAAAGCTGA 14761 GAG GATC
TCAGCTTTG GCA TGG
||||||| ||| |||
AGTCGAAAC CGT ACC
A__ GAA_
GAM2402 C20orf110 3' TCGGCACCTCCAAGAGCTGA 80366 _ CAGAT
TCAGCTTT GGAGG CTGG
||||||| ||||| |||||
AGTCGAGA CCTCC GGCT
A AC____
GAM2402 C8orf17 3' TCCAGATCCACCTTACGTAGC 40000 TTG_ CA
GCT GAGG GATCTGGA
||| ||||| |||||
CGA TTCC CTAGACCT
TGCA AC
GAM2402 CBARA1 3' TCCAGGATGGGCCTCTAAAGCT 21396 AG _
GA TCAGCTTTGGAGGC ATC TGGA
||||||| ||| |||||
AGTCGAAATCTCCG TAG ACCT
GG G
GAM2402 DKFZp434B1222 5' CCAGAGTCCCCAAAATTGA 34551 C A CAGA
TCAG TTTGG GG TCTGG
||||| ||||| ||| |||||
AGTT AAACC CC AGACC
A _ TG__
GAM2402 DKFZP564A1164 3' CCTTACTCCTCCAAAACCTGA 71536 C C ATCT
TCAG TTTGGAGG AG GG
||||| ||||| ||| |||
AGTC AAACCTCC TC CC
A _ ATT_
GAM2402 DKFZP564D172 3' TCCACACACACTCCAAAGCCGA 50198 A GCAGATC
TC GCTTTGGAG TGGA
|| ||||| |||||
AG CGAAACCTC ACCT
C ACACAC_
GAM2402 FLJ20619 3' CCAGACCTGCCTCCTAGAG 35892 _ A
CTTT GGAGGCAG TCTGG
||||| ||||| |||||
GAGA CCTCCGTC AGACC
T C
GAM2402 FLJ22037 5' TCAGGACCCGCCTCCAAGCTGA 95537 T AGA_
TCAGCTT GGAGGC TCTGG
||||| ||||| |||||

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			AGTCGAA CCTCCG G	GGACT	
			—	CCCA	
GAM2402	FLJ23093	3'	CCAGATCTGCCTGCAGAGCT	45322	G
			AGCTTTG AGGCAGATCTGG		
			TCGAGAC TCCGTCTAGACC		
			G		
GAM2402	FLJ32865	3'	CCAGATGGCTCCAAGGC	58803	G GA
			GCTTTGGAG CA TCTGG		
			CGGAACCTC GT AGACC		
			G —		
GAM2402	KIAA0254	3'	TCCAGAAGACTTCAAAGCTGA	29284	GCAGA
			TCAGCTTTGGAG TCTGGA		
			AGTCGAAACTTC AGACCT		
			AGA—		
GAM2402	KIAA0828	3'	CCAGATTATCAAAGCT	82111	AGGCA
			AGCTTTGG GATCTGG		
			TCGAAACT TTAGACC		
			A—		
GAM2402	KIAA1328	3'	TCCAGATAGATCCAAAGCT	62333	GGCAG
			AGCTTTGGA ATCTGGA		
			TCGAAACCT TAGACCT		
			AGA—		
GAM2402	MGC2647	3'	CCGCTGTCACCTTCAAAGCTGA	74077	CA C—
			TCAGCTTTGGAGG GAT TGG		
			AGTCGAAACTTCC CTG GCC		
			A_ TC		
GAM2402	NRF	5'	CCATCCTCCAAAGGTGA	34506	G CAGATC
			TCA CTTTGGAGG TGG		
			AGT GAAACCTCC ACC		
			G T—		
GAM2402	PDE10A	5'	CCTGAGCCCCAAAGCT	22843	A AGA T
			AGCTTTGG GGC TC GG		
			TCGAAACC CCG AG CC		
			— — T		
GAM2402	PLP1	3'	CCAAATCTGCCTATTGCAGCTG	6756	TTGG_ C
			CAGCT AGGCAGAT TGG		
			GTCGA TCCGTCTA ACC		
			CGTTA A		
GAM2402	SEMA5A	3'	TCCAAATCTGGATAAAGCTG	15597	GAGG C
			CAGCTTTG CAGAT TGGA		

GTCGAAAT GTCTA ACCT
 AG__ A
 GAM2402 ZNF185 3' CCATGAAAATGCCTCCAAACTG 24092 C GA_ _
 A TCAG TTTGGAGGCA TC TGG
 |||| ||||| || |||
 AGTC AAACCTCCGT AG ACC
 _ AAA T
 GAM2402 LOC113201 3' CCAGCTACTCCAGAAGCTGA 57353 _ GC AT
 TCAGCT TTGGAG AG CTGG
 ||||| ||||| || ||||
 AGTCGA GACCTC TC GACC
 A A_ _
 GAM2402 LOC120114 3' CCAGTCCTCAAAACTGA 76043 C G CAGAT
 TCAG TTT GAGG CTGG
 |||| ||||| ||||
 AGTC AAA CTCC GACC
 _ A T____
 GAM2402 LOC146373 3' TCCAGATCCACCCTCCCTAG 84651 TT CA_
 CT GGAGG GATCTGGA
 || ||||| |||||
 GA CCTCC CTAGACCT
 TC CAC
 GAM2402 LOC147178 5' CCAGCACTGACCTCCAAGC 61996 T _ AT
 GCTT GGAGG CAG CTGG
 |||| ||||| || ||||
 CGAA CCTCC GTC GACC
 _ A AC
 GAM2402 LOC149267 3' CCAGATGGGGGTCCAGAGCT 57475 GGCAG
 AGCTTTGGA ATCTGG
 ||||| |||||
 TCGAGACCT TAGACC
 GGGGG
 GAM2402 LOC149345 3' CCAGGACCCCAAAGCTGG 80082 A CAGA
 TCAGCTTTGG GG TCTGG
 ||||| || |||||
 GGTCGAAACC CC GGACC
 _ A____
 GAM2402 LOC158987 3' TCATGTTACTCCCAAAGCT 88332 AG CA C
 AGCTTTGG G GAT TGG
 ||||| | |||||
 TCGAAACC C TTG ACT
 CT A_ T
 GAM2402 LOC164714 3' TCCAGATCTGCCCTTTGA 88589 CTTT A
 TCAG GG GGCAGATCTGGA
 |||| || |||||
 AGTT CC CCGTCTAGACCT
 T____ _
 GAM2402 LOC201771 5' CCAGATCTGCACTAGC 70517 TT AG
 GCT GG GCAGATCTGG
 ||| || |||||

		CGA TC CGTCTAGACC		
		__ A_		
GAM2402	LOC221814 5'	TCCAAAAATTGCAAAGCTGA 95562	G	GCAGATC
		TCAGCTTTG AG TGGA		
		AGTCGAAAC TT ACCT		
		G AAAA__		
GAM2402	LOC253962 5'	CCAGACTGTTCCAAAGC 98478	G	A
		GCTTTGGAG CAG TCTGG		
		CGAAACCTT GTC AGACC		
		- -		
GAM2402	LOC255271 5'	TCCAGAGCAGCCTCCAAAATGA 97243	GC	AGA
		TCA TTTGGAGGC TCTGGA		
		AGT AAACCTCCG AGACCT		
		A_ ACG		
GAM2402	LOC91561 5'	CCAGATCCGCCTCTTCTCTGA 67040	CTTT	A
		TCAG GGAGGC GATCTGG		
		AGTC TCTCCG CTAGACC		
		TCT_ C		
GAM2403	CDH12 3'	CTTATCATTTAAAGTGGTGTA 15777	CCCAA	GA
		TACACCACT GAA ATAAG		
		ATGTGGTGA TTT TATTC		
		AA__ AC		
GAM2403	GOCAP1 3'	ATTGTTCTTGGGAGCAGTGTA 43007	CA	G
		TACAC CTCCCAAGAA AAT		
		ATGTG GAGGGTTCTT TTA		
		AC G		
GAM2403	DKFZp434N2435 5'	CTTATTACTGTGGGGTGGT 98090	T	AGAAG
		ACCAC CCCA AATAAG		
		TGGTG GGGT TTATTC		
		_ GTCA_		
GAM2403	DKFZP564I122 3'	CTTATTCTTCTCCCTCATGTGT 63877	CACTCCCA	
	A	TACAC AGAAGAATAAG		
		ATGTG TCTTCTTATTC		
		TACTCCC_		
GAM2403	FLJ21791 3'	CTTATTTGCAGAAGTGGTGTA 62126	CCCAAGAA	
		TACACCACT GAATAAG		
		ATGTGGTGA TTTATTC		
		AGACG__		
GAM2403	HMP19 3'	CTTATTCTTTGTTAGGAAAATG 88860	CCAC	CAA_
	TA	TACA TCC GAAGAATAAG		

		ATGT AGG TTTCTTATTC	
		AAA_ ATTG	
GAM2403 KIAA1579	3'	TACTCTTAGTGGTGTA 37154	CCCAAG A
		TACACCACT AAGA TA	
		ATGTGGTGGA TTCT AT	
		_____ C	
GAM2403 KIAA1719	3'	TCTGTCTTGGGAGTGGTGTA 68742	_
		TACACCACTCCCAAGA AGA	
		ATGTGGTGAGGGTTCT TCT	
		G	
GAM2403 KIAA1853	3'	TTTTTCTTGGAAGCAGTG 69929	CA C
		CAC CT CCAAGAAGAA	
		GTG GA GGTTCCTTTT	
		AC A	
GAM2403 KIAA1877	3'	CTTATTCTTCTGCCATGAGT 66748	CCA__
		ACTC AGAAGAATAAG	
		TGAG TCTTCTTATTC	
		TACCG	
GAM2403 KIAA1906	3'	CTTATTCTTCTTGACTTTTGG 73571	CTCC_
		CCA CAAGAAGAATAAG	
		GGT GTTCTTCTTATTC	
		TTTCA	
GAM2403 OSBPL11	3'	CTTAATTTCCCAAGAGTGGTG 43206	CCAA AA
		CACCACTC GAAG TAAG	
		GTGGTGAG CTTT ATTC	
		AACC A_	
GAM2403 YME1L1	3'	TCATTCTTGATGTGGTGTA 58438	TCC _
		TACACCAC CAAGAA GA	
		ATGTGGTG GTTCTT CT	
		TA_ A	
GAM2403 YME1L1	3'	TCATTCTTGATGTGGTGTA 27323	TCC _
		TACACCAC CAAGAA GA	
		ATGTGGTG GTTCTT CT	
		TA_ A	
GAM2403 ZNF262	3'	CTTATTTTGTGTTGGGAGT 18723	A
		ACTCCCAAG AGAATAAG	
		TGAGGGTTT TTTTATTC	
		G	
GAM2403 LOC91960	3'	TGTGGCTTGGAACGTGGTGTA 68294	TC_ AAGA
		TACACCAC CCAAG ATA	

ATGTGGTG GGTTC TGT
 CAA GG__
 GAM2404 OVOL1 5' CCAGTTTCCGCTAAGACACA 17064 C TT GG
 TGTGTCT AGC G GCTGG
 ||||| ||| | |||||
 ACACAGA TCG C TGACC
 A C_ TT
 GAM2404 TTC3 3' CCAGCCGTGCTGAGCACACA 13882 _ TT G
 TGTGT CTCAGC G GGCTGG
 |||| ||||| | |||||
 ACACA GAGTCG T CCGACC
 C _ G
 GAM2404 ASB13 3' CAGCCCCAAGCCTGCAC 45542 CTCA
 GTGT GCTTGGGGCTG
 ||| |||||
 CACG CGAACCCCGAC
 TC__
 GAM2404 CFLAR 5' CCAGTGACAGCTGAGACAACA 15272 _ T GG
 TGT GTCTCAGCT G GCTGG
 || ||||| | |||||
 ACA CAGAGTCGA C TGACC
 A _ AG
 GAM2404 CX46.6 3' CCAGCCCCAAACTGAGACA 40309 C
 TGTCTCAG TTGGGGCTGG
 ||||| |||||
 ACAGAGTC AACCCCGACC
 A
 GAM2404 DKFZP564P1916 5' CAGCCCCTAGACATACAG 32237 A CAGCTT
 CT TGTGTCT GGGGCTG
 || ||||| |||||
 GA ATACAGA CCCCGAC
 C T____
 GAM2404 DKFZp761F2014 3' CCAGCCCCAAAATGCCAATAG 39940 G TCT GC
 CTAT TG CA TTGGGGCTGG
 ||| || || |||||
 GATA AC GT AACCCCGACC
 _ C_ AA
 GAM2404 FLJ11939 3' CCAGGGGGCTGAGGCACACAG 45495 A GGGG
 CT TGTGTCTCAGCTT CTGG
 || ||||| |||||
 GA ACACGGAGTCGGG GACC
 C G__
 GAM2404 FLJ21156 3' CAGCCCCGCAGACCCACA 45119 TC A TT
 TGTG TC GC GGGGCTG
 ||| || || |||||
 ACAC AG CG CCCCGAC
 CC A _
 GAM2404 FLJ22349 3' CCAGCCCCTCTGCAGAGACACA 46107 A TT_
 TGTGTCTC GC GGGGCTGG
 ||||| || |||||

			ACACAGAG CG CCCCCGACC		
			A TCT		
GAM2404 FOXJ1	3'		CCAGCCCCACCTTGTACACACA 9375	A	CT CT
G			CT TGTGT CAG TGGGGCTGG		
			GA ACACA GTT ACCCCGACC		
			C T_ CC		
GAM2404 HEY1	3'		CAGCCCCAGCAACACA 92886	CTCA	T
			TGTGT GCT GGGGCTG		
			ACACA CGA CCCCCGAC		
			A__ _		
GAM2404 HS6ST	3'		CCAGCCCCATCACCGAAACACA 62728	C	AGCT_
TA			TATGTGT TC TGGGGCTGG		
			ATACACA AG ACCCCGACC		
			A CCACT		
GAM2404 JM4	3'		CAGCCCCAACTAAGATAT 24260	C	C
			GTGTCT AG TTGGGGCTG		
			TATAGA TC AACCCCGAC		
			A A		
GAM2404 KIAA0211	3'		CAACCCCAAGCTGCTTAT 28281	TCT	C
			GTG CAGCTTGGGG TG		
			TAT GTCGAACCCC AC		
			TC_ A		
GAM2404 LOC115051	3'		CCAGCCCCATCACCGAAACACA 60677	C	AGCT_
TA			TATGTGT TC TGGGGCTGG		
			ATACACA AG ACCCCGACC		
			A CCACT		
GAM2404 LOC126564	5'		CCAACCCCAAGCTCTGGGCACA 76212	C_	C
T			ATGTGTCT AGCTTGGGG TGG		
			TACACGGG TCGAACCCC ACC		
			TC A		
GAM2404 LOC145609	5'		CCATCAGGTGAAACACATAG 84364	C	G _
			CTATGTGT TCA CTTGG GG		
			GATACACA AGT GGA CT CC		
			A _ A		
GAM2404 LOC148183	5'		CCAGCTTTCTCTGAAACACA 85262	C	CTT
			TGTGT TCAG GGGGCTGG		
			ACACA AGTC TTTCGACC		
			A TC_		
GAM2404 LOC165229	5'		CCAGAAAGCTGAGCCACA 83361	T	GGGG
			TGTG CTCAGCTT CTGG		

		ACAC GAGTCGAA GACC		
		C A__		
GAM2404	LOC220515 5'	CCAACCTAGACTCTGAAAAACA 92755	C__ C__ GC	
	CA	TGTGT TCAG TTGGG TGG		
		ACACA AGTC GATCC ACC		
		AAA TCA A_		
GAM2404	LOC221810 3'	CCAGCCCCCAGGAAAACAC 95545	CTCAG _	
		GTGT CTTGGGG CTGG		
		CACA GGACCCC GACC		
		AAA__ C		
GAM2404	LOC91759 5'	CCAGGGGGCATGAGACACACAG 67691	A _ GGGG	
		CT TGTGTCTCA GCTT CTGG		
		GA ACACAGAGT CGGG GACC		
		C A G__		
GAM2404	LOC92710 3'	CCAGCCCCAGCCAAACACACA 70863	CTCA_ T	
		TGTGT GCT GGGGCTGG		
		ACACA CGA CCCC GACC		
		CAAAC _		
GAM2405	ABCC5 3'	TTGCTGTGTGGTTTGGTGTGT 20299	G GAGA	
		GCACACCGGG CTAT AGCAA		
		TGTGTGGTTT GGTG TCGTT		
		_ TG__		
GAM2405	ACP5 3'	TGCTGAGTTCCGGGGTGC 9659	A ATGAGA	
		GCAC CCGGGGCT AGCA		
		CGTG GGCCTTGA TCGT		
		G G__		
GAM2405	B4GALT6 3'	TTCCATGTACCTCTGGTGTGT 60556	C__ A	
		GCACACCGGGG TATG GAA		
		TGTGTGGTCTC GTAC CTT		
		CAT _		
GAM2405	BACH2 3'	TTGTTTTTCTTGTGTGTGT 41792	CG TAT	
	GT	GCACAC GGGC GAGAAGCAA		
		TGTGTG TTTG TTTTTTGT		
		TG TTC		
GAM2405	BCL9 5'	TTGCTTTGATGTTGTCCTGGTG 16326	TATGA_	
	T	ACACCGGGGC GAAGCAA		
		TGTGGTCCTG TTTCGTT		
		TTGTAG		
GAM2405	CDKN2D 3'	TTGTTTTTCTCACTCCTTTTGG 10161	____ CTAT	
	TGTGT	GCACACC GGGG GAGAAGCAA		

			TGTGTGG	CCTC	CTTTTGT	
			TTTT	ACT_		
GAM2405	CST2	3'	TTGCTTCTCATAGCCCTGGT	8999		
			ACCGGGGCTATGAGAAGCAA			
			TGGTCCCGATACTCTTCGTT			
GAM2405	CST3	3'	CTTGCTTCTCATAGCCCCGGTG	5436		
	TGC		GCACACCGGGGCTATGAGAAGCAA			
			CGTGTGGCCCCGATACTCTTCGTT			
			CT			
GAM2405	DUT	3'	TTGCTTCAAGTGT	10463	T GA	
			ACACCGGGGC AT GAAGCAA			
			TGTGGTTTTG TG CTTCGTT			
			_ AA			
GAM2405	DVL3	3'	TTCCTGGGGTTTTGGTGTGC	16655	ATGA	
			GCACACCGGGGCT GAA			
			CGTGTGGTTTTGG CTT			
			GGTC			
GAM2405	EMX2	3'	TTGTTTTTGCACCTCGCTGTG	88957	C CTA	
	T		GCACA CGGGG TGAGAAGCAA			
			TGTGT GCTTC GTTTTTGT			
			C AC_			
GAM2405	HMG20A	3'	TTGTTTTTTAAGAAGTTGATGT	37075	C GG_ A	
	GC		GCACA CGG CT TGAGAAGCAA			
			CGTGT GTT GA ATTTTTTGT			
			A GAA _			
GAM2405	LEP	3'	TTGTTGGAAGGTTTGGTGTGT	5873	G ATGAGA	
			GCACACCGGG CT AGCAA			
			TGTGTGGTTT GA TTGTT			
			G AGG_			
GAM2405	LIFR	3'	TTGTTTTTTTGGTTGGTTGT	11314	C GG T	
			GCA ACCG GCTA GAGAAGCAA			
			TGT TGGT TGGT TTTTTTGT			
			_ _ T			
GAM2405	MAP3K7IP1	3'	TTGCTTCTCCTTCTGGTGCTG	21493	_ CTAT	
	T		GCA CACCGGGG GAGAAGCAA			
			TGT GTGGTCTT TTCTTCGTT			
			C CC_			
GAM2405	MEN1	5'	TTGTTTTTTCCTTTTGGTGAG	56364	A CTAT	
	T		GC CACCGGGG GAGAAGCAA			

			TG GTGGTTTT TTTTTGTT		
			A CCT_		
GAM2405	MLLT2	3'	TTGCCTGGTAGGTTTGGTGTGT 21034	G G AA	
			GCACACCGGG CTAT AG GCAA		
			TGTGTGGTTT GATG TC CGTT		
			G G _		
GAM2405	MMP9	3'	TGTTTTTTGTTGGAGTGT 18425	A GGGCT TG	
			GCAC CCG A AGAAGCA		
			TGTG GGT T TTTTGT		
			A ____ GT		
GAM2405	MRE11A	3'	TTGTTTTTTTAACCTGGTTGT 20005	C GCTAT	
			GCA ACCGGG GAGAAGCAA		
			TGT TGGTCC TTTTTGTT		
			_ AAT_		
GAM2405	NEU3	3'	TTGCTTTTGGACCTTGGATGTG 22837	_ _ TGA	
	T		GCACA CCGGGG CTA GAAGCAA		
			TGTGT GGTTCC GGT TTTCGTT		
			A A _		
GAM2405	P53AIP1	3'	TTGTTTTTATCCCTGGTCTGT 42341	C CTATG	
			GCA ACCGGGG AGAAGCAA		
			TGT TGGTCCC TTTTTGTT		
			C TA_		
GAM2405	PKP2	3'	TTGTTTTTATCCCCTTGGTTGT 17111	C CTATG	
			GCA ACCGGGG AGAAGCAA		
			TGT TGGTTCC TTTTTGTT		
			_ CCTA_		
GAM2405	SLC7A6	3'	TTGTTTTTTTCACCGGTTGC 15645	C GCTAT	
			GCA ACCGGG GAGAAGCAA		
			CGT TGGCCC TTTTTGTT		
			_ ACT_		
GAM2405	STK38	5'	TTGCTTCTGGTTTCTGGTTGT 24403	C CT G	
			GCA ACCGGGG AT AGAAGCAA		
			TGT TGGTCTT TG TCTTCGTT		
			_ T_ G		
GAM2405	TGM4	3'	TGCTTCCTCCCTGGTGTG 13724	CTATGA	
			CACACCGGGG GAAGCA		
			GTGTGGTCCC CTTCGT		
			TC_		
GAM2405	ABTB1	3'	TTGCTTCTCTAAGCTGGTGT 51703	GG AT	
			ACACC GGCT GAGAAGCAA		

TGTGG TCGA CTCTTCGTT
 — AT
 GAM2405 CLGN 3' TTGTTTGGAGATAGTTTTGGTT 16417 C GAG_
 TGT GCA ACCGGGGCTAT AAGCAA
 ||| ||||| |||||
 TGT TGGTTTTGATA TTTGTT
 T GAGG
 GAM2405 DKFZP761F241 3' TGCTTGAGTCTTGGTGGC 49585 A ATGAG
 GC CACCGGGGCT AAGCA
 || ||||| |||||
 CG GTGGTTCTGA TTCGT
 — G—
 GAM2405 ENPP4 3' TTCACATTAAGGTTTTGGTGTG 30719 — A GCAA
 T GCACACCGGGGCT ATG GAA
 ||||| ||| |||
 TGTGTGGTTTTGG TAC CTT
 AAT A A
 GAM2405 FLJ10407 3' TGCTTTTTGTGTGTGTG 36580 CGGG T TG
 CACAC GC A AGAAGCA
 |||| ||| |||||
 GTGTG TG T TTTTCGT
 — — GT
 GAM2405 FLJ13848 3' TGCTTTTCTCTCTGGTGT 45833 CTAT
 ACACCGGGG GAGAAGCA
 ||||| |||||
 TGTGGTCTC CTTTCGT
 T—
 GAM2405 FLJ14084 3' TTGTTTTTCCTTGTTAGGTGTG 41599 GG TAT
 C GCACACC GGC GAGAAGCAA
 ||||| ||| |||||
 CGTGTGG TTG CTTTTTGTT
 A_ TTC
 GAM2405 FLJ20546 3' GCTTCAGTTCTGGTGTGC 35810 ATGA
 GCACACCGGGGCT GAAGC
 ||||| |||||
 CGTGTGGTCTTGA CTTCG
 —
 GAM2405 FLJ20695 3' TTGTTTTTTTTTAGTCTTGCTG 35988 C T_
 TGT GCACA CGGGGCTA GAGAAGCAA
 ||||| ||||| |||||
 TGTGT GTTCTGAT TTTTTTGTT
 C TT
 GAM2405 FLJ20793 3' TTTTATGTTTCTGGTGTGT 93455 C
 GCACACCGGGG TATGAGAA
 ||||| |||||
 TGTGTGGTCTT GTATTTT
 T
 GAM2405 FLJ22127 3' TGCTTCTCGACTGGTGGC 43203 A GGCTAT
 GC CACCGG GAGAAGCA
 || ||||| |||||

CG GTGGTC CTCTTCGT
 _ AG____
 GAM2405 FLJ23519 3' TTGCTCTCGGGGTGGCCTTGGG 50967 A ____ A
 GTGC GCAC CCGGGGCTAT GAGA GCAA
 |||| ||||| |||| ||||
 CGTG GGTTCGGTG CTCT CGTT
 G GGG _

GAM2405 GPR74 3' TTGCTTTTTGTGGCTTTG 54897 TG
 CGGGGCTA AGAAGCAA
 ||||| |||||
 GTTTCGGT TTTTCGTT
 GT

GAM2405 GRP3 3' TTGTTTTGTTCTTCTTGGTGTG 31743 CTATGA
 C GCACACCGGGG GAAGCAA
 ||||| |||||
 CGTGTGGTTCT TTTTGT
 TCTTG_

GAM2405 HABP4 3' CTCGTGGTTTCTGTGTGT 71084 C GG
 GCACAC G GCTATGAG
 ||||| |||||
 TGTGTG C TGGTGCTC
 T TT

GAM2405 HSPCA 5' TTGCTTCAGCGTCCCGGTGTG 19293 TATGA
 CACACCGGGGC GAAGCAA
 ||||| |||||
 GTGTGGCCCTG CTTCGTT
 CGA__

GAM2405 KIAA0121 3' TTGCTTCTTGAGACCGGGGTGT 73047 A GG A
 GCAC CCGG CT TGAGAAGCAA
 |||| |||| |||||
 TGTG GGCC GA GTTCTTCGTT
 G A_ _

GAM2405 KIAA0459 3' TGTTTTTGACTTTGGTGGC 61665 A CTATG
 GC CACCGGGG AGAAGCA
 || ||||| |||||
 CG GTGGTTTC TTTTGT
 _ AG____

GAM2405 KIAA0775 3' TTGTTTCTTGTGGTTCCCTGC 28959 CACC TG
 GCA GGGGCTA AGAAGCAA
 || ||||| |||||
 CGT CCTTGGT TCTTTGTT
 C__ GT

GAM2405 KIAA1076 3' TTGGTGGTTTTGTTGTGT 66130 C G
 GCACA CGGGGCTAT AG
 |||| ||||| |||||
 TGTGT GTTTTGGTG TT
 T G

GAM2405 KIAA1078 3' TTGTTTTTTAAGATGCTGTGC 65718 C GGGG A
 GCACA C CT TGAGAAGCAA
 |||| | |||||

CGTGT G GA ATTTTTTGTT
 C TA__ _
 GAM2405 KIAA1371 3' TGTTTTTCATGTGGTATGT 90479 C GGGC
 GCA ACCG TATGAGAAGCA
 ||| ||| |||||
 TGT TGGT GTACTTTTGT
 A ____
 GAM2405 KIAA1437 3' TTGTTTTTTGGGTTTTTTTGGT 61224 ____ A
 GT ACACCGGG GCT TGAGAAGCAA
 ||||| ||| |||||
 TGTGGTTT TGG GTTTTTTGT
 TTT _
 GAM2405 LCHN 3' TGTTTTTCCTTCTGGTGGC 87481 A CTAT
 GC CACCGGGG GAGAAGCA
 || ||||| |||||
 CG GTGGTCTT CTTTTGT
 _ C__
 GAM2405 MGC13138 3' TTGCTTTTAGTGTTTTTTGGTGT 54167 C G
 ACACCGGGG TAT AGAAGCAA
 ||||| ||| |||||
 TGTGGTTT GTG TTTTCGTT
 T A
 GAM2405 MGC3178 3' CTCTGGCCCTGGTGTGC 48716 T
 GCACACCGGGGCTA GAG
 ||||| |||
 CGTGTGGTCCCGGT CTC
 _
 GAM2405 NOL4 3' TTGCTTTTTGTTTTAGTGTGT 15036 CG TAT
 GCACAC GGGC GAGAAGCAA
 |||| ||| |||||
 TGTGTG TTTG TTTTCGTT
 AT ____
 GAM2405 NPGPR 3' TTGCTTTTTGTGGCTTTG 18085 TG
 CGGGGCTA AGAAGCAA
 ||||| |||||
 GTTTCGGT TTTTCGTT
 GT
 GAM2405 NR2F1 3' TGCTTCTTATAATGAGTGC 97644 ACCGGGGC
 GCAC TATGAGAAGCA
 ||| |||||
 CGTG ATATTCTTCGT
 AGTA__ _
 GAM2405 PCDHB10 3' TTCATATACTTTTGGTGTGT 38910 C A
 GCACACCGGGG TATG GAA
 ||||| ||| |||
 TGTGTGGTTTT ATAT CTT
 C A
 GAM2405 PGR1 3' TTGTTCCCGGGCTTTGGTGGT 53908 A A A G
 GC CACCGGGGCT TG GAA CAA
 || ||||| || ||| |||

TG GTGGTTTCGG GC CTT GTT
 _ _ C _
 GAM2405 PRO1489 5' TTGTTTTTCGTGTGTGTGTGTG 38333 CGGG _
 T GCACAC GC TATGAGAAGCAA
 ||||| || |||||
 TGTGTG TG GTGCTTTTGT
 TG_ T
 GAM2405 RAB1B 3' TTGAGTCTGTGGCTTTGGGGTG 49119 A G AG
 T GCAC CCGGGGCTAT AGA CAA
 ||| ||||| ||| |||
 TGTG GGTTTCGGTG TCT GTT
 G _ GA
 GAM2405 RP4-622L5 3' TTGCTTCTTGGCTGAATGGTCT 39432 C G_ AT
 GC GCA ACCG GGCT GAGAAGCAA
 ||| ||| ||| |||||
 CGT TGGT TCGG TTCTTCGTT
 C AAG _
 GAM2405 SERF1B 3' TGAGGTCTCCTGGCCCTGGTGT 43706 T AG_ A
 GC GCACACCGGGGCTA GAGA CA
 ||||| ||| |||
 CGTGTGGTCCCGGT CTCT GT
 C GGA
 GAM2405 SH3BGRL2 3' TTGTTTTTCCAAATTCGGGTGT 49680 CTAT
 ACACCGGGG GAGAAGCAA
 ||||| |||||
 TGTGGCCTT CTTTTGT
 AAAC
 GAM2405 SP2 5' TTGTTTTAAATTCTTGTGTGC 13334 C CTATGA
 GCACAC GGGG GAAGCAA
 ||||| ||| |||||
 CGTGTG TCTT TTTTGT
 T AAA_
 GAM2405 SPUVE 3' TTGTTTTTTGTCATTGGCGTGC 24139 A _ TAT
 GCAC CCGG GGC GAGAAGCAA
 ||| ||| ||| |||||
 CGTG GGTT CTG TTTTTGT
 C A _
 GAM2405 SRPK2 3' TTGTTTCTTGTGTTGTGTG 13415 CGG T TG
 CACAC GGC A AGAAGCAA
 |||| ||| |||||
 GTGTG TTG T TCTTTGT
 _ _ GT
 GAM2405 STRBP 5' TTGCTTCTTATAAAGGTGTGT 37822 GGGGC
 GCACACC TATGAGAAGCAA
 ||||| |||||
 TGTGTGG ATATTCTTCGTT
 AA_
 GAM2405 UBE4B 3' TGTTTTTTTAATTGGTGT 21288 GGCTAT
 ACACCGG GAGAAGCA
 ||||| |||||

		TGTGGTT	TTTTTTGT		
		AAT__			
GAM2405	LOC115509 3'	TTGTTTCAGCAGCTTTGGTTGC	73845	C	ATGA
		GCA ACCGGGGCT	GAAGCAA		
		CGT TGGTTTCGA	CTTTGTT		
		_	CGA_		
GAM2405	LOC122524 3'	TTGAGAAAGTAGTTTTGGTTGC	74587	C	GAGAAG
		GCA ACCGGGGCTAT	CAA		
		CGT TGGTTTTGATG	GTT		
		_	AAGA_		
GAM2405	LOC135932 5'	TTGTGTCCCTGTGGCTTTGGTG	76702	A	A_ A
	CGC	GC CACCGGGGCTATG	GA GCAA		
		CG GTGGTTTCGGTGT	CT TGTT		
		C	CC G		
GAM2405	LOC147658 3'	TTGCTTAAAGTGTTTTGGTGT	79052		T GAG
		ACACCGGGGC	AT AAGCAA		
		TGTGGTTTTG	TG TTCGTT		
		_	AAA		
GAM2405	LOC149840 5'	TTGCTTCCGCGTTCCGTTGC	80348	C	TA A
		GCA ACCGGGGC	TG GAAGCAA		
		CGT TGGCCTTG	GC CTTCGTT		
		_	C_ _		
GAM2405	LOC151162 5'	TTGCTTTTTTGTGTGTTTGCTG	86433	C	_ TAT
	TGC	GCACA CGGG	GC GAGAAGCAA		
		CGTGT GTTT	TG TTTTCGTT		
		C	G TGT		
GAM2405	LOC154739 5'	TTGCTTTTTGTATTTGGATGTG	87451	_	GC TG
	T	GCACA CCGGG	TA AGAAGCAA		
		TGTGT GGT	AT TTTTCGTT		
		A	_ GT		
GAM2405	LOC154760 5'	TTGTGTCCCTGTGGCTTTGGTG	87458	A	A_ A
	CGC	GC CACCGGGGCTATG	GA GCAA		
		CG GTGGTTTCGGTGT	CT TGTT		
		C	CC G		
GAM2405	LOC154865 3'	TTGTTTTTCATAGTATTTTGAG	82064	A	CCGGG
	T	GC CA	GCTATGAGAAGCAA		
		TG GT	TGATACTTTTGTT		
		A	TTTA_		
GAM2405	LOC158014 5'	TTGTTTTTTTAATTTGGGGTG	82573	A	GC T
	T	GCAC CCGGG	TA GAGAAGCAA		

TGTG GGTTT AT TTTTTGT
 G A T
 GAM2405 LOC158293 3' TTGTTTTTGTGCTTGGTTTGT 82749 C GT G
 GCA ACCGGG C AT AGAAGCAA
 ||| ||||| | || |||||
 TGT TGGTTC G TG TTTTTGT
 T _ T _
 GAM2405 LOC158332 3' TTGTTTTTGGTACATGTCCTG 82767 C TA____
 GTTGT GCA ACCGGGGC TGAGAAGCAA
 ||| ||||| |||||
 TGT TGGTCCTG GTTTTTTGT
 _ TACATG
 GAM2405 LOC200058 5' TTGTTAAGGCAAGCATTGGTGT 89967 G A AGA_
 GT GCACACCGG GCT TG AGCAA
 ||||| ||| || |||||
 TGTGTGGTT CGA AC TTGTT
 A _ GGAA
 GAM2405 LOC200609 5' TGTTTCTTTATTGGTGAGT 91671 A GGCTAT
 GC CACCGG GAGAAGCA
 || ||||| |||||
 TG GTGGTT TTCTTTGT
 A AT____
 GAM2405 LOC200830 5' TGTTTCCTTCTGGTGGGT 91732 A CTATGA
 GC CACCGGGG GAAGCA
 || ||||| |||||
 TG GTGGTCTT CTTTGT
 G C____
 GAM2405 LOC202347 3' TTGTTAGAGAGCTCTGGTTGT 91953 C ATGAGA
 GCA ACCGGGGCT AGCAA
 ||| ||||| |||||
 TGT TGGTCTCGA TTGTT
 _ GAGA_
 GAM2405 LOC202559 3' TTGTTTTTCATTGTTGTGTGT 90689 CGG T
 GCACAC GGC ATGAGAAGCAA
 ||||| ||| |||||
 TGTGTG TTG TACTTTTTGT
 _ T
 GAM2405 LOC203377 5' TTGCTTTTTTGTGTGTTTGCTG 92262 C _ TAT
 TGC GCACA CGGG GC GAGAAGCAA
 ||||| ||||| |||||
 CGTGT GTTT TG TTTTCGTT
 C G TGT
 GAM2405 LOC219654 3' TTGTTTTTTACTATGCTTTGGT 92943 C TA____
 CTGT GCA ACCGGGGC TGAGAAGCAA
 ||| ||||| |||||
 TGT TGGTTTCG ATTTTTTGT
 C TATC
 GAM2405 LOC219738 3' TGCTGGGCCTTGGTGTG 59936 ATGAGA
 CACACCGGGGCT AGCA
 ||||| ||||| |||||

GTGTGGTTCCGG TCGT
 G____
 GAM2405 LOC256126 3' TTGTTTTTCATGGTTCTATAAT 97016 CACC
 GC GCA GGGGCTATGAGAAGCAA
 ||| |||||
 CGT TCTTGGTACTTTTTGTT
 AATA
 GAM2405 LOC256714 3' TTGTTTCTTGTGGCGAAATGTG 98050 A CGGG_ TG
 GC GC CAC GCTA AGAAGCAA
 || ||| |||||
 CG GTG CGGT TCTTTGTT
 _ TAAAG GT
 GAM2405 LOC81558 3' TTGTTTTTTGCAGATCTTGGTG 48682 _ AT
 T ACACCGGGG CT GAGAAGCAA
 ||||| || |||||
 TGTGGTTCT GA TTTTTTGT
 A CG
 GAM2406 SP4 3' AAGTGGATTACAGAGTA 13335 G TAGTG
 TACT TGTAAT CCACTT
 ||| ||||| |||||
 ATGA ACATTA GGTGAA
 G ____
 GAM2406 EDG2 3' AAGTACATTCTAATTACCAGTA 9169 T TGCC_
 TACTG GTAATTAG ACTT
 |||| ||||| |||||
 ATGAC CATTAATC TGAA
 _ TTACA
 GAM2406 EDG2 3' AAGTACATTCTAATTACCAGTA 55129 T TGCC_
 TACTG GTAATTAG ACTT
 |||| ||||| |||||
 ATGAC CATTAATC TGAA
 _ TTACA
 GAM2406 FLJ10540 3' TAAGTGGCCACACACA 36767 AATTA _
 TGTGT GTG CCACTTA
 |||| ||| |||||
 ACACA CAC GGTGAAT
 _ C
 GAM2406 KIAA0555 5' AAGGAGCACCACACAGTA 29540 AATTA CA
 TACTGTGT GTGC CTT
 ||||| ||| |||
 ATGACACA CACG GAA
 C____ AG
 GAM2406 KIAA0976 3' TAAGTAACTGATTACA 30554 GCC
 TGTAAATTAGT ACTTA
 ||||| |||||
 ACATTAGTCA TGAAT
 A____
 GAM2406 MGC11324 3' TTAAATGGTGAGATTACACA 52150 AG C
 TGTGTAATT TGCCA TTAA
 ||||| ||||| |||||

			ACACATTAG GTGGT AATT	
			A_ A	
GAM2406	NAV3	3'	AAGCAACACCAGTTAACATAGT 30449	_ A CCA
	A		TACTGTGT AATT GTG CTT	
			ATGATACA TTGA CAC GAA	
			A C AAC	
GAM2406	POF1B	3'	TAAGTCCACTAAATTATACAGT 46772	_ CC
	A		TACTGTGTAATT AGTG ACTTA	
			ATGACATATTAA TCAC TGAAT	
			A C_	
GAM2407	A1BG	3'	AACTCCTGAGCTCAGGTGATCC 56274	G
	A		TGGATCACCTGAG TCAGGAGTT	
			ACCTAGTGGACTC AGTCCTCAA	
			G	
GAM2407	A1BG	3'	GAACTCTTGGGCTCAAGTGATC 56290	C G
	C		GGATCAC TGAG TCAGGAGTTC	
			CCTAGTG ACTC GGTCTCAAG	
			A G	
GAM2407	ADAMTS4	3'	GAACTCCTGACCTCAGGTAATC 18758	C
			GAT ACCTGAGGTCAGGAGTTC	
			CTA TGGACTCCAGTCCTCAAG	
			A	
GAM2407	ADAMTS4	3'	GAACTCCTGACCTTAGGTGATC 18759	
	CA		TGGATCACCTGAGGTCAGGAGTTC	
			ACCTAGTGGATTCCAGTCCTCAAG	
GAM2407	AGL	5'	GAACTCCTGGACTCAAGCAACC 7213	ATCACC GT
	C		GG TGAG CAGGAGTTC	
			CC ACTC GTCCTCAAG	
			CAACGA AG	
GAM2407	ALDH1B1	3'	GAACTCCTGACCTCAGGTGATC 7324	
	CA		TGGATCACCTGAGGTCAGGAGTTC	
			ACCTAGTGGACTCCAGTCCTCAAG	
GAM2407	APAF1	3'	GAACTCTTGGCCTCAAGTAATC 25972	C C
	C		GGAT AC TGAGGTCAGGAGTTC	
			CCTA TG ACTCCGGTTCTCAAG	
			A A	
GAM2407	APM1	3'	AACTCCTGACTTTGTGATCCA 17749	CT
			TGGATCAC GAGGTCAGGAGTT	

ACCTAGTG TTTCAGTCCTCAA

GAM2407 APM1 3' GAACTCCTGGCCTAGGTGATCC 17781 G
A TGGATCACCT AGGTCAGGAGTTC
||||||| |||||||||
ACCTAGTGGA TCCGGTCCTCAAG

GAM2407 AQP6 3' TCCTGACCCCAGATGCCCA 55016 AT C A
TGG CA CTG GGT CAGGA
||| || ||| |||||||
ACC GT GAC CCAGTCCT
C_ A C

GAM2407 AQP6 3' TCCTGACCCCAGATGCCCA 55017 AT C A
TGG CA CTG GGT CAGGA
||| || ||| |||||||
ACC GT GAC CCAGTCCT
C_ A C

GAM2407 ARCN1 3' GAACTCCTGAGCTCAGGCAATC 9752 CA G
C GGAT CCTGAG TCAGGAGTTC
|||| ||||| |||||||
CCTA G GACTC AGTCCTCAAG
AC G

GAM2407 ARSF 5' GAACTCCCGACCTCAAGTGATC 65208 C A
C GGATCAC TGAGGTC GGAGTTC
||||||| ||||| |||||||
CCTAGTG ACTCCAG CCTCAAG
A C

GAM2407 ATP1B2 3' GAACTCCCGACCTCAGGTGATC 9834 A
CA TGGATCACCTGAGGTC GGAGTTC
||||||| ||||| |||||||
ACCTAGTGGACTCCAG CCTCAAG
C

GAM2407 ATP6V1A1 3' GAACTCCAGACCTCAGGTGATC 9868 A
C GGATCACCTGAGGTC GGAGTTC
||||||| ||||| |||||||
CCTAGTGGACTCCAG CCTCAAG
A

GAM2407 ATP7A 3' AACTCCTAACCTCAGGTGATCC 5307 C
A TGGATCACCTGAGGT AGGAGTT
||||||| ||||| |||||||
ACCTAGTGGACTCCA TCCTCAA
A

GAM2407 AXL 3' AACTCCTGACCTCAAGTGATCT 41868 C
GGATCAC TGAGGTCAGGAGTT
||||| |||||||||
TCTAGTG ACTCCAGTCCTCAA
A

GAM2407 B4GALT5 3' GAACTCCTGGACTCAAGCAATC 17687 CACC GT
C GGAT TGAG CAGGAGTTC
||| ||| |||||||

			CCTA ACTC GTCCTCAAG		
			ACGA AG		
GAM2407	C7	3'	AACTCCTGACCTCAGGTAATCC 6973	C	
			GGAT ACCTGAGGTCAGGAGTT		
			CCTA TGGACTCCAGTCCTCAA		
			A		
GAM2407	CASP10	3'	AACTCCTGGGCTCAAGCGATCC 53192	ACC	G
			GGATC TGAG TCAGGAGTT		
			CCTAG ACTC GGTCCTCAA		
			CGA G		
GAM2407	CASP10	3'	AACTCCTGGGCTCAAGCGATCC 53233	ACC	G
			GGATC TGAG TCAGGAGTT		
			CCTAG ACTC GGTCCTCAA		
			CGA G		
GAM2407	CBFA2T2	3'	AACCCCGGACCTCAGGTGATCC 18696	A	A
			GGATCACCTGAGGTC GG GTT		
			CCTAGTGGACTCCAG CC CAA		
			G C		
GAM2407	CBFB	3'	GAACTCCTGGCATCAAGCGATC 10037	ACC	G
	C		GGATC TGA GTCAGGAGTTC		
			CCTAG ACT CGGTCCTCAAG		
			CGA A		
GAM2407	CBFB	3'	GAACTCCTGGCATCAAGCGATC 10038	ACC	G
	C		GGATC TGA GTCAGGAGTTC		
			CCTAG ACT CGGTCCTCAAG		
			CGA A		
GAM2407	CCNF	3'	GAACTCATGACCTCAAGTGATC 10074	C	G
	C		GGATCAC TGAGGTCA GAGTTC		
			CCTAGTG ACTCCAGT CTCAAG		
			A A		
GAM2407	CDH1	3'	AACTCCTGGCCTCAAGCAATCC 16395	CACC	
			GGAT TGAGGTCAGGAGTT		
			CCTA ACTCCGGTCCTCAA		
			ACGA		
GAM2407	CDH1	3'	AACTCCTGGGCTCAAGTGATCC 16396	C	G
			GGATCAC TGAG TCAGGAGTT		
			CCTAGTG ACTC GGTCCTCAA		
			A G		
GAM2407	CHRN4	3'	GAACTCCTGACCTCAGATGACC 7449	A	C
	CA		TGG TCA CTGAGGTCAGGAGTTC		

			ACC AGT GACTCCAGTCCTCAAG	
			C A	
GAM2407	CLECSF12	3'	GAACTCCTGACCTCAAGTGATC 77211	C
	T		GGATCAC TGAGGTCAGGAGTTC	
			TCTAGTG ACTCCAGTCCTCAAG	
			A	
GAM2407	CNP	3'	GAACTCCTGGGCTCAAGCAATC 53621	CACC G
	C		GGAT TGAG TCAGGAGTTC	
			CCTA ACTC GGCCTCAAG	
			ACGA G	
GAM2407	COX15	3'	GAACTCCTGACCTCAGGTAATC 55284	C
	C		GGAT ACCTGAGGTCAGGAGTTC	
			CCTA TGGACTCCAGTCCTCAAG	
			A	
GAM2407	CRTAP	3'	GAACTCTTGACTTCAGATGATC 22078	C
	CA		TGGATCA CTGAGGTCAGGAGTTC	
			ACCTAGT GACTTCAGTTCTCAAG	
			A	
GAM2407	CXCL16	3'	GAACTCCTGAGTCAAGTGATCC 42167	C GG
			GGATCAC TGA TCAGGAGTTC	
			CCTAGTG ACT AGTCCTCAAG	
			A G_	
GAM2407	CYP1A2	3'	AACTCCTGACCTCAAGTGATCT 69653	C
			GGATCAC TGAGGTCAGGAGTT	
			TCTAGTG ACTCCAGTCCTCAA	
			A	
GAM2407	CYP1A2	3'	GAACTCCTGACCCCAAGTTATC 7514	C C A
	CA		TGGAT AC TG GGTGAGGAGTTC	
			ACCTA TG AC CCAGTCCTCAAG	
			T A C	
GAM2407	CYP2B6	3'	CCTGGCCTCAGGTGATCCA 7558	
			TGGATCACCTGAGGTCAGG	
			ACCTAGTGGACTCCGGTCC	
GAM2407	CYP2B6	3'	GAACTCCTGAACTCAAGTGATT 7561	C G
	CA		TGGATCAC TGAG TCAGGAGTTC	
			ACTTAGTG ACTC AGTCCTCAAG	
			A A	
GAM2407	CYP4F3	3'	GAACTCCTAACCTCAGGTGATC 8007	C
	CA		TGGATCACCTGAGGT AGGAGTTC	

			ACCTAGTGGACTCCA TCCTCAAG		
			A		
GAM2407	DFFB	3'	AACTCCTGACCTCAGGTGATCC 88746		
			GGATCACCTGAGGTCAGGAGTT		
			CCTAGTGGACTCCAGTCCTCAA		
GAM2407	DFFB	3'	GAACCTCCTGACCTCAGGTGATC 88770		
	T		GGATCACCTGAGGTCAGGAGTTC		
			TCTAGTGGACTCCAGTCCTCAAG		
GAM2407	DIAPH2	3'	GAACCTCCTAGCCTCAAGCAATC 24592	CACC	TC
	CA		TGGAT TGAGG AGGAGTTC		
			ACCTA ACTCC TCCTCAAG		
			ACGA GA		
GAM2407	DISC1	3'	AACTCCTGACCTCAGGCGATCC 38494	A	
	A		TGGATC CCTGAGGTCAGGAGTT		
			ACCTAG GGA CTCCAGTCCTCAA		
			C		
GAM2407	DSCR3	3'	GAACCTCCTAGACTCAAGTGATC 21312	C	G _
	C		GGATCAC TGAG TC AGGAGTTC		
			CCTAGTG ACTC AG TCCTCAAG		
			A _ A		
GAM2407	DSCR3	3'	GAACCTCCTGACCTCGTGACCCA 21313	A	CT
			TGG TCAC GAGGTCAGGAGTTC		
			ACC AGTG CTCCAGTCCTCAAG		
			C _		
GAM2407	EPB72	3'	GAACCTCCTAACCTCAGGTGATC 15873		C
	CA		TGGATCACCTGAGGT AGGAGTTC		
			ACCTAGTGGACTCCA TCCTCAAG		
			A		
GAM2407	F2RL2	3'	GAACCTCCTGACCTCAAGTGATC 15896		C
	T		GGATCAC TGAGGTCAGGAGTTC		
			TCTAGTG ACTCCAGTCCTCAAG		
			A		
GAM2407	F3	3'	GAATTCCTGACCTCAGTTGATC 67677		C
	CA		TGGATCA CTGAGGTCAGGAGTTC		
			ACCTAGT GACTCCAGTCCTTAAG		
			T		
GAM2407	FABP2	3'	GAACCCCTGGCCTCAAGCAATC 5535	CACC	A
	C		GGAT TGAGGTCAGG GTTC		

			CCTA	ACTCCGGTCC	CAAG	
			ACGA	C		
GAM2407	FCAR	3'	GA	ACTCCTGACCTCAGGTGATC	10587	
	CA			TGGATCACCTGAGGTCAGGAGTTC		
				ACCTAGTGGACTCCAGTCCTCAAG		
GAM2407	FCAR	3'	GA	ACTCCCGACCTCAGGTGATC	56571	A
	CA			TGGATCACCTGAGGTC	GGAGTTC	
				ACCTAGTGGACTCCAG	CCTCAAG	
				C		
GAM2407	G6PC	3'	GA	ACTCCTGACCTCAAGTGATC	5660	C
	CA			TGGATCAC	TGAGGTCAGGAGTTC	
				ACCTAGTG	ACTCCAGTCCTCAAG	
				A		
GAM2407	GNE	3'	GA	ACTCCTGACCTCAGGTGATC	19669	
	C			GGATCACCTGAGGTCAGGAGTTC		
				CCTAGTGGACTCCAGTCCTCAAG		
GAM2407	GPR81	3'	CCTGACCTCAGGTGATCC	51745		
				GGATCACCTGAGGTCAGG		
				CCTAGTGGACTCCAGTCC		
GAM2407	GRAF	3'	GA	ACTCCTGACCTCAAGTGATC	31236	C
	T			GGATCAC	TGAGGTCAGGAGTTC	
				TCTAGTG	ACTCCAGTCCTCAAG	
				A		
GAM2407	HCS	3'	AA	CTCCTGAGCTCAAGCAATCC	38956	CACC G
				GGAT	TGAG TCAGGAGTT	
				CCTA	ACTC AGTCCTCAA	
				ACGA	G	
GAM2407	HLCS	5'	GA	ACTCCTGACCTCGTGATCCA	6412	CT
				TGGATCAC	GAGGTCAGGAGTTC	
				ACCTAGTG	CTCCAGTCCTCAAG	
				—		
GAM2407	IFNAR2	3'	GA	ACTCCTGACCTCAAGTGATC	7900	C
	T			GGATCAC	TGAGGTCAGGAGTTC	
				TCTAGTG	ACTCCAGTCCTCAAG	
				A		
GAM2407	IL11	3'	GA	ACTCCTGACCTCAGGTGATC	7183	
	C			GGATCACCTGAGGTCAGGAGTTC		

CCTAGTGGACTCCAGTCCTCAAG

GAM2407 JAK3 3' GAACTCCTAACCTCAAGTGATC 5830 C C
C GGATCAC TGAGGT AGGAGTTC

||||| ||||| |||||
CCTAGTG ACTCCA TCCTCAAG
A A

GAM2407 JRK 3' GAACTCTTGGCCTCAAGCGATC 87826 ACC
C GGATC TGAGGTCAGGAGTTC

|||| |||||
CCTAG ACTCCGGTTCTCAAG
CGA

GAM2407 LNK 3' GAATGTCTGACCTCAGGTGATC 19644 GA
CA TGGATCACCTGAGGTCAG GTTC

||||| ||||| ||||
ACCTAGTGGACTCCAGTC TAAG
TG

GAM2407 LZTS1 3' AACTTGTGGCCTCAAGCAATCC 41019 CACC G
A TGGAT TGAGGTCA GAGTT

|||| ||||| ||||
ACCTA ACTCCGGT TTCAA
ACGA G

GAM2407 MAK 3' AACTCCTGACCTCAGGTGATCC 20933
A TGGATCACCTGAGGTCAGGAGTT

|||||
ACCTAGTGGACTCCAGTCCTCAA

GAM2407 MEFV 3' AACTCCTGACCTCAGGTGATGC 5917 G
A TG ATCACCTGAGGTCAGGAGTT

|| |||||
AC TAGTGGACTCCAGTCCTCAA
G

GAM2407 MEFV 3' GAACTCCTGACCTCAGGTGATC 5937
CA TGGATCACCTGAGGTCAGGAGTTC

|||||
ACCTAGTGGACTCCAGTCCTCAAG

GAM2407 MHC2TA 3' GAACTCTTGACCTCGGGTGATC 5983
CA TGGATCACCTGAGGTCAGGAGTTC

|||||
ACCTAGTGGGCTCCAGTTCTCAAG

GAM2407 MICB 3' AACTCCTGACCTCAGGTGATCT 21016
GGATCACCTGAGGTCAGGAGTT

|||||
TCTAGTGGACTCCAGTCCTCAA

GAM2407 MLANA 3' AACTCCTGACCTCAGGTGATCT 19752
GGATCACCTGAGGTCAGGAGTT

|||||

TCTAGTGGACTCCAGTCCTCAA

GAM2407 MPL 3' GAACTCCTAACCTCGGGTGATC 19354 C
CA TGGATCACCTGAGGT AGGAGTTC

|||||
ACCTAGTGGGCTCCA TCCTCAAG

A

GAM2407 MRPL49 3' AACTCCTGACTCGAAGTGATCC 70154 CTGA
GGATCAC GGTCAGGAGTT

|||||
CCTAGTG TCAGTCCTCAA

AAGC

GAM2407 MYCL2 3' CCTGACCTAGGTGATCCA 19373 G
TGGATCACCT AGGTCAGG

|||||
ACCTAGTGGA TCCAGTCC

GAM2407 NCOA6 5' AACTCCTGACCTCAAGTGATCC 26816 C
A TGGATCAC TGAGGTCAGGAGTT

|||||
ACCTAGTG ACTCCAGTCCTCAA

A

GAM2407 NCOA6 5' GAACTCCTGAGCTCAAGCAGTC 26835 CACC G
CA TGGAT TGAG TCAGGAGTTC

|||||
ACCTG ACTC AGTCCTCAAG

ACGA G

GAM2407 NDRG3 3' AACTCCTGACCTCAGGTGATCC 42759
A TGGATCACCTGAGGTCAGGAGTT

|||||
ACCTAGTGGACTCCAGTCCTCAA

GAM2407 NQO1 3' AACTCCTGACCTCAGGTGATCC 8037
GGATCACCTGAGGTCAGGAGTT

|||||
CCTAGTGGACTCCAGTCCTCAA

GAM2407 NT5C2 5' CCTGACGTCAAGTGATCCA 25262 C G
TGGATCAC TGA GTCAGG

|||||
ACCTAGTG ACT CAGTCC

A G

GAM2407 PDE6B 3' GAACTCCTGACCTCAGGTGATC 6076
GATCACCTGAGGTCAGGAGTTC

|||||
CTAGTGGACTCCAGTCCTCAAG

GAM2407 PER2 3' GAACTCCTGACCTCAAGCGATC 43351 ACC
CA TGGATC TGAGGTCAGGAGTTC

|||||

			ACCTAG ACTCCAGTCCTCAAG		
			CGA		
GAM2407	PIK3CD	3'	GAACCTCCTGACCTCAGGTGATC 18491		
	CA		TGGATCACCTGAGGTCAGGAGTTC		
			ACCTAGTGGACTCCAGTCCTCAAG		
GAM2407	PMCHL1	3'	GAACCTCCTGACCTCGTGATCCA 49916	CT	
			TGGATCAC GAGGTCAGGAGTTC		
			ACCTAGTG CTCCAGTCCTCAAG		
GAM2407	PPEF2	3'	GAACCTCCCAACCTCAGGTGATC 21775	CA	
	CA		TGGATCACCTGAGGT GGAGTTC		
			ACCTAGTGGACTCCA CCTCAAG		
			AC		
GAM2407	PPID	3'	GAACCTCCTGACCTTGTGATCCA 88825	CT	
			TGGATCAC GAGGTCAGGAGTTC		
			ACCTAGTG TTCCAGTCCTCAAG		
GAM2407	PRKR	3'	AACTCCTGACCTCAAGTAATCC 12334	C C	
	A		TGGAT AC TGAGGTCAGGAGTT		
			ACCTA TG ACTCCAGTCCTCAA		
			A A		
GAM2407	PRKWNK3	3'	AACTCCTAACCTTGTGATCC 62221	CT C	
			GGATCAC GAGGT AGGAGTT		
			CCTAGTG TTCCA TCCTCAA		
			A		
GAM2407	PTGES	3'	GAACCTCCTGGCCTCAAGTGATC 18060	C	
	CA		TGGATCAC TGAGGTCAGGAGTTC		
			ACCTAGTG ACTCCGGTCCTCAAG		
			A		
GAM2407	RBBP9	3'	GAACCTCCTGGCCTCAAGTGATC 70690	C	
	CA		TGGATCAC TGAGGTCAGGAGTTC		
			ACCTAGTG ACTCCGGTCCTCAAG		
			A		
GAM2407	RGS9	5'	AACTCCTGGGCTCAAGCGATCC 15166	ACC G	
			GGATC TGAG TCAGGAGTT		
			CCTAG ACTC GGTCTCAA		
			CGA G		
GAM2407	RHD	3'	AACTCCTGACCTCAAGTGATCT 32797	C	
			GGATCAC TGAGGTCAGGAGTT		

			TCTAGTG ACTCCAGTCCTCAA	
			A	
GAM2407	RHD	3'	AACTCCTGACCTCAAGTGATCT 32798	C
			GGATCAC TGAGGTCAGGAGTT	
			TCTAGTG ACTCCAGTCCTCAA	
			A	
GAM2407	RP2	3'	GAACCTCCTGACCTCAGGTGATC 23602	
	C		GGATCACCTGAGGTCAGGAGTTC	
			CCTAGTGGACTCCAGTCCTCAAG	
GAM2407	RPH3AL	3'	GAACCTCCTGGTCTCAAGTGATC 23733	C GT
	C		GGATCAC TGAG CAGGAGTTC	
			CCTAGTG ACTC GTCCTCAAG	
			A TG	
GAM2407	SAS	3'	GAACCTCCTGACCTCAGGTGATC 21100	
	CA		TGGATCACCTGAGGTCAGGAGTTC	
			ACCTAGTGGACTCCAGTCCTCAAG	
GAM2407	SCML2	3'	AACTCCTGACCTCAGGTGATCC 21417	
			GGATCACCTGAGGTCAGGAGTT	
			CCTAGTGGACTCCAGTCCTCAA	
GAM2407	SEDL	3'	AACTCCTGACCTCAGTTGATCC 28064	C
	A		TGGATCA CTGAGGTCAGGAGTT	
			ACCTAGT GACTCCAGTCCTCAA	
			T	
GAM2407	SEDL	3'	GAACCTCCTGACCTCGTGATCCA 28098	CT
			TGGATCAC GAGGTCAGGAGTTC	
			ACCTAGTG CTCCAGTCCTCAAG	
GAM2407	SEPN1	3'	GAACCTCTGACCTCAGGTGATC 66971	
	CA		TGGATCACCTGAGGTCAGGAGTTC	
			ACCTAGTGGACTCCAGTCTTCAAG	
GAM2407	SERPINB9	3'	GAACCTCCTGGCCTCAAGCAATC 16020	CACC
	C		GGAT TGAGGTCAGGAGTTC	
			CCTA ACTCCGGTCCTCAAG	
			ACGA	
GAM2407	SH3BP2	3'	GAACCTCCTGACCTCAACTGATC 13071	CC
	C		GGATCA TGAGGTCAGGAGTTC	

			CCTAGT ACTCCAGTCCTCAAG	
			CA	
GAM2407	SH3BP2	3'	GAATCCTGACCTCAGGTGATC 13072	
	T		GGATCACCTGAGGTCAGGAGTTC	
			TCTAGTGGACTCCAGTCCTCAAG	
GAM2407	SHOX	3'	AACTCCTGGGCTCAAGCAATCC 6556	CACC G
			GGAT TGAG TCAGGAGTT	
			CCTA ACTC GGCCTCAA	
			ACGA G	
GAM2407	SHOX	3'	GAATCCTGACCTCAGGTGATC 6573	
	CA		TGGATCACCTGAGGTCAGGAGTTC	
			ACCTAGTGGACTCCAGTCCTCAAG	
GAM2407	SHOX	3'	GAATCCTGACCTCAGGTGATC 6574	
	T		GGATCACCTGAGGTCAGGAGTTC	
			TCTAGTGGACTCCAGTCCTCAAG	
GAM2407	SIL	3'	AACTCCCGACCTCAGGTGATCC 13147	A
			GGATCACCTGAGGTC GGAGTT	
			CCTAGTGGACTCCAG CCTCAA	
			C	
GAM2407	SIL	5'	TCCTGACTTCAGGTGATCCA 13164	
			TGGATCACCTGAGGTCAGGA	
			ACCTAGTGGACTTCAGTCCT	
GAM2407	SLA2	3'	GAATCCTGACCTCAGGTGATC 50889	
	CA		TGGATCACCTGAGGTCAGGAGTTC	
			ACCTAGTGGACTCCAGTCCTCAAG	
GAM2407	SLC14A2	5'	GAATTCTGACGTCAAGTGATC 24117	C G
	CA		TGGATCAC TGA GTCAGGAGTTC	
			ACCTAGTG ACT CAGTCTTCAAG	
			A G	
GAM2407	SLC17A5	3'	GAATCCTGGCTTCAAGCGATC 25831	ACC
	C		GGATC TGAGGTCAGGAGTTC	
			CCTAG ACTTCGGTCCTCAAG	
			CGA	
GAM2407	SLC3A2	5'	GAATCCTTGGCCTCAGGTGATC 11520	
	C		GGATCACCTGAGGTCAGGAGTTC	

CCTAGTGGACTCCGGTTCTCAAG

GAM2407 SMAC 5' GAACTCCTGGGCTCAAGTGATC 57999 C G
C GGATCAC TGAG TCAGGAGTTC

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CCTAGTG ACTC GGTCCTCAAG
A G

GAM2407 SMAC 5' GAATTCCTGACCTCAAGTGATC 58000 C
CA TGGATCAC TGAGGTCAGGAGTTC

||||| |||||
ACCTAGTG ACTCCAGTCCTTAAG
A

GAM2407 SNX15 3' GAACTCCTGACCTCAAGTGATC 74119 C
CA TGGATCAC TGAGGTCAGGAGTTC

||||| |||||
ACCTAGTG ACTCCAGTCCTCAAG
A

GAM2407 SPN 3' AACTCCTGACCTCAGGTGATCT 13361
A TGGATCACCTGAGGTCAGGAGTT

|||||
ATCTAGTGGACTCCAGTCCTCAA

GAM2407 SULT2B1 5' AACTCCTGACCTCAGGTGATCC 17218
A TGGATCACCTGAGGTCAGGAGTT

|||||
ACCTAGTGGACTCCAGTCCTCAA

GAM2407 TAF11 3' GAACTCCTGGGCTTAAGTGACC 20120 A C G
C GG TCAC TGAG TCAGGAGTTC

|| ||| ||| |||||
CC AGTG ATTG GGTCCTCAAG
C A G

GAM2407 TAT 3' AACTCCTGACCTCAGGCAATCT 6243 CA
GGAT CCTGAGGTCAGGAGTT

||| |||||
TCTA GGA CTCCAGTCCTCAA
AC

GAM2407 TBXA2R 3' GAACTCCTGACCTCAGGTGATT 8357
CA TGGATCACCTGAGGTCAGGAGTTC

|||||
ACTTAGTGGACTCCAGTCCTCAAG

GAM2407 TES 3' AACTCCTGACCTCAGATGATCC 72454 C
GGATCA CTGAGGTCAGGAGTT

|||||
CCTAGT GACTCCAGTCCTCAA
A

GAM2407 TMPRSS3 3' AACCCCTGACCTCAAATGAT 44008 CC A
ATCA TGAGGTCAGG GTT

||| ||||| |||

			TAGT ACTCCAGTCC CAA		
			AA C		
GAM2407	TNFRSF10B	3'	CCTGACCTCAGGTGATCCA 15222		
			TGGATCACCTGAGGTCAGG		
			ACCTAGTGGACTCCAGTCC		
GAM2407	TNFRSF10B	3'	GAACCTCCTGACCTCAGGTGATC 15226		
		CA	TGGATCACCTGAGGTCAGGAGTTC		
			ACCTAGTGGACTCCAGTCCTCAAG		
GAM2407	TNFSF9	3'	GAACCTCCTGGACTTAGACGATC 15097	AC	GT
		C	GGATC CTGAG CAGGAGTTC		
			CCTAG GATTC GTCCTCAAG		
			CA AG		
GAM2407	TP53	3'	AACTCCTGGGCTCAGGCGATCC 6789	A	G
		A	TGGATC CCTGAG TCAGGAGTT		
			ACCTAG GGACTC GGTCTCAA		
			C G		
GAM2407	TPMT	3'	GAGCTCCTGACCTCAGGTGATC 6312		
		TA	TGGATCACCTGAGGTCAGGAGTTC		
			ATCTAGTGGACTCCAGTCCTCGAG		
GAM2407	TRAF5	3'	AACTCCTGACCTCAAGTGATCT 17262	C	
			GGATCAC TGAGGTCAGGAGTT		
			TCTAGTG ACTCCAGTCCTCAA		
			A		
GAM2407	TRPM6	3'	AACTCCTGACCTCAGATGATCC 35017	C	
		A	TGGATCA CTGAGGTCAGGAGTT		
			ACCTAGT GACTCCAGTCCTCAA		
			A		
GAM2407	TRPV1	3'	GAACCTCCTGACCTCAGGTGATC 55672		
		C	GGATCACCTGAGGTCAGGAGTTC		
			CCTAGTGGACTCCAGTCCTCAAG		
GAM2407	TUFT1	3'	GAATTCCTGACCTCAGGTGATC 39674		
		CA	TGGATCACCTGAGGTCAGGAGTTC		
			ACCTAGTGGACTCCAGTCCTTAAG		
GAM2407	VENTX2	3'	AACTCCTGACCCTGTGATCC 27849	CTGA	
			GGATCAC GGTCAGGAGTT		

			CCTAGTG CCAGTCCTCAA	
			TC__	
GAM2407	VHL	3'	AACTCCTGACCTCAGGTGATCC 6812	
			GGATCACCTGAGGTCAGGAGTT	
			CCTAGTGGACTCCAGTCCTCAA	
GAM2407	WHSC1	3'	GAACCTCCTGACCTCGTGATCCA 56706	CT
			TGGATCAC GAGGTCAGGAGTTC	
			ACCTAGTG CTCCAGTCCTCAAG	
GAM2407	XRCC2	3'	GAACCTCCTGACCTCAAGTGATC 19500	C
	CA		TGGATCAC TGAGGTCAGGAGTTC	
			ACCTAGTG ACTCCAGTCCTCAAG	
			A	
GAM2407	ZNF133	5'	GAACCTGCTGACCTCAGGTGATC 14296	G
	CA		TGGATCACCTGAGGTCAG AGTTC	
			ACCTAGTGGACTCCAGTC TCAAG	
			G	
GAM2407	ZNF157	3'	AACTCCTGACCTCAGGTGATCC 14318	
	A		TGGATCACCTGAGGTCAGGAGTT	
			ACCTAGTGGACTCCAGTCCTCAA	
GAM2407	ZNF264	3'	AACTCCTGACCTTGTGATCC 14177	CT
			GGATCAC GAGGTCAGGAGTT	
			CCTAGTG TTCCAGTCCTCAA	
GAM2407	AAK1	3'	GAACCTCCTGACCTCAGGTGATC 30522	
	C		GGATCACCTGAGGTCAGGAGTTC	
			CCTAGTGGACTCCAGTCCTCAAG	
GAM2407	AP3S2	3'	GAACCTCCTGGACCTCAAGTGAT 20651	C
	CTA		TGGATCAC TGAGGTC AGGAGTTC	
			ATCTAGTG ACTCCAG TCCTCAAG	
			A G	
GAM2407	ARHF	3'	GAACCTCCTGACCTCGTGATCCA 39268	CT
			TGGATCAC GAGGTCAGGAGTTC	
			ACCTAGTG CTCCAGTCCTCAAG	
GAM2407	ARHGAP5	5'	GAACCTCCCAACCTCAGGTGATC 77601	CA
	C		GGATCACCTGAGGT GGAGTTC	

			CCTAGTGGACTCCA	CCTCAAG	
			AC		
GAM2407	ASB16	3'	CTGACCTCAGGTGATCCA	55982	
			TGGATCACCTGAGGTCAG		
			ACCTAGTGGACTCCAGTC		
GAM2407	ASE-1	3'	GAACCTCCTGACCTCGTGATCCA	24979	CT
			TGGATCAC	GAGGTCAGGAGTTC	
			ACCTAGTG	CTCCAGTCCTCAAG	
GAM2407	ATP1B4	3'	GAACCTCCTGACCTCAAGTGATC	24843	C
	C		GGATCAC	TGAGGTCAGGAGTTC	
			CCTAGTG	ACTCCAGTCCTCAAG	
			A		
GAM2407	BA108L7.2	3'	GAACCTCCTGACCTCAGGTGATC	49074	
	CA		TGGATCACCTGAGGTCAGGAGTTC		
			ACCTAGTGGACTCCAGTCCTCAAG		
GAM2407	C13orf1	3'	AACTCCTGACCTCATGATCCA	40343	CC
			TGGATCA	TGAGGTCAGGAGTT	
			ACCTAGT	ACTCCAGTCCTCAA	
GAM2407	C1QTNF6	3'	GAACCTCCTGACTTCAGGTGACC	49992	A
	CA		TGG	TCACCTGAGGTCAGGAGTTC	
			ACC	AGTGGACTTCAGTCCTCAAG	
			C		
GAM2407	C20orf142	3'	AACTCCTGACCGCAGGTGATCC	75266	A
	A		TGGATCACCTG	GGTCAGGAGTT	
			ACCTAGTGGAC	CCAGTCCTCAA	
			G		
GAM2407	C21orf25	3'	GAACCTCCTGACCTCAGGTGATC	64293	
	CA		TGGATCACCTGAGGTCAGGAGTTC		
			ACCTAGTGGACTCCAGTCCTCAAG		
GAM2407	C3F	3'	GAACCTCCTGACCGCAAGTGATC	20476	C A
	CA		TGGATCAC	TG GGTCAGGAGTTC	
			ACCTAGTG	AC CCAGTCCTCAAG	
			A	G	
GAM2407	C6orf33	3'	GAACCTCCTGAACCTCAAGTGATC	56715	C G
	C		GGATCAC	TGAG TCAGGAGTTC	

			CCTAGTG ACTC AGTCCTCAAG	
			A A	
GAM2407	C9orf14	5'	GAACTCCTGACCTGAAGTGATG 87957	G CTG
	CA		TG ATCAC AGGTCAGGAGTTC	
			AC TAGTG TCCAGTCCTCAAG	
			G AAG	
GAM2407	C9orf9	3'	GAACTCCTGACCTCAACTGGTC 39019	CC
	CA		TGGATCA TGAGGTCAGGAGTTC	
			ACCTGGT ACTCCAGTCCTCAAG	
			CA	
GAM2407	CARD6	3'	GAACTCCCGACCTCAGGTGATC 51841	A
	C		GGATCACCTGAGGTC GGAGTTC	
			CCTAGTGGACTCCAG CCTCAAG	
			C	
GAM2407	CDC14B	3'	GAACTCCTGACCTCAAGTGATC 14776	C
	T		GGATCAC TGAGGTCAGGAGTTC	
			TCTAGTG ACTCCAGTCCTCAAG	
			A	
GAM2407	CENPH	3'	GAACTCCTGAGCTCAGGCAGTC 43565	CA G
	CA		TGGAT CCTGAG TCAGGAGTTC	
			ACCTG GGA CTC AGTCCTCAAG	
			AC G	
GAM2407	CIP29	3'	GAACTCCTGAGCTCAGGTGATC 51376	G
	CA		TGGATCACCTGAG TCAGGAGTTC	
			ACCTAGTGGACTC AGTCCTCAAG	
			G	
GAM2407	COLEC12	3'	AACTTCTGGCCTCAAGTGATCC 48603	C
	A		TGGATCAC TGAGGTCAGGAGTT	
			ACCTAGTG ACTCCGGTCTTCAA	
			A	
GAM2407	COLEC12	3'	GAACTCCTGGCCTCAAGCAACC 56102	ATCACC
	C		GG TGAGGTCAGGAGTTC	
			CC ACTCCGGTCCTCAAG	
			CAACGA	
GAM2407	CPSF2	3'	AACTCCCGACCTCAGGTGATCC 62252	A
			GGATCACCTGAGGTC GGAGTT	
			CCTAGTGGACTCCAG CCTCAA	
			C	
GAM2407	CPSF2	3'	AACTCCTGACCTCAAGCGATCC 62253	ACC
	A		TGGATC TGAGGTCAGGAGTT	

		ACCTAG ACTCCAGTCCTCAA	
		CGA	
GAM2407	DBR1	3' AACTCCTGACCTCAGGCGATCC 33054	A
	A	TGGATC CCTGAGGTCAGGAGTT	
		ACCTAG GGA	
		CTCCAGTCCTCAA	
		C	
GAM2407	DCO	3' AACTCCTGGCCTCAAGTGATCC 50503	C
	HM	GGATCAC TGAGGTCAGGAGTT	
		CCTAGTG ACTCCGGTCCTCAA	
		A	
GAM2407	DKFZp434A2417	3' AACTCCCAACCTCAGGTGATCT 66671	CA
		GGATCACCTGAGGT GGAGTT	
		TCTAGTGGACTCCA CCTCAA	
		AC	
GAM2407	DKFZP434B044	3' GAACTCCTTACCTCAGGTGATC 49717	C
	CA	TGGATCACCTGAGGT AGGAGTTC	
		ACCTAGTGGACTCCA TCCTCAAG	
		T	
GAM2407	DKFZP434D146	3' AACTCCTGCCCTCAAGTGATCC 32128	C T
	A	TGGATCAC TGAGG CAGGAGTT	
		ACCTAGTG ACTCC GTCCTCAA	
		A C	
GAM2407	DKFZP434J037	3' AACTCCCGACCTCAGGTGATCC 48933	A
	A	TGGATCACCTGAGGTC GGAGTT	
		ACCTAGTGGACTCCAG CCTCAA	
		C	
GAM2407	DKFZp547H025	3' AACTCTTGACTTCAAGTGATCC 39762	C
	A	TGGATCAC TGAGGTCAGGAGTT	
		ACCTAGTG ACTTCAGTTCTCAA	
		A	
GAM2407	DKFZP564G092	5' GAACTCCTGACCTCAAGTAATC 32159	C C
	T	GGAT AC TGAGGTCAGGAGTTC	
		TCTA TG ACTCCAGTCCTCAAG	
		A A	
GAM2407	DKFZP564K0322	3' AACTTCTGGCCTCAAGTGATCC 50183	C
		GGATCAC TGAGGTCAGGAGTT	
		CCTAGTG ACTCCGGTCTTCAA	
		A	
GAM2407	DKFZP564O0423	3' AACTCCTGGCCTCAGGCGATCC 93335	A
	A	TGGATC CCTGAGGTCAGGAGTT	

		ACCTAG GGA	CTCCGGTCCTCAA		
		C			
GAM2407	DKFZP564O0523	3'	GAACTCCTGACCTTGTGATACA 50420	G	CT
			TG ATCAC GAGGTCAGGAGTTC		
			AC TAGTG TTCCAGTCCTCAAG		
			A		
GAM2407	DKFZP566I1024	3'	GAACTCCTGGCCTCAAGCGATC 70649	ACC	
		C	GGATC TGAGGTCAGGAGTTC		
			CCTAG ACTCCGGTCCTCAAG		
			CGA		
GAM2407	DKFZp761O0113	5'	GAACTCCCGGACTCGGGTGATC 37892		GT A
		CA	TGGATCACCTGAG C GGAGTTC		
			ACCTAGTGGGCTC G CCTCAAG		
			AG C		
GAM2407	DKFZp762P2111	3'	GAACTCCTGATGTTAGGTGACC 87634	A	G
		C	GG TCACCTGA GTCAGGAGTTC		
			CC AGTGGATT TAGTCCTCAAG		
			C G		
GAM2407	DSCR6	3'	GAACTCCTGACCTCAGGTGATC 39067		
		CA	TGGATCACCTGAGGTCAGGAGTTC		
			ACCTAGTGGACTCCAGTCCTCAAG		
GAM2407	EVI5	3'	AACTTCTGACCTCAGGTGATCC 20187		
		A	TGGATCACCTGAGGTCAGGAGTT		
			ACCTAGTGGACTCCAGTCTTCAA		
GAM2407	EVI5	3'	GAACTCCTAACCTCAAGTGATC 20207	C	C
		CA	TGGATCAC TGAGGT AGGAGTTC		
			ACCTAGTG ACTCCA TCCTCAAG		
			A A		
GAM2407	FBP17	3'	AACTCCTGACCTCAGGTGATCC 73137		
			GGATCACCTGAGGTCAGGAGTT		
			CCTAGTGGACTCCAGTCCTCAA		
GAM2407	FER1L4	3'	GAACCCCTGACCTCAAGTGATC 48121	C	A
		CA	TGGATCAC TGAGGTCAGG GTTC		
			ACCTAGTG ACTCCAGTCC CAAG		
			A C		
GAM2407	FLB6421	3'	GAACTCCTGAGCTCAAGTGATC 39644	C	G
		C	GGATCAC TGAG TCAGGAGTTC		

		CCTAGTG ACTC AGTCCTCAAG	
		A G	
GAM2407	FLJ10232	3' GAACTCCTGACCTCAGGTGATC 36379	
	CA	TGGATCACCTGAGGTCAGGAGTTC	
		ACCTAGTGGACTCCAGTCCTCAAG	
GAM2407	FLJ10298	3' AACTCCTGACCTAGTGATCCA 36448	CTG
		TGGATCAC AGGTCAGGAGTT	
		ACCTAGTG TCCAGTCCTCAA	
		A__	
GAM2407	FLJ10607	3' AACTCCTGAGCTCAAGTGATCC 77618	C G
		GGATCAC TGAG TCAGGAGTT	
		CCTAGTG ACTC AGTCCTCAA	
		A G	
GAM2407	FLJ10713	3' AACTCCTGGACTCAAGTGATC 36992	C GT
		GATCAC TGAG CAGGAGTT	
		CTAGTG ACTC GTCCTCAA	
		A AG	
GAM2407	FLJ10901	3' GAACTCCTGACCTCAAGTGATC 37360	C
	CA	TGGATCAC TGAGGTCAGGAGTTC	
		ACCTAGTG ACTCCAGTCCTCAAG	
		A	
GAM2407	FLJ11186	3' GAACTCCTGGCTACAAGTGATC 37725	C A
	C	GGATCAC TG GGTCAGGAGTTC	
		CCTAGTG AC TCGGTCCTCAAG	
		A A	
GAM2407	FLJ11193	3' AACTCCTGGGCACAAGCAATCC 37742	CAC GAG _
	A	TGGAT CT GTC AGGAGTT	
		ACCTA GA CGG TCCTCAA	
		AC_ ACA G	
GAM2407	FLJ12363	3' AACTCCTGACCTCAGGTGATCT 50623	
		GGATCACCTGAGGTCAGGAGTT	
		TCTAGTGGACTCCAGTCCTCAA	
GAM2407	FLJ12668	3' AACTCCTGACCTCAGGGGATCC 47151	A
	A	TGGATC CCTGAGGTCAGGAGTT	
		ACCTAG GGA CTCCAGTCCTCAA	
		G	
GAM2407	FLJ12687	3' AACTCCTGACCTCAAGTGATCC 46737	C
	A	TGGATCAC TGAGGTCAGGAGTT	

		ACCTAGTG ACTCCAGTCCTCAA	
		A	
GAM2407	FLJ12747 3'	GATTCCCACCTCAGGTGATCC 50666	A
		GGATCACCTGAGGTC GGAGTT	
		CCTAGTGGACTCCAG CCTTAG	
		C	
GAM2407	FLJ12787 3'	AACTCCTGACCTCAAGTGATCT 50685	C
	A	TGGATCAC TGAGGTCAGGAGTT	
		ATCTAGTG ACTCCAGTCCTCAA	
		A	
GAM2407	FLJ12903 3'	GAATCCTGACCTCAGGTGATC 43070	
	T	GGATCACCTGAGGTCAGGAGTTC	
		TCTAGTGGACTCCAGTCCTCAAG	
GAM2407	FLJ12975 3'	GAATCCTGACCTCATGATCC 70194	CC
		GGATCA TGAGGTCAGGAGTTC	
		CCTAGT ACTCCAGTCCTCAAG	
GAM2407	FLJ13072 5'	GAATCCTGACCTCAGGTAATC 91390	C
	C	GGAT ACCTGAGGTCAGGAGTTC	
		CCTA TGGACTCCAGTCCTCAAG	
		A	
GAM2407	FLJ13102 3'	GAATCCTGACCTCAGGTGATT 46532	
	C	GGATCACCTGAGGTCAGGAGTTC	
		CTTAGTGGACTCCAGTCCTCAAG	
GAM2407	FLJ13197 3'	GAATCCTGACCTCAAGTGATC 45179	C
	CA	TGGATCAC TGAGGTCAGGAGTTC	
		ACCTAGTG ACTCCAGTCCTCAAG	
		A	
GAM2407	FLJ13305 5'	GATTCCTGACCTCAAGTGACCC 91712	A C
	A	TGG TCAC TGAGGTCAGGAGTT	
		ACC AGTG ACTCCAGTCCTTAG	
		C A	
GAM2407	FLJ13590 5'	GAATCCTGACCTCAAGTGATC 46206	C
	C	GGATCAC TGAGGTCAGGAGTTC	
		CCTAGTG ACTCCAGTCCTCAAG	
		A	
GAM2407	FLJ13952 3'	CCTGACGTCAGGTGATCCA 46011	G
		TGGATCACCTGA GTCAGG	

			ACCTAGTGGACT CAGTCC		
			G		
GAM2407	FLJ14351	3'	GAACTCCTGAGCTCAAGCAATC 45648	CACC	G
		C	GGAT TGAG TCAGGAGTTC		
			CCTA ACTC AGTCCTCAAG		
			ACGA G		
GAM2407	FLJ14950	3'	GAACTCCTGACCGCAGGTAATC 52788	C	A
		CA	TGGAT ACCTG GGTCAGGAGTTC		
			ACCTA TGGAC CCAGTCCTCAAG		
			A G		
GAM2407	FLJ14957	3'	GAACTCCTGACCTCAGGTGATC 52818		
		CA	TGGATCACCTGAGGTCAGGAGTTC		
			ACCTAGTGGACTCCAGTCCTCAAG		
GAM2407	FLJ20034	3'	AACTCCCGACCTCAGGTGATCC 34827		A
			GGATCACCTGAGGTC GGAGTT		
			CCTAGTGGACTCCAG CCTCAA		
			C		
GAM2407	FLJ20045	3'	GAACTCCTGACCTCGTGATCCA 34884	CT	
			TGGATCAC GAGGTCAGGAGTTC		
			ACCTAGTG CTCCAGTCCTCAAG		
GAM2407	FLJ20344	3'	GAACTCCTGACCTCAAGTGATC 35481		C
		C	GGATCAC TGAGGTCAGGAGTTC		
			CCTAGTG ACTCCAGTCCTCAAG		
			A		
GAM2407	FLJ20452	3'	GAACTCCTGACCTCAGGTGATC 35648		
		CA	TGGATCACCTGAGGTCAGGAGTTC		
			ACCTAGTGGACTCCAGTCCTCAAG		
GAM2407	FLJ20507	3'	GAACTCCTAACCTCAGGTTATC 35739	C	C
		CA	TGGAT ACCTGAGGT AGGAGTTC		
			ACCTA TGGACTCCA TCCTCAAG		
			T A		
GAM2407	FLJ20671	3'	GAACTGCTGGCCTCAAGCGATC 35938	ACC	G
		CA	TGGATC TGAGGTCAG AGTTC		
			ACCTAG ACTCCGGTC TCAAG		
			CGA G		
GAM2407	FLJ20813	3'	AACTCCTGACCTCATGATCCA 36123	CC	
			TGGATCA TGAGGTCAGGAGTT		

ACCTAGT ACTCCAGTCCTCAA

—
GAM2407 FLJ21324 5' AACTCCTGACCTCAAGTGATCT 92837 C
GGATCAC TGAGGTCAGGAGTT
||||| |||||||||
TCTAGTG ACTCCAGTCCTCAA
A

GAM2407 FLJ21459 3' GAACTCCTGACCTCAGGTGATC 44804
C GGATCACCTGAGGTCAGGAGTTC
||||| |||||||||
CCTAGTGGACTCCAGTCCTCAAG

GAM2407 FLJ22002 3' GAACCTCTGACCTCAGGTGATC 46197 GA
CA TGGATCACCTGAGGTCAG GTTC
||||| ||||| |||
ACCTAGTGGACTCCAGTC CAAG
TC

GAM2407 FLJ22329 3' GAACTCCTGACCTCAAGTGATC 45400 C
T GGATCAC TGAGGTCAGGAGTTC
||||| |||||||||
TCTAGTG ACTCCAGTCCTCAAG
A

GAM2407 FLJ22529 3' GAACTCCTGACCTCAAGTGATC 45943 C
T GGATCAC TGAGGTCAGGAGTTC
||||| |||||||||
TCTAGTG ACTCCAGTCCTCAAG
A

GAM2407 FLJ22625 3' AACTGCTGACTTCAGGTGATCC 45584 G
A TGGATCACCTGAGGTCAG AGTT
||||| ||||| |||
ACCTAGTGGACTTCAGTC TCAA
G

GAM2407 FLJ22684 3' AACTCCTGACCTCAGGTGATCC 47459
GGATCACCTGAGGTCAGGAGTT
||||| |||||||||
CCTAGTGGACTCCAGTCCTCAA

GAM2407 FLJ22794 3' GAACTCCTGACCTCGTGATCCA 93246 CT
TGGATCAC GAGGTCAGGAGTTC
||||| |||||||||
ACCTAGTG CTCCAGTCCTCAAG

—
GAM2407 FLJ23416 3' GAACTCCTGAGCTCAAGCAATC 50932 CACC G
C GGAT TGAG TCAGGAGTTC
||| ||| |||||||
CCTA ACTC AGTCCTCAAG
ACGA G

GAM2407 FLJ23556 3' GAACTCCTGACCTCAGGTGA 46440
TCACCTGAGGTCAGGAGTTC
||||| |||||||||

AGTGGACTCCAGTCCTCAAG

GAM2407 FLJ23563 3' CCTGACCTCAGGTGATCC 68214
GGATCACCTGAGGTCAGG
|||||
CCTAGTGGACTCCAGTCC

GAM2407 FLJ30532 3' AGCTCCTGACCTCAGATGATCT 59215 C
A TGGATCA CTGAGGTCAGGAGTT
|||||
ATCTAGT GACTCCAGTCCTCGA
A

GAM2407 FLJ31101 3' GAACTCCTGACCTCATGATCCA 36161 CC
TGGATCA TGAGGTCAGGAGTTC
|||||
ACCTAGT ACTCCAGTCCTCAAG

—
GAM2407 FLJ31153 3' GAACTCCTGACCTCAGGTGATC 58747
T GGATCACCTGAGGTCAGGAGTTC
|||||
TCTAGTGGACTCCAGTCCTCAAG

GAM2407 FLJ32865 3' AAGCCCTGACCTCAGGCAATCT 58792 CA A
GGAT CCTGAGGTCAGG GTT
|||
TCTA GGAAGTCAGTCC CAA
AC C

GAM2407 FLJ32894 3' GAACTCCTGACCTCGGGATCCA 58997 A T
TGGATC CC GAGGTCAGGAGTTC
|||||
ACCTAG GG CTCCAGTCCTCAAG

— —
GAM2407 GAL3ST-4 3' GAACTCCTCACCTCAGGTGATC 45279 C
CA TGGATCACCTGAGGT AGGAGTTC
|||||
ACCTAGTGGACTCCA TCCTCAAG
C

GAM2407 GGA2 3' GAACTCCTGACCTCAGGTGATC 57667
C GGATCACCTGAGGTCAGGAGTTC
|||||
CCTAGTGGACTCCAGTCCTCAAG

GAM2407 GGA2 3' GAACTCCTGACCTCAGGTGATC 57668
C GGATCACCTGAGGTCAGGAGTTC
|||||
CCTAGTGGACTCCAGTCCTCAAG

GAM2407 GMPPB 5' GAATTCCTGACCTCAGGTGATC 42022
CA TGGATCACCTGAGGTCAGGAGTTC
|||||

ACCTAGTGGACTCCAGTCCTTAAG

GAM2407 GNG4 3' AACTCCTGACCTCGTGATCCA 16833 CT
TGGATCAC GAGGTCAGGAGTT
||||| |||||
ACCTAGTG CTCCAGTCCTCAA

GAM2407 H2AV 3' AACTCCTGACCTCAGGCGATCC 25753 A
GGATC CCTGAGGTCAGGAGTT
||||| |||||
CCTAG GGACTCCAGTCCTCAA
C

GAM2407 HRH4 3' AACTCCTGGGCTGAAACAATCC 41518 CACCTG G
GGAT AG TCAGGAGTT
||| || |||||
CCTA TC GGTCCTCAA
ACAAAG G

GAM2407 HRH4 3' GAACTCCTTGGCTCAAGCAATC 41538 CAC GA _
C GGAT CT GGTCA GGAGTTC
||| || |||||
CCTA GA TCGGT CCTCAAG
AC_ AC T

GAM2407 HSMPP8 3' GAACTCCTGACCTCAGGTGATC 95133
C GGATCACCTGAGGTCAGGAGTTC
|||||
CCTAGTGGACTCCAGTCCTCAAG

GAM2407 HSPC065 3' GAACTCCTGACCTCATGATCCA 27151 CC
TGGATCA TGAGGTCAGGAGTTC
||||| |||||
ACCTAGT ACTCCAGTCCTCAAG

GAM2407 JAM1 3' AACTCCTGACCTCTTGATCC 34205 CCT
GGATCA GAGGTCAGGAGTT
||||| |||||
CCTAGT CTCCAGTCCTCAA
T_

GAM2407 JAM1 3' AACTCCTGACCTCTTGATCC 34206 CCT
GGATCA GAGGTCAGGAGTT
||||| |||||
CCTAGT CTCCAGTCCTCAA
T_

GAM2407 KIAA0022 3' AACTCCTGACCTCAAGTGATCC 30273 C
A TGGATCAC TGAGGTCAGGAGTT
||||| |||||
ACCTAGTG ACTCCAGTCCTCAA
A

GAM2407 KIAA0063 3' AACTCCCGACCTCAAGTGATCT 30245 C A
GGATCAC TGAGGTC GGAGTT
||||| |||||

TCTAGTG ACTCCAG CCTCAA
 A C
 GAM2407 KIAA0161 3' AACTCCTGACCTCAGGTGATCT 29183
 GGATCACCTGAGGTCAGGAGTT
 |||||
 TCTAGTGGACTCCAGTCCTCAA

GAM2407 KIAA0186 3' AACTCCTGACCTCAAGTGACCC 41089 A C
 A TGG TCAC TGAGGTCAGGAGTT
 ||| ||| |||||
 ACC AGTG ACTCCAGTCCTCAA
 C A

GAM2407 KIAA0186 3' CCTGACCTCAAGTGACCCA 41104 A C
 TGG TCAC TGAGGTCAGG
 ||| ||| |||||
 ACC AGTG ACTCCAGTCC
 C A

GAM2407 KIAA0205 3' GAACTCCTGACCTCAGGTGATC 30213
 T GGATCACCTGAGGTCAGGAGTTC
 |||||
 TCTAGTGGACTCCAGTCCTCAAG

GAM2407 KIAA0210 5' GAACTGCTGACCTCAAGTAATC 29158 C C G
 C GGAT AC TGAGGTCAG AGTTC
 |||| || ||||| |||||
 CCTA TG ACTCCAGTC TCAAG
 A A G

GAM2407 KIAA0391 3' AACTCCTGACCTCAGGTGATCC 28594
 A TGGATCACCTGAGGTCAGGAGTT
 |||||
 ACCTAGTGGACTCCAGTCCTCAA

GAM2407 KIAA0447 3' GAACTCCTCGGCTCAAGCAATC 72122 CAC GA _
 C GGAT CT GGTC AGGAGTTC
 |||| || ||| |||||
 CCTA GA TCGG TCCTCAAG
 AC_ AC C

GAM2407 KIAA0472 5' GAACTCCTGACCTCAAACGATC 72351 ACC
 T GGATC TGAGGTCAGGAGTTC
 |||| |||||
 TCTAG ACTCCAGTCCTCAAG
 CAA

GAM2407 KIAA0475 3' GACTCCTGACCCAGGTGATCC 30117 A
 A TGGATCACCTG GGTCAGGAGTT
 ||||| |||||
 ACCTAGTGGAC CCAGTCCTCAG
 C

GAM2407 KIAA0513 5' GAACTCCTGACCTCAGGTGAGC 29029 A
 CA TGG TCACCTGAGGTCAGGAGTTC
 ||| |||||

		ACC AGTGGACTCCAGTCCTCAAG		
		G		
GAM2407	KIAA0513	3' GAACTCCTGACCTCAGGTGATC 29030		
	C	GGATCACCTGAGGTCAGGAGTTC		
		CCTAGTGGACTCCAGTCCTCAAG		
GAM2407	KIAA0527	3' GAACTCCTGACCTCAAGTGATC 97497	C	
	T	GGATCAC TGAGGTCAGGAGTTC		
		TCTAGTG ACTCCAGTCCTCAAG		
		A		
GAM2407	KIAA0555	3' GAACTCCTGACCTCAAGTGATC 60741	C	
	T	GGATCAC TGAGGTCAGGAGTTC		
		TCTAGTG ACTCCAGTCCTCAAG		
		A		
GAM2407	KIAA0557	3' GAACTCCCGACCTTGTGATCCA 78561	CT	A
		TGGATCAC GAGGTC GGAGTTC		
		ACCTAGTG TTCCAG CCTCAAG		
		— C		
GAM2407	KIAA0562	3' AACTCCTGACCTTGTGATCCA 28810	CT	
		TGGATCAC GAGGTCAGGAGTT		
		ACCTAGTG TTCCAGTCCTCAA		
		—		
GAM2407	KIAA0594	3' GAACTCCTGACCTTGTGATCCA 65512	CT	
		TGGATCAC GAGGTCAGGAGTTC		
		ACCTAGTG TTCCAGTCCTCAAG		
		—		
GAM2407	KIAA0599	3' GAACTTCTGACCTCAGGTGATC 77692		
	CA	TGGATCACCTGAGGTCAGGAGTTC		
		ACCTAGTGGACTCCAGTCTTCAAG		
GAM2407	KIAA0682	3' GAACTCCCAACCTCAAGTGATC 30021	C	CA
	CA	TGGATCAC TGAGGT GGAGTTC		
		ACCTAGTG ACTCCA CCTCAAG		
		A AC		
GAM2407	KIAA0682	3' GAATTCCTGACCTCAAGTGATC 30022	C	
	CA	TGGATCAC TGAGGTCAGGAGTTC		
		ACCTAGTG ACTCCAGTCCTTAAG		
		A		
GAM2407	KIAA0720	3' GAACTCCTGACCCCAAGTGTTT 62984	T	C A
	C	GGA CAC TG GGTGAGGAGTTC		

			CCT GTG AC CCAGTCCTCAAG		
			T A C		
GAM2407	KIAA0737	3'	GAAGTCCTGACCTCATGATCC 29808	CC	
			GGATCA TGAGGTCAGGAGTTC		
			CCTAGT ACTCCAGTCCTCAAG		
			—		
GAM2407	KIAA0828	3'	AACTCCTGGGCTCAAGCAATCC 82106	CACC	G
			GGAT TGAG TCAGGAGTT		
			CCTA ACTC GGCCTCAA		
			ACGA G		
GAM2407	KIAA0841	3'	GAAGTCCTGACCTCAAGTGATC 71895	C	
	T		GGATCAC TGAGGTCAGGAGTTC		
			TCTAGTG ACTCCAGTCCTCAAG		
			A		
GAM2407	KIAA0889	3'	GAAGTCCCGACCTCAAGTGATC 31776	C	A
	C		GGATCAC TGAGGTC GGAGTTC		
			CCTAGTG ACTCCAG CCTCAAG		
			A C		
GAM2407	KIAA0924	3'	AACTCCTGACCTTGTGATCC 30345	CT	
			GGATCAC GAGGTCAGGAGTT		
			CCTAGTG TTCCAGTCCTCAA		
			—		
GAM2407	KIAA0931	3'	GAAGTCTTGACCTCAGGTGATC 68011		
	CA		TGGATCACCTGAGGTCAGGAGTTC		
			ACCTAGTGGAAGTCCAGTTCTCAAG		
			—		
GAM2407	KIAA0961	3'	AACTCCTGACCTCAGGTGATCC 30381		
	A		TGGATCACCTGAGGTCAGGAGTT		
			ACCTAGTGGAAGTCCAGTCCTCAA		
			—		
GAM2407	KIAA1040	3'	GAAGTCTGACCTCAGGTGATC 72686		
	T		GGATCACCTGAGGTCAGGAGTTC		
			TCTAGTGGAAGTCCAGTCCTCAAG		
			—		
GAM2407	KIAA1054	3'	GAAGTCTGACCTCAAGTGATC 68964	C	
			GATCAC TGAGGTCAGGAGTTC		
			CTAGTG ACTCCAGTCCTCAAG		
			A		
GAM2407	KIAA1128	3'	GAAGTCTGACCTCAAGTGATC 69005	C	
	CA		TGGATCAC TGAGGTCAGGAGTTC		

ACCTAGTG ACTCCAGTCCTCAAG
 A
 GAM2407 KIAA1161 5' AACTCCTGACCTAGTGATGCA 82634 G CTG
 TG ATCAC AGGTCAGGAGTT
 || |||| |||||
 AC TAGTG TCCAGTCCTCAA
 G A__
 GAM2407 KIAA1170 3' AACTCCTGACCTCAGGTGATCC 70402
 GGATCACCTGAGGTCAGGAGTT
 |||||
 CCTAGTGGACTCCAGTCCTCAA

 GAM2407 KIAA1198 3' AACTCCTGACCTCAGGTGATCT 63970
 GGATCACCTGAGGTCAGGAGTT
 |||||
 TCTAGTGGACTCCAGTCCTCAA

 GAM2407 KIAA1198 3' AACTCTTGACCTCAAATGATCC 63971 CC
 A TGGATCA TGAGGTCAGGAGTT
 ||||| |||||
 ACCTAGT ACTCCAGTTCTCAA
 AA
 GAM2407 KIAA1198 3' GAACTCCTGACCTCAGGTAATC 64035 C
 CA TGGAT ACCTGAGGTCAGGAGTTC
 |||| |||||
 ACCTA TGGACTCCAGTCCTCAAG
 A
 GAM2407 KIAA1200 3' GAACTCCTGACCTCAGGTGATC 63037
 T GGATCACCTGAGGTCAGGAGTTC
 |||||
 TCTAGTGGACTCCAGTCCTCAAG

 GAM2407 KIAA1243 3' CTTGACCTCAAGTAACCA 74025 ATC C
 TGG AC TGAGGTCAGG
 || || |||||
 ACC TG ACTCCAGTTC
 AA_ A
 GAM2407 KIAA1254 3' TCCTGACCTCAAGTGATCCA 70567 C
 TGGATCAC TGAGGTCAGGA
 ||||| |||||
 ACCTAGTG ACTCCAGTCCT
 A
 GAM2407 KIAA1257 3' AACTCCCGACTTCAGGTGATCC 63382 A
 GGATCACCTGAGGTC GGAGTT
 ||||| |||||
 CCTAGTGGACTTCAG CCTCAA
 C
 GAM2407 KIAA1257 3' AACTCCTGGTCACAAGTAATCC 63383 C C A GT
 GGAT AC TG G CAGGAGTT
 |||| || || |||||

			CCTA TG AC C GTCCTCAA		
			A A A TG		
GAM2407	KIAA1320	5'	GAATTCCTGACCTCAAGTGATC 69840	C	
		TA	TGGATCAC TGAGGTCAGGAGTTC		
			ATCTAGTG ACTCCAGTCCTTAAG		
			A		
GAM2407	KIAA1396	3'	AACTCCTGTGCTCAAGTGACCC 63666	A C	GT
			GG TCAC TGAG CAGGAGTT		
			CC AGTG ACTC GTCCTCAA		
			C A GT		
GAM2407	KIAA1465	3'	GATCTCTTGACCTCAGGTGATC 61498		T
		CA	TGGATCACCTGAGGTCAGGAG TC		
			ACCTAGTGGACTCCAGTTCTC AG		
			T		
GAM2407	KIAA1467	3'	GAATCCTGACCTCAGATAATC 72067	CAC	
		CA	TGGAT CTGAGGTCAGGAGTTC		
			ACCTA GACTCCAGTCCTCAAG		
			ATA		
GAM2407	KIAA1493	3'	AACTCCTGACCTCAGGTGATCC 64827		
		A	TGGATCACCTGAGGTCAGGAGTT		
			ACCTAGTGGACTCCAGTCCTCAA		
GAM2407	KIAA1508	3'	GAATCCTGACCTCAGGTAATC 62550	C	
		CA	TGGAT ACCTGAGGTCAGGAGTTC		
			ACCTA TGGACTCCAGTCCTCAAG		
			A		
GAM2407	KIAA1530	3'	GAATCCTAGCCTCAAGCGATC 68560	ACC	TC
		C	GGATC TGAGG AGGAGTTC		
			CCTAG ACTCC TCCTCAAG		
			CGA GA		
GAM2407	KIAA1571	3'	AACTCCTGACCTTGTGGTCCA 61609		CT
			TGGATCAC GAGGTCAGGAGTT		
			ACCTGGTG TTCCAGTCCTCAA		
GAM2407	KIAA1615	3'	AACTCCCGACCTCAGGTGATCC 69261		A
		A	TGGATCACCTGAGGTC GGAGTT		
			ACCTAGTGGACTCCAG CCTCAA		
			C		
GAM2407	KIAA1617	3'	GAATCCCAACCTCAAGTGATC 93077	C	CA
		T	GGATCAC TGAGGT GGAGTTC		

		TCTAGTG ACTCCA CCTCAAG	
		A AC	
GAM2407	KIAA1649	3' GAACTCCTGGGCACAAGTGATC 51236	C AG _
	C	GGATCAC TG GTC AGGAGTTC	
		CCTAGTG AC CGG TCCTCAAG	
		A A_ G	
GAM2407	KIAA1655	3' AACTCCTGACCTCCAGTGATCC 67167	CT
	A	TGGATCAC GAGGTCAGGAGTT	
		ACCTAGTG CTCCAGTCCTCAA	
		AC	
GAM2407	KIAA1712	3' AACTCCTGACCTCAGGTGATCT 68142	
		GGATCACCTGAGGTCAGGAGTT	
		TCTAGTGGA CTCCAGTCCTCAA	
GAM2407	KIAA1737	3' GAACTCCTGACCTCAGTTGATC 67941	C
	C	GGATCA CTGAGGTCAGGAGTTC	
		CCTAGT GACTCCAGTCCTCAAG	
		T	
GAM2407	KIAA1755	3' AACTCCTGGGCTCAAGTGATCC 62002	C G
		GGATCAC TGAG TCAGGAGTT	
		CCTAGTG ACTC GGTCCTCAA	
		A G	
GAM2407	KIAA1829	3' GAACTCCTGACTTTAGGTGATC 62643	
	CA	TGGATCACCTGAGGTCAGGAGTTC	
		ACCTAGTGGA TTT CAGTCCTCAAG	
GAM2407	KIAA1922	5' GAACTCCTGACCTCAGGTGATC 73993	
	C	GGATCACCTGAGGTCAGGAGTTC	
		CCTAGTGGA CTCCAGTCCTCAAG	
GAM2407	KIAA1962	3' GAACTCCTGGGCTCAAGTGATC 82801	C G
	C	GGATCAC TGAG TCAGGAGTTC	
		CCTAGTG ACTC GGTCCTCAA	
		A G	
GAM2407	KIAA1971	3' GAACTCCTGACCTCGTGATCCA 74679	CT
		TGGATCAC GAGGTCAGGAGTTC	
		ACCTAGTG CTCCAGTCCTCAAG	
GAM2407	KIAA1987	5' GAACTTCTGACCTCAGGTGATC 89383	
	CA	TGGATCACCTGAGGTCAGGAGTTC	

ACCTAGTGGACTCCAGTCTTCAAG

GAM2407	KLK7	3'	GAACGCCTGACCTCAGATGATC 18543	C	A
	CA		TGGATCA CTGAGGTCAGG GTTC		
			ACCTAGT GACTCCAGTCC CAAG		
			A G		
GAM2407	LAMP3	3'	GAACCTTTGACCTCAGGTGATC 60203		
	CA		TGGATCACCTGAGGTCAGGAGTTC		
			ACCTAGTGGACTCCAGTTCTCAAG		
GAM2407	LIECG3	3'	GAACCTCCTGGGCTCAAGCGGTC 88798	ACC	G
	CA		TGGATC TGAG TCAGGAGTTC		
			ACCTGG ACTC GGTCTCAAG		
			CGA G		
GAM2407	LNIR	3'	GAACCTCCTGGGCTCAAGCAATC 48871	CACC	G
	C		GGAT TGAG TCAGGAGTTC		
			CCTA ACTC GGTCTCAAG		
			ACGA G		
GAM2407	MAP-1	3'	GAACCTCCTGACCTCAAGTGATC 42440	C	
	CA		TGGATCAC TGAGGTCAGGAGTTC		
			ACCTAGTG ACTCCAGTCCTCAAG		
			A		
GAM2407	MCLC	3'	GAACCTCCTGACCTCAAGTGACC 31381	A	C
	C		GG TCAC TGAGGTCAGGAGTTC		
			CC AGTG ACTCCAGTCCTCAAG		
			C A		
GAM2407	MCM10	3'	AACTCCTGAGCACTAGCAATCC 38171	CAC	AG_
	A		TGGAT CTG G TCAGGAGTT		
			ACCTA GAT C AGTCCTCAA		
			AC_ CA G		
GAM2407	MEF-2	3'	AACTCCTGACCTCGTGATCCA 65012	CT	
			TGGATCAC GAGGTCAGGAGTT		
			ACCTAGTG CTCCAGTCCTCAA		
GAM2407	MGC10200	3'	GAGCTCCTGAGCTCAAACAATC 59645	CACC	G
	CA		TGGAT TGAG TCAGGAGTTC		
			ACCTA ACTC AGTCCTCGAG		
			ACAA G		
GAM2407	MGC11386	3'	AACTCCTGGGCTCAAGCAATCC 53049	CACC	G
			GGAT TGAG TCAGGAGTT		

			CCTA	ACTC	GGTCCTCAA		
			ACGA	G			
GAM2407	MGC13159	3'	GA	ACTCCTGGGATCAAGTGATC	53037	C	GG
		C		GGATCAC TGA TCAGGAGTTC			
			CCTAGTG	ACT	GGTCCTCAAG		
			A	AG			
GAM2407	MGC1842	3'	GA	ACCCCTGAGCTCAGGTGATC	66255	G	A
		CA		TGGATCACCTGAG TCAGG GTTC			
			ACCTAGTGGACTC	AGTCC CAAG			
			G	C			
GAM2407	MGC20235	3'	GA	ACTCCTGGGCTCAAGCGATC	59553	ACC	G
		C		GGATC TGAG TCAGGAGTTC			
			CCTAG	ACTC	GGTCCTCAAG		
			CGA	G			
GAM2407	MGC21675	3'	GA	ACTCCTGACCTCAGGTGATC	54591		
		CA		TGGATCACCTGAGGTCAGGAGTTC			
			ACCTAGTGGACTCCAGTCCTCAAG				
GAM2407	MGC21738	3'	GA	ACTCCTGACCTCAAGTGATC	59576	C	
		C		GGATCAC TGAGGTCAGGAGTTC			
			CCTAGTG	ACTCCAGTCCTCAAG			
			A				
GAM2407	MGC2474	3'	GA	ACTCCTGCCCTCAGGTGATC	43957		T
		CA		TGGATCACCTGAGG CAGGAGTTC			
			ACCTAGTGGACTCC	GTCCTCAAG			
			C				
GAM2407	MKRN4	3'	GA	ACTCCTGACCTCAGGTGATC	48462		
		CA		TGGATCACCTGAGGTCAGGAGTTC			
			ACCTAGTGGACTCCAGTCCTCAAG				
GAM2407	MLZE	5'	GA	ACTCCTGACCTCGGGATCCA	49451	A	T
				TGGATC CC GAGGTCAGGAGTTC			
			ACCTAG	GG CTCCAGTCCTCAAG			
			— —				
GAM2407	MMPL1	3'	GA	ACTCTTGGGCTCAAGCGATC	15964	ACC	G
		C		GGATC TGAG TCAGGAGTTC			
			CCTAG	ACTC	GGTTCTCAAG		
			CGA	G			
GAM2407	moblak	3'	AA	CTCCTGACTTCAGGTGATCC	56377		
				GGATCACCTGAGGTCAGGAGTT			

CCTAGTGGACTTCAGTCCTCAA

GAM2407 MRPL44 3' GAACTCCTGACCTCAGGTGATC 43597
CA TGGATCACCTGAGGTCAGGAGTTC
|||||
ACCTAGTGGACTCCAGTCCTCAAG

GAM2407 NFAT5 3' GAACTCCTAACCTCCAGTGATC 57769 CT C
CA TGGATCAC GAGGT AGGAGTTC
||||| |||| |||||
ACCTAGTG CTCCA TCCTCAAG
AC A

GAM2407 NINJ2 3' GAACTCCTGACCTCAGGTGATC 33724
T GGATCACCTGAGGTCAGGAGTTC
|||||
TCTAGTGGACTCCAGTCCTCAAG

GAM2407 Nup43 3' GAACTCCTGACCACAGGTAATC 45346 C A
GAT ACCTG GGTCAGGAGTTC
||| |||| |||||
CTA TGGAC CCAGTCCTCAAG
A A

GAM2407 NXN 3' GAACTCCTGACCTCAGGTGATC 42674
CA TGGATCACCTGAGGTCAGGAGTTC
|||||
ACCTAGTGGACTCCAGTCCTCAAG

GAM2407 OCT11 3' GAACTCCTGACCTCCTGATCCA 27589 CCT
TGGATCA GAGGTCAGGAGTTC
||||| |||||
ACCTAGT CTCCAGTCCTCAAG
C_

GAM2407 PELI1 5' AACTCCCAACCTCAAGTGATCC 40614 C CA
GGATCAC TGAGGT GGAGTT
||||| ||||| |||||
CCTAGTG ACTCCA CCTCAA
A AC

GAM2407 PELI1 5' GAACTCCTGACCTCAAGTGATC 40639 C
T GGATCAC TGAGGTCAGGAGTTC
||||| |||||
TCTAGTG ACTCCAGTCCTCAAG
A

GAM2407 PIG7 3' GAACTCCTGGGCTCAAGCGATC 17969 ACC G
C GGATC TGAG TCAGGAGTTC
|||| |||| |||||
CCTAG ACTC GGTCCTCAAG
CGA G

GAM2407 PIP3-E 3' AACTCCTGACCTCAGGTGATCT 67339
GGATCACCTGAGGTCAGGAGTT
|||||

TCTAGTGGACTCCAGTCCTCAA

GAM2407 POLR2D 3' AACTCCTGGGCTCAAGTGATCC 17837 C G
GGATCAC TGAG TCAGGAGTT
||||| ||| |||||
CCTAGTG ACTC GGTCCTCAA
A G

GAM2407 PRO0899 5' GAACTCCTGGGCCCAAGCAATC 38310 CAC GA _
C GGAT CT GGTC AGGAGTTC
||| || ||| |||||
CCTA GA CCGG TCCTCAAG
AC_ AC G

GAM2407 PRO1992 3' GAACTCAACCTCAGGTGATCC 26904 CAG
GGATCACCTGAGGT GAGTTC
||||||| |||||
CCTAGTGGACTCCA CTCAAG
A_

GAM2407 PRO2955 3' AACTCCTGACCTCAGGTGATCC 38228
A TGGATCACCTGAGGTCAGGAGTT
|||||||
ACCTAGTGGACTCCAGTCCTCAA

GAM2407 PSTPIP2 3' AACTCCTGACCTCAGGTGATCC 44644
A TGGATCACCTGAGGTCAGGAGTT
|||||||
ACCTAGTGGACTCCAGTCCTCAA

GAM2407 RASSF2 3' GAACTCCTGACCTCGTGATCCA 29098 CT
TGGATCAC GAGGTCAGGAGTTC
||||| |||||
ACCTAGTG CTCCAGTCCTCAAG

GAM2407 RES4-25 3' GAATTCCCGACCTCAGGTAATC 65266 C A
CA TGGAT ACCTGAGGTC GGAGTTC
|||| ||||| |||||
ACCTA TGGACTCCAG CCTTAAG
A C

GAM2407 RNF8 3' AATTCCTGACCTTAAGTGATCC 15552 C
A TGGATCAC TGAGGTCAGGAGTT
||||| |||||
ACCTAGTG ATTCCAGTCCTTAA
A

GAM2407 Rpo1-2 3' GACCCTGACCTCAAGTGATCCA 39220 C A
TGGATCAC TGAGGTCAGG GTT
||||| ||||| |||
ACCTAGTG ACTCCAGTCC CAG
A _

GAM2407 Rpo1-2 3' GACCCTGACCTCAAGTGATCCA 39221 C A
TGGATCAC TGAGGTCAGG GTT
||||| ||||| |||

			ACCTAGTG ACTCCAGTCC CAG	
			A _	
GAM2407	SARM	3'	GAAGTCTGGGCTCAAGTGATC 31290	C G
	C		GGATCAC TGAG TCAGGAGTTC	
			CCTAGTG ACTC GGTCCTCAAG	
			A G	
GAM2407	SCAMP-4	3'	GAAGTCTGACCTCAAGTGATC 55347	C
	CA		TGGATCAC TGAGGTCAGGAGTTC	
			ACCTAGTG ACTCCAGTCCTCAAG	
			A	
GAM2407	SCYA22	3'	AACTCCTGGGCTCAAGCGATCC 92565	ACC G
			GGATC TGAG TCAGGAGTT	
			CCTAG ACTC GGTCCTCAA	
			CGA G	
GAM2407	SCYA22	3'	GAAGTCTGACCTCAAGTGATC 92593	C
	CA		TGGATCAC TGAGGTCAGGAGTTC	
			ACCTAGTG ACTCCAGTCCTCAAG	
			A	
GAM2407	SCYA22	3'	GAAGTCTGTCCTCAGGTAATC 92594	C T
	C		GGAT ACCTGAGG CAGGAGTTC	
			CCTA TGGACTCC GTCCTCAAG	
			A T	
GAM2407	SCYA28	3'	GAAGTTCTGATCTCAAGTGATC 39542	C
	CA		TGGATCAC TGAGGTCAGGAGTTC	
			ACCTAGTG ACTCTAGTCTTCAAG	
			A	
GAM2407	SFXN2	3'	GAAGTCTGACCTCAGGTGATC 74375	
	C		GGATCACCTGAGGTCAGGAGTTC	
			CCTAGTGGACTCCAGTCCTCAAG	
GAM2407	SIRPB1	3'	GAAGTCCCGACCTCAGGTGATC 21366	A
	CA		TGGATCACCTGAGGTC GGAGTTC	
			ACCTAGTGGACTCCAG CCTCAAG	
			C	
GAM2407	SLC12A8	3'	GAAGTCTGACCTCGTGATCCA 45236	CT
			TGGATCAC GAGGTCAGGAGTTC	
			ACCTAGTG CTCCAGTCCTCAAG	
GAM2407	SLC2A10	3'	GAAGTCTGAGCTCAAGTGATC 48551	C G
	CA		TGGATCAC TGAG TCAGGAGTTC	

			ACCTAGTG ACTC AGTCCTCAAG		
			A G		
GAM2407	SLC6A14	3'	GAAC TCCCGACCTCAAGTGATC 24308	C	A
	T		GGATCAC TGAGGTC GGAGTTC		
			TCTAGTG ACTCCAG CCTCAAG		
			A C		
GAM2407	STAF65(gamma)	3'	AACTCCTGACCTCAAGTGATCT 30056	C	
			GGATCAC TGAGGTCAGGAGTT		
			TCTAGTG ACTCCAGTCCTCAA		
			A		
GAM2407	STRBP	5'	GAAC TCTGAACGCAAGTGATC 37818	C	AGG
	C		GGATCAC TG TCAGGAGTTC		
			CCTAGTG AC AGTCCTCAAG		
			A GCA		
GAM2407	TBCC	3'	GAAC TCTGACCTCAGGTGATC 13603		
	CA		TGGATCACCTGAGGTCAGGAGTTC		
			ACCTAGTGGACTCCAGTCCTCAAG		
GAM2407	TCL6	3'	AACTCCTGAGCTCAAGCGATCC 40453	ACC	G
			GGATC TGAG TCAGGAGTT		
			CCTAG ACTC AGTCCTCAA		
			CGA G		
GAM2407	TCL6	5'	GAAC TCTGACCAAGTGATCCA 40473	CTGA	
			TGGATCAC GGTGAGGAGTTC		
			ACCTAGTG CCAGTCCTCAAG		
			AA__		
GAM2407	TGIF2	3'	GAAC TCTGACCTCGTGAGCCA 41750	A	CT
			TGG TCAC GAGGTCAGGAGTTC		
			ACC AGTG CTCCAGTCCTCAAG		
			G __		
GAM2407	TRIM16	3'	AACTCCTGACCTCGTGATGCA 22359	G	CT
			TG ATCAC GAGGTCAGGAGTT		
			AC TAGTG CTCCAGTCCTCAA		
			G __		
GAM2407	TRIM5	3'	GAAC CTCTGACCTCAGGTGATC 53468		GA
	CA		TGGATCACCTGAGGTCAG GTTC		
			ACCTAGTGGACTCCAGTC CAAG		
			TC		
GAM2407	TRIM5	3'	GAAC CTCTGACCTCAGGTGATC 53469		GA
	CA		TGGATCACCTGAGGTCAG GTTC		

			ACCTAGTGGACTCCAGTC CAAG	
			TC	
GAM2407	TRIM6	3'	GAACTCCTGACCGCAAGTGATC 55179	C A
	CA		TGGATCAC TG GGTCAGGAGTTC	
			ACCTAGTG AC CCAGTCCTCAAG	
			A G	
GAM2407	TU12B1-TY	3'	GAACTCCTGACCTCAGATAATC 33847	CAC
	T		GGAT CTGAGGTCAGGAGTTC	
			TCTA GACTCCAGTCCTCAAG	
			ATA	
GAM2407	TU12B1-TY	3'	GAACTCCTGACCTTGGGTAATC 33848	C TG
	CA		TGGAT ACC AGGTCAGGAGTTC	
			ACCTA TGG TCCAGTCCTCAAG	
			A GT	
GAM2407	TUCAN	3'	GAACTCCTGGCCTCAAGTGATC 30976	C
	CA		TGGATCAC TGAGGTCAGGAGTTC	
			ACCTAGTG ACTCCGGTCCTCAAG	
			A	
GAM2407	TUSP	3'	GAACTCCTGACCTCAGGTGATC 40025	
	C		GGATCACCTGAGGTCAGGAGTTC	
			CCTAGTGGACTCCAGTCCTCAAG	
GAM2407	UBF-fl	3'	AACTCCTGACCTCAAGTGATCC 52613	C
	A		TGGATCAC TGAGGTCAGGAGTT	
			ACCTAGTG ACTCCAGTCCTCAA	
			A	
GAM2407	VDU1	3'	AACTCCTGACCTCAGGTGATCC 31111	
	A		TGGATCACCTGAGGTCAGGAGTT	
			ACCTAGTGGACTCCAGTCCTCAA	
GAM2407	VMP	3'	GAACTCCTGGGCTCAAGCGATC 55762	ACC G
	C		GGATC TGAG TCAGGAGTTC	
			CCTAG ACTC GGTCTCAAG	
			CGA G	
GAM2407	VPS33A	3'	AACTCCTGACCTCAGGTGATCC 43604	
	A		TGGATCACCTGAGGTCAGGAGTT	
			ACCTAGTGGACTCCAGTCCTCAA	
GAM2407	WBSCR23	3'	AACTCCTGACCTCAGGTGATCC 47405	
	A		TGGATCACCTGAGGTCAGGAGTT	

ACCTAGTGGACTCCAGTCCTCAA

GAM2407 WIT-1 3' GAACTCCTGACCCCAGATTCA 32398 ACC A
TGGATC TG GGTGAGGAGTTC
||||| || |||||
ACTTAG AC CCAGTCCTCAAG
___ C

GAM2407 ZNF177 5' AACTCCTGCTCTCAAGTGATCC 14355 C GT
GGATCAC TGAG CAGGAGTT
||||| ||| |||||
CCTAGTG ACTC GTCCTCAA
A TC

GAM2407 ZNF338 3' GAACTCCTGACCTCAAGTGATC 42255 C
T GGATCAC TGAGGTCAGGAGTTC
||||| |||||
TCTAGTG ACTCCAGTCCTCAAG
A

GAM2407 ZTL1 3' GAACTCCTGACCTCAGGTGATC 43519
T GGATCACCTGAGGTCAGGAGTTC
|||||
TCTAGTGGACTCCAGTCCTCAAG

GAM2407 LOC112687 3' AACTCCTGACCTCATGTAATCC 73214 C C
A TGGAT AC TGAGGTCAGGAGTT
||||| || |||||
ACCTA TG ACTCCAGTCCTCAA
A T

GAM2407 LOC112817 3' GAACTCCTGACCTCAGGTGATC 57325
CA TGGATCACCTGAGGTCAGGAGTTC
|||||
ACCTAGTGGACTCCAGTCCTCAAG

GAM2407 LOC113026 3' CCTGACCTCAAGTGATCC 56727 C
GGATCAC TGAGGTCAGG
||||| |||||
CCTAGTG ACTCCAGTCC
A

GAM2407 LOC113523 3' GAACTCCTGACCTCACACAATC 73422 CACC
C GGAT TGAGGTCAGGAGTTC
||| |||||
CCTA ACTCCAGTCCTCAAG
ACAC

GAM2407 LOC115098 5' GAACTCCTGGCCTCAAGCAATC 57394 CACC
C GGAT TGAGGTCAGGAGTTC
||| |||||
CCTA ACTCCGGTCCTCAAG
ACGA

GAM2407 LOC115219 5' AACTCCTGACGTCGTGATCC 73680 CT G
GGATCAC GA GTCAGGAGTT
||||| || |||||

		CCTAGTG CT CAGTCCTCAA	
		— G	
GAM2407	LOC115648 3'	GAACCTCCTGACCTCAGGTGATC 60021	
	CA	TGGATCACCTGAGGTCAGGAGTTC	
		ACCTAGTGGACTCCAGTCCTCAAG	
GAM2407	LOC119392 3'	GAACCTCCTGACCTCAGGTGATC 59813	
	CA	TGGATCACCTGAGGTCAGGAGTTC	
		ACCTAGTGGACTCCAGTCCTCAAG	
GAM2407	LOC120114 3'	AACTCCTGACCTCGTAATCCA 76031	C CT
		TGGAT AC GAGGTCAGGAGTT	
		ACCTA TG CTCCAGTCCTCAA	
		A —	
GAM2407	LOC120224 5'	GAACCTCCTGACCTCAGGTGATC 57887	
	T	GGATCACCTGAGGTCAGGAGTTC	
		TCTAGTGGACTCCAGTCCTCAAG	
GAM2407	LOC120939 3'	GAACCTCCTGACGTCAGGTGATC 76761	G
	C	GGATCACCTGA GTCAGGAGTTC	
		CCTAGTGGACT CAGTCCTCAAG	
		G	
GAM2407	LOC121504 3'	GAACCTCCTGGCCTCAAGTGATT 74545	C
	CA	TGGATCAC TGAGGTCAGGAGTTC	
		ACTTAGTG ACTCCGGTCCTCAAG	
		A	
GAM2407	LOC124216 3'	AACTCCTGACCTCGTGATCC 74730	CT
		GGATCAC GAGGTCAGGAGTT	
		CCTAGTG CTCCAGTCCTCAA	
		—	
GAM2407	LOC125194 5'	AACTCCTGGCTTCAAGTGATCC 74859	C
		GGATCAC TGAGGTCAGGAGTT	
		CCTAGTG ACTTCGGTCCTCAA	
		A	
GAM2407	LOC126364 3'	GAACCTCCTGACCTCAAGCGATC 76191	ACC
	T	GGATC TGAGGTCAGGAGTTC	
		TCTAG ACTCCAGTCCTCAAG	
		CGA	
GAM2407	LOC126661 3'	GAACCTCCTGGGCTCAACTGATC 75056	CC G
	CA	TGGATCA TGAG TCAGGAGTTC	

		ACCTAGT ACTC GGTCTCAAG		
		CA G		
GAM2407	LOC126669 3'	AACTCCTGACCTCAAATGATCC 75916	CC	
	A	TGGATCA TGAGGTCAGGAGTT		
		ACCTAGT ACTCCAGTCCTCAA		
		AA		
GAM2407	LOC128077 3'	GAACCTCCTGACATAAGGTAATC 75214	C	GAG
	CA	TGGAT ACCT GTCAGGAGTTC		
		ACCTA TGGA CAGTCCTCAAG		
		A ATA		
GAM2407	LOC128989 3'	GAACCTCCTGACGTGGTGATCCA 75315		TGAG
		TGGATCACG GTCAGGAGTTC		
		ACCTAGTGG CAGTCCTCAAG		
		TG__		
GAM2407	LOC130639 5'	GAACCTCCTGACCTCAAGTGATC 75479	C	
	C	GGATCAC TGAGGTCAGGAGTTC		
		CCTAGTG ACTCCAGTCCTCAAG		
		A		
GAM2407	LOC130813 3'	AACTCCCAACTTCAGGTGATCC 76257		CA
		GGATCACCTGAGGT GGAGTT		
		CCTAGTGGACTTCA CCTCAA		
		AC		
GAM2407	LOC132241 5'	GAACGCCTGACCTCAAGTGATC 75561	C	A
	C	GGATCAC TGAGGTCAGG GTTC		
		CCTAGTG ACTCCAGTCC CAAG		
		A G		
GAM2407	LOC135154 3'	GAACCTCCTGACCTCAGTTGATC 75730	C	
	CA	TGGATCA CTGAGGTCAGGAGTTC		
		ACCTAGT GACTCCAGTCCTCAAG		
		T		
GAM2407	LOC135293 3'	AACTCCTGGGCTCAAGCAATCC 76673	CACC	G
		GGAT TGAG TCAGGAGTT		
		CCTA ACTC GGTCTCAA		
		ACGA G		
GAM2407	LOC135293 3'	GAACCTCCTGACCTCAGGTGATG 76684	G	
	CA	TG ATCACCTGAGGTCAGGAGTTC		
		AC TAGTGGACTCCAGTCCTCAAG		
		G		
GAM2407	LOC135818 3'	GAACCTCCTGACCTCAGGTGATC 75747		
	T	GGATCACCTGAGGTCAGGAGTTC		

TCTAGTGGACTCCAGTCCTCAAG

GAM2407 LOC139422 5' GAACTCCTGAGCTCAAGCAATC 76350 CACC G
C GGAT TGAG TCAGGAGTTC

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CCTA ACTC AGTCCTCAAG
ACGA G

GAM2407 LOC142927 5' AACTCCTGGCCTCAAGTGATCC 76937 C
GGATCAC TGAGGTCAGGAGTT

||||| |||||
CCTAGTG ACTCCGGTCCTCAA
A

GAM2407 LOC143916 3' AACTTCTGACCTCAGGTGATCC 77131
A TGGATCACCTGAGGTCAGGAGTT

|||||
ACCTAGTGGACTCCAGTCTTCAA

GAM2407 LOC144305 3' AACTCCTGGACCCAAGCGATCC 83965 AC GA _
GGATC CT GGTC AGGAGTT

|||| || ||| |||||
CCTAG GA CCAG TCCTCAA
C_ AC G

GAM2407 LOC144317 5' GAACTCCTGACCTCAGGTGATC 77294
CA TGGATCACCTGAGGTCAGGAGTTC

|||||
ACCTAGTGGACTCCAGTCCTCAAG

GAM2407 LOC144519 3' GAACTCCTGACCTGAAGCGATC 77372 AC G_
C GGATC CT AGGTCAGGAGTTC

|||| || |||||
CCTAG GA TCCAGTCCTCAAG
C_ AG

GAM2407 LOC144519 5' GAACTCCTGGGCTCAAGTGGTC 77373 C G
CA TGGATCAC TGAG TCAGGAGTTC

||||| ||| |||||
ACCTGGTG ACTC GGTCTCAAG
A G

GAM2407 LOC144524 5' AACTCCTGAACTCAGGTGATCC 84044 G
GGATCACCTGAG TCAGGAGTT

||||| |||||
CCTAGTGGACTC AGTCCTCAA
A

GAM2407 LOC144742 5' GAACTCATGGCCTCAAATGATC 77459 CC G
CA TGGATCA TGAGGTCA GAGTTC

||||| ||||| |||||
ACCTAGT ACTCCGGT CTCAAG
AA A

GAM2407 LOC145009 3' GAACTCCTGACCTCGTGATCCA 60974 CT
TGGATCAC GAGGTCAGGAGTTC

||||| |||||

ACCTAGTG CTCCAGTCCTCAAG

GAM2407 LOC145082 5' CCTAACCTAAGGTGATCCA 84185 G C
TGGATCACCT AGGT AGG
||||||| ||| |||
ACCTAGTGGA TCCA TCC
A A

GAM2407 LOC145268 5' GAACTCCTAACCTCGGGTGATC 77578 C
CA TGGATCACCTGAGGT AGGAGTTC
||||||| |||||
ACCTAGTGGGCTCCA TCCTCAAG
A

GAM2407 LOC145453 5' AACTCCTGACCTCAAGGATCT 77649 ACC
GGATC TGAGGTCAGGAGTT
||| |||||
TCTAG ACTCCAGTCCTCAA
GA_

GAM2407 LOC145725 3' GAACTCCTGGGCTCAAGTGATC 77882 C G
C GGATCAC TGAG TCAGGAGTTC
||||| ||| |||||
CCTAGTG ACTC GGTCTCAAG
A G

GAM2407 LOC145732 3' GAACTCCTGGGCTCAAGTGATC 77894 C G
C GGATCAC TGAG TCAGGAGTTC
||||| ||| |||||
CCTAGTG ACTC GGTCTCAAG
A G

GAM2407 LOC145813 5' GAACTCCTGGGCTCAAGCGATC 84508 ACC G
C GGATC TGAG TCAGGAGTTC
||| ||| |||||
CCTAG ACTC GGTCTCAAG
CGA G

GAM2407 LOC145873 5' GAACTCCTGAACTCAAGTAATC 78011 C C G
CA TGGAT AC TGAG TCAGGAGTTC
|||| || ||| |||||
ACCTA TG ACTC AGTCCTCAAG
A A A

GAM2407 LOC146050 3' AACTCCCGACCTCAGGTGATCT 78094 A
GGATCACCTGAGGTC GGAGTT
||||||| |||||
TCTAGTGGA CTCCAG CCTCAA
C

GAM2407 LOC146108 3' AACTCCTGGCTTCAAGCAATCC 78145 CACC
GGAT TGAGGTCAGGAGTT
||| |||||
CCTA ACTTCGGTCCTCAA
ACGA

GAM2407 LOC146229 3' AACTCCTGACCTCAAGTGATCC 78237 C
A TGGATCAC TGAGGTCAGGAGTT
||||| |||||

		ACCTAGTG ACTCCAGTCCTCAA	
		A	
GAM2407	LOC146229 3'	AACTCCTGACCTCAGGTGATCC 78238	
	A	TGGATCACCTGAGGTCAGGAGTT	
		ACCTAGTGGACTCCAGTCCTCAA	
GAM2407	LOC146229 3'	AACTCCTGACTTCAAATGATCC 78239	CC
	A	TGGATCA TGAGGTCAGGAGTT	
		ACCTAGT ACTTCAGTCCTCAA	
		AA	
GAM2407	LOC146336 3'	GAACTCTTGGGCTCAAGTGATC 78372	C G
	C	GGATCAC TGAG TCAGGAGTTC	
		CCTAGTG ACTC GGTCTCAAG	
		A G	
GAM2407	LOC146346 5'	GAACTCCTGACCACATGTGGTC 78396	C A
	CA	TGGATCAC TG GGTCAGGAGTTC	
		ACCTGGTG AC CCAGTCCTCAAG	
		T A	
GAM2407	LOC146894 3'	GAACTCCTGACCTCAAATGAGC 59861	A CC
	C	GG TCA TGAGGTCAGGAGTTC	
		CC AGT ACTCCAGTCCTCAAG	
		G AA	
GAM2407	LOC146901 3'	GAACTCCTGACCTCAGGTGATC 84900	
	CA	TGGATCACCTGAGGTCAGGAGTTC	
		ACCTAGTGGACTCCAGTCCTCAAG	
GAM2407	LOC146909 3'	GAACTCCTGACCTCAGGTGATC 78771	
	C	GGATCACCTGAGGTCAGGAGTTC	
		CCTAGTGGACTCCAGTCCTCAAG	
GAM2407	LOC146952 5'	AACTCCTGACCTCAGATGATCT 84918	C
	A	TGGATCA CTGAGGTCAGGAGTT	
		ATCTAGT GACTCCAGTCCTCAA	
		A	
GAM2407	LOC147054 3'	GAACTCCCGATCTCAGGTGATC 85006	A
	C	GGATCACCTGAGGTC GGAGTTC	
		CCTAGTGGACTCTAG CCTCAAG	
		C	
GAM2407	LOC147276 3'	GAACTCCTGACCTCAAGTGATC 78961	C
	CA	TGGATCAC TGAGGTCAGGAGTTC	

		ACCTAGTG ACTCCAGTCCTCAAG		
		A		
GAM2407	LOC147817 3'	AACTCCTGACCTTATAATCC 79161	CACC	
		GGAT TGAGGTCAGGAGTT		
		CCTA ATTCCAGTCCTCAA		
		AT__		
GAM2407	LOC147817 3'	AACTCCTGGCTTCAAGTGATCC 79162	C	
		GGATCAC TGAGGTCAGGAGTT		
		CCTAGTG ACTTCGGTCCTCAA		
		A		
GAM2407	LOC147841 3'	GAACCTCCTGACCTCAGGTGATC 79227		
	CA	TGGATCACCTGAGGTCAGGAGTTC		
		ACCTAGTGGACTCCAGTCCTCAAG		
GAM2407	LOC147935 3'	AACTCCTGGGCTCAAGTGATCC 85202	C G	
		GGATCAC TGAG TCAGGAGTT		
		CCTAGTG ACTC GGTCTCAA		
		A G		
GAM2407	LOC147990 3'	GAACCTCCTGGGCTCAAGCGATC 85222	ACC G	
	C	GGATC TGAG TCAGGAGTTC		
		CCTAG ACTC GGTCTCAAG		
		CGA G		
GAM2407	LOC148195 3'	GAACCTCCTGACCTCAGGTGAGC 85282	A	
	C	GG TCACCTGAGGTCAGGAGTTC		
		CC AGTGGACTCCAGTCCTCAAG		
		G		
GAM2407	LOC148645 5'	GAACCTCCTGGGCCCAAGTGATC 85334	C A _	
	C	GGATCAC TG GGTC AGGAGTTC		
		CCTAGTG AC CCGG TCCTCAAG		
		A _ G		
GAM2407	LOC148709 3'	AACTCCCGACCTTAGGTGATGC 79685	G A	
	A	TG ATCACCTGAGGTC GGAGTT		
		AC TAGTGGATTCCAG CCTCAA		
		G C		
GAM2407	LOC148918 5'	GAACCTCCTGACCTCAGGTGATC 79827		
	CA	TGGATCACCTGAGGTCAGGAGTTC		
		ACCTAGTGGACTCCAGTCCTCAAG		
GAM2407	LOC149478 3'	GAACCTCCTGACTTCATGTGATC 80169	C	
	C	GGATCAC TGAGGTCAGGAGTTC		

		CCTAGTG ACTTCAGTCCTCAAG	
		T	
GAM2407	LOC149577 3'	ACTCCTGACCTCAAGTGATCCA 85663	C
		TGGATCAC TGAGGTCAGGAGT	
		ACCTAGTG ACTCCAGTCCTCA	
		A	
GAM2407	LOC149577 3'	GAACCTCCTGACCTCAAGTGATC 85675	C
	CA	TGGATCAC TGAGGTCAGGAGTTC	
		ACCTAGTG ACTCCAGTCCTCAAG	
		A	
GAM2407	LOC149692 3'	GAACCTCCTGACCTCAGGTGATC 85734	
	CA	TGGATCACCTGAGGTCAGGAGTTC	
		ACCTAGTGGACTCCAGTCCTCAAG	
GAM2407	LOC149711 3'	AACTCCTGACCTCAGGTGATCC 85829	
	A	TGGATCACCTGAGGTCAGGAGTT	
		ACCTAGTGGACTCCAGTCCTCAA	
GAM2407	LOC150054 5'	GAACCTTATGACCTCAGGTGATC 85972	G
	C	GGATCACCTGAGGTCA GAGTTC	
		CCTAGTGGACTCCAGT TTCAAG	
		A	
GAM2407	LOC150225 3'	AACTCCTGACCTCAGATGATTC 86174	C
	A	TGGATCA CTGAGGTCAGGAGTT	
		ACTTAGT GACTCCAGTCCTCAA	
		A	
GAM2407	LOC150282 5'	GAACCTCCTGACCTCAGGTGATC 80543	
	CA	TGGATCACCTGAGGTCAGGAGTTC	
		ACCTAGTGGACTCCAGTCCTCAAG	
GAM2407	LOC150290 3'	AACTCCTGGCCTCAAGCAATCC 80581	CACC
		GGAT TGAGGTCAGGAGTT	
		CCTA ACTCCGGTCCTCAA	
		ACGA	
GAM2407	LOC150397 3'	GAACCCCTGACCTCAGGTGATC 80662	A
	C	GGATCACCTGAGGTCAGG GTTC	
		CCTAGTGGACTCCAGTCC CAAG	
		C	
GAM2407	LOC150407 3'	AACTCCTGGGCTCAAGTAATCC 80634	C C G
		GGAT AC TGAG TCAGGAGTT	

		CCTA TG ACTC GGCCTCAA	
		A A G	
GAM2407	LOC150587 3'	AACTCCTGGGCTCAAGCAATCC 86238	CACC G
		GGAT TGAG TCAGGAGTT	
		CCTA ACTC GGCCTCAA	
		ACGA G	
GAM2407	LOC150587 3'	AACTCCTGGGCTCAAGCGATCC 86239	ACC G
		GGATC TGAG TCAGGAGTT	
		CCTAG ACTC GGCCTCAA	
		CGA G	
GAM2407	LOC150960 3'	AATTCCTGACCTCAGGTGATCC 80859	
	A	TGGATCACCTGAGGTCAGGAGTT	
		ACCTAGTGGACTCCAGTCCTTAA	
GAM2407	LOC151201 3'	GAACCTCCTGGTTTCAAGCGATC 86476	ACC GT
	C	GGATC TGAG CAGGAGTTC	
		CCTAG ACTT GTCCTCAAG	
		CGA TG	
GAM2407	LOC151701 3'	GAACCTCCTGACCTCAGATGATC 86671	C
	T	GGATCA CTGAGGTCAGGAGTTC	
		TCTAGT GACTCCAGTCCTCAAG	
		A	
GAM2407	LOC151826 3'	GAACCTCCTGACATCAGGTGATC 81181	G
	CA	TGGATCACCTGA GTCAGGAGTTC	
		ACCTAGTGGACT CAGTCCTCAAG	
		A	
GAM2407	LOC152137 3'	GAACCCCTGACCTCAAGTGATC 81316	C A
	CA	TGGATCAC TGAGGTCAGG GTTC	
		ACCTAGTG ACTCCAGTCC CAAG	
		A C	
GAM2407	LOC152343 3'	GAACCTCCTGTGCTCAAGTGATC 81426	C GT
	C	GGATCAC TGAG CAGGAGTTC	
		CCTAGTG ACTC GTCCTCAAG	
		A GT	
GAM2407	LOC152794 5'	GAACCTCCTGACCTCAGGTGATC 81558	
	C	GGATCACCTGAGGTCAGGAGTTC	
		CCTAGTGGACTCCAGTCCTCAAG	
GAM2407	LOC153077 3'	GAACCTCCTGACCTCAGGTGATC 87125	
	CA	TGGATCACCTGAGGTCAGGAGTTC	

ACCTAGTGGACTCCAGTCCTCAAG

GAM2407	LOC153443	3'	AACTCCTGGGCTCAAGTGATCC	81686	C	G
			GGATCAC TGAG TCAGGAGTT			
			CCTAGTG ACTC GGTCCTCAA			
			A G			
GAM2407	LOC153606	5'	GAACCTCCTGACTGCAGGTGATC	87256	A	
	C		GGATCACCTG GGTCAGGAGTTC			
			CCTAGTGGAC TCAGTCCTCAAG			
			G			
GAM2407	LOC153688	3'	GAACCTCCCAACCTCAGGTGATC	87311	CA	
	C		GGATCACCTGAGGT GGAGTTC			
			CCTAGTGGACTCCA CCTCAAG			
			AC			
GAM2407	LOC153688	3'	GAACCTCCTGGGCTCAAGCGATC	87312	ACC	G
	CA		TGGATC TGAG TCAGGAGTTC			
			ACCTAG ACTC GGTCCTCAAG			
			CGA G			
GAM2407	LOC153811	3'	AACTCCTGACCTCAAATGATCC	81816	CC	
	A		TGGATCA TGAGGTCAGGAGTT			
			ACCTAGT ACTCCAGTCCTCAA			
			AA			
GAM2407	LOC153883	5'	GAACCTCCTGACCTCAAGTGATC	81894	C	
	CA		TGGATCAC TGAGGTCAGGAGTTC			
			ACCTAGTG ACTCCAGTCCTCAAG			
			A			
GAM2407	LOC154007	3'	GAACCTCCTGGGCTCAGATGATC	81927	C	G
	C		GGATCA CTGAG TCAGGAGTTC			
			CCTAGT GACTC GGTCCTCAAG			
			A G			
GAM2407	LOC154726	3'	AACTCCTGGGCTCAGATGATCC	82003	C	G
	A		TGGATCA CTGAG TCAGGAGTT			
			ACCTAGT GACTC GGTCCTCAA			
			A G			
GAM2407	LOC154877	3'	AACTCCTGGGCTCAAGTGATCC	87512	C	G
			GGATCAC TGAG TCAGGAGTT			
			CCTAGTG ACTC GGTCCTCAA			
			A G			
GAM2407	LOC154877	3'	GAACCTCCCGACCTCAGGTGATC	87547	A	
	TA		TGGATCACCTGAGGTC GGAGTTC			

		ATCTAGTGGACTCCAG CCTCAAG	
		C	
GAM2407	LOC154877 5'	GAACCTCCTAGGCTCAAGTGATC 87548	C G _
	C	GGATCAC TGAG TC AGGAGTTC	
		CCTAGTG ACTC GG TCCTCAAG	
		A _ A	
GAM2407	LOC154877 3'	GAACCTCCTGACCTTACGTGATC 87549	C
	CA	TGGATCAC TGAGGTCAGGAGTTC	
		ACCTAGTG ATTCCAGTCCTCAAG	
		C	
GAM2407	LOC154930 3'	GAACCTCCTGACTTGAAATGATC 82090	CCTG
	CA	TGGATCA AGGTCAGGAGTTC	
		ACCTAGT TTCAGTCCTCAAG	
		AAAG	
GAM2407	LOC157247 5'	GAACCTCCTGACCTCAGGTGATC 82296	
	CA	TGGATCACCTGAGGTCAGGAGTTC	
		ACCTAGTGGACTCCAGTCCTCAAG	
GAM2407	LOC157623 3'	AACTCCTGGGCTCAAGTGATCC 82405	C G
		GGATCAC TGAG TCAGGAGTT	
		CCTAGTG ACTC GGTCCTCAA	
		A G	
GAM2407	LOC157867 5'	AACTCCTGGCTTCAAGCAATCC 87871	CACC
		GGAT TGAGGTCAGGAGTT	
		CCTA ACTTCGGTCCTCAA	
		ACGA	
GAM2407	LOC158310 5'	GAACCTCCTGACCTTAAGTGATC 88081	C
	CA	TGGATCAC TGAGGTCAGGAGTTC	
		ACCTAGTG ATTCCAGTCCTCAAG	
		A	
GAM2407	LOC158476 3'	GAACCTCCTGACCCCAGGTGATC 88193	A
	C	GGATCACCTG GGTCAGGAGTTC	
		CCTAGTGGAC CCAGTCCTCAAG	
		C	
GAM2407	LOC158865 5'	GAACCTCCTGACCTCAAGTGAT 88307	C
		ATCAC TGAGGTCAGGAGTTC	
		TAGTG ACTCCAGTCCTCAAG	
		A	
GAM2407	LOC160646 3'	GAACCTCCTGACCTTCAGGTGAT 83111	_
	CCA	TGGATCACCTGA GGTCAGGAGTTC	

		ACCTAGTGGACT CCAGTCCTCAAG	
		T	
GAM2407	LOC162427 3'	AACTCCTGACCTCAAGTGAGCT 83217	A C
		GG TCAC TGAGGTCAGGAGTT	
		TC AGTG ACTCCAGTCCTCAA	
		G A	
GAM2407	LOC162461 5'	GAACCTCCTAGGCTCAAGTGATC 83238	C G _
	C	GGATCAC TGAG TC AGGAGTTC	
		CCTAGTG ACTC GG TCCTCAAG	
		A _ A	
GAM2407	LOC169611 3'	AACTCCTGACCTCAGGTGATCC 83627	
	A	TGGATCACCTGAGGTCAGGAGTT	
		ACCTAGTGGACTCCAGTCCTCAA	
GAM2407	LOC169611 3'	GAACCTCCTGACCTTAGGTGATC 83648	
	C	GGATCACCTGAGGTCAGGAGTTC	
		CCTAGTGGATTCCAGTCCTCAAG	
GAM2407	LOC196047 5'	AACTCCTGACCTCAGGTGATCC 91133	
	A	TGGATCACCTGAGGTCAGGAGTT	
		ACCTAGTGGACTCCAGTCCTCAA	
GAM2407	LOC196529 3'	GAACCTCCTGATCTCAGGCAATC 89132	CA
	CA	TGGAT CCTGAGGTCAGGAGTTC	
		ACCTA GGACTCTAGTCCTCAAG	
		AC	
GAM2407	LOC196957 3'	GAACCTCCTGGGCTCAAGTGATC 89187	C G
	C	GGATCAC TGAG TCAGGAGTTC	
		CCTAGTG ACTC GGTCCTCAAG	
		A G	
GAM2407	LOC196961 3'	GAACCTCCTGGGCTCAAGTGATC 89201	C G
	C	GGATCAC TGAG TCAGGAGTTC	
		CCTAGTG ACTC GGTCCTCAAG	
		A G	
GAM2407	LOC197138 3'	GAACCTCCTGGGCTCAAGTGATC 89250	C G
	C	GGATCAC TGAG TCAGGAGTTC	
		CCTAGTG ACTC GGTCCTCAAG	
		A G	
GAM2407	LOC197358 3'	AACTCCTGACCTCAAGTGATCC 89403	C
	A	TGGATCAC TGAGGTCAGGAGTT	

	ACCTAGTG ACTCCAGTCCTCAA	
	A	
GAM2407 LOC197358 3'	GAACCTCCTGACCTCAGGTGATC 89431	
CA	TGGATCACCTGAGGTCAGGAGTTC	
	ACCTAGTGGACTCCAGTCCTCAAG	
GAM2407 LOC199725 5'	GAACCTCCTGACCTCGTGATC 91418	CT
	GATCAC GAGGTCAGGAGTTC	
	CTAGTG CTCCAGTCCTCAAG	
GAM2407 LOC199786 3'	AACTCCTGGACTCAAGCAATCC 89729	CACC GT
	GGAT TGAG CAGGAGTT	
	CCTA ACTC GTCCTCAA	
	ACGA AG	
GAM2407 LOC199786 3'	GAACCTCCTGACCTCATGATCC 89752	CC
	GGATCA TGAGGTCAGGAGTTC	
	CCTAGT ACTCCAGTCCTCAAG	
GAM2407 LOC199906 3'	AACTCCTGACCTCAGGCGATCC 89838	A
	GGATC CCTGAGGTCAGGAGTT	
	CCTAG GGACTCCAGTCCTCAA	
	C	
GAM2407 LOC200014 3'	GAACCTCCTGACCTCATGATCCA 89934	CC
	TGGATCA TGAGGTCAGGAGTTC	
	ACCTAGT ACTCCAGTCCTCAAG	
GAM2407 LOC200314 3'	GAACCTCCTGACCTCAGGTGATC 91599	
CA	TGGATCACCTGAGGTCAGGAGTTC	
	ACCTAGTGGACTCCAGTCCTCAAG	
GAM2407 LOC200316 3'	GAACCTCCTGACCTCAGGTGATC 90180	
T	GGATCACCTGAGGTCAGGAGTTC	
	TCTAGTGGACTCCAGTCCTCAAG	
GAM2407 LOC200339 3'	GAACCTCCTGGCCTCAAGCGATC 91615	ACC
CA	TGGATC TGAGGTCAGGAGTTC	
	ACCTAG ACTCCGGTCCTCAAG	
	CGA	
GAM2407 LOC200407 3'	AACTCCTGACCTCAGGTGATCC 91621	
A	TGGATCACCTGAGGTCAGGAGTT	

ACCTAGTGGACTCCAGTCCTCAA

GAM2407 LOC201164 3' AACTCCTGACCTCAAGTGATCC 89480 C
A TGGATCAC TGAGGTCAGGAGTT

||||||| |||||||||
ACCTAGTG ACTCCAGTCCTCAA

A

GAM2407 LOC201411 3' GAACTCCAGACCTCAGGTGATC 63641 A
TA TGGATCACCTGAGGTC GGAGTTC

||||||||||| |||||
ATCTAGTGGACTCCAG CCTCAAG

A

GAM2407 LOC201510 3' AACTCCTGGTCTCAAGTGATCC 89627 C GT
GGATCAC TGAG CAGGAGTT

||||| ||| |||||||
CCTAGTG ACTC GTCCTCAA

A TG

GAM2407 LOC201626 3' GAACTCCTGACCTCAGGTGATC 90432
CA TGGATCACCTGAGGTCAGGAGTTC

|||||||||||
ACCTAGTGGACTCCAGTCCTCAAG

GAM2407 LOC201627 3' AACTCCCGACCTCAGGTGATCC 90442 A
GGATCACCTGAGGTC GGAGTT

||||||||||| |||||
CCTAGTGGACTCCAG CCTCAA

C

GAM2407 LOC203197 3' ACTCCTGACCTCAGGTGATCCA 90799
TGGATCACCTGAGGTCAGGAGT

|||||||||||
ACCTAGTGGACTCCAGTCCTCA

GAM2407 LOC203197 3' GAACTCCTGACCTCAGGTGATC 90811
CA TGGATCACCTGAGGTCAGGAGTTC

|||||||||||
ACCTAGTGGACTCCAGTCCTCAAG

GAM2407 LOC203378 3' AACTCCTCCACTCAGGTGATCC 92267 GTC
A TGGATCACCTGAG AGGAGTT

||||||||| |||||
ACCTAGTGGACTC TCCTCAA

ACC

GAM2407 LOC204804 3' GAACTCCTGGCCTCAGGTGATC 91042
CA TGGATCACCTGAGGTCAGGAGTTC

|||||||||||
ACCTAGTGGACTCCGGTCCTCAAG

GAM2407 LOC219529 5' AACTCCTGAGCCCAGGTGATCC 94560 A _
GGATCACCTG GG TCAGGAGTT

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		CCTAGTGGAC CC AGTCCTCAA		
		— G		
GAM2407	LOC219673 5'	AACGCCTGACCTCAAGTAATCC 94603	C C	A
	A	TGGAT AC TGAGGTCAGG GTT		
		ACCTA TG ACTCCAGTCC CAA		
		A A G		
GAM2407	LOC219673 5'	GAACCTCCTGGGCTCAAGTGATC 94624	C G	
	C	GGATCAC TGAG TCAGGAGTTC		
		CCTAGTG ACTC GGTCCTCAAG		
		A G		
GAM2407	LOC220074 3'	AACTCCTGACCTCAGGTGATCT 59949		
		GGATCACCTGAGGTCAGGAGTT		
		TCTAGTGGACTCCAGTCCTCAA		
GAM2407	LOC220074 3'	GAACCTCCTGACCTCAGGTGATC 59977		
	C	GGATCACCTGAGGTCAGGAGTTC		
		CCTAGTGGACTCCAGTCCTCAAG		
GAM2407	LOC220662 3'	GAACCTCCTGGACTCAAGCAATC 92818	CACC	GT
	C	GGAT TGAG CAGGAGTTC		
		CCTA ACTC GTCCTCAAG		
		ACGA AG		
GAM2407	LOC221060 3'	GAACCTCCTGACCTCAGGTGATC 94831		
	C	GGATCACCTGAGGTCAGGAGTTC		
		CCTAGTGGACTCCAGTCCTCAAG		
GAM2407	LOC221964 3'	GAACCTCCTGACCTCAGGTGATC 95605		
	CA	TGGATCACCTGAGGTCAGGAGTTC		
		ACCTAGTGGACTCCAGTCCTCAAG		
GAM2407	LOC222031 3'	GAACCTCCTGACCTCAGGTGATC 95680		
	CA	TGGATCACCTGAGGTCAGGAGTTC		
		ACCTAGTGGACTCCAGTCCTCAAG		
GAM2407	LOC222068 3'	GACTCCTGACCTCAGTTGATCC 94275	C	
	A	TGGATCA CTGAGGTCAGGAGTT		
		ACCTAGT GACTCCAGTCCTCAG		
		T		
GAM2407	LOC222070 5'	GAACCTCCTGGCCTCAAGTGACC 95814	A C	
	C	GG TCAC TGAGGTCAGGAGTTC		

		CC AGTG ACTCCGGTCCTCAAG	
		C A	
GAM2407	LOC245771 5'	GAACCTCCTGACCTCAAGTGATC 94473	C
	CA	TGGATCAC TGAGGTCAGGAGTTC	
		ACCTAGTG ACTCCAGTCCTCAAG	
		A	
GAM2407	LOC253805 3'	GAACCTCCTGACCTCAGATGATT 98174	C
	CA	TGGATCA CTGAGGTCAGGAGTTC	
		ACTTAGT GACTCCAGTCCTCAAG	
		A	
GAM2407	LOC253981 3'	GAACCTCCTGACCTCAGGCGATC 97536	A
	TA	TGGATC CCTGAGGTCAGGAGTTC	
		ATCTAG GGA CTCCAGTCCTCAAG	
		C	
GAM2407	LOC254268 3'	AACTCCTGACCTCAAGTGATCC 97133	C
		GGATCAC TGAGGTCAGGAGTT	
		CCTAGTG ACTCCAGTCCTCAA	
		A	
GAM2407	LOC254351 5'	AGCTCCTGACCTCGGGTGATCC 96681	
	A	TGGATCACCTGAGGTCAGGAGTT	
		ACCTAGTGGGCTCCAGTCCTCGA	
GAM2407	LOC254532 5'	AACTCCTGACCTCAAGTGATCC 98441	C
	A	TGGATCAC TGAGGTCAGGAGTT	
		ACCTAGTG ACTCCAGTCCTCAA	
		A	
GAM2407	LOC254655 3'	GAACCTCCTGACCTCAGGTGATC 97219	
	CA	TGGATCACCTGAGGTCAGGAGTTC	
		ACCTAGTGGACTCCAGTCCTCAAG	
GAM2407	LOC254672 3'	GAACCTCCTGACCCTGTGATCCA 96294	CTGA
		TGGATCAC GGT CAGGAGTTC	
		ACCTAGTG CCAGTCCTCAAG	
		TC__	
GAM2407	LOC254778 3'	AACTCCTGGGTTCAAGAGATCC 97825	ACC G
	A	TGGATC TGAG TCAGGAGTT	
		ACCTAG ACTT GGT CCTCAA	
		AGA G	
GAM2407	LOC255065 5'	AACTCCTGACCTCAAGTAATCC 98367	C C
	A	TGGAT AC TGAGGTCAGGAGTT	

	ACCTA TG ACTCCAGTCCTCAA		
	A A		
GAM2407 LOC255065 5'	CCTGACCTCAAGTAATCCA 98370	C C	
	TGGAT AC TGAGGTCAGG		
	ACCTA TG ACTCCAGTCC		
	A A		
GAM2407 LOC255458 5'	AACTCCTGGGCTCAAGCGATCC 98930	ACC G	
	GGATC TGAG TCAGGAGTT		
	CCTAG ACTC GGTCCTCAA		
	CGA G		
GAM2407 LOC255497 3'	AACTCCTGACCTCAGGTG 98978		
	CACCTGAGGTCAGGAGTT		
	GTGGACTCCAGTCCTCAA		
GAM2407 LOC255707 3'	TCTTGAAGTCAAGTGATCCA 98733	C G	
	TGGATCAC TGAG TCAGGA		
	ACCTAGTG ACTC AGTTCT		
	A A		
GAM2407 LOC256306 3'	GAACACCTGACCTCAAATGATC 98514	CC A	
C	GGATCA TGAGGTCAGG GTTC		
	CCTAGT ACTCCAGTCC CAAG		
	AA A		
GAM2407 LOC256364 5'	AACTCCTGGCCTCAGGTGACCC 96440	A	
	GG TCACCTGAGGTCAGGAGTT		
	CC AGTGGACTCCGGTCCTCAA		
	C		
GAM2407 LOC257127 5'	GAACCTCCTGACCTCAGGTGATC 98496		
C	GGATCACCTGAGGTCAGGAGTTC		
	CCTAGTGGACTCCAGTCCTCAAG		
GAM2407 LOC257465 3'	GAACCTCCTGACCTTGGTGATCC 82495	T	
A	TGGATCACC GAGGTCAGGAGTTC		
	ACCTAGTGG TTCCAGTCCTCAAG		
GAM2407 LOC51008 5'	GAACCTCCCGACCTCAGGTGATC 32532	A	
CA	TGGATCACCTGAGGTC GGAGTTC		
	ACCTAGTGGACTCCAG CCTCAAG		
	C		
GAM2407 LOC51193 3'	AACTCCTGGACTCAAGCAATCC 33352	CACC GT	
	GGAT TGAG CAGGAGTT		

		CCTA ACTC GTCCTCAA		
		ACGA AG		
GAM2407	LOC51200 3'	AACTCCCAACCTCAGGTGATCT 33430	CA	
		GGATCACCTGAGGT GGAGTT		
		TCTAGTGGACTCCA CCTCAA		
		AC		
GAM2407	LOC51219 5'	GAACTCCCGACCTCAGGTGATC 33544	A	
	T	GGATCACCTGAGGTC GGAGTTC		
		TCTAGTGGACTCCAG CCTCAAG		
		C		
GAM2407	LOC57107 3'	GAACTCCTGACCTCAGGTGATC 40187		
	C	GGATCACCTGAGGTCAGGAGTTC		
		CCTAGTGGACTCCAGTCCTCAAG		
GAM2407	LOC57146 3'	AACTCCTGACCTCAGGTGCTCC 40285	T	
	A	TGGA CACCTGAGGTCAGGAGTT		
		ACCT GTGGACTCCAGTCCTCAA		
		C		
GAM2407	LOC89231 3'	GAACTCCTGGACTCAAGCAATC 94298	CACC GT	
	C	GGAT TGAG CAGGAGTTC		
		CCTA ACTC GTCCTCAAG		
		ACGA AG		
GAM2407	LOC89932 3'	GAACTCCCGACCTCAGGTAATC 61459	C A	
	C	GGAT ACCTGAGGTC GGAGTTC		
		CCTA TGGACTCCAG CCTCAAG		
		A C		
GAM2407	LOC90072 3'	GAACTCCCGACCTCAAGTGATC 61958	C A	
	C	GGATCAC TGAGGTC GGAGTTC		
		CCTAGTG ACTCCAG CCTCAAG		
		A C		
GAM2407	LOC90110 5'	GAACTTCTGACCTCAAGTGGTC 62178	C	
	CA	TGGATCAC TGAGGTCAGGAGTTC		
		ACCTGGTG ACTCCAGTCTTCAAG		
		A		
GAM2407	LOC90288 3'	GAACTACTGACCTCAGCTGATC 62788	C G	
	CA	TGGATCA CTGAGGTCAG AGTTC		
		ACCTAGT GACTCCAGTC TCAAG		
		C A		
GAM2407	LOC90408 5'	GAACTCCTGACTTCAAGTGATC 63344	C	
	CA	TGGATCAC TGAGGTCAGGAGTTC		

		ACCTAGTG ACTTCAGTCCTCAAG	
		A	
GAM2407	LOC90459 3'	GAACTCCTGACCTCAAGTGATT 63555	C
	T	GGATCAC TGAGGTCAGGAGTTC	
		TTTAGTG ACTCCAGTCCTCAAG	
		A	
GAM2407	LOC90591 3'	GAACTCCTGACCTCAGGTGATC 64166	
	CA	TGGATCACCTGAGGTCAGGAGTTC	
		ACCTAGTGGACTCCAGTCCTCAAG	
GAM2407	LOC90591 3'	GAACTCCTGACCTGAAGTGATC 64167	CTG
	CA	TGGATCAC AGGTCAGGAGTTC	
		ACCTAGTG TCCAGTCCTCAAG	
		AAG	
GAM2407	LOC91115 3'	AACTCCTGACCTCAGATGGTCC 65532	C
	A	TGGATCA CTGAGGTCAGGAGTT	
		ACCTGGT GACTCCAGTCCTCAA	
		A	
GAM2407	LOC91547 3'	GAACTCCTGGGCTCAAGTGATC 67002	C G
	C	GGATCAC TGAG TCAGGAGTTC	
		CCTAGTG ACTC GGTCCTCAAG	
		A G	
GAM2407	LOC91561 5'	GAACTCCTGACCTCAGGTGATC 67043	
	T	GGATCACCTGAGGTCAGGAGTTC	
		TCTAGTGGACTCCAGTCCTCAAG	
GAM2407	LOC92267 3'	AACTCCTGACCTCAAGTGATCC 69159	C
		GGATCAC TGAGGTCAGGAGTT	
		CCTAGTG ACTCCAGTCCTCAA	
		A	
GAM2407	LOC92303 3'	GAATTCCAGACCTCAGGTGATC 69391	A
	CA	TGGATCACCTGAGGTC GGAGTTC	
		ACCTAGTGGACTCCAG CCTTAAG	
		A	
GAM2407	LOC92697 5'	GAACTCCCAACCTCAGGTGATC 70810	CA
	C	GGATCACCTGAGGT GGAGTTC	
		CCTAGTGGACTCCA CCTCAAG	
		AC	
GAM2407	LOC92841 3'	GAACTCCTGACCTCAAGTGATC 71252	C
	C	GGATCAC TGAGGTCAGGAGTTC	

		CCTAGTG ACTCCAGTCCTCAAG		
		A		
GAM2407	LOC92876	5' GACTCCTGACCTCAGGTGATCC 71349		
	A	TGGATCACCTGAGGTCAGGAGTT		
		ACCTAGTGGACTCCAGTCCTCAG		
GAM2407	LOC93408	5' AACTCCTGGCCTCAAGTGATCC 57281		C
		GGATCAC TGAGGTCAGGAGTT		
		CCTAGTG ACTCCGGTCCTCAA		
		A		
GAM2408	ADAMTS4	3' GGGGTTTCACCATGTTGGCCA 18766		
		TGGCCAACATGGTGAAATCCC		
		ACCGGTTGTACCACTTTGGGG		
GAM2408	ADAMTS4	3' GGGTTTCACCATGTTGGCCA 18768		
		TGGCCAACATGGTGAAATCC		
		ACCGGTTGTACCACTTTGGG		
GAM2408	ADCY6	5' GGTTTCACCATCTTGGCCA 31591		C
		TGGCCAA ATGGTGAAATC		
		ACCGGTT TACCACTTTGG		
		C		
GAM2408	ALDH1B1	3' ATGAGGTTTCACCATTTTGGCC 7316		C
	A	TGGCCAA ATGGTGAAATC CAT		C
		ACCGGTT TACCACTTTGG GTA		
		T A		
GAM2408	APAF1	3' GGGGTTTCACCATGTTGGCC 8589		
		GGCCAACATGGTGAAATCCC		
		CCGGTTGTACCACTTTGGGG		
GAM2408	APAF1	3' GGGGTTTCACCATGTTGGCC 25976		
		GGCCAACATGGTGAAATCCC		
		CCGGTTGTACCACTTTGGGG		
GAM2408	APM1	3' GGGTTTCACCATATTGGCCA 17786		C
		TGGCCAA ATGGTGAAATCC		
		ACCGGTT TACCACTTTGGG		
		A		
GAM2408	APOL1	3' ATGGGGTTTCACCATGTTGGCC 14728		
	A	TGGCCAACATGGTGAAATCCCAT		

ACCGGTTGTACCACTTTGGGGTA

GAM2408 APPL 3' GGGGTTTCACCGTGTTAGCCA 24950 C
TGGC AACATGGTGAAATCCC
|||||
ACCG TTGTGCCACTTTGGGG
A

GAM2408 ARSF 5' GGCTCTCACCATGTTGACCA 65209 C AAT
TGG CAACATGGTGA CC
||| ||||| ||
ACC GTTGTACCACT GG
A CTC

GAM2408 ATM 3' GTTTCACCATATTGCCCA 57148 C C
TGG CAA ATGGTGAAAT
||| ||| |||||
ACC GTT TACCACTTTG
C A

GAM2408 ATP6V1A1 3' GGGGTTTCACCATATTGGTCA 9870 C
TGGCCAA ATGGTGAAATCCC
||||| |||||
ACTGGTT TACCACTTTGGGG
A

GAM2408 ATP8B2 3' GTTTCACCATGTTGGCCA 65847
TGGCCAACATGGTGAAAT
|||||
ACCGGTTGTACCACTTTG

GAM2408 AXL 3' GGGTTTCACCATGTTGGCCA 41889
TGGCCAACATGGTGAAATCC
|||||
ACCGGTTGTACCACTTTGGG

GAM2408 AXL 3' GGGTTTCACCATGTTGGCCA 9907
TGGCCAACATGGTGAAATCC
|||||
ACCGGTTGTACCACTTTGGG

GAM2408 BRIP1 3' ATGGGGTTTCACCATGTTGGCC 50206
A TGGCCAACATGGTGAAATCCCAT
|||||
ACCGGTTGTACCACTTTGGGGTA

GAM2408 C7 3' ATGGGGTTTCACCATGTTGGCCA 6980 T
TGGCCAACATGGTGAAA CCCAT
||||| |||||
ACCGGTTGTACCACTTT GGGTA

GAM2408 CASP2 3' GGGTTTCACCATGTTAGCC 8715 C
—
GGC AACATGGTGAAATCC
||| |||||

			CCG TTGTACCACTTTGGG		
			A		
GAM2408	CASP2	3'	GGGTTTCACCATGTTAGCC 53291	C	
			GGC AACATGGTGAAATCC		
			CCG TTGTACCACTTTGGG		
			A		
GAM2408	CASP2	3'	GGGTTTCACCATGTTAGCC 53307	C	
			GGC AACATGGTGAAATCC		
			CCG TTGTACCACTTTGGG		
			A		
GAM2408	CASP2	3'	GGGTTTCACCATGTTAGCC 53339	C	
			GGC AACATGGTGAAATCC		
			CCG TTGTACCACTTTGGG		
			A		
GAM2408	CCNF	3'	GGGATTTACCATGTTGGCCA 10080		
			TGGCCAACATGGTGAAATCCC		
			ACCGGTTGTACCACTTTAGGG		
GAM2408	CDC6	3'	GGGTTTACCATGTTGGCCA 8823		
			TGGCCAACATGGTGAAATCC		
			ACCGGTTGTACCATTTTGGG		
GAM2408	CLECSF11	5'	ATGGGGTTTCACTATGTTGGCC 56146		
	A		TGGCCAACATGGTGAAATCCCAT		
			ACCGGTTGTATCACTTTGGGGTA		
GAM2408	CNGA1	5'	ATGGGATTTACCATGTTGGCC 60233		
	A		TGGCCAACATGGTGAAATCCCAT		
			ACCGGTTGTACCACTTTAGGGTA		
GAM2408	CNN2	3'	ATGGGGTTTCCCATGTTGGCC 16456	T	
	A		TGGCCAACATGG GAAATCCCAT		
			ACCGGTTGTACC CTTTGGGGTA		
			C		
GAM2408	CPM	3'	GACTTCACCATAAGGCCA 60408	AAC	A
			TGGCC ATGGTGAA TC		
			ACCGG TACCACTT AG		
			AA_ C		
GAM2408	CR1	3'	GGGGTTTCACCATGTTAGCCA 6945	C	
			TGGC AACATGGTGAAATCCC		

			ACCG TTGTACCACTTTGGGG		
			A		
GAM2408	CXCL16	3'	GGGGTTTCACCATGTTGACCA 42173	C	
			TGG CAACATGGTGAAATCCC		
			ACC GTTGTACCACTTTGGGG		
			A		
GAM2408	CYP1A2	3'	ATGGGGTTTCACCATGTTGGCC 7502		
	A		TGGCCAACATGGTGAAATCCCAT		
			ACCGGTTGTACCACTTTGGGGTA		
GAM2408	CYP1A2	3'	GGGTTTCACCATGTTGGTCA 7519		
			TGGCCAACATGGTGAAATCC		
			ACTGGTTGTACCACTTTGGG		
GAM2408	DFFB	3'	GGGGTTTCACCATGTTGGCCA 88776		
			TGGCCAACATGGTGAAATCCC		
			ACCGGTTGTACCACTTTGGGG		
GAM2408	DFFB	3'	GGGGTTTCACCATGTTGGTCA 88778		
			TGGCCAACATGGTGAAATCCC		
			ACTGGTTGTACCACTTTGGGG		
GAM2408	DHFR	3'	ATGGGGTTTCACCATGTTGGTC 7642		
	A		TGGCCAACATGGTGAAATCCCAT		
			ACTGGTTGTACCACTTTGGGGTA		
GAM2408	DISC1	3'	GGGCTTCACCATGTTGGCTA 38510	AT	
			TGGCCAACATGGTGAA CCC		
			ATCGGTTGTACCACTT GGG		
			C_		
GAM2408	DSCR3	3'	GGGGCTTCACCATCTTGGCCA 21319	C	AT
			TGGCCAA ATGGTGAA CCC		
			ACCGGTT TACCACTT GGG		
			C CG		
GAM2408	EHD2	3'	ATGGGATTACAGGCATGAGCCA 28215	CAA	G_ A
			TGGC CATG TG AATCCCAT		
			ACCG GTAC AC TTAGGGTA		
			A_ GG A		
GAM2408	EHD2	3'	GGGGTTTCACCATGTTGGCCA 28225		
			TGGCCAACATGGTGAAATCCC		

ACCGGTTGTACCACTTTGGGG

GAM2408 EPB72 3' GGGGTTTCACCATGTTGGCCA 15878
TGGCCAACATGGTGAAATCCC
|||||
ACCGGTTGTACCACTTTGGGG

GAM2408 F2RL2 3' GGGGTTTCACCATGTTGACCA 15898 C
TGG CAACATGGTGAAATCCC
||| |||||
ACC GTTGTACCACTTTGGGG
A

GAM2408 F2RL3 3' GGAGTTTCACCATGTTGGCCA 15522 TC
TGGCCAACATGGTGAAA CC
||||| ||
ACCGGTTGTACCACTTT GG
GA

GAM2408 F3 3' ATGGGGTTTCACCATCTTGGCC 67673 C
A TGGCCAA ATGGTGAAATCCCAT
||||| |||||
ACCGGTT TACCACTTTGGGGTA
C

GAM2408 FANCF 3' GGGGTTTCACCATGCTGGCCA 42982 A
TGGCCA CATGGTGAAATCCC
||||| |||||
ACCGGT GTACCACTTTGGGG
C

GAM2408 FCAR 3' GGGTTTCACCATGTTGGCCA 56638
TGGCCAACATGGTGAAATCC
|||||
ACCGGTTGTACCACTTTGGG

GAM2408 FCRH1 3' GATTTCACCGTTTTGCCCA 54728 C C
TGG CAA ATGGTGAAATC
||| ||| |||||
ACC GTT TGCCACTTTAG
C T

GAM2408 FEZ1 3' ATGGGAGTTTCACCATGTTGGC 42867 —
CA TGGCCAACATGGTGAAA TCCCAT
||||| |||||
ACCGGTTGTACCACTTT AGGGTA
G

GAM2408 FGF5 3' GGGGTTTCACCATGTTGGTCA 16761
TGGCCAACATGGTGAAATCCC
|||||
ACTGGTTGTACCACTTTGGGG

GAM2408 FGF5 3' GGGGTTTCACCATGTTGGTCA 53663
TGGCCAACATGGTGAAATCCC
|||||

ACTGGTTGTACCACTTTGGGG

GAM2408 FUT1 3' GGGTTTCACCATGTTGGCC 5604
GGCCAACATGGTGAAATCC
|||||
CCGGTTGTACCACTTTGGG

GAM2408 G6PC 3' ATGGGATTTTCATCATGTTGGCC 5653
A TGGCCAACATGGTGAAATCCCAT
|||||
ACCGTTGTACTACTTTAGGGTA

GAM2408 GHR 3' GGGGTTTCACCATGTTGGCCA 5704
TGGCCAACATGGTGAAATCCC
|||||
ACCGTTGTACCACTTTGGGG

GAM2408 GM2A 3' ATGGGGTTTCACCATGTTGGCC 68375
A TGGCCAACATGGTGAAATCCCAT
|||||
ACCGTTGTACCACTTTGGGGTA

GAM2408 GNE 3' GGGTTTCACCATGTTGGCCA 19674
TGGCCAACATGGTGAAATCC
|||||
ACCGTTGTACCACTTTGGG

GAM2408 GRM7 5' GTTTCACCATGTTGGCCA 7789
TGGCCAACATGGTGAAAT
|||||
ACCGTTGTACCACTTTG

GAM2408 HCS 3' ATGGTGTTTCACCATGTTGGCC 38968 TC
A TGGCCAACATGGTGAAA CCAT
||||| ||||
ACCGTTGTACCACTTT GGTA
GT

GAM2408 HTR1D 3' GGGGTTTCATCATGTTGGCCA 7845
TGGCCAACATGGTGAAATCCC
|||||
ACCGTTGTACTACTTTGGGG

GAM2408 HTR1E 5' GGGATTTTCACCATGTTGGCCA 7862
TGGCCAACATGGTGAAATCCC
|||||
ACCGTTGTACCACTTTAGGG

GAM2408 HYAL4 5' ATGGGGTTTCACCGTGTGGCC 25364
A TGGCCAACATGGTGAAATCCCAT
|||||

ACCGGTTGTGCCACTTTGGGGTA

GAM2408 IFNAR2 3' GGATTTTACCATGTTGGCCA 7902
TGGCCAACATGGTGAAATCC
|||||
ACCGGTTGTACCATTTTAGG

GAM2408 IGF1 3' GGGGTTTTACCATGTTGGCCA 7077
TGGCCAACATGGTGAAATCCC
|||||
ACCGGTTGTACCATTTTGGGG

GAM2408 IL11 3' GGGTTTCACCATGTTGGCCA 7192
TGGCCAACATGGTGAAATCC
|||||
ACCGGTTGTACCACTTTGGG

GAM2408 INMT 3' ATGGGGTTTCACCGTGTTAGCC 23208 C
A TGGC AACATGGTGAAATCCCAT
||| |||||
ACCG TTGTGCCACTTTGGGGTA
A

GAM2408 JAK3 3' ATGAGGTTTCACCATGATGGCC 5826 A C
A TGGCCA CATGGTGAAATC CAT
||||| ||||| |||
ACCGGT GTACCACTTTGG GTA
A A

GAM2408 LLGL1 3' ATGGGGTTTCACCATGTTAGCC 67414 C
A TGGC AACATGGTGAAATCCCAT
||| |||||
ACCG TTGTACCACTTTGGGGTA
A

GAM2408 LNK 3' GGGTTTCACCATGTTGGCCA 19648
TGGCCAACATGGTGAAATCC
|||||
ACCGGTTGTACCACTTTGGG

GAM2408 LTB4R 5' GGGGTTTCACCATGTTGGCCA 7469
TGGCCAACATGGTGAAATCCC
|||||
ACCGGTTGTACCACTTTGGGG

GAM2408 LYZ 3' GGGTTTCACCGTGTTAGCCA 5898 C
TGGC AACATGGTGAAATCC
||| |||||
ACCG TTGTGCCACTTTGGG
A

GAM2408 MAK 3' GGGTTTCACCATGTTGGTCA 20949
TGGCCAACATGGTGAAATCC
|||||

ACTGGTTGTACCACTTTGGG

GAM2408	MDM2	3'	GGGTTTCACCGTGTTAGCCA	23459	C	
			TGGC AACATGGTGAAATCC			
			ACCG TTGTGCCACTTTGGG			
			A			
GAM2408	MDM2	3'	GGGTTTCACCGTGTTAGCCA	23472	C	
			TGGC AACATGGTGAAATCC			
			ACCG TTGTGCCACTTTGGG			
			A			
GAM2408	MDM2	3'	GGGTTTCACCGTGTTAGCCA	23485	C	
			TGGC AACATGGTGAAATCC			
			ACCG TTGTGCCACTTTGGG			
			A			
GAM2408	MDM2	3'	GGGTTTCACCGTGTTAGCCA	23498	C	
			TGGC AACATGGTGAAATCC			
			ACCG TTGTGCCACTTTGGG			
			A			
GAM2408	MDM2	3'	GGGTTTCACCGTGTTAGCCA	11496	C	
			TGGC AACATGGTGAAATCC			
			ACCG TTGTGCCACTTTGGG			
			A			
GAM2408	MEF2A	5'	ATGGAGTTTCACCATGTTGGCC	19991		TC
	A		TGGCCAACATGGTGAAA CCAT			
			ACCGTTGTACCACTTT GGTA			
			GA			
GAM2408	MEFV	3'	ATGAGGTTTCATCATGTTGGCC	5927		C
	A		TGGCCAACATGGTGAAATC CAT			
			ACCGTTGTACTACTTTGG GTA			
			A			
GAM2408	MEFV	3'	GGGGTTTCACCATGTTAGCCA	5940	C	
			TGGC AACATGGTGAAATCCC			
			ACCG TTGTACCACTTTGGGG			
			A			
GAM2408	MFI2	3'	GGGGTCTCACCATGTTGCCCA	53971	C	A
			TGG CAACATGGTGA ATCCC			
			ACC GTTGTACCACT TGGGG			
			C C			
GAM2408	MRPL49	3'	ATGGGGTTTCACCATGTTGGCC	70161		
	A		TGGCCAACATGGTGAAATCCCAT			

ACCGGTTGTACCACTTTGGGGTA

GAM2408	MTR	3'	GGATTTC	ACTGTG	TTAGCCA	6022	C	
			TGGC	AACATGGT	GAAATCC			
			ACCG	TTGTGTCACT	TTTAGG			
			A					
GAM2408	MYCL2	3'	ATGGGGT	TTTCACCACATT	TGGCC	19370	CA	
	A		TGGCCAA	TGGT	GAAATCCC	AT		
			ACCGGTT	ACCACTTT	GGGGTA			
			AC					
GAM2408	NCOA6	5'	ATGGGGT	TTTCATCATGTT	TGGCC	26828		
	A		TGGCCAACATGGT	GAAATCCC	AT			
			ACCGGTTGTACTACTTT	GGGGTA				
GAM2408	NCOA6IP	3'	GGTCCCACCATGTT	TGCCCA	46156	C	AA	
			TGG	CAACATGGTG	ATC			
			ACC	GTTGTACCAC	TGG			
			C	CC				
GAM2408	NDRG3	3'	ATGGAGTTTCACCATGTT	TGGCC	50117		TC	
	A		TGGCCAACATGGT	GAAA	CCAT			
			ACCGGTTGTACCACTTT	GGTA				
			GA					
GAM2408	NQO1	3'	GGCGTTTCACCATGTT	TGGCCA	8050		C	
			TGGCCAACATGGT	GAAAT	CC			
			ACCGGTTGTACCACTTTG	GG				
			C					
GAM2408	ORC1L	3'	GGGCTTCACCATGTT	TGCCA	15983	C	AT	
			TGGC	AACATGGTGAA	CCC			
			ACCG	TTGTACCACTT	GGG			
			—	C—				
GAM2408	PCDHA9	3'	ATGGGGT	TTTCATCATGTT	TGGCC	26611		
	A		TGGCCAACATGGT	GAAATCCC	AT			
			ACCGGTTGTACTACTTT	GGGGTA				
GAM2408	PCDHB11	3'	GGGGTTTCACCACGTT	TGGCC	38927		A	
			GGCCAAC	TGGT	GAAATCCC			
			CCGGTTG	ACCACTTT	GGGG			
			C					
GAM2408	PDE6B	3'	ATGGGGT	TTTCACCATATT	TGGGC	6070	G	C
	A		TG	CCAA	ATGGT	GAAATCCC	AT	

			AC GGTT TACCACTTTGGGGTA		
			G A		
GAM2408	PER2	3'	GGGTTTCACCATGTTGGCCA 43356		
			TGGCCAACATGGTGAAATCC		
			ACCGGTTGTACCACTTTGGG		
GAM2408	PIGR	3'	GGGTTTCACCGTGTTAGCCA 73004	C	
			TGGC AACATGGTGAAATCC		
			ACCG TTGTGCCACTTTGGG		
			A		
GAM2408	PIK3C2B	3'	GGGGTTTCACCATGTTGGCCA 12105		
			TGGCCAACATGGTGAAATCCC		
			ACCGGTTGTACCACTTTGGGG		
GAM2408	POU2AF1	3'	GGGGTTTCACCATGTTGGCCA 21746		
			TGGCCAACATGGTGAAATCCC		
			ACCGGTTGTACCACTTTGGGG		
GAM2408	PPID	3'	ATGGGGTTTCACCATATTGGTC 88820	C	
	A		TGGCCAA ATGGTGAAATCCCAT		
			ACTGGTT TACCACTTTGGGGTA		
			A		
GAM2408	PRKR	3'	GGGTTTCACCATGTTGGCCA 12350		
			TGGCCAACATGGTGAAATCC		
			ACCGGTTGTACCACTTTGGG		
GAM2408	PRKWNK3	3'	ATGGGGTTTCACTATGTTGGCC 62225		
	A		TGGCCAACATGGTGAAATCCCAT		
			ACCGGTTGTATCACTTTGGGGTA		
GAM2408	PTGES	3'	GGGTTTCACCATGTTGCCCA 18066	C	AT
			TGG CAACATGGTGAA CCC		
			ACC GTTGTACCACTT GGG		
			C		
GAM2408	PTGIS	3'	ATGGGATTTACCGTATTAGCC 8193	C C	
	A		TGGC AA ATGGTGAAATCCCAT		
			ACCG TT TGCCACTTTAGGGTA		
			A A		
GAM2408	RAB36	3'	GGTTTCACCATGTTAGCCA 18176	C	
			TGGC AACATGGTGAAATC		

			ACCG TTGTACCACTTTGG	
			A	
GAM2408	RABL2A	3'	GGGGTTTCACCATGTTGCCCA 26410	C
			TGG CAACATGGTCAAATCCC	
			ACC GTTGTACCACTTTGGGG	
			C	
GAM2408	RABL2B	3'	GGGGTTTCACCATGTTGCCCA 23981	C
			TGG CAACATGGTCAAATCCC	
			ACC GTTGTACCACTTTGGGG	
			C	
GAM2408	RBBP9	3'	GGGTTTCACCATGTTGGCCA 70694	
			TGGCCAACATGGTCAAATCC	
			ACCGGTTGTACCACTTTGGG	
GAM2408	RHD	3'	ATGGGGTTTCACCATGTTGGCC 32815	
	A		TGGCCAACATGGTCAAATCCCAT	
			ACCGGTTGTACCACTTTGGGGTA	
GAM2408	RHD	3'	GGGTTTCACCATGTTGGCTA 32830	
			TGGCCAACATGGTCAAATCC	
			ATCGGTTGTACCACTTTGGG	
GAM2408	RHD	3'	ATGGGGTTTCACCATGTTGGCC 33135	
	A		TGGCCAACATGGTCAAATCCCAT	
			ACCGGTTGTACCACTTTGGGGTA	
GAM2408	RHD	3'	GGGTTTCACCATGTTGGCTA 33144	
			TGGCCAACATGGTCAAATCC	
			ATCGGTTGTACCACTTTGGG	
GAM2408	RPH3AL	3'	ATGGGGTTTCTCCATGTTGGCC 23729	T
	A		TGGCCAACATGG GAAATCCCAT	
			ACCGGTTGTACC CTTTGGGGTA	
			T	
GAM2408	RPP30	3'	GGGGTTTCACCGTGTTAGCCA 22202	C
			TGGC AACATGGTCAAATCCC	
			ACCG TTGTGCCACTTTGGGG	
			A	
GAM2408	SAS	3'	GGGTTTCACCATGTTAGTCA 21104	C
			TGGC AACATGGTCAAATCC	

			ACTG TTGTACCACTTTGGG		
			A		
GAM2408	SCNN1G	3'	GGATCTCACTATGTTGCCCA 8301	C	A
			TGG CAACATGGTGA ATCC		
			ACC GTTGTATCACT TAGG		
			C C		
GAM2408	SED1	3'	GGGTTTCACCATATTGGTCA 28101	C	
			TGGCCAA ATGGTGAAATCC		
			ACTGGTT TACCACTTTGGG		
			A		
GAM2408	SED1	3'	GGGTTTCACCATATTGGTCA 28102	C	
			TGGCCAA ATGGTGAAATCC		
			ACTGGTT TACCACTTTGGG		
			A		
GAM2408	SEPN1	3'	ATGGGGTTTCACCATATTGGTC 66960	C	
	A		TGGCCAA ATGGTGAAATCCCAT		
			ACTGGTT TACCACTTTGGGGTA		
			A		
GAM2408	SEPX1	3'	TGAGGCCACACGTTGGCCA 33381	ATG	AAAT _
			TGGCCAAC GTG CC CA		
			ACCGGTTG CAC GG GT		
			CA_ C__ A		
GAM2408	SERPINB9	3'	GGGGTTTCACCGTGTTAGCCA 16024	C	
			TGGC AACATGGTGAAATCCC		
			ACCG TTGTGCCACTTTGGGG		
			A		
GAM2408	SH3BP2	3'	GGGATTTTATCATGTTGGCCA 13079		
			TGGCCAACATGGTGAAATCCC		
			ACCGGTTGTACTATTTTAGGG		
GAM2408	SH3BP2	3'	GTTTCACCATGTTGGCCA 13085		
			TGGCCAACATGGTGAAAT		
			ACCGGTTGTACCACTTTG		
GAM2408	SH3GL3	5'	ATGGGGTTTCACCATGTTGGCCA 13105		T
			TGGCCAACATGGTGAAA CCCAT		
			ACCGGTTGTACCACTTT GGGTA		
GAM2408	SHOX	3'	GGCGTTTCACCGTGTTGGCCA 6579		C
			TGGCCAACATGGTGAAAT CC		

			ACCGGTTGTGCCACTTTG GG	
			C	
GAM2408	SHOX	3'	ATGGGGTTTGACCATGTTGGCC 23515	G
	A		TGGCCAACATGGT AAATCCCAT	
			ACCGGTTGTACCA TTTGGGGTA	
			G	
GAM2408	SLA2	3'	ATGGGGTTTCACCACATTGGCC 50880	CA
	A		TGGCCAA TGGTGAAATCCCAT	
			ACCGGTT ACCACTTTGGGGTA	
			AC	
GAM2408	SLC14A2	5'	GGGGTTTCACCACATTGGCCA 24121	CA
			TGGCCAA TGGTGAAATCCC	
			ACCGGTT ACCACTTTGGGG	
			AC	
GAM2408	SLC15A1	3'	ATGGGGTTTCACCATGTTAACC 18635	CC
	A		TGG AACATGGTGAAATCCCAT	
			ACC TTGTACCACTTTGGGGTA	
			AA	
GAM2408	SMAC	5'	ATGGGGTTTCACCATGTTGGTC 58016	
	A		TGGCCAACATGGTGAAATCCCAT	
			ACTGGTTGTACCACTTTGGGGTA	
GAM2408	SNX15	3'	GGGGTTACACCATGTTGGCCA 74126	A
			TGGCCAACATGGTG AATCCC	
			ACCGGTTGTACCAC TTGGGG	
			A	
GAM2408	SPN	3'	ATGGGGTTTCACCATGTTGGCT 13369	
	A		TGGCCAACATGGTGAAATCCCAT	
			ATCGGTTGTACCACTTTGGGGTA	
GAM2408	SULT2B1	5'	GTTTCACCATGTTGGCCA 17226	
			TGGCCAACATGGTGAAAT	
			ACCGGTTGTACCACTTTG	
GAM2408	TAPBP	3'	GGGGTTTCACCATGTTGGCCA 13571	
			TGGCCAACATGGTGAAATCCC	
			ACCGGTTGTACCACTTTGGGG	
GAM2408	TAPBP	3'	GGGGTTTCACCGTGTTAGCCA 13573	C
			TGGC AACATGGTGAAATCCC	

			ACCG TTGTGCCACTTTGGGG		
			A		
GAM2408	TAPBP	3'	GGGGTTTCACCGTGTTAGCCA 13574	C	
			TGGC AACATGGTGAAATCCC		
			ACCG TTGTGCCACTTTGGGG		
			A		
GAM2408	TAT	3'	GGGGTTTCACCATGTTAGCCA 6257	C	
			TGGC AACATGGTGAAATCC		
			ACCG TTGTACCACTTTGGG		
			A		
GAM2408	TBXA2R	3'	GGGGTTTCACCGTGTTGGCCA 8360		
			TGGCCAACATGGTGAAATCCC		
			ACCGGTTGTGCCACTTTGGGG		
GAM2408	TDGF1	3'	GGGGTTTCACCATATTGGCCA 13658	C	
			TGGCCAA ATGGTGAAATCCC		
			ACCGGTT TACCACTTTGGGG		
			A		
GAM2408	TERF1	3'	GTTTCACCATGCTGGTCA 34400	A	
			TGGCCA CATGGTGAAAT		
			ACTGGT GTACCACTTTG		
			C		
GAM2408	TERF2	3'	GGGGTTTCACCGTGTTAGCCA 20157	C	
			TGGC AACATGGTGAAATCCC		
			ACCG TTGTGCCACTTTGGGG		
			A		
GAM2408	TES	3'	GGTTTTCACCATGTTAGCCA 72464	C	T
			TGGC AACATGGTGAAA CC		
			ACCG TTGTACCACTTT GG		
			A T		
GAM2408	TGFBR1	3'	TGGGATTGTACTATACCA 17240	CCAAC	A
			TGG ATGGTG AATCCCA		
			ACC TATCAT TTAGGGT		
			A G		
GAM2408	TIM3	3'	GGGGTTTCACCATGTTGGCCA 52357		
			TGGCCAACATGGTGAAATCC		
			ACCGGTTGTACCACTTTGGG		
GAM2408	TMPRSS3	3'	GGGGTTTCACCATGTTGGCCA 51519		
			TGGCCAACATGGTGAAATCC		

ACCGGTTGTACCACTTTGGG

GAM2408 TMPRSS3 3' GGGTTTCACCATGTTGGCCA 51546
TGGCCAACATGGTGAAATCC
|||||||
ACCGGTTGTACCACTTTGGG

GAM2408 TMPRSS3 3' GGGTTTCACCATGTTGGCCA 44029
TGGCCAACATGGTGAAATCC
|||||||
ACCGGTTGTACCACTTTGGG

GAM2408 TNFRSF10B 3' GGGGTTTCACCATGTTGGTCA 15228
TGGCCAACATGGTGAAATCCC
|||||||
ACTGGTTGTACCACTTTGGGG

GAM2408 TNFRSF11A 3' GGTCCCACCATGTTACCCA 15196 CC AA
TGG AACATGGTG ATC
||| ||||| |||
ACC TTGTACCAC TGG
CA CC

GAM2408 TP53BP2 5' GTTTCATCATGTTGGCCA 19466
TGGCCAACATGGTGAAAT
|||||||
ACCGGTTGTACTACTTTG

GAM2408 TPMT 3' GGGGTTTCACCATGTTGGTCA 6315
TGGCCAACATGGTGAAATCCC
|||||||
ACTGGTTGTACCACTTTGGGG

GAM2408 TRIM9 5' GGGGTTTCACCATACTGGCC 31459 AC
GGCCA ATGGTGAAATCCC
||||| |||||
CCGGT TACCACTTTGGGG
CA

GAM2408 TRIP15 3' ATGGGATTTATGCTGTATTGAC 16175 GC C _
A TG CAA ATGGTG AAATCCCAT
|| ||| ||||| |||||
AC GTT TGTCGT TTTAGGGTA
A_ A A

GAM2408 TRPM6 3' ATGGGGTTTCACCATGTTGGCC 35026
A TGGCCAACATGGTGAAATCCCAT
|||||||
ACCGGTTGTACCACTTTGGGGTA

GAM2408 TRPV1 3' ATGGGGTTTCGCCATGTTGGCC 38688
A TGGCCAACATGGTGAAATCCCAT
|||||||

ACCGGTTGTACCGCTTTGGGGTA

GAM2408 TRPV1 3' GGGGTTTCACCATGTTGGCCA 38700
TGGCCAACATGGTGAAATCCC
|||||
ACCGGTTGTACCACTTTGGGG

GAM2408 TRPV1 3' ATGGGGTTTCGCCATGTTGGCC 55659
A TGGCCAACATGGTGAAATCCCAT
|||||
ACCGGTTGTACCGCTTTGGGGTA

GAM2408 TRPV1 3' GGGGTTTCACCATGTTGGCCA 55681
TGGCCAACATGGTGAAATCCC
|||||
ACCGGTTGTACCACTTTGGGG

GAM2408 TRPV1 3' ATGGGGTTTCGCCATGTTGGCC 55704
A TGGCCAACATGGTGAAATCCCAT
|||||
ACCGGTTGTACCGCTTTGGGGTA

GAM2408 TRPV1 3' GGGGTTTCACCATGTTGGCCA 55716
TGGCCAACATGGTGAAATCCC
|||||
ACCGGTTGTACCACTTTGGGG

GAM2408 TRPV1 3' ATGGGGTTTCGCCATGTTGGCC 55735
A TGGCCAACATGGTGAAATCCCAT
|||||
ACCGGTTGTACCGCTTTGGGGTA

GAM2408 TRPV1 3' GGGGTTTCACCATGTTGGCCA 55747
TGGCCAACATGGTGAAATCCC
|||||
ACCGGTTGTACCACTTTGGGG

GAM2408 TTR 3' ATGGGATTTTCATGTAACCA 6323 CCA TGG
TGG ACA TGAAATCCCAT
||| ||| |||||
ACC TGT ACTTTAGGGTA
AA_ _

GAM2408 TUFT1 3' ATGGGGTTTCACCATACTGGCT 39669 AC
A TGGCCA ATGGTGAAATCCCAT
||||| |||||
ATCGGT TACCACTTTGGGGTA
CA

GAM2408 UGDH 3' GGGTTTCACCATGTGAGCCA 14000 CA
TGGC ACATGGTGAAATCC
||| |||||

			ACCG TGTACCACTTTGGG	
			AG	
GAM2408	VENTX2	3'	ATGGGGTTTCACCATGTTAGCC 27856	C
	A		TGGC AACATGGTGAAATCCCAT	
			ACCG TTGTACCACTTTGGGGTA	
			A	
GAM2408	VHL	3'	GGGGTTTCACCATGTTGTCCA 6869	C
			TGG CAACATGGTGAAATCCC	
			ACC GTTGTACCACTTTGGGG	
			T	
GAM2408	VHL	3'	GTTTCGCCATGTTGGCCA 6872	
			TGGCCAACATGGTGAAAT	
			ACCGGTTGTACCGCTTTG	
GAM2408	VIPR2	3'	GGGTTTCACCATGTTAGCCA 14070	C
			TGGC AACATGGTGAAATCC	
			ACCG TTGTACCACTTTGGG	
			A	
GAM2408	WHSC1	5'	GATTTCGCCATGTTGCCCA 24674	C
			TGG CAACATGGTGAAATC	
			ACC GTTGTACCGCTTTAG	
			C	
GAM2408	WHSC1	5'	GATTTCGCCATGTTGCCCA 30583	C
			TGG CAACATGGTGAAATC	
			ACC GTTGTACCGCTTTAG	
			C	
GAM2408	WHSC1	5'	GATTTCGCCATGTTGCCCA 56670	C
			TGG CAACATGGTGAAATC	
			ACC GTTGTACCGCTTTAG	
			C	
GAM2408	WHSC1	5'	GATTTCGCCATGTTGCCCA 56681	C
			TGG CAACATGGTGAAATC	
			ACC GTTGTACCGCTTTAG	
			C	
GAM2408	WHSC1	3'	GGGTTTCGCCATATTGGCCA 56698	C
			TGGCCAA ATGGTGAAATCC	
			ACCGGTT TACCGCTTTGGG	
			A	
GAM2408	XRCC2	3'	GGGGTTTCACCATGTTGGCCA 19506	
			TGGCCAACATGGTGAAATCCC	

ACCGGTTGTACCACTTTGGGG

GAM2408	YES1	3'	GTTTCACCGTGTTAGCCA	19543	C
			TGGC AACATGGTGAAAT		
			ACCG TTGTGCCACTTTG		
			A		
GAM2408	ZNF157	3'	GGGTTTCACCATGTTGGCCA	14334	
			TGGCCAACATGGTGAAATCC		
			ACCGGTTGTACCACTTTGGG		
GAM2408	ZNF264	3'	GGGGTTTCACCATCTTGGCCA	14217	C
			TGGCCAA ATGGTGAAATCCC		
			ACCGGTT TACCACTTTGGGG		
			C		
GAM2408	AP3S2	3'	GGGTTTCACCATGTTGGCCA	20654	
			TGGCCAACATGGTGAAATCC		
			ACCGGTTGTACCACTTTGGG		
GAM2408	ARHF	3'	GGGTTTCACCATGTTGGCCA	39273	
			TGGCCAACATGGTGAAATCC		
			ACCGGTTGTACCACTTTGGG		
GAM2408	ARHGAP11A	3'	GGTTTCACCGTGTTAGCCA	29453	C
			TGGC AACATGGTGAAATC		
			ACCG TTGTGCCACTTTGG		
			A		
GAM2408	ASB16	3'	GGGGTCTCGCCATGTTGGCCA	55984	A
			TGGCCAACATGGTGA ATCCC		
			ACCGGTTGTACCGCT TGGGG		
			C		
GAM2408	ASE-1	3'	ATGGGGTTTCACCACGTTAGCC	24970	C A
	A		TGGC AAC TGGTGAAATCCCAT		
			ACCG TTG ACCACTTTGGGGTA		
			A C		
GAM2408	ASE-1	3'	GGGGTTTCACCATATTGGCCA	24984	C
			TGGCCAA ATGGTGAAATCCC		
			ACCGGTT TACCACTTTGGGG		
			A		
GAM2408	ATP1B4	3'	GGGTTTCACCATGTTGGCCA	24848	
			TGGCCAACATGGTGAAATCC		

ACCGGTTGTACCACTTTGGG

GAM2408 BA108L7.2 3' GGGGTTTCACCATGTTGGCCA 49078
TGGCCAACATGGTGAAATCCC
|||||||
ACCGGTTGTACCACTTTGGGG

GAM2408 BNIP-S 3' GGGGTTTCACCATGTTGGCCA 57092
TGGCCAACATGGTGAAATCCC
|||||||
ACCGGTTGTACCACTTTGGGG

GAM2408 BTN3A1 3' ATGAGGGTTCACATGTTGGCC 23887 A _
A TGGCCAACATGGTGAA TCC CAT
||||||| ||| |||
ACCGGTTGTATCACTT GGG GTA
_ A

GAM2408 C11orf17 3' GGGGTTTAACCATGTTGGCCA 40583 G
TGGCCAACATGGT AAATCCC
||||||| |||||
ACCGGTTGTACCA TTTGGGG
A

GAM2408 C13orf1 3' ATGGGGTTTCACCATGTTGTCC 40353 C
A TGG CAACATGGTGAAATCCCAT
||| |||||||||
ACC GTTGTACCACTTTGGGGTA
T

GAM2408 C1orf24 3' ATGGGGTTTTCACCATGTTGGCC 54782 T
A TGGCCAACATGGTGAAA CCCAT
||||||| |||||
ACCGGTTGTACCACTTT GGGTA
T

GAM2408 C1QTNF6 3' ATGGGGTTTTCACCATATTGGCC 49988 C
A TGGCCAA ATGGTGAAATCCCAT
||||| |||||||||
ACCGGTT TACCACTTTGGGGTA
A

GAM2408 C21orf25 3' ATGGAGTCTCACCATGTTGGTC 64283 A TC
A TGGCCAACATGGTGA A CCAT
||||||| | |||
ACTGGTTGTACCACT T GGTA
C GA

GAM2408 C3F 3' GGGATTTCACCACGTTGGCCA 20479 A
TGGCCAAC TGGTGAAATCCC
||||| |||||||||
ACCGGTTG ACCACTTTAGGG
C

GAM2408 C9orf14 5' GGTTTCACCCTGTTGGCCA 87959 T
TGGCCAACA GGTGAAATC
||||||| |||||||

			ACCGGTTGT CCACTTTGG		
			C		
GAM2408	C9orf9	3'	GGGGCTTCACCACGTTGGCCA 39028	A	AT
			TGGCCAAC TGGTGAA CCC		
			ACCGGTTG ACCACTT GGG		
			C CG		
GAM2408	C9orf9	3'	GTTTCACCATGTTAGCCA 39033 C		
			TGGC AACATGGTGAAAT		
			ACCG TTGTACCACTTTG		
			A		
GAM2408	CCRN4L	3'	GGGGTTTCACCGTGTTAGCCA 25071 C		
			TGGC AACATGGTGAAATCCC		
			ACCG TTGTGCCACTTTGGGG		
			A		
GAM2408	CDC14B	3'	GGGTTTCACCATGTTGGCCA 54009		
			TGGCCAACATGGTGAAATCC		
			ACCGGTTGTACCACTTTGGG		
GAM2408	CHRA1	3'	GGGGTTCACCATGTTGGCCA 34336	A	
			TGGCCAACATGGTGAA TCCC		
			ACCGGTTGTACCACTT GGGG		
GAM2408	CHST3	3'	ATGGGATTCGCTATAATCAGCC 16230	CAAC_	A
			GGC ATGGTGAA TCCCAT		
			CCG TATCGCTT AGGGTA		
			ACTAA _		
GAM2408	CIP29	3'	GGGGTTTCACCATGTTGCCCA 51379 C		
			TGG CAACATGGTGAAATCCC		
			ACC GTTGTACCACTTTGGGG		
			C		
GAM2408	CNOT3	5'	ATGGGGTCCCCTGTTGGCCA 27982	T T	AA
			TGGCCAACA GG GA TCCCAT		
			ACCGGTTGT CC CT GGGGTA		
			C _ _		
GAM2408	CPSF2	3'	GGGTTTCACCATGTTGGCCA 62276		
			TGGCCAACATGGTGAAATCC		
			ACCGGTTGTACCACTTTGGG		
GAM2408	DBR1	3'	GGGTTTCACCGTGTTGGCCA 33068		
			TGGCCAACATGGTGAAATCC		

ACCGGTTGTGCCACTTTGGG

GAM2408 DKFZP434C128 3' ATGGGATTTCTGTTGCGCA 65467 C TGGT
TGGC AACAA GAAATCCCAT
||||| |||||
ACCG TTGT CTTTAGGGTA
C _____

GAM2408 DKFZP434C212 3' GGGGTTTCACCATGTTGGCCA 69493
TGGCCAACATGGTGAAATCCC
|||||||
ACCGGTTGTACCACTTTGGGG

GAM2408 DKFZP434D146 3' GGGTTTCATCATGTTGGCCA 32137
TGGCCAACATGGTGAAATCC
|||||||
ACCGGTTGTACTACTTTGGG

GAM2408 DKFZP434F0318 3' GGGTTTCGCCATGTTGGCCA 48762
TGGCCAACATGGTGAAATCC
|||||||
ACCGGTTGTACCGCTTTGGG

GAM2408 DKFZp434F1719 3' ATGGGATTTCGCCATGTTGGCC 51012
A TGGCCAACATGGTGAAATCCCAT
|||||||
ACCGGTTGTACCGCTTTAGGGTA

GAM2408 DKFZp547H025 3' ATGAGGTTTCACCATGTTGGCC 39770 C
A TGGCCAACATGGTGAAATC CAT
||||||| |||
ACCGGTTGTACCACTTTGG GTA
A

GAM2408 DKFZP564G092 5' GGATTTACCATGTTGGCCA 32164
TGGCCAACATGGTGAAATCC
|||||||
ACCGGTTGTACCACTTTAGG

GAM2408 DKFZP564O0523 3' ATGGGTTTTACCATATTGGTC 50418 C T
A TGGCCAA ATGGTGAAA CCCAT
||||| ||||| |||||
ACTGGTT TACCACTTT GGGTA
A T

GAM2408 DKFZp761J139 5' ATGGGGTTTGACCATGTTGGCC 51100 G
A TGGCCAACATGGT AAATCCCAT
||||||| |||||
ACCGGTTGTACCA TTTGGGGTA
G

GAM2408 DKFZp761N1114 3' GGGATTTACCGTGTTAGCCA 79788 C
TGGC AACATGGTGAAATCCC
|||||

			ACCG TTGTGCCACTTTAGGG		
			A		
GAM2408	DRIM	3'	GGATTTCGCCATGTTGGCCA 27953		
			TGGCCAACATGGTGAAATCC		
			ACCGGTTGTACCGCTTTAGG		
GAM2408	DSCR6	3'	GGTTTCACCATGTTGGTCA 39071		
			TGGCCAACATGGTGAAATC		
			ACTGGTTGTACCACTTTGG		
GAM2408	EREG	3'	GTTTCACCATGTTGGCCA 9316		
			TGGCCAACATGGTGAAAT		
			ACCGGTTGTACCACTTTG		
GAM2408	FER1L4	3'	GGGTTTCACCATGTTGTCCA 48127	C	
			TGG CAACATGGTGAAATCC		
			ACC GTTGTACCACTTTGGG		
			T		
GAM2408	FKBP9	3'	GGGGTTTCACCGTGTGGCCA 95717		
			TGGCCAACATGGTGAAATCCC		
			ACCGGTTGTGCCACTTTGGGG		
GAM2408	FLJ00060	5'	ATGGAATTTACCATGTTAGCC 61736	C	C
			A TGGC AACATGGTGAAAT CCAT		
			ACCG TTGTACCACTTTA GGTA		
			A A		
GAM2408	FLJ10298	3'	GGGGTTTCACCATGTTGGTCA 36459		
			TGGCCAACATGGTGAAATCCC		
			ACTGGTTGTACCACTTTGGGG		
GAM2408	FLJ10346	5'	GTTTCACCATGTTGACCA 36530	C	
			TGG CAACATGGTGAAAT		
			ACC GTTGTACCACTTTG		
			A		
GAM2408	FLJ10535	3'	ATGGGGTTTCACCATGTTGGCC 36738		
			A TGGCCAACATGGTGAAATCCCAT		
			ACCGGTTGTACCACTTTGGGGTA		
GAM2408	FLJ10713	3'	ATGGGGTTTCACCATGTTGGCC 36998		
			A TGGCCAACATGGTGAAATCCCAT		

ACCGGTTGTACCACTTTGGGGTA

GAM2408 FLJ10846 3' GGGTCTCACCATGTTAGCCA 37288 C AAT
TGGC AACATGGTGA CCC
||||| ||||| |||
ACCG TTGTACCACT GGG
A CT_

GAM2408 FLJ10901 3' ATGGGGTTTCATCATGTTGGCC 37353
A TGGCCAACATGGTGAAATCCCAT
|||||
ACCGGTTGTACTACTTTGGGGTA

GAM2408 FLJ10956 3' GGGGTTTCACCATGTTGGCCA 37470
TGGCCAACATGGTGAAATCCC
|||||
ACCGGTTGTACCACTTTGGGG

GAM2408 FLJ11193 3' ATGGGGTCTCACCATGTTACCC 37746 CC A
A TGG AACATGGTGA ATCCCAT
||| ||||| |||||
ACC TTGTACCACT TGGGGTA
CA C

GAM2408 FLJ12363 3' ATGGGGTTTCACCATGTTGGCC 50628
A TGGCCAACATGGTGAAATCCCAT
|||||
ACCGGTTGTACCACTTTGGGGTA

GAM2408 FLJ12687 3' GGGTTTCACCATGTTGGCCA 46753
TGGCCAACATGGTGAAATCC
|||||
ACCGGTTGTACCACTTTGGG

GAM2408 FLJ12688 3' ATGGAATTTCACTAATTGCCCA 73551 C CA C
TGG CAA TGGTGAAAT CCAT
||| ||| ||||| |||
ACC GTT ATCACTTTA GGTA
C A_ A

GAM2408 FLJ12903 3' GGATTTCTCCATGTTGGTCA 43073 T
TGGCCAACATGG GAAATCC
||||| |||||
ACTGGTTGTACC CTTTAGG
T

GAM2408 FLJ12973 3' ATGGGGTTTCATCATGTTGGCC 46639
A TGGCCAACATGGTGAAATCCCAT
|||||
ACCGGTTGTACTACTTTGGGGTA

GAM2408 FLJ13072 5' GGGTTTCACCATGTTGGACA 91393 G
TG CCAACATGGTGAAATCC
|| |||||

AC GGTTGTACCACTTTGGG
 A
 GAM2408 FLJ13114 3' ATGGAGTTTCACCATGTTACCC 44895 CC TC
 A TGG AACATGGTGAAA CCAT
 ||| ||||| ||||
 ACC TTGTACCACTTT GGTA
 CA GA
 GAM2408 FLJ13197 3' GTTTCACCATGTTGGCCA 45185
 TGGCCAACATGGTGAAAT
 |||||
 ACCGGTTGTACCACTTTG

 GAM2408 FLJ13305 5' ATGGGGTTTCACCATGTTGGCC 91706
 A TGGCCAACATGGTGAAATCCCAT
 |||||
 ACCGGTTGTACCACTTTGGGGTA

 GAM2408 FLJ13952 3' GGGTTTCACCACGTTGGCCA 46016 A
 TGGCCAAC TGGTGAAATCC
 ||||| |||||
 ACCGGTTG ACCACTTTGGG
 C
 GAM2408 FLJ14950 3' GGGTTTCACCATGTTGGCCA 52794
 TGGCCAACATGGTGAAATCC
 |||||
 ACCGGTTGTACCACTTTGGG

 GAM2408 FLJ14957 3' GGGGTTTCACCATGTTGGTCA 52824
 TGGCCAACATGGTGAAATCCC
 |||||
 ACTGGTTGTACCACTTTGGGG

 GAM2408 FLJ20033 3' ATGGGATTCCTTTCTTGTCCA 34818 C CAT T A
 TGG CAA GG GAA TCCCAT
 ||| || || |||||
 ACC GTT TC CTT AGGGTA
 T CTT _ _
 GAM2408 FLJ20045 3' ATGGGGATTCACCATGTTGGTC 34873 A
 A TGGCCAACATGGTGAA TCCCAT
 ||||| |||||
 ACTGGTTGTACCACTT GGGGTA
 A
 GAM2408 FLJ20136 3' GTTTCACCATGTTGGTCA 35102
 TGGCCAACATGGTGAAAT
 |||||
 ACTGGTTGTACCACTTTG

 GAM2408 FLJ20344 3' GGGTTTCACCATGTTGGCCA 35483
 TGGCCAACATGGTGAAATCC
 |||||

ACCGGTTGTACCACTTTGGG

GAM2408 FLJ20507 3' GGGTTTCACCATGTTGGCCA 35747
TGGCCAACATGGTGAAATCC
|||||||
ACCGGTTGTACCACTTTGGG

GAM2408 FLJ20507 3' GGGTTTCACCATGTTGGCCA 60851
TGGCCAACATGGTGAAATCC
|||||||
ACCGGTTGTACCACTTTGGG

GAM2408 FLJ20511 3' GTTTCACCGTGTTAGCCA 35781 C
TGGC AACATGGTGAAAT
||| |||||
ACCG TTGTGCCACTTTG
A

GAM2408 FLJ20700 3' GGGTTTCACCATATTGACCA 36016 C C
TGG CAA ATGGTGAAATCC
||| ||| |||||
ACC GTT TACCACTTTGGG
A A

GAM2408 FLJ20813 3' ATGGGCTTTCACCTACGTTAGCC 36126 C A T
A TGGC AAC TGGTGAAA CCCAT
||| ||| ||||| |||||
ACCG TTG ATCACTTT GGGTA
A C C

GAM2408 FLJ21302 3' GGGTTTCACCATGTTGGCCA 43510
TGGCCAACATGGTGAAATCC
|||||||
ACCGGTTGTACCACTTTGGG

GAM2408 FLJ21324 5' ATGGGGTTTCACCATGTTGGCC 92843
A TGGCCAACATGGTGAAATCCCAT
|||||||
ACCGGTTGTACCACTTTGGGGTA

GAM2408 FLJ21459 3' GGGTGTTACCATGTTGGCCA 44808 AAT
TGGCCAACATGGTGA CCC
||||||| |||
ACCGGTTGTACCATT GGG
GT_

GAM2408 FLJ21603 3' ATGGGGTTTCACCCTGTTAGCC 45767 C T
A TGGC AACA GGTGAAATCCCAT
||| ||| |||||
ACCG TTGT CCACTTTGGGGTA
A C

GAM2408 FLJ22329 3' GGGGTTTCACCATGTTGGCCA 45404
TGGCCAACATGGTGAAATCCC
|||||||

ACCGGTTGTACCACTTTGGGG

GAM2408 FLJ22529 3' GGGTTTCACCACATTGGCCA 45946 CA
TGGCCAA TGGTGAAATCC
||||| ||||||||
ACCGGTT ACCACTTTGGG
AC

GAM2408 FLJ22529 3' GGGTTTCATCATGTTGGCCA 45948
TGGCCAACATGGTGAAATCC
||||||||||||||
ACCGGTTGTACTACTTTGGG

GAM2408 FLJ22684 3' GGGTTTCACCATGTTGGCCA 47470
TGGCCAACATGGTGAAATCC
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ACCGGTTGTACCACTTTGGG

GAM2408 FLJ22794 3' GGGTTTCACCATGTTGGTCA 93250
TGGCCAACATGGTGAAATCC
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ACTGGTTGTACCACTTTGGG

GAM2408 FLJ22969 3' GGGTTTCACCATGTTGCCCA 69213 C
TGG CAACATGGTGAAATCC
||| ||||||||||||
ACC GTTGTACCACTTTGGG
C

GAM2408 FLJ23024 3' GGGGTTTCACCATGTTGGCCA 46843
TGGCCAACATGGTGAAATCCC
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ACCGGTTGTACCACTTTGGGG

GAM2408 FLJ23392 3' GGGTTTCACCATGTTGGCCA 45898
TGGCCAACATGGTGAAATCC
||||||||||||||
ACCGGTTGTACCACTTTGGG

GAM2408 FLJ23392 3' GGGTTTCACCGTGTTAGCCA 45900 C
TGGC AACATGGTGAAATCC
||| ||||||||||||
ACCG TTGTGCCACTTTGGG
A

GAM2408 FLJ23519 3' ATGGGGTTTCACCGTGTTAGCC 50944 C
A TGGC AACATGGTGAAATCCCAT
||| ||||||||||||
ACCG TTGTGCCACTTTGGGGTA
A

GAM2408 FLJ23556 3' GGGGTTTCACCGTGTTAGCCA 46448 C
TGGC AACATGGTGAAATCCC
||| ||||||||||||

ACCG TTGTGCCACTTTGGGG
 A
 GAM2408 FLJ25416 5' ATGGGGTTTCACCATGTTGGCC 59449
 A TGGCCAACATGGTGAAATCCCAT
 |||||
 ACCGGTTGTACCACTTTGGGGTA

GAM2408 FLJ30532 3' GGATTTCACATGTTGGCCA 59222
 TGGCCAACATGGTGAAATCC
 |||||
 ACCGGTTGTATCACTTTAGG

GAM2408 FLJ31101 3' GGGATTTACCATGTTGGCCA 36165
 TGGCCAACATGGTGAAATCCC
 |||||
 ACCGGTTGTACCACTTTAGGG

GAM2408 FLJ31153 3' ATGGGGTTTCACCATGCTGGCC 58743 A
 A TGGCCA CATGGTGAAATCCCAT
 ||||| |||||
 ACCGGT GTACCACTTTGGGGTA
 C

GAM2408 FLJ32894 3' ATGGGATTTCACTGTGTTGGCC 58993
 A TGGCCAACATGGTGAAATCCCAT
 |||||
 ACCGGTTGTGTCACCTTTAGGGTA

GAM2408 GGA2 3' GGATTTCACCATGTTGGCCA 31168
 TGGCCAACATGGTGAAATCC
 |||||
 ACCGGTTGTACCACTTTAGG

GAM2408 GGA2 3' GGATTTCACCATGTTGGCCA 57672
 TGGCCAACATGGTGAAATCC
 |||||
 ACCGGTTGTACCACTTTAGG

GAM2408 GMPPB 5' GGGTTTCACCAGGTTGGCCA 97457 A
 TGGCCAAC TGGTGAAATCC
 ||||| |||||
 ACCGGTTG ACCACTTTGGG
 G

GAM2408 GNG4 3' GGGGTTTCACCATGTTGGTCA 16849
 TGGCCAACATGGTGAAATCCC
 |||||
 ACTGGTTGTACCACTTTGGGG

GAM2408 GOLGA3 3' ATGGGGTTTCACCATGTTGGCC 20882
 A TGGCCAACATGGTGAAATCCCAT
 |||||

ACCGGTTGTACCACTTTGGGGTA

GAM2408 GREB1	3'	GGGGTTTCACCATGTTAGCCA	28573	C
		TGGC AACATGGTGAAATCCC		
		ACCG TTGTACCACTTTGGGG		
		A		
GAM2408 GRWD	3'	GGGGTTTCACCATGTTGGCCA	49785	
		TGGCCAACATGGTGAAATCCC		
		ACCGGTTGTACCACTTTGGGG		
GAM2408 GTF2E1	3'	GTTTCACCATGTTAGCCA	19803	C
		TGGC AACATGGTGAAAT		
		ACCG TTGTACCACTTTG		
		A		
GAM2408 GTPBG3	3'	GGTTTCACCATGTTGACCA	51901	C
		TGG CAACATGGTGAAATC		
		ACC GTTGTACCACTTTGG		
		A		
GAM2408 H2AV	3'	GTTTCACCATGTTGGCCA	57634	
		TGGCCAACATGGTGAAAT		
		ACCGGTTGTACCACTTTG		
GAM2408 HARS2	3'	GGGGTTTTACCATGTTAGCCA	55866	C
		TGGC AACATGGTGAAATCCC		
		ACCG TTGTACCATTTTGGGG		
		A		
GAM2408 HSNV1	3'	ATGGGGTTTCACCATGTTGCCC	34427	C
A		TGG CAACATGGTGAAATCCCAT		
		ACC GTTGTACCACTTTGGGGTA		
		C		
GAM2408 HSPC065	3'	ATGGGGTTTCACCATGTTGGCC	27141	
A		TGGCCAACATGGTGAAATCCCAT		
		ACCGGTTGTACCACTTTGGGGTA		
GAM2408 HSPC065	3'	ATGGGGTTTCACGATGTTGGCC	27142	G
A		TGGCCAACAT GTGAAATCCCAT		
		ACCGGTTGTA CACTTTGGGGTA		
		G		
GAM2408 HSPC232	3'	ATGGGGTTTCACCATGTTGGCCA	33655	A
		TGGCCAACATGGTGAA TCCCAT		

ACCGGTTGTACCACTT GGGGTA

GAM2408 HT002 3' GGGTTTCACCGTGTGAGCCA 26796
TGGCCAACATGGTGAAATCC
|||||
ACCGGTTGTGCCACTTTGGG

GAM2408 JAM1 3' ATGGGATTACAGATGTGAGCCA 58496 CA GG A
TGGC ACAT TG AATCCCAT
||| ||| || |||||
ACCG TGTA AC TTAGGGTA
AG G_ A

GAM2408 JAM1 3' ATGGGATTACAGATGTGAGCCA 58511 CA GG A
TGGC ACAT TG AATCCCAT
||| ||| || |||||
ACCG TGTA AC TTAGGGTA
AG G_ A

GAM2408 JAM1 3' ATGGGATTACAGATGTGAGCCA 58539 CA GG A
TGGC ACAT TG AATCCCAT
||| ||| || |||||
ACCG TGTA AC TTAGGGTA
AG G_ A

GAM2408 JAM1 3' ATGGGATTACAGATGTGAGCCA 58567 CA GG A
TGGC ACAT TG AATCCCAT
||| ||| || |||||
ACCG TGTA AC TTAGGGTA
AG G_ A

GAM2408 JAM1 3' ATGGGATTACAGATGTGAGCCA 34220 CA GG A
TGGC ACAT TG AATCCCAT
||| ||| || |||||
ACCG TGTA AC TTAGGGTA
AG G_ A

GAM2408 JM11 3' GGTTTCACCATATTGGCCA 54367 C
TGGCCAA ATGGTGAAATC
||||| |||||
ACCGGTT TACCACTTTGG
A

GAM2408 KIAA0087 3' ATGGGGTTTCACCATCTTGGCC 29339 C
A TGGCCAA ATGGTGAAATCCCAT
||||| |||||
ACCGGTT TACCACTTTGGGGTA
C

GAM2408 KIAA0161 3' GGGGTTTCACCATGTTGGCCA 29204
TGGCCAACATGGTGAAATCCC
||||| |||||
ACCGGTTGTACCACTTTGGGG

GAM2408 KIAA0186 3' ATGGGGTTTCACCATGTTGGCC 41098
A TGGCCAACATGGTGAAATCCCAT
||||| |||||

ACCGGTTGTACCACTTTGGGGTA

GAM2408 KIAA0186 3' GTTTTACCATGTTGGCCA 41114
TGGCCAACATGGTGAAAT
|||||||
ACCGGTTGTACCATTG

GAM2408 KIAA0205 3' ATGGGGTTTCACCATGTTGGCC 30202
A TGGCCAACATGGTGAAATCCCAT
|||||||
ACCGGTTGTACCACTTTGGGGTA

GAM2408 KIAA0210 5' GGAGTTTCACCATGTTGGCCA 29166 TC
TGGCCAACATGGTGAAA CC
||||||| ||
ACCGGTTGTACCACTTT GG
GA

GAM2408 KIAA0210 5' GGGGTTTCACTATATTGGCCA 29168 C
TGGCCAA ATGGTGAAATCCC
||||| |||||
ACCGGTT TATCACTTTGGGG
A

GAM2408 KIAA0280 3' ATGGGATTCCACACCGGAGCC 93290 CAACA A__
GGC TGGTG AATCCCAT
||| ||||| |||||
CCG GCCAC TTAGGGTA
AG__ ACC

GAM2408 KIAA0426 3' GGGGTTTCACCATGTTGGCCA 28928
TGGCCAACATGGTGAAATCCC
|||||||
ACCGGTTGTACCACTTTGGGG

GAM2408 KIAA0459 3' GGGGTTTCACCATGTTAGCCA 61655 C
TGGC AACATGGTGAAATCCC
||| |||||
ACCG TTGTACCACTTTGGGG
A

GAM2408 KIAA0469 3' GGGATTTCACCTGTGTTAGCCA 29988 C
TGGC AACATGGTGAAATCCC
||| |||||
ACCG TTGTGTCACCTTTAGGG
A

GAM2408 KIAA0475 3' GTTTCACCATGTTGGCCA 30129
TGGCCAACATGGTGAAAT
|||||||
ACCGGTTGTACCACTTTG

GAM2408 KIAA0495 3' ATGGGATTTACCATGTTGGCC 63259
A TGGCCAACATGGTGAAATCCCAT
|||||||

ACCGGTTGTACCACTTTAGGGTA

GAM2408 KIAA0513 3' ATGGGGTTTCACCATGCTGGCC 29018 A
A TGGCCA CATGGTGAAATCCCAT

||||| |||||||||
ACCGGT GTACCACTTTGGGGTA
C

GAM2408 KIAA0513 5' GGGTTTCGCCATGTTGGCCA 29044
TGGCCAACATGGTGAAATCC
||||| |||||||||
ACCGGTTGTACCGCTTTGGG

GAM2408 KIAA0527 3' ATGGAGTTTCACCATGTTGGCC 97489 TC
A TGGCCAACATGGTGAAA CCAT

||||| |||||
ACCGGTTGTACCACTTT GGTA
GA

GAM2408 KIAA0544 3' GGGATTTACCATGTTGGCC 71471
GGCCAACATGGTGAAATCCC
||||| |||||||||
CCGGTTGTACCACTTTAGGG

GAM2408 KIAA0561 3' GGGGTTTCACCATGTTGGTCA 66483
TGGCCAACATGGTGAAATCCC
||||| |||||||||
ACTGGTTGTACCACTTTGGGG

GAM2408 KIAA0562 3' GGGGTTTCACCATATTGGCCA 28827 C
TGGCCAA ATGGTGAAATCCC

||||| |||||||||
ACCGGTT TACCACTTTGGGG
A

GAM2408 KIAA0594 3' ATGGGGTTTCAGCATATTGGCC 65505 C G
A TGGCCAA ATG TGAAATCCCAT

||||| ||| |||||||||
ACCGGTT TAC ACTTTGGGGTA
A G

GAM2408 KIAA0682 3' GGGGTTTCACCATGTGGGCCA 30025 A
TGGCC ACATGGTGAAATCCC

||||| |||||||||
ACCGG TGTACCACTTTGGGG
G

GAM2408 KIAA0682 3' GTTTCACCATGTAGACCA 30027 CCA
TGG ACATGGTGAAAT

||| |||||||||
ACC TGTACCACTTTG
AGA

GAM2408 KIAA0720 3' GGCATTTACCATATTGGTCA 62986 C C
TGGCCAA ATGGTGAAAT CC

||||| ||||||||| ||

ACTGGTT TACCACTTTA GG
 A C
 GAM2408 KIAA0737 3' GGGTTTCACCATGTTGGCCA 29813
 TGGCCAACATGGTGAAATCC
 |||||
 ACCGGTTGTACCACTTTGGG

GAM2408 KIAA0831 3' GGGGTTTTTCACCATGTTGGCCA 30646 —
 TGGCCAACATGGTGAAA TCCC
 |||||
 ACCGGTTGTACCACTTT GGGG
 T

GAM2408 KIAA0831 5' GTTTCACCATGTTGGCCA 30653
 TGGCCAACATGGTGAAAT
 |||||
 ACCGGTTGTACCACTTTG

GAM2408 KIAA0841 3' GGGGTTTCATCATGTTGGCCA 71899
 TGGCCAACATGGTGAAATCCC
 |||||
 ACCGGTTGTACTACTTTGGGG

GAM2408 KIAA0843 3' TATGAGATTCCAAAATGAAGTG 30804 GG_____ A C ____
 TTGGCCA TGGCCAACAT TG AATC CAT A
 ||||| || ||| ||| |
 ACCGGTTGTG AC TTAG GTA T
 AAGTAAA C A ____

GAM2408 KIAA0884 3' GGTTCACCATGTTGCCCA 70756 C
 TGG CAACATGGTGAAATC
 ||| |||||
 ACC GTTGTACCACTTTGG
 C

GAM2408 KIAA0924 3' ATGGGGTTTTACCATATTGGCC 30354 C
 A TGGCCAA ATGGTGAAATCCCAT
 ||||| |||||
 ACCGGTT TACCACTTTGGGGTA
 A

GAM2408 KIAA0931 3' GGGGTTTCACCATGTTGGCCA 68014
 TGGCCAACATGGTGAAATCCC
 |||||
 ACCGGTTGTACCACTTTGGGG

GAM2408 KIAA0961 3' ATGGGGTTTTACCATGTTGGCC 30391
 A TGGCCAACATGGTGAAATCCCAT
 ||||| |||||
 ACCGGTTGTACCACTTTGGGGTA

GAM2408 KIAA1026 3' ATGAGATTTTCACCATGTTGGCC 71731 C
 A TGGCCAACATGGTGAAATC CAT
 ||||| |||||

			ACCGGTTGTACCACTTTAG GTA		
			A		
GAM2408	KIAA1040	3'	ATGGGGTTTCACCATTTTGGCC 72681	C	
	A		TGGCCAA ATGGTGAAATCCCAT		
			ACCGGTT TACCACTTTGGGGTA		
			T		
GAM2408	KIAA1128	3'	ATGAGATTTACCTTGTTGGTC 68996	T	C
	A		TGGCCAACA GGTGAAATC CAT		
			ACTGGTTGT CCACTTTAG GTA		
			T A		
GAM2408	KIAA1161	5'	ATGGGGTTTACCATGTTGGCCA 82640		A
			TGGCCAACATGGTGAA TCCCAT		
			ACCGGTTGTACCATTG GGGGTA		
			—		
GAM2408	KIAA1170	3'	GGGTTTCACCATGTTAGCCA 70419	C	
			TGGC AACATGGTGAAATCC		
			ACCG TTGTACCACTTTGGG		
			A		
GAM2408	KIAA1185	3'	GGGGTTTCACCATTTTGACCA 63290	C	C
			TGG CAA ATGGTGAAATCCC		
			ACC GTT TACCACTTTGGGG		
			A T		
GAM2408	KIAA1198	3'	ATGGGGTTTCACCATGTTGACC 64003	C	
	A		TGG CAACATGGTGAAATCCCAT		
			ACC GTTGTACCACTTTGGGGTA		
			A		
GAM2408	KIAA1198	3'	GGGGTTTCACCATGTTGGCCA 64046		
			TGGCCAACATGGTGAAATCCC		
			ACCGGTTGTACCACTTTGGGG		
GAM2408	KIAA1198	3'	GGGGTTTCACCATGTTGGCCA 64047		
			TGGCCAACATGGTGAAATCCC		
			ACCGGTTGTACCACTTTGGGG		
GAM2408	KIAA1198	3'	GGGGTTTCACCGTGTTAGCCA 64050	C	
			TGGC AACATGGTGAAATCCC		
			ACCG TTGTGCCACTTTGGGG		
			A		
GAM2408	KIAA1198	3'	GTTTCACCATGTTGACCA 64058	C	
			TGG CAACATGGTGAAAT		

ACC GTTGTACCACTTTG

A

GAM2408 KIAA1200 3' GGGGTTTTCACCATGTTGGCCA 63039
TGGCCAACATGGTGAAATCCC
|||||
ACCGGTTGTACCACTTTGGGG

GAM2408 KIAA1209 3' GTTTCATCATGTTGGCCA 61409
TGGCCAACATGGTGAAAT
|||||
ACCGGTTGTACTACTTTG

GAM2408 KIAA1210 3' GGGGTTTTCACCATGTTGGCCA 98076
TGGCCAACATGGTGAAATCCC
|||||
ACCGGTTGTACCACTTTGGGG

GAM2408 KIAA1254 3' ATGGGGTTTTCACCATGTTGGCC 70555
A TGGCCAACATGGTGAAATCCCAT
|||||
ACCGGTTGTACCACTTTGGGGTA

GAM2408 KIAA1320 5' TATGGGATTTCAATTCACCATG 69848
TTGGCCA TGGCCAACATGGTGAA ATCCCAT A
||||| |||||
ACCGGTTGTACCACTT TAGGGTA T
AACTT

GAM2408 KIAA1328 5' GTTTCACCGTGTTAGCCA 62331 C
TGGC AACATGGTGAAAT
||| |||||
ACCG TTGTGCCACTTTG
A

GAM2408 KIAA1443 3' GGGTTTTCATCATGTTAGCCA 64575 C
TGGC AACATGGTGAAATCC
||| |||||
ACCG TTGTACTACTTTGGG
A

GAM2408 KIAA1456 3' GGGGTTTTCACCGTGTTAGCCA 67563 C
TGGC AACATGGTGAAATCCC
||| |||||
ACCG TTGTGCCACTTTGGGG
A

GAM2408 KIAA1465 3' GGGGTTTTCACCATGTTGGCCA 61504
TGGCCAACATGGTGAAATCCC
|||||
ACCGGTTGTACCACTTTGGGG

GAM2408 KIAA1467 3' GGGGTTTTCACCATGTTGGCCA 72071
TGGCCAACATGGTGAAATCCC
|||||

ACCGGTTGTACCACTTTGGGG

GAM2408 KIAA1497 5' GGGTTTCACCATGTTGGTCA 68124
TGGCCAACATGGTGAAATCC
|||||
ACTGGTTGTACCACTTTGGG

GAM2408 KIAA1508 3' GGTTTCACCATGTTGGTCA 62557
TGGCCAACATGGTGAAATC
|||||
ACTGGTTGTACCACTTTGG

GAM2408 KIAA1571 3' GTTTCACATGTTGGCCA 61623
TGGCCAACATGGTGAAAT
|||||
ACCGGTTGTATCACTTTG

GAM2408 KIAA1615 3' ATGGAGTTTCACCACGTTGGCC 69266 A TC
A TGGCCAAC TGGTGAAA CCAT
||||| ||||| ||||
ACCGGTTG ACCACTTT GGTA
C GA

GAM2408 KIAA1617 3' GGGTTTCACCATGTTGGTCA 93079
TGGCCAACATGGTGAAATCC
|||||
ACTGGTTGTACCACTTTGGG

GAM2408 KIAA1655 3' GGTTTCACCATGTTGGCCA 67195
TGGCCAACATGGTGAAATC
|||||
ACCGGTTGTACCACTTTGG

GAM2408 KIAA1668 3' GGGGTTTCACCGTGTTAACCA 67074 CC
TGG AACATGGTGAAATCCC
||| |||||
ACC TTGTGCCACTTTGGGG
AA

GAM2408 KIAA1712 3' GGGTTTCACCATGTTGCCCA 68162 C
TGG CAACATGGTGAAATCC
||| |||||
ACC GTTGTACCACTTTGGG
C

GAM2408 KIAA1829 3' GGGGTTTCACCACATTGGTCA 62651 CA
TGGCCAA TGGTGAAATCCC
||||| |||||
ACTGGTT ACCACTTTGGGG
AC

GAM2408 KIAA1877 3' GGGTTTCACCGTGTTAGCCA 66755 C
TGGC AACATGGTGAAATCC
||| |||||

			ACCG TTGTGCCACTTTGGG	
			A	
GAM2408	KIAA1971	3'	GGTTTCACCGTGTTAGCCA 74687	C
			TGGC AACATGGTGAAATC	
			ACCG TTGTGCCACTTTGG	
			A	
GAM2408	KIAA1975	5'	ATGGGGTTTCACCATGTTAACC 74414	CC
	A		TGG AACATGGTGAAATCCCAT	
			ACC TTGTACCACTTTGGGGTA	
			AA	
GAM2408	KIAA1987	5'	GGTTTCACCATATTGGCCA 89386	C
			TGGCCAA ATGGTGAAATC	
			ACCGGTT TACCACTTTGG	
			A	
GAM2408	KLK7	3'	GGGTTTCACCATGTTGGCCA 18546	
			TGGCCAACATGGTGAAATCC	
			ACCGGTTGTACCACTTTGGG	
GAM2408	KLK7	3'	GGGTTTCACCATGTTGGCCA 58392	
			TGGCCAACATGGTGAAATCC	
			ACCGGTTGTACCACTTTGGG	
GAM2408	LAMP3	3'	GGGGTTTCACCATGTTGGCCA 60206	
			TGGCCAACATGGTGAAATCCC	
			ACCGGTTGTACCACTTTGGGG	
GAM2408	LEC3	3'	ATGGGATTTTTAGGTCAGCC 31533	CA ATGGT
			GGC AC GAAATCCCAT	
			CCG TG TTTTAGGGTA	
			AC GAT__	
GAM2408	LY75	3'	ATGGGGTTTCACCATGTTGGCC 11388	
	A		TGGCCAACATGGTGAAATCCCAT	
			ACCGGTTGTACCACTTTGGGGTA	
GAM2408	MAP-1	3'	GGGGTTTCACCATGTTGGCCA 42445	
			TGGCCAACATGGTGAAATCCC	
			ACCGGTTGTACCACTTTGGGG	
GAM2408	MCLC	3'	ATGGGGTTTCACCATGTTGGTC 31378	
	A		TGGCCAACATGGTGAAATCCCAT	

ACTGGTTGTACCACTTTGGGGTA

GAM2408 MEF-2 3' GTTTCACCATGTTGGTCA 65029
TGGCCAACATGGTGAAAT
|||||||
ACTGGTTGTACCACTTTG

GAM2408 MGC12518 3' GTTTCACCATGTTGGCCA 64780
TGGCCAACATGGTGAAAT
|||||||
ACCGGTTGTACCACTTTG

GAM2408 MGC13204 3' ATGTGGTTTCTCCATGTTGGCC 49625 T C
A TGGCCAACATGG GAAATC CAT
||||||| ||||| ||
ACCGGTTGTACC CTTTGG GTA
T T

GAM2408 MGC15563 3' ATGGGATCTCACCATGTTGCCC 52860 C A
A TGG CAACATGGTGA ATCCCAT
||| ||||| |||||
ACC GTTGTACCACT TAGGGTA
C C

GAM2408 MGC1842 3' GGCTTCGCCATGTTGGCCA 66257 AT
TGGCCAACATGGTGAA C
||||||| |
ACCGGTTGTACCGCTT G
CG

GAM2408 MGC21675 3' ATGGGGTTTCACCATGTTGGTC 54586
A TGGCCAACATGGTGAAATCCCAT
|||||||
ACTGGTTGTACCACTTTGGGGTA

GAM2408 MGC2474 3' ATGGGGTTTCACCATGTTGGCT 43950
A TGGCCAACATGGTGAAATCCCAT
|||||||
ATCGGTTGTACCACTTTGGGGTA

GAM2408 MGC2603 3' GGTTTCACCATATTAGCCA 44079 C C
TGGC AA ATGGTGAAATC
||| || |||||
ACCG TT TACCACTTTGG
A A

GAM2408 MGC2615 3' GGATTTTCATCATGTTGCCCA 44322 C
TGG CAACATGGTGAAATCC
||| |||||
ACC GTTGTACTACTTTAGG
C

GAM2408 MGC4638 3' GGTTTCAACATGTTGGCCA 49741 G
TGGCCAACATG TGAAATC
||||||| |||||

			ACCGGTTGTAC ACTTTGG	
			A	
GAM2408	MGC4766	5'	GGGGTTTCACCGTGTTAGCCA 49560	C
			TGGC AACATGGTGAAATCCC	
			ACCG TTGTGCCACTTTGGGG	
			A	
GAM2408	MGC5149	3'	ATGGGGTTTCACCACATTGGCC 72754	CA
	A		TGGCCAA TGGTGAAATCCCAT	
			ACCGGTT ACCACTTTGGGGTA	
			AC	
GAM2408	MKRN4	3'	GGGGTTTCACCATATTGGTCA 48469	C
			TGGCCAA ATGGTGAAATCCC	
			ACTGGTT TACCACTTTGGGG	
			A	
GAM2408	moblak	3'	GATTTACCATGTTGGCCA 56403	
			TGGCCAACATGGTGAAATC	
			ACCGGTTGTACCACTTTAG	
GAM2408	moblak	3'	GGGTTTCACCGTGTTAGCCA 56406	C
			TGGC AACATGGTGAAATCC	
			ACCG TTGTGCCACTTTGGG	
			A	
GAM2408	MRPS27	3'	ATGGGGTTTCACCATGTTGGTC 31322	
	A		TGGCCAACATGGTGAAATCCCAT	
			ACTGGTTGTACCACTTTGGGGTA	
GAM2408	MtFMT	3'	ATGGGGTTTCACCATGTTGGTC 58330	
	A		TGGCCAACATGGTGAAATCCCAT	
			ACTGGTTGTACCACTTTGGGGTA	
GAM2408	MYO5C	3'	GGTTTCACCATGTTGGCCA 38724	
			TGGCCAACATGGTGAAATC	
			ACCGGTTGTACCACTTTGG	
GAM2408	NDP52	3'	GGGTTTCACTATGTTGGCCA 20673	
			TGGCCAACATGGTGAAATCC	
			ACCGGTTGTATCACTTTGGG	
GAM2408	NDUFC2	3'	GGGGTTTCACCATGTTGGCCA 17032	
			TGGCCAACATGGTGAAATCCC	

ACCGGTTGTACCACTTTGGGG

GAM2408 Nup43 3' GGGTTTCACCATGTTGGCCA 45349

TGGCCAACATGGTGAAATCC

|||||

ACCGGTTGTACCACTTTGGG

GAM2408 NXN 3' ATGGGGTTTCACCATGTTGGCT 42667

A

TGGCCAACATGGTGAAATCCCAT

|||||

ATCGGTTGTACCACTTTGGGGTA

GAM2408 OCT11 3' ATGGGGTTTCACCATGTTGGTC 27583

A

TGGCCAACATGGTGAAATCCCAT

|||||

ACTGGTTGTACCACTTTGGGGTA

GAM2408 OR51E2 3' GTTTCACCATGTTGGCCA 48517

TGGCCAACATGGTGAAAT

|||||

ACCGGTTGTACCACTTTG

GAM2408 OSBPL2 3' GGGTTTTACCATGTTGGTCA 58489

T

TGGCCAACATGGTGAAA CCC

|||||

ACTGGTTGTACCACTTT GGG

T

GAM2408 OSBPL2 3' GGGTTTTACCATGTTGGTCA 29903

T

TGGCCAACATGGTGAAA CCC

|||||

ACTGGTTGTACCACTTT GGG

T

GAM2408 PELI1 5' ATGGGGTTTCACCATGTTGGCC 40625

A

TGGCCAACATGGTGAAATCCCAT

|||||

ACCGGTTGTACCACTTTGGGGTA

GAM2408 PELI1 5' GGGGTTTCACCATGTTGCCCA 40644 C

TGG CAACATGGTGAAATCCC

||| |||||

ACC GTTGTACCACTTTGGGG

C

GAM2408 PRO0365 5' GGGGTTTCACTATGTTGGCCA 26989

TGGCCAACATGGTGAAATCCC

|||||

ACCGGTTGTATCACTTTGGGG

GAM2408 PRO0800 5' GGTTTCATCATGTTGACCA 38349 C

TGG CAACATGGTGAAATC

||| |||||

ACC GTTGTACTACTTTGG
 A
 GAM2408 RAB21 3' GGGGTTTCACCAGGTTAGCCA 31093 C A
 TGGC AAC TGGTGAAATCCC
 |||| ||| |||||
 ACCG TTG ACCACTTTGGGG
 A G
 GAM2408 RAB33B 3' ATGGGGTTTCACCATGTTGGCC 49319
 A TGGCCAACATGGTGAAATCCCAT
 |||||
 ACCGGTTGTACCACTTTGGGGTA

 GAM2408 RAI 5' GGGTTCTTACCATGTTGGCCA 22855 AAT
 TGGCCAACATGGTGA CCC
 ||||| |||
 ACCGGTTGTACCATT GGG
 CTT
 GAM2408 RASSF2 3' GTTTCACCATCTTGGCCA 29109 C
 TGGCCAA ATGGTGAAAT
 ||||| |||||
 ACCGGTT TACCACTTTG
 C
 GAM2408 RNF8 3' GGGTTTCACCATGTTGGCCA 15570
 TGGCCAACATGGTGAAATCC
 |||||
 ACCGGTTGTACCACTTTGGG

 GAM2408 RNO2 5' ATGGGGTGTACCATGTTGGCC 53922 A
 A TGGCCAACATGGTGA ATCCCAT
 ||||| |||||
 ACCGGTTGTACCACT TGGGGTA
 G
 GAM2408 SCAMP-4 3' ATGGGGTTTCACCATGTTGGCC 55338
 A TGGCCAACATGGTGAAATCCCAT
 |||||
 ACCGGTTGTACCACTTTGGGGTA

 GAM2408 SCAMP5 3' ATGGGATTTTCAGGTTAGGC 58052 _ ATGG
 GCC AAC TGAAATCCCAT
 ||| ||| |||||
 CGG TTG ACTTTAGGGTA
 A G__
 GAM2408 SCYA16 3' GGGATTCTACCATGTTGCCCA 17173 C A
 TGG CAACATGGTG AATCCC
 ||| ||||| |||||
 ACC GTTGTACCAT TTAGGG
 C C
 GAM2408 SCYA22 3' GGCTTCACCATGTTGGCCA 92599 AT
 TGGCCAACATGGTGAA C
 ||||| |

			ACCGGTTGTACCACTT	G	
			CG		
GAM2408	SCYA22	3'	GGTTTCACCATATTGGCCA	92602	C
			TGGCCAA ATGGTGAAATC		
			ACCGGTT TACCACTTTGG		
			A		
GAM2408	SERF1B	3'	ATGGGGTTTCACCATGTTGGCC	43690	
	A		TGGCCAACATGGTGAAATCCCAT		
			ACCGGTTGTACCACTTTGGGGTA		
GAM2408	SFXN2	3'	GGGGTTTCACCATGCTGGCCA	74379	A
			TGGCCA CATGGTGAAATCCC		
			ACCGGT GTACCACTTTGGGG		
			C		
GAM2408	SLC12A8	3'	GGGTTTCACCATGTTGGCCA	45241	
			TGGCCAACATGGTGAAATCC		
			ACCGGTTGTACCACTTTGGG		
GAM2408	SLC16A4	3'	GTTTCACCATGTTAGCCA	17458	C
			TGGC AACATGGTGAAAT		
			ACCG TTGTACCACTTTG		
			A		
GAM2408	SLC19A3	3'	ATGGGGTTTCACAATGTTGGCC	48236	G
	A		TGGCCAACAT GTGAAATCCCAT		
			ACCGGTTGTA CACTTTGGGGTA		
			A		
GAM2408	SLC6A14	3'	GTTTCCCCATGTTGGCCA	24311	T
			TGGCCAACATGG GAAAT		
			ACCGGTTGTACC CTTTG		
			C		
GAM2408	SREC	3'	GGGTTTCACCATGTTAGCCA	14906	C
			TGGC AACATGGTGAAATCC		
			ACCG TTGTACCACTTTGGG		
			A		
GAM2408	SS-56	3'	GGAGTTTCACCATGTTAGCTA	60354	C TC
			TGGC AACATGGTGAAA CC		
			ATCG TTGTACCACTTT GG		
			A GA		
GAM2408	STAF65(gamma)	3'	ATGAGGTTTCACCGTGTGGCC	30061	C
	A		TGGCCAACATGGTGAAATC CAT		

			ACCGGTTGTGCCACTTTGG	GTA	
			A		
GAM2408	SULT1C2	3'	GGTTTCACCGTGTTAGCCA	22717	C
			TGGC AACATGGTGAAATC		
			ACCG TTGTGCCACTTTGG		
			A		
GAM2408	SYT13	3'	ATGGGGTTTCACCATGTTGGCC	95096	
	A		TGGCCAACATGGTGAAATCCCAT		
			ACCGGTTGTACCACTTTGGGGTA		
GAM2408	TADA3L	3'	GGGGTTTCACCGTGTTAGCCA	56810	C
			TGGC AACATGGTGAAATCCC		
			ACCG TTGTGCCACTTTGGGG		
			A		
GAM2408	TCL6	3'	GGGTTTCACCGTGTTAGCCA	25911	C
			TGGC AACATGGTGAAATCC		
			ACCG TTGTGCCACTTTGGG		
			A		
GAM2408	TCL6	5'	GGTTTCACCATGTTGGCCA	25913	
			TGGCCAACATGGTGAAATC		
			ACCGGTTGTACCACTTTGG		
GAM2408	TCL6	3'	GGGTTTCACCGTGTTAGCCA	27763	C
			TGGC AACATGGTGAAATCC		
			ACCG TTGTGCCACTTTGGG		
			A		
GAM2408	TCL6	5'	GGTTTCACCATGTTGGCCA	27765	
			TGGCCAACATGGTGAAATC		
			ACCGGTTGTACCACTTTGG		
GAM2408	TCL6	5'	GGTTTCACCATGTTGGCCA	40488	
			TGGCCAACATGGTGAAATC		
			ACCGGTTGTACCACTTTGG		
GAM2408	TCL6	5'	GGTTTCACCATGTTGGCCA	40515	
			TGGCCAACATGGTGAAATC		
			ACCGGTTGTACCACTTTGG		
GAM2408	TERA	3'	GGGGTTTCACCACGTTGGCCA	41419	A
			TGGCCAAC TGGTGAAATCCC		

			ACCGGTTG ACCACTTTGGGG	
			C	
GAM2408	TGIF2	3'	GGGGTTTCACCATCTTGGCCA 41754	C
			TGGCCAA ATGGTGAAATCCC	
			ACCGGTT TACCACTTTGGGG	
			C	
GAM2408	TRIM16	3'	ATGGGGTTTCACCATGTTGGCC 22365	
	A		TGGCCAACATGGTGAAATCCCAT	
			ACCGGTTGTACCACTTTGGGGTA	
GAM2408	TRIM6	3'	GGGTTTCACCGTGTTGGCCA 55183	
			TGGCCAACATGGTGAAATCC	
			ACCGGTTGTGCCACTTTGGG	
GAM2408	TU12B1-TY	3'	ATGGGGTTTCACCATGTTGGCC 33828	
	A		TGGCCAACATGGTGAAATCCCAT	
			ACCGGTTGTACCACTTTGGGGTA	
GAM2408	TU12B1-TY	3'	GGGGTTTCACCATGTTGGCCA 33855	
			TGGCCAACATGGTGAAATCCC	
			ACCGGTTGTACCACTTTGGGG	
GAM2408	TUCAN	3'	GGGTTTCACCATTTTGGCCA 30982	C
			TGGCCAA ATGGTGAAATCC	
			ACCGGTT TACCACTTTGGG	
			T	
GAM2408	UBF-fl	3'	ATGGGGTTTCACCATGCTGGCC 52616	A
	A		TGGCCA CATGGTGAAATCCCAT	
			ACCGGT GTACCACTTTGGGGTA	
			C	
GAM2408	UBF-fl	3'	ATGGGGTTTACCATGTTGGCC 52618	
	A		TGGCCAACATGGTGAAATCCCAT	
			ACCGGTTGTACCATTTTGGGGTA	
GAM2408	UBF-fl	3'	GTTTCACCATGCTGGCCA 52633	A
			TGGCCA CATGGTGAAAT	
			ACCGGT GTACCACTTTG	
			C	
GAM2408	VDU1	3'	ATGGGGTTTCACCATGTTGGCC 31119	
	A		TGGCCAACATGGTGAAATCCCAT	

ACCGGTTGTACCACTTTGGGGTA

GAM2408 VPS33A 3' ATGGTGTTCACCATGTTGGCC 43609 TC
A TGGCCAACATGGTGAAA CCAT

|||||
ACCGGTTGTACCACTTT GGTA
GT

GAM2408 WBSCR23 3' GGGGTTTCACCATGTTGGCCA 47439
TGGCCAACATGGTGAAATCCC
|||||
ACCGGTTGTACCACTTTGGGG

GAM2408 ZNF17 3' GGGGTCTTACCATGTTGGCCA 83272 A
TGGCCAACATGGTGA ATCCC
|||||
ACCGGTTGTACCATT TGGGG
C

GAM2408 ZNF221 3' GGGGTTTCACCGTGTTAGCCA 26269 C
TGGC AACATGGTGAAATCCC
||| |||||
ACCG TTGTGCCACTTTGGGG
A

GAM2408 LOC112817 3' ATGGGGTTTCACCGTGTTGGCC 57316
A TGGCCAACATGGTGAAATCCCAT
|||||
ACCGGTTGTGCCACTTTGGGGTA

GAM2408 LOC113523 5' GGGTTTCACCATGTTAGCCA 73428 C
TGGC AACATGGTGAAATCC
||| |||||
ACCG TTGTACCACTTTGGG
A

GAM2408 LOC115219 5' GGGGTTTCATCATGTTGGCCA 73700
TGGCCAACATGGTGAAATCCC
|||||
ACCGGTTGTACTACTTTGGGG

GAM2408 LOC115648 3' GGGGTTTCACCATGTTGGCTA 60027
TGGCCAACATGGTGAAATCCC
|||||
ATCGGTTGTACCACTTTGGGG

GAM2408 LOC119392 3' GTTTCACCACGTTGGCCA 59816 A
TGGCCAAC TGGTGAAAT
||||| |||||
ACCGGTTG ACCACTTTG
C

GAM2408 LOC120114 3' ATGGGGTTTCACCATGTTGGCC 76040
A TGGCCAACATGGTGAAATCCCAT
|||||

ACCGGTTGTACCACTTTGGGGTA

GAM2408 LOC120939 3' GTTTCACCATGTTGGCCA 76770
TGGCCAACATGGTGAAAT
|||||||
ACCGGTTGTACCACTTTG

GAM2408 LOC121504 3' GGGGTTTCACCATGTTGGCCA 74550
TGGCCAACATGGTGAAATCCC
|||||||
ACCGGTTGTACCACTTTGGGG

GAM2408 LOC124216 3' GGTTTCACCATGTTGGCCA 74737
TGGCCAACATGGTGAAATC
|||||||
ACCGGTTGTACCACTTTGG

GAM2408 LOC124222 3' GGAAGGGCCATGTTGCCA 74752 C GAAA
TGGC AACATGGT TCC
||| ||||| |||
ACCG TTGTACCG AGG
_ GGA_

GAM2408 LOC126364 3' ATGGGGTTTCGCCATGTTGGCC 76183
A TGGCCAACATGGTGAAATCCCAT
|||||||
ACCGGTTGTACCGCTTTGGGGTA

GAM2408 LOC126661 3' ATGGGGTTTCACCATGTTGGCC 75050
A TGGCCAACATGGTGAAATCCCAT
|||||||
ACCGGTTGTACCACTTTGGGGTA

GAM2408 LOC126661 3' GGTTTTACCATGTTGCCCA 75061 C T
TGG CAACATGGTGAAA CC
||| ||||| |||
ACC GTTGTACCACTTT GG
C T

GAM2408 LOC128077 3' GGGGTTTCACCATGTTAGCCA 75222 C
TGGC AACATGGTGAAATCCC
||| |||||
ACCG TTGTACCACTTTGGGG
A

GAM2408 LOC128077 3' GGGTTTCACCATGTTGGCCA 75224
TGGCCAACATGGTGAAATCC
|||||||
ACCGGTTGTACCACTTTGGG

GAM2408 LOC128989 3' GGGGTTTCACCATGTTGGTCA 75321
TGGCCAACATGGTGAAATCCC
|||||||

ACTGGTTGTACCACTTTGGGG

GAM2408 LOC130813 3' GGGTCTCACTATGTTGACCA 76277 C AAT
TGG CAACATGGTGA CCC
||| ||||| |||
ACC GTTGTATCACT GGG
A CT_

GAM2408 LOC132241 5' GTTTCACATGTTGGCCA 75565
TGGCCAACATGGTGAAAT
||||| |||||
ACCGGTTGTATCACTTTG

GAM2408 LOC132625 3' ATGGGGTTTCACCATGTTGGCC 76434
A TGGCCAACATGGTGAAATCCCAT
||||| |||||
ACCGGTTGTACCACTTTGGGGTA

GAM2408 LOC133686 3' ATGGGGATTACCATGTTGGTC 75611 A
A TGGCCAACATGGTGAA TCCCAT
||||| |||||
ACTGGTTGTACCACTT GGGGTA
A

GAM2408 LOC135154 3' GGTTCACCATGTTAGCCA 75732 C
TGGC AACATGGTGAAATC
||| |||||
ACCG TTGTACCACTTTGG
A

GAM2408 LOC135293 3' GGCATTTACCATGTTGGCCA 76687 C
TGGCCAACATGGTGAAAT CC
||||| |||
ACCGGTTGTACCACTTTA GG
C

GAM2408 LOC143187 3' ATGGAGTTTCACCATGTTGGCC 59755 TC
A TGGCCAACATGGTGAAA CCAT
||||| |||||
ACCGGTTGTACCACTTT GGTA
GA

GAM2408 LOC143916 3' ATGGGGTTTCACCTTGTTGGCC 77138 T
A TGGCCAACA GGTGAAATCCCAT
||||| |||||
ACCGGTTGT CCACTTTGGGGTA
T

GAM2408 LOC144524 5' GTTTCACCGTGTTAGCCA 84062 C
TGGC AACATGGTGAAAT
||| |||||
ACCG TTGTGCCACTTTG
A

GAM2408 LOC144742 5' GGTTTTACCATGTTGGCCA 77463 T
TGGCCAACATGGTGAAA CC
||||| |||

		ACCGGTTGTACCACTTT GG	
		T	
GAM2408	LOC145268 5'	GTTTCACCATGTTGGCCA 77583	
		TGGCCAACATGGTGAAAT	
		ACCGGTTGTACCACTTTG	
GAM2408	LOC145384 3'	GGCAAGGTTTCACTACATTGAC 77715	C CA
	CA	TGG CAA TGGTGAAATC CC	
		ACC GTT ATCACTTTGG GG	
		A AC AAC	
GAM2408	LOC145622 3'	GTTTCACCACGTTGGCCA 77824	A
		TGGCCAAC TGGTGAAAT	
		ACCGGTTG ACCACTTTG	
		C	
GAM2408	LOC146050 3'	ATGGGGTTTCACCATGTTGGCC 78102	
	A	TGGCCAACATGGTGAAATCCCAT	
		ACCGGTTGTACCACTTTGGGGTA	
GAM2408	LOC146229 3'	GGGGTTTCACCATGTTGGCCA 78293	
		TGGCCAACATGGTGAAATCCC	
		ACCGGTTGTACCACTTTGGGG	
GAM2408	LOC146229 3'	GGGGTTTCACCATGTTGGCCA 78294	
		TGGCCAACATGGTGAAATCCC	
		ACCGGTTGTACCACTTTGGGG	
GAM2408	LOC146229 3'	GGGTTTCACCATATTGGCCA 78297	C
		TGGCCAA ATGGTGAAATCC	
		ACCGGTT TACCACTTTGGG	
		A	
GAM2408	LOC146346 5'	GGATTTCATCATGTTGGCCA 78398	
		TGGCCAACATGGTGAAATCC	
		ACCGGTTGTACTACTTTAGG	
GAM2408	LOC146429 5'	GGGTTTCACCATGATAGCCA 84671	CAA
		TGGC CATGGTGAAATCC	
		ACCG GTACCACTTTGGG	
		ATA	
GAM2408	LOC146603 5'	GGGGTTTCACCGTGTTAGCCA 78599	C
		TGGC AACATGGTGAAATCCC	

		ACCG TTGTGCCACTTTGGGG	
	A		
GAM2408	LOC146784 5'	ATGGGGTTTCACCATGTTGGCC 78706	
	A	TGGCCAACATGGTGAAATCCCAT	
		ACCGGTTGTACCACTTTGGGGTA	
GAM2408	LOC146839 3'	GGGGTTTCACCGTGTTAGCCA 84843	C
		TGGC AACATGGTGAAATCCC	
		ACCG TTGTGCCACTTTGGGG	
	A		
GAM2408	LOC146894 3'	ATGGGGTTTCACCATGTTGGCC 59854	
	A	TGGCCAACATGGTGAAATCCCAT	
		ACCGGTTGTACCACTTTGGGGTA	
GAM2408	LOC146901 3'	GGGGTTTCACCATGTTGGCCA 84907	
		TGGCCAACATGGTGAAATCCC	
		ACCGGTTGTACCACTTTGGGG	
GAM2408	LOC146909 3'	ATGGGGTTTCACCGTGTTAGCC 78760	C
	A	TGGC AACATGGTGAAATCCCAT	
		ACCG TTGTGCCACTTTGGGGTA	
	A		
GAM2408	LOC146952 5'	GGGTTTCACCACATTGGCCA 84930	CA
		TGGCCAA TGGTGAAATCC	
		ACCGGTT ACCACTTTGGG	
	AC		
GAM2408	LOC147080 5'	GGTTTCACCATGTTAGCCA 85043	C
		TGGC AACATGGTGAAATC	
		ACCG TTGTACCACTTTGG	
	A		
GAM2408	LOC147166 3'	ATGGGGTTTCACCATGTTGGCC 78882	
	A	TGGCCAACATGGTGAAATCCCAT	
		ACCGGTTGTACCACTTTGGGGTA	
GAM2408	LOC147429 3'	ATGGGGTTTCACCATGTTAGTC 78992	C
	A	TGGC AACATGGTGAAATCCCAT	
		ACTG TTGTACCACTTTGGGGTA	
	A		
GAM2408	LOC147694 3'	GGGGTTTCACCGTGTTAGCCA 79100	C
		TGGC AACATGGTGAAATCCC	

		ACCG TTGTGCCACTTTGGGG		
		A		
GAM2408	LOC147817 3'	GGGCTTCACCATGTTGGC 79185	AT	
		GCCAACATGGTGAA CCC		
		CGGTTGTACCACTT GGG		
		C_		
GAM2408	LOC147990 3'	GGGGTTTCAGCATATTGACCA 85227	C C G	
		TGG CAA ATG TGAAATCCC		
		ACC GTT TAC ACTTTGGGG		
		A A G		
GAM2408	LOC148147 3'	ATGAGGTTTCACCTTGTTGGCC 79390	T C	
	A	TGGCCAACA GGTGAAATC CAT		
		ACCGGTTGT CCACTTTGG GTA		
		T A		
GAM2408	LOC148189 5'	GGGGTTTCACCATGTTGACCA 79451	C	
		TGG CAACATGGTGAAATCCC		
		ACC GTTGTACCACTTTGGGG		
		A		
GAM2408	LOC148195 3'	GGTTTCACCACATTGGTCA 85286	CA	
		TGGCCAA TGGTGAAATC		
		ACTGGTT ACCACTTTGG		
		AC		
GAM2408	LOC148443 3'	GGGTCTCACCATGTTGCCCA 79603	C AAT	
		TGG CAACATGGTGGA CCC		
		ACC GTTGTACCACT GGG		
		C CT_		
GAM2408	LOC148887 5'	GGGTTTCACCATGTTGGTCA 85407		
		TGGCCAACATGGTGAAATCC		
		ACTGGTTGTACCACTTTGGG		
GAM2408	LOC149194 3'	ATGGGATCTCATTTTGTGCCC 79979	C TG A	
	A	TGG CAACA GTGA ATCCCAT		
		ACC GTTGT TACT TAGGGTA		
		C TT C		
GAM2408	LOC149421 3'	GGGGTTTCACCGCATTAGCCA 80147	C CA	
		TGGC AA TGGTGAAATCCC		
		ACCG TT GCCACTTTGGGG		
		A AC		
GAM2408	LOC149478 3'	GGGGTTTCACCATGTTGGCCA 80173		
		TGGCCAACATGGTGAAATCCC		

ACCGGTTGTACCACTTTGGGG

GAM2408 LOC149506 3' GGGTTCACCACGTTGGCCA 85641 A AT
TGGCCAAC TGGTGAA CCC
||||| ||||| ||
ACCGGTTG ACCACTT GGG
C _

GAM2408 LOC149692 3' GGGTTTCACCATGTTGGCCA 85740
TGGCCAACATGGTGAAATCC
|||||||
ACCGGTTGTACCACTTTGGG

GAM2408 LOC149711 3' ATGGGGTTTTACCATGTTGGCC 85839
A TGGCCAACATGGTGAAATCCCAT
|||||||
ACCGGTTGTACCATTTTGGGGTA

GAM2408 LOC149821 5' GGAGTTTCACCGTGTTAGCCA 85934 C TC
TGGC AACATGGTGAAA CC
||| ||||| ||
ACCG TTGTGCCACTTT GG
A GA

GAM2408 LOC150054 5' ATGGGGTTTCCCATGTTGGCCA 85968 T
TGGCCAACATGG GAAATCCCAT
||||||| |||||
ACCGGTTGTACC CTTTGGGGTA

GAM2408 LOC150166 5' ATGGGGTTTCACCATGTTGTCC 86035 C
A TGG CAACATGGTGAAATCCCAT
||| |||||
ACC GTTGTACCACTTTGGGGTA
T

GAM2408 LOC150225 3' GGTTCACCATGTCTGGCCA 86199 A
TGGCC ACATGGTGAAATC
||||| |||||
ACCGG TGTACCACTTTGG
C

GAM2408 LOC150282 5' ATGGCGTTTCACCATGTTGGCC 80536 C
A TGGCCAACATGGTGAAAT CCAT
||||||| |||||
ACCGGTTGTACCACTTTG GGTA
C

GAM2408 LOC150290 3' ATGAGATTTTACTATGTCTGCC 80585 CA C
GGC ACATGGTGAAATC CAT
||| ||||| |||
CCG TGTATCATTTTAG GTA
C_ A

GAM2408 LOC150397 3' GTTTCACCGTGTTGACCA 80667 C
TGG CAACATGGTGAAAT
||| |||||

		ACC GTTGTGCCACTTTG	
		A	
GAM2408	LOC150960 3'	ATGGGGTCTCACCCTGTTGGCC 80867	T A
	A	TGGCCAACA GGTGA ATCCCAT	
		ACCGGTTGT CCACT TGGGGTA	
		C C	
GAM2408	LOC151050 5'	GTTTCACCATGTTGGCCA 80919	
		TGGCCAACATGGTGAAAT	
		ACCGGTTGTACCACTTTG	
GAM2408	LOC151057 3'	GGGGTTTCACCATGTTGGCCA 86390	
		TGGCCAACATGGTGAAATCCC	
		ACCGGTTGTACCACTTTGGGG	
GAM2408	LOC151201 3'	GGGGTTTCACCATGTTGGCTA 86478	
		TGGCCAACATGGTGAAATCCC	
		ATCGGTTGTACCACTTTGGGG	
GAM2408	LOC151475 5'	GGTTTCACCATGTTGGCCA 86598	
		TGGCCAACATGGTGAAATC	
		ACCGGTTGTACCACTTTGG	
GAM2408	LOC151701 3'	GGGGTTTCACCATGTTGGCCA 86676	
		TGGCCAACATGGTGAAATCCC	
		ACCGGTTGTACCACTTTGGGG	
GAM2408	LOC152137 3'	GTTTCACCATGTTGGCCA 81324	
		TGGCCAACATGGTGAAAT	
		ACCGGTTGTACCACTTTG	
GAM2408	LOC152300 3'	GGGTTTCACCATATTGGCCA 81385	C
		TGGCCAA ATGGTGAAATCC	
		ACCGGTT TACCACTTTGGG	
		A	
GAM2408	LOC152343 3'	GTTTCACCATGTTGCCCA 81433	C
		TGG CAACATGGTGAAAT	
		ACC GTTGTACCACTTTG	
		C	
GAM2408	LOC152445 3'	GGGTTTCACCATGTTAGCCA 86957	C
		TGGC AACATGGTGAAATCC	

ACCG TTGTACCACTTTGGG
 A
 GAM2408 LOC152719 5' GGGGTTTCACCATGTTGGTCA 87034
 TGGCCAACATGGTGAAATCCC
 |||||
 ACTGGTTGTACCACTTTGGGG

GAM2408 LOC152719 5' GGGTTTCACCATGTTAGCCA 87036 C
 TGGC AACATGGTGAAATCC
 ||| |||||
 ACCG TTGTACCACTTTGGG
 A

GAM2408 LOC152794 5' ATGGGGTTTCATCATGTTGGCC 81554
 A TGGCCAACATGGTGAAATCCCAT
 |||||
 ACCGGTTGTACTACTTTGGGGTA

GAM2408 LOC152851 3' GGATTTCACTATGTTGGTCA 81593
 TGGCCAACATGGTGAAATCC
 |||||
 ACTGGTTGTATCACTTTAGG

GAM2408 LOC153077 3' ATGGGGCTTCACCATGTTGGCC 87111 AT
 A TGGCCAACATGGTGAA CCCAT
 ||||| ||||
 ACCGGTTGTACCACTT GGGTA
 CG

GAM2408 LOC153469 3' ATGGGATTACTGTACTAACCA 81698 CCAAC AA
 TGG ATGGTGA TCCCAT
 || ||||| ||||
 ACC TGTCACTT AGGGTA
 AATCA —

GAM2408 LOC153606 5' GGGTTTCACCATGTTGGCCA 87258
 TGGCCAACATGGTGAAATCC
 |||||
 ACCGGTTGTACCACTTTGGG

GAM2408 LOC153688 3' GGATTTCATCGTGTTGCCCA 87321 C
 TGG CAACATGGTGAAATCC
 ||| |||||
 ACC GTTGTGCTACTTTAGG
 C

GAM2408 LOC153688 3' GGGTTTCACCATGTTGGCC 87326
 GGCCAACATGGTGAAATCC
 |||||
 CCGGTTGTACCACTTTGGG

GAM2408 LOC153811 3' GGTTTCACCACGTTGGCCA 81844 A
 TGGCCAAC TGGTGAAATC
 ||||| |||||

		ACCGGTTG ACCACTTTGG			
		C			
GAM2408	LOC154282 5'	ATGGTGTTCACCATGTTGGCC 87400		TC	
	A	TGGCCAACATGGTGAAC CCAT			
		ACCGGTTGTACCACTTT GGTA			
		GT			
GAM2408	LOC154877 3'	GGATCTCACTATGTTGCCA 87558	C	A	
		TGG CAACATGGTGA ATCC			
		ACC GTTGTATCACT TAGG			
		C C			
GAM2408	LOC154877 3'	GGGTCTCACCATGTTGGCTA 87565		AAT	
		TGGCCAACATGGTGA CCC			
		ATCGGTTGTACCACT GGG			
		CT_			
GAM2408	LOC154877 3'	GTTTCACCATGTTGCCA 87572	C		
		TGG CAACATGGTGAAT			
		ACC GTTGTACCACTTTG			
		C			
GAM2408	LOC154930 3'	GGATTTTACTGTGTTGGCCA 82093			
		TGGCCAACATGGTGAATCC			
		ACCGGTTGTGTCATTTTAGG			
GAM2408	LOC155372 3'	GGAATTTACCATGGTGGCCA 82259	A	C	
		TGGCCA CATGGTGAAT CC			
		ACCGGT GTACCACTTTA GG			
		G A			
GAM2408	LOC157247 5'	GGGGTTTCACCAAGTGTGGCCA 82302		_	
		TGGCCAACA TGGTGAATCCC			
		ACCGGTTGT ACCACTTTGGGG			
		G			
GAM2408	LOC157506 3'	GGGGTTTCACCATGTTGGTCA 82370			
		TGGCCAACATGGTGAATCCC			
		ACTGGTTGTACCACTTTGGGG			
GAM2408	LOC157623 3'	ATGGAGTTTCACCATATTGCC 82410	C C	TC	
	A	TGG CAA ATGGTGAAC CCAT			
		ACC GTT TACCACTTT GGTA			
		C A GA			
GAM2408	LOC157798 5'	GGGGTTTCACCTTGTGGCCA 87862		T	
		TGGCCAACA GGTGAATCCC			

		ACCGGTTGT CCACTTTGGGG		
		T		
GAM2408	LOC158014 5'	GGAGTTTCACCATGTTAGCCA 82562	C	TC
		TGGC AACATGGTGAAA CC		
		ACCG TTGTACCACTTT GG		
		A GA		
GAM2408	LOC158310 5'	GGGTTTCACAATGTTGACCA 88084	C	G
		TGG CAACAT GTGAAATCC		
		ACC GTTGTA CACTTTGGG		
		A A		
GAM2408	LOC158402 5'	GTTTCACCGTGTTGGCCA 88153		
		TGGCCAACATGGTGAAAT		
		ACCGGTTGTGCCACTTTG		
GAM2408	LOC158476 3'	GGGTTTCACCATATTGGCCA 88197	C	
		TGGCCAA ATGGTGAAATCC		
		ACCGGTT TACCACTTTGGG		
		A		
GAM2408	LOC158476 3'	GGGTTTCACCATGTTGGTCA 88199		
		TGGCCAACATGGTGAAATCC		
		ACTGGTTGTACCACTTTGGG		
GAM2408	LOC158549 5'	GGGGTTTCACCGTGTTAGCCA 88225	C	
		TGGC AACATGGTGAAATCCC		
		ACCG TTGTGCCACTTTGGGG		
		A		
GAM2408	LOC158668 3'	GTTTCACCATGCTGGTCA 69906	A	
		TGGCCA CATGGTGAAAT		
		ACTGGT GTACCACTTTG		
		C		
GAM2408	LOC158865 5'	GGGACTTCACCGTGTTGGCCA 88310		A
		TGGCCAACATGGTGAA TCCC		
		ACCGGTTGTGCCACTT AGGG		
		C		
GAM2408	LOC160646 3'	ATGGGGCTTCACCATGTTGGCC 83106		AT
	A	TGGCCAACATGGTGAA CCCAT		
		ACCGGTTGTACCACTT GGGTA		
		CG		
GAM2408	LOC161829 3'	ATGGGGTTTCACCATGTTGGCC 83183		
	A	TGGCCAACATGGTGAAATCCCAT		

ACCGGTTGTACCACTTTGGGGTA

GAM2408 LOC162427 3' ATGGGGTTTCACCATGTTGGCC 83223
A TGGCCAACATGGTGAAATCCCAT
|||||||
ACCGGTTGTACCACTTTGGGGTA

GAM2408 LOC169611 3' GGATTTACCATGTTGGCCA 83652
TGGCCAACATGGTGAAATCC
|||||||
ACCGGTTGTACCACTTTAGG

GAM2408 LOC169611 3' GGGGTTTCACCACGTTGGCCA 83654 A
TGGCCAAC TGGTGAAATCCC
||||| |||||
ACCGGTTG ACCACTTTGGGG
C

GAM2408 LOC170082 5' ATGGGGTTTCACCATGTTAGCC 83439 C
A TGGC AACATGGTGAAATCCCAT
||| |||||
ACCG TTGTACCACTTTGGGGTA
A

GAM2408 LOC196047 5' GTTTCACCATGTCTGGCCA 91164 A
TGGCC ACATGGTGAAAT
|||| |||||
ACCGG TGTACCACTTTG
C

GAM2408 LOC196264 3' GGGGTTTCACCATTTTGGCCA 88988 C
TGGCCAA ATGGTGAAATCCC
||||| |||||
ACCGGTT TACCACTTTGGGG
T

GAM2408 LOC196411 3' ATGGGGTTTCACTATGTTGGCC 89040
A TGGCCAACATGGTGAAATCCCAT
|||||||
ACCGGTTGTATCACTTTGGGGTA

GAM2408 LOC196529 3' GGGTTTCACTACGTTGGCCA 89136 A
TGGCCAAC TGGTGAAATCC
||||| |||||
ACCGGTTG ATCACTTTGGG
C

GAM2408 LOC197358 3' ATGGGGTTTCACCATGTTGATC 89421 GC
A TG CAACATGGTGAAATCCCAT
|| |||||
AC GTTGTACCACTTTGGGGTA
TA

GAM2408 LOC197358 3' GGGGTTTCATCATGTTGGCCA 89438
TGGCCAACATGGTGAAATCCC
|||||||

ACCGGTTGTACTACTTTGGGG

GAM2408 LOC199699 3' GGGTTTCACCGTGTTAGCCA 89677 C
TGGC AACATGGTGAAATCC
|||||
ACCG TTGTGCCACTTTGGG
A

GAM2408 LOC199725 5' GGGATTTTACCATGTTGGTCA 91422
TGGCCAACATGGTGAAATCCC
|||||
ACTGGTTGTACCACTTTAGGG

GAM2408 LOC199786 3' ATGGGGTTTCACCATGTTGGCC 89742
A TGGCCAACATGGTGAAATCCCAT
|||||
ACCGGTTGTACCACTTTGGGGTA

GAM2408 LOC199786 3' GGTGGTTTCACCATGTTGGTCA 89761
TGGCCAACATGGTGAAATC CC
||||| ||
ACTGGTTGTACCACTTTGG GG
T

GAM2408 LOC200014 3' GGTGTTTCACCATGTTGGTCA 89941 TC
TGGCCAACATGGTGAAA CC
||||| ||
ACTGGTTGTACCACTTT GG
GT

GAM2408 LOC200169 5' GGAGTTTCACCATGTTGGCCA 91558 TC
TGGCCAACATGGTGAAA CC
||||| ||
ACCGGTTGTACCACTTT GG
GA

GAM2408 LOC200268 3' ATGGGATTTTGCCATGTTGCCC 90082 C TG
A TGG CAACATGG AAATCCCAT
||| ||| |||
ACC GTTGTAACC TTTAGGGTA
C GT

GAM2408 LOC200301 5' GGGGTTTCACCGTGTTAGCCA 90146 C
TGGC AACATGGTGAAATCCC
|||||
ACCG TTGTGCCACTTTGGGG
A

GAM2408 LOC200310 3' GGGGTTTCACCATGTTGGTCA 66330
TGGCCAACATGGTGAAATCCC
|||||
ACTGGTTGTACCACTTTGGGG

GAM2408 LOC200314 3' ATGGGGTTTCACCACGTTGGCC 91589 A
A TGGCCAAC TGGTGAAATCCCAT
||||| |||

	ACCGGTTG ACCACTTTGGGGTA	
	C	
GAM2408 LOC200316 3'	GTTTCACCATGTTGGCCA 90191	
	TGGCCAACATGGTGAAAT	
	ACCGGTTGTACCACTTTG	
GAM2408 LOC201173 5'	GGAGTTTCACCATGTTGGTCA 88688	TC
	TGGCCAACATGGTGAAA CC	
	ACTGGTTGTACCACTTT GG	
	GA	
GAM2408 LOC201220 5'	ATGGAGTTTCACCATGTTGGTC 88705	TC
A	TGGCCAACATGGTGAAA CCAT	
	ACTGGTTGTACCACTTT GGTA	
	GA	
GAM2408 LOC201294 3'	GGGGTTTCACCATGTTGGCCA 89590	
	TGGCCAACATGGTGAAATCCC	
	ACCGGTTGTACCACTTTGGGG	
GAM2408 LOC201411 3'	GGGTTTCACCATGTTGGTCA 63645	
	TGGCCAACATGGTGAAATCC	
	ACTGGTTGTACCACTTTGGG	
GAM2408 LOC201626 3'	ATGGGGTTTCGCCACGTTGGCC 90426	A
A	TGGCCAAC TGGTGAAATCCCAT	
	ACCGGTTG ACCGCTTTGGGGTA	
	C	
GAM2408 LOC202460 5'	ATGGGGTTTCACCATGTAGGCC 90666	A
A	TGGCC ACATGGTGAAATCCCAT	
	ACCGG TGTACCACTTTGGGGTA	
	A	
GAM2408 LOC202934 3'	GGGTTTCACCACGTTGGCCA 92044	A
	TGGCCAAC TGGTGAAATCC	
	ACCGGTTG ACCACTTTGGG	
	C	
GAM2408 LOC203197 3'	ATGGGGTTTCGCCATGTTGGCC 90805	
A	TGGCCAACATGGTGAAATCCCAT	
	ACCGGTTGTACCGCTTTGGGGTA	
GAM2408 LOC203339 3'	ATGGGGTTTCACCATGTTTGCC 92206	C
A	TGGC AACATGGTGAAATCCCAT	

	ACCG TTGTACCACTTTGGGGTA		
	T		
GAM2408 LOC203350 3'	GGGGTTTCACCGTGTTGGCCA 92242		
	TGGCCAACATGGTGAAATCCC		
	ACCGGTTGTGCCACTTTGGGG		
GAM2408 LOC203378 3'	ATGGGATTTTACCACATTGGTC 92277	CA	
A	TGGCCAA TGGTGAAATCCCAT		
	ACTGGTT ACCATTTTAGGGTA		
	AC		
GAM2408 LOC204804 3'	ATGAGGTTTTCACCTTGTTGGCC 91034	T	C
A	TGGCCAACA GGTGAAATC CAT		
	ACCGGTTGT CCACTTTGG GTA		
	T A		
GAM2408 LOC205251 5'	GGGTTTCACCATGTTAACCA 92358	CC	
	TGG AACATGGTGAAATCC		
	ACC TTGTACCACTTTGGG		
	AA		
GAM2408 LOC219445 5'	GGGGTTTCACCGTGTTAGCCA 93209	C	
	TGGC AACATGGTGAAATCCC		
	ACCG TTGTGCCACTTTGGGG		
	A		
GAM2408 LOC219445 5'	GGTGTTCACCATATTGGCCA 93213	C	TC
	TGGCCAA ATGGTGAAA CC		
	ACCGGTT TACCACTTT GG		
	A GT		
GAM2408 LOC219673 5'	GTTTCACCATGTTGGCCA 94632		
	TGGCCAACATGGTGAAAT		
	ACCGGTTGTACCACTTTG		
GAM2408 LOC219735 3'	GGGGTTTCACCGTGTTAGCCA 94730	C	
	TGGC AACATGGTGAAATCCC		
	ACCG TTGTGCCACTTTGGGG		
	A		
GAM2408 LOC219894 3'	ATGGGGTTTCACCGTGTTAGCC 94898	C	
A	TGGC AACATGGTGAAATCCCAT		
	ACCG TTGTGCCACTTTGGGGTA		
	A		
GAM2408 LOC220074 3'	ATGGGGTTTCGCCATGTTGGCC 59963		
A	TGGCCAACATGGTGAAATCCCAT		

ACCGGTTGTACCGCTTTGGGGTA

GAM2408	LOC220074	3'	GGGGTTTCACCATGTTAGCCA	59986	C	
			TGGC AACATGGTGAAATCCC			
			ACCG TTGTACCACTTTGGGG			
			A			
GAM2408	LOC220074	3'	GGTTTCGCCATGTTGGCCA	59989		
			TGGCCAACATGGTGAAATC			
			ACCGGTTGTACCGCTTTGG			
GAM2408	LOC221060	3'	GGTGTTCACCATGTTAGTCA	94833	C	TC
			TGGC AACATGGTGAAA	CC		
			ACTG TTGTACCACTTT	GG		
			A	GT		
GAM2408	LOC221296	3'	GGGGTTTCACCATGCTGGCCA	93612	A	
			TGGCCA CATGGTGAAATCCC			
			ACCGGT GTACCACTTTGGGG			
			C			
GAM2408	LOC222031	3'	GGTTTCAACATGTTGGCCA	95682	G	
			TGGCCAACATG TGAAATC			
			ACCGGTTGTAC ACTTTGG			
			A			
GAM2408	LOC222068	3'	ATGGGGTTTTACCATGTTGGCC	94269		
	A		TGGCCAACATGGTGAAATCCCAT			
			ACCGGTTGTACCATTTTGGGGTA			
GAM2408	LOC222070	5'	GGTGTTCACCATGTTGGCCA	95818		TC
			TGGCCAACATGGTGAAA	CC		
			ACCGGTTGTACCACTTT	GG		
			GT			
GAM2408	LOC222224	5'	GGGTTTCACCATGTTGGCCA	95874		
			TGGCCAACATGGTGAAATCC			
			ACCGGTTGTACCACTTTGGG			
GAM2408	LOC245771	5'	ATGGGGTTTCATCATGTTGGCC	94467		
	A		TGGCCAACATGGTGAAATCCCAT			
			ACCGGTTGTACTACTTTGGGGTA			
GAM2408	LOC253664	3'	ATGGGGTTTCCCATGTTGGCC	96458		T
	A		TGGCCAACATGG GAAATCCCAT			

ACCGGTTGTACC CTTTGGGGTA
 C
 GAM2408 LOC253666 3' GGGGTTTCACCATGTTGCGCA 96762 C
 TGGC AACATGGTGAAATCCC
 |||| ||||||||
 ACCG TTGTACCACTTTGGGG
 C
 GAM2408 LOC253805 3' GGGTTTCACAATGTTGGCCA 98181 G
 TGGCCAACAT GTGAAATCC
 ||||||| |||||||
 ACCGGTTGTA CACTTTGGG
 A
 GAM2408 LOC253842 5' GTTTCACCACGTTAGCCA 99240 C A
 TGGC AAC TGGTGAAAT
 |||| || |||||||
 ACCG TTG ACCACTTTG
 A C
 GAM2408 LOC254018 5' ATGGGGTTTCGCCATGTTAGCC 98737 C
 A TGGC AACATGGTGAAATCCCAT
 |||| ||||||||
 ACCG TTGTACCGCTTTGGGGTA
 A
 GAM2408 LOC254268 3' ATGGGGTTTCACCATGTTGGCC 97138
 A TGGCCAACATGGTGAAATCCCAT
 |||||||||
 ACCGGTTGTACCACTTTGGGGTA
 A
 GAM2408 LOC254295 5' GGGGTTTCACCGTGTTAGCCA 97892 C
 TGGC AACATGGTGAAATCCC
 |||| ||||||||
 ACCG TTGTGCCACTTTGGGG
 A
 GAM2408 LOC254655 3' GGGGTTTCACCATGTTGGCCA 97221
 TGGCCAACATGGTGAAATCCC
 |||||||||
 ACCGGTTGTACCACTTTGGGG
 A
 GAM2408 LOC254778 3' ATGGAACATTTTACTTGGCCA 97829 ACAT C__
 TGGCCA GGTGAAAT CCAT
 |||| ||||| |||
 ACCGGT TCATTTTA GGTA
 CAA
 GAM2408 LOC254778 3' GGATTTTGCTGTGTTGCCCA 97835 C TG
 TGG CAACATGG AAATCC
 || ||||| |||||
 ACC GTTGTGTC TTTAGG
 C GT
 GAM2408 LOC255465 3' GGGTTTCACCATGTTGGCCA 99119
 TGGCCAACATGGTGAAATCC
 |||||||||

ACCGGTTGTACCACTTTGGG

GAM2408 LOC255497 3' GGGGTTTCACCATGTTGGCCA 98988
TGGCCAACATGGTGAAATCCC
|||||
ACCGGTTGTACCACTTTGGGG

GAM2408 LOC255927 5' GGGGTTTCACCATCTTGGCCA 97711 C
TGGCCAA ATGGTGAAATCCC
||||| |||||
ACCGGTT TACCACTTTGGGG
C

GAM2408 LOC256221 3' GGGGTTTCACCGTGTTAGCCA 96915 C
TGGC AACATGGTGAAATCCC
||| |||||
ACCG TTGTGCCACTTTGGGG
A

GAM2408 LOC256306 3' GGGGTTTCACCATGTTGGCCA 98518
TGGCCAACATGGTGAAATCCC
|||||
ACCGGTTGTACCACTTTGGGG

GAM2408 LOC257465 3' ATGGTGTTTCACCATGTTGGCC 82490 TC
A TGGCCAACATGGTGAAA CCAT
||||| |||
ACCGGTTGTACCACTTT GGTA
GT

GAM2408 LOC257486 3' GGGGTTTCACCATGTTGGCCA 69776
TGGCCAACATGGTGAAATCCC
|||||
ACCGGTTGTACCACTTTGGGG

GAM2408 LOC51159 5' GGGATTTACCATGTTGGCCA 33031
TGGCCAACATGGTGAAATCCC
|||||
ACCGGTTGTACCACTTTAGGG

GAM2408 LOC51193 3' ATGAGATCTCGCTATGTTGCC 33359 C A C
A TGG CAACATGGTGA ATC CAT
||| ||||| ||| |||
ACC GTTGTATCGCT TAG GTA
C C A

GAM2408 LOC51696 3' GTTTCACCATGTTAGCTA 33089 C
TGGC AACATGGTGAAAT
||| |||||
ATCG TTGTACCACTTTG
A

GAM2408 LOC57146 3' ATGGGGTTTCACCATGTTGGTC 40292
A TGGCCAACATGGTGAAATCCCAT
|||||

ACTGGTTGTACCACTTTGGGGTA

GAM2408 LOC81034 3' ATGGGGTTTCACCATGTTAGCC 48584 C
A TGGC AACATGGTGAAATCCCAT

|||||
ACCG TTGTACCACTTTGGGGTA
A

GAM2408 LOC89932 3' ATGGGGTTTCACCATGTTGGCC 61447
A TGGCCAACATGGTGAAATCCCAT

|||||
ACCGGTTGTACCACTTTGGGGTA

GAM2408 LOC90288 3' ATGGGGTTTCACCATATTGGTC 62773 C
A TGGCCAA ATGGTGAAATCCCAT

|||||
ACTGGTT TACCACTTTGGGGTA
A

GAM2408 LOC90333 3' GTTTCACCGTGTTAGCCA 62963 C
TGGC AACATGGTGAAAT

|||||
ACCG TTGTGCCACTTTG
A

GAM2408 LOC90459 3' GTTTCACCATGTTGGTCA 63562
TGGCCAACATGGTGAAAT

|||||
ACTGGTTGTACCACTTTG

GAM2408 LOC90485 3' GTTTCACCATGTTGGCCA 63709
TGGCCAACATGGTGAAAT

|||||
ACCGGTTGTACCACTTTG

GAM2408 LOC90485 3' GTTTCACCATGTTGGCTA 63710
TGGCCAACATGGTGAAAT

|||||
ATCGGTTGTACCACTTTG

GAM2408 LOC90591 3' GGGGCTTCACTATGTTGGCCA 64177 AT
TGGCCAACATGGTGAA CCC

|||||
ACCGGTTGTATCACTT GGG
CG

GAM2408 LOC91250 5' ATGGGGTTTCATCATGTTGGCC 65907
A TGGCCAACATGGTGAAATCCCAT

|||||
ACCGGTTGTACTACTTTGGGGTA

GAM2408 LOC91893 3' GGTTTCACCGTGTTAGCCA 68077 C
TGGC AACATGGTGAAATC

|||||

		ACCG TTGTGCCACTTTGG		
		A		
GAM2408	LOC92267 3'	ATGGGGTTTCACCATATTGGCC 69163	C	
	A	TGGCCAA ATGGTGAAATCCCAT		
		ACCGGTT TACCACTTTGGGGTA		
		A		
GAM2408	LOC92303 3'	ATGGGTTTCACCATGTTGGCCA 69385	T	
		TGGCCAACATGGTGAAA CCCAT		
		ACCGGTTGTACCACTTT GGGTA		
		—		
GAM2408	LOC92689 3'	GGGTTTCACCATGTTGGCCA 70777		
		TGGCCAACATGGTGAAATCC		
		ACCGGTTGTACCACTTTGGG		
		—		
GAM2408	LOC92841 3'	GGGGTTTCACCATGTTAGCCA 71258	C	
		TGGC AACATGGTGAAATCCC		
		ACCG TTGTACCACTTTGGGG		
		A		
GAM2408	LOC92841 3'	GGGGTTTCACCATGTTGGCCA 71260		
		TGGCCAACATGGTGAAATCC		
		ACCGGTTGTACCACTTTGGG		
		—		
GAM2408	LOC93349 3'	GGGGTTTCACTATGTTGGCCA 57272		
		TGGCCAACATGGTGAAATCCC		
		ACCGGTTGTATCACTTTGGGG		
		—		
GAM2409	CDH12 3'	CTTATCATTTAAAGTGGTGTA 15777	CCCAA GA	
		TACACCACT GAA ATAAG		
		ATGTGGTGA TTT TATTC		
		AA__ AC		
GAM2409	GOCAP1 3'	ATTGTTCTTGGGAGCAGTGTA 43007	CA G	
		TACAC CTCCCAAGAA AAT		
		ATGTG GAGGGTTCTT TTA		
		AC G		
GAM2409	DKFZp434N2435 5'	CTTATTACTGTGGGGTGGT 98090	T AGAAG	
		ACCAC CCCA AATAAG		
		TGGTG GGGT TTATTC		
		_ GTCA_		
GAM2409	DKFZP564I122 3'	CTTATTCTTCTCCCTCATGTGT 63877	CACTCCCA	
	A	TACAC AGAAGAATAAG		

		ATGTG	TCTTCTTATTC		
		TACTCCC_			
GAM2409	FLJ21791	3'	CTTATTTGCAGAAAGTGGTGTA	62126	CCCAAGAA
			TACACCACT	GAATAAG	
			ATGTGGTGA	TTTATTC	
			AGACG__		
GAM2409	HMP19	3'	CTTATTCTTTGTTAGGAAAATG	88860	CCAC CAA_
	TA		TACA TCC	GAAGAATAAG	
			ATGT AGG	TTTCTTATTC	
			AAA_	ATTG	
GAM2409	KIAA1719	3'	TCTGTCTTGGGAGTGGTGTA	68742	_
			TACACCACTCCCAAGA	AGA	
			ATGTGGTGAGGGTTCT	TCT	
			G		
GAM2409	KIAA1853	3'	TTTTTCTTGGAAGCAGTG	69929	CA C
			CAC CT	CCAAGAAGAA	
			GTG GA	GGTTCTTTTT	
			AC A		
GAM2409	KIAA1877	3'	CTTATTCTTCTGCCATGAGT	66748	CCA_
			ACTC	AGAAGAATAAG	
			TGAG	TCTTCTTATTC	
			TACCG		
GAM2409	KIAA1906	3'	CTTATTCTTCTTGACTTTTGG	73571	CTCC_
			CCA	CAAGAAGAATAAG	
			GGT	GTTCTTCTTATTC	
			TTTCA		
GAM2409	OSBPL11	3'	CTTAATTTCCCAAGAGTGGTG	43206	CCAA AA
			CACCACTC	GAAG TAAG	
			GTGGTGAG	CTTT ATTC	
			AACC	A_	
GAM2409	YME1L1	3'	TCATTCTTGATGTGGTGTA	58438	TCC _
			TACACCAC	CAAGAA GA	
			ATGTGGTG	GTTCTT CT	
			TA_	A	
GAM2409	ZNF262	3'	CTTATTTTGTGTTGGGAGT	18723	A
			ACTCCCAAG	AGAATAAG	
			TGAGGGTTT	TTTTATTC	
			G		
GAM2409	LOC91960	3'	TGTGGCTTGGAACGTGGTGTA	68294	TC_ AAGA
			TACACCAC	CCAAG ATA	

			ATGTGGTG	GGTTC	TGT		
			CAA	GG__			
GAM2410	OLR1	3'	TTCAAGCTT	GAAAACCCTC	11893	TT C	A
			GAG	TT TTCAGGCTT	AA		
			CTC	AA AAGTTCGAA	TT		
			CC	_	C		
GAM2410	C8orf17	3'	AAGCAGAAA	ACTCCAC	39986	A	TCAG
			GT	GAGTTTTCT	GCTT		
			CA	CTCAAAAGA	CGAA		
			C	_____			
GAM2410	FLJ10511	3'	CCTAGAAAA	CAACTCTAC	36687	_ C	_
			G	TAGAGTT	TT TTC AGG		
			CATCTCAA	AA AAG	TCC		
			C	A	A		
GAM2410	KIAA1854	3'	AGTCCAAAG	AACTCTAC	72198	T	CA
			G	TAGAGTTT	CTT GGCT		
			CATCTCAA	GAA	CTGA		
			_	AC			
GAM2410	MGC16025	3'	AAGCCTGAGT	GACACTCTA	53019	T	C
			T	AGAGT	TT TTCAGGCTT		
			ATCTCA	AG GAGTCCGAA			
			C	T			
GAM2410	ST6GalNAcI	3'	CTTTAAGCTATTT	GACAACTCT	37912	T	TTCA
	AC		G	TAGAGTT	TC GGCTTAAAG		
			CATCTCAA	AG	TCGAATTTC		
			C	TTTA			
GAM2410	TRIM2	3'	CTTTAGGGT	TAAAAAACTCT	31600	C	C G
			A	GAGTTTT	TT AG CTTAAAG		
			TCTCAAAA	AA TT GGATTTC			
			A	A	G		
GAM2410	WDR5B	5'	CTTTAAGCTTT	CAAAACTGTAC	39345	G	CTTC
			G	TAGTTTT	AGGCTTAAAG		
			CAT	TCAAAA	TTCGAATTTC		
			G	CT__			
GAM2410	LOC124739	3'	CTTTAGGTCG	AAAGAAAACCTT	74809	A	CA
	AC		G	TAG GTTTTCTT	GGCTTAAAG		
			CATT	CAAAAGAA	CTGGATTTC		
			C	AG			
GAM2410	LOC152078	3'	AAGACCCAG	AGAAAACCTC	81284	A	CA _
			G	TAGTTTTCTT	GG	CTT	

			CA CTCAAAAGAG CC GAA		
			C AC A		
GAM2411	AGXT	3'	CCCGGGAGGCAGAACCAGGCAG 5257	AAAC_ CA	
			CTGC TC CCTCCCGGG		
			GACG AG GGAGGGCCC		
			GACCA AC		
GAM2411	AICDA	3'	CCCAGGAGGTGGAGGTTGCAGT 40691	A C	
			ACTGCAA CTCCACCTCC GGG		
			TGACGTT GAGGTGGAGG CCC		
			G A		
GAM2411	AIRE	3'	GAGGTGGAGGTTGCAGTGA 6352	A	
			TCACTGCAA CTCCACCTC		
			AGTGACGTT GAGGTGGAG		
			G		
GAM2411	AK1	3'	CCCGGGAGTGGAGCTTGCAATG 6637	C A C	
	A		TCA TGCAA CTCCAC TCCCGGG		
			AGT ACGTT GAGGTG AGGGCCC		
			A C _		
GAM2411	ALDH3B1	3'	CCCGGGAGGTGGAGGTTGCCGT 93154	T A	
	GA		TCAC GCAA CTCCACCTCCCGGG		
			AGTG CGTT GAGGTGGAGGGCCC		
			C G		
GAM2411	ALPP	3'	CCCGGGCGGCGGAGATTGCAGT 69412	A A T	
	GA		TCACTGCAA CTCC CC CCCGGG		
			AGTGACGTT GAGG GG GGGCCC		
			A C C		
GAM2411	APOL1	3'	CCTGGGAGGTGGAGCTTGCAAGT 14736	A	
	GA		TCACTGCAA CTCCACCTCCCGGG		
			AGTGACGTT GAGGTGGAGGGTCC		
			C		
GAM2411	ARHGEF6	3'	CCCAGGAGGTCAAGGCTGCAGT 68755	AA CC C	
	GA		TCACTGCA CT ACCTCC GGG		
			AGTGACGT GA TGGAGG CCC		
			CG AC A		
GAM2411	ASNA1	3'	CCCTCGGGGCAGAGTTTGCA 63664	CA CC	
			TGCAAATC CCTC GGG		
			ACGTTTGAG GGGG CCC		
			AC CT		
GAM2411	BCAS1	3'	CCCAGGAGGTGGAGGTTGCAGT 14709	A C	
	GA		TCACTGCAA CTCCACCTCC GGG		

			AGTGACGTT GAGGTGGAGG CCC	
			G A	
GAM2411 BHMT2	3'	CCCAGGAGGCGGAGCTTGCAGT 34730		A A C
GA		TCACTGCAA CTCC CCTCC GGG		
		AGTGACGTT GAGG GGAGG CCC		
		C C A		
GAM2411 BRCA1	3'	CCCGGGAGGTGGAGGTTGCAGT 24446		A
GA		TCACTGCAA CTCCACCTCCCGGG		
		AGTGACGTT GAGGTGGAGGGCCC		
		G		
GAM2411 BRCA1	5'	CCCGGGAGGCGGAGGTTGCAGT 24457		A A
GA		TCACTGCAA CTCC CCTCCCGGG		
		AGTGACGTT GAGG GGAGGGCCC		
		G C		
GAM2411 BRCA1	3'	CCCGGGAGGTGGAGGTTGCAGT 24458		A
GA		TCACTGCAA CTCCACCTCCCGGG		
		AGTGACGTT GAGGTGGAGGGCCC		
		G		
GAM2411 BRCA1	3'	CCCGGGAGGTGGAGGTTGCAGT 24469		A
GA		TCACTGCAA CTCCACCTCCCGGG		
		AGTGACGTT GAGGTGGAGGGCCC		
		G		
GAM2411 BRCA1	3'	CCCGGGAGGTGGAGGTTGCAGT 24478		A
GA		TCACTGCAA CTCCACCTCCCGGG		
		AGTGACGTT GAGGTGGAGGGCCC		
		G		
GAM2411 BRCA1	3'	CCCGGGAGGTGGAGGTTGCAGT 24486		A
GA		TCACTGCAA CTCCACCTCCCGGG		
		AGTGACGTT GAGGTGGAGGGCCC		
		G		
GAM2411 BRCA1	3'	CCCGGGAGGTGGAGGTTGCAGT 24494		A
GA		TCACTGCAA CTCCACCTCCCGGG		
		AGTGACGTT GAGGTGGAGGGCCC		
		G		
GAM2411 BRCA1	3'	CCCGGGAGGTGGAGGTTGCAGT 24503		A
GA		TCACTGCAA CTCCACCTCCCGGG		
		AGTGACGTT GAGGTGGAGGGCCC		
		G		
GAM2411 BRCA1	3'	CCCGGGAGGTGGAGGTTGCAGT 24513		A
GA		TCACTGCAA CTCCACCTCCCGGG		

			AGTGACGTT GAGGTGGAGGGCCC		
			G		
GAM2411	BRCA1	3'	CCCGGGAGGTGGAGGTTGCAGT 24521	A	
	GA		TCACTGCAA CTCCACCTCCCGGG		
			AGTGACGTT GAGGTGGAGGGCCC		
			G		
GAM2411	BRCA1	3'	CCCGGGAGGTGGAGGTTGCAGT 24529	A	
	GA		TCACTGCAA CTCCACCTCCCGGG		
			AGTGACGTT GAGGTGGAGGGCCC		
			G		
GAM2411	BRCA1	3'	CCCGGGAGGTGGAGGTTGCAGT 24554	A	
	GA		TCACTGCAA CTCCACCTCCCGGG		
			AGTGACGTT GAGGTGGAGGGCCC		
			G		
GAM2411	CARKL	3'	GAGGCAGAGGTTGCAGTGA 26102	A	CA
			TCACTGCAA CTC CCTC		
			AGTGACGTT GAG GGAG		
			G AC		
GAM2411	CASP6	3'	CCCAGGAGGTGGAGGCTGCGGT 53363	AA	C
	GA		TCACTGCA CTCCACCTCC GGG		
			AGTGGCGT GAGGTGGAGG CCC		
			CG A		
GAM2411	CASP6	3'	CCCAGGAGGTGGAGGCTGCGGT 8732	AA	C
	GA		TCACTGCA CTCCACCTCC GGG		
			AGTGGCGT GAGGTGGAGG CCC		
			CG A		
GAM2411	CASP8	3'	CCCAAGAGGTCCAAGGCTGCAG 8748	AA	CC_ CC
	TGA		TCACTGCA CT ACCTC GGG		
			AGTGACGT GA TGGAG CCC		
			CG ACC AA		
GAM2411	CASP8	3'	CCCAAGAGGTCCAAGGCTGCAG 54072	AA	CC_ CC
	TGA		TCACTGCA CT ACCTC GGG		
			AGTGACGT GA TGGAG CCC		
			CG ACC AA		
GAM2411	CASP8	3'	CCCAAGAGGTCCAAGGCTGCAG 54097	AA	CC_ CC
	TGA		TCACTGCA CT ACCTC GGG		
			AGTGACGT GA TGGAG CCC		
			CG ACC AA		
GAM2411	CASP8	3'	CCCAAGAGGTCCAAGGCTGCAG 54113	AA	CC_ CC
	TGA		TCACTGCA CT ACCTC GGG		

			AGTGACGT GA TGGAG CCC		
			CG ACC AA		
GAM2411	CD28	3'	AGGCGGAGGTTGCAGTGA 21549	A	A
			TCACTGCAA CTCC CCT		
			AGTGACGTT GAGG GGA		
			G C		
GAM2411	CD68	3'	CCCAGGAGGTGGAGGTTGCAGT 60504	A	C
	GA		TCACTGCAA CTCCACCTCC GGG		
			AGTGACGTT GAGGTGGAGG CCC		
			G A		
GAM2411	CEACAM5	3'	CCCGGGAGGTGGAGATTGCAGT 16422	A	
	GA		TCACTGCAA CTCCACCTCCCGGG		
			AGTGACGTT GAGGTGGAGGGCCC		
			A		
GAM2411	CHST5	3'	CCAAAGGTGGAGGTTGCAGT 25086	A	CCC
			ACTGCAA CTCCACCT GG		
			TGACGTT GAGGTGGA CC		
			G AA_		
GAM2411	CPM	3'	CCCTAGAGGCGGAGTTTGCAGT 60405	A	CC
	GA		TCACTGCAA ACTCC CCTC GGG		
			AGTGACGTTTGAGG GGAG CCC		
			C AT		
GAM2411	CPT2	3'	CCCAGGAGGTGGAGGTTGCAGT 5422	A	C
	GA		TCACTGCAA CTCCACCTCC GGG		
			AGTGACGTT GAGGTGGAGG CCC		
			G A		
GAM2411	CRACC	3'	GAGGTGGAGGTTGCAGTGA 41311	A	
			TCACTGCAA CTCCACCTC		
			AGTGACGTT GAGGTGGAG		
			G		
GAM2411	CROT	3'	CCCAGGAGGTTGTGGCTGCAGT 41257	AA TC _	C
	GA		TCACTGCA C CA CCTCC GGG		
			AGTGACGT G GT GGAGG CCC		
			C_ GT T A		
GAM2411	CTMP	3'	CCCAGGAGGAAGAGGTTGCAGT 54949	A CA	C
	GA		TCACTGCAA CTC CCTCC GGG		
			AGTGACGTT GAG GGAGG CCC		
			G AA A		
GAM2411	CUBN	3'	CCCAGGAGGCAGAGGTTGCAGT 8420	A CA	C
	GA		TCACTGCAA CTC CCTCC GGG		

			AGTGACGTT GAG GGAGG CCC		
			G AC A		
GAM2411	DAPP1	3'	CCCGGGAGGTGGAGGTTGCAGT 27681	A	
	GA		TCACTGCAA CTCCACCTCCCGGG		
			AGTGACGTT GAGGTGGAGGGCCC		
			G		
GAM2411	DBT	3'	CCCAAGAGGTGGAGGTTACAGT 10370	CAAA	CC
	GA		TCACTG CTCCACCTC GGG		
			AGTGAC GAGGTGGAG CCC		
			ATTG AA		
GAM2411	DBT	3'	GAGGTGGAGGTTGCAGTGA 10373	A	
			TCACTGCAA CTCCACCTC		
			AGTGACGTT GAGGTGGAG		
			G		
GAM2411	DCLRE1C	3'	CCCAGGAGATTGAGGCTGCAGT 42821	AA CAC	C
	GA		TCACTGCA CTC CTCC GGG		
			AGTGACGT GAG GAGG CCC		
			CG TTA A		
GAM2411	DDOST	3'	CCAGGAGGCAGAGCTTGCAGTG 19062	A CA	C
	A		TCACTGCAA CTC CCTCC GG		
			AGTGACGTT GAG GGAGG CC		
			C AC A		
GAM2411	DFFA	3'	CCTGGGAGGCAGAGCTTGCAGT 16592	A CA	
	GA		TCACTGCAA CTC CCTCCCGGG		
			AGTGACGTT GAG GGAGGGTCC		
			C AC		
GAM2411	DMC1	3'	CCCAGGAGGCAGAGATTGCGGT 23943	A CA	C
	GA		TCACTGCAA CTC CCTCC GGG		
			AGTGGCGTT GAG GGAGG CCC		
			A AC A		
GAM2411	DSC1	3'	GAGGCGGAGGTTGCAGTGA 44605	A A	
			TCACTGCAA CTCC CCTC		
			AGTGACGTT GAGG GGAG		
			G C		
GAM2411	DSC1	3'	GAGGCGGAGGTTGCAGTGA 18241	A A	
			TCACTGCAA CTCC CCTC		
			AGTGACGTT GAGG GGAG		
			G C		
GAM2411	DVL3	3'	CCTCCCGGGCAAGCGGAGGTTG 16641	A A_____	TCCC
	CAGTGA		TCACTGCAA CTCC	CC	GG

			AGTGACGTT GAGG	GG	CC	
			G	CGAAC	G	CCCT
GAM2411	EDAR	5'	AGGTGAGTTT	GCAATGA	42522	C C
			TCA	TGCAA	ACTC	ACCT
			AGT	ACGTTT	GAG	TGGA
			A	—		
GAM2411	EGFL4	3'	CCCAGGAGGCGGAGGTT	GCAGT	62461	A A C
	GA		TCACTGCAA	CTCC	CCTCC	GGG
			AGTGACGTT	GAGG	GGAGG	CCC
			G	C	A	
GAM2411	ENPP3	3'	CCCGGGAGGCAGAGGTT	GCAGT	18470	A CA
	GA		TCACTGCAA	CTC	CCTCCCGGG	
			AGTGACGTT	GAG	GGAGGGCCC	
			G	AC		
GAM2411	F2R	3'	CCCAGGAGGCGGACCTT	GTAGT	10563	AC A C
	GA		TCACTGCAA	TCC	CCTCC	GGG
			AGTGATGTT	AGG	GGAGG	CCC
			CC	C	A	
GAM2411	F2RL3	3'	GAGGCAGAGGTT	GCAGTGA	15516	A CA
			TCACTGCAA	CTC	CCTC	
			AGTGACGTT	GAG	GGAG	
			G	AC		
GAM2411	FANCC	3'	CCCGGGAGGTGGGAGTT	GTAGT	71036	AC
	GA		TCACTGCAA	TCCACCTCCCGGG		
			AGTGATGTT	GGGTGGAGGGCCC		
			GA			
GAM2411	FBXL7	5'	CCCGGGAGACGGCGGGCATGA	25489	C	AACT AC
			TCA	TGC	CC	CTCCCGGG
			AGT	ACG	GG	GAGGGCCC
			—	GGC	—	CA
GAM2411	FCAR	3'	CCCAGGAGGCAGCTGTT	GCAGT	56633	ACTCCA C
	GA		TCACTGCAA	CCTCC	GGG	
			AGTGACGTT	GGAGG	CCC	
			GTCGAC	A		
GAM2411	FCAR	3'	CCCAGGAGGCAGCTGTT	GCAGT	56646	ACTCCA C
	GA		TCACTGCAA	CCTCC	GGG	
			AGTGACGTT	GGAGG	CCC	
			GTCGAC	A		
GAM2411	FCMD	3'	CCCGGGAAGCAGAGTCT	GCAGT	23033	A CACC
	GA		TCACTGCA	ACTC	TCCCGGG	

			AGTGACGT TGAG AGGGCCC	
			C ACGA	
GAM2411 FGFR1	3'	CCCAGAAGGCAGAGGTTGCAGT 43875		A CA CCC
GA		TCACTGCAA CTC CCT GGG		
		AGTGACGTT GAG GGA CCC		
		G AC AGA		
GAM2411 FGFR1	3'	CCCAGAAGGCAGAGGTTGCAGT 43880		A CA CCC
GA		TCACTGCAA CTC CCT GGG		
		AGTGACGTT GAG GGA CCC		
		G AC AGA		
GAM2411 FLRT2	5'	CCCAAGAGTCCAAGGCTGCAGT 25995		AA CCAC CC
GA		TCACTGCA CT CTC GGG		
		AGTGACGT GA GAG CCC		
		CG ACCT AA		
GAM2411 FUT6	3'	GAGGTGGAGCTTGCAGTGA 5638	A	
		TCACTGCAA CTCCACCTC		
		AGTGACGTT GAGGTGGAG		
		C		
GAM2411 GALNT7	3'	CCCAGGAGGCAGAGGTTGCAGT 55088		A CA C
GA		TCACTGCAA CTC CCTCC GGG		
		AGTGACGTT GAG GGAGG CCC		
		G AC A		
GAM2411 GAS7	3'	GAGGCGGAGATTGCAGTGA 20849	A A	
		TCACTGCAA CTCC CCTC		
		AGTGACGTT GAGG GGAG		
		A C		
GAM2411 GGCX	3'	CCCAGGAGGTGGAGGTTGCAGT 7702	A	C
GA		TCACTGCAA CTCCACCTCC GGG		
		AGTGACGTT GAGGTGGAGG CCC		
		G A		
GAM2411 GPRK7	3'	CCCAGGAGGCGGAGGTTGTAGT 58312	A A	C
GA		TCACTGCAA CTCC CCTCC GGG		
		AGTGATGTT GAGG GGAGG CCC		
		G C A		
GAM2411 GRAF	3'	CCCGGGAGGCGGAGATTGCGGT 31230	A	A
GA		TCACTGCAA CTCC CCTCCCGGG		
		AGTGGCGTT GAGG GGAGGGCCC		
		A C		
GAM2411 GRM6	3'	GAGGTGGAGGTTGCAGTGA 7766	A	
		TCACTGCAA CTCCACCTC		

			AGTGACGTT GAGGTGGAG	
			G	
GAM2411	GTF2F1	3'	CCCAGTTCAAGGCTGCAGTGA 10890	AA CCAC CCC
			TCACTGCA CT CT GGG	
			AGTGACGT GA GA CCC	
			CG ACTT ____	
GAM2411	HCS	3'	CTTGGGAGGTGGAGGTTGCAGT 38979	A
	GA		TCACTGCAA CTCCACCTCCCGGG	
			AGTGACGTT GAGGTGGAGGGTTC	
			G	
GAM2411	HIP1	3'	CCCAGAGGCAGAGGTTGCAGTG 19252	A CA CC
	A		TCACTGCAA CTC CCTC GGG	
			AGTGACGTT GAG GGAG CCC	
			G AC A_	
GAM2411	HLA-E	3'	CCCGGGAGGCGGAGGTTGCAGT 92672	A A
	GA		TCACTGCAA CTCC CCTCCCGGG	
			AGTGACGTT GAGG GGAGGGCCC	
			G C	
GAM2411	HRH1	3'	CCCGGGAGGTGGAGGTTGCCGT 7818	T A
	GA		TCAC GCAA CTCCACCTCCCGGG	
			AGTG CGTT GAGGTGGAGGGCCC	
			C G	
GAM2411	HSPA5	3'	CCCGGGAGGCGAGGTTGCAGT 19284	A CA
	GA		TCACTGCAA CTC CCTCCCGGG	
			AGTGACGTT GAG GGAGGGCCC	
			G AC	
GAM2411	HTR2A	3'	CCCAGAAGCTCAAGGCTGCAGT 7102	AA CCAC CCC
	GA		TCACTGCA CT CT GGG	
			AGTGACGT GA GA CCC	
			CG ACTC AGA	
GAM2411	IAPP	3'	CCCAGGAGGCGGAGGTTGCAGT 6441	A A C
	GA		TCACTGCAA CTCC CCTCC GGG	
			AGTGACGTT GAGG GGAGG CCC	
			G C A	
GAM2411	IFNAR1	3'	GAGGTGGAGGTTGCAGTGA 7139	A
			TCACTGCAA CTCCACCTC	
			AGTGACGTT GAGGTGGAG	
			G	
GAM2411	IFNGR2	5'	GAGGCGGAGGTTGCAGTGA 19849	A A
			TCACTGCAA CTCC CCTC	

			AGTGACGTT GAGG GGAG	
			G C	
GAM2411 IL10	3'	CCCAGGAGATGGAAGTTGCAGT 6924		AC C C
	GA	TCACTGCAA TCCA CTCC GGG		
		AGTGACGTT AGGT GAGG CCC		
		GA A A		
GAM2411 IL13RA1	3'	GAGGTGGAGGTTGCAGTGA 9570		A
		TCACTGCAA CTCCACCTC		
		AGTGACGTT GAGGTGGAG		
		G		
GAM2411 IL17R	3'	GAGGCAGAGGTTGCAGTGA 27555		A CA
		TCACTGCAA CTC CCTC		
		AGTGACGTT GAG GGAG		
		G AC		
GAM2411 IL1R1	3'	GAGACGGAGGTTGCAGTGA 7923		A AC
		TCACTGCAA CTCC CTC		
		AGTGACGTT GAGG GAG		
		G CA		
GAM2411 IPP	3'	CCCAGGAGGTCAGGGCTGCAGT 20905		AA CC C
	GA	TCACTGCA CT ACCTCC GGG		
		AGTGACGT GG TGGAGG CCC		
		CG AC A		
GAM2411 IRAK4	3'	GAGGTAGAGGTTGCAGTGA 61845		A C
		TCACTGCAA CTC ACCTC		
		AGTGACGTT GAG TGGAG		
		G A		
GAM2411 ITGAL	3'	GAGGTGGAGGTTGCAGTGA 11044		A
		TCACTGCAA CTCCACCTC		
		AGTGACGTT GAGGTGGAG		
		G		
GAM2411 KAI1	3'	CCCGGGAGCGGAGGTTGCAGTG 11121		A AC
	A	TCACTGCAA CTCC CTCCCGGG		
		AGTGACGTT GAGG GAGGGCCC		
		G C_		
GAM2411 KCNA7	3'	CCTGGGAGGCGGAGCTTGCAGT 49897		A A
	GA	TCACTGCAA CTCC CCTCCCGGG		
		AGTGACGTT GAGG GGAGGGTCC		
		C C		
GAM2411 KCNJ5	3'	GAGGTGGAGGTTGCAGTGA 7974		A
		TCACTGCAA CTCCACCTC		

		AGTGACGTT GAGGTGGAG		
		G		
GAM2411	KIF1B	3' CCCAGGAGGCAGAGGTTGCAGT 31266	A CA C	
	GA	TCACTGCAA CTC CCTCC GGG		
		AGTGACGTT GAG GGAGG CCC		
		G AC A		
GAM2411	KIF3B	3' GAGGCGGAGGTTGCAGTGA 17804	A A	
		TCACTGCAA CTCC CCTC		
		AGTGACGTT GAGG GGAG		
		G C		
GAM2411	KLRG1	3' CCCAGGAGTTTGAGGCTGCAGT 20556	AA CAC C	
	GA	TCACTGCA CTC CTCC GGG		
		AGTGACGT GAG GAGG CCC		
		CG TTT A		
GAM2411	KNSL1	3' CCCAGGAAGCGGGGTTGCAGTG 16943	A ACC C	
	A	TCACTGCAA CTCC TCC GGG		
		AGTGACGTT GGGG AGG CCC		
		— CGA A		
GAM2411	LAMP2	3' CCCGGGAGGCAGAGGTTGCGGT 26570	A CA	
	GA	TCACTGCAA CTC CCTCCCGGG		
		AGTGCGGTT GAG GGAGGGCCC		
		G AC		
GAM2411	LDLR	3' CCCAGGAGGTGGAGGTTGCAGT 6731	A C	
	GA	TCACTGCAA CTCCACCTCC GGG		
		AGTGACGTT GAGGTGGAGG CCC		
		G A		
GAM2411	LDLR	3' CCCGGGAAGCGGAGCTTGCAGT 6732	A ACC	
	GA	TCACTGCAA CTCC TCCCGGG		
		AGTGACGTT GAGG AGGGCCC		
		C CGA		
GAM2411	LRRC2	3' GAGGTGGAGTTGCAGTGA 44747	A	
		TCACTGCAA CTCCACCTC		
		AGTGACGTT GAGGTGGAG		
		—		
GAM2411	LUZP1	3' CCCAGGAGGCGGAGGTTGCAGT 54399	A A C	
	GA	TCACTGCAA CTCC CCTCC GGG		
		AGTGACGTT GAGG GGAGG CCC		
		G C A		
GAM2411	MAFF	3' CCCAGAAGGCAGAGGTTGTAGT 25579	A CA CCC	
	GA	TCACTGCAA CTC CCT GGG		

			AGTGATGTT GAG GGA CCC	
			G AC AGA	
GAM2411	MCM4	3'	CCCAGGCGGCAGAGGTTGCAGT 62577	A CA T C
	GA		TCACTGCAA CTC CC CC GGG	
			AGTGACGTT GAG GG GG CCC	
			G AC C A	
GAM2411	MOG	3'	CCCAGGAGGCAGAGGTTGCAGT 11670	A CA C
	GA		TCACTGCAA CTC CCTCC GGG	
			AGTGACGTT GAG GGAGG CCC	
			G AC A	
GAM2411	MS4A1	3'	GAGGCGGAGGTTGCAGTGA 5548	A A
			TCACTGCAA CTCC CCTC	
			AGTGACGTT GAGG GGAG	
			G C	
GAM2411	MSH3	3'	GAGGCGGAGGTTGCAATGA 11691	C A A
			TCA TGCAA CTCC CCTC	
			AGT ACGTT GAGG GGAG	
			A G C	
GAM2411	MSL3L1	3'	CCCAGAGTCTAAGACTGCAGTG 55319	AA CCAC CC
	A		TCACTGCA CT CTC GGG	
			AGTGACGT GA GAG CCC	
			CA ATCT A_	
GAM2411	MTMR8	3'	CCCGGGAGGCAGAGCTTGCAGT 31908	A CA
	GA		TCACTGCAA CTC CCTCCCGGG	
			AGTGACGTT GAG GGAGGGCCC	
			C AC	
GAM2411	MYO1B	3'	GAGGCAGAGGTTGCAGTGA 25244	A CA
			TCACTGCAA CTC CCTC	
			AGTGACGTT GAG GGAG	
			G AC	
GAM2411	MYO1C	3'	CCCGGGAAGTGGAGGTTGCAGT 61860	A C
	GA		TCACTGCAA CTCCAC TCCCGGG	
			AGTGACGTT GAGGTG AGGGCCC	
			G A	
GAM2411	NEO1	5'	CCCGGGAGCCGAGCTTGCAGCG 11770	A A CAC
	A		TC CTGCAA CTC CTCCCGGG	
			AG GACGTT GAG GAGGGCCC	
			C C CC_	
GAM2411	NFKBIL2	3'	CCCGGGAGGCGGAGCTTGCAGT 26449	A A
	GA		TCACTGCAA CTCC CCTCCCGGG	

			AGTGACGTT GAGG GGAGGGCCC		
			C C		
GAM2411	NPHP1	3'	GAGGTGGAGGTTGCAGTGA 63144	A	
			TCACTGCAA CTCCACCTC		
			AGTGACGTT GAGGTGGAG		
			G		
GAM2411	NPHS1	3'	CCCAGGAGGCGGAGGTTGCAGT 17369	A A C	
	GA		TCACTGCAA CTCC CCTCC GGG		
			AGTGACGTT GAGG GGAGG CCC		
			G C A		
GAM2411	NT5C2	3'	CCCAGGAGGCGGAGGTTGCAGT 25261	A A C	
	GA		TCACTGCAA CTCC CCTCC GGG		
			AGTGACGTT GAGG GGAGG CCC		
			G C A		
GAM2411	NUP62	3'	CCAGGAGGTGTTGCAGTGA 33783	ACTC C	
			TCACTGCAA CACCTCC GG		
			AGTGACGTT GTGGAGG CC		
			— A		
GAM2411	OGG1	5'	CCCGGGAGGCGGAGCTTGCAGT 34151	A A	
	GA		TCACTGCAA CTCC CCTCCCGGG		
			AGTGACGTT GAGG GGAGGGCCC		
			C C		
GAM2411	OGG1	5'	CCCGGGAGGCGGAGCTTGCAGT 34163	A A	
	GA		TCACTGCAA CTCC CCTCCCGGG		
			AGTGACGTT GAGG GGAGGGCCC		
			C C		
GAM2411	OGG1	5'	CCCGGGAGGCGGAGCTTGCAGT 11889	A A	
	GA		TCACTGCAA CTCC CCTCCCGGG		
			AGTGACGTT GAGG GGAGGGCCC		
			C C		
GAM2411	OPTN	3'	CCCAGGAAGTGGCAGTTGCAGT 42052	A _ C C	
	GA		TCACTGCAA CT CCAC TCC GGG		
			AGTGACGTT GA GGTG AGG CCC		
			_ C A A		
GAM2411	P2RX7	3'	CCCGGGAGGCAGAGGTTGTAGT 11926	A CA	
	GA		TCACTGCAA CTC CCTCCCGGG		
			AGTGATGTT GAG GGAGGGCCC		
			G AC		
GAM2411	PA2G4	3'	CCCGGGAGGTGGAGGTTGCAGT 71827	A	
	GA		TCACTGCAA CTCCACCTCCCGGG		

			AGTGACGTT GAGGTGGAGGGCCC		
			G		
GAM2411	PAICS	3'	CCCGGGAGGCGGAGGTTGCAGT 22259	A	A
	GA		TCACTGCAA CTCC CCTCCCGGG		
			AGTGACGTT GAGG GGAGGGCCC		
			G C		
GAM2411	PCDH11X	3'	CCCGGGAGGCGGAGCTTGCAGT 53127	A	A
	GA		TCACTGCAA CTCC CCTCCCGGG		
			AGTGACGTT GAGG GGAGGGCCC		
			C C		
GAM2411	PCDH11Y	3'	CCCGGGAGGCGGAGCTTGCAGT 53158	A	A
	GA		TCACTGCAA CTCC CCTCCCGGG		
			AGTGACGTT GAGG GGAGGGCCC		
			C C		
GAM2411	PCDH11Y	3'	CCCGGGAGGCGGAGCTTGCAGT 53178	A	A
	GA		TCACTGCAA CTCC CCTCCCGGG		
			AGTGACGTT GAGG GGAGGGCCC		
			C C		
GAM2411	PDE4C	3'	GAGGTGGAGGTTGCAGTGA 8104	A	
			TCACTGCAA CTCCACCTC		
			AGTGACGTT GAGGTGGAG		
			G		
GAM2411	PHKB	3'	GAGACGGAGGTTGCAGTGA 6098	A	AC
			TCACTGCAA CTCC CTC		
			AGTGACGTT GAGG GAG		
			G CA		
GAM2411	PIK3CG	3'	CCCAGGAGGTGGAACTGCAGA 12121	A	AAC C
	GA		TC CTGCA TCCACCTCC GGG		
			AG GACGT AGGTGGAGG CCC		
			A CAA A		
GAM2411	PPP1R12B	3'	CCCGGGAGGCGGAGCTTGCAGT 50384	A	A
	GA		TCACTGCAA CTCC CCTCCCGGG		
			AGTGACGTT GAGG GGAGGGCCC		
			C C		
GAM2411	PSMB2	3'	CCCGGGAGAGGGAGGTTGCAGT 12464	A	AC
	GA		TCACTGCAA CTCC CTCCCGGG		
			AGTGACGTT GAGG GAGGGCCC		
			G GA		
GAM2411	PSMB2	3'	CCCGGGAGGCGGAGGTTGCAGT 12465	A	A
	GA		TCACTGCAA CTCC CCTCCCGGG		

			AGTGACGTT GAGG GGAGGGCCC		
			G C		
GAM2411	PSMB9	3'	CCCAGGAGGCGGAGGTTGCGGT 12499	A A C	
	GA		TCACTGCAA CTCC CCTCC GGG		
			AGTGGCGTT GAGG GGAGG CCC		
			G C A		
GAM2411	PSMB9	3'	CCCGGGAGGCGGGGGTTGCAGT 12500	A A	
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			G C		
GAM2411	PSMB9	3'	CCCGGGAGGTAGAGTTTGCAGT 12501	C	
	GA		TCACTGCAAACCTC ACCTCCCGGG		
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			A		
GAM2411	PSMD5	3'	GAGGCAGAGGTTGCAGTGA 18559	A CA	
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			AGTGACGTT GAG GGAG		
			G AC		
GAM2411	PTAFR	3'	GAGGCAGAGGTTGCAGTGA 8165	A CA	
			TCACTGCAA CTC CCTC		
			AGTGACGTT GAG GGAG		
			G AC		
GAM2411	PTGIS	3'	CCCAGGAGGTGGAGGTTGCAGT 8202	A C	
	GA		TCACTGCAA CTCCACCTCC GGG		
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GAM2411	RAB7L1	3'	GAGGCAGAGGTTGCAGTGA 15405	A CA	
			TCACTGCAA CTC CCTC		
			AGTGACGTT GAG GGAG		
			G AC		
GAM2411	RAD1	3'	CCCGGGAGGCGGAGGTTGTGG 12642	TG A A	
			C CAA CTCC CCTCCCGGG		
			G GTT GAGG GGAGGGCCC		
			GT G C		
GAM2411	RAD1	3'	CCCGGGAGGCGGAGGTTGTGG 56654	TG A A	
			C CAA CTCC CCTCCCGGG		
			G GTT GAGG GGAGGGCCC		
			GT G C		
GAM2411	RAD1	3'	CCCGGGAGGCGGAGGTTGTGG 56751	TG A A	
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			G GTT GAGG GGAGGGCCC	
			GT G C	
GAM2411	RBBP5	3'	TGGGAGGCAGAGGTTGCAGTGA 18581	A CA
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			G AC	
GAM2411	RBM3	3'	CCCGGGAGGCGGAGGTTGCAGT 71008	A A
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GAM2411	RFC2	3'	GGAGGTGGAGGTTGCAGTGA 12844	A
			TCACTGCAA CTCCACCTCC	
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GAM2411	ROCK2	3'	CCCAGGAGACGGTGGTTGCAGT 66616	ACT _ _ _
	GA		TCACTGCAA CCACC TC CC GGG	
			AGTGACGTT GGTGG AG GG CCC	
			_ C A A	
GAM2411	RPN1	5'	CCCGGGAGGCAGAGGTTGCAG 12906	A CA
			CTGCAA CTC CCTCCCGGG	
			GACGTT GAG GGAGGGCCC	
			G AC	
GAM2411	SCAP2	3'	AGGCAGAGGTTGCAGTGA 15421	A CA
			TCACTGCAA CTC CCT	
			AGTGACGTT GAG GGA	
			G AC	
GAM2411	SHOC2	3'	CCCCGGGAAGAGAACTTGCAG 24783	A__ CA__ TCCC
	TGA		TCACTGCAA CTC CC G	
			AGTGACGTT GAG GG C	
			CAAA AA__G CCCT	
GAM2411	SIGLEC11	3'	CCCGGGAGGTGGAGGTTGCAGT 54651	A
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GAM2411	SIP	3'	CCCAGGAGTTTAAGGCTGCAGT 27731	AA CCAC C
	GA		TCACTGCA CT CTCC GGG	

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			CG ATTT A		
GAM2411	SLC14A1	3'	CCCAGGAGGAGGAGGCTGCAGT 32412	AA A C	
	GA		TCACTGCA CTCC CCTCC GGG		
			AGTGACGT GAGG GGAGG CCC		
			CG A A		
GAM2411	SLC14A2	3'	CCCGGGAGGTGGAGCTTGCAGT 24115	A	
	GA		TCACTGCAA CTCCACCTCCCGGG		
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GAM2411	SLC17A5	3'	GAGATGGAAGTTGCAGTGA 25832	AC C	
			TCACTGCAA TCCA CTC		
			AGTGACGTT AGGT GAG		
			GA A		
GAM2411	SLC25A15	3'	CCCGGGAGGCAGAAGTTGCAGT 27292	AC CA	
	GA		TCACTGCAA TC CCTCCCGGG		
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			GA AC		
GAM2411	SLC26A4	3'	CCCGGGAGGCGGAGCTTGCAGT 6525	A A	
	GA		TCACTGCAA CTCC CCTCCCGGG		
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GAM2411	SLC28A2	3'	CCGGGAGGCGGAGCTTGCAGCG 16147	A A A	
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			C C C		
GAM2411	SLC2A6	3'	CCCGGGAGGTGGAGGCTGCAAT 34568	C AA	
	GA		TCA TGCA CTCCACCTCCCGGG		
			AGT ACGT GAGGTGGAGGGCCC		
			A CG		
GAM2411	SLC31A1	3'	GAGGCGGAGGTTGCAGTGA 10277	A A	
			TCACTGCAA CTCC CTC		
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			G C		
GAM2411	SMG1	3'	CCCAGGAGGCGGAGCTTGCAGT 31345	A A C	
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			C C A		
GAM2411	STAT3	3'	GAGGCGGAGGTTGCAGTGA 58378	A A	
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			G C		
GAM2411	STAT3	3'	GAGGCGGAGGTTGCAGTGA 13436	A A	
			TCACTGCAA CTCC CCTC		
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			G C		
GAM2411	SUDD	3'	CCCGGGAGGCAGAGGTTGCAGT 15157	A CA	
	GA		TCACTGCAA CTC CCTCCCGGG		
			AGTGACGTT GAG GGAGGGCCC		
			G AC		
GAM2411	SULT2A1	3'	CCCAGGGATGCAAAGGTTGCAG 72225	A CCACC _	
	TGA		TCACTGCAA CT TCCC GGG		
			AGTGACGTT GA AGGG CCC		
			G AACGT A		
GAM2411	SUV39H2	3'	GAGGCGGAGGTTGCAGTGA 45457	A A	
			TCACTGCAA CTCC CCTC		
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			G C		
GAM2411	TBX6	3'	CCCAGGAGGTGGAGGTTGCAGT 55811	A C	
	GA		TCACTGCAA CTCCACCTCC GGG		
			AGTGACGTT GAGGTGGAGG CCC		
			G A		
GAM2411	TCF7	3'	CCCGGGAGGCGGAGGTTCCAGT 13620	CAAA A	
	GA		TCACTG CTCC CCTCCCGGG		
			AGTGAC GAGG GGAGGGCCC		
			CTTG C		
GAM2411	TCTA	3'	GAGGCAGAGGTTGCAGTGA 42496	A CA	
			TCACTGCAA CTC CCTC		
			AGTGACGTT GAG GGAG		
			G AC		
GAM2411	TEM7	3'	GAGGCAGAGGTTGCAGTGA 40263	A CA	
			TCACTGCAA CTC CCTC		
			AGTGACGTT GAG GGAG		
			G AC		
GAM2411	TNFSF10	3'	CCCGGGAGGCAGAGGTTGCAGT 15091	A CA	
	G		CACTGCAA CTC CCTCCCGGG		
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			G AC		
GAM2411	TNFSF14	3'	CCCGGGAGGCGGAGGTTGCAGT 15079	A A	
	GA		TCACTGCAA CTCC CCTCCCGGG		

			AGTGACGTT GAGG GGAGGGCCC		
			G C		
GAM2411	TPM4	3'	CCCAGGAAGTGGAGACTGCAGT 13832	AA	C C
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			CA A A		
GAM2411	TRIM14	3'	CCCGGGCAGCGGAGGTTGCAGT 53773	A	AC _
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			AGTGACGTT GAGG GA GGGCCC		
			G C_ C		
GAM2411	TRIM14	3'	CCCAGGAGGCGGAGATTGCAGT 29508	A	A C
	GA		TCACTGCAA CTCC CCTCC GGG		
			AGTGACGTT GAGG GGAGG CCC		
			A C A		
GAM2411	TRPM8	3'	GAGGCGGAGGTTGCAGTGA 44206	A	A
			TCACTGCAA CTCC CCTC		
			AGTGACGTT GAGG GGAG		
			G C		
GAM2411	TSNAX	3'	GAGGCAGAGGTTGCAGTGA 21157	A	CA
			TCACTGCAA CTC CCTC		
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			G AC		
GAM2411	UBE2G2	3'	CCCAGGAGGCGGAGCTTGCAGT 65484	A	A C
	GA		TCACTGCAA CTCC CCTCC GGG		
			AGTGACGTT GAGG GGAGG CCC		
			C C A		
GAM2411	UBE2G2	3'	CCCGGGAGGCAGAGGTAGCAGT 65485	AAA	CA
	GA		TCACTGC CTC CCTCCCGGG		
			AGTGACG GAG GGAGGGCCC		
			ATG AC		
GAM2411	UC28	3'	CCCGGAAGGTGGAGGTTGTTGC 41585	A__	C
	GGTGA		TCACTGCAA CTCCACCT CCGGG		
			AGTGCGCTT GAGGTGGA GGCCC		
			GTTG A		
GAM2411	UPK1B	3'	GAGACAGAGGTTGCAGTGA 23701	A	CAC
			TCACTGCAA CTC CTC		
			AGTGACGTT GAG GAG		
			G ACA		
GAM2411	VDR	3'	CCCAGGAGGTGGAGGTTGCAGT 6339	A	C
	GA		TCACTGCAA CTCCACCTCC GGG		

			AGTGACGTT GAGGTGGAGG CCC		
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GAM2411	VHL	3'	CCCAGGAGGCGAAGATTGCAGT 6844	A CCA	C
	GA		TCACTGCAA CT CCTCC GGG		
			AGTGACGTT GA GGAGG CCC		
			A AGC A		
GAM2411	VHL	3'	CCCGGGAGGCGGAGGTTGCAGT 6846	A A	
	GA		TCACTGCAA CTCC CCTCCCGGG		
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			G C		
GAM2411	VHL	3'	CCTGGAAGGTGGAGCTTGCAGT 6850	A C	
	GA		TCACTGCAA CTCCACCT CCGGG		
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GAM2411	WIG1	3'	CCCGGGAGGCGGAGCTTGCAGT 96098	A A	
	GA		TCACTGCAA CTCC CCTCCCGGG		
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GAM2411	XRCC2	3'	CCCAGGAGGTGGAGGTTGCAGT 19496	A C	
	GA		TCACTGCAA CTCCACCTCC GGG		
			AGTGACGTT GAGGTGGAGG CCC		
			G A		
GAM2411	ZNF14	3'	GAGACAGAGGTTGCAGTGA 41057	A CAC	
			TCACTGCAA CTC CTC		
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			G ACA		
GAM2411	ZNF264	3'	TGGGAGGCGGAGGTTGCAGTGA 14236	A A	
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GAM2411	ZNF36	3'	CCCAGGAGGCAGAGGTTGCAGT 95580	A CA C	
	GA		TCACTGCAA CTC CCTCC GGG		
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			G AC A		
GAM2411	ZNF91	3'	CCCGGGAGGCGGAGCTTGCAGT 14279	A A	
	GA		TCACTGCAA CTCC CCTCCCGGG		
			AGTGACGTT GAGG GGAGGGCCC		
			C C		
GAM2411	AF020591	3'	GAGGCGTAGCTTGCAGTGA 27913	A CCA	
			TCACTGCAA CT CTC		

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			C TGC		
GAM2411	AGMAT	3'	CCCAGGAAGCGGAGGCTGCAGT 45739	AA	ACC C
	GA		TCACTGCA CTCC TCC GGG		
			AGTGACGT GAGG AGG CCC		
			CG CGA A		
GAM2411	AKAP11	3'	GAGGCAGAGATTGCAGTGA 58461	A	CA
			TCACTGCAA CTC CCTC		
			AGTGACGTT GAG GGAG		
			A AC		
GAM2411	AKR1B10	5'	CCCAGGAGACAGAGGTTGTAGT 40080	A	CAC C
	GA		TCACTGCAA CTC CTCC GGG		
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			G ACA A		
GAM2411	AKR1D1	3'	CCCGGGAGGAGGAGCTTGCAGT 21130	A	A
	GA		TCACTGCAA CTCC CCTCCCGGG		
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GAM2411	ALTE	3'	CCCAGGAGGTGGAGGTTGCAGT 17580	A	C
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GAM2411	APXL2	3'	CCTGGGAGGTGGAGCTTGCAGT 75676	A	
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			C		
GAM2411	ARNTL2	3'	GAGGCAGAGGTTGCAGTGA 39850	A	CA
			TCACTGCAA CTC CCTC		
			AGTGACGTT GAG GGAG		
			G AC		
GAM2411	ATP1B4	3'	CCCAGGAGGTCAAGGCTGCAGT 24840	AA	CC C
	GA		TCACTGCA CT ACCTCC GGG		
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			CG AC A		
GAM2411	ATP9A	3'	TCCGGGCCTGTGGATTTTGCAG 62739	C	_____ CCGG
	T		ACTGCAAA TCCAC CT G		
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GAM2411	BIRC1	3'	CCCGGGAGGCAGAGGTTGCAGT 16991	A	CA
	GA		TCACTGCAA CTC CCTCCCGGG		

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			C		
GAM2411	BLOV1	3'	CCCGGGAGGCGGCGGTTGCAGT 76794	ACT A	
	GA		TCACTGCAA CC CCTCCCGGG		
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			GGC C		
GAM2411	BLOV1	3'	GAGGCGGAGGTTGCAATGA 76795	C A A	
			TCA TGCAA CTCC CCTC		
			AGT ACGTT GAGG GGAG		
			A G C		
GAM2411	BTN3A2	3'	CCCGGAAGGCAGAGCTTGCAGT 23874	A CA C	
	GA		TCACTGCAA CTC CCT CCGGG		
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			C AC A		
GAM2411	C12orf2	3'	CCCGGGAGGTGGAGGTTGCAGT 83682	A	
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GAM2411	C13orf1	3'	CCCGGGAGACGGCGCTTGCAGT 40360	ACT AC	
	GA		TCACTGCAA CC CTCCCGGG		
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			CGC CA		
GAM2411	C1orf33	3'	CCCGGGAGGTGGAGGTTGCCGT 32981	T A	
	GA		TCAC GCAA CTCCACCTCCCGGG		
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			C G		
GAM2411	C1orf34	3'	GAGGCGGAGGTTGCAGTGA 61310	A A	
			TCACTGCAA CTCC CCTC		
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			G C		
GAM2411	C1QTNF2	3'	CCCAGGAGGTGGAGGTTGCAGT 49971	A C	
			ACTGCAA CTCCACCTCC GGG		
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GAM2411	C20orf108	3'	CCCAGGAGGTGGAGGTTGCAGT 55878	A C	
	GA		TCACTGCAA CTCCACCTCC GGG		

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GAM2411 C20orf12 3' CCCGGGAGGCAGAGGTTACAGT 36847      CAAA CA
      GA      TCACTG CTC CCTCCCGGG
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      ATTG AC
GAM2411 C20orf121 3' CCCACTGGTTGAAGTTTGCA 44524      _C TCCC
      TGCAAAC T C ACC GGG
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      A T TCA_
GAM2411 C20orf142 3' CCCAGGAGGCAGAGGTTGCAGT 75279      A CA C
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GAM2411 C20orf172 3' CCCAGGAGGTTGAGGCTGCAGT 46765      AA C C
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GAM2411 C20orf175 3' CCCGGGAGGCGGAGGTTGCAGT 55924      A A
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GAM2411 C20orf177 3' CCCGGGAGGCGGAGGTTGTGG 62831 TG A A
      C CAA CTCC CCTCCCGGG
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      GT G C
GAM2411 C20orf183 3' CCCGGGAGGTGGAGCTTCCAGT 48531      C A
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GAM2411 C20orf29 3' CCTGGGAGGCAGAGTTTGCAGT 37708      CA
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GAM2411 C21orf108 3' GAGGTGGAGGCTACAGTGA 90115      CAAA
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GAM2411 C22orf19 3' CCCATGAGGCGGAGGTTGCAGT 14822      A A CC
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GAM2411	C6orf29	3'	CCCGGGAGGCAGAGGTTGCAGT 52456	A CA	
	GA		TCACTGCAA CTC CCTCCCGGG		
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GAM2411	C6orf5	3'	CCCGGGAGGCAGAGGTTGCAGT 31982	A CA	
	GA		TCACTGCAA CTC CCTCCCGGG		
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GAM2411	C6orf5	3'	CCCGGGAGGCGGAGCTTGCAGT 31983	A A	
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GAM2411	C8orf17	3'	CCCAGAGGTGGAGGTTGCAGTG 39993	A CC	
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GAM2411	C8orf2	3'	GAGGCAGAGGTTGCAGTGA 24152	A CA	
			TCACTGCAA CTC CCTC		
			AGTGACGTT GAG GGAG		
			G AC		
GAM2411	CAM-KIIN	5'	CCGGGAGGCGGAGGCGCGG 53833	AAA A	
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			CG_ C		
GAM2411	CAMKK2	5'	GAGGCAGAGGTTGCAGTGA 22622	A CA	
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GAM2411	CBCIP2	3'	CCCGGGAGGCAGAGCTTGCAGT 52655	A CA	
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GAM2411	CCR6	3'	CCCAGGAGGCAGAGGTTGCAGT 16441	A CA C	
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GAM2411	CCR6	3'	CCCAGGAGGCAGAGGTTGCAGT 49399	A CA	C
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			G AC A		
GAM2411	CDT1	3'	CCCAGGAGGCACAGCTTGCAGT 78159	A CCA	C
	GA		TCACTGCAA CT CCTCC GGG		
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			C CAC A		
GAM2411	cerk	3'	CCCAAGAGGTGGAGGTTGCGGT 43164	A	CC
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GAM2411	CG012	5'	CCCAGGACACGGAGATTGCAGT 84152	A ACC	C
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GAM2411	CG012	5'	CCCAGGAGGTGGAGGTTGAAAT 84154	CTG A	C
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GAM2411	CHRFAM7A	3'	CCCAAAAGGTGGAGGCTGCAGT 96716	AA	CCC
	GA		TCACTGCA CTCCACCT GGG		
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			CG AAA		
GAM2411	CNNM1	3'	GAGGCAGAGGTTGCAGTGA 40120	A CA	
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GAM2411	COE2	3'	CCCAGGAGGCACAGATTGCAGT 64908	A CCA	C
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GAM2411	CPR2	3'	CCCGGGAGGTGGAGGCTGCAGT 48830	AA	
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GAM2411	CRTAM	3'	GAGGTGGAGATTGCAGTGA 39472	A	
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GAM2411	CYP4F12	3'	CCTGAATGTAAGCTTGCAGTGA 62185	A CC CTCC
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GAM2411	DAPK2	3'	CCCAGAAGGTCGAGGCTGCAGT 27512	AA C CCC
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GAM2411	DDX34	3'	CCCGGGAGGCAGAGCTTGCAGT 28667	A CA
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GAM2411	DEGS	3'	CCAGGAGGCGGAGGCAG 59266	AAA A C
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GAM2411	DEGS	3'	CCAGGAGGCGGAGGCAG 14801	AAA A C
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GAM2411	DIS3	3'	GAGGCAGAGGTTGCAGTGA 30916	A CA
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GAM2411	DIS3	3'	GAGGCGGAAGTTGCAGTGA 30917	AC A
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GAM2411	DJ122O8.2	3'	CCCAGGAAGTGGAGGTTGCAGT 40394	A C C
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GAM2411 dJ383J4.3 3'	CCCAGAAGACAGGCTGCAGTGA 67493	AA CCACC CC
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	CG CAGA_ A_	
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	CG A A	
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GAM2411 DKFZP434C171 3'	CCCAGGAGGCGGAGCTTGCAGT 32188	A A C
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	C C A	
GAM2411 DKFZp434E0519 3'	GAGGCGGAAGTTGCAGTGA 50991	AC A
	TCACTGCAA TCC CCTC	
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	GA C	
GAM2411 DKFZp434E169 3'	CCCGGGAGGCGGAGCTTGCAGT 51075	A A
GA	TCACTGCAA CTCC CCTCCCGGG	
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	C C	
GAM2411 DKFZp434E2220 5'	GAGGCGGAGGTTGCAGTGA 34712	A A
	TCACTGCAA CTCC CCTC	
	AGTGACGTT GAGG GGAG	
	G C	
GAM2411 DKFZp434G171 3'	AGGCAGAGGTTGCAGTGA 80230	A CA
	TCACTGCAA CTC CCT	
	AGTGACGTT GAG GGA	
	G AC	
GAM2411 DKFZp434G171 3'	CCCGGGAGGCAGAGGTTGCAGT 80240	A CA
GA	TCACTGCAA CTC CCTCCCGGG	
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	G AC	
GAM2411 DKFZP434I1735 3'	AGGCAGAGGTTGCAGTGA 89163	A CA
	TCACTGCAA CTC CCT	

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	G AC		
GAM2411 DKFZP434N1511 3'	CCCTGGAGGCAGAGCTTGCAGT 93056	A CA C	
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	C AC T		
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	ATTG		
GAM2411 DKFZp547G183 3'	GAGGCGGAGGTTGCAGTGA 38644	A A	
	TCACTGCAA CTCC CCTC		
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	G C		
GAM2411 DKFZP564I122 3'	GAGGCAGAGATTGCAGTGA 63878	A CA	
	TCACTGCAA CTC CCTC		
	AGTGACGTT GAG GGAG		
	A AC		
GAM2411 DKFZP564M182 3'	CCCGGGAGGTAGAGGCTGCAAT 78623	C AA C	
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	GGT ACGT GAG TGGAGGGCCC		
	A CG A		
GAM2411 DKFZP564M182 3'	CCCGGGAGGTGGAGGTTGCAGT 78624	A	
GA	TCACTGCAA CTCCACCTCCCGGG		
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	G		
GAM2411 DKFZP564M182 3'	GAGGCGGAGGTTGCAGTGA 78630	A A	
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	G C		
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GA	TCACTGCAA CTCCACCTCC GGG		
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	G A		
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	C CGA		
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			AGTGAC TT GAGG GGAGGGCCC		
			A C C		
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			TCACTGCAA CTCC CCT		
			AGTGACGTT GAGG GGA		
			G C		
GAM2411	DKFZP586D2223	3'	GAGGCAGAGGTTGCAGTGA	38291	A CA
			TCACTGCAA CTC CCTC		
			AGTGACGTT GAG GGAG		
			G AC		
GAM2411	DKFZp727G131	3'	AGGCAGAGATTGCAGTGA	59691	A CA
			TCACTGCAA CTC CCT		
			AGTGACGTT GAG GGA		
			A AC		
GAM2411	DKFZp761J139	5'	CGGCAGAGGTTGCAGTGA	51105	AACTCC _
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			AGTGACGT TGGAG GGC		
			AC		
GAM2411	DRF1	3'	GAGGTGGAGGTTGCAGTGA	47750	A
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			G		
GAM2411	DSCR6	3'	CCCGGGAGGCGGAGGTTGCCGT	39063	T A A
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			AGTG CGTT GAGG GGAGGGCCC		
			C G C		
GAM2411	ET	3'	GAGGCGGAGGTTGCAGTGA	44470	A A
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			AGTGACGTT GAGG GGAG		
			G C		
GAM2411	FADS1	3'	GAGGTGGAGGTTGCAGTGA	26379	A
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			AGTGACGTT GAGGTGGAG		
			G		
GAM2411	FBXO27	3'	CCCGGGAGGCAGAGGCTGCAGT	75009	AA CA
	GA		TCACTGCA CTC CCTCCCGGG		
			AGTGACGT GAG GGAGGGCCC		
			CG AC		
GAM2411	FBXO6	3'	CCCGGAAGGCAGAGCTTGCAGT	37990	A CA C
	GA		TCACTGCAA CTC CCT CCGGG		

			AGTGACGTT GAG GGA GGCCC		
			C AC A		
GAM2411	FBXO9	3'	GAAGTGGAAGTTGCAGTGA 54246	AC	C
			TCACTGCAA TCCAC TC		
			AGTGACGTT AGGTG AG		
			GA A		
GAM2411	FKBP14	3'	CCCGGGAGGCGGAGGTTGCAGT 36066	A	A
			GA TCACTGCAA CTCC CCTCCCGGG		
			AGTGACGTT GAGG GGAGGGCCC		
			G C		
GAM2411	FKSG17	3'	AGGCGGAGGTTGCAGTGA 50151	A	A
			TCACTGCAA CTCC CCT		
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			G C		
GAM2411	FLJ00060	3'	CCCAGGAGGCAGAGCTTGCAGT 61743	A	CA C
			GA TCACTGCAA CTC CCTCC GGG		
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			C AC A		
GAM2411	FLJ10008	3'	CCTGGGAGGCAGAGCTTGCAGT 36184	A	CA
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			C AC		
GAM2411	FLJ10043	3'	CCCAGGAGGTGGAGGTTGTGG 36232	TG A	C
			C CAA CTCCACCTCC GGG		
			G GTT GAGGTGGAGG CCC		
			GT G A		
GAM2411	FLJ10058	3'	CCCAGGAGGTGGAGGTTGCA 36262	A	C
			TGCAA CTCCACCTCC GGG		
			ACGTT GAGGTGGAGG CCC		
			G A		
GAM2411	FLJ10244	3'	GAGGCAGAGGTTGCAGTGA 36401	A	CA
			TCACTGCAA CTC CCTC		
			AGTGACGTT GAG GGAG		
			G AC		
GAM2411	FLJ10314	3'	CCCGGGAGGCAGAGGTTGCAGT 36488	A	CA
			GA TCACTGCAA CTC CCTCCCGGG		
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			G AC		
GAM2411	FLJ10439	5'	CCCGGGAGGCGGAGGTTGAGCA 36598	AAA__	A
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		ACG GAGG GGAGGGCCC	
		AGTTG C	
GAM2411	FLJ10520	3' GAGGCAGAGGTTGCAGTGA 36709	A CA
		TCACTGCAA CTC CCTC	
		AGTGACGTT GAG GGAG	
		G AC	
GAM2411	FLJ10607	3' CCCGGGAGGCAAAGGTTGCAGT 77629	A CCA
	GA	TCACTGCAA CT CCTCCCGGG	
		AGTGACGTT GA GGAGGGCCC	
		G AAC	
GAM2411	FLJ10613	3' GAGGCAGAGGTTGCAGTGA 39338	A CA
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		AGTGACGTT GAG GGAG	
		G AC	
GAM2411	FLJ10803	3' CCCGGGAGGTGGAGGTTGCAGT 37200	A
	GA	TCACTGCAA CTCCACCTCCCGGG	
		AGTGACGTT GAGGTGGAGGGCCC	
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GAM2411	FLJ10826	3' CCCAGGAGGCGGAGGTTGCAGT 37246	A A C
	GA	TCACTGCAA CTCC CCTCC GGG	
		AGTGACGTT GAGG GGAGG CCC	
		G C A	
GAM2411	FLJ10932	3' GAGGTGGAGGTTGCAGTGA 37428	A
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		AGTGACGTT GAGGTGGAG	
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GAM2411	FLJ10989	3' CCCTGGAGGTGGAGGTTGCAGT 37500	A C
	GA	TCACTGCAA CTCCACCTCC GGG	
		AGTGACGTT GAGGTGGAGG CCC	
		G T	
GAM2411	FLJ11036	3' CCCAGGAGTTCAGGGCTGCAGT 37554	AA CCAC C
	GA	TCACTGCA CT CTCC GGG	
		AGTGACGT GG GAGG CCC	
		CG ACTT A	
GAM2411	FLJ11106	3' CCTGGGAGGTGGAGCTTGCAGT 37622	A
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GAM2411	FLJ11151	3' GAGGCAGAGGTTGCAGTGA 68477	A CA
		TCACTGCAA CTC CCTC	

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		G AC		
GAM2411	FLJ11259	3' CCCAGGAGGTGGAGGCTGCAGT 37765	AA	C
	GA	TCACTGCA CTCCACCTCC GGG		
		AGTGACGT GAGGTGGAGG CCC		
		CG A		
GAM2411	FLJ11301	3' CCAGGGAGGCAGAGTTTGCAGT 37805	CA	_
	GA	TCACTGCAAACTC CCTCCC GG		
		AGTGACGTTTGAG GGAGGG CC		
		AC A		
GAM2411	FLJ11577	3' GAGGCAGAGGTTGCAGTGA 47959	A CA	
		TCACTGCAA CTC CCTC		
		AGTGACGTT GAG GGAG		
		G AC		
GAM2411	FLJ11700	3' CCCGGGAAGTGGAGGTTGCAGT 46560	A C	
	GA	TCACTGCAA CTCCAC TCCCGGG		
		AGTGACGTT GAGGTG AGGGCCC		
		G A		
GAM2411	FLJ11726	3' CCCTGGAGGCGGAAGTTGCAGT 47018	AC A C	
	GA	TCACTGCAA TCC CCTCC GGG		
		AGTGACGTT AGG GGAGG CCC		
		GA C T		
GAM2411	FLJ11996	3' CCCGGGAGGCAGAGGTTGCAGT 47059	A CA	
	GA	TCACTGCAA CTC CCTCCCGGG		
		AGTGACGTT GAG GGAGGGCCC		
		G AC		
GAM2411	FLJ11996	3' GGAGGCGGAGGTTGCAGTGA 47066	A A	
		TCACTGCAA CTCC CCTCC		
		AGTGACGTT GAGG GGAGG		
		G C		
GAM2411	FLJ12056	3' CCCAGGAGATGGAGGTTGCGGT 46820	A C C	
	GA	TCACTGCAA CTCCA CTCC GGG		
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		G A A		
GAM2411	FLJ12078	3' GAGGCAGAGGTTGCAGTGA 47080	A CA	
		TCACTGCAA CTC CCTC		
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GAM2411	FLJ12190	3' CCCGGGAGGCAGAGGTTGCAGT 47566	A CA	
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GAM2411	FLJ12298	3' CCCAGGAGGCGGAAGTTGCAGT 50597	AC A C
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		GA C A	
GAM2411	FLJ12331	3' CCCGGGAGGCAAAGGTTGCGGT 47110	A CCA
		ACTGCAA CT CCTCCCGGG	
		TGGCGTT GA GGAGGGCCC	
		G AAC	
GAM2411	FLJ12448	3' CCCAGGAGGTGCAGGTTGCAGT 43476	A C C
	GA	TCACTGCAA CT CACCTCC GGG	
		AGTGACGTT GA GTGGAGG CCC	
		G C A	
GAM2411	FLJ12586	3' GAGGTGGAGGTTGCAGTGA 45210	A
		TCACTGCAA CTCCACCTC	
		AGTGACGTT GAGGTGGAG	
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GAM2411	FLJ12606	3' CCCGGGAGGCGGAAGTTGCGGT 46064	AC A
	GA	TCACTGCAA TCC CCTCCCGGG	
		AGTGGCGTT AGG GGAGGGCCC	
		CA C	
GAM2411	FLJ12618	3' CCCAGGAGGTCTAGGCTGCAGT 46505	AA CC C
	GA	TCACTGCA CT ACCTCC GGG	
		AGTGACGT GA TGGAGG CCC	
		CG TC A	
GAM2411	FLJ12660	3' CCCGGGAGGCTGAGGTTGCAGT 47894	A CA
	GA	TCACTGCAA CTC CCTCCCGGG	
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		G TC	
GAM2411	FLJ12671	3' CCCAGGAGGCGGAGATTGCAGT 49106	A A C
	GA	TCACTGCAA CTCC CCTCC GGG	
		AGTGACGTT GAGG GGAGG CCC	
		A C A	
GAM2411	FLJ12800	3' CCTGGAAGCAGAGTTTGCAGT 43528	CACC
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GAM2411	FLJ12921	3' CCTGGAAGGCGGAGCTTGCAGT 46396	A A C
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			CG C A			
GAM2411	FLJ13162	3'	CCCAGGAGGCGGAGGTTGCGGT 47184	A	A	C
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GAM2411	FLJ13193	3'	CCCAGGAGGTGGAGGTTGCAGT 50716	A		C
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GAM2411	FLJ13241	3'	GAGGTGGAGGCTGCAGTGA 47653	AA		
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GAM2411	FLJ13448	3'	CCCGGGAGGCGGAGGTTGCAGT 47881	A	A	
			ACTGCAA CTCC CCTCCCGGG			
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GAM2411	FLJ13456	3'	CCCAGGAAGTGGAGGTTGCAGT 66540	A	C	C
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GAM2411	FLJ13621	3'	CCCGGGAGGCGGAGCTTGCAGT 47221	A	A	
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GAM2411	FLJ13659	3'	CCCGGGAGGCAGAGGTTGAAGT 48029	G	A	CA
	GA		TCACT CAA CTC CCTCCCGGG			
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			A G AC			
GAM2411	FLJ13848	3'	CCCAGGAGGTGGAGGTTGTGG 45819	TG	A	C
			C CAA CTCCACCTCC GGG			
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			GT G A			
GAM2411	FLJ13984	3'	GGAGGCGGAGGTTGCAGTGA 45809	A	A	
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GAM2411 FLJ14011 3' CCCAGGAGGTGGGGGTTGCACC 42316  AC  A      C
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                  CC   G      A
GAM2411 FLJ14100 3' CCTGGGAGGTGGAGCTTGCAGT 47332      A
      GA          TCACTGCAA CTCCACCTCCCGGG
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GAM2411 FLJ14117 3' CCCGCGAGGCGGAGACTGCAGT 43221      AA  A  C
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GAM2411 FLJ14117 3' GAGGCAGAGGTTGCAGTGA  43226      A  CA
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GAM2411 FLJ14129 3' GAGGCGGAGGTTGCAGTGA  48808      A  A
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GAM2411 FLJ14251 3' CCCAGGAGGTGGAGGTTTCAGC 46477  A  C  _      C
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GAM2411 FLJ14345 3' GAGGCGGAGGTTGCAGTGA  45658      A  A
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                  G   C
GAM2411 FLJ14346 3' CTTGGGAGGTGGAGCTTACAGT 47364      C  A
      GA          TCACTG AA CTCCACCTCCCGGG
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GAM2411	FLJ14397 3'	CCTGGGAGGCGGAGCTTGCAGT 52324	A	A
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	GA	TCACTGCAA CTCC CCTCC GGG		
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	GA	TCACTGCAA CTCC CCTCC GGG		
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		C C A		
GAM2411	FLJ14621 3'	CCCGGGAGGCAGAGGTTGCAGT 52536	A	CA
	GA	TCACTGCAA CTC CCTCCCGGG		
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GAM2411	FLJ14768 3'	CCCAAGACATGGGGACTTTGCA 52674	—	CC CC
	GTGA	TCACTGCAAA CTCCA TC GGG		
		AGTGACGTTT GGGGT AG CCC		
		CA AC AA		
GAM2411	FLJ20004 3'	CCTCCCGGGGAAGCGGAGGTTG 34755	A	A_____ TCCC
	CAGTGA	TCACTGCAA CTCC CC GG		
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		G CGAAG__G CCCT		
GAM2411	FLJ20004 3'	CCCAGGAGGCAGAGGTTGCAGT 97002	A	CA C
	GA	TCACTGCAA CTC CCTCC GGG		
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GAM2411 FLJ20006 3'	GAGGCAGAGATTGCAGTGA 34783	A CA	
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GAM2411 FLJ20006 3'	GAGGCGGAGGTTGCAGTGA 34784	A A	
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GAM2411 FLJ20013 3'	GAGGCGGAGGTTGCAGTGA 34797	A A	
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GAM2411 FLJ20045 3'	CCCAGGAGGTGAAGGTTGCAGT 34881	A C C	
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GAM2411 FLJ20055 3'	CCCAGGAGGCAGAGGTTGCAGT 34906	A CA C	
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	G AC A		
GAM2411 FLJ20059 3'	CCCGGGAGGTGGAGGTCGCGGT 34926	AAA	
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GAM2411 FLJ20069 3'	CCCAGGAGGCAGAGGTTGCAGT 34950	A CA C	
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GAM2411 FLJ20081 3'	CCCGGGAGTTTGAAGTTGCAGT 34989	AC CAC	
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GAM2411 FLJ20139 3'	CCCAGGAGGTGGAGGCTGCAAT 35116	C AA C	
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GAM2411	FLJ20241	3' CCCAGGAGGCGGAGCTTGCAGT 35290	A A C
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		C C A	
GAM2411	FLJ20280	3' CCCAGGAGACGGAGGTTGCGGT 35327	A AC C
	GA	TCACTGCAA CTCC CTCC GGG	
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		G CA A	
GAM2411	FLJ20296	3' CCCAGAAATGGCATTTCAGT 35364	CT CC CC
		ACTGCAAA CCA TC GGG	
		TGACGTTT GGT AG CCC	
		AC AA A_	
GAM2411	FLJ20340	3' CCCGGGAGGTGGAGGTTGCAG 35457	A
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GAM2411	FLJ20413	3' CCAGGGAGGAGGAGCTTGCAGT 35592	A A _
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GAM2411	FLJ20456	3' CCCGGGAGGCGGAGGTTGCAGT 35663	A A
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GAM2411	FLJ20464	3' CCCGGGAGGCGGAGTTGCGGTG 35694	A A
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GAM2411	FLJ20627	3' CTTGGGAGGCGGAGGTTGCAGT 35910	A A
	GA	TCACTGCAA CTCC CCTCCCGGG	
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GAM2411	FLJ20694	3' CCCAGGAGGCAGAGGTTGCAGT 35975	A CA C
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GAM2411	FLJ20700	3'	CCCGGGTGGCGGCGCTTGCAGT 36005	ACT	A T
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			CGC C T		
GAM2411	FLJ20783	3'	CCCAGGAGGCGGAGCTTGCAGT 36097	A A	C
	GA		TCACTGCAA CTCC CCTCC GGG		
			AGTGACGTT GAGG GGAGG CCC		
			C C A		
GAM2411	FLJ20802	3'	AGGCAGAGGTTGCAGTGA 36104	A	CA
			TCACTGCAA CTC CCT		
			AGTGACGTT GAG GGA		
			G AC		
GAM2411	FLJ20972	3'	CCCAGGAGGCAGAGATTGCAGT 47385	A CA	C
	GA		TCACTGCAA CTC CCTCC GGG		
			AGTGACGTT GAG GGAGG CCC		
			A AC A		
GAM2411	FLJ21240	3'	CCCAGGAGGTGGAGTTTGCAGT 46263		C
	GA		TCACTGCAA ACTCCACCTCC GGG		
			AGTGACGTTTGAGGTGGAGG CCC		
			A		
GAM2411	FLJ21551	3'	CCCAGGAGGTGGAGGTTGCAGT 46034	A	C
	GA		TCACTGCAA CTCCACCTCC GGG		
			AGTGACGTT GAGGTGGAGG CCC		
			G A		
GAM2411	FLJ21603	3'	GAGGCAGAGGTTGCAGTGA 45773	A	CA
			TCACTGCAA CTC CCTC		
			AGTGACGTT GAG GGAG		
			G AC		
GAM2411	FLJ21687	3'	GAGGTGGAGGTTGCAGCGA 46298	A	A
			TC CTGCAA CTCCACCTC		
			AG GACGTT GAGGTGGAG		
			C G		
GAM2411	FLJ21777	5'	CCCGGGAGGCGGAGGTTTCAGT 50839	C _	A
	GA		TCACTG AAAC TCC CCTCCCGGG		
			AGTGAC TTTG AGG GGAGGGCCC		
			_ G C		
GAM2411	FLJ21777	3'	CCCTGGAGGCGGAGGTTGCAGT 50840	A A	C
	GA		TCACTGCAA CTCC CCTCC GGG		

			AGTGACGTT GAGG GGAGG CCC	
			G C T	
GAM2411	FLJ21791	3'	CCCAGGAAATTGACTTTGCAGT 62124	C CACC C
	G		CACTGCAA TC TCC GGG	
			GTGACGTTT AG AGG CCC	
			C TTAA A	
GAM2411	FLJ22009	3'	CCCAGGAGGTTGAGGCTGCAGT 60917	AA C C
	GA		TCACTGCA CTC ACCTCC GGG	
			AGTGACGT GAG TGGAGG CCC	
			CG T A	
GAM2411	FLJ22054	3'	GAGGTGGAGGTTGCAGTGA 96048	A
			TCACTGCAA CTCCACCTC	
			AGTGACGTT GAGGTGGAG	
			G	
GAM2411	FLJ22167	3'	CCAGAGGTGGAGGTTGCAGT 44864	A CC
			ACTGCAA CTCCACCTC GG	
			TGACGTT GAGGTGGAG CC	
			G A_	
GAM2411	FLJ22313	3'	CCCAGGAGGCGGAGGTTGCAGT 42578	A A C
	GA		TCACTGCAA CTCC CCTCC GGG	
			AGTGACGTT GAGG GGAGG CCC	
			G C A	
GAM2411	FLJ22415	3'	AGGTGGAGGTTGCAGTGA 93116	A
			TCACTGCAA CTCCACCT	
			AGTGACGTT GAGGTGGA	
			G	
GAM2411	FLJ22474	3'	GAGGCGGAGGTTGCAGTGA 45615	A A
			TCACTGCAA CTCC CCTC	
			AGTGACGTT GAGG GGAG	
			G C	
GAM2411	FLJ22692	3'	CCCAGGAGGCAGAGCTTGCAGT 47479	A CA C
	GA		TCACTGCAA CTC CCTCC GGG	
			AGTGACGTT GAG GGAGG CCC	
			C AC A	
GAM2411	FLJ22814	3'	CCCAGGAGGCGGAGCTTGCAGT 46722	A A C
	GA		TCACTGCAA CTCC CCTCC GGG	
			AGTGACGTT GAGG GGAGG CCC	
			C C A	
GAM2411	FLJ22965	3'	GAGGTGGAGGTTGCAGTGA 42297	A
			TCACTGCAA CTCCACCTC	

			AGTGACGTT GAGGTGGAG		
			G		
GAM2411	FLJ23022	3'	CCCGGGAGGTGGAGGTTGCAGT 47493	A	
	GA		TCACTGCAA CTCCACCTCCCGGG		
			AGTGACGTT GAGGTGGAGGGCCC		
			G		
GAM2411	FLJ23229	3'	GAGGCGGAGGTTGCAGTGA 47531	A	A
			TCACTGCAA CTCC CCTC		
			AGTGACGTT GAGG GGAG		
			G C		
GAM2411	FLJ23235	3'	AGGCAGAGTTTGCAGTGA 46874	CA	
			TCACTGCAA ACTC CCT		
			AGTGACGTTTGAG GGA		
			AC		
GAM2411	FLJ23360	3'	GAGGCAGAGGTTGCAGTGA 43830	A	CA
			TCACTGCAA CTC CCTC		
			AGTGACGTT GAG GGAG		
			G AC		
GAM2411	FLJ23499	3'	CCCAGGAAGCAGAGGTTGCAGT 43131	A	CACC C
	GA		TCACTGCAA CTC TCC GGG		
			AGTGACGTT GAG AGG CCC		
			G ACGA A		
GAM2411	FLJ23537	3'	GAGGCGGAAGTTGCAGTGA 46542	AC	A
			TCACTGCAA TCC CCTC		
			AGTGACGTT AGG GGAG		
			GA C		
GAM2411	FLJ23878	3'	CCCGGAAGGCGGAGCTTGCAGT 59369	A	A C
	GA		TCACTGCAA CTCC CCT CCGGG		
			AGTGACGTT GAGG GGA GGCCC		
			C C A		
GAM2411	FLJ25006	3'	CCCAGGAGATGGAGGTTGCGGT 58788	A	C C
	GA		TCACTGCAA CTCCA CTCC GGG		
			AGTGCGCTT GAGGT GAGG CCC		
			G A A		
GAM2411	FLJ31455	3'	GAGGCGAAGGTTGCAGTGA 59285	A	CCA
			TCACTGCAA CT CCTC		
			AGTGACGTT GA GGAG		
			G AGC		
GAM2411	FLJ31737	3'	CCCAGGAGGCAAAGGCTGCAGT 59348	AA	CCA C
	GA		TCACTGCA CT CCTCC GGG		

			AGTGACGT GA GGAGG CCC		
			CG AAC A		
GAM2411	FLJ31952	3'	GAGGCAGAGGTTGCAGTGA 59046	A CA	
			TCACTGCAA CTC CCTC		
			AGTGACGTT GAG GGAG		
			G AC		
GAM2411	FLJ32915	5'	CCCGGGAGGCGGAGGCTGCAGT 59430	AA A	
			GA TCACTGCA CTCC CCTCCCGGG		
			AGTGACGT GAGG GGAGGGCCC		
			CG C		
GAM2411	FUSIP1	3'	GAGGTAGAAGTTGCAGTGA 55040	AC C	
			TCACTGCAA TC ACCTC		
			AGTGACGTT AG TGGAG		
			GA A		
GAM2411	GALNT6	3'	CCCAGGAGGCAGAGGTTGCAGT 24245	A CA C	
			GA TCACTGCAA CTC CCTCC GGG		
			AGTGACGTT GAG GGAGG CCC		
			G AC A		
GAM2411	GLTP	3'	CCCGGGAGGTGGAGGTTGCAGT 33583	A	
			GA TCACTGCAA CTCCACCTCCCGGG		
			AGTGACGTT GAGGTGGAGGGCCC		
			G		
GAM2411	GNB4	3'	CCCGGGAGGCAGAGGTTGCAGT 41567	A CA	
			GA TCACTGCAA CTC CCTCCCGGG		
			AGTGACGTT GAG GGAGGGCCC		
			G AC		
GAM2411	GP5	3'	CCCGGGAGGCGGAGGTTGCAGT 16870	A A	
			GA TCACTGCAA CTCC CCTCCCGGG		
			AGTGACGTT GAGG GGAGGGCCC		
			G C		
GAM2411	GTPBP5	3'	CCTGGGAGGCGGAGCTTGCAGT 65973	A A	
			GA TCACTGCAA CTCC CCTCCCGGG		
			AGTGACGTT GAGG GGAGGGTCC		
			C C		
GAM2411	HCGIX	3'	CCCAGGAGTTCGAGGCTGCAGT 20714	AA CAC C	
			GA TCACTGCA CTC CTCC GGG		
			AGTGACGT GAG GAGG CCC		
			CG CTT A		
GAM2411	HES2	3'	CCTGGGAGGTGGAGCTTGCAGT 39372	A	
			GA TCACTGCAA CTCCACCTCCCGGG		

AGTGACGTT GAGGTGGAGGGTCC

C

GAM2411 HIC 3' CCCGAGAGGCGGAAGTTGCAGT 68047 AC A C
GA TCACTGCAA TCC CCTC CGGG

||||||| ||| ||| |||

AGTGACGTT AGG GGAG GCCC

GA C A

GAM2411 HIG2 3' CCCGGGGACGGAGGTTGCAGTG 26199 A ACC
A TCACTGCAA CTCC TCCCGGG

||||||| ||| |||||

AGTGACGTT GAGG GGGGCCC

G CA_

GAM2411 HRH4 3' CCCGGGAGGCGGAGTTTTGCCA 41533 _ _ A
G CTG CAAA CTCC CCTCCCGGG

||| ||| ||| |||||

GAC GTTT GAGG GGAGGGCCC

C T C

GAM2411 HSA250303 3' CCCAGGAAGCAGAGGTTGCAGT 38020 A CACC C
GA TCACTGCAA CTC TCC GGG

||||||| ||| ||| |||

AGTGACGTT GAG AGG CCC

G ACGA A

GAM2411 HSD17B7 3' GAGGCAGAGGTTGCAGTGA 33482 A CA
TCACTGCAA CTC CCTC

||||||| ||| |||

AGTGACGTT GAG GGAG

G AC

GAM2411 HSH2 3' CCCGGGAGGCAGAGGTTGCAGT 52737 A CA
GA TCACTGCAA CTC CCTCCCGGG

||||||| ||| |||||

AGTGACGTT GAG GGAGGGCCC

G AC

GAM2411 HYPK 3' CCTCCCGGGAAAGCAGAGGTTG 33514 A CA_____ TCCC
CAGTGA TCACTGCAA CTC CC GG

||||||| ||| || ||

AGTGACGTT GAG GG CC

G ACGAAA__G CCCT

GAM2411 IMAGE:4907098 3' GAGGCGGAGGTTGCAGTGA 93325 A A
TCACTGCAA CTCC CCTC

||||||| ||| |||

AGTGACGTT GAGG GGAG

G C

GAM2411 KALI 3' CCCAGGAGGTGGAGGTTCCAGT 54691 CAAA C
GA TCACTG CTCCACCTCC GGG

||||| ||||| |||

AGTGAC GAGGTGGAGG CCC

CTTG A

GAM2411 KBRAS2 3' AGGCGGAGGCTGCAGTGA 34618 AA A
TCACTGCA CTCC CCT

||||||| ||| |||

			AGTGACGT GAGG GGA			
			CG C			
GAM2411	KCNH6	3'	CCCGGGAGGTGGAGGTTGCAGG 48571	A	A	
	GA		TC CTGCAA CTCCACCTCCCGGG			
			AG GACGTT GAGGTGGAGGGCCC			
			G G			
GAM2411	KIAA0042	3'	GAGGCAGAGGTTGCAGTGA 30236	A	CA	
			TCACTGCAA CTC CCTC			
			AGTGACGTT GAG GGAG			
			G AC			
GAM2411	KIAA0057	3'	AGGTGGAGGTTGCAGTGA 25400	A		
			TCACTGCAA CTCCACCT			
			AGTGACGTT GAGGTGGA			
			G			
GAM2411	KIAA0184	3'	CCAGGGAGGCGGAGCTTGCAGT 65807	A	A	_
	GA		TCACTGCAA CTCC CCTCCC GG			
			AGTGACGTT GAGG GGAGGG CC			
			C C A			
GAM2411	KIAA0186	3'	CCCAGAGGTCAAGACTGCAGTG 41103	AA	CC	CC
	A		TCACTGCA CT ACCTC GGG			
			AGTGACGT GA TGGAG CCC			
			CA AC A_			
GAM2411	KIAA0226	3'	GAGGCAGAGGTTGCAGTGA 64259	A	CA	
			TCACTGCAA CTC CCTC			
			AGTGACGTT GAG GGAG			
			G AC			
GAM2411	KIAA0266	3'	AGGCAGAGGTTGCAGTGA 41636	A	CA	
			TCACTGCAA CTC CCT			
			AGTGACGTT GAG GGA			
			G AC			
GAM2411	KIAA0355	3'	CCCGGGAGGCGGAGGTTACAGT 28705	CAAA	A	
	GA		TCACTG CTCC CCTCCCGGG			
			AGTGAC GAGG GGAGGGCCC			
			ATTG C			
GAM2411	KIAA0391	3'	CCCAGAGGTCAAGGCTGCAGTG 28603	AA	CC	CC
	A		TCACTGCA CT ACCTC GGG			
			AGTGACGT GA TGGAG CCC			
			CG AC A_			
GAM2411	KIAA0408	3'	CCCGGGAGGCAGAGCTTGCAGT 28797	A	CA	
	GA		TCACTGCAA CTC CCTCCCGGG			

		AGTGACGTT GAG GGAGGGCCC		
		C AC		
GAM2411	KIAA0419	3' GAGGCAGAGGTTGCAGTGA 28861	A CA	
		TCACTGCAA CTC CCTC		
		AGTGACGTT GAG GGAG		
		G AC		
GAM2411	KIAA0441	3' CCCAGGAGGCGGAGGCTGCAGT 29629	AA A C	
	GA	TCACTGCA CTCC CCTCC GGG		
		AGTGACGT GAGG GGAGG CCC		
		CG C A		
GAM2411	KIAA0446	5' GCCCGGGAGGTGGAGCTTGCAG 69453	A	—
	TGG	TCACTGCAA CTCCACCTCCCGGG C		
		GGTGACGTT GAGGTGGAGGGCCC G		
		C		
GAM2411	KIAA0447	3' CCCGGAGATGGAGGTTGCAGTG 72113	A C C	
	A	TCACTGCAA CTCCA CTCC GGG		
		AGTGACGTT GAGGT GAGG CCC		
		G A _		
GAM2411	KIAA0451	5' CCCAGGAGGTCGAGGCTGCAGT 29768	AA C C	
	GA	TCACTGCA CTC ACCTCC GGG		
		AGTGACGT GAG TGGAGG CCC		
		CG C A		
GAM2411	KIAA0472	3' GAGGCGGAGGTTGCAGTGA 72354	A A	
		TCACTGCAA CTCC CCTC		
		AGTGACGTT GAGG GGAG		
		G C		
GAM2411	KIAA0475	3' GAGGCGAAGGTTGCAGTGA 30118	A CCA	
		TCACTGCAA CT CCTC		
		AGTGACGTT GA GGAG		
		G AGC		
GAM2411	KIAA0514	3' CCCAGGAGGTTGAGGTTGCAGT 28743	A C	
	GA	TCACTGCAA CTCCACCTCC GGG		
		AGTGACGTT GAGGTGGAGG CCC		
		G A		
GAM2411	KIAA0557	3' CCCAGGAAGTTGAGGCTGCAGT 78548	AA C C C	
	GA	TCACTGCA CTC AC TCC GGG		
		AGTGACGT GAG TG AGG CCC		
		CG T A A		
GAM2411	KIAA0557	3' GAGGCGGAGGTTGCAGTGA 78565	A A	
		TCACTGCAA CTCC CCTC		

			AGTGACGTT GAGG GGAG	
			G C	
GAM2411	KIAA0563	3'	CCTGGGAGGCAGAGCTTGCAGT 29878	A CA
	GA		TCACTGCAA CTC CCTCCCGGG	
			AGTGACGTT GAG GGAGGGTCC	
			C AC	
GAM2411	KIAA0565	3'	GAGGCAAAGGTTGCAGTGA 67438	A CCA
			TCACTGCAA CT CCTC	
			AGTGACGTT GA GGAG	
			G AAC	
GAM2411	KIAA0596	3'	GAGGTGGAGGTTGCAGTGA 63492	A
			TCACTGCAA CTCCACCTC	
			AGTGACGTT GAGGTGGAG	
			G	
GAM2411	KIAA0635	3'	CCCGGGAGGTGGAGGCTGCGGT 28414	AA
	GA		TCACTGCA CTCCACCTCCCGGG	
			AGTGGCGT GAGGTGGAGGGCCC	
			CG	
GAM2411	KIAA0794	3'	GAGGCAGAGGTTGCAGTGA 81230	A CA
			TCACTGCAA CTC CCTC	
			AGTGACGTT GAG GGAG	
			G AC	
GAM2411	KIAA0825	3'	CCCGGGAGGTGGAGGTTGCAGT 61684	A
	GA		TCACTGCAA CTCCACCTCCCGGG	
			AGTGACGTT GAGGTGGAGGGCCC	
			G	
GAM2411	KIAA0831	3'	GAGGCGGAGGTTGCAGTGA 30639	A A
			TCACTGCAA CTCC CCTC	
			AGTGACGTT GAGG GGAG	
			G C	
GAM2411	KIAA0853	3'	CCCAGGAAATTGAGGCTGCAGT 31214	AA CACC C
	GA		TCACTGCA CTC TCC GGG	
			AGTGACGT GAG AGG CCC	
			CG TTAA A	
GAM2411	KIAA0872	3'	CCCGAGAGGCGGAGGTTGCAGT 30749	A A C
	GA		TCACTGCAA CTCC CCTC CGGG	
			AGTGACGTT GAGG GGAG GCCC	
			G C A	
GAM2411	KIAA0872	3'	CCCGGGAGGCAGAGGTTATCGT 30750	TGCAAA CA
	GA		TCAC CTC CCTCCCGGG	

		AGTG GAG GGAGGGCCC	
		CTATTG AC	
GAM2411 KIAA0889	3'	CCCAGGAGGCGGAGGCTGCAGT 31769	AA A C
	GA	TCACTGCA CTCC CCTCC GGG	
		AGTGACGT GAGG GGAGG CCC	
		CG C A	
GAM2411 KIAA0889	5'	CCCAGGAGTTTGAGGCTGCAGT 31770	AA CAC C
	GA	TCACTGCA CTC CTCC GGG	
		AGTGACGT GAG GAGG CCC	
		CG TTT A	
GAM2411 KIAA0889	3'	CCCAGTAGGCGGAAGTTGCAGT 31771	AC A CCC
	GA	TCACTGCAA TCC CCT GGG	
		AGTGACGTT AGG GGA CCC	
		GA C TGA	
GAM2411 KIAA0892	3'	CCCAGGAGATTGAGGCTGCAGT 71569	AA CAC C
	GA	TCACTGCA CTC CTCC GGG	
		AGTGACGT GAG GAGG CCC	
		CG TTA A	
GAM2411 KIAA0907	3'	GAGGCAGAGGTTGCAGTGA 30874	A CA
		TCACTGCAA CTC CCTC	
		AGTGACGTT GAG GGAG	
		G AC	
GAM2411 KIAA0924	3'	CCCAGGAGGCGGAGCTTGCAGT 30357	A A C
	GA	TCACTGCAA CTCC CCTCC GGG	
		AGTGACGTT GAGG GGAGG CCC	
		C C A	
GAM2411 KIAA0930	3'	AGGCAGAGGTTGCAGTGA 71063	A CA
		TCACTGCAA CTC CCT	
		AGTGACGTT GAG GGA	
		G AC	
GAM2411 KIAA0937	5'	CCCGGGAGGCGGGCCGCGCAG 93223	AAAC A
		CTGC TCC CCTCCCGGG	
		GACG GGG GGAGGGCCC	
		CGCC C	
GAM2411 KIAA0961	3'	CCCGGGAGGCAGAGGTTGCAGT 30398	A CA
	GA	TCACTGCAA CTC CCTCCCGGG	
		AGTGACGTT GAG GGAGGGCCC	
		G AC	
GAM2411 KIAA0981	3'	GAGGCGGAGGCTGCAGTGA 62088	AA A
		TCACTGCA CTCC CCTC	

		AGTGACGT GAGG GGAG	
		CG C	
GAM2411 KIAA1001	3'	GAGGTGGAGGCTGCAGTGA 31007	AA
		TCACTGCA CTCCACCTC	
		AGTGACGT GAGGTGGAG	
		CG	
GAM2411 KIAA1001	3'	GAGGTGGAGGTTGCAGTGA 31008	A
		TCACTGCAA CTCCACCTC	
		AGTGACGTT GAGGTGGAG	
		G	
GAM2411 KIAA1056	3'	AGGCGGAGGTTGCAGTGA 30309	A A
		TCACTGCAA CTCC CCT	
		AGTGACGTT GAGG GGA	
		G C	
GAM2411 KIAA1130	3'	CCCGGGAGGCAGAGGTAGCAGT 63083	AAA CA
	GA	TCACTGC CTC CCTCCCGGG	
		AGTGACG GAG GGAGGGCCC	
		ATG AC	
GAM2411 KIAA1143	3'	CCCAGGAGTTCAACGCTGCAGT 69236	AACTCCAC C
	GA	TCACTGCA CTCC GGG	
		AGTGACGT GAGG CCC	
		CGCAACTT A	
GAM2411 KIAA1160	3'	CCCGAGAGGTGGAGGTTGAAGT 40754	G A C
	GA	TCACT CAA CTCCACCTC CGGG	
		AGTGA GTT GAGGTGGAG GCCC	
		A G A	
GAM2411 KIAA1164	3'	CCCAGGAGGCAGTGATTGCAGT 70039	__ CCA C
	GA	TCACTGCAA ACT CCTCC GGG	
		AGTGACGTT TGA GGAGG CCC	
		AG C__ A	
GAM2411 KIAA1164	3'	CCCGGCAGGCAGAGGTTGCAGT 70040	A CA C
	GA	TCACTGCAA CTC CCT CCGGG	
		AGTGACGTT GAG GGA GGCCC	
		G AC C	
GAM2411 KIAA1202	3'	AGGCAGAGATTGCAGTGA 72483	A CA
		TCACTGCAA CTC CCT	
		AGTGACGTT GAG GGA	
		A AC	
GAM2411 KIAA1228	3'	CCCAGGAGGCGGAGGTTGCAGT 65673	A A C
	GA	TCACTGCAA CTCC CCTCC GGG	

		AGTGACGTT GAGG GGAGG CCC	
		G C A	
GAM2411 KIAA1244	3'	CCCAGGAGGCGGACGTTGCAGT 72443	AC A C
	GA	TCACTGCAA TCC CCTCC GGG	
		AGTGACGTT AGG GGAGG CCC	
		GC C A	
GAM2411 KIAA1253	3'	CCCAGGAGGCAGAGGTTGCAGT 93549	A CA C
	GA	TCACTGCAA CTC CCTCC GGG	
		AGTGACGTT GAG GGAGG CCC	
		G AC A	
GAM2411 KIAA1271	3'	CCCAGAAGCTTGAAGCTGCAGT 70134	AA C C_ CCC
	GA	TCACTGCA CT CA CT GGG	
		AGTGACGT GA GT GA CCC	
		C_ A TC AGA	
GAM2411 KIAA1271	3'	CCCAGGATGCGGAGGTTGCAGT 70135	A ACC C
	GA	TCACTGCAA CTCC TCC GGG	
		AGTGACGTT GAGG AGG CCC	
		G CGT A	
GAM2411 KIAA1276	3'	GAGGCAGAGGTTGCAGTGA 67031	A CA
		TCACTGCAA CTC CCTC	
		AGTGACGTT GAG GGAG	
		G AC	
GAM2411 KIAA1328	3'	CCCGGGAGGCGGAGGTTGCAGT 62319	A A
	GA	TCACTGCAA CTCC CCTCCCGGG	
		AGTGACGTT GAGG GGAGGGCCC	
		G C	
GAM2411 KIAA1340	3'	CCCTTCAGGCGGAGGTTGCAGT 69694	A A CCC
	GA	TCACTGCAA CTCC CCT GGG	
		AGTGACGTT GAGG GGA CCC	
		G C CTT	
GAM2411 KIAA1348	3'	CCCGGGAGGCGGAGGTTGCGGT 69121	A A
	GA	TCACTGCAA CTCC CCTCCCGGG	
		AGTGCGTT GAGG GGAGGGCCC	
		G C	
GAM2411 KIAA1364	3'	GAGGCGGAGGTTGCAGCGA 64349	A A A
		TC CTGCAA CTCC CCTC	
		AG GACGTT GAGG GGAG	
		C G C	
GAM2411 KIAA1364	3'	GAGGCGGAGGTTGCAGTGA 64350	A A
		TCACTGCAA CTCC CCTC	

		AGTGACGTT GAGG GGAG	
		G C	
GAM2411 KIAA1404	3'	CCCAGGAGGCGGAGGTTGCAGT 62686	A A C
	GA	TCACTGCAA CTCC CCTCC GGG	
		AGTGACGTT GAGG GGAGG CCC	
		G C A	
GAM2411 KIAA1456	3'	CCCAGGAATTCAAGGCTGCAGT 67543	AA CCACC C
	GA	TCACTGCA CT TCC GGG	
		AGTGACGT GA AGG CCC	
		CG ACTTA A	
GAM2411 KIAA1456	5'	CCCGTGAGGCAGAGGTTGCAGT 67544	A CA C
	GA	TCACTGCAA CTC CCTC CGGG	
		AGTGACGTT GAG GGAG GCCC	
		G AC T	
GAM2411 KIAA1456	3'	GAGGCGGAGGTTGCAGTGA 67557	A A
		TCACTGCAA CTCC CCTC	
		AGTGACGTT GAGG GGAG	
		G C	
GAM2411 KIAA1473	3'	CCCGGGAAGCAGAGGTTGCGGT 71209	A CACC
	GA	TCACTGCAA CTC TCCCGGG	
		AGTGCGGTT GAG AGGGCCC	
		G ACGA	
GAM2411 KIAA1486	3'	CCTGGGAGGTGGAGCTTGCAGT 67972	A
	GA	TCACTGCAA CTCCACCTCCCGGG	
		AGTGACGTT GAGGTGGAGGGTCC	
		C	
GAM2411 KIAA1503	3'	CCCGGGAGGCAGAGGCTGCAGT 68898	AA CA
	GA	TCACTGCA CTC CCTCCCGGG	
		AGTGACGT GAG GGAGGGCCC	
		CG AC	
GAM2411 KIAA1508	3'	CTTGGGAGGCAGAGGTTGCAGT 62549	A CA
	GA	TCACTGCAA CTC CCTCCCGGG	
		AGTGACGTT GAG GGAGGGTTC	
		G AC	
GAM2411 KIAA1559	3'	CCCAAGAGGCAGAGTTTGCAGT 73453	CA CC
	GA	TCACTGCAA ACTC CCTC GGG	
		AGTGACGTTTGAG GGAG CCC	
		AC AA	
GAM2411 KIAA1586	5'	CCCGGGAGGTGGAGTTTACGGT 93937	C
	GA	TCACTG AA ACTCCACCTCCCGGG	

			AGTGGC TTTGAGGTGGAGGGCCC		
			A		
GAM2411	KIAA1594	3'	CCCAGGAGGCAGAGGTTGCAGT 72550	A	CA C
	GA		TCACTGCAA CTC CCTCC GGG		
			AGTGACGTT GAG GGAGG CCC		
			G AC A		
GAM2411	KIAA1614	3'	CCCGGGAGGTAGAGGTTGCAGT 70665	A	C
	GA		TCACTGCAA CTC ACCTCCCGGG		
			AGTGACGTT GAG TGGAGGGCCC		
			G A		
GAM2411	KIAA1630	3'	GAGGCGGAGGTTGCAGTGA 38655	A	A
			TCACTGCAA CTCC CCTC		
			AGTGACGTT GAGG GGAG		
			G C		
GAM2411	KIAA1641	3'	CCCGGGAGGCAGAGGTTTCAGT 81018	C	_ CA
	GA		TCACTG AAAC TC CCTCCCGGG		
			AGTGAC TTTG AG GGAGGGCCC		
			_ G AC		
GAM2411	KIAA1644	3'	CCCAGAAGGCAGAGCTTGCAGT 86219	A	CA CCC
	GA		TCACTGCAA CTC CCT GGG		
			AGTGACGTT GAG GGA CCC		
			C AC AGA		
GAM2411	KIAA1649	3'	CCCGGGAGGCGGAGTTTGCAGT 51229	A	
	GA		TCACTGCAA ACTCC CCTCCCGGG		
			AGTGACGTTTGAGG GGAGGGCCC		
			C		
GAM2411	KIAA1656	5'	CCCAGGAGGTGGAGGTTGCAGT 66364	A	C
	GA		TCACTGCAA CTCCACCTCC GGG		
			AGTGACGTT GAGGTGGAGG CCC		
			G A		
GAM2411	KIAA1674	3'	CCCAGGAGACGGAGCTTGCAGT 69334	A	AC C
	GA		TCACTGCAA CTCC CTCC GGG		
			AGTGACGTT GAGG GAGG CCC		
			C CA A		
GAM2411	KIAA1715	3'	GAGGCAGAGGTTGCAGTGA 68686	A	CA
			TCACTGCAA CTC CCTC		
			AGTGACGTT GAG GGAG		
			G AC		
GAM2411	KIAA1724	3'	GAGATGGAGATTGCAGTGA 67615	A	C
			TCACTGCAA CTCCA CTC		

		AGTGACGTT GAGGT GAG	
		A A	
GAM2411	KIAA1735	3' CCCAGGAGTTTGAGGTTGCAGT 89002	A CAC C
	GA	TCACTGCAA CTC CTCC GGG	
		AGTGACGTT GAG GAGG CCC	
		G TTT A	
GAM2411	KIAA1751	3' CCCGGGAGGCGGAGGTTGCAGT 72152	A A
	GA	TCACTGCAA CTCC CCTCCCGGG	
		AGTGACGTT GAGG GGAGGGCCC	
		G C	
GAM2411	KIAA1771	3' CCCAAGAGGTTGAGGCTGCAGT 79865	AA C CC
	GA	TCACTGCA CTC ACCTC GGG	
		AGTGACGT GAG TGGAG CCC	
		CG T AA	
GAM2411	KIAA1841	3' CCCGGGTGGCAGAGGTTGCAGT 80849	A CA T
	GA	TCACTGCAA CTC CC CCCGGG	
		AGTGACGTT GAG GG GGGCCC	
		G AC T	
GAM2411	KIAA1870	3' GAGGCAGAGGTTGCAGTGA 52902	A CA
		TCACTGCAA CTC CCTC	
		AGTGACGTT GAG GGAG	
		G AC	
GAM2411	KIAA1872	3' CCCAGGAGGCAGAGGTTGCAGT 63606	A CA C
	GA	TCACTGCAA CTC CCTCC GGG	
		AGTGACGTT GAG GGAGG CCC	
		G AC A	
GAM2411	KIAA1879	3' CCCGGGAGGCAGAACCTGCAGT 73935	AAC CA
	GA	TCACTGCA TC CCTCCCGGG	
		AGTGACGT AG GGAGGGCCC	
		CCA AC	
GAM2411	KIAA1904	3' CCCGGGAGGCAGCTGGGGCAGC 73864	AAA ____
	AG	CTGC CTCCA CCTCCCGGG	
		GACG GGGGT GGAGGGCCC	
		AC_ CGAC	
GAM2411	KIAA1941	3' GAGGTGGAGGTTGCAGTGA 75338	A
		TCACTGCAA CTCCACCTC	
		AGTGACGTT GAGGTGGAG	
		G	
GAM2411	KIAA1948	5' CCCAGGAGGCAGAGGCTGCAGT 83300	AA CA C
	GA	TCACTGCA CTC CCTCC GGG	

			AGTGACGT GAG GGAGG CCC		
			CG AC A		
GAM2411	KIAA1948	3'	CCCGGGAGGCGGAGCTTGCAGT 83301	A	A
	GA		TCACTGCAA CTCC CCTCCCGGG		
			AGTGACGTT GAGG GGAGGGCCC		
			C C		
GAM2411	KIAA1951	3'	CCCGGGAGGCGGAGCTTGCAGT 74150	A	A
	GA		TCACTGCAA CTCC CCTCCCGGG		
			AGTGACGTT GAGG GGAGGGCCC		
			C C		
GAM2411	KIAA1954	3'	CCCGGGAGCAGAGACTGCAGTG 78224	AA	CAC
	A		TCACTGCA CTC CTCCCGGG		
			AGTGACGT GAG GAGGGCCC		
			CA AC_		
GAM2411	KIAA1958	3'	GAGGCGGAGGTTGCAGTGA 82783	A	A
			TCACTGCAA CTCC CCTC		
			AGTGACGTT GAGG GGAG		
			G C		
GAM2411	KIAA1969	3'	GAGGTGGAAGTTGCAGTGA 79479	AC	
			TCACTGCAA TCCACCTC		
			AGTGACGTT AGGTGGAG		
			GA		
GAM2411	KIAA1979	3'	CCCAGGAGGTGGAGGATGCAGT 89650	AA	C
	GA		TCACTGCA CTCCACCTCC GGG		
			AGTGACGT GAGGTGGAGG CCC		
			AG A		
GAM2411	KLHL8	3'	CCCAGGAGGTGGAGGTTGCAAT 63510	C	A C
	GA		TCA TGCAA CTCCACCTCC GGG		
			AGT ACGTT GAGGTGGAGG CCC		
			A G A		
GAM2411	KR18	3'	CCCAGGAGGCGGAGGTTGTGG 53889	TG A A C	
			C CAA CTCC CCTCC GGG		
			G GTT GAGG GGAGG CCC		
			GT G C A		
GAM2411	KREMEN	3'	CCCAGGAGGTTCGAGGCTGCAGT 50231	AA C C	
	GA		TCACTGCA CTC ACCTCC GGG		
			AGTGACGT GAG TGGAGG CCC		
			CG C A		
GAM2411	KREMEN	3'	CCTGGGAGGCGGAGTTTGCAGT 50232	A	
	GA		TCACTGCAAACCTCC CCTCCCGGG		

			AGTGACGTTTGAGG GGAGGGTCC	
			C	
GAM2411 LANO	3'	CCCGGGAGGCTAAGGTTGCAGT 47971	A CCA	
GA		TCACTGCAA CT CCTCCCGGG		
		AGTGACGTT GA GGAGGGCCC		
		G ATC		
GAM2411 LAP1B	3'	CCCGGGAGGCGGAGGTTGCAGT 65189	A A	
		ACTGCAA CTCC CCTCCCGGG		
		TGACGTT GAGG GGAGGGCCC		
		G C		
GAM2411 LIM	3'	CCCAGGAGACGGAAGTTGCAGT 22321	AC AC C	
GA		TCACTGCAA TCC CTCC GGG		
		AGTGACGTT AGG GAGG CCC		
		GA CA A		
GAM2411 LIM	3'	CCCGGGAGGGAGAGGTTGCAGT 22322	A CA	
GA		TCACTGCAA CTC CCTCCCGGG		
		AGTGACGTT GAG GGAGGGCCC		
		G AG		
GAM2411 LIN-28	3'	CCCAGGCAGAGGTTGCAGTGA 45468	A CA CCC	
		TCACTGCAA CTC CCT GGG		
		AGTGACGTT GAG GGA CCC		
		G AC ____		
GAM2411 LRG	3'	GAGGCGGAGCTTGCGGTGA 54820	A A	
		TCACTGCAA CTCC CCTC		
		AGTGGCGTT GAGG GGAG		
		C C		
GAM2411 LRRFIP1	3'	GAGGCAGAGATTGCAGTGA 17613	A CA	
		TCACTGCAA CTC CCTC		
		AGTGACGTT GAG GGAG		
		A AC		
GAM2411 LSR68	3'	CCCAAAAGGCGGAGGTTGCAGT 38553	A A CCC	
GA		TCACTGCAA CTCC CCT GGG		
		AGTGACGTT GAGG GGA CCC		
		G C AAA		
GAM2411 MAL2	5'	CCGGGAGGCGGAGGCGGGA 54661	A AAA A	
		TC CTGC CTCC CCTCCCGG		
		AG GGCG GAGG GGAGGGCC		
		— — C		
GAM2411 MAWBP	3'	CCCAGGAGGCAGAAGTTGCAGT 42381	AC CA C	
GA		TCACTGCAA TC CCTCC GGG		

			AGTGACGTT AG GGAGG CCC		
			GA AC A		
GAM2411	MCAM	3'	CCAGGAGGTGGAGCTTGCAGTG 22459	A	C
	A		TCACTGCAA CTCCACCTCC GG		
			AGTGACGTT GAGGTGGAGG CC		
			C A		
GAM2411	MESDC2	3'	CCCGGGAGGCGGAGGTTGCAGT 72911	A	A
	GA		TCACTGCAA CTCC CCTCCCGGG		
			AGTGACGTT GAGG GGAGGGCCC		
			G C		
GAM2411	MGC10200	3'	GAGGTGGAGGTTGCAGTGA 59646	A	
			TCACTGCAA CTCCACCTC		
			AGTGACGTT GAGGTGGAG		
			G		
GAM2411	MGC10765	3'	CCCGGGAGGCAGAGGGTGCAGT 44558	AA	CA
			ACTGCA CTC CCTCCCGGG		
			TGACGT GAG GGAGGGCCC		
			GG AC		
GAM2411	MGC10771	3'	GAGGCAGAGGTTGCAGTGA 44714	A	CA
			TCACTGCAA CTC CCTC		
			AGTGACGTT GAG GGAG		
			G AC		
GAM2411	MGC10814	3'	CCCGGGAGGTGGAGGTTGCGGT 52017	A	
	GA		TCACTGCAA CTCCACCTCCCGGG		
			AGTGGCGTT GAGGTGGAGGGCCC		
			G		
GAM2411	MGC10999	3'	AGGTGGAGGTTGCAGTGA 51190	A	
			TCACTGCAA CTCCACCT		
			AGTGACGTT GAGGTGGA		
			G		
GAM2411	MGC10999	3'	CCCAGGGGTTTGAGGCTGCAGT 51192	AA	C_ T C
	GA		TCACTGCA CTC ACC CC GGG		
			AGTGACGT GAG TGG GG CCC		
			CG TT _ A		
GAM2411	MGC11352	3'	CCCAGGAGGCGGAGCTTGCAGT 65429	A	A C
	GA		TCACTGCAA CTCC CCTCC GGG		
			AGTGACGTT GAGG GGAGG CCC		
			C C A		
GAM2411	MGC11386	3'	GAGGCGGAGGTTGCAGTGA 53066	A	A
			TCACTGCAA CTCC CCTC		

		AGTGACGTT GAGG GGAG	
		G C	
GAM2411	MGC12945 3'	CCCAGGAAGCGGAGGTTGCAGT 51265	A ACC C
	GA	TCACTGCAA CTCC TCC GGG	
		AGTGACGTT GAGG AGG CCC	
		G CGA A	
GAM2411	MGC13053 3'	CCCGGGGGGCGGAGGTTGCAGT 52104	A A
	GA	TCACTGCAA CTCC CCTCCCGGG	
		AGTGACGTT GAGG GGGGGGCCC	
		G C	
GAM2411	MGC13053 3'	CCCGGGGGGTGGAGCCTGCAGT 52105	AA
	GA	TCACTGCA CTCCACCTCCCGGG	
		AGTGACGT GAGGTGGGGGGCCC	
		CC	
GAM2411	MGC14407 3'	CCCAGGAGGCAGAGGTTGCAGT 52972	A CA C
	GA	TCACTGCAA CTC CCTCC GGG	
		AGTGACGTT GAG GGAGG CCC	
		G AC A	
GAM2411	MGC14436 3'	CCCGGGAGGCGGAGCTTACAGT 52925	C A A
	GA	TCACTG AA CTCC CCTCCCGGG	
		AGTGAC TT GAGG GGAGGGCCC	
		A C C	
GAM2411	MGC16037 3'	CCCGGGAGGCAGAGGTTGCAGT 52892	A CA
	GA	TCACTGCAA CTC CCTCCCGGG	
		AGTGACGTT GAG GGAGGGCCC	
		G AC	
GAM2411	MGC16175 3'	CCTGGGAGGCGGAGCTTGCAGT 52276	A A
		ACTGCAA CTCC CCTCCCGGG	
		TGACGTT GAGG GGAGGGTCC	
		C C	
GAM2411	MGC16384 3'	GCCCAGGAGGTCAGGTCAAGGC 54934	AA ____ C ____
	TGCAGTGA	TCACTGCA CT CC ACCTCC GGG C	
		AGTGACGT GA GG TGGAGG CCC G	
		CG ACT AC A ____	
GAM2411	MGC16703 3'	CCCGGGAGGCAGAGCTTGCAGT 73492	A CA
	GA	TCACTGCAA CTC CCTCCCGGG	
		AGTGACGTT GAG GGAGGGCCC	
		C AC	
GAM2411	MGC20235 3'	AGGCAGAGGTTGCAGTGA 59548	A CA
		TCACTGCAA CTC CCT	

		AGTGACGTT GAG GGA	
		G AC	
GAM2411	MGC23244	3' GAGGCGGAGGTTGCAGTGA 58832	A A
		TCACTGCAA CTCC CCTC	
		AGTGACGTT GAGG GGAG	
		G C	
GAM2411	MGC2562	3' CCCAGCAGGCAGAGGTTGCAGT 51436	A CA CCC
	GA	TCACTGCAA CTC CCT GGG	
		AGTGACGTT GAG GGA CCC	
		G AC CGA	
GAM2411	MGC2562	3' CCCAGGAGGCGGAGGTTGCAGT 51437	A A C
	GA	TCACTGCAA CTCC CCTCC GGG	
		AGTGACGTT GAGG GGAGG CCC	
		G C A	
GAM2411	MGC2562	3' CCCGGTAGGTGGAGGTTGCAGT 51438	A C
	GA	TCACTGCAA CTCCACCT CCGGG	
		AGTGACGTT GAGGTGGA GGCCC	
		G T	
GAM2411	MGC2663	3' CCCAGGAAGCAGAGGTTGCAGT 44333	A CACC C
	GA	TCACTGCAA CTC TCC GGG	
		AGTGACGTT GAG AGG CCC	
		G ACGA A	
GAM2411	MGC26641	3' GAAGTGGAAGCTGCAGTGA 59323	AAC C
		TCACTGCA TCCAC TC	
		AGTGACGT AGGTG AG	
		CGA A	
GAM2411	MGC26877	5' GAGGCAGAGGTTGCAGTGA 58891	A CA
		TCACTGCAA CTC CCTC	
		AGTGACGTT GAG GGAG	
		G AC	
GAM2411	MGC29891	3' CCCGGGAGGCGGAGGTTGCAGT 58858	A A
	GA	TCACTGCAA CTCC CCTCCCGGG	
		AGTGACGTT GAGG GGAGGGCCC	
		G C	
GAM2411	MGC29891	3' GAGGTGGAGGTTGCAGTGA 58863	A
		TCACTGCAA CTCCACCTC	
		AGTGACGTT GAGGTGGAG	
		G	
GAM2411	MGC3169	3' GAGGTGGAGGTTGCAGTGA 44187	A
		TCACTGCAA CTCCACCTC	

			AGTGACGTT GAGGTGGAG		
			G		
GAM2411	MGC3207	3'	CTGGGAGGCAGAGCTTGCAGTG 63237	A	CA
	A		TCACTGCAA CTC CCTCCCGG		
			AGTGACGTT GAG GGAGGGTC		
			C AC		
GAM2411	MGC3329	3'	GAGGTGGAGGTTGCAGTGA 44247	A	
			TCACTGCAA CTCCACCTC		
			AGTGACGTT GAGGTGGAG		
			G		
GAM2411	MGC4562	3'	CCCAGGAAGAGGAGGTTGCAGT 56737	A	ACC C
	GA		TCACTGCAA CTCC TCC GGG		
			AGTGACGTT GAGG AGG CCC		
			G AGA A		
GAM2411	MGC4663	3'	CCCGGGAGGCGGAGCTTTCAGT 44785	C	_ A
	GA		TCACTG AAA CTCC CCTCCCGGG		
			AGTGAC TTT GAGG GGAGGGCCC		
			_ C C		
GAM2411	MGC4840	3'	CCCAGGAGGTGGAGGTTGCAGT 72019	A	C
	GA		TCACTGCAA CTCCACCTCC GGG		
			AGTGACGTT GAGGTGGAGG CCC		
			G A		
GAM2411	MGC5457	3'	CCCAGCAGATGGAGGTTGCAGT 51938	A	C CCC
	GA		TCACTGCAA CTCCA CT GGG		
			AGTGACGTT GAGGT GA CCC		
			G A CGA		
GAM2411	MKRN4	3'	CCTGGGAGGCGGAGCTTGCAAT 48459	C	A A
	GA		TCA TGCAA CTCC CCTCCCGGG		
			AGT ACGTT GAGG GGAGGGTCC		
			A C C		
GAM2411	MRP63	3'	CCTCCCGGGGAAGCGGAGGTTG 44044	A	A_____ TCCC
	CAGTGA		TCACTGCAA CTCC CC GG		
			AGTGACGTT GAGG GG CC		
			G CGAAG__G CCCT		
GAM2411	MRP63	3'	GAGGCAGAGGTTGCAATGA 44045	C	A CA
			TCA TGCAA CTC CCTC		
			AGT ACGTT GAG GGAG		
			A G AC		
GAM2411	MRPL48	5'	CCCGAGAGGCGGAGGTGGCAGT 32657	AAA	A C
	GA		TCACTGC CTCC CCTC CGGG		

			AGTGACG GAGG GGAG GCCC		
			GTG C A		
GAM2411	MRPL56	3'	CCCAGGAGGTGGAGTTGCAGT 52754	A	C
			ACTGCAA CTCCACCTCC GGG		
			TGACGTT GAGGTGGAGG CCC		
			— A		
GAM2411	MRPS18B	3'	CCCAGGAGGCGGAGGTTCAGT 26749	A	A C
	GA		TCACTGCAA CTCC CCTCC GGG		
			AGTGACGTT GAGG GGAGG CCC		
			G C A		
GAM2411	N4BP2	3'	GAGGTGGAGGTTCAGTGA 36941	A	
			TCACTGCAA CTCCACCTC		
			AGTGACGTT GAGGTGGAG		
			G		
GAM2411	NMNAT	3'	CCCAGGTGGTGGAGGTTCAGT 43285	A	T C
	GA		TCACTGCAA CTCCACC CC GGG		
			AGTGACGTT GAGGTGG GG CCC		
			G T A		
GAM2411	NPTXR	3'	CTGAGGAGGTGGAGGTTCAGT 27433	A	—
	GA		TCACTGCAA CTCCACCTCC CGG		
			AGTGACGTT GAGGTGGAGG GTC		
			G A		
GAM2411	NPTXR	3'	CTGAGGAGGTGGAGGTTCAGT 55210	A	—
	GA		TCACTGCAA CTCCACCTCC CGG		
			AGTGACGTT GAGGTGGAGG GTC		
			G A		
GAM2411	Nup43	3'	CCCGGGAGGCAGAGGTTCAGT 45345	A	CA
	GA		TCACTGCAA CTC CCTCCCGGG		
			AGTGACGTT GAG GGAGGGCCC		
			G AC		
GAM2411	ORC6L	3'	TGGGAGGCAGAGGTTCAGTGA 27497	A	CA
			TCACTGCAA CTC CCTCCCG		
			AGTGACGTT GAG GGAGGGT		
			G AC		
GAM2411	PAFAH2	3'	GAGGCGGAGGTTCAGTGA 6503	A	A
			TCACTGCAA CTCC CCTC		
			AGTGACGTT GAGG GGAG		
			G C		
GAM2411	PB1	3'	CCCAGGAGGCAGAGGTTCAGT 37575	A	CA C
	GA		TCACTGCAA CTC CCTCC GGG		

			AGTGACGTT GAG GGAGG CCC		
			G AC A		
GAM2411	PB1	3'	GAGGCGGAGGCTGCAGTGA 37577	AA	A
			TCACTGCA CTCC CCTC		
			AGTGACGT GAGG GGAG		
			CG C		
GAM2411	PDCD7	3'	CCCAGGAGGCAGAGCTTGCAGT 72601	A	CA C
	GA		TCACTGCAA CTC CCTCC GGG		
			AGTGACGTT GAG GGAGG CCC		
			C AC A		
GAM2411	phorbolin-1	3'	CCCGGGAGGCAGAGCTTGCGGT 90207	A	CA
	GA		TCACTGCAA CTC CCTCCCGGG		
			AGTGGCGTT GAG GGAGGGCCC		
			C AC		
GAM2411	PIP5K2B	3'	CCCAGGAGGCGGAGGTTGCGGT 57690	A	A C
	GA		TCACTGCAA CTCC CCTCC GGG		
			AGTGGCGTT GAGG GGAGG CCC		
			G C A		
GAM2411	PIWIL2	3'	CCCGGGAGGTGGAGGTTGCAGT 36542	A	
	GA		TCACTGCAA CTCCACCTCCCGGG		
			AGTGACGTT GAGGTGGAGGGCCC		
			G		
GAM2411	PNPASE	3'	CCCAGGAGGTGGAGGTTGTAGT 71437	A	C
	GA		TCACTGCAA CTCCACCTCC GGG		
			AGTGATGTT GAGGTGGAGG CCC		
			G A		
GAM2411	POFUT1	3'	GAGGTGGAGGTTGCAGTGA 70978	A	
			TCACTGCAA CTCCACCTC		
			AGTGACGTT GAGGTGGAG		
			G		
GAM2411	PPP1R3B	3'	CCCAGGAGGTGGAGGTTGCAGT 45137	A	C
	GA		TCACTGCAA CTCCACCTCC GGG		
			AGTGACGTT GAGGTGGAGG CCC		
			G A		
GAM2411	PPP1R3B	3'	CCTGGGAGGCGGAGCTTACAGT 45140	C	A A
	GA		TCACTG AA CTCC CCTCCCGGG		
			AGTGAC TT GAGG GGAGGGTCC		
			A C C		
GAM2411	PRO0255	3'	GAGATGGAGGTTGCAGTGA 26967	A	C
			TCACTGCAA CTCCA CTC		

			AGTGACGTT GAGGT GAG	
			G A	
GAM2411	PRO0478	3'	CCCAGAAGTTTGAGGCTGCAGT 27028	AA C_ C CC
	GA		TCACTGCA CTC AC TC GGG	
			AGTGACGT GAG TG AG CCC	
			CG TT A A_	
GAM2411	PRO0478	3'	CCCGGGAGGCATAGCTTGCAGT 27029	A CCA
	GA		TCACTGCAA CT CCTCCCGGG	
			AGTGACGTT GA GGAGGGCCC	
			C TAC	
GAM2411	PRO0618	3'	CCCGGGAGGCAGAGGTTGCAGT 27051	A CA
	GA		TCACTGCAA CTC CCTCCCGGG	
			AGTGACGTT GAG GGAGGGCCC	
			G AC	
GAM2411	PRO1048	5'	CCCAGGAGGCAGAGCTTGCAGT 38107	A CA C
	GA		TCACTGCAA CTC CCTCC GGG	
			AGTGACGTT GAG GGAGG CCC	
			C AC A	
GAM2411	PRO1048	3'	CCCGGGAGGCAGAGCTTGTGGT 38108	TG A CA
	GA		TCAC CAA CTC CCTCCCGGG	
			AGTG GTT GAG GGAGGGCCC	
			GT C AC	
GAM2411	PRO1048	5'	CCCGGGAGGTCAAGGTTGCAGT 38109	A CC
	GA		TCACTGCAA CT ACCTCCCGGG	
			AGTGACGTT GA TGGAGGGCCC	
			G AC	
GAM2411	PRO2015	3'	CCCGGGAGGCGGAGGTTGTAGT 38159	A A
	GA		TCACTGCAA CTCC CCTCCCGGG	
			AGTGATGTT GAGG GGAGGGCCC	
			G C	
GAM2411	PRO2198	5'	GAGGCGGAGGTTGCAGTGA 38407	A A
			TCACTGCAA CTCC CCTC	
			AGTGACGTT GAGG GGAG	
			G C	
GAM2411	PRO2730	3'	CCCAGGAGGCGGAGGTTGCGGT 48182	A A C
	GA		TCACTGCAA CTCC CCTCC GGG	
			AGTGGCGTT GAGG GGAGG CCC	
			G C A	
GAM2411	PRO2893	3'	CCCGGGAGGTGGAGGTTGCAGT 38432	A
	GA		TCACTGCAA CTCCACCTCCCGGG	

			AGTGACGTT GAGGTGGAGGGCCC	
			G	
GAM2411	PRO2964	3'	CCCGGGAGGCGGAGCTTGCAGT 38257	A A
	GA		TCACTGCAA CTCC CCTCCCGGG	
			AGTGACGTT GAGG GGAGGGCCC	
			C C	
GAM2411	PRPF4	3'	GAGGCAGAGGTTGCAGTGA 17466	A CA
			TCACTGCAA CTC CCTC	
			AGTGACGTT GAG GGAG	
			G AC	
GAM2411	PSP1	3'	CCCGAAGTTCAGCTTGCAGTG 37457	A CC CTCC
			CACTGCAA CT AC CGGG	
			GTGACGTT GA TG GCCC	
			C CT AA__	
GAM2411	PSR	3'	CCCAGGAGGCAGAGGTTGCAGT 65783	A CA C
	GA		TCACTGCAA CTC CCTCC GGG	
			AGTGACGTT GAG GGAGG CCC	
			G AC A	
GAM2411	PTK6	3'	CCCGGGAGGTGGAGCTTGCAGT 21071	A
	GA		TCACTGCAA CTCCACCTCCCGGG	
			AGTGACGTT GAGGTGGAGGGCCC	
			C	
GAM2411	PTRF	3'	CCCAGGAGTTTGAGGCTGCAGT 64236	AA CAC C
	GA		TCACTGCA CTC CTCC GGG	
			AGTGACGT GAG GAGG CCC	
			CG TTT A	
GAM2411	PTRF	3'	GAGGTGGAGGTTGCAGTGA 64241	A
			TCACTGCAA CTCCACCTC	
			AGTGACGTT GAGGTGGAG	
			G	
GAM2411	R32184_3	3'	TTGGTAGGTCTGCAGTGA 54202	AACTCC C
			TCACTGCA ACCT CCGG	
			AGTGACGT TGGA GGTT	
			C_____ T	
GAM2411	Rabip4R	3'	CCCGGGAAGCAGAGGTTGCAGT 36276	A CACC
	GA		TCACTGCAA CTC TCCCGGG	
			AGTGACGTT GAG AGGGCCC	
			G ACGA	
GAM2411	RAD51	3'	AGGTGGAAGTTGCAGTGA 56829	AC
			TCACTGCAA TCCACCT	

			AGTGACGTT AGGTGGA		
			GA		
GAM2411	RAD51	3'	AGGTGGAAGTTGCAGTGA 12745	AC	
			TCACTGCAA TCCACCT		
			AGTGACGTT AGGTGGA		
			GA		
GAM2411	RHOBTB3	3'	GAGGTGGAAGTTGCAGTGA 30426	AC	
			TCACTGCAA TCCACCTC		
			AGTGACGTT AGGTGGAG		
			GA		
GAM2411	RNO2	5'	CCCGGGAGGCGGAGGTTGTGG 53930	TG A A	
			C CAA CTCC CCTCCCGGG		
			G GTT GAGG GGAGGGCCC		
			GT G C		
GAM2411	RoXaN	3'	CCCAGGAGGCACAGTTTGCAGT 47282	CCA C	
	GA		TCACTGCAA ACT CCTCC GGG		
			AGTGACGTTTGA GGAGG CCC		
			CAC A		
GAM2411	Rpo1-2	3'	CCCAAGAGGTCGAGGCTGCAGT 39216	AA C CC	
	GA		TCACTGCA CTC ACCTC GGG		
			AGTGACGT GAG TGGAG CCC		
			CG C AA		
GAM2411	RRP4	3'	GAGGCGGAGGTTGCAGTGA 27356	A A	
			TCACTGCAA CTCC CCTC		
			AGTGACGTT GAGG GGAG		
			G C		
GAM2411	SAMHD1	3'	GAGGCAGAGGTTGCAGTGA 61986	A CA	
			TCACTGCAA CTC CCTC		
			AGTGACGTT GAG GGAG		
			G AC		
GAM2411	SAMHD1	3'	GAGGCGGAGGTTGCAGTGA 61987	A A	
			TCACTGCAA CTCC CCTC		
			AGTGACGTT GAGG GGAG		
			G C		
GAM2411	SC65	3'	CCCAGGAGGCGGAGCTTGCAGT 22292	A A C	
	GA		TCACTGCAA CTCC CCTCC GGG		
			AGTGACGTT GAGG GGAGG CCC		
			C C A		
GAM2411	SCIN	3'	CCCAGGAGGCTGAGGTTGCAGT 53602	A CA C	
	GA		TCACTGCAA CTC CCTCC GGG		

			AGTGACGTT GAG GGAGG CCC		
			G TC A		
GAM2411	SCN12A	3'	GAGACGGAGGTTGCAGTGA 27081	A	AC
			TCACTGCAA CTCC CTC		
			AGTGACGTT GAGG GAG		
			G CA		
GAM2411	SCYA5	3'	CCCAGGAGGTGGAGGCTGCAGT 12965	AA	C
	GA		TCACTGCA CTCCACCTCC GGG		
			AGTGACGT GAGGTGGAGG CCC		
			CG A		
GAM2411	SCYA5	3'	CCCGGGAGCGGAGCTTGCAGTG 12966	A	AC
	A		TCACTGCAA CTCC CTCCCGGG		
			AGTGACGTT GAGG GAGGGCCC		
			C C_		
GAM2411	SEMA3E	3'	CCCGGGAAGCGGAGCTTGCAGT 25805	A	ACC
	GA		TCACTGCAA CTCC TCCCGGG		
			AGTGACGTT GAGG AGGGCCC		
			C CGA		
GAM2411	SGKL	3'	CCCACGAGATGGAAGTTGCAGT 26057	AC	C CC
	GA		TCACTGCAA TCCA CTC GGG		
			AGTGACGTT AGGT GAG CCC		
			GA A CA		
GAM2411	SGKL	3'	CCCGGGAGGCGGAGGTTGCAGT 26058	A	A
	GA		TCACTGCAA CTCC CCTCCCGGG		
			AGTGACGTT GAGG GGAGGGCCC		
			G C		
GAM2411	SLC7A11	3'	CCCGGGAGGCGGAGGTTGCAGT 27531	A	A
	GA		TCACTGCAA CTCC CCTCCCGGG		
			AGTGACGTT GAGG GGAGGGCCC		
			G C		
GAM2411	SMA3	3'	CCTGGGAGGCAGAGTCTGCAGT 23260	A	CA
	GA		TCACTGCA ACTC CCTCCCGGG		
			AGTGACGT TGAG GGAGGGTCC		
			C AC		
GAM2411	SMAP-5	3'	CCCAGGAGGCGGAGCTTGCAGT 48658	A	A C
	GA		TCACTGCAA CTCC CCTCC GGG		
			AGTGACGTT GAGG GGAGG CCC		
			C C A		
GAM2411	SPRY4	3'	CCCGGGAGGTGGAGGTTACAGT 49009	CAAA	
	GA		TCACTG CTCCACCTCCCGGG		

			AGTGAC GAGGTGGAGGGCCC		
			ATTG		
GAM2411	SPTLC2	3'	CCCAGGAGGCGGAGGTTGCAGT 17988	A A C	
	GA		TCACTGCAA CTCC CCTCC GGG		
			AGTGACGTT GAGG GGAGG CCC		
			G C A		
GAM2411	SSR3	3'	CCCAGGAGGCAGAGGTTGCAGT 24032	A CA C	
	GA		TCACTGCAA CTC CCTCC GGG		
			AGTGACGTT GAG GGAGG CCC		
			G AC A		
GAM2411	TA-LRRP	3'	GAGGTGGAGGTTGCAGTGA 31713	A	
			TCACTGCAA CTCCACCTC		
			AGTGACGTT GAGGTGGAG		
			G		
GAM2411	TACTILE	3'	CCCGGGAGGCAGAGCTTGCAGT 20584	A CA	
	GA		TCACTGCAA CTC CCTCCCGGG		
			AGTGACGTT GAG GGAGGGCCC		
			C AC		
GAM2411	TADA3L	3'	GAGGCGGAGGTTGCAGTGA 56808	A A	
			TCACTGCAA CTCC CCTC		
			AGTGACGTT GAGG GGAG		
			G C		
GAM2411	TAF9L	5'	CCCGCAGGGGTGGAGCCTGAGC 32560	A G AA C_	
	GA		TC CT CA CTCCACCTC CGGG		
			AG GA GT GAGGTGGGG GCCC		
			C _ CC AC		
GAM2411	THEA	3'	TGGGAGGTGGAGGCTGCAGTGA 66901	AA	
			TCACTGCA CTCCACCTCCCG		
			AGTGACGT GAGGTGGAGGGT		
			CG		
GAM2411	TIP47	3'	GAGGCGGAGGTTGCAGTGA 20603	A A	
			TCACTGCAA CTCC CCTC		
			AGTGACGTT GAGG GGAG		
			G C		
GAM2411	TRIAD3	3'	GAGGCAGAGGTTGCAGTGA 96134	A CA	
			TCACTGCAA CTC CCTC		
			AGTGACGTT GAG GGAG		
			G AC		
GAM2411	TU12B1-TY	5'	CCCGGGAGGCGAAGAGAAGCA 33842	AAA CA__	
			TGC CTC CCTCCCGGG		

		ACG GAG GGAGGGCCC		
		AA_ AAGC		
GAM2411	UBCE7IP5	3' GAGGCAGAGGTTGCAGTGA	30847	A CA
		TCACTGCAA CTC CCTC		
		AGTGACGTT GAG GGAG		
		G AC		
GAM2411	UST	3' CCCAGGAGTTTGAGGTTGCAGT	20351	A CAC C
	GA	TCACTGCAA CTC CTCC GGG		
		AGTGACGTT GAG GAGG CCC		
		G TTT A		
GAM2411	VPS4B	3' GAGGCAGAGGTTGCAGTGA	18022	A CA
		TCACTGCAA CTC CCTC		
		AGTGACGTT GAG GGAG		
		G AC		
GAM2411	WBSCR23	5' CCCAGGAATTGGAGGCTGCAGT	47428	AA CC C
	GA	TCACTGCA CTCCA TCC GGG		
		AGTGACGT GAGGT AGG CCC		
		CG TA A		
GAM2411	WBSCR23	3' CCCAGGAGTTCAAGTCTGCAGT	47429	A CCAC C
	GA	TCACTGCA ACT CTCC GGG		
		AGTGACGT TGA GAGG CCC		
		C ACTT A		
GAM2411	WSB1	3' CCCAGGAGGTGGAGGTTGCAGT	56971	A C
		ACTGCAA CTCCACCTCC GGG		
		TGACGTT GAGGTGGAGG CCC		
		G A		
GAM2411	WSB1	3' CCCAGGAGGTGGAGGTTGCAGT	56990	A C
		ACTGCAA CTCCACCTCC GGG		
		TGACGTT GAGGTGGAGG CCC		
		G A		
GAM2411	YME1L1	3' CCCAGGAGGTGGAGGTTGCAGT	58430	A C
	GA	TCACTGCAA CTCCACCTCC GGG		
		AGTGACGTT GAGGTGGAGG CCC		
		G A		
GAM2411	YME1L1	3' GAGATGGAGGTTGCAGTGA	58434	A C
		TCACTGCAA CTCCA CTC		
		AGTGACGTT GAGGT GAG		
		G A		
GAM2411	YME1L1	3' CCCAGGAGGTGGAGGTTGCAGT	27320	A C
	GA	TCACTGCAA CTCCACCTCC GGG		

			AGTGACGTT GAGGTGGAGG CCC	
			G A	
GAM2411	YME1L1	3'	GAGATGGAGGTTGCAGTGA 27321	A C
			TCACTGCAA CTCCA CTC	
			AGTGACGTT GAGGT GAG	
			G A	
GAM2411	ZAK	3'	CCCGGGAGGCAGAGGTTGCAGT 56940	A CA
	GA		TCACTGCAA CTC CCTCCCGGG	
			AGTGACGTT GAG GGAGGGCCC	
			G AC	
GAM2411	ZFD25	3'	GAGGCGAAGATTGCAGTGA 33111	A CCA
			TCACTGCAA CT CTC	
			AGTGACGTT GA GGAG	
			A AGC	
GAM2411	ZFP106	3'	CCCGGGAGGCAGAGATTGCAGT 42722	A CA
			ACTGCAA CTC CCTCCCGGG	
			TGACGTT GAG GGAGGGCCC	
			A AC	
GAM2411	ZFP106	3'	CCCTGGAGGTAGAAGTTGCAGT 42724	AC C C
	GA		TCACTGCAA TC ACCTCC GGG	
			AGTGACGTT AG TGGAGG CCC	
			GA A T	
GAM2411	ZIM3	3'	GAGGTAGAGGTTGCAGTGA 54638	A C
			TCACTGCAA CTC ACCTC	
			AGTGACGTT GAG TGGAG	
			G A	
GAM2411	ZNF271	3'	CCCAGGAGTTTGAGGCTGCAGT 96963	AA CAC C
	GA		TCACTGCA CTC CTCC GGG	
			AGTGACGT GAG GAGG CCC	
			CG TTT A	
GAM2411	ZNF297B	5'	CCCAAGAGTTCAAGGCTGCAGT 26653	AA CCAC CC
	GA		TCACTGCA CT CTC GGG	
			AGTGACGT GA GAG CCC	
			CG ACTT AA	
GAM2411	ZNF297B	3'	GAGGCGGAGGTTGCAGTGA 26658	A A
			TCACTGCAA CTCC CTC	
			AGTGACGTT GAGG GGAG	
			G C	
GAM2411	ZNF333	3'	CCCAGGAGGCAGAGGTTGCAGT 51591	A CA C
	GA		TCACTGCAA CTC CCTCC GGG	

		AGTGACGTT GAG GGAGG CCC	
		G AC A	
GAM2411 ZNF347	3'	CCCAGGAGGCGGAGGTTGCAGT 51823	A A C
	GA	TCACTGCAA CTCC CCTCC GGG	
		AGTGACGTT GAGG GGAGG CCC	
		G C A	
GAM2411 LOC112687	3'	CCCAGGAGATGGAGGTTGCAGT 73229	A C C
	GA	TCACTGCAA CTCCA CTCC GGG	
		AGTGACGTT GAGGT GAGG CCC	
		G A A	
GAM2411 LOC114987	3'	CCCAGGAGGCGGAGGTTGCGGT 59794	A A C
	GA	TCACTGCAA CTCC CCTCC GGG	
		AGTGGCGTT GAGG GGAGG CCC	
		G C A	
GAM2411 LOC115129	5'	CCCAGGAGACAGGTTGCAGTGA 73614	A CCAC C
		TCACTGCAA CT CTCC GGG	
		AGTGACGTT GA GAGG CCC	
		G CA__ A	
GAM2411 LOC115129	3'	CCCAGGAGGTGGTGGTTGCAGT 73615	ACT C
	GA	TCACTGCAA CCACCTCC GGG	
		AGTGACGTT GGTGGAGG CCC	
		GGT A	
GAM2411 LOC115129	5'	GAGGTGGAGGTTGCAGCGA 73618	A A
		TC CTGCAA CTCCACCTC	
		AG GACGTT GAGGTGGAG	
		C G	
GAM2411 LOC115196	3'	CCCGGGAGGTGGAGCTTGCAGT 73655	A
	GA	TCACTGCAA CTCCACCTCCCGGG	
		AGTGACGTT GAGGTGGAGGGCCC	
		C	
GAM2411 LOC115273	3'	GAGGCAGAGATTGCAGTGA 73751	A CA
		TCACTGCAA CTC CCTC	
		AGTGACGTT GAG GGAG	
		A AC	
GAM2411 LOC115761	3'	CCCAAGAGGTAGAGGTTGCAGT 93397	A C CC
	GA	TCACTGCAA CTC ACCTC GGG	
		AGTGACGTT GAG TGGAG CCC	
		G A AA	
GAM2411 LOC116143	3'	CCCAGGAGGTGGAGATTGCAGT 74181	A C
	GA	TCACTGCAA CTCCACCTCC GGG	

		AGTGACGTT GAGGTGGAGG CCC		
		A A		
GAM2411	LOC116143 3'	CCCGGGAGGCGGAGGTTGCAGT 74182	A	A
	GA	TCACTGCAA CTCC CCTCCCGGG		
		AGTGACGTT GAGG GGAGGGCCC		
		G C		
GAM2411	LOC116236 3'	CCCGGGAGGCGGAGCTTGCAGT 74241	A	A
	GA	TCACTGCAA CTCC CCTCCCGGG		
		AGTGACGTT GAGG GGAGGGCCC		
		C C		
GAM2411	LOC116349 3'	CCCGGGAGGCGGAGCTTGCAGT 74273	A	A
	GA	TCACTGCAA CTCC CCTCCCGGG		
		AGTGACGTT GAGG GGAGGGCCC		
		C C		
GAM2411	LOC119180 3'	CCCCGGGCCCTAGGGTTTGCAG 74405	CA_____	TCCC
	TGA	TCACTGCAA ACTC CC G		
		AGTGACGTTTGGG GG C		
		ATCCC__G CCCT		
GAM2411	LOC120406 3'	GAGGTGGAGGTTGCAGTGA 76065	A	
		TCACTGCAA CTCCACCTC		
		AGTGACGTT GAGGTGGAG		
		G		
GAM2411	LOC121219 5'	CCCTGGAAAGTTTGCAG 74485	CCACC	C
		CTGCAA ACT TCC GGG		
		GACGTTTGA AGG CCC		
		A__ T		
GAM2411	LOC122704 3'	GAGGTAGAGGTTGCAGTGA 74606	A	C
		TCACTGCAA CTC ACCTC		
		AGTGACGTT GAG TGGAG		
		G A		
GAM2411	LOC126282 3'	CCCAGGAGTTAAGAGGCTGCAG 74952	AA	CAC_ C
	TGA	TCACTGCA CTC CTCC GGG		
		AGTGACGT GAG GAGG CCC		
		CG AATT A		
GAM2411	LOC126282 3'	GAGGCGGAGGTTGCAGTGA 74959	A	A
		TCACTGCAA CTCC CCTC		
		AGTGACGTT GAGG GGAG		
		G C		
GAM2411	LOC126297 5'	GAGGTGGAGGTTGCAGTGA 74978	A	
		TCACTGCAA CTCCACCTC		

		AGTGACGTT GAGGTGGAG			
		G			
GAM2411	LOC126669 3'	CCCAGGAGGTGGAGGTTGCAGT 75929	A	C	
	GA	TCACTGCAA CTCCACCTCC GGG			
		AGTGACGTT GAGGTGGAGG CCC			
		G A			
GAM2411	LOC127262 3'	CCCAGGAGGCGGAGGTTGCAGT 76595	A	A	C
	GA	TCACTGCAA CTCC CCTCC GGG			
		AGTGACGTT GAGG GGAGG CCC			
		G C A			
GAM2411	LOC130026 3'	CCCGGGAGGCGGAGCTTGCAGT 57435	A	A	
	GA	TCACTGCAA CTCC CCTCCCGGG			
		AGTGACGTT GAGG GGAGGGCCC			
		C C			
GAM2411	LOC130535 3'	CCCAGGAGGCAGAAGTTGCAGT 76649	AC	CA	C
	GA	TCACTGCAA TC CCTCC GGG			
		AGTGACGTT AG GGAGG CCC			
		GA AC A			
GAM2411	LOC130535 3'	CCCGGGAGGCAGAGGTTGCTGT 76650	T	A	CA
		AC GCAA CTC CCTCCCGGG			
		TG CGTT GAG GGAGGGCCC			
		T G AC			
GAM2411	LOC130589 3'	GAGGTGGAGGTTGCAGTGA 57932	A		
		TCACTGCAA CTCCACCTC			
		AGTGACGTT GAGGTGGAG			
		G			
GAM2411	LOC131744 3'	CTGGGGAGGCAGAGGTTGCAGT 76390	A	CA	G
	GA	TCACTGCAA CTC CCTCCC GG			
		AGTGACGTT GAG GGAGGG TC			
		G AC G			
GAM2411	LOC131965 3'	CCCAAGAGGCGGAGACTGCAGT 75521	AA	A	CC
	GA	TCACTGCA CTCC CCTC GGG			
		AGTGACGT GAGG GGAG CCC			
		CA C AA			
GAM2411	LOC133926 3'	CCCAGGAGGCAGAGGTTGCAGT 75630	A	CA	C
	GA	TCACTGCAA CTC CCTCC GGG			
		AGTGACGTT GAG GGAGG CCC			
		G AC A			
GAM2411	LOC134147 3'	CCCAGGAGGTGGAGACTGCAGT 57957	AA		C
	GA	TCACTGCA CTCCACCTCC GGG			

	AGTGACGT GAGGTGGAGG CCC		
	CA A		
GAM2411 LOC134147 3'	GAGGCAGAGGTTGCAGTGA 57960	A CA	
	TCACTGCAA CTC CCTC		
	AGTGACGTT GAG GGAG		
	G AC		
GAM2411 LOC135154 3'	CCCAGGAGGTGGAGGTTGCGGT 75727	A C	
GA	TCACTGCAA CTCCACCTCC GGG		
	AGTGGCGTT GAGGTGGAGG CCC		
	G A		
GAM2411 LOC135818 3'	CCCAGGAGTCAAAAGCTGCAGT 75745	AACTCCAC C	
GA	TCACTGCA CTCC GGG		
	AGTGACGT GAGG CCC		
	CGAAAACT A		
GAM2411 LOC137362 3'	GAGGCGAAGGTTGCAGTGA 75785	A CCA	
	TCACTGCAA CT CCTC		
	AGTGACGTT GA GGAG		
	G AGC		
GAM2411 LOC137829 3'	CCTGGCAGAAGTTTGCAG 75797	CCAC C	
	CTGCAAAC CT CCGGG		
	GACGTTTGA GA GGTCC		
	A__ C		
GAM2411 LOC138389 3'	CCCTGGAGGCAGAGGTTGCAGT 76731	A CA C	
GA	TCACTGCAA CTC CCTCC GGG		
	AGTGACGTT GAG GGAGG CCC		
	G AC T		
GAM2411 LOC139422 3'	CCCGGGAGGCGGAGCTTGCAGT 76345	A A	
GA	TCACTGCAA CTCC CCTCCCGGG		
	AGTGACGTT GAGG GGAGGGCCC		
	C C		
GAM2411 LOC142948 3'	CCCGGGAGGTGGAGCTTGCAGT 83774	A	
GA	TCACTGCAA CTCCACCTCCCGGG		
	AGTGACGTT GAGGTGGAGGGCCC		
	C		
GAM2411 LOC143310 3'	CCCGGGAGGTGGAGCTTGCAGT 77042	A	
GA	TCACTGCAA CTCCACCTCCCGGG		
	AGTGGCGTT GAGGTGGAGGGCCC		
	C		
GAM2411 LOC143465 3'	CCCAGGAGGTGGAGGTTGCAGT 83871	A C	
GG	TCACTGCAA CTCCACCTCC GGG		

		GGTGACGTT GAGGTGGAGG CCC		
		G A		
GAM2411	LOC143888 3'	GAGGCAGAGGTTGCAGTGA 77172	A	CA
		TCACTGCAA CTC CCTC		
		AGTGACGTT GAG GGAG		
		G AC		
GAM2411	LOC143943 3'	CCTGGGAGGTGGAGCTTGCAGT 83917	A	
	GA	TCACTGCAA CTCCACCTCCCGGG		
		AGTGACGTT GAGGTGGAGGGTCC		
		C		
GAM2411	LOC144289 3'	CCCGGCAGGCGGAGGTTGCAGT 83956	A	A C
	GA	TCACTGCAA CTCC CCT CCGGG		
		AGTGACGTT GAGG GGA GGCCC		
		G C C		
GAM2411	LOC144289 3'	CCCGGGAGGTGGAGGTTGCAG 83957	A	
		CTGCAA CTCCACCTCCCGGG		
		GACGTT GAGGTGGAGGGCCC		
		G		
GAM2411	LOC144481 3'	CCCAGGAGGTGGAGGTTACAGT 84016	CAAA	C
	GA	TCACTG CTCCACCTCC GGG		
		AGTGAC GAGGTGGAGG CCC		
		ATTG A		
GAM2411	LOC144481 3'	CCCAGGAGGTTGAGGCTGCAGT 84017	AA	C C
	GA	TCACTGCA CTC ACCTCC GGG		
		AGTGACGT GAG TGGAGG CCC		
		CG T A		
GAM2411	LOC144558 3'	CCCAGGAGGTAGAGGCTGCAGT 84076	AA	C C
	GA	TCACTGCA CTC ACCTCC GGG		
		AGTGACGT GAG TGGAGG CCC		
		CG A A		
GAM2411	LOC144563 3'	CCCAGGAGGTGGAGGTTGCAGT 77394	A	C
	GA	TCACTGCAA CTCCACCTCC GGG		
		AGTGACGTT GAGGTGGAGG CCC		
		G A		
GAM2411	LOC144845 3'	CCCGGGAGGCGGAGGTTGCAGT 57458	A	A
	GA	TCACTGCAA CTCC CCTCCCGGG		
		AGTGACGTT GAGG GGAGGGCCC		
		G C		
GAM2411	LOC145082 5'	CCAGAGGCGGAGGTTGCAGTGA 84184	A	A CC
		TCACTGCAA CTCC CTC GG		

		AGTGACGTT GAGG GGAG CC	
		G C A_	
GAM2411	LOC145216 3'	CCCGGAAGCGAAGGTTGCAGTG 84220	A CCAC C
	A	TCACTGCAA CT CT CCGGG	
		AGTGACGTT GA GA GGCCC	
		G AGC_ A	
GAM2411	LOC145231 3'	CCCGGGAGGCGGAGGTTGCGGT 84246	A A
	GA	TCACTGCAA CTCC CCTCCCGGG	
		AGTGCGCTT GAGG GGAGGGCCC	
		G C	
GAM2411	LOC145231 3'	GAGATGGAGGTTGCAGTGA 84248	A C
		TCACTGCAA CTCCA CTC	
		AGTGACGTT GAGGT GAG	
		G A	
GAM2411	LOC145299 3'	CCCGGGAAGCGGAGCTTGCAGT 84274	A ACC
	GA	TCACTGCAA CTCC TCCCGGG	
		AGTGACGTT GAGG AGGGCCC	
		C CGA	
GAM2411	LOC145333 3'	CCTGGGAGGCAGAGCTTGCAGT 84294	A CA
	GA	TCACTGCAA CTC CCTCCCGGG	
		AGTGACGTT GAG GGAGGGTCC	
		C AC	
GAM2411	LOC145387 3'	GAGGCGGAGGTTGCAGTGA 84335	A A
		TCACTGCAA CTCC CCTC	
		AGTGACGTT GAGG GGAG	
		G C	
GAM2411	LOC145387 3'	GAGGTGGAGGCTGCAGTGA 84336	AA
		TCACTGCA CTCCACCTC	
		AGTGACGT GAGGTGGAG	
		CG	
GAM2411	LOC145438 3'	CCCGGGAGGCGGAGCTTGCAGT 84311	A A
	GA	TCACTGCAA CTCC CCTCCCGGG	
		AGTGACGTT GAGG GGAGGGCCC	
		C C	
GAM2411	LOC145453 3'	GAGGCAGAGGTTGCAGTGA 77666	A CA
		TCACTGCAA CTC CCTC	
		AGTGACGTT GAG GGAG	
		G AC	
GAM2411	LOC145608 5'	CCCGGGAGGCGGAGCTTGCAGT 84380	A A
	GA	TCACTGCAA CTCC CCTCCCGGG	

	AGTGACGTT GAGG GGAGGGCCC	
	C C	
GAM2411 LOC145609 3'	CCCGGGAGGCGGAGCTTGCAGT 84365	A A
GA	TCACTGCAA CTCC CCTCCCGGG	
	AGTGACGTT GAGG GGAGGGCCC	
	C C	
GAM2411 LOC145662 3'	GAGGTGGAGGTTGCAGTGA 77835	A
	TCACTGCAA CTCCACCTC	
	AGTGACGTT GAGGTGGAG	
	G	
GAM2411 LOC145663 3'	CCCGGGAGGCGGAGCTTGTAGT 84419	A A
GA	TCACTGCAA CTCC CCTCCCGGG	
	AGTGATGTT GAGG GGAGGGCCC	
	C C	
GAM2411 LOC145757 3'	CCCAGGAGGCAAAGGTTGCAGT 77926	A CCA C
GA	TCACTGCAA CT CCTCC GGG	
	AGTGACGTT GA GGAGG CCC	
	G AAC A	
GAM2411 LOC145820 3'	CCCGGGAGGCGGAGCTTGCAGT 77975	A A
GA	TCACTGCAA CTCC CCTCCCGGG	
	AGTGACGTT GAGG GGAGGGCCC	
	C C	
GAM2411 LOC145945 5'	CCCAACTGAGAGTTTGCAGT 84564	_ CCTCCC
	ACTGCAA ACTC CA GGG	
	TGACGTTTGAG GT CCC	
	A CAA__	
GAM2411 LOC145988 5'	CCTAGGAGGCGGAGCTTGCAGT 78065	A A CG
GA	TCACTGCAA CTCC CCTCC GG	
	AGTGACGTT GAGG GGAGG CC	
	C C AT	
GAM2411 LOC146059 3'	GAGGTGGAGGTTGCAGTGA 78087	A
	TCACTGCAA CTCCACCTC	
	AGTGACGTT GAGGTGGAG	
	G	
GAM2411 LOC146229 3'	CCCGGAAGGCGGAGGTTGCAGT 78272	A A C
GA	TCACTGCAA CTCC CCT CCGGG	
	AGTGACGTT GAGG GGA GGCCC	
	G C A	
GAM2411 LOC146512 3'	CCCAGGAGTTTGAGGCTGCAGT 78498	AA CAC C
GA	TCACTGCA CTC CTCC GGG	

		AGTGACGT GAG GAGG CCC	
		CG TTT A	
GAM2411	LOC146713 3'	CCCGGGAGGCAGAGGTTGCAGT 84726	A CA
	GA	TCACTGCAA CTC CCTCCCGGG	
		AGTGACGTT GAG GGAGGGCCC	
		G AC	
GAM2411	LOC146713 3'	CCCGGGAGGCGGAGGTTGCATG 84727	C A A
	A	TCA TGCAA CTCC CCTCCCGGG	
		AGT ACGTT GAGG GGAGGGCCC	
		_ G C	
GAM2411	LOC146723 3'	GAGGTGGAGATTGCAGTGA 78680	A
		TCACTGCAA CTCCACCTC	
		AGTGACGTT GAGGTGGAG	
		A	
GAM2411	LOC146728 5'	GAGGTGGAGGTTGCAGTGA 84767	A
		TCACTGCAA CTCCACCTC	
		AGTGACGTT GAGGTGGAG	
		G	
GAM2411	LOC146756 3'	CCCGGGAGGCGGAGCTTGCAGT 84798	A A
	GA	TCACTGCAA CTCC CCTCCCGGG	
		AGTGACGTT GAGG GGAGGGCCC	
		C C	
GAM2411	LOC146901 3'	CCCAGGAGACAGAGGTTGCAGT 84897	A CAC C
	GA	TCACTGCAA CTC CTCC GGG	
		AGTGACGTT GAG GAGG CCC	
		G ACA A	
GAM2411	LOC146923 3'	CCCAGGAGGCGGAGCTTGCAGT 78798	A A C
	GA	TCACTGCAA CTCC CCTCC GGG	
		AGTGACGTT GAGG GGAGG CCC	
		C C A	
GAM2411	LOC146958 3'	GAGGCAGAGGTTGCAGTGA 84942	A CA
		TCACTGCAA CTC CCTC	
		AGTGACGTT GAG GGAG	
		G AC	
GAM2411	LOC147057 3'	CCCAGGAGGTGGAGGTAGCAGT 84978	AAA C
	GA	TCACTGC CTCCACCTCC GGG	
		AGTGACG GAGGTGGAGG CCC	
		ATG A	
GAM2411	LOC147071 3'	CCTGGGAGGCAGAGCTTGCAGT 73361	A CA
	GA	TCACTGCAA CTC CCTCCCGGG	

	AGTGACGTT GAG GGAGGGTCC	
	C AC	
GAM2411 LOC147080 3'	CCCGGGAGGCAGCAGTTGCAGT 85030	ACTCCA
GA	TCACTGCAA CCTCCCGGG	
	AGTGACGTT GGAGGGCCC	
	GACGAC	
GAM2411 LOC147180 5'	GAGGTGGAGGTTGCAGTGA 85100	A
	TCACTGCAA CTCCACCTC	
	AGTGACGTT GAGGTGGAG	
	G	
GAM2411 LOC147599 3'	CCCAGGAGGCAGAGGTTGCAGT 85161	A CA C
GA	TCACTGCAA CTC CCTCC GGG	
	AGTGACGTT GAG GGAGG CCC	
	G AC A	
GAM2411 LOC147649 3'	CCCGGGAGGCGGAGCTTGCAGT 79058	A A
GA	TCACTGCAA CTCC CCTCCCGGG	
	AGTGACGTT GAGG GGAGGGCCC	
	C C	
GAM2411 LOC147664 3'	CCCGGGAGGCAGAGGTTGT 79047	A CA
	GCAA CTC CCTCCCGGG	
	TGTT GAG GGAGGGCCC	
	G AC	
GAM2411 LOC147700 3'	CCCAGGAGGTGGAGGTTGCTGT 59882	T A C
GA	TCAC GCAA CTCCACCTCC GGG	
	AGTG CGTT GAGGTGGAGG CCC	
	T G A	
GAM2411 LOC147727 5'	AGGCGGAGGTTGCAGTGA 79125	A A
	TCACTGCAA CTCC CCT	
	AGTGACGTT GAGG GGA	
	G C	
GAM2411 LOC147727 5'	CCCAGGAGGCGGAGGTTGCAGT 79134	A A C
GA	TCACTGCAA CTCC CCTCC GGG	
	AGTGACGTT GAGG GGAGG CCC	
	G C A	
GAM2411 LOC148147 3'	CCTGGGAGGCGGAGCTTGCGGT 79395	A A
GA	TCACTGCAA CTCC CCTCCCGGG	
	AGTGGCGTT GAGG GGAGGGTCC	
	C C	
GAM2411 LOC148166 3'	GAGACGGAGGTTGCAGTGA 79415	A AC
	TCACTGCAA CTCC CTC	

		AGTGACGTT GAGG GAG		
		G CA		
GAM2411	LOC148198 3'	CCCAGGAGGCAGAGGTTGCGGT 71223	A CA C	
	GA	TCACTGCAA CTC CCTCC GGG		
		AGTGGCGTT GAG GGAGG CCC		
		G AC A		
GAM2411	LOC148206 3'	GAGGCAGAGGTTGCAGTGA 79463	A CA	
		TCACTGCAA CTC CCTC		
		AGTGACGTT GAG GGAG		
		G AC		
GAM2411	LOC148254 3'	GAGGCGGAGGTTGCAGTGA 79503	A A	
		TCACTGCAA CTCC CCTC		
		AGTGACGTT GAGG GGAG		
		G C		
GAM2411	LOC148343 3'	CCCAGGAGGTGGAGGCTGCAGT 79541	AA C	
	GA	TCACTGCA CTCCACCTCC GGG		
		AGTGACGT GAGGTGGAGG CCC		
		CG A		
GAM2411	LOC148397 3'	CCCGGGAGGCGGAGGTTATGG 79568	GC A A	
		CT AA CTCC CCTCCCGGG		
		GG TT GAGG GGAGGGCCC		
		TA G C		
GAM2411	LOC148534 3'	CCCGAGAGACGGAGGTTGCAGT 79637	A AC C	
	GA	TCACTGCAA CTCC CTC CGGG		
		AGTGACGTT GAGG GAG GCCC		
		G CA A		
GAM2411	LOC148734 3'	CCCGGGAGGCGGAGCTTGCAGT 79710	A A	
	GA	TCACTGCAA CTCC CCTCCCGGG		
		AGTGACGTT GAGG GGAGGGCCC		
		C C		
GAM2411	LOC148758 5'	CCCGGGAGGTAGAGGTTGCAGT 79722	A C	
	GA	TCACTGCAA CTC ACCTCCCGGG		
		AGTGACGTT GAG TGGAGGGCCC		
		G A		
GAM2411	LOC148809 5'	CCCAGGAGGTGGAGGTTGCAGC 79750	A A C	
	GA	TC CTGCAA CTCCACCTCC GGG		
		AG GACGTT GAGGTGGAGG CCC		
		C G A		
GAM2411	LOC148938 3'	CCTCCCGGGTAGACAGAGGTTG 85432	A CA_____ TCCC	
	CAGTGA	TCACTGCAA CTC CC GG		

		AGTGACGTT GAG GG CC	
		G ACAGAT__G CCCT	
GAM2411	LOC149113 3'	CCCAAAAGGCAGACATTGCAGT 79906	AC CA CCC
	GA	TCACTGCAA TC CCT GGG	
		AGTGACGTT AG GGA CCC	
		AC AC AAA	
GAM2411	LOC149113 5'	CCCGGGAGGTGGAGGTTGTAGT 79907	A
	GA	TCACTGCAA CTCCACCTCCCGGG	
		AGTGATGTT GAGGTGGAGGGCCC	
		G	
GAM2411	LOC149175 3'	CCCGGGAGGCGGAGCTTGCAGT 79951	A A
	GA	TCACTGCAA CTCC CCTCCCGGG	
		AGTGACGTT GAGG GGAGGGCCC	
		C C	
GAM2411	LOC149194 5'	CCCGGGAGGCAGAGGTTGCAGT 79982	A CA
	GA	TCACTGCAA CTC CCTCCCGGG	
		AGTGACGTT GAG GGAGGGCCC	
		G AC	
GAM2411	LOC149271 3'	CCCAGGAGGCAGAGTTTGCAGT 80002	CA C
	GA	TCACTGCAA ACTC CCTCC GGG	
		AGTGACGTTTGAG GGAGG CCC	
		AC A	
GAM2411	LOC149464 5'	CCCAGGAGGCAGAGGTTGCAGT 85589	A CA C
	GA	TCACTGCAA CTC CCTCC GGG	
		AGTGACGTT GAG GGAGG CCC	
		G AC A	
GAM2411	LOC149529 3'	CCCAAAAGGCAAAAGTTTGCAG 80206	CCA_ CCC
		CTGCAA ACT CCT GGG	
		GACGTTTGA GGA CCC	
		AAAC AAA	
GAM2411	LOC149628 3'	GAGGTGGAGGTTGCAGTGA 80279	A
		TCACTGCAA CTCCACCTC	
		AGTGACGTT GAGGTGGAG	
		G	
GAM2411	LOC149705 3'	CCCAGGTGGCGGAGGTTGCAGT 85776	A A T C
	GA	TCACTGCAA CTCC CC CC GGG	
		AGTGACGTT GAGG GG GG CCC	
		G C T A	
GAM2411	LOC149711 5'	CCCTTGTAGAATTTGCAGT 85847	C C CTCCC
		ACTGCAAA TC AC GGG	

		TGACGTTT AG TG CCC	
		A A TT___	
GAM2411	LOC150095 3'	CCCGGGAGGCAGAGGTTGCAGT 85993	A CA
	GA	TCACTGCAA CTC CCTCCCGGG	
		AGTGACGTT GAG GGAGGGCCC	
		G AC	
GAM2411	LOC150142 5'	CCCAGGAAGTCAAGGCTGCAGT 80405	AA CC C C
	GA	TCACTGCA CT AC TCC GGG	
		AGTGACGT GA TG AGG CCC	
		CG AC A A	
GAM2411	LOC150185 3'	CCCAGGAGGCAGAGGTTGCAGT 86066	A CA C
	GA	TCACTGCAA CTC CCTCC GGG	
		AGTGACGTT GAG GGAGG CCC	
		G AC A	
GAM2411	LOC150225 3'	CCCGGGAGGCGGAGGTTGCAGT 86187	A A
	GA	TCACTGCAA CTCC CCTCCCGGG	
		AGTGACGTT GAGG GGAGGGCCC	
		G C	
GAM2411	LOC150244 3'	CTGGGAGGCAGAGTTTGCCGTG 80549	T CA
	A	TCAC GCAAATC CCTCCCGG	
		AGTG CGTTTGAG GGAGGGTC	
		C AC	
GAM2411	LOC150358 3'	CCCGGGAGGCAGAGTTTGCACT 86092	CA
	GA	TCACTGCAAATC CCTCCCGGG	
		AGTGACGTTTGAG GGAGGGCCC	
		AC	
GAM2411	LOC150372 3'	GAGACAGAGGTTGCAGTGA 80611	A CAC
		TCACTGCAA CTC CTC	
		AGTGACGTT GAG GAG	
		G ACA	
GAM2411	LOC150481 3'	GAGGCGGAGGTTGCAGTGA 80704	A A
		TCACTGCAA CTCC CCTC	
		AGTGACGTT GAGG GGAG	
		G C	
GAM2411	LOC150577 3'	CCCAGAAGGTTGAGACTGCAGT 86253	AA C CCC
	GA	TCACTGCA CTC ACCT GGG	
		AGTGACGT GAG TGGA CCC	
		CA T AGA	
GAM2411	LOC150622 3'	CCCAGGAGGCGGAGGTTGCAGT 80760	A A C
	GA	TCACTGCAA CTCC CCTCC GGG	

		AGTGACGTT GAGG GGAGG CCC	
		G C A	
GAM2411	LOC150622 3'	CCGGGAGGCTAATGCAGGA 80761 A	AACTCCA
		TC CTGCA CCTCCCGG	
		AG GACGT GGAGGGCC	
		_ AATC__	
GAM2411	LOC150889 3'	CCCGGGAGGCAGACTTTGCAGT 80813	C CA
	GA	TCACTGCAA TC CCTCCCGG	
		AGTGACGTTT AG GGAGGGCCC	
		C AC	
GAM2411	LOC151248 5'	CCCAAGGCGGAGCTTGCAGTGA 80989	A A CCC
		TCACTGCAA CTCC CCT GGG	
		AGTGACGTT GAGG GGA CCC	
		C C A__	
GAM2411	LOC151248 3'	CCCAGGAGGCAGAGATTGCAGT 80990	A CA C
	GA	TCACTGCAA CTC CCTCC GGG	
		AGTGACGTT GAG GGAGG CCC	
		A AC A	
GAM2411	LOC151248 3'	CCCGGGAGGCGGAACTTGCAGT 80991	AC A
	GA	TCACTGCAA TCC CCTCCCGG	
		AGTGACGTT AGG GGAGGGCCC	
		CA C	
GAM2411	LOC151429 3'	CCCGGGAGGCGGAGCTTGCAGT 86529	A A
	GA	TCACTGCAA CTCC CCTCCCGG	
		AGTGACGTT GAGG GGAGGGCCC	
		C C	
GAM2411	LOC151429 3'	CCCGGGAGGTGGAGGTTGCAGT 86530	A
	GA	TCACTGCAA CTCCACCTCCCGG	
		AGTGACGTT GAGGTGGAGGGCCC	
		G	
GAM2411	LOC151446 3'	CCCAGGAGGGGGAGTTTGCAGT 86569	A C
	GA	TCACTGCAA ACTCC CCTCC GGG	
		AGTGACGTTTGAGG GGAGG CCC	
		G A	
GAM2411	LOC151602 3'	CCCGGGAGGCGGAGGTTGCAGT 81108	A A
	GA	TCACTGCAA CTCC CCTCCCGG	
		AGTGACGTT GAGG GGAGGGCCC	
		G C	
GAM2411	LOC151623 3'	CCCAGGAGGTAGAGGCTGCAGT 86632	AA C C
	GA	TCACTGCA CTC ACCTCC GGG	

		AGTGACGT GAG TGGAGG CCC		
		CG A A		
GAM2411	LOC151632 3'	CCCAGGAGGTGGAGGTTGCAGT 86643	A	C
	GA	TCACTGCAA CTCCACCTCC GGG		
		AGTGACGTT GAGGTGGAGG CCC		
		G A		
GAM2411	LOC151720 3'	CCCAGGAGGCAGAGCTTGTAGT 81149	A CA	C
	GA	TCACTGCAA CTC CCTCC GGG		
		AGTGATGTT GAG GGAGG CCC		
		C AC A		
GAM2411	LOC151904 3'	CCCGGGAGGCGGAGGTTGCAGT 81204	A A	
	GA	TCACTGCAA CTCC CCTCCCGGG		
		AGTGACGTT GAGG GGAGGGCCC		
		G C		
GAM2411	LOC152106 3'	CCCAGGAAGTGGAGATTGCAGT 70593	A C C	
	GA	TCACTGCAA CTCCAC TCC GGG		
		AGTGACGTT GAGGTG AGG CCC		
		A A A		
GAM2411	LOC152271 3'	CCCAGGAGGTGGAGGTTGCAGT 81357	A	C
	GA	TCACTGCAA CTCCACCTCC GGG		
		AGTGACGTT GAGGTGGAGG CCC		
		G A		
GAM2411	LOC152283 3'	GAGGCGGAGGTTGCAGTGA 86871	A A	
		TCACTGCAA CTCC CCTC		
		AGTGACGTT GAGG GGAG		
		G C		
GAM2411	LOC152313 3'	AGGTGGAGCTTGCAGTGA 86844	A	
		TCACTGCAA CTCCACCT		
		AGTGACGTT GAGGTGGA		
		C		
GAM2411	LOC152316 3'	CCCAGGAGGTGGAGGTTGCAGT 86791	A	C
	GA	TCACTGCAA CTCCACCTCC GGG		
		AGTGACGTT GAGGTGGAGG CCC		
		G A		
GAM2411	LOC152453 3'	CCCAGGAGGCGGAGGTTGCGGT 81469	A A C	
	GA	TCACTGCAA CTCC CCTCC GGG		
		AGTGCGGTT GAGG GGAGG CCC		
		G C A		
GAM2411	LOC152627 5'	GAGGCAGAGGTTGCAGTGA 81510	A CA	
		TCACTGCAA CTC CCTC		

	AGTGACGTT GAG GGAG		
	G AC		
GAM2411 LOC152804 3'	GAGGCAGAGGTTGCAGTGA 87081	A	CA
	TCACTGCAA CTC CCTC		
	AGTGACGTT GAG GGAG		
	G AC		
GAM2411 LOC152804 3'	GAGGTGGAGGTTGCAGTGA 87082	A	
	TCACTGCAA CTCCACCTC		
	AGTGACGTT GAGGTGGAG		
	G		
GAM2411 LOC153077 3'	CCTGGGAGGCGGAGCTTGCAGT 87122	A	A
GA	TCACTGCAA CTCC CCTCCCGGG		
	AGTGACGTT GAGG GGAGGGTCC		
	C C		
GAM2411 LOC153260 3'	CCCAGGAGGTGGAGGTTGCAGT 81670	A	C
GA	TCACTGCAA CTCCACCTCC GGG		
	AGTGACGTT GAGGTGGAGG CCC		
	G A		
GAM2411 LOC153338 3'	CCCAGGAGGTGGAGGTTGCAGT 87195	A	C
GA	TCACTGCAA CTCCACCTCC GGG		
	AGTGACGTT GAGGTGGAGG CCC		
	G A		
GAM2411 LOC153579 3'	CCCGGGAAGCGGAGCTTGCAGT 81768	A	ACC
GA	TCACTGCAA CTCC TCCCGGG		
	AGTGACGTT GAGG AGGGCCC		
	C CGA		
GAM2411 LOC153642 3'	CCCGGGAGGCAGCAGTTGCAGT 81784	ACTCCA	
GA	TCACTGCAA CCTCCCGGG		
	AGTGACGTT GGAGGGCCC		
	GACGAC		
GAM2411 LOC153682 3'	CCTGGGAGGCAGAGCTTGCAGT 87272	A	CA
GA	TCACTGCAA CTC CCTCCCGGG		
	AGTGACGTT GAG GGAGGGTCC		
	C AC		
GAM2411 LOC153688 3'	CCCGGAAGGTGGAGTTTGCAGT 87305		C
GA	TCACTGCAA ACTCCACCT CCGGG		
	AGTGACGTTTGAGGTGGA GGCCC		
	A		
GAM2411 LOC154403 3'	CCCAAAGGCAGACATTGCAGT 81972	AC	CA CCC
GA	TCACTGCAA TC CCT GGG		

		AGTGACGTT AG GGA CCC	
		AC AC AAA	
GAM2411	LOC154403 5'	CCCGGGAGGTGGAGGTTGTAGT 81973	A
	GA	TCACTGCAA CTCCACCTCCCGGG	
		AGTGATGTT GAGGTGGAGGGCCC	
		G	
GAM2411	LOC154791 3'	CCCGGGAGGTGGAGGTTGCGAT 82052	C A
	GA	TCA TGCAA CTCCACCTCCCGGG	
		AGT GCGTT GAGGTGGAGGGCCC	
		A G	
GAM2411	LOC154877 3'	CCCGGGAGGCGGAGGTTGCAGT 87541	A A
	GA	TCACTGCAA CTCC CCTCCCGGG	
		AGTGACGTT GAGG GGAGGGCCC	
		G C	
GAM2411	LOC154992 3'	CCCAAAGGCAGACATTGCAGT 82133	AC CA CCC
	GA	TCACTGCAA TC CCT GGG	
		AGTGACGTT AG GGA CCC	
		AC AC AAA	
GAM2411	LOC154992 5'	CCCGGGAGGTGGAGGTTGCAGT 82134	A
	GA	TCACTGCAA CTCCACCTCCCGGG	
		AGTGACGTT GAGGTGGAGGGCCC	
		G	
GAM2411	LOC155006 3'	GGAGGCGGAGGTTGCAGTGA 82173	A A
		TCACTGCAA CTCC CCTCC	
		AGTGACGTT GAGG GGAGG	
		G C	
GAM2411	LOC155054 3'	CCCAGGAGGCAGAGGCTGCAGT 82204	AA CA C
	GA	TCACTGCA CTC CCTCC GGG	
		AGTGACGT GAG GGAGG CCC	
		CG AC A	
GAM2411	LOC155072 3'	CCCGGGAGGCAGAGCTTGCAGT 87659	A CA
	GA	TCACTGCAA CTC CCTCCCGGG	
		AGTGACGTT GAG GGAGGGCCC	
		C AC	
GAM2411	LOC155072 3'	CCTGGGAGGCAGAGCTTGCAGT 87662	A CA
	GA	TCACTGCAA CTC CCTCCCGGG	
		AGTGACGTT GAG GGAGGGTCC	
		C AC	
GAM2411	LOC157278 3'	CCCAGGAGGTAGAGGCTGCAGT 87706	AA C C
	GA	TCACTGCA CTC ACCTCC GGG	

		AGTGACGT GAG TGGAGG CCC		
		CG A A		
GAM2411	LOC157464 5'	GAGGTGGAGGTTGCAGTGA 87747	A	
		TCACTGCAA CTCCACCTC		
		AGTGACGTT GAGGTGGAG		
		G		
GAM2411	LOC157737 3'	CCCAGGAGACGGAGGTTGCAGT 87843	A	AC C
	GA	TCACTGCAA CTCC CTCC GGG		
		AGTGACGTT GAGG GAGG CCC		
		G CA A		
GAM2411	LOC157983 3'	CCCGGGAGGCGGAGCTTGCAGT 82539	A	A
	GA	TCACTGCAA CTCC CCTCCCGGG		
		AGTGACGTT GAGG GGAGGGCCC		
		C C		
GAM2411	LOC158088 3'	CCCGGGAGGCGGAGCTTGCAGT 87972	A	A
	GA	TCACTGCAA CTCC CCTCCCGGG		
		AGTGACGTT GAGG GGAGGGCCC		
		C C		
GAM2411	LOC158160 3'	GAGGCGGAGGTTGCAGTGA 73472	A	A
		TCACTGCAA CTCC CCTC		
		AGTGACGTT GAGG GGAG		
		G C		
GAM2411	LOC158187 3'	CCCGGGAGGCAGAGGTTGCAGT 87991	A	CA
	GA	TCACTGCAA CTC CCTCCCGGG		
		AGTGACGTT GAG GGAGGGCCC		
		G AC		
GAM2411	LOC158191 3'	GAGGCGGAGGTTGCAGTGA 82676	A	A
		TCACTGCAA CTCC CCTC		
		AGTGACGTT GAGG GGAG		
		G C		
GAM2411	LOC158292 5'	CCCAGGAGGCGGAGGTTGCAGT 88044	A	A C
	GA	TCACTGCAA CTCC CCTCC GGG		
		AGTGACGTT GAGG GGAGG CCC		
		G C A		
GAM2411	LOC158292 5'	CCCGGGAGGCGGAGCTTGCAGT 88045	A	A
	GA	TCACTGCAA CTCC CCTCCCGGG		
		AGTGACGTT GAGG GGAGGGCCC		
		C C		
GAM2411	LOC158677 5'	GAGGCGGAGGTTGCAGTGA 88249	A	A
		TCACTGCAA CTCC CCTC		

		AGTGACGTT GAGG GGAG	
		G C	
GAM2411	LOC158819 3'	CCCAGGAGGCGGAGGTTGCAGT 88274	A A C
	GA	TCACTGCAA CTCC CCTCC GGG	
		AGTGACGTT GAGG GGAGG CCC	
		G C A	
GAM2411	LOC158987 3'	CCCAGGAGGTGGAGGCTGCAGT 88322	AA C
	GA	TCACTGCA CTCCACCTCC GGG	
		AGTGACGT GAGGTGGAGG CCC	
		CG A	
GAM2411	LOC159053 3'	CCCGGGAGGTGGAGGTTGCAGT 88368	A
	GA	TCACTGCAA CTCCACCTCCCGGG	
		AGTGACGTT GAGGTGGAGGGCCC	
		G	
GAM2411	LOC159110 3'	CCCAGGAGGCAGAGTTTGCAGT 82988	CA C
	GA	TCACTGCAAACCTC CCTCC GGG	
		AGTGACGTTTGAG GGAGG CCC	
		AC A	
GAM2411	LOC159116 3'	CCCAGGAGGCAGAGTTTGCAGT 82971	CA C
	GA	TCACTGCAAACCTC CCTCC GGG	
		AGTGACGTTTGAG GGAGG CCC	
		AC A	
GAM2411	LOC170395 3'	CCCAGGAGGTCGAGGCTGCAGT 76867	AA C C
	GA	TCACTGCA CTC ACCTCC GGG	
		AGTGACGT GAG TGGAGG CCC	
		CG C A	
GAM2411	LOC170395 3'	CCCGGAAGGCAGAGGTTGCAGT 76868	A CA C
	GA	TCACTGCAA CTC CCT CCGGG	
		AGTGACGTT GAG GGA GGCCC	
		G AC A	
GAM2411	LOC196047 5'	GAGGTGGAGGTTGCAGTGA 91155	A
		TCACTGCAA CTCCACCTC	
		AGTGACGTT GAGGTGGAG	
		G	
GAM2411	LOC196529 3'	CCCAGAAGGCGAAGGTTGCAGT 89128	A CCA CCC
	GA	TCACTGCAA CT CCT GGG	
		AGTGACGTT GA GGA CCC	
		G AGC AGA	
GAM2411	LOC197196 3'	CCCAGAAGGTGCAGGTTGCAGT 91301	A C CCC
	GA	TCACTGCAA CT CACCT GGG	

	AGTGACGTT GA GTGGA CCC	
	G C AGA	
GAM2411 LOC197408 5'	CCCAAAAGTTTGAGGCTGCAGT 91317	AA CAC CCC
GA	TCACTGCA CTC CT GGG	
	AGTGACGT GAG GA CCC	
	CG TTT AAA	
GAM2411 LOC199676 3'	CCCAGGAGGCAGAGGTTGCAGT 91359	A CA C
GA	TCACTGCAA CTC CCTCC GGG	
	AGTGACGTT GAG GGAGG CCC	
	G AC A	
GAM2411 LOC199858 3'	CCCGGGAGGCGGAGCTTGCAGT 89795	A A
GA	TCACTGCAA CTCC CCTCCCGGG	
	AGTGACGTT GAGG GGAGGGCCC	
	C C	
GAM2411 LOC200014 3'	CCCAGGAAGCAGAGGTTGCAGT 89927	A CACC C
GA	TCACTGCAA CTC TCC GGG	
	AGTGACGTT GAG AGG CCC	
	G ACGA A	
GAM2411 LOC200251 3'	GAGGCGGAGGTTGCAGTGA 90063	A A
	TCACTGCAA CTCC CCTC	
	AGTGACGTT GAGG GGAG	
	G C	
GAM2411 LOC200317 3'	GGAGGCGGAGTTTGCAGTGA 90225	A
	TCACTGCAA ACTCC CCTCC	
	AGTGACGTTTGAGG GGAGG	
	C	
GAM2411 LOC200470 3'	CCCAGGAAATTGGGGCTGCAGT 91641	AA CC_ C
GA	TCACTGCA CTCCA TCC GGG	
	AGTGACGT GGGGT AGG CCC	
	C_ TAA A	
GAM2411 LOC200728 3'	CCCAGGAGGCAGAGCTTGCAGT 91682	A CA C
GA	TCACTGCAA CTC CCTCC GGG	
	AGTGACGTT GAG GGAGG CCC	
	C AC A	
GAM2411 LOC200904 3'	CCCAGGAGGTGGAGGTTGCACT 91778	C A C
GA	TCA TGCAA CTCCACCTCC GGG	
	AGT ACGTT GAGGTGGAGG CCC	
	C G A	
GAM2411 LOC201173 3'	CCTGGGAGGCAGAGCTTGCAGT 88681	A CA
GA	TCACTGCAA CTC CCTCCCGGG	

	AGTGACGTT GAG GGAGGGTCC	
	C AC	
GAM2411 LOC201182 5'	AGGCGGAGGCTGCAGTGA 91332	AA A
	TCACTGCA CTCC CCT	
	AGTGACGT GAGG GGA	
	CG C	
GAM2411 LOC201220 3'	CCTGGGAGGCAGAGCTTGCAGT 88716	A CA
GA	TCACTGCAA CTC CCTCCCGGG	
	AGTGACGTT GAG GGAGGGTCC	
	C AC	
GAM2411 LOC201252 3'	CCTCCCGGGGAAGCAGAGGTTG 89552	A CA_____ TCCC
CAGTGA	TCACTGCAA CTC CC GG	
	AGTGACGTT GAG GG CC	
	G ACGAAG__G CCCT	
GAM2411 LOC201564 3'	CCCGGGAGGCAGAGGTTGCAGT 81274	A CA
GA	TCACTGCAA CTC CCTCCCGGG	
	AGTGACGTT GAG GGAGGGCCC	
	G AC	
GAM2411 LOC201627 3'	GAGGCGGAGGTTGCAGTGA 90456	A A
	TCACTGCAA CTCC CCTC	
	AGTGACGTT GAGG GGAG	
	G C	
GAM2411 LOC201868 3'	CCCAAAGGCAGACATTGCAGT 90519	AC CA CCC
GA	TCACTGCAA TC CCT GGG	
	AGTGACGTT AG GGA CCC	
	AC AC AAA	
GAM2411 LOC201868 5'	CCCGGGAGGTGGAGGTTGTAGT 90521	A
GA	TCACTGCAA CTCCACCTCCCGGG	
	AGTGATGTT GAGGTGGAGGGCCC	
	G	
GAM2411 LOC201895 3'	CCCGGGAGGTGGAGGTTGCAGT 90543	A
GA	TCACTGCAA CTCCACCTCCCGGG	
	AGTGACGTT GAGGTGGAGGGCCC	
	G	
GAM2411 LOC201911 3'	CCCGGGAGGCGGAGATTGCGGT 91862	A A
GA	TCACTGCAA CTCC CCTCCCGGG	
	AGTGGCGTT GAGG GGAGGGCCC	
	A C	
GAM2411 LOC201931 3'	CCCAGGAGGCGGAGCTTGCAGT 90563	A A C
GA	TCACTGCAA CTCC CCTCC GGG	

	AGTGACGTT GAGG GGAGG CCC	
	C C A	
GAM2411 LOC202020 3'	GAGGCGGAGGTTGCAGTGA 90600	A A
	TCACTGCAA CTCC CCTC	
	AGTGACGTT GAGG GGAG	
	G C	
GAM2411 LOC202400 3'	CCCGGGACTTCAATGCTGCAGT 91954	AACTCCACC
GA	TCACTGCA TCCCGGG	
	AGTGACGT AGGGCCC	
	CGTAACTTC	
GAM2411 LOC202868 3'	CCCGGGAGGCAGAGCTTGCAGT 91995	A CA
GA	TCACTGCAA CTC CCTCCCGGG	
	AGTGACGTT GAG GGAGGGCCC	
	C AC	
GAM2411 LOC202868 3'	CCCGGGAGGCGGAGCTTGCAGT 91996	A A
GA	TCACTGCAA CTCC CCTCCCGGG	
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	C C	
GAM2411 LOC203025 3'	GAGGCGAAGGTTGCAGTGA 90747	A CCA
	TCACTGCAA CT CCTC	
	AGTGACGTT GA GGAG	
	G AGC	
GAM2411 LOC203083 3'	CCCAGGAGGTGGAGGTTGCAGT 92085	A C
GA	TCACTGCAA CTCCACCTCC GGG	
	AGTGACGTT GAGGTGGAGG CCC	
	G A	
GAM2411 LOC203246 3'	CCCGGAAGGCGGAGCTTGCAGT 90829	A A C
GA	TCACTGCAA CTCC CCT CCGGG	
	AGTGACGTT GAGG GGA GGCCC	
	C C A	
GAM2411 LOC203289 3'	CCCGGGAGGCGGAGCTTGCAGT 90866	A A
GA	TCACTGCAA CTCC CCTCCCGGG	
	AGTGACGTT GAGG GGAGGGCCC	
	C C	
GAM2411 LOC219347 3'	CCCGGGAGGCAGAGCTTGCAGT 94576	A CA
GA	TCACTGCAA CTC CCTCCCGGG	
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	C AC	
GAM2411 LOC219376 3'	CCCAGGAGGTGGAGGTTGTAGT 95513	A C
GA	TCACTGCAA CTCCACCTCC GGG	

		AGTGATGTT GAGGTGGAGG CCC		
		G A		
GAM2411	LOC219540 3'	GAGGTGGAGGTTGCAATGA 95243	C	A
		TCA TGCAA CTCCACCTC		
		AGT ACGTT GAGGTGGAG		
		A G		
GAM2411	LOC219627 3'	CCCAGGAGGCAGAGATTGCAGT 93804	A	CA C
	GA	TCACTGCAA CTC CCTCC GGG		
		AGTGACGTT GAG GGAGG CCC		
		A AC A		
GAM2411	LOC219627 3'	GAGGTGGAAGTTGCAGTGA 93807	AC	
		TCACTGCAA TCCACCTC		
		AGTGACGTT AGGTGGAG		
		GA		
GAM2411	LOC219649 3'	CCCAGGAGGCGGAGGTTGCAGT 94548	A	A C
	GA	TCACTGCAA CTCC CCTCC GGG		
		AGTGACGTT GAGG GGAGG CCC		
		G C A		
GAM2411	LOC219649 3'	CCCGGGCGGTGGAGCTTGCAGT 94549	A	T
	GA	TCACTGCAA CTCCACC CCCGGG		
		AGTGACGTT GAGGTGG GGGCCC		
		C C		
GAM2411	LOC219672 5'	CCCGGGAGGCAGAGGTTGCAGT 92967	A	CA
	GA	TCACTGCAA CTC CCTCCCGGG		
		AGTGACGTT GAG GGAGGGCCC		
		G AC		
GAM2411	LOC219722 5'	CCCAGGAGTTTGAAGCTGCAGT 94678	AA	C C_ C
	GA	TCACTGCA CT CA CTCC GGG		
		AGTGACGT GA GT GAGG CCC		
		C_ A TT A		
GAM2411	LOC219722 5'	GAGGCAGAGGTTGCAGTGA 94680	A	CA
		TCACTGCAA CTC CCTC		
		AGTGACGTT GAG GGAG		
		G AC		
GAM2411	LOC219919 3'	CCCAGGAGGTGGAGGTTGCAGT 94924	A	C
	GA	TCACTGCAA CTCCACCTCC GGG		
		AGTGACGTT GAGGTGGAGG CCC		
		G A		
GAM2411	LOC220038 3'	CCCAGGGGTGGAGGCTGCAATG 93375	C	AA T C
	A	TCA TGCA CTCCACC CC GGG		

		AGT ACGT GAGGTGG GG CCC	
		A CG _ A	
GAM2411	LOC220070 3'	CCCAGGAGTTTGAGGCTGCAGT 59941	AA CAC C
	GA	TCACTGCA CTC CTCC GGG	
		AGTGACGT GAG GAGG CCC	
		CG TTT A	
GAM2411	LOC220164 5'	CCCGAGAGACAAAGAAGCATGC 93444	AA _ CAC__ C
	GG	CTGCA CT C CTC CGGG	
		GGCGT GA G GAG GCCC	
		AC A AAACA A	
GAM2411	LOC220370 3'	CCCAGATAGCAGAGGTTGCAGT 94398	A CACC_ CC
	GA	TCACTGCAA CTC TC GGG	
		AGTGACGTT GAG AG CCC	
		G ACGAT A_	
GAM2411	LOC220506 3'	CCCGGGAGGCGGAGGTTGCAGT 74518	A A
	GA	TCACTGCAA CTCC CCTCCCGGG	
		AGTGACGTT GAGG GGAGGGCCC	
		G C	
GAM2411	LOC220549 3'	CCCAGGAGGTTGAGGCTGCAGT 94506	AA C C
	GA	TCACTGCA CTC ACCTCC GGG	
		AGTGACGT GAG TGGAGG CCC	
		CG T A	
GAM2411	LOC220662 3'	GAGGCAGAGGTTGCAGTGA 92819	A CA
		TCACTGCAA CTC CCTC	
		AGTGACGTT GAG GGAG	
		G AC	
GAM2411	LOC220662 3'	GAGGTGGAGGTTGCAGTGA 92820	A
		TCACTGCAA CTCCACCTC	
		AGTGACGTT GAGGTGGAG	
		G	
GAM2411	LOC220906 3'	CCCAGGAGGCAGAGATTGCGGT 93034	A CA C
	GA	TCACTGCAA CTC CCTCC GGG	
		AGTGGCGTT GAG GGAGG CCC	
		A AC A	
GAM2411	LOC221042 3'	CCCGGGAGGCAGAGGTTGCAGT 94797	A CA
	GA	TCACTGCAA CTC CCTCCCGGG	
		AGTGACGTT GAG GGAGGGCCC	
		G AC	
GAM2411	LOC221069 3'	CCCGGGAGGCAGAGGTTGCACT 94820	C A CA
	GA	TCA TGCAA CTC CCTCCCGGG	

		AGT ACGTT GAG GGAGGGCCC		
		C G AC		
GAM2411	LOC221178 3'	CCTCCCGGGGAAGCGGAGGTTG 95169	A	A_____ TCCC
		CAGTGA TCACTGCAA CTCC CC GG		
		AGTGACGTT GAGG GG CC		
		G CGAAG__G CCCT		
GAM2411	LOC221271 3'	CCCAGGAGGCGGAGCTTGCAGT 93505	A	A C
		GA TCACTGCAA CTCC CCTCC GGG		
		AGTGACGTT GAGG GGAGG CCC		
		C C A		
GAM2411	LOC221271 3'	CCCGGGAGGTGGAGCTTGCAGT 93506	A	
		GA TCACTGCAA CTCCACCTCCCGGG		
		AGTGACGTT GAGGTGGAGGGCCC		
		C		
GAM2411	LOC221288 3'	CCCGGGAGGCGGAGCTTGCAGT 95258	A	A
		GA TCACTGCAA CTCC CCTCCCGGG		
		AGTGACGTT GAGG GGAGGGCCC		
		C C		
GAM2411	LOC221477 3'	GAGGCGGAGATTGCAGTGA 93771	A	A
		TCACTGCAA CTCC CCTC		
		AGTGACGTT GAGG GGAG		
		A C		
GAM2411	LOC221489 3'	GAGGCAGAGGTTGCAGTGA 95288	A	CA
		TCACTGCAA CTC CCTC		
		AGTGACGTT GAG GGAG		
		G AC		
GAM2411	LOC221490 3'	CCCAGGAGGTGGATGTTGCAGT 95303	AC	C
		GA TCACTGCAA TCCACCTCC GGG		
		AGTGACGTT AGGTGGAGG CCC		
		GT A		
GAM2411	LOC221543 5'	CCGGGGAGGCGGAGCTTGCAGT 95370	A	A G
		GA TCACTGCAA CTCC CCTCCC GG		
		AGTGACGTT GAGG GGAGGG CC		
		C C G		
GAM2411	LOC221543 3'	GAGGCAGAGGTTGCAGTGA 95377	A	CA
		TCACTGCAA CTC CCTC		
		AGTGACGTT GAG GGAG		
		G AC		
GAM2411	LOC221795 3'	CCCAGGAGGTGGAGGTTGCAGT 94072	A	C
		GA TCACTGCAA CTCCACCTCC GGG		

		AGTGACGTT GAGGTGGAGG CCC	
		G A	
GAM2411	LOC221943 5'	CCCAGGAGGCGGAGGTTGCAGT 95620	A A C
	GA	TCACTGCAA CTCC CCTCC GGG	
		AGTGACGTT GAGG GGAGG CCC	
		G C A	
GAM2411	LOC221954 5'	CCCAGGAGGCAGAGGCTGCAGT 95644	AA CA C
	GA	TCACTGCA CTC CCTCC GGG	
		AGTGACGT GAG GGAGG CCC	
		CG AC A	
GAM2411	LOC221962 3'	CCCAGGAGGTAGAGGCTGCAGT 94239	AA C C
	GA	TCACTGCA CTC ACCTCC GGG	
		AGTGACGT GAG TGGAGG CCC	
		CG A A	
GAM2411	LOC222060 5'	CCCGGGAGGCGGAGGTTGCAGT 95752	A A
	GA	TCACTGCAA CTCC CCTCCCGGG	
		AGTGACGTT GAGG GGAGGGCCC	
		G C	
GAM2411	LOC222066 3'	CCCAGGAGGCAGAGGTTGCAGT 94318	A CA C
	GA	TCACTGCAA CTC CCTCC GGG	
		AGTGACGTT GAG GGAGG CCC	
		G AC A	
GAM2411	LOC222160 5'	CCCAGGAGGTGGAGGTTGCAGT 95780	A C
	GA	TCACTGCAA CTCCACCTCC GGG	
		AGTGACGTT GAGGTGGAGG CCC	
		G A	
GAM2411	LOC222160 3'	CCCAGGAGGTTGAGGCTGCAGT 95781	AA C C
	GA	TCACTGCA CTC ACCTCC GGG	
		AGTGACGT GAG TGGAGG CCC	
		CG T A	
GAM2411	LOC222160 3'	CCTGGGAGGCAGAGTTTGCAGT 95783	CA
	GA	TCACTGCAAACCTC CCTCCCGGG	
		AGTGACGTTTGAG GGAGGGTCC	
		AC	
GAM2411	LOC222256 3'	GAGGTGGAGGTTACAGTGA 95911	CAAA
		TCACTG CTCCACCTC	
		AGTGAC GAGGTGGAG	
		ATTG	
GAM2411	LOC222865 3'	CCCGGGAGGCGGAGCTTGCAGT 94443	A A
	GA	TCACTGCAA CTCC CCTCCCGGG	

		AGTGACGTT GAGG GGAGGGCCC		
		C C		
GAM2411	LOC253003 3'	CCCGGGAGGTGGAGCTTGCAGT 98675	A	
	GA	TCACTGCAA CTCCACCTCCCGGG		
		AGTGACGTT GAGGTGGAGGGCCC		
		C		
GAM2411	LOC253612 5'	CCCGGAAGGTGGAGGTTGCAGT 98545	A	C
	GA	TCACTGCAA CTCCACCT CCGGG		
		AGTGACGTT GAGGTGGA GGCCC		
		G A		
GAM2411	LOC253639 3'	CCCTGAGGCAGAGGTTGCAGTG 97513	A	CA CC
	A	TCACTGCAA CTC CCTC GGG		
		AGTGACGTT GAG GGAG CCC		
		G AC T_		
GAM2411	LOC253664 3'	CCCAGGAAGTCAAGGCTGCAGT 96463	AA	CC C C
	GA	TCACTGCA CT AC TCC GGG		
		AGTGACGT GA TG AGG CCC		
		CG AC A A		
GAM2411	LOC253786 3'	CCCAGGAGGCTGAGGTTGCAGT 98832	A	CA C
	GA	TCACTGCAA CTC CCTCC GGG		
		AGTGACGTT GAG GGAGG CCC		
		G TC A		
GAM2411	LOC254041 5'	CGGCAGAGGTTGCAGTGA 96556	AACTCC	___
		TCACTGCA ACCTC CCG		
		AGTGACGT TGGAG GGC		
		_____ AC		
GAM2411	LOC254045 3'	CCCAGGAGGTGGAGGTTACAGT 98266	CAAA	C
	GA	TCACTG CTCCACCTCC GGG		
		AGTGAC GAGGTGGAGG CCC		
		ATTG A		
GAM2411	LOC254045 3'	CCCAGGAGGTTGAGGCTGCAGT 98267	AA	C C
	GA	TCACTGCA CTC ACCTCC GGG		
		AGTGACGT GAG TGGAGG CCC		
		CG T A		
GAM2411	LOC254100 3'	GAGGCAGAAGTTGCAGTGA 98156	AC	CA
		TCACTGCAA TC CCTC		
		AGTGACGTT AG GGAG		
		GA AC		
GAM2411	LOC254176 3'	CCCAGGAGGTGGAGGTTGCAGT 99166	A	C
	GA	TCACTGCAA CTCCACCTCC GGG		

		AGTGACGTT GAGGTGGAGG CCC	
		G A	
GAM2411	LOC254249 5'	GAGGTGGAGGTTGCAGTGA 97184	A
		TCACTGCAA CTCCACCTC	
		AGTGACGTT GAGGTGGAG	
		G	
GAM2411	LOC254266 3'	CCCAGGAGGAGGAGCTTGCAGT 99198	A A C
	GA	TCACTGCAA CTCC CCTCC GGG	
		AGTGACGTT GAGG GGAGG CCC	
		C A A	
GAM2411	LOC254531 5'	GAGGTGGAGGTTGCAGTGA 96668	A
		TCACTGCAA CTCCACCTC	
		AGTGACGTT GAGGTGGAG	
		G	
GAM2411	LOC254659 3'	GAGGTGGAGGTTGCAGTGA 96820	A
		TCACTGCAA CTCCACCTC	
		AGTGACGTT GAGGTGGAG	
		G	
GAM2411	LOC254685 3'	CCCAGGAGGCGGAGGTTGCAGT 98241	A A C
	GA	TCACTGCAA CTCC CCTCC GGG	
		AGTGACGTT GAGG GGAGG CCC	
		G C A	
GAM2411	LOC254808 3'	CCCGGGAGGCGGAGCTTGCAGT 98804	A A
	GA	TCACTGCAA CTCC CCTCCCGGG	
		AGTGACGTT GAGG GGAGGGCCC	
		C C	
GAM2411	LOC255042 3'	CCCGGGAGGTGGAGGTTGCAGT 97041	A
	GA	TCACTGCAA CTCCACCTCCCGGG	
		AGTGACGTT GAGGTGGAGGGCCC	
		G	
GAM2411	LOC255042 3'	GAAGTGGAGGTTGCAGTGA 97045	A C
		TCACTGCAA CTCCAC TC	
		AGTGACGTT GAGGTG AG	
		G A	
GAM2411	LOC255177 3'	TGGGAGGCGGAGGTTGCAGTGA 98403	A A
		TCACTGCAA CTCC CCTCCCG	
		AGTGACGTT GAGG GGAGGGT	
		G C	
GAM2411	LOC255252 3'	CCCAGGAGGTGGAGGTTGCAGT 96707	A C
	GA	TCACTGCAA CTCCACCTCC GGG	

	AGTGACGTT GAGGTGGAGG CCC		
	G A		
GAM2411 LOC255326 3'	CCCAGGAGGCAGAGGTTGCAGT 98118	A CA C	
GA	TCACTGCAA CTC CCTCC GGG		
	AGTGACGTT GAG GGAGG CCC		
	G AC A		
GAM2411 LOC255328 3'	TGGGAGGCAGAAGTTGCAGTGA 98351	AC CA	
	TCACTGCAA TC CCTCCCG		
	AGTGACGTT AG GGAGGGT		
	GA AC		
GAM2411 LOC255374 5'	CCCAGGAGGTTGAGGCTGCAGT 97790	AA C C	
GA	TCACTGCA CTC ACCTCC GGG		
	AGTGACGT GAG TGGAGG CCC		
	CG T A		
GAM2411 LOC255461 3'	CCCAGGAGGTAGAGGCTGCAGT 99138	AA C C	
GA	TCACTGCA CTC ACCTCC GGG		
	AGTGACGT GAG TGGAGG CCC		
	CG A A		
GAM2411 LOC255463 3'	GAGGCAAAGGTTGCAGTGA 96541	A CCA	
	TCACTGCAA CT CCTC		
	AGTGACGTT GA GGAG		
	G AAC		
GAM2411 LOC255516 3'	CCCAGGAGGTAGAGGCTGCAGT 99152	AA C C	
GA	TCACTGCA CTC ACCTCC GGG		
	AGTGACGT GAG TGGAGG CCC		
	CG A A		
GAM2411 LOC255671 3'	CCCGGGAGGCGGAGGTTGCAGT 99071	A A	
GA	TCACTGCAA CTCC CCTCCCGGG		
	AGTGACGTT GAGG GGAGGGCCC		
	G C		
GAM2411 LOC255937 3'	CCCAGGAGGTGGAGGTTGCAGT 97678	A C	
GA	TCACTGCAA CTCCACCTCC GGG		
	AGTGACGTT GAGGTGGAGG CCC		
	G A		
GAM2411 LOC256207 3'	GAGGCAAAGGTTGCAGTGA 96877	A CCA	
	TCACTGCAA CT CCTC		
	AGTGACGTT GA GGAG		
	G AAC		
GAM2411 LOC256267 3'	CCCGGGAGGCAGAGGTTGCAGT 98610	A CA	
GA	TCACTGCAA CTC CCTCCCGGG		

		AGTGACGTT GAG GGAGGGCCC		
		G AC		
GAM2411	LOC256515 3'	CCCAGGAAGTGGAGGTTGCAGT 98209	A	C C
	GA	TCACTGCAA CTCCAC TCC GGG		
		AGTGACGTT GAGGTG AGG CCC		
		G A A		
GAM2411	LOC256520 3'	CCCGGGAGGCGGAGTTTGCAGA 97664	A	A
	GA	TC CTGCAAACCTCC CCTCCCGGG		
		AG GACGTTTGAGG GGAGGGCCC		
		A C		
GAM2411	LOC256544 3'	CCCGGGAGGCGGAGCTTGCAGT 97930	A	A
	GA	TCACTGCAA CTCC CCTCCCGGG		
		AGTGACGTT GAGG GGAGGGCCC		
		C C		
GAM2411	LOC256594 3'	CCCAGGAGGTGGAGGTTGCAGT 98861	A	C
	GA	TCACTGCAA CTCCACCTCC GGG		
		AGTGACGTT GAGGTGGAGG CCC		
		G A		
GAM2411	LOC257115 3'	CCCAGAAAGTTGAGGCTGCAGT 98292	AA	C C_ CC
	GA	TCACTGCA CTC AC TC GGG		
		AGTGACGT GAG TG AG CCC		
		CG T AA A_		
GAM2411	LOC257539 3'	CCCGGGAGGCGGAGGTTGCAGT 99546	A	A
	GA	TCACTGCAA CTCC CCTCCCGGG		
		AGTGACGTT GAGG GGAGGGCCC		
		G C		
GAM2411	LOC257578 3'	CCCGGGAGGCGGAGGTTGCAGT 99658	A	A
	GA	TCACTGCAA CTCC CCTCCCGGG		
		AGTGACGTT GAGG GGAGGGCCC		
		G C		
GAM2411	LOC257596 5'	CCGGGGAGGCGGAGCTTGCAGT 99773	A	A G
	GA	TCACTGCAA CTCC CCTCCC GG		
		AGTGACGTT GAGG GGAGGG CC		
		C C G		
GAM2411	LOC257596 3'	GAGGCAGAGGTTGCAGTGA 99780	A	CA
		TCACTGCAA CTC CCTC		
		AGTGACGTT GAG GGAG		
		G AC		
GAM2411	LOC51145 3'	CCCAGGAGGTGGAGGTTGCGGT 32921	A	C
	GA	TCACTGCAA CTCCACCTCC GGG		

		AGTGGCGTT GAGGTGGAGG CCC		
		G A		
GAM2411	LOC51212 3'	CCCGGGAGGCAGAGCTTGCAGT 33500	A	CA
	GA	TCACTGCAA CTC CCTCCCGGG		
		AGTGACGTT GAG GGAGGGCCC		
		C AC		
GAM2411	LOC51279 3'	GAGGCGGAGGTTGCAGTGA 33758	A	A
		TCACTGCAA CTCC CCTC		
		AGTGACGTT GAGG GGAG		
		G C		
GAM2411	LOC51759 3'	CCCAAGAGGCGGAGGTTGTGG 73170	TG	A A CC
		C CAA CTCC CCTC GGG		
		G GTT GAGG GGAG CCC		
		GT G C AA		
GAM2411	LOC55974 3'	CCCAGGAGGTGGAGGTTGCAGT 38743	A	C
	GA	TCACTGCAA CTCCACCTCC GGG		
		AGTGACGTT GAGGTGGAGG CCC		
		G A		
GAM2411	LOC63929 3'	GAGGTGGAGGTTGCAGTGA 42281	A	
		TCACTGCAA CTCCACCTC		
		AGTGACGTT GAGGTGGAG		
		G		
GAM2411	LOC64167 3'	CCCGGGAGGTGGAGCTTGCAGT 42537	A	
	GA	TCACTGCAA CTCCACCTCCCGGG		
		AGTGACGTT GAGGTGGAGGGCCC		
		C		
GAM2411	LOC85479 5'	CCTGGGAGGCGGAGCTTGCAGT 53564	A	A
	GA	TCACTGCAA CTCC CCTCCCGGG		
		AGTGACGTT GAGG GGAGGGTCC		
		C C		
GAM2411	LOC90072 5'	CCCAGGAGTTTGAGGCTGCAGT 61956	AA	CAC C
	GA	TCACTGCA CTC CTCC GGG		
		AGTGACGT GAG GAGG CCC		
		CG TTT A		
GAM2411	LOC90092 3'	CCCAGAAGGCGGAAGTTGCAGT 62058	AC	A CCC
	GA	TCACTGCAA TCC CCT GGG		
		AGTGACGTT AGG GGA CCC		
		GA C AGA		
GAM2411	LOC90092 3'	CCTGGGAGCGGAGATTGCAGTG 62060	A	AC
	A	TCACTGCAA CTCC CTCCCGGG		

		AGTGACGTT GAGG GAGGGTCC	
		A C_	
GAM2411 LOC90155 5'	CCCGGGAGGCGGAGGTTGCAGT 62366		A A
GA	TCACTGCAA CTCC CCTCCCGGG		
	AGTGACGTT GAGG GGAGGGCCC		
	G C		
GAM2411 LOC90233 3'	CCCAGAAGGCGGAAGTTGCAGT 57192		AC A CCC
GA	TCACTGCAA TCC CCT GGG		
	AGTGACGTT AGG GGA CCC		
	GA C AGA		
GAM2411 LOC90393 5'	CCCGGGAGGCGGAGCTTGCAGT 63306		A A
GA	TCACTGCAA CTCC CCTCCCGGG		
	AGTGACGTT GAGG GGAGGGCCC		
	C C		
GAM2411 LOC90573 5'	AGGTAGAGGTTGCAGTGA 63953		A C
	TCACTGCAA CTC ACCT		
	AGTGACGTT GAG TGGA		
	G A		
GAM2411 LOC90573 3'	CCCATAAGGCAGAGGTTGCAGT 63956		A CA CCC
GA	TCACTGCAA CTC CCT GGG		
	AGTGACGTT GAG GGA CCC		
	G AC ATA		
GAM2411 LOC90591 3'	CCAGGAGGCAGAGCTTGCAGTG 64156		A CA C
A	TCACTGCAA CTC CCTCC GG		
	AGTGACGTT GAG GGAGG CC		
	C AC A		
GAM2411 LOC90591 3'	CCCAGGAGCTGGATGTTGCAGT 64160		AC C C
GA	TCACTGCAA TCCA CTCC GGG		
	AGTGACGTT AGGT GAGG CCC		
	GT C A		
GAM2411 LOC90591 3'	GAGGCGGAGGTTGCAGTGA 64172		A A
	TCACTGCAA CTCC CCTC		
	AGTGACGTT GAGG GGAG		
	G C		
GAM2411 LOC90624 3'	CCCGGGAGGTGGAGGTTGCAGT 64369		A
GA	TCACTGCAA CTCCACCTCCCGGG		
	AGTGACGTT GAGGTGGAGGGCCC		
	G		
GAM2411 LOC90639 3'	CCAGAGGTTAAGTCTGCAGTGA 64408		A CC CC
	TCACTGCA ACT ACCTC GG		

	AGTGACGT TGA TGGAG CC	
	C AT A_	
GAM2411 LOC90785 3'	GAGGTAGAGGTTGCAGTGA 64716	A C
	TCACTGCAA CTC ACCTC	
	AGTGACGTT GAG TGGAG	
	G A	
GAM2411 LOC91035 3'	GAGGCAGAGGTTGCAGTGA 65299	A CA
	TCACTGCAA CTC CCTC	
	AGTGACGTT GAG GGAG	
	G AC	
GAM2411 LOC91056 3'	GAGGCAGAAGTTGCAGTGA 96405	AC CA
	TCACTGCAA TC CCTC	
	AGTGACGTT AG GGAG	
	GA AC	
GAM2411 LOC91250 5'	TCCGGGCTAGTGTAAGCTTGCA 65923	A C_ _____ CCGG
	GTGA TCACTGCAA CT CAC CT G	
	AGTGACGTT GA GTG GG T	
	C AT ATC_ GCCC	
GAM2411 LOC91286 3'	GAGGCGGAGGTTGCAGTGA 66059	A A
	TCACTGCAA CTCC CCTC	
	AGTGACGTT GAGG GGAG	
	G C	
GAM2411 LOC91380 3'	CCCGGGAGGCGGAGGTTGCAGT 66443	A A
	GA TCACTGCAA CTCC CCTCCCGGG	
	AGTGACGTT GAGG GGAGGGCCC	
	G C	
GAM2411 LOC91380 3'	CGGCAAAGGTTGCAGTGA 66445	AACTCC C_
	TCACTGCA ACCT CCG	
	AGTGACGT TGGA GGC	
	_____ AAC	
GAM2411 LOC91442 3'	CCCGGGAGGCGGAGGTTGCAGT 66643	A A
	GA TCACTGCAA CTCC CCTCCCGGG	
	AGTGACGTT GAGG GGAGGGCCC	
	G C	
GAM2411 LOC91547 3'	CCCGGGAGGCGGAGCTTGCAG 66999	A A
	CTGCAA CTCC CCTCCCGGG	
	GACGTT GAGG GGAGGGCCC	
	C C	
GAM2411 LOC91574 3'	CCCAGGAGCTCAAGATTGCAGT 67109	A CCAC C
	GA TCACTGCAA CT CTCC GGG	

		AGTGACGTT GA GAGG CCC	
		A ACTC A	
GAM2411	LOC91660 3'	CCCGGGAGACGGAGGTTGCAGT 67401	A AC
	GA	TCACTGCAA CTCC CTCCCGGG	
		AGTGACGTT GAGG GAGGGCCC	
		G CA	
GAM2411	LOC91750 3'	GAGGTGGAGGTTGCAGTGA 67653	A
		TCACTGCAA CTCCACCTC	
		AGTGACGTT GAGGTGGAG	
		G	
GAM2411	LOC91796 5'	GAGGTGGAGGTTGCAGTGA 67786	A
		TCACTGCAA CTCCACCTC	
		AGTGACGTT GAGGTGGAG	
		G	
GAM2411	LOC91812 3'	GAGGCGGAGGCTGCAGTGA 67816	AA A
		TCACTGCA CTCC CCTC	
		AGTGACGT GAGG GGAG	
		CG C	
GAM2411	LOC91813 3'	GAGGCGGAGGCTGCAGTGA 67840	AA A
		TCACTGCA CTCC CCTC	
		AGTGACGT GAGG GGAG	
		CG C	
GAM2411	LOC91862 3'	GAGGCGGAGATTGCAGTGA 54573	A A
		TCACTGCAA CTCC CCTC	
		AGTGACGTT GAGG GGAG	
		A C	
GAM2411	LOC91963 5'	GAGGCAGAGGTTGCAGTGA 68320	A CA
		TCACTGCAA CTC CCTC	
		AGTGACGTT GAG GGAG	
		G AC	
GAM2411	LOC92223 3'	GAGGCAGAGGTTGCAGTGA 69050	A CA
		TCACTGCAA CTC CCTC	
		AGTGACGTT GAG GGAG	
		G AC	
GAM2411	LOC92228 3'	GAGGCGGAGGTTGCAGTGA 69076	A A
		TCACTGCAA CTCC CCTC	
		AGTGACGTT GAGG GGAG	
		G C	
GAM2411	LOC92299 3'	CCCGGGCGGCGGAAGTTGCAGT 69363	AC A T
	GA	TCACTGCAA TCC CC CCCGGG	

	AGTGACGTT AGG GG GGGCCC	
	GA C C	
GAM2411 LOC92405 3'	CCCGGGAGGCAGAGGCTGCA 69711	AA CA
	TGCA CTC CCTCCCGGG	
	ACGT GAG GGAGGGCCC	
	CG AC	
GAM2411 LOC92421 3'	CCCAGGAGATGGAGGTTGCAGT 69725	A C C
GA	TCACTGCAA CTCCA CTCC GGG	
	AGTGACGTT GAGGT GAGG CCC	
	G A A	
GAM2411 LOC92465 5'	CCCAGGGGGCGGAGGTTGCAGT 69946	A A C
GA	TCACTGCAA CTCC CCTCC GGG	
	AGTGACGTT GAGG GGGGG CCC	
	G C A	
GAM2411 LOC92465 5'	CCCGGAGGCGGAGGTTGCAGTG 69947	A A C
A	TCACTGCAA CTCC CCTCC GGG	
	AGTGACGTT GAGG GGAGG CCC	
	G C _	
GAM2411 LOC92466 3'	CCCGGGAGGCAGAGGTTGCAGT 69966	A CA
GA	TCACTGCAA CTC CCTCCCGGG	
	AGTGACGTT GAG GGAGGGCCC	
	G AC	
GAM2411 LOC92499 5'	CGGCAGAGGTTGCAGTGA 70107	AACTCC _
	TCACTGCA ACCTC CCG	
	AGTGACGT TGGAG GGC	
	_____ AC	
GAM2411 LOC92521 3'	CCCAGGAGTTCGAGGCTGCAGT 70202	AA CAC C
GA	TCACTGCA CTC CTCC GGG	
	AGTGACGT GAG GAGG CCC	
	CG CTT A	
GAM2411 LOC92568 3'	CCCAGGAGTTCAAAGCTGCAGT 70327	AACTCCAC C
GA	TCACTGCA CTCC GGG	
	AGTGACGT GAGG CCC	
	CGAAACTT A	
GAM2411 LOC92573 3'	CCCATGAGGTGGAAGTTGCAGT 70374	AC CC
GA	TCACTGCAA TCCACCTC GGG	
	AGTGACGTT AGGTGGAG CCC	
	GA TA	
GAM2411 LOC93132 5'	CCCGGGAGGCAGAGGTTGCAGT 71984	A CA
GA	TCACTGCAA CTC CCTCCCGGG	

		AGTGACGTT GAG GGAGGGCCC		
		G AC		
GAM2411	LOC93132 5'	GAGGCGGAGGTTGCAGTGA 71990	A A	
		TCACTGCAA CTCC CCTC		
		AGTGACGTT GAGG GGAG		
		G C		
GAM2411	LOC93613 3'	CCCAGGAGGCACAGGCTGCAGT 73072	AA CCA C	
	GA	TCACTGCA CT CCTCC GGG		
		AGTGACGT GA GGAGG CCC		
		CG CAC A		
GAM2411	LOC96597 5'	CCCAGGCAGTGGAGGTTGCAGT 67451	A CT C	
	GA	TCACTGCAA CTCCAC CC GGG		
		AGTGACGTT GAGGTG GG CCC		
		G AC A		
GAM2412	ABCD3 3'	CTTGTGGTTAAAAACCT 12664 C C		
		AGG TTTTA ACCACAAG		
		TCC AAAAT TGGTGTTC		
		A _		
GAM2412	CDH19 3'	TTGTATGAATAAAAGCCT 41259	CACCACAA	
		AGGCTTTTA GTGCAG		
		TCCGAAAAT TATGTT		
		AAG_____		
GAM2412	LRRC2 5'	GCCTCTGCGGTGTAAACAGCCT 44749	_ A _ T	
		AGGCT TTTACACC CA AG GC		
		TCCGA AAATGTGG GT TC CG		
		C C C _		
GAM2412	NCYM 5'	ACCGCACTCGCAGCGGTGTGGG 21970	T ACA_ A	
	GCC	GGCTTT ACACC AGTGC GT		
		CCGGGG TGTGG TCACG CA		
		_ CGACGC C		
GAM2412	PPP1R12B 3'	ACTCAATGGTATAAAAGCT 50342	C CA_	
		GGCTTTTA ACCA AGT		
		TCGAAAAT TGGT TCA		
		A AAC		
GAM2412	APOARGC 3'	ACACACTGATGCAGAAGCCT 44672	A CCACA CA	
		AGGCTTTT CA AGTG GT		
		TCCGAAGA GT TCAC CA		
		C AG_ AC		
GAM2412	C20orf183 5'	GCACAGTGCAGAAGCCT 48534	A CACAA _	
		AGGCTTTT CAC GTG C		

TCCGAAGA GTG CAC G
 C A ____ C
 GAM2412 KCNT1 3' ACTGCTACGGCGCAAGAGCCT 62484 ACA ACAA _
 AGGCTTTT CC GT GCAGT
 ||||| || |||||
 TCCGAGAA GG CA CGTCA
 CGC ____ T
 GAM2412 MGC33182 3' CATTTAGTTGGTGTAAAAAACT 76092 GC _ _
 AG TTTTACACCA C AAGTG
 || ||||| |||||
 TC AAAATGTGGT G TTTAC
 AA T A
 GAM2412 LOC255056 5' ACACACTTGTGACAAGGCTT 99464 TACAC CA
 AGGCTTT CACAAGTG GT
 ||||| ||||| ||
 TTCGGAA GTGTTCAC CA
 CA ____ AC
 GAM2413 GRF2 3' TGACGCCTTAGCAGCCCCGCA 19202 A TT _
 TGTGG GCTGCTAA CG CA
 |||| ||||| ||||
 ACGCC CGACGATT GC GT
 C CC A
 GAM2413 HUNK 3' TGAACAGAGCTCCACA 28193 G AA
 TGTGGAGCT CT TTCG
 ||||| || ||||
 ACACCTCGA GA AAGT
 _ C_
 GAM2413 FLJ14082 5' GACTGCACTGCAGCCCACA 47320 A TAATTC A
 TGTGG GCTGC GCA TC
 |||| |||| ||||
 ACACC CGACG CGT AG
 _ TCA ____ C
 GAM2413 KIAA1332 3' TGCTTGGAGCTCCACA 71709 G TTC
 TGTGGAGCT CTAA GCA
 ||||| |||| ||||
 ACACCTCGA GGTT CGT
 _ _
 GAM2414 CCNA1 3' TGCACGTTGGATCAACTA 15345 GC TATGAA
 TAGT GATCCAAC GCA
 |||| ||||| ||||
 ATCA CTAGGTTG CGT
 A_ CA ____
 GAM2414 CYR61 3' TTGCTTCATAGTATTGGAGCAC 9557 GA _
 GTGC TCCA ACTATGAAGCAA
 |||| |||| |||||
 CACG AGGT TGATACTTCGTT
 _ TA
 GAM2414 MAFF 3' TTGTAGTGAGCTGAGATCGCAC 25587 _ _ TG
 GTGCGATC CA ACTA A
 ||||| || |||| |

		CACGCTAG GT TGAT T	
		A CGAG GT	
GAM2414 RAB7L1	3'	TTGCAGTGAGCTGAGATCACAC 15417	C _ A ATGAA
		GTG GATC CA CT GCAA	
		CAC CTAG GT GA CGTT	
		A A C GTGA_	
GAM2414 VHL	3'	TTGCAGTGAGCTGATATCGCAC 6883	C_ A ATGAA
		GTGCGAT CA CT GCAA	
		CACGCTA GT GA CGTT	
		TA C GTGA_	
GAM2414 WW45	3'	TTGCAGGGTCAAGATCGCAC 41816	CA_ ATGAA
		GTGCGATC ACT GCAA	
		CACGCTAG TGG CGTT	
		AAC GA__	
GAM2414 AKR1B10	5'	TTGTAGTGAGCTGAGATCGCAC 40082	_ _ _ _ TG
		GTGCGATC CA ACTA A	
		CACGCTAG GT TGAT T	
		A CGAG GT	
GAM2414 CDC16	3'	GCCTTAAGAGACTGGATCGCAC 15336	A_ A_ A
		GTGCGATCCA CT TGA GC	
		CACGCTAGGT GA ATT CG	
		CA GA C	
GAM2414 DSCR6	3'	TTGCCGTGAGTCGAGATCGCAC 39078	CA_ _ AA
		GTGCGATC ACT ATG GCAA	
		CACGCTAG TGA TGC CGTT	
		AGC G _	
GAM2414 FLJ10058	3'	TTGCAAGTGAGCTGAGATCGCA 36268	_ A ATGAA
C		GTGCGATC CA CT GCAA	
		CACGCTAG GT GA CGTT	
		A C GTGAA	
GAM2414 FLJ10900	3'	TTAGCATTGAATTGCACTA 37346	C CTA
		TAGTGCGAT CAA TGA	
		ATCACGTTA GTT ATT	
		A ACG	
GAM2414 FLJ10900	3'	TTAGCATTGAATTGCACTA 66208	C CTA
		TAGTGCGAT CAA TGA	
		ATCACGTTA GTT ATT	
		A ACG	
GAM2414 FLJ21240	3'	TTGCAGTGAGCTGAGATCACAC 46271	C _ A ATGAA
		GTG GATC CA CT GCAA	

	CAC CTAG GT GA CGTT	
	A A C GTGA_	
GAM2414 FLJ21687 3'	TTGCAGCGAGCCAAGATCGCAC 46305	CAA_ A AA
	GTGCGATC CT TG GCAA	
	CACGCTAG GA GC CGTT	
	AACC _ GA	
GAM2414 FLJ22814 3'	TTGCAGTGAGCTGAGATCGCAC 46734	_ A ATGAA
	GTGCGATC CA CT GCAA	
	CACGCTAG GT GA CGTT	
	A C GTGA_	
GAM2414 FLJ23042 3'	TGCGGTGAGTTGTGATCGCAC 47952	_ ATGAA
	GTGCGATC CAACT GCA	
	CACGCTAG GTTGA CGT	
	T GTGG_	
GAM2414 GLTP 3'	TTGCAGTGAGCTGAGATCGCAC 33592	_ A ATGAA
	GTGCGATC CA CT GCAA	
	CACGCTAG GT GA CGTT	
	A C GTGA_	
GAM2414 HSU79303 3'	GCTTCAAGCGGTGATCGCAC 26152	CA A__
	GTGCGATC ACT TGAAGC	
	CACGCTAG TGG ACTTCG	
	_ CGA	
GAM2414 KHDRBS1 5'	GCTCCTTGGATCGCAC 22662	CTAT A
	GTGCGATCCAA GA GC	
	CACGCTAGGTT CT CG	
	C__ _	
GAM2414 KIAA0445 5'	TTGCAGTCAGCCAGGATCGCAC 28644	AACTA A_
	GTGCGATCC TGA GCAA	
	CACGCTAGG ACT CGTT	
	ACCG_ GA	
GAM2414 KIAA0931 3'	TTGCCCCATAGTTGGGGTAAGC 68024	GA__ AA
A	TGC TCCAACATATG GCAA	
	ACG GGGTTGATAC CGTT	
	AATG CC	
GAM2414 KIAA1486 3'	TTGCAGTGAGCTGAGATCGCAC 67983	_ A ATGAA
	GTGCGATC CA CT GCAA	
	CACGCTAG GT GA CGTT	
	A C GTGA_	
GAM2414 KIAA1644 3'	TTGCAGTGAGCTGAGATCGCAC 86224	_ A ATGAA
	GTGCGATC CA CT GCAA	

		CACGCTAG GT GA CGTT	
		A C GTGA_	
GAM2414 LIN-28	3'	TTGCAGTGAGCTGAGATCGCAC 45474	_ A ATGAA
		GTGCGATC CA CT GCAA	
		CACGCTAG GT GA CGTT	
		A C GTGA_	
GAM2414 MGC29891	3'	TTGCAGTGAGCTGAGATCGCAC 58877	_ A ATGAA
		GTGCGATC CA CT GCAA	
		CACGCTAG GT GA CGTT	
		A C GTGA_	
GAM2414 PLP1	3'	TTGCTTCATAGCTGGTTC 6761 T A	
		GA CCA CTATGAAGCAA	
		CT GGT GATACTTCGTT	
		T C	
GAM2414 WBSCR23	3'	TTGCCGTGAGCCAAGATCGCAC 47453	CAA_ _ AA
		GTGCGATC CT ATG GCAA	
		CACGCTAG GA TGC CGTT	
		AACC G _	
GAM2414 LOC116236	3'	TTGCAGTGAGCTGAGATCGCAC 74250	_ A ATGAA
		GTGCGATC CA CT GCAA	
		CACGCTAG GT GA CGTT	
		A C GTGA_	
GAM2414 LOC126669	3'	TGCAGCGAGCCATGATCGCAC 75954	CAA_ A AA
		GTGCGATC CT TG GCA	
		CACGCTAG GA GC CGT	
		TACC _ GA	
GAM2414 LOC142779	3'	TTGCAGTGAGCTGAGATCGCAC 76910	_ A ATGAA
		GTGCGATC CA CT GCAA	
		CACGCTAG GT GA CGTT	
		A C GTGA_	
GAM2414 LOC146475	5'	TTGCAGTGAGCTGAGATCGCAC 84694	_ A ATGAA
		GTGCGATC CA CT GCAA	
		CACGCTAG GT GA CGTT	
		A C GTGA_	
GAM2414 LOC146958	3'	TGCAGTGAGCTGTGATCGCAC 84951	_ A ATGAA
		GTGCGATC CA CT GCA	
		CACGCTAG GT GA CGT	
		T C GTGA_	
GAM2414 LOC147700	3'	TTGCTGTGAGCCAAGATCGCAC 59887	CAA_ ATGA
		GTGCGATC CT AGCAA	

	CACGCTAG GA TCGTT	
	AACC GTG_	
GAM2414 LOC149579 5'	TTGCAGTCAGCCAGGATCGCAC 71697	AACTA A_
	GTGCGATCC TGA GCAA	
	CACGCTAGG ACT CGTT	
	ACCG_ GA	
GAM2414 LOC149628 3'	TTGCAGTGAGCTGAGATCGCAC 80282	_ A ATGAA
	GTGCGATC CA CT GCAA	
	CACGCTAG GT GA CGTT	
	A C GTGA_	
GAM2414 LOC155072 3'	TTGCAGTGAGCTGAGATCGCAC 87674	_ A ATGAA
	GTGCGATC CA CT GCAA	
	CACGCTAG GT GA CGTT	
	A C GTGA_	
GAM2414 LOC202868 3'	TTGCAGTGAGCTGAGATCGCAC 92011	_ A ATGAA
	GTGCGATC CA CT GCAA	
	CACGCTAG GT GA CGTT	
	A C GTGA_	
GAM2414 LOC221178 3'	TTGCAGTGAGCTGAGATCGCAC 95180	_ A ATGAA
	GTGCGATC CA CT GCAA	
	CACGCTAG GT GA CGTT	
	A C GTGA_	
GAM2414 LOC221410 3'	TTGCAGTGGGCCAAGATCGCAC 93702	CAA__ GAA
	GTGCGATC CTAT GCAA	
	CACGCTAG GGTG CGTT	
	AACCG A__	
GAM2414 LOC221543 3'	TTGCAGTGAGCTGAGATCGCAC 95392	_ A ATGAA
	GTGCGATC CA CT GCAA	
	CACGCTAG GT GA CGTT	
	A C GTGA_	
GAM2414 LOC253639 3'	TTGCAGTGAGCTGAGATCGCAC 97521	_ A ATGAA
	GTGCGATC CA CT GCAA	
	CACGCTAG GT GA CGTT	
	A C GTGA_	
GAM2414 LOC253778 5'	TGCAGTGAGCTGAGATCGCAC 96529	_ A ATGAA
	GTGCGATC CA CT GCA	
	CACGCTAG GT GA CGT	
	A C GTGA_	
GAM2414 LOC255030 5'	TTGCAGTAAGTTGAGATCGCAC 99088	_ A AA
	GTGCGATC CAACT TG GCAA	

		CACGCTAG GTTGA AT CGTT	
		A _ GA	
GAM2414	LOC255042 3'	TTGCAGTGAGTCAGGATCGCAC 97064	A_ ATGAA
		GTGCGATCC ACT GCAA	
		CACGCTAGG TGA CGTT	
		AC GTGA_	
GAM2414	LOC255042 3'	TTGTGGTGAGCTGAGATCGCAC 97065	_ A ATGAA
		GTGCGATC CA CT GCAA	
		CACGCTAG GT GA TGTT	
		A C GTGG_	
GAM2414	LOC256658 3'	TTGCAGTCAGCCGAGATCGCAC 99149	CAACTA A_
		GTGCGATC TGA GCAA	
		CACGCTAG ACT CGTT	
		AGCCG_ GA	
GAM2414	LOC257596 3'	TTGCAGTGAGCTGAGATCGCAC 99795	_ A ATGAA
		GTGCGATC CA CT GCAA	
		CACGCTAG GT GA CGTT	
		A C GTGA_	
GAM2414	LOC90784 5'	TGCAATGAGCTGTGATCGCAC 64704	_ A ATGAA
		GTGCGATC CA CT GCA	
		CACGCTAG GT GA CGT	
		T C GTAA_	
GAM2415	FGB 3'	TCATTTCTCTTGCTCACCAAGA 18911	_ CC
	A	TTCTTGGTGAG AAGGG GGATGA	
		AAGAACCACTC TTCTC TTTACT	
		G _	
GAM2415	FLOT2 3'	CACCCGGCCCTCCCTCCAG 16796	TGA A A
		TTGG GA GGGCCGG TG	
		GACC CT CCCGGCC AC	
		TCC _ C	
GAM2415	MCL1 3'	CCTCCCTCCCCACCAAGAG 41988	AGA CC
		TTCTTGGTG AGGG GG	
		GAGAACCAC TCCC CC	
		CCC T_	
GAM2415	PLA2G2D 3'	CCACCTCTCCCAACCAAGAG 25711	A AG CC
		TTCTTGGTG GA GG GG	
		GAGAACCAC CT CC CC	
		C CT A_	
GAM2415	PPP3CA 5'	CATCCCCCTTCCCCCAAGAA 8135	TGA CC
		TTCTTGG GAAGGG GGATG	

		AAGAACC CTTCCC CCTAC		
		CC_ _		
GAM2415 SAG	5'	CACCCGGCCCTTCCCACCTGG 6772	T A	A
		CT GGTG GAAGGGCCGG TG		
		GG CCAC CTTCCCGGCC AC		
		T C C		
GAM2415 TNR	3'	TCACCTCCTTTCCCACCAAGGA 13824	A	CC A
		TTCTTGGTG GAAGGG GG TGA		
		AGGAACCAC CTTTCC CC ACT		
		C T_ _		
GAM2415 CEACAM4	3'	CCACCCGGGGTCACCAGGAA 10192		GAA_ CC
		TTCTTGGTGA GGG GG		
		AAGGACCACT CCC CC		
		GGGG A_		
GAM2415 FBXO30	3'	CATAGGCTTCACCACCAAGAA 50489	AGAA	GG
		TTCTTGGTG GGGCC ATG		
		AAGAACCAC TTCGG TAC		
		CAC_ A_		
GAM2415 FLJ11286	3'	CCATGTCCTCTCACCAGAA 37792	T A	C_
		TTCT GGTGAGA GGGC GG		
		AAGA CCACTCT CCTG CC		
		_ _ TA		
GAM2415 FLJ12389	3'	GGACCCTCCTCACCAGGAA 60901	A	_
		TTCTTGGTGAG AGGG CC		
		AAGGACCACTC TCCC GG		
		C A		
GAM2415 FLJ13154	3'	CCACCCACACTCACCAGAA 45104	T	AA_ CC
		TTCT GGTGAG GGG GG		
		AAGA CCACTC CCC CC		
		_ ACA A_		
GAM2415 GRWD	3'	CAGTGACCCCTCTCACCAGAA 49777	_	A C GA
		TCTT GGTGAGA GGG CG TG		
		AGAA CCACTCT CCC GT AC		
		A C A G_		
GAM2415 moblak	3'	CCACCCTACTCCTCACCAGAA 56388	T	A_ CC
		TTCT GGTGAG AGGG GG		
		AAGA CCACTC TCCC CC		
		_ CTCA A_		
GAM2415 STMN3	3'	CATCTCCCTCTCCCCACCAAGA 32464	A_ _	CC
		TCTTGGTG GA AGGG GGATG		

			AGAACCAC CT TCCC TCTAC		
			CC C _		
GAM2415	TU3A	3'	CCAGGCCTTCCCACCAGGAA 24179	A	G _
			TTCTTGGTG GAAGG CC GG		
			AAGGACCAC CTTCC GG CC		
			C _ A		
GAM2415	LOC220143	5'	CACCAGCCTCTCACCAGAA 95233	T	AG C A
			TTCT GGTGAGA GGC GG TG		
			AAGA CCACTCT CCG CC AC		
			_ _ A _		
GAM2415	LOC96652	5'	CATCGCGACCTCACCAAGAA 66073		AAGG C
			TTCTTGGTGAG GC GGATG		
			AAGAACCACTC CG CCTAC		
			CAG_ _		
GAM2416	LDLR	3'	AGCCAAACCCCTAAACTCA 6723	T	C ATGA
			TG AGTT AG GGTTTGGCT		
			AC TCAA TC CCAAACCGA		
			_ A C_		
GAM2416	ROBO1	3'	AAGCCAAACAAAACCTGAACCAC 12891	A	ATGAG
	A		TGT GTTCAG GTTTGGCTT		
			ACA CAAGTC CAAACCGAA		
			C AAAA_		
GAM2416	ATP6V1G3	3'	CCAGAAATCCATGTGAACTACA 56658	G	_ GG
			TGTAGTTCA ATG A TTTGG		
			ACATCAAGT TAC T AGACC		
			G C AA		
GAM2416	PI4KII	3'	CCAAACCTGACCTGAACTTACA 37949	_	ATG
			TGTA GTTCAG AGGTTTGG		
			ACAT CAAGTC TCCAAACC		
			T CAG		
GAM2416	LOC151701	5'	AGGACTAGCTTCATCTGAACCA 86666	A	TGG
	CA		TGT GTTCAGATGAGGTT CTT		
			ACA CAAGTCTACTTCGA GGA		
			C TCA		
GAM2417	BHMT2	3'	CTGACCAACATGGTGAAACCC 34731		
			GGGTTTCACCATGTTGGTCAG		
			CCCAAAGTGGTACAACCAGTC		
GAM2417	C21orf5	3'	CTGACCAACATGGTGAGACCC 18884		
			GGGTTTCACCATGTTGGTCAG		

CCCAGAGTGGTACAACCAGTC

GAM2417 CHST5 3' CTGGCCAACATAGTGAAACCC 25088 C
GGGTTTCAC ATGTTGGTCAG
||||||| |||||||||
CCCAAAGTG TACAACCGGTC

A

GAM2417 COG7 3' CTGACCAACATGGTGAAACCC 68251
GGGTTTCACCATGTTGGTCAG
||||||| |||||||||
CCCAAAGTGGTACAACCAGTC

GAM2417 CORO2A 3' CTGACCAACATGGTGAAACCC 54494
GGGTTTCACCATGTTGGTCAG
||||||| |||||||||
CCCAAAGTGGTACAACCAGTC

GAM2417 CORO2A 3' CTGACCAACATGGTGAAACCC 14102
GGGTTTCACCATGTTGGTCAG
||||||| |||||||||
CCCAAAGTGGTACAACCAGTC

GAM2417 CPM 3' CTGACCAACATGGTGAAACCC 60406
GGGTTTCACCATGTTGGTCAG
||||||| |||||||||
CCCAAAGTGGTACAACCAGTC

GAM2417 F2R 3' CTAACACGGTGAAACCCGTC 10565 A
GATGGGTTTCACC TGTGG
||||||| |||||
CTGCCCAAAGTGG ACAATC

C

GAM2417 FUT6 3' CCAATATGGTGAAACCCGTC 5632
GATGGGTTTCACCATGTTGG
||||||| |||||||||
CTGCCCAAAGTGGTATAACC

GAM2417 HIP1 3' CTGTCCAACATGGTGAAACCC 19256 T
GGGTTTCACCATGTTGG CAG
||||||| |||||
CCCAAAGTGGTACAACC GTC

T

GAM2417 IL18 3' CTGACCAACATGGTGAAACCTC 9592 _
AT ATG GGTTCACCATGTTGGTCAG
||| |||||||||
TAC CCAAAGTGGTACAACCAGTC

T

GAM2417 MASP1 3' CTGACCACTTATCAAACCCATC 58212 CACCAT T
GATGGGTTT GT GGTCAG
||||||| || |||||

			CTACCCAAA	CA CCAGTC	
			CTATT_ _		
GAM2417	MUC3B	3'	CCA	ACTTGGCTGAAACCCA	95919 _ T
			TGGGTTTCA	CCA GTTGG	
			ACCCAAAGT	GGT CAACC	
			C	T	
GAM2417	P2RY6	5'	TGA	ACATAGGAAACCCA	16001 ACC TGG
			TGGGTTTC	ATGT TCA	
			ACCCAAAG	TACA AGT	
			GA_ _ _		
GAM2417	PA2G4	3'	ACCA	ACATGGCGAAACCC	71819 A
			GGGTTTC	CCATGTTGGT	
			CCCAAAG	GGTACAACCA	
			C		
GAM2417	POLH	3'	CCA	ACATGGCAAAACCATC	22477 G CA
			GATGG	TTT CCATGTTGG	
			CTACC	AAA GGTACAACC	
			_	AC	
GAM2417	PSMB2	3'	CTG	ACCAACATGGTGAAACCC	12470
			GGGTTTC	ACCATGTTGGTCAG	
			CCCAAAGTGGTACAACCAGTC		
GAM2417	RBM3	3'	CTG	ACCAACATGGTGAAACCC	71009
			GGGTTTC	ACCATGTTGGTCAG	
			CCCAAAGTGGTACAACCAGTC		
GAM2417	SLC14A2	3'	CTGG	CGAACATGGTGAGACCCA	24116 G
	TC		GATGGGTTTC	ACCATGTT GTCAG	
			CTACCCAGAGTGGTACAA	CGGTC	
			G		
GAM2417	TCTA	3'	CTG	ACCAACATGGTGAAAACCC	42495 _
			GGGTTT	CACCATGTTGGTCAG	
			CCCAA	GTGGTACAACCAGTC	
			A		
GAM2417	ALTE	3'	ACCA	ACATGGTGAAACCTCGT	17572 _
			ATG	GGTTTCACCATGTTGGT	
			TGC	CCAAAGTGGTACAACCA	
			T		
GAM2417	C1QTNF2	3'	CTG	ACCAACATGGCAAAACATC	49974 GG TCA
			GATG	TT CCATGTTGGTCAG	

CTAC AA GGTACAACCAGTC
 AA C__
 GAM2417 CCR6 3' CTGGCCAACATGGCGAAACCCC 49401 T A
 TC GA GGGTTTC CCATGTTGGTCAG
 || ||||| |||||
 CT CCCAAAG GGTACAACCGGTC
 C C
 GAM2417 CCR6 3' CTGGCCAACATGGCGAAACCCC 16442 T A
 TC GA GGGTTTC CCATGTTGGTCAG
 || ||||| |||||
 CT CCCAAAG GGTACAACCGGTC
 C C
 GAM2417 CHRFAM7A 3' CTGACCAATGTGATAAAACCC 96720 CAC
 GGGTTT CATGTTGGTCAG
 ||||| |||||
 CCCAAA GTGTAACCAGTC
 ATA
 GAM2417 CNNM1 3' CTGGCCAACATGGTGAAACCC 40118
 GGGTTTCACCATGTTGGTCAG
 |||||
 CCCAAAGTGGTACAACCGGTC

 GAM2417 DKFZP434I1735 3' CTGACCAACATGGTGAAACCC 89168
 GGGTTTCACCATGTTGGTCAG
 |||||
 CCCAAAGTGGTACAACCGTC

 GAM2417 DKFZP434N161 3' CTGGGCAACACAGCAAGACCCA 79216 CACCA G
 TC GATGGGTTT TGTG TCAG
 ||||| |||||
 CTACCCAGA ACAAC GGTC
 ACGAC G
 GAM2417 FLJ10520 3' CTGACCAACATGGTGAAACCC 36705
 GGGTTTCACCATGTTGGTCAG
 |||||
 CCCAAAGTGGTACAACCGTC

 GAM2417 FLJ10547 3' GCTGACCAACATGGTGAAATGA 36776 _____
 AACCCCAT ATGGG TTTCACCATGTTGGTCAG C
 ||||| |||||
 TACCC AAAGTGGTACAACCGTC G
 CAAAGT _____
 GAM2417 FLJ10803 3' CTGACCAACATGGCAAAACCC 37201 CA
 GGGTTT CCATGTTGGTCAG
 ||||| |||||
 CCCAAA GGTACAACCGTC
 AC
 GAM2417 FLJ10971 3' CCAGTATGAATAGTGGAACCC 37482 - _____
 ATC GATGGGTTTC AC CATGTTGG
 ||||| || |||||

	CTACCCAAAG TG GTATGACC		
	G ATAA		
GAM2417 FLJ11700 3'	CTGGCCAACATGGTGAAACCC 46562		
	GGGTTTCACCATGTTGGTCAG		
	CCCAAAGTGGTACAACCGGTC		
GAM2417 FLJ11996 3'	CTGACCAACATGGTGAAAT 47060		
	GTTTCACCATGTTGGTCAG		
	TAAAGTGGTACAACCGGTC		
GAM2417 FLJ12178 3'	CTTACACGGTGAAACCCA 47828	A	T
	TGGGTTTCACC TGT GG		
	ACCCAAAGTGG ACA TC		
	C T		
GAM2417 FLJ12294 3'	CTGGCCAACATGGTGAAACCC 47715		
	GGGTTTCACCATGTTGGTCAG		
	CCCAAAGTGGTACAACCGGTC		
GAM2417 FLJ12363 3'	CTGACCAACATGGTGAAACCC 50635		
	GGGTTTCACCATGTTGGTCAG		
	CCCAAAGTGGTACAACCGGTC		
GAM2417 FLJ12660 3'	CTGACCAACATGGTGAAACCC 47895		
	GGGTTTCACCATGTTGGTCAG		
	CCCAAAGTGGTACAACCGGTC		
GAM2417 FLJ13659 3'	CTGACCAACATGGTGAAATCC 48030		
	GGGTTTCACCATGTTGGTCAG		
	CCTAAAGTGGTACAACCGGTC		
GAM2417 FLJ13848 3'	CTGGTCAACATGGCAAAGCCC 45820	CA_	GT
ATC	GATGGGTTT CCATGTTG CAG		
	CTACCCGAA GGTACAAC GTC		
	AAC TG		
GAM2417 FLJ14129 3'	CTGGCCAACATGGCAAACCC 48807	CA	
	GGGTTT CCATGTTGGTCAG		
	CCCAA GGTACAACCGGTC		
	AC		
GAM2417 FLJ14326 3'	CCAACAGGTGAAACCCCATC 50763	_	A
	GATGGG TTTCACC TGTTGG		

			CTACCC AAAGTGG ACAACC		
			C _		
GAM2417	FLJ20004	3'	CTGGCCAACATGGTGAAACCCA 34760		
	TC		GATGGGTTTCACCATGTTGGTCAG		
			CTACCCAAAGTGGTACAACCGGTC		
GAM2417	FLJ20045	3'	CCAAATGGTGAAACCCCATC 34878	_	G
			GATGGG TTTACCAT TTGG		
			CTACCC AAAGTGGTA AACC		
			C _		
GAM2417	FLJ20069	3'	CTGACCAACATGGTGAAACCC 34951		
			GGGTTTCACCATGTTGGTCAG		
			CCCAAAGTGGTACAACCAGTC		
GAM2417	FLJ22167	3'	CTGGCCAACATAGTGAAACCC 44870		C
			GGGTTTCAC ATGTTGGTCAG		
			CCCAAAGTG TACAACCGGTC		
			A		
GAM2417	FLJ23499	3'	CTGACCAACATGGTGAAACACT 43134	_	
	GT		ATGG GTTTCACCATGTTGGTCAG		
			TGTC CAAAGTGGTACAACCAGTC		
			A		
GAM2417	FLJ30681	3'	CTGACCAACATGGTGAAACCC 93434		
			GGGTTTCACCATGTTGGTCAG		
			CCCAAAGTGGTACAACCAGTC		
GAM2417	FLJ31455	3'	CTGGCCAACATGGTGAAACCCT 59284	T	
	TC		GA GGGTTTCACCATGTTGGTCAG		
			CT CCCAAAGTGGTACAACCGGTC		
			T		
GAM2417	FRSB	3'	CTGACCAACATGATGAAATGCC 20291	_	C
	AT		ATGG GTTTCA CATGTTGGTCAG		
			TACC TAAAGT GTACAACCAGTC		
			G A		
GAM2417	FUSIP1	3'	CTGACCAACACGGTGAAACCC 55037		A
			GGGTTTCACC TGTTGGTCAG		
			CCCAAAGTGG ACAACCAGTC		
			C		
GAM2417	HAPIP	3'	CTAATCTGAAAAACCCATC 15465	CA	T
			GATGGGTTT CCA GTTGG		

		CTACCCAAA GGT TAATC	
		AA C	
GAM2417	KIAA0441	3' CTGACCAACATAGTGAAACCC 29633	C
		GGGTTTCAC ATGTTGGTCAG	
		CCCAAAGTG TACAACCAGTC	
		A	
GAM2417	KIAA0798	3' CTGACCAACATGGTGAGGCC 28446	
		GGGTTTCACCATGTTGGTCAG	
		CCCGGAGTGGTACAACCAGTC	
GAM2417	KIAA0872	3' CTGACCAACATGGTGAAACACC 30754	_
	AT	ATGG GTTTCACCATGTTGGTCAG	
		TACC CAAAGTGGTACAACCAGTC	
		A	
GAM2417	KIAA1404	3' CTGACCAACATGGCGAAACCC 62688	A
		GGGTTTC CCATGTTGGTCAG	
		CCCAAAG GGTACAACCAGTC	
		C	
GAM2417	KIAA1456	5' CTGACCAACATGGAGAAACCCA 67549	A
	TC	GATGGGTTTC CCATGTTGGTCAG	
		CTACCCAAAG GGTACAACCAGTC	
		A	
GAM2417	KIAA1456	3' CTGACCAACATGGTGAAACCC 67550	
		GGGTTTCACCATGTTGGTCAG	
		CCCAAAGTGGTACAACCAGTC	
GAM2417	KIAA1614	3' CCACATGGTGAAACCCAT 70664	T
		ATGGGTTTCACCATGT GG	
		TACCCAAAGTGGTACA CC	
GAM2417	KIAA1811	5' CTGACCAACATGGTGAAACCC 65417	
		GGGTTTCACCATGTTGGTCAG	
		CCCAAAGTGGTACAACCAGTC	
GAM2417	KLHL8	3' CTGACCAACATGGTGAAACCC 63513	
		GGGTTTCACCATGTTGGTCAG	
		CCCAAAGTGGTACAACCAGTC	
GAM2417	KREMEN	3' CCAACATGGCGAAAACCCATC 50230	_ A
		GATGGGTTT C CCATGTTGG	

CTACCCAAA G GGTACAACC
 A C
 GAM2417 MGC10765 3' CTGACCAACATGGTGAAACGCC 44561 _
 AT ATGG GTTTCACCATGTTGGTCAG
 |||| ||||||||||||||
 TACC CAAAGTGGTACAACCAGTC
 G
 GAM2417 MGC13053 3' GCCAACATGGTGAAACCC 52110
 GGGTTTCACCATGTTGGT
 ||||||||||||||
 CCCAAAGTGGTACAACCG

 GAM2417 MGC14799 3' GACCAACATGGTGAAACCC 51328
 GGGTTTCACCATGTTGGTC
 ||||||||||||||
 CCCAAAGTGGTACAACCAG

 GAM2417 MGC29937 3' CTGACCAACATGGTGAAACCC 58728
 GGGTTTCACCATGTTGGTCAG
 ||||||||||||||
 CCCAAAGTGGTACAACCAGTC

 GAM2417 MGC4771 3' CTGACCAACATAGTGAAACCC 52003 C
 GGGTTTCAC ATGTTGGTCAG
 |||||| ||||||||
 CCCAAAGTG TACAACCAGTC
 A
 GAM2417 MRP63 3' CCAAGGTGATAAAACCCGTC 44043 CAC G
 GATGGGTTT CAT TTGG
 |||||| ||| ||||
 CTGCCCAA GTG AACC
 ATA G
 GAM2417 MYO3B 3' CTGACCAACATGGTGAAACCC 58110
 GGGTTTCACCATGTTGGTCAG
 ||||||||||||||
 CCCAAAGTGGTACAACCAGTC

 GAM2417 PB1 3' CTGACCAACATGGTGAAACCTC 37576 _
 AT ATG GGTTCACCATGTTGGTCAG
 || ||||||||||||||
 TAC CCAAAGTGGTACAACCAGTC
 T
 GAM2417 SPRY4 3' CCAATATGGTAAACCCCATC 49005 T C
 GATGGG TT ACCATGTTGG
 |||| || ||||||||
 CTACCC AA TGGTATAACC
 C A
 GAM2417 ZNF197 3' CTGACCAACATGGTGAAACCC 23754
 GGGTTTCACCATGTTGGTCAG
 ||||||||||||||

CCCAAAGTGGTACAACCAGTC

GAM2417 ZNF271 3' CTGACCAACATGGTGAAACCC 96964
GGGTTTCACCATGTTGGTCAG
|||||
CCCAAAGTGGTACAACCAGTC

GAM2417 ZNF297B 3' CTGACCAACATAGTGAAACCC 26654 C
GGGTTTCAC ATGTTGGTCAG
|||||
CCCAAAGTG TACAACCAGTC
A

GAM2417 ZNF33A 3' CTGGTCAACATGGTGAAACCC 92995 GT
GGGTTTCACCATGTTG CAG
|||||
CCCAAAGTGGTACAAC GTC
TG

GAM2417 ZNF347 3' CTGACCAACATGGCGAAACCC 51824 A
GGGTTTC CCATGTTGGTCAG
|||||
CCCAAAG GGTACAACCAGTC
C

GAM2417 LOC127262 3' CTGGGCAACATGGTGAAACCCG 76597 G
TC GATGGGTTTCACCATGTTG TCAG
|||||
CTGCCCAAAGTGGTACAAC GGTC
G

GAM2417 LOC131744 3' CTGACCAACATGGTGAAACCC 76388
GGGTTTCACCATGTTGGTCAG
|||||
CCCAAAGTGGTACAACCAGTC

GAM2417 LOC145082 5' CTGACCAACATGGCAAAACCC 84187 CA
GGGTTT CCATGTTGGTCAG
|||||
CCCAA GGTACAACCAGTC
AC

GAM2417 LOC145216 3' CTGACCAACATGACAAAACCC 84221 CAC
GGGTTT CATGTTGGTCAG
|||||
CCCAA GTACAACCAGTC
ACA

GAM2417 LOC145231 3' CTGACCAACATGGTGAAACT 84247
GGTTTCACCATGTTGGTCAG
|||||
TCAAAGTGGTACAACCAGTC

GAM2417 LOC146545 5' CTGACCAACACAGCTGCTCA 78533 TTCACCA
TGGGT TGTTGGTCAG
|||||

	ACTCG	ACAACCAGTC	
	TCGAC__		
GAM2417 LOC146756 3'	CTGACCAACATGGTGAAACCTC	84802	—
A	TG GGTTCACCATGTTGGTCAG		
	AC CCAAAGTGGTACAACCAGTC		
	T		
GAM2417 LOC148758 5'	CCACATGGTGAAACCCAT	79721	T
	ATGGGTTTCACCATGT GG		
	TACCCAAAGTGGTACA CC		
GAM2417 LOC148946 3'	GGCCAACATGGTGAAACCCGTC	85470	
	GATGGGTTTCACCATGTTGGTC		
	CTGCCCAAAGTGGTACAACCGG		
GAM2417 LOC149073 3'	CTGACCAACATGGCGAAACCC	85483	A
	GGGTTTC CCATGTTGGTCAG		
	CCCAAAG GGTACAACCAGTC		
	C		
GAM2417 LOC149113 5'	CTGACCAACATGGTGAAACCC	79909	
	GGGTTTCACCATGTTGGTCAG		
	CCCAAAGTGGTACAACCAGTC		
GAM2417 LOC149194 3'	ACCAGTAAAACCCATC	79973	C CATGT
	GATGGGTTT AC TGGT		
	CTACCCAAA TG ACCA		
	A		
GAM2417 LOC150185 3'	CTGACCAACATGGTAGAACCC	86068	TC
	GGGTT ACCATGTTGGTCAG		
	CCCAA TGGTACAACCAGTC		
	GA		
GAM2417 LOC153260 3'	CTGACCAACATGGTGAAACCC	81671	
	GGGTTTCACCATGTTGGTCAG		
	CCCAAAGTGGTACAACCAGTC		
GAM2417 LOC154403 5'	CTGACCAACATGGTGAAACCC	81975	
	GGGTTTCACCATGTTGGTCAG		
	CCCAAAGTGGTACAACCAGTC		
GAM2417 LOC154739 5'	CTGACCAACATGGTGAAACCC	87438	
	GGGTTTCACCATGTTGGTCAG		

CCCAAAGTGGTACAACCAGTC

GAM2417 LOC154992 5' CTGACCAACATGGTGAAACCC 82136
GGGTTTCACCATGTTGGTCAG
|||||||
CCCAAAGTGGTACAACCAGTC

GAM2417 LOC157660 3' CTGACCAACATGGTGAAACCC 87802
GGGTTTCACCATGTTGGTCAG
|||||||
CCCAAAGTGGTACAACCAGTC

GAM2417 LOC197201 3' CTGGGCAACATGGCGAAAACCC 89273 _ A G
ATC GATGGGTTT C CCATGTTG TCAG
||||||| | ||||| ||||
CTACCCAAA G GGTACAAC GGTC
A C G

GAM2417 LOC200251 5' CTGACCAACACGATGAAACCC 90061 CCA
GGGTTTCA TGTTGGTCAG
||||||| |||||
CCCAAAGT ACAACCAGTC
AGC

GAM2417 LOC200728 3' CTAACACGGTGAAACCCA 91684 A
TGGGTTTCACC TGTTGG
||||||| |||||
ACCCAAAGTGG ACAATC
C

GAM2417 LOC200731 3' CCAACATGATGAAACCATC 91694 G C
GATGG TTTCA CATGTTGG
|||| |||| |||||
CTACC AAAGT GTACAACC
_ A

GAM2417 LOC201810 3' CTGACCAACATGGTGAAACCC 90501
GGGTTTCACCATGTTGGTCAG
|||||||
CCCAAAGTGGTACAACCAGTC

GAM2417 LOC201868 5' CTGACCAACATGGTGAAACCC 90524
GGGTTTCACCATGTTGGTCAG
|||||||
CCCAAAGTGGTACAACCAGTC

GAM2417 LOC219722 5' CTGACCAACATGGTGAAACTC 94679
GGGTTTCACCATGTTGGTCAG
|||||||
CTCAAAGTGGTACAACCAGTC

GAM2417 LOC221550 3' CCAACATGGCAAAAACCCATC 93743 CA_
GATGGGTTT CCATGTTGG
||||||| |||||

	CTACCCAAA GGTACAACC		
	AAC		
GAM2417 LOC221641 5'	CTGACCAACATGGTGAAACGCT 95344	_	
AT	ATGG GTTTCACCATGTTGGTCAG		
	TATC CAAAGTGGTACAACCAGTC		
	G		
GAM2417 LOC221893 3'	CAACAGGATGAAACCCATC 94095	_ A	
	GATGGGTTTCA CC TGTTG		
	CTACCCAAAGT GG ACAAC		
	A _		
GAM2417 LOC221954 5'	CTGGCCAACATGGTGAAACCCG 95647		
TC	GATGGGTTTCACCATGTTGGTCAG		
	CTGCCCAAAGTGGTACAACCGGTC		
GAM2417 LOC253612 5'	CTGACCAACATGGTGAAACCC 98547		
	GGGTTTCACCATGTTGGTCAG		
	CCCAAAGTGGTACAACCAGTC		
GAM2417 LOC254531 5'	CTGACCAACATGGCAAAACCC 96666	CA	
	GGGTTT CCATGTTGGTCAG		
	CCCAA GGTACAACCAGTC		
	AC		
GAM2417 LOC255196 3'	CTGGGGAACATAATGAGACCCA 98957	CC GG	
TC	GATGGGTTTCA ATGTT TCAG		
	CTACCCAGAGT TACAA GGTC		
	AA GG		
GAM2417 LOC255196 3'	GGCCAACATGGTGAAACCC 98961		
	GGGTTTCACCATGTTGGTC		
	CCCAAAGTGGTACAACCGG		
GAM2417 LOC255937 3'	CTGACCAACATGGTGAAACTCC 97681	_	
AT	ATGG GTTTCACCATGTTGGTCAG		
	TACC CAAAGTGGTACAACCAGTC		
	T		
GAM2417 LOC257495 3'	CCAACATGGCAAAAACCCATC 99570	CA_	
	GATGGGTTT CCATGTTGG		
	CTACCCAAA GGTACAACC		
	AAC		
GAM2417 LOC257576 3'	CCAACATGGCAAAAACCCATC 99707	CA_	
	GATGGGTTT CCATGTTGG		

CTACCCAAA GGTACAACC
 AAC
 GAM2417 LOC51267 3' ACCAACCTCAGAAACCCAT 33672 ACCAT
 ATGGGTTTC GTTGGT
 ||||| |||||
 TACCCAAAG CAACCA
 ACTC_
 GAM2417 LOC57118 3' CTGACCAACATGGTGAAACCC 40221
 GGGTTTCACCATGTTGGTCAG
 |||||
 CCCAAAGTGGTACAACCAGTC

 GAM2417 LOC85479 5' CTAACACAGTGAAAGCCCATC 53566 _ CA
 GATGGGTTT CAC TGTTGG
 ||||| || |||||
 CTACCCGAA GTG ACAATC
 A AC
 GAM2417 LOC90918 5' CTGACCAACATGGTGAAACCC 65000
 GGGTTTCACCATGTTGGTCAG
 |||||
 CCCAAAGTGGTACAACCAGTC

 GAM2417 LOC93132 5' CTGACCAACATGGTGAAACCC 71985
 GGGTTTCACCATGTTGGTCAG
 |||||
 CCCAAAGTGGTACAACCAGTC

 GAM2418 HRH1 3' CTCAAACATGTTTAGAGTGGA 7819 A TGG
 TCCA TCTGA GCATGTTTGAG
 ||| |||| |||||
 AGGT AGATT TGTACAAACTC
 G _
 GAM2418 TRIM37 3' CTCAAATTTGTCATCAG 31625 G T
 CTGATGG CA GTTTGAG
 ||||| || |||||
 GACTACT GT TAAACTC
 _ T
 GAM2418 HTMP10 3' CTCAAAAAAGCCATCAGATCTG 53758 CA G ATG
 A TC ATCTGATGG C TTTGAG
 || ||||| | |||||
 AG TAGACTACC G AAACTC
 TC _ AAA
 GAM2418 PAK2 5' CTCAAATATCACCAAACTAGA 67140 A_ GC
 TCTG TGG ATGTTTGAG
 ||| || |||||
 AGAT ACC TATAAACTC
 CAA AC
 GAM2418 SEMA6A 3' CTCGAGTACCCACCAGA 40818 A CA
 TCTG TGGG TGTTTGAG
 ||| ||| |||||

AGAC ACCC ATGAGCTC
 C ____
 GAM2418 TTY7 3' TCAAACATGCAGGCTGGA 50019 AT GATGG
 TCCA CT GCATGTTTGA
 |||| || |||||
 AGGT GA CGTACAACT
 CG ____
 GAM2418 LOC144766 3' CTCAAACATGAGAAGACTGGG 77481 A GATGGG
 TCCA TCT CATGTTTGAG
 |||| || |||||
 GGGT AGA GTACAACTC
 C AGA ____
 GAM2418 LOC201685 5' TAAACACCCATCAGATGGA 91845 A CA
 TCCA TCTGATGGG TGTTTG
 |||| ||||| ||||
 AGGT AGACTACCC ACAAAT
 - -
 GAM2418 LOC221596 5' CTCAAACAAAACCTCAGATT 93623 TG GCA
 AATCTGA G TGTTTGAG
 ||||| | |||||
 TTAGACT C ACAAACCTC
 - AAA
 GAM2418 LOC93622 3' CTCTGCAGACCATCAGAT 57729 GCA TT
 ATCTGATGG TGT GAG
 ||||| ||| |||
 TAGACTACC ACG CTC
 AG_ T_
 GAM2419 GPD1 3' TCATGCCACCACATTTG 60398 C C
 TAAATG GGTGGCAT GA
 ||||| ||||| ||
 GTTTAC CCACCGTA CT
 A -
 GAM2419 IL5RA 5' TCGCATGGCCACCGCATTT 6906 AT__
 AAATGCGGTGGC CGA
 ||||| |||
 TTTACGCCACCG GCT
 GTAC
 GAM2419 MYO1C 3' TGCCGATGCCAAATATTTG 61873 CGG A
 TAAATG TGGCATCG CA
 |||| ||||| ||
 GTTTAT ACCGTAGC GT
 AA_ C
 GAM2419 C6orf37 3' TGTCACACTGCATTTA 68097 GCATC
 TAAATGCGGTG GACA
 ||||| |||
 ATTTACGTCAC CTGT
 A ____
 GAM2419 DNAJC6 3' TTGCAGAACCACCGCATT 29498 CA GA
 AATGCGGTGG TC CAA
 ||||| || |||

	TTACGCCACC AG GTT	
	A_ AC	
GAM2419 FLJ11210 3'	GTCGATGTGCATGCTTTTA 60319	T GTG
	TAAA GCG GCATCGAC	
	ATTT CGT TGTAGCTG	
	T ACG	
GAM2419 FLJ12476 3'	TCGATCTTCTGCATTTA 43270	T C
	TAAATGCGG GG ATCGA	
	ATTTACGTC TC TAGCT	
	T _	
GAM2419 KIAA1034 3'	TCGATGGCATCCGCATTTG 63134	_ G
	TAAATGCGG TG CATCGA	
	GTTTACGCC AC GTAGCT	
	T G	
GAM2419 KIAA1987 3'	TCATGTAAGTGCATTTA 89391	G C
	TAAATGCGGT GCAT GA	
	ATTTACGTCA TGTA CT	
	A _	
GAM2419 MGC16063 3'	TGTCCTGGCCACTGCATT 54929	ATC
	AATGCGGTGGC GACA	
	TTACGTCACCG CTGT	
	GTC	
GAM2419 LOC147949 3'	TGTCAGATGTCCACATTGCA 79279	_ _ _
	TGCG GTGG CATC GACA	
	ACGT CACC GTAG CTGT	
	TA T A	
GAM2419 LOC150577 3'	GTCCTCACCGCATTTG 86258	CATC
	TAAATGCGGTGG GAC	
	GTTTACGCCACT CTG	
	C_	
GAM2419 LOC158219 3'	TGTGTGTCACCACATT 82694	C CG
	AAATG GGTGGCAT ACA	
	TTTAC CCACTGTG TGT	
	A _	
GAM2419 LOC202020 3'	TGTCTCACCACATTTA 90605	C CATC
	TAAATG GGTGG GACA	
	ATTTAC CCACT CTGT	
	A _	
GAM2419 LOC90826 5'	TGTCGATGCAGGTTTATTTG 64788	CGGTG
	TAAATG GCATCGACA	

GTTTAT CGTAGCTGT
 TTGGA
 GAM2419 LOC93587 3' TTGTCTTTACCTGCATTTA 73042 _ CATC
 TAAATGC GGTGG GACAA
 ||||| |||| ||||
 ATTTACG CCATT CTGTT
 T T__
 GAM2420 EPAC 3' GGCCAAGGAAGGGAGGACAGAG 21456 GG__ AA
 AGG TCTCTC TCCCTTCCTT CC
 ||||| ||||| ||
 GGAGAG AGGGAAGGAA GG
 ACAGG CC
 GAM2420 NCAM2 3' GGTTAAGGAAAAAAAAACGTTGA 17002 T_ GTCCC_
 G CTC CG TTCCTTAACC
 ||| || |||||
 GAG GC AAGGAATTGG
 TT AAAAAA
 GAM2420 DKFZp434N035 3' GGCCAGGGCGGACCGAGAGA 51064 CTT AA
 TCTCTCGGTCC CCTT CC
 ||||| ||| ||
 AGAGAGCCAGG GGGA GG
 C__ CC
 GAM2420 FLJ13615 3' TTAAGGAAATGCAGAAAGATC 47799 C G CCC
 GATCT TC GT TTCCTTAA
 |||| || |||||
 CTAGA AG CG AAGGAATT
 A A TA_
 GAM2420 GREB1 3' GGTTAAGGAAAGAATGCAAGA 28576 CT G CC
 TCT CG TC TTCCTTAACC
 ||| || |||||
 AGA GT AG AAGGAATTGG
 AC A A_
 GAM2420 KIAA1163 3' GGTATAAGAAAAGGCCGAGAGA 79653 CC C _
 TC GATCTCTCGGTC TTC TTA ACC
 ||||| ||| ||| |||
 CTAGAGAGCCGG AAG AAT TGG
 AA _ A
 GAM2420 PIWIL2 5' GGTTAAGGAAGTAACCAGAGA 36546 C CC
 TCTCT GGT CTTCTTAACC
 |||| || |||||
 AGAGA CCA GAAGGAATTGG
 _ AT
 GAM2420 PPAP2C 3' GGTTAAGGAAGGGACCGAGAGA 14932
 TC GATCTCTCGGTCCCTTCCTTAACC
 |||||
 CTAGAGAGCCAGGGAAGGAATTGG
 GAM2420 REA 3' TTAAGGAAGACTGAAGA 24404 C CC
 TCT TCGGTC TTCCTTAA
 ||| |||| |||||

AGA AGTCAG AAGGAATT

GAM2420 LOC149832 5' AGTTGGGGACCAGAAATC 85860 C C TC
GAT TCT GGTCCCT CT
||| ||| ||||| ||
CTA AGA CCAGGGG GA
A _ TT

GAM2420 LOC157226 5' GGAAAAGACCGAGGGATC 64639 CC
GATCTCTCGGTC TTCC
||||||| |||
CTAGGGAGCCAG AAGG
AA

GAM2421 FANCF 3' ACCCAGTGAAGAGTTCTAC 42968 TC_ C
GTAGA CTTC ACTGGGT
|||| ||| |||||
CATCT GAAG TGACCCA
TGA _

GAM2421 KIAA1244 3' ACCCAGTGAAGTGGCTGGTA 72437 AGATC C
TATCAGT CTT CACTGGGT
||||| ||| |||||
ATGGTCG GAA GTGACCCA
GT_ A

GAM2421 LOC148534 3' CCCAGCATATCTGCTGATA 79636 CCTTCCA
TATCAGTAGAT CTGGG
||||||| |||
ATAGTCGTCTA GACCC
TAC_

GAM2422 EHF 3' TCCAAAACCCAAGGTTGGCT 25127 AT _ C
AGT GCCT GGGT TTGGA
||| ||| ||| |||
TCG TGGA CCCA AACCT
GT A A

GAM2422 EPHA2 3' CCATCGGCCAAGAATACTTGAA 16675 GC G T_
G CTTCAAGTAT CT GGTC TGG
||||||| || ||| |||
GAAGTTCATA GA CCGG ACC
A_ A CT

GAM2422 ITGA5 3' CCCAGAGACATACTTGAAG 61933 C_
CTTCAAGTATG CTGGG
||||||| |||
GAAGTTCATAC GACCC
AGA

GAM2422 TREM2 3' TCCAAGACTGTCATATTT 39098 CCTG
AAGTATG GGTCTTGGA
||||| |||||
TTTATAC TCAGAACCT
TG_

GAM2422 UQCRB 3' CCAACATAGGCATACTTAAG 21939 C GGTC
CTT AAGTATGCCTG TTGG
||| ||||| |||

GAA TTCATACGGAT AACC
 _ AC_
 GAM2422 ATP10D 3' CAGAGACCACTTGAAG 73526 ATGCCTG _
 CTTCAAGT GGTCT TG
 ||||| |||||
 GAAGTTCA CCAGA AC
 _____ G
 GAM2422 B3GNT7 3' CCCTTCCAGGCAACCTGAA 71678 A A TCTT
 TTCA GT TGCCTGGG GG
 ||| || ||||| ||
 AAGT CA ACGGACCT CC
 C _ TC_
 GAM2422 DKFZp547I224 3' TCCAAAATTGACCACATACTTG 39963 CCTG ____
 GA TTCAAGTATG GGTC TTGGA
 ||||| ||| |||||
 AGGTTCATAC CCAG AACCT
 A_ TTAA
 GAM2422 FLJ22341 3' CCAAGCTCAGGCACACCCAAG 45114 CAA A T
 CTT GT TGCCTGGG CTTGG
 ||| || ||||| |||||
 GAA CA ACGGACTC GAACC
 CC_ C _
 GAM2422 KIAA0779 3' CCGAACAGCATACTTGAAG 86908 C GGTC
 CTTCAAGTATGC TG TTGG
 ||||| || |||||
 GAAGTTCATACG AC AGCC
 _ A_
 GAM2422 LOC144233 3' CCAAGGCACATAATTGAA 77246 G CCTGG
 TTCAA TATG GTCTTGG
 |||| ||| |||||
 AAGTT ATAC CGGAACC
 A A_
 GAM2422 LOC147341 3' ACCCAGGCATAACTGAAG 85116 AG
 CTTCA TATGCCTGGGT
 |||| |||||
 GAAGT ATACGGACCCA
 CA
 GAM2422 LOC221088 5' TCCAAGGTGCTGGCCACTCGAA 94888 A AT TGGG
 G CTTT AGT GCC TCTTGGA
 |||| ||| ||| |||||
 GAAG TCA CGG GGAACCT
 C C_ TCGT
 GAM2423 ELF3 3' TGACCTTGACCTTGACCAA 16685 T GAT AAA
 TTGGT CAAGG GG GTCA
 |||| |||| || |||||
 AACCA GTTCC TC CAGT
 _ AGT _
 GAM2423 JAK2 3' TGACCTTCATTCTGAGACCAA 18318 CAA AA
 TTGGTT GGGATGGA GTCA
 ||||| ||||| |||||

			AACCAG TCTTACTT CAGT		
			AG_ C_		
GAM2423	SLC10A2	5'	ACTCTCTGTCTTGACCAA 6590	CAA	A
			TTGGTT GGGATGGA AGT		
			AACCAG TTCTGTCT TCA		
			_____ C		
GAM2423	FLJ10803	3'	GTGACTTTTCAGTTAAAGCCAA 37205	CAAGG	G
			TTGGTT GAT GAAAGTCAC		
			AACCGA TTG CTTTCAGTG		
			AA_____ A		
GAM2423	KIAA1958	5'	GTGACTTTGAACCCCAAACC 82788	CAA	ATGG
			GGTT GGG AAAGTCAC		
			CCAA CCC TTTTCAGTG		
			A_____ CAAG		
GAM2423	MARCKS	3'	ACTTTCCACCCTGCCCA 11411	TTCA	A
			TGG AGGG TGGAAAGT		
			ACC TCCC ACCTTTCA		
			CG_____		
GAM2423	TUB	5'	GTGGGACCATCCCTTAAACC 13898	C	AAAG
			GGTT AAGGGATGG TCAC		
			CCAA TTCCCTACC GGTG		
			A AG_____		
GAM2423	LOC80298	3'	ACTTTTACCTTGAACCA 48062	GATG	
			TGGTTCAAGG GAAAGT		
			ACCAAGTTCC TTTTCA		
			A_____		
GAM2424	DDX9	3'	GATCTCTTAAAAATACC 89952	A	C
			GGTAT TTT AAGAGATT		
			CCATA AAA TTCTCTAG		
			A _____		
GAM2424	NCOA3	3'	AATCTCTTAAATACACGTA 22558	GTA	C
			TACG TATTT AAGAGATT		
			ATGC ATAAA TTCTCTAA		
			AC_____		
GAM2424	VNN1	3'	AGAATCTCTTGACATTAC 17421	TATT	
			GTA TCAAGAGATTCT		
			CAT AGTTCTCTAAGA		
			TAC_____		
GAM2424	C20orf21	3'	AATCTCTTGAAAATACTG 35567	A	
			CGGTAT TTTCAAGAGATT		

GTCATA AAAGTTCTCTAA

GAM2424 FLJ13187 3' AATCTGAATATACCG 45159 CAAG
CGGTATATTT AGATT
||||||| ||||
GCCATATAAG TCTAA

GAM2424 FLJ30294 3' TAGAATCTCTCCAGACACC 58897 ATA CA
GGT TTT AGAGATTCTA
||| ||| ||||||||
CCA AGA TCTCTAAGAT
C__ CC

GAM2424 KIAA0256 3' AATTTCTAAATATACC 65046 CA
GGTATATTT AGAGATT
||||||| ||||||
CCATATAAA TCTTTAA

GAM2424 KIAA1243 3' TAGGGTTTGAAACATGCC 74029 A AGA
GGTAT TTTCA GATTCTA
||||| ||||| |||||||
CCGTA AAAGT TTGGGAT
C ____

GAM2424 KIAA1257 3' AGAACCTCTTGAGAGGCAAC 63387 ATA_ A
GT TTTCAAGAG TTCT
|| ||||||| ||||
CA AGAGTTCTC AAGA
ACGG C

GAM2425 FUT1 3' TGGGTCCTCCAAAGA 5616 G G G
TCT TTGGAGGA C CCA
||| ||||||| | |||
AGA AACCTCCT G GGT

GAM2425 LDB1 5' TGGTGCCCCCAGCAGA 15313 A A
TCTGTTGG GG GCGCCA
||||||| || |||||||
AGACGACC CC CGTGGT

GAM2425 LTA 3' TTTGGCCATTCCAACAG 6993 GAGC
CTGTTGGAG GCCAAA
||||||| |||||
GACAACCTT CGGTTT
AC__

GAM2425 NAT1 5' TTGGGAGTCCTCCAAAGA 7261 G G G_
TCT TTGGAGGA C CCAA
||| ||||||| | ||||
AGA AACCTCCT G GGTT

GAM2425 RBL2 3' TTGACGTCTCCAACAGA 20042 GA C
TCTGTTGGAG GCG CAA
||||||| ||| |||

			AGACAACCTC TGC GTT		
			— A		
GAM2425	SLC21A9	3'	TTTGCGCCCCCTGGAGG 24385	GTT A A	
			TCT GG GG GCGCCAAA		
			GGA CC CC CGCGGTTT		
			GGT _ _		
GAM2425	SLC4A7	3'	CTTTTGGTTTATTCCAACA 14617	GAGC	
			TGTTGGAG GCCAAAAG		
			ACAACCTT TGGTTTTC		
			ATT_		
GAM2425	TBXA2R	3'	CTTTTGAACCTCCAACAGG 8356	AGCGC	
			TCTGTTGGAGG CAAAAG		
			GGACAACCTCC GTTTTC		
			AA_		
GAM2425	TFDP2	3'	CTTCTGGAAGCCCCCAATAGA 21890	A A G_ A	
			TCTGTTGG GG GC CCA AAG		
			AGATAACC CC CG GGT TTC		
			_ _ AA C		
GAM2425	TLR1	3'	CTTTTGAAGTTCCAACAAT 13776	GA G_	
			GTTG GGAGC CCAAAG		
			TAAC CCTTG GGTTTTC		
			AA AA		
GAM2425	XRCC5	3'	TTTGCCTGATCCTCCAACAG 41242	GCGC_	
			CTGTTGGAGGA CAAA		
			GACAACCTCCT GTTT		
			AGTCC		
GAM2425	AGPAT1	5'	TTGGCACCGACACCCCGACAGA 22181	A AG_	
			TCTGTTGG GG C GCCAA		
			AGACAGCC CC G CGGTT		
			_ ACA CCA		
GAM2425	dA141H5.1	3'	CTTGAACATCTCCTCCAAAGA 59780	G CGCCAA	
			TCT TTGGAGGAG AAG		
			AGA AACCTCCTC TTC		
			_ TACAAG		
GAM2425	DKFZP434L0117	3'	CTTTTGGCAGGTACAACAGA 43242	GAGGAGC	
			TCTGTTG GCCAAAAG		
			AGACAAC CGGTTTTC		
			ATGGA_		
GAM2425	DKFZp762E1312	5'	TTTGCATCCTTCCTCCACAGA 37906	T CGC_	
			TCTGT GGAGGAG CAAA		

		AGACA CCTCCTT	GTTT		
		— CCTAC			
GAM2425	FLJ14888	3'	CTTTTGGTGGCCCCACA	52748	T A AG
			TGT GG GG CGCCAAAAG		
			ACA CC CC GTGGTTTTC		
			— — G—		
GAM2425	FLJ20113	3'	TGAGCTTCCCCAACAGG	35059	A GC
			TCTGTTGG GGAGC CA		
			GGACAACC CTTCG GT		
			C A—		
GAM2425	FLJ22955	5'	CTTCTGGCACTCCTCTGGTGGA	96825	TG TG C A
			TC T GAGGAG GCCA AAG		
			AG G CTCCTC CGGT TTC		
			GT GT A C		
GAM2425	HUMZD58C02	3'	TTGGCCGTCCCAATAGA	80579	A AGC
			TCTGTTGG GG GCCAA		
			AGATAACC CT CGGTT		
			— GC—		
GAM2425	KIAA0321	5'	TTTGTTCGTGCTGCAACAGA	63066	G G CGC
			TCTGTTG AG AG CAAA		
			AGACAAC TC TC GTTT		
			G G TT—		
GAM2425	KIAA1061	3'	CTTTTGGCAGGAAAACCAATAG	71720	AGGAGC—
A			TCTGTTGG GCCAAAAG		
			AGATAACC CGGTTTTC		
			AAAAGGA		
GAM2425	LHFPL2	3'	CTTCAAGTTGTCTCCAACG	70498	— GCCA
			TGTTGGAGG AGC AAAG		
			GCAACCTCT TTG TTTC		
			G AAC—		
GAM2425	PRKRI	5'	GTGCCTCCTGCCAACAGA	21830	— —
			TCTGTTGG AGGAG CGC		
			AGACAACC TCCTC GTG		
			G C		
GAM2425	RNF8	3'	CTTTTTCAGCTTCTCCAACA	15567	GCC
			TGTTGGAGGAGC AAAAG		
			ACAACCTCTTCG TTTC		
			ACT		
GAM2425	LOC129676	5'	TGAGTTCCTCCCACAGA	76238	T GC
			TCTGT GGAGGAGC CA		

			AGACA CCTCCTTG GT		
			C A_		
GAM2425	LOC91179	3'	TTGGCCGTCCCAATAGA 65768	A AGC	
			TCTGTTGG GG GCCAA		
			AGATAACC CT CGGTT		
			_ GC_		
GAM2426	B2M	3'	TGAGTGCTGTCTCCATGT 15751	A_ CC	
			ACA AGACAGCAC TCA		
			TGT TCTGTCGTG AGT		
			ACC _		
GAM2426	CLASP2	3'	ATGGTGCCAAGGCTGTCTTTGT 65200	ACCCT	
	AT		ATACAAAGACAGC CATCAT		
			TATGTTTCTGTGCG GTGGTA		
			GAACC		
GAM2426	CSN2	3'	ATGATGCCTTTTCCGTCTTTGT 10309	AGCACCCCT	
	AT		ATACAAAGAC CATCAT		
			TATGTTTCTG GTAGTA		
			CCTTTTCC		
GAM2426	DAPP1	3'	ATGATGAAACCTTGTCTTT 27679	CACCC	
			AAAGACAG TCATCAT		
			TTTCTGTT AGTAGTA		
			CCAA_		
GAM2426	FUT1	3'	ATGAAGGAAGTTGGTCTTTGT 5583	_ AC _	
			ACAAAGAC AGC CCT CAT		
			TGTTTCTG TTG GGA GTA		
			G AA A		
GAM2426	IRAK1	3'	ATGATGAGACCCTGTCTCTG 9610	A CACC	
			CA AGACAG CTCATCAT		
			GT TCTGTC GAGTAGTA		
			C CCA_		
GAM2426	MAT1A	3'	ATGATGAGGTAGTACCTTT 92495	ACA AC	
			AAAG GC CCTCATCAT		
			TTTC TG GGAGTAGTA		
			CA_ AT		
GAM2426	OPA1	3'	ATGATATTGCCCTCTTTGTAT 56427	CA CCC	
			ATACAAAGA GCA TCAT		
			TATGTTTCT CGT AGTA		
			CC TAT		
GAM2426	OPA1	3'	ATGATATTGCCCTCTTTGTAT 56431	CA CCC	
			ATACAAAGA GCA TCAT		

		TATGTTTCT CGT AGTA	
		CC TAT	
GAM2426 OPA1	3'	ATGATATTGCCCTCTTTGTAT 56433	CA CCC
		ATACAAAGA GCA TCAT	
		TATGTTTCT CGT AGTA	
		CC TAT	
GAM2426 OPA1	3'	ATGATATTGCCCTCTTTGTAT 56435	CA CCC
		ATACAAAGA GCA TCAT	
		TATGTTTCT CGT AGTA	
		CC TAT	
GAM2426 OPA1	3'	ATGATATTGCCCTCTTTGTAT 56437	CA CCC
		ATACAAAGA GCA TCAT	
		TATGTTTCT CGT AGTA	
		CC TAT	
GAM2426 TRAF5	3'	TGAAGTGCTGTCTTTTAA 17286	C CC
		TA AAAGACAGCAC TCA	
		AT TTTCTGTCGTG AGT	
		T A_	
GAM2426 VIL2	3'	ATGAAGGATCCATCTTTGTAT 14051	CAGCA C
		ATACAAAGA CC TCAT	
		TATGTTTCT GG AGTA	
		ACCTA A	
GAM2426 FLJ20330	3'	TGAGGGTGTGTCTTTGTA 39146	G
		TACAAAGACA CACCCTCA	
		ATGTTTCTGT GTGGGAGT	
		—	
GAM2426 FLJ32894	3'	ATGATGAGGATGACGACCTTT 58992	ACAG_ C
		AAAG CA CCTCATCAT	
		TTTC GT GGAGTAGTA	
		CAGCA A	
GAM2426 HCNGP	3'	GTGGGAGGCGCCACTTTGTAT 26073	ACA A _
		ATACAAAG GC CC CTCAT	
		TATGTTTC CG GG GGGTG	
		AC_ C A	
GAM2426 KIAA0237	3'	ATGACTCAGAGCGTCTGTCTTT 29214	C C A__
	GTAT	ATACAAAGACAG AC CTC TCAT	
		TATGTTTCTGTC TG GAG AGTA	
		_ C ACTC	
GAM2426 MGC18079	5'	ATGATGAGGGGCAGTCCCTG 59031	AA A A
		CA GAC GC CCCTCATCAT	

			GT CTG CG GGGAGTAGTA		
			CC A _		
GAM2426	SE70-2	5'	ATGATGAAAAGGGTTTTGTAT 42346	AGCACCC	
			ATACAAAGAC TCATCAT		
			TATGTTTTTG AGTAGTA		
			GGAAA_		
GAM2426	Spir-2	3'	ATGATGAAATGTTGTCT 71155	CCC	
			AGACAGCA TCATCAT		
			TCTGTTGT AGTAGTA		
			AA_		
GAM2426	SYPL	3'	ATGATGAGTGTATTGTCTTTG 94500	C C	
			CAAAGACAG AC CTCATCAT		
			GTTTCTGTT TG GAGTAGTA		
			A T		
GAM2426	LOC200558	3'	AGTGTGCTGTCTTTATAT 90250	C C	
			ATA AAAGACAGCAC CT		
			TAT TTTCTGTCGTG GA		
			A T		
GAM2426	LOC203414	3'	TGTTGATGCTGTCTTT 90914	CCC T	
			AAAGACAGCA TCA CA		
			TTTCTGTCGT AGT GT		
			_ T		
GAM2426	LOC222194	5'	ATGATCCTGTTTTTGTAT 95833	CACCC	
			ATACAAAGACAG TCAT		
			TATGTTTTTGTC AGTA		
			CT_		
GAM2427	ANXA8	3'	ACAGAAGAACAAGAGCAA 73465	AAC	
			TTGCTCTT TTTTCTGT		
			AACGAGAA AGAAGACA		
			CA_		
GAM2427	CDH18	5'	ACAGAAACAGGGAGCCAG 18215	T AACT	
			CT GCTCTT TTTCTGT		
			GA CGAGGG AAAGACA		
			C AC_		
GAM2427	CORO1C	3'	ACAGAAAAAATGGGAGCAAG 27505	AC	
			CTTGCTCTTA TTTTCTGT		
			GAACGAGGGT AAAAGACA		
			AA		
GAM2427	DIAPH2	3'	ACAGAAAAGTTAATCTGC 24585	TC_	
			GC TTAACTTTTCTGT		

			CG AATTGAAAAGACA		
			TCT		
GAM2427	FCER2	3'	ACAGCCAGGCCAGAGCAAG	10598	TAA TT
			CTTGCTCT CTT CTGT		
			GAACGAGA GGA GACA		
			CCC CC		
GAM2427	ICMT	3'	ACAGAAAACAAGGCAGCA	25732	_ AAC
			TGCT CTT TTTTCTGT		
			ACGA GGA AAAAGACA		
			C AC_		
GAM2427	KCNA7	3'	ACAGAGACCAAGAGCAGG	49881	AACT
			CTTGCTCTT TTTCTGT		
			GGACGAGAA AGAGACA		
			CC__		
GAM2427	LILRB1	5'	ACAGAAAAGAAAAGAAAAG	22866	GC AA
			CTT TCTT CTTTTCTGT		
			GAA AGAA GAAAAGACA		
			A_ AA		
GAM2427	MCSP	3'	ACAGAAATAAAGAGCAA	48407	AACT
			TTGCTCTT TTTCTGT		
			AACGAGAA AAAGACA		
			AT__		
GAM2427	MF12	3'	ACAGAAAGATTGGTAAGAGCCA	53969	_ AC__
	AG		CTTG CTCTTA TTTTCTGT		
			GAAC GAGAAT GAAAGACA		
			C GGTTA		
GAM2427	PCDHA9	3'	ATGGGTAGTAAGAGCAA	49832	A TT
			TTGCTCTTA CT TCTGT		
			AACGAGAAT GA GGGTA		
			_ T_		
GAM2427	POU3F2	5'	ACAGAAAGAGCGAGCGAG	20024	TTAAC
			CTTGCTC TTTTCTGT		
			GAGCGAG GAAAGACA		
			CGA__		
GAM2427	RNMT	3'	ACAGAAAGGAGCAGAGAGCAAG	15046	AA__
			CTTGCTCTT CTTTTCTGT		
			GAACGAGAG GGAAAGACA		
			ACGA		
GAM2427	SELP	3'	ACAGAAGCCAGGAGCAA	13010	AACT
			TTGCTCTT TTTCTGT		

			AACGAGGA GAAGACA		
			CC__		
GAM2427	SFRP1	3'	ACAGAATACGGAAGAGCAGG 13024		AACTT
			CTTGCTCTT TTCTGT		
			GGACGAGAA AAGACA		
			GGCAT		
GAM2427	SIM1	3'	ACAAGTAGTTAAGAGCTAAG 18617	_	TTTC
			CTT GCTCTTAACT TGT		
			GAA CGAGAATTGA ACA		
			T TGA_		
GAM2427	SLC7A7	5'	ACAGAAAGTGCTGAGCCAAG 15632	_	TTA T
			CTTG CTC ACTTT CTGT		
			GAAC GAG TGAAA GACA		
			C TCG _		
GAM2427	SPAG8	3'	ACAGAAAGTAGGGAGGAAG 25838	G TA T	
			CTT CTCT ACTTT CTGT		
			GAA GAGG TGAAA GACA		
			G GA _		
GAM2427	STAT6	3'	ACAGAAGACAGCAGCAAG 13445	_	TAAC
			CTTGCT CT TTTTCTGT		
			GAACGA GA AGAAGACA		
			C C__		
GAM2427	SYBL1	3'	ACAAGGAGTTAAAAGCAA 20108	C C	
			TTGCT TTAACTTTT TGT		
			AACGA AATTGAGGA ACA		
			A _		
GAM2427	SYT4	3'	ACAAAATCGTTCAAGAGCAA 63107	_	TT C
			TTGCTCTT AAC TT TGT		
			AACGAGAA TTG AA ACA		
			C CT A		
GAM2427	UCP1	5'	ACAGGCGTGAAGAGCAAG 41849	A TTT	
			CTTGCTCTT AC TCTGT		
			GAACGAGAA TG GGACA		
			G C__		
GAM2427	ALK7	3'	ACAGAAAAGGAAGAGGAAG 76239	G AA	
			CTT CTCTT CTTTTCTGT		
			GAA GAGAA GAAAAGACA		
			G G_		
GAM2427	AQP10	3'	ACAGAGACAGAGAGCAAG 55390		AACT
			CTTGCTCTT TTTCTGT		

GAACGAGAG AGAGACA
AC__

GAM2427 ARHGEF3 3' ACAGAAAAGAAAGCAGTAA 39456 _ AA
TTGCT CTT CTTTCTGT
||||| ||| |||||
AATGA GAA GAAAAGACA
C A_

GAM2427 ARPC3 3' ACAGAAGAGAGAAGAGCA 20362 AA
TGCTCTT CTTTCTGT
||||| |||||
ACGAGAA GAGAAGACA
GA

GAM2427 BNIP-S 5' ACAGAAAAGAGGTAAG 57097 T TAA
CTTGC CT CTTTCTGT
||||| || |||||
GAATG GA GAAAAGACA

GAM2427 DCNP1 3' ACAGAAACGTGTAGAGCAAG 56453 TA T
CTTGCTCT AC TTTCTGT
||||| || |||||
GAACGAGA TG AAAGACA
TG C

GAM2427 DKFZP434B103 5' ACAGTGGGAGCCAAGGGCAAG 32222 AA _
CTTGCTCTT CTTT CTGT
||||| ||||| |||||
GAACGGGAA GAGGG GACA
CC T

GAM2427 DKFZp547H025 3' ACAGAAAAGCAAATAGCAA 39763 C AA
TTGCT TT CTTTCTGT
||||| || |||||
AACGA AA GAAAAGACA
T AC

GAM2427 DMTF1 3' ACAGAAGGGTTAAGGCAA 41244 T
TTGC CTTAACTTTTCTGT
||| |||||
AACG GAATTGGGAAGACA

GAM2427 ENPP4 3' ACAGAAAAGATATAGCAA 30713 CT A
TTGCT TA CTTTCTGT
||||| || |||||
AACGA AT GAAAAGACA
T_ A

GAM2427 ESAM 3' ACAGAAGGAGAAGAGGAAG 58044 G AAC
CTT CTCTT TTTTCTGT
||| ||||| |||||
GAA GAGAA GGAAGACA
G GA_

GAM2427 FLJ20752 5' ACAGAAATGCTGTCTGAGAGCA 39304 _ T__
AG CTTGCTCTTA AC TTTCTGT
||||| || |||||

			GAACGAGAGT TG AAAGACA	
			C TCGT	
GAM2427	FLJ21034	5'	ACAGAAAAGTACTTGCAGG 46862	TCTTA
			CTTGC ACTTTTCTGT	
			GGACG TGAAAAGACA	
			TTCA_	
GAM2427	FLJ33069	3'	ACAGAAAAATGCCTTGAGGGCA 58967	C_____
	A		TTGCTCTTAA TTTTCTGT	
			AACGGGAGTT AAAAGACA	
			CCGTA	
GAM2427	G2	5'	ACACTGGGTCAAGAGCAAG 67238	A TTC
			CTTGCTCTT ACTT TGT	
			GAACGAGAA TGGG ACA	
			C TC_	
GAM2427	KIAA0368	3'	ACAGAGTTGCAGAGCAAG 65761	_ TTT
			CTTGCTCT TAAC TCTGT	
			GAACGAGA GTTG AGACA	
			C _	
GAM2427	KIAA0410	3'	ACAGAACAGCAAGAGCAGG 29421	AA T
			CTTGCTCTT CT TTCTGT	
			GGACGAGAA GA AAGACA	
			C_ C	
GAM2427	KIAA0427	3'	ACGGTGAGCTCAGAGCAAG 29368	TAA TT
			CTTGCTCT CTT CTGT	
			GAACGAGA GAG GGCA	
			CTC T_	
GAM2427	KIAA0461	3'	ACAGAGAAAAGGAGCAA 71391	AAC
			TTGCTCTT TTTTCTGT	
			AACGAGGA AAGAGACA	
			A_	
GAM2427	KIAA0565	3'	ACAGAAAAGTAGCGCAGG 67427	T TA
			CTTGC CT ACTTTTCTGT	
			GGACG GA TGAAAAGACA	
			C _	
GAM2427	KIAA0662	3'	ACAGAAAGAGGAGGAGCAAG 82737	AAC
			CTTGCTCTT TTTTCTGT	
			GAACGAGGA GAAAGACA	
			GGA	
GAM2427	KIAA0853	3'	ACAGAAAAGTTGGGAAAAG 31210	GC
			CTT TCTTAACTTTTCTGT	

			GAA AGGGTTGAAAAGACA		
			A_		
GAM2427	KIAA1357	3'	ACAGAAATAGAAGAAAGCAAG 72430	___	AACT
			CTTGC TCTT TTTCTGT		
			GAACG AGAA AAAGACA		
			AA GAT_		
GAM2427	KIAA1494	3'	ACAGAAACTTGAGAGAAG 68978	G	CT
			CTT CTCTTAA TTTCTGT		
			GAA GAGAGTT AAAGACA		
			_ C_		
GAM2427	KIAA1500	3'	ACAGGAGATTTAGAGCAA 64805	T	C
			TTGCTCT AA TTTTCTGT		
			AACGAGA TT AGAGGACA		
			_ T		
GAM2427	LHFPL2	3'	ACAGATTAAGGGCTAAGGGCAA 70495	A_	___
			TTGCTCTTA CTTT TCTGT		
			AACGGGAAT GGAA AGACA		
			CG TT		
GAM2427	MYLE	3'	ACAGAAGGGGGAACGCAAG 26690	TC	AA
			CTTGC TT CTTTTCTGT		
			GAACG AA GGGAAGACA		
			C_ GG		
GAM2427	NASP	3'	ACAGAAAAGACAGAAGATGCAA 68575	_	AA__
			TTGC TCTT CTTTTCTGT		
			AACG AGAA GAAAAGACA		
			T GACA		
GAM2427	NFAT5	5'	ACAGAAAAGCAAGAGCAA 57760	AA	
			TTGCTCTT CTTTTCTGT		
			AACGAGAA GAAAAGACA		
			C_		
GAM2427	NR1H3	3'	ACAGACTGAGAAGGGCAA 20302	AA	T_
			TTGCTCTT CTT TCTGT		
			AACGGGAA GAG AGACA		
			_ TC		
GAM2427	PP591	5'	ACAGAAAGAAGAAAGCAGG 48143	C	AAC
			CTTGCT TT TTTTCTGT		
			GGACGA AG GAAAGACA		
			A AA_		
GAM2427	PRO1257	3'	ACAGAAATCAAGAGTAAG 38325		AACT
			CTTGCTCTT TTTCTGT		

			GAATGAGAA AAAGACA	
			CT__	
GAM2427	SMA3	5'	ACAGAGTGAAAGAGCAGG 23253	AACTT
			CTTGCTCTT TTCTGT	
			GGACGAGAA GAGACA	
			AGT__	
GAM2427	TM4-B	5'	ACAGAGGGGCAGAGCAAG 25887	TAA
			CTTGCTCT CTTTCTGT	
			GAACGAGA GGGGAGACA	
			C__	
GAM2427	LOC120114	3'	ACAGAAAAGTGGAAGCAG 76033	CTTA
			TTGCT ACTTTTCTGT	
			GACGA TGAAAAGACA	
			AGG_	
GAM2427	LOC122786	3'	ACAGAAAATGTACAGCAAG 74618	CTTA _
			CTTGCT AC TTTTCTGT	
			GAACGA TG AAAAGACA	
			CA__ T	
GAM2427	LOC123036	3'	ACAGAAAAATTGAGAGGAAG 74646	G C
			CTT CTCTTAA TTTTCTGT	
			GAA GAGAGTT AAAAGACA	
			G A	
GAM2427	LOC132241	5'	ACAGAAAAGTGAGAGCCAAG 75550	CT A
			CTTG CTT ACTTTTCTGT	
			GAAC GAG TGAAAAGACA	
			CG G	
GAM2427	LOC142972	3'	ACAGAAGAACAAGAGCAA 65720	AAC
			TTGCTCTT TTTTCTGT	
			AACGAGAA AGAAGACA	
			CA_	
GAM2427	LOC146237	3'	ACAGAGCATGAGAGCAAG 84603	ACTT
			CTTGCTCTTA TTCTGT	
			GAACGAGAGT GAGACA	
			AC__	
GAM2427	LOC148132	5'	ACAGAGACGCAGAGCAAG 85254	TAACT
			CTTGCTCT TTTCTGT	
			GAACGAGA AGAGACA	
			CGC__	
GAM2427	LOC148293	3'	ACAGAAGCAGAGAGCAG 79525	AACT
			TTGCTCTT TTTCTGT	

	GACGAGAG GAAGACA	
	AC__	
GAM2427 LOC149182 5'	ACAGAAGGAGTAGAGTAA 85531	TA _
	TTGCTCT ACTT TTCTGT	
	AATGAGA TGAG AAGACA	
	_ G	
GAM2427 LOC150225 5'	ATGGAAATCCAGAGCAAG 86180	TAACT
	CTTGCTCT TTTCTGT	
	GAACGAGA AAAGGTA	
	CCT__	
GAM2427 LOC153277 3'	ACAGAGTCCAAGATGCAAG 87185	_ AACTT
	CTTGC TCTT TTCTGT	
	GAACG AGAA GAGACA	
	T CCT__	
GAM2427 LOC153966 5'	ACAGAGTGAAAGAGCAGG 71629	AACTT
	CTTGCTCTT TTCTGT	
	GGACGAGAA GAGACA	
	AGT__	
GAM2427 LOC155435 3'	ACAGAAAAGGAAAGAAGCA 82266	_ AA
	TGCT CTT CTTTTCTGT	
	ACGA GAA GAAAAGACA	
	A AG	
GAM2427 LOC157381 3'	ACAGAAGTGGGTGAGAGCAA 87729	A _
	TTGCTCTTA CT TTTCTGT	
	AACGAGAGT GG GAAGACA	
	G T	
GAM2427 LOC158257 5'	ACAGAAAAGTTCTCCAAG 88013	CTCTT
	CTTG AACTTTTCTGT	
	GAAC TTGAAAAGACA	
	CTC__	
GAM2427 LOC158490 3'	ACAGAAGAAGAGAGGAAG 82819	G AAC
	CTT CTCTT TTTTCTGT	
	GAA GAGAG AGAAGACA	
	G A__	
GAM2427 LOC158714 5'	ACAAAAAGGTTAGAGCAG 82867	T C
	TTGCTCT AACTTTT TGT	
	GACGAGA TTGGAAA ACA	
	_ A	
GAM2427 LOC166793 5'	ACAGAAATACGCAGAGCAAG 59915	TAACT
	CTTGCTCT TTTCTGT	

			GAACGAGA	AAAGACA		
			CGCAT			
GAM2427	LOC199982	3'	ACAGAGGAGAGAAGCAAG	89897	_	TAA
			CTTGCT CT	CTTTTCTGT		
			GAACGA GA	GAGGAGACA		
			A	__		
GAM2427	LOC203084	5'	ACAGAAAGGATGAGACAA	88874	C	A
			TTG TCTTA	CTTTTCTGT		
			AAC AGAGT	GGAAAGACA		
			-	A		
GAM2427	LOC221632	3'	ACAGAAACAGAGAGTAAG	95444		AACT
			CTTGCTCTT	TTTCTGT		
			GAATGAGAG	AAAGACA		
			AC	__		
GAM2427	LOC256207	3'	ACAGAAAAGTAGCGCAGG	96866	T	TA
			CTTGC CT	ACTTTTCTGT		
			GGACG GA	TGAAAAGACA		
			C	__		
GAM2427	LOC57805	3'	ACGGAATTGAAGAGCAAG	41286		AACTT
			CTTGCTCTT	TTCTGT		
			GAACGAGAA	AAGGCA		
			GTT	__		
GAM2427	LOC90785	3'	ACAGAAAAGTTCCCAAG	64705		CTCTT
			CTTG	AACTTTTCTGT		
			GAAC	TTGAAAAGACA		
			CCC	__		
GAM2427	LOC91694	3'	ACAAAAAAGCCATAGAGAGCAG	67505	AA	__ C
			TTGCTCTT	CTTTT TGT		
			GACGAGAG	GAAAA ACA		
			ATACC	A		
GAM2427	LOC93320	3'	ACAGAAGAAGAGAGGAAG	72512	G	AAC
			CTT CTCTT	TTTTCTGT		
			GAA GAGAG	AGAAGACA		
			G	A	__	
GAM2428	LENG4	5'	GAACATCTCCCTAGCAACCGTG	44420	C	GGAC
			CACGGT GT	GAGATGTTT		
			GTGCCA CG	CTCTACAAG		
			A	ATCC		
GAM2428	ODF2	5'	GAACACCCCTGTCCACGTCC	11886	T	AGA
			GG CGTGGACG	TGTTT		

CC GCACCTGT ACAAG
 T CCCC
 GAM2428 FLJ10300 5' AACATCTCTGGGCCATAC 36466 C A__
 GT GTGG C GAGATGTT
 || ||| | |||||
 CA TACC G CTCTACAA
 _ GG T
 GAM2428 KIAA0014 3' AACATCTCGTGGCCGCGCT 28535 T __
 GG CGTGG ACGAGATGTT
 || ||| |||||
 TC GCGCC TGCTCTACAA
 _ GG
 GAM2428 LOC158263 3' GAACATCTCACCCAGCATCC 82728 TC _ AC
 GG G TGG GAGATGTTC
 || | || |||||
 CC C ACC CTCTACAAG
 TA G CA
 GAM2429 ALMS1 3' GCTTATTCTTTGTCCATGTGTA 31365 CATCCCAA
 TACAC GAAGAATAAGC
 |||| |||||
 ATGTG TTTCTTATTCG
 TACCTG__
 GAM2429 CCR9 3' GCTTATTCCTTGGTATGGTG 49125 C AA
 CACCAT CCAAG GAATAAGC
 |||| ||| |||||
 GTGGTA GGTC CTTATTCG
 T __
 GAM2429 DIAPH2 3' TCTGCTCTCGGGATGGTG 24596 A __
 CACCATCCC AGA AGA
 ||||| ||| ||
 GTGGTAGGG TCT TCT
 C CG
 GAM2429 GALNT3 3' GCTTATTCCTCTTTTGGG 16827 __ A
 CCCA AGA GAATAAGC
 ||| || |||||
 GGGT TCT CTTATTCG
 TT C
 GAM2429 IL1F9 3' GCTTTATTCCCTCTTGGGATG 39512 A_ _
 CATCCCAAGA GAATAA GC
 ||||| ||||| ||
 GTAGGGTTCT CTTATT CG
 CC T
 GAM2429 MKKS 5' GCTCATACATTTGGGGTGGT 38750 AAGA A
 ACCATCCCAAG AT AGC
 ||||| || |||
 TGGTGGGGTTT TA TCG
 ACA_ C
 GAM2429 MLANA 3' GTTCTCCTTTGGAATGGTGTA 19767 _ C A
 TACACCAT CC AAG AGAAT
 ||||| || ||| |||||

			ATGTGGTA GG TTC TCTTG		
			A T C		
GAM2429	OGN	3'	GCTCATTCTTCTTTTATG 26767	CCC	A
			CAT AAGAAGAAT AGC		
			GTA TTCTTCTTA TCG		
			TT_ C		
GAM2429	PRSS8	3'	CCATTCTTCTGGGTGTG 12420	CAT	A AA
			CAC CCCA GAAGAAT G		
			GTG GGGT CTTCTTA C		
			T_ _ CC		
GAM2429	TOP2B	3'	GCTTATTTTAATGTGATGATGT 8409	C	C AGA
	A		TACA CATC CA AGAATAAGC		
			ATGT GTAG GT TTTTATTCG		
			A T AA_		
GAM2429	BRD4	3'	GCTTATCTCCGAAATGGTGTG 55252	CCCAA	A A
			TACACCAT GA GA TAAGC		
			GTGTGGTA CT CT ATTCG		
			AAGC_ _ _		
GAM2429	C5orf4	5'	GCTTATTCTGATGCAGATGGTC 51492	C	CCAAGA
	A		A ACCATC AGAATAAGC		
			A TGGTAG TCTTATTCG		
			C ACGTAG		
GAM2429	C5orf4	3'	GCTTATTCTGATGCAGATGGTC 51493	C	CCAAGA
	A		A ACCATC AGAATAAGC		
			A TGGTAG TCTTATTCG		
			C ACGTAG		
GAM2429	CHIC1	3'	CTTATTCTTTATAATGGT 82899	CCCAA	
			ACCAT GAAGAATAAG		
			TGGTA TTTCTTATTC		
			ATA_		
GAM2429	DKFZp434N2435	5'	CTTATTACTGTGGGGTGGT 98089		AGAAG
			ACCATCCCA AATAAG		
			TGGTGGGGT TTATTC		
			GTCA_		
GAM2429	DKFZP564I122	3'	GCTTATTCTTCTCCCTCATGTG 63879		CATCCCA
	TA		TACAC AGAAGAATAAGC		
			ATGTG TCTTCTTATTCG		
			TACTCCC		
GAM2429	FLJ21791	3'	CTTATTTGCAGAAGTGGTGTA 62125		CCCAAGAA
			TACACCAT GAATAAG		

ATGTGGTG TTTATTC
 AAGACG__
 GAM2429 FLJ22794 5' CTTATTCTGGGACAGTG 93245 CA AGAA
 CAC TCCCA GAATAAG
 ||| |||| |||||
 GTG AGGGT CTTATTC
 AC ____
 GAM2429 HN1L 3' GCTCACTCAGCTAATGGGATGG 58618 __ AA ATA
 CCATCCCA AG GA AGC
 ||||| || || |||
 GGTAGGGT TC CT TCG
 AA GA CAC
 GAM2429 HYPH 3' CTTATTCTATTGACAGACATGG 96567 CC__ GA
 TGTA TACACCAT CAA AGAATAAG
 ||||| || |||||
 ATGTGGTA GTT TCTTATTC
 CAGACA A_
 GAM2429 ITGB8 3' GCTTATTTTTGCAAGATGG 11057 CCAAG
 CCATC AAGAATAAGC
 |||| |||||
 GGTAG TTTTATTTCG
 AACG_
 GAM2429 KIAA0342 3' GCTCATCACTGTGGGATGGTG 71141 AGAA ATA
 CACCATCCCA GA AGC
 ||||| || |||
 GTGGTAGGGT CT TCG
 GTCA AC_
 GAM2429 KIAA1579 3' CTTACTCTTAGTGGTGTA 37149 CCCAAG A
 TACACCAT AAGA TAAG
 ||||| || ||||
 ATGTGGTG TTCT ATTC
 A__ C
 GAM2429 KIAA1719 3' TCTGTCTTGGGAGTGGTGTA 68741 _ _
 TACACCA TCCCAAGA AGA
 ||||| ||||| |||
 ATGTGGT AGGGTTCT TCT
 G G
 GAM2429 KIAA1877 3' CTTATTCTTCTGCCATGAGT 66747 _ CCCA
 AC CAT AGAAGAATAAG
 || ||| |||||
 TG GTA TCTTCTTATTC
 A CCG_
 GAM2429 MLZE 5' GCTTATTTTTCCAGGATACTG 49452 CC CAA
 CA ATCC GAAGAATAAGC
 || ||| |||||
 GT TAGG CTTTTTATTTCG
 CA AC_
 GAM2429 POLD3 3' GCTTCTTTTGCCTCAAGATGGT 93314 CCA A_ T
 GTA TACACCATC AG AGAA AAGC
 ||||| || ||| |||

		ATGTGGTAG TC TTTT TTCG	
		AAC CG C	
GAM2429	LOC145946 3'	CTAGTCCTGGAATGGTGTA 84560	C A AGAATA
		TACACCAT CCA GA AG	
		ATGTGGTA GGT CT TC	
		A C GA____	
GAM2429	LOC149322 3'	CTTATACCCAGGATGGTGTG 60287	CAAGAAGA
		TACACCATCC ATAAG	
		GTGTGGTAGG TATTC	
		ACCCA____	
GAM2429	LOC149910 3'	CTTACATTCAGATGGTGTA 80355	CCAA GAA
		TACACCATC GAA TAAG	
		ATGTGGTAG CTT ATTC	
		A__ AC_	
GAM2429	LOC220635 3'	CTTATACCCAGGATGGTGTG 92454	CAAGAAGA
		TACACCATCC ATAAG	
		GTGTGGTAGG TATTC	
		ACCCA____	
GAM2429	LOC253868 3'	GCTTATTCAAGTGGGGGAGGTG 97323	A AAGAA
		CACC TCCC GAATAAGC	
		GTGG AGGG CTTATTCG	
		_ GGTGA	
GAM2429	LOC90826 5'	GCTTATTCTTCTGTAGAT 64786	CCA
		ATC AGAAGAATAAGC	
		TAG TCTTCTTATTCG	
		ATG	
GAM2430	ELF3 3'	TGACCTTGACCTTGACCAA 16685	T GAT AAA
		TTGGT CAAGG GG GTCA	
		AACCA GTTCC TC CAGT	
		_ AGT ____	
GAM2430	JAK2 3'	TGACCTTCATTCTGAGACCAA 18318	CAA AA
		TTGGTT GGGATGGA GTCA	
		AACCAG TCTTACTT CAGT	
		AG_ C_	
GAM2430	SLC10A2 5'	ACTCTCTGTCTTGACCAA 6590	CAA A
		TTGGTT GGGATGGA AGT	
		AACCAG TTCTGTCT TCA	
		____ C	
GAM2430	FLJ10803 3'	GTGACTTTCAGTTAAAGCCAA 37205	CAAGG G
		TTGGTT GAT GAAAGTCAC	

			AACCGA	TTG CTTTCAGTG		
			AA__	A		
GAM2430	KIAA1958	5'	GTGACTTTGAACCCCAAACC	82788	CAA	ATGG
			GGTT GGG	AAAGTCAC		
			CCAA CCC	TTTCAGTG		
			A__	CAAG		
GAM2430	MARCKS	3'	ACTTTCCACCCTGCCCA	11411	TTCA	A
			TGG AGGG	TGGAAAGT		
			ACC TCCC	ACCTTTCA		
			CG__	_		
GAM2430	TUB	5'	GTGGGACCATCCCTTAAACC	13898	C	AAAG
			GGTT AAGGG	GATGG TCAC		
			CCAA TTCCCTACC	GGTG		
			A	AG__		
GAM2430	LOC80298	3'	ACTTTTACCTTGAACCA	48062	GATG	
			TGGTTCAAGG	GAAAGT		
			ACCAAGTTCC	TTTTCA		
			A__			
GAM2431	HLA-G	3'	TGGGGGAGCTCACCCACCCAC	10938	CA	G
			GTG GTGGGTGAGCTTT	CTG		
			CAC CACCCACTCGAGG	GGT		
			CC	G		
GAM2431	MGEA5	3'	GTAAAACTCACCCATCACAC	25224	CA	C
			GTG GTGGGTGAG	TTTGC		
			CAC TACCCACTC	AAATG		
			AC	A		
GAM2431	NUP62	3'	AAGATCACACCACTGCAC	33776	_	G
			GTGCAGTGG	GTGA CTT		
			CACGTCACC	CACT GAA		
			A	A		
GAM2431	SLC17A5	3'	AAGATCACGCCACTGCAC	25819	_	G
			GTGCAGTGG	GTGA CTT		
			CACGTCACC	CACT GAA		
			G	A		
GAM2431	LOC148709	5'	GTAACCTCACCCACTCAC	79699	C	CT
			GTG AGTGGGTGAG	TTGC		
			CAC TCACCCACTC	AATG		
			_	_		
GAM2431	LOC150372	5'	TGGCAGCTCACCCACCGC	80623	A	TT
			GC GTGGGTGAGCT	GCTG		

CG CACCCACTCGA CGGT
C _

GAM2431 LOC151610 3' ATCAACAAAGCTCCTGTTCTGC 81090 TG_ T C
A TGCAG GG GAGCTTTG TGAT
|||| || |||||| |||
ACGTC TC CTCGAAAC ACTA
TTG _ A

GAM2431 LOC254057 3' CAGGGTTCCCACCCACCCAC 98779 CA _
GTG GTGGGT GAGCTTTG
|| |||| ||||||
CAC CACCCA CTTGGGAC
C_ CC

GAM2431 LOC57118 3' ATCAGCTGAGATCACACCACTG 40214 _ G T
CAC GTGCAGTGG GTGA CTT GCTGAT
|||||| ||| || |||||
CACGTCACC CACT GAG CGACTA
A A T

GAM2431 LOC57826 3' GCAGCTCACCTACTGCAC 41318 TT
GTGCAGTGGGTGAGCT GC
|||||||||| ||
CACGTCATCCACTCGA CG

GAM2432 ELF3 3' TGACCTTGACCTTGACCAA 16685 T GAT CAA
TTGGT CAAGG GG GTCA
|||| |||| || |||
AACCA GTTCC TC CAGT
_ AGT _

GAM2432 KIAA1228 3' ACTTACACTTTGAACCA 65661 GA GC
TGGTTCAAGG TG AAGT
|||||| || |||
ACCAAGTTTC AC TTCA
_ A_

GAM2432 TUB 5' GTGGGACCATCCCTTAAACC 13898 C CAAG
GGTT AAGGGATGG TCAC
||| |||||| |||
CCAA TTCCCTACC GGTG
A AG_

GAM2432 LOC197423 5' TGACTTGTGCCCTAAAC 78427 CA ATG
GTT AGGG GCAAGTCA
|| ||| ||||||
CAA TCCC TGTTCAGT
A_ G_

GAM2433 SCAMP1 3' GCTAAATAAATATTCTCC 18014 T C
GGA AATATT ATTTAGC
|| |||| ||||||
CCT TTATAA TAAATCG
C A

GAM2433 SCAMP1 3' GCTAAATAAATATTCTCC 54500 T C
GGA AATATT ATTTAGC
|| |||| ||||||

CCT TTATAA TAAATCG
 C A
 GAM2433 NX-17 3' TGAATATCAGCCCCTAATA 40706 ATA_
 TATTAGGG ATATTCA
 ||||| |||||
 ATAATCCC TATAAGT
 CGAC
 GAM2433 LOC161589 3' GCTAAATGAATATTATCCCTAA 83159
 TA TATTAGGGATAATATTCATTTAGC
 |||||
 ATAATCCCTATTATAAGTAAATCG

 GAM2434 AKAP1 3' ACTATGGGTTCTCTTCGCAAA 14472 A CTT C
 TTTGT GA GGAACCCA AGT
 ||||| || ||||| |||
 AAACG CT TCTTGGGT TCA
 _ TC_ A
 GAM2434 AKAP1 3' ACTATGGGTTCTCTTCGCAAA 58373 A CTT C
 TTTGT GA GGAACCCA AGT
 ||||| || ||||| |||
 AAACG CT TCTTGGGT TCA
 _ TC_ A
 GAM2434 EGF 3' ACTATAGGTTTTGGTTCCACAA 10488 A C TG CAC
 TTGT GA T GAACC AGT
 ||||| || ||||| |||
 AACA CT G TTTGG TCA
 C T GT ATA
 GAM2434 EZH1 3' GACTGTGGGTTCCAAATTAC 10551 AC
 GTAG TTGGAACCCACAGTC
 ||||| |||||
 CATT AACCTTGGGTGTCAG
 A_
 GAM2434 STAC 3' GACTGTGGAGTAATAGCCACAA 13427 AGA TGGA _
 A TTTGT CT AC CCACAGTC
 ||||| || |||||
 AAACA GA TG GGTGTCAG
 CC_ TAA_ A
 GAM2434 CCR1 3' GACTGTGGGCTCCATTC 8927 CT A
 GA TGGA CCCACAGTC
 || |||||
 CT ACCT GGGTGTGTCAG
 T_ C
 GAM2434 FLJ10483 3' GACTGTGGAAGAGATTACAAA 36652 A GGAAC
 TTTGTAG CTT CCACAGTC
 ||||| || |||||
 AAACATT GAG GGTGTCAG
 A AA_
 GAM2434 KIAA1871 3' ACTGTAAGAGTCTACAAA 61890 GGAACCC
 TTTGTAGACTT ACAGT
 ||||| |||||

		AAACATCTGAG	TGTCA	
		AA_____		
GAM2434	LOC150821 3'	GGGTTCCACATCCACAAA	60944	A CT
		TTTGT GA TGGAACCC		
		AAACA CT ACCTTGGG		
		C AC		
GAM2434	LOC151057 3'	ACTGTGGGTACACCTATAAA	86379	ACT GA
		TTTGTAG TG ACCCACAGT		
		AAATATC AC TGGGTGTCA		
		C__ A_		
GAM2434	LOC157507 5'	ACTGTAAAAGTCTGCAAA	82377	GGAACCC
		TTTGTAGACTT ACAGT		
		AAACGTCTGAA TGTCA		
		AA_____		
GAM2434	LOC203339 5'	GGATTCCCAGTCTACAAA	92214	T C
		TTTGTAGACT GGAA CC		
		AAACATCTGA CCTT GG		
		C A		
GAM2434	LOC51030 3'	ACTGTAAATTAACCAATCTAC	32695	C AACCC__
	AAA	TTTGTAGA TTGG ACAGT		
		AAACATCT AACC TGTCA		
		_ AAATTA		
GAM2434	LOC90906 3'	GACTGTGGATCCCAAACCTTTGC	64951	C_ AAC
	A	TGTAGA TTGG CCACAGTC		
		ACGTTT AACC GGTGTCAG		
		CA CTA		
GAM2435	ATF7 3'	TCCCAGCCCCGAGCCTCATA	23404	_ TAGA CC
		TATGAGGC CC GCT GGGA		
		ATACTCCG GG CGA CCCT		
		A CCC_ _		
GAM2435	CREBBP 5'	CCCGCCGGTCCCGGGCCCCA	16495	A TA G C_
		TG GGCC GA CT CGGG		
		AC CCGGG CT GG GCCC		
		C CC _ CC		
GAM2435	EGLN2 5'	TTGGGGCTCCAGAACCTC	54926	CC A
		GAGG CT GAGCTCCGG		
		CTCC GA CTCGGGGTT		
		AA C		
GAM2435	GNA11 5'	CCCAGTGA CTCTGGGCCTCA	10810	T C C_
		TGAGGCC AGAG TC GGG		

ACTCCGGG TCTC AG CCC
 _ _ TGA
 GAM2435 LATS2 3' GTCCCGGAGCCGGTGCCCTCA 28135 _ _ TAGA
 TGAGG C CC GCTCCGGGAC
 ||||| || |||||
 ACTCC G GG CGAGGCCCTG
 C T C _
 GAM2435 NLGN3 3' GTCTCTCTGGCTCTAGGACC 39121 C CC_
 GG CCTAGAGCT GGGAC
 || ||||| |||||
 CC GGATCTCGG CTCTG
 A TCT
 GAM2435 NOTCH1 5' GTCCCGGAGCCCCAAGTGCTT 92138 C AGA_
 AGGC CT GCTCCGGGAC
 ||| || |||||
 TTCG GA CGAGGCCCTG
 T ACCC
 GAM2435 RBBP9 3' TCCGGAGTCTAGAGCCCCA 70699 A C G
 TG GGC CTAGA CTCCGGG
 || ||| ||||| |||||
 AC CCG GATCT GAGGCCT
 C A _
 GAM2435 UBQLN1 5' CCGAGCTCCGGGGGCCCA 26473 A TA C
 TG GGCCG GAGCTC GG
 || |||| ||||| ||
 AC CCGGG CTCGAG CC
 C GC _
 GAM2435 ARTN 5' CCCGGGCCTGGAGCCCCA 15612 A C A T
 TG GGC CTAG GC CCGGG
 || ||| |||| |||||
 AC CCG GGTC CG GGCCC
 C A _ _
 GAM2435 CNTNAP1 3' CCCAAAGGAGAAGCCTCATG 14641 CCTAGAG _
 TATGAGGC CTCC GGG
 ||||| ||| |||
 GTACTCCG GAGG CCC
 AA _ AAA
 GAM2435 FLJ10898 5' CCCCAAGCCAGGCACAGCCTCA 60130 _ AGA CC
 TA TATGAGGC CCT GCT GGG
 ||||| ||| ||| |||
 ATACTCCG GGA CGA CCC
 ACAC C _ AC
 GAM2435 KIAA1977 5' CGAAGGCTCAGGGCCTCA 74765 A C_
 TGAGGCCCT GAGCT CG
 ||||| ||||| ||
 ACTCCGGGA CTCGG GC
 _ AA
 GAM2435 P24B 3' TCCTGCTCTAGGGCCCCTCA 24774 _ TCC
 TGA GGCCCTAGAGC GGGA
 ||| ||||| ||||| |||||

ACT CCGGGATCTCG TCCT
 CC ____
 GAM2435 LOC146669 3' GTCTTTCTCCAGGGGCCTCA 78664 A_ CTCC
 TGAGGCCCT GAG GGGAC
 ||||| ||| ||||
 ACTCCGGGG CTC TTCTG
 AC T____
 GAM2435 LOC170127 5' CCCGGAGCCCCAGGGGCCCA 83456 A AGA_
 TG GGCCCT GCTCCGGG
 || ||||| |||||
 AC CCGGGG CGAGGCCC
 _ ACCC
 GAM2435 LOC256812 5' CCCGGAGCCCCCTGGGCCCA 99406 A TAGA_
 TG GGCCG GCTCCGGG
 || ||||| |||||
 AC CCGGG CGAGGCCC
 C TCCCC
 GAM2435 LOC90408 5' CCCCTCTCCGAGGCCTCATA 63342 CTA CTCC
 TATGAGGCC GAG GGG
 ||||| ||| |||
 ATACTCCGG CTC CCC
 AGC TC____
 GAM2436 ACVRL1 5' TTTATTAGGAGGGAGTGGTG 5240 AAGAAG
 CACCACTCCC AATAAG
 ||||| |||||
 GTGGTGAGGG TTATTT
 AGGA____
 GAM2436 BCL11B 3' TTTGTTTTTGGGGTGGGGGGTG 57582 A_ _ G TAAG
 TG TACACC CT CCCAAGAA AA
 ||||| || ||||| ||
 GTGTGG GG GGGTTTTT TT
 GG TG G T
 GAM2436 C18orf1 3' CTTCGTGTGGGAGTGGTGTG 60865 A_
 TACACCACTCCCA GAAG
 ||||| |||||
 GTGTGGTGAGGGT CTTC
 GTG
 GAM2436 ITPR3 3' CTTGTTTTTCTCCTTTTGGTGT 11085 CTCCCA
 A TACACCA AGAAGAATAAG
 ||||| |||||
 ATGTGGT TCTTTTGTTC
 TTTCC_
 GAM2436 KCNAB1 3' GTTTGTTTTTTTTTGAAGGGGG 61585 ____
 TGGTGTG TACACCACTCCC AAGAAGAATAAG T
 ||||| ||||| |
 GTGTGGTGAGGGG TTTTTTTGTTT G
 AAGT
 GAM2436 KRAS2 3' CTTATTTTTCTTACCAAGTGTG 54123 C CCC_
 CAC ACT AAGAAGAATAAG
 ||| ||| |||||

			GTG TGA TTCTTTTATTC		
			_ ACCA		
GAM2436	KRAS2	3'	CTTATTTTCTTACCAAGTGTG 54124	C CCC_	
			CAC ACT AAGAAGAATAAG		
			GTG TGA TTCTTTTATTC		
			_ ACCA		
GAM2436	LIFR	3'	TTTGTTTTTTTGGTTGGTTG 11315	C CTC	
			A ACCA CCAAGAAGAATAAG		
			G TGGT GGTTTTTTTGT		
			T T_		
GAM2436	MEN1	5'	CTTGTTTTTTTCTTTTGGTG 56348	CTCCCA	
			CACCA AGAAGAATAAG		
			GTGGT TTTTTTGTTC		
			TTTCC_		
GAM2436	MLLT7	3'	TTGTGCCTGGGAGTGTGTG 21043	_ AGAAGA	
			CAC CACTCCCA ATAA		
			GTG GTGAGGGT TGTT		
			T CCG_		
GAM2436	SIAH1	3'	TTTGTTTTTGCCGTGGGAGTGT 13128	_ AG_	
	GTG		CAC CACTCCCA AAGAATAAG		
			GTG GTGAGGGT TTTTGT		
			T GCCG		
GAM2436	SLC7A6	3'	TTTGTTTTTGTTGGTGGGTGCTG 15646	C _ AG	
	TG		TACA CACTC CCA AAGAATAAG		
			GTGT GTGGG GGT TTTTGT		
			C T G_		
GAM2436	STAT6	5'	TTTTCTTTTGGTGGTGGTG 13453	TC TAAG	
			CACCAC CCAAGAAGAA		
			GTGGTG GGTTTTCTT		
			GT TTTA		
GAM2436	TCF8	3'	CTTGTTTTTTAAGAGTGTGTG 48429	_ CCA	
			CAC CACTC AGAAGAATAAG		
			GTG GTGAG TTTTTTGTTC		
			T AA_		
GAM2436	B3GNT7	3'	TTGTTCTTGCTGGTGGGTG 71685	A C_ G	
			TAC CCACT CCAAGAA AA		
			GTG GGTGG GGTTCTT TT		
			_ TC G		
GAM2436	BCDO	3'	TTATTCTTCTGTGGGTG 34287	C AG	
			CACTC CA AAGAATAA		

			GTGGG GT TTCTTATT		
			T CT		
GAM2436	DKFZP564I122	3'	CTTATTCTTCTCCCTCATGTGT 63877	CACTCCCA	
	A		TACAC AGAAGAATAAG		
			ATGTG TCTTCTTATTC		
			TACTCCC_		
GAM2436	EPN2	3'	TTTATTTTCTTTGACTCGTGT 31046	CAC CC	
	G		TACAC TC AAGAAGAATAAG		
			GTGTG AG TTCTTTTATTT		
			CTC T_		
GAM2436	FLJ13855	3'	GGGTATTTTCTTGGGGGTGGA 43853	A AG	
	GTA		TAC CCACTCCCAAGAAGAATA		
			ATG GGTGGGGGTTCTTTTAT		
			A GGA		
GAM2436	FLJ21791	3'	CTTATTTGCAGAAGTGGTGTA 62126	CCCAAGAA	
			TACACCACT GAATAAG		
			ATGTGGTGA TTTATTC		
			AGACG__		
GAM2436	FLJ32865	3'	TTTGTTGGGGGTGGGGTG 58824	A G	
			TAC CCACTCCCAA AAG		
			GTG GGTGGGGGTT TTT		
			G G		
GAM2436	HAND1	3'	TTTGTTCTTCGAATCGTGGTG 17880	TCCCAA	
			CACCAC GAAGAATAAG		
			GTGGTG CTTCTTGTTT		
			CTAAG_		
GAM2436	KIAA0562	3'	TTTGTTTTGCGGGGTGGTG 28834	AAGA	
			CACCACTCCC AGAATAAG		
			GTGGTGCGGGG TTTGTTT		
			CG__		
GAM2436	KIAA0871	5'	TTATTTTTTTGGTGTGTGTGTG 31022	_ TC ATAAG	
			TACAC CAC CCAAGAAGA		
			GTGTG GTG GGTTTTTTT		
			T T_ ATTT		
GAM2436	KIAA0970	3'	TTTGTTTTTTTGTAGGGTG 30622	A CC	
			CACC CT CAAGAAGAATAAG		
			GTGG GA GTTTTTTTTGTTT		
			_ TT		
GAM2436	KIAA1240	3'	TTTATTTTTAGGGAGTGGGTA 67297	A AAG	
			TAC CCACTCCC AAGAATAAG		

			ATG GGTGAGGG TTTTATTT	
			— A—	
GAM2436	KIAA1719	3'	TCTGTCTTGGGAGTGGTGTA 68742	—
			TACACCACTCCCAAGA AGA	
			ATGTGGTGAGGGTTCT TCT	
			G	
GAM2436	KIAA1750	3'	TTTATTTTTTTTGTCTAGGTGT 68815	ACTCCCA
			G TACACC AGAAGAATAAG	
			GTGTGG TTTTTTATTT	
			ATCTTG_	
GAM2436	MAP2K3	3'	CTTGTTTTTCTTGCATGGT 12323	CTCC
			ACCA CAAGAAGAATAAG	
			TGGT GTTCTTTTGTTC	
			AC_	
GAM2436	MLN64	3'	CTTGTTGGGGAGTGGGTG 96062	A _ G
			TAC CCACTCCC AA AAG	
			GTG GGTGAGGG TT TTC	
			_ G G	
GAM2436	NY-REN-41	3'	TTTGTTTTTCTATCCTGGTGG 55564	CCCA_
			CCACT AGAAGAATAAG	
			GGTGG TCTTTTGTTT	
			TCCTA	
GAM2436	PRO1489	5'	TTTGTTTTTTCGTGTGTGTGTG 38334	_ TCCCAA
			TACAC CAC GAAGAATAAG	
			GTGTG GTG CTTTTGTTT	
			T TG_	
GAM2436	SEC15L	3'	TTTGTTCCTACTTGGGTGGT 72731	CT A
			ACCA CCAAG AGAATAAG	
			TGGT GGGTTC TCTTGTTT	
			_ A	
GAM2436	SHAPY	3'	TTTGTTCCTTTTGGAACTGTG 57915	TC_
			CAC CCAAGAAGAATAAG	
			GTG GGTTTTTCTTGTTT	
			TCAA	
GAM2436	STAM2	3'	GTTTTTCTTCCTGCAATGTGGT 20707	TCC_ A TAAG
			GTG TACACCAC CA GAAGAA	
			GTGTGGTG GT CTTCTT	
			TAAC C TTTGT	
GAM2436	TUBGCP3	3'	TTTATTTTTTTTTAGTGTTGTA 21982	C CCC
			TACA CACT AAGAAGAATAAG	

	ATGT GTGA TTTTTTTTATTT	
	T T__	
GAM2436 ZNF220	3' CTTGTTTTTTTACCACCTGGTG 23157	CTCCCA
	CACCA AGAAGAATAAG	
	GTGGT TTTTTTTGTTC	
	CCACCA	
GAM2436 LOC121219	5' TTGTTCTATGGGTGGGTG 74493	ACT AGA
	CACC CCCA AGAATAA	
	GTGG GGGT TCTTGTT	
	GT_ A__	
GAM2436 LOC143146	3' TTTGTTGGAGGTGGTGTA 60767	TC G
	TACACCAC CCAA AAG	
	ATGTGGTG GGTT TTT	
	GA G	
GAM2436 LOC146445	3' TTGTTCTTTGTGTGGTTG 84687	C TCCCAA
	A ACCAC GAAGAATAA	
	G TGGTG TTTCTTGTT	
	T TG____	
GAM2436 LOC150174	3' TTTATTTTTTTTACAATGGTG 80444	CTCCC
	CACCA AAGAAGAATAAG	
	GTGGT TTTTTTTTATTT	
	AACAT	
GAM2436 LOC150213	3' TTTATTTTTTTTACAATGGTG 75363	CTCCC
	CACCA AAGAAGAATAAG	
	GTGGT TTTTTTTTATTT	
	AACA_	
GAM2436 LOC150236	3' TTTATTTTTTTTACAATGGTG 80505	CTCCC
	CACCA AAGAAGAATAAG	
	GTGGT TTTTTTTTATTT	
	AACA_	
GAM2436 LOC154084	3' CTTGTTTTTTTAGTAGGTGTG 87378	_ CCCA
	TACACC ACT AGAAGAATAAG	
	GTGTGG TGA TTTTTTTGTTC	
	A ____	
GAM2436 LOC170261	3' TTTATTCTTTGTGAAAGTGGT 83472	CC A
	ACCACT CA GAAGAATAAG	
	TGGTGA GT TTTCTTATTT	
	AA G	
GAM2436 LOC199692	3' CTTGTTCTTCTGCTGTAGTGTG 59926	C TCCCA
	TACAC AC AGAAGAATAAG	

			GTGTG TG TCTTCTTGTC		
			A TCG__		
GAM2436	LOC203414	3'	CTTGTCAACTGGGGGTGATGTG 90913	C	A AA A
			TACA CACTCCCA G GA TAAG		
			GTGT GTGGGGGT C CT GTTC		
			A _AA _		
GAM2436	LOC257051	3'	TTTATTCTTTGTGAAAGTGGT 98054	CC	A
			ACCACT CA GAAGAATAAG		
			TGGTGA GT TTTCTTATTT		
			AA G		
GAM2436	LOC92303	3'	TTATTTTTTTTGAGGTGG 69400	CC	
			CCACT CAAGAAGAATAA		
			GGTGG GTTTTTTTTATT		
			A_		
GAM2437	ADCY2	3'	CTGGGAGAACTAACAGAGGAGA 65649	GCC_	T
			TCTCCTT AGTT CTCCCAG		
			AGAGGAG TCAA GAGGGTC		
			ACAA _		
GAM2437	ARF4L	5'	GGGAAAGGCTCGAGGAGA 70390	CC	C
			TCTCCTTG AGTTT TCCC		
			AGAGGAGC TCGGA AGGG		
			_ A		
GAM2437	ARNT2	3'	TGCTGGGAAAATGGGCAAGCAG 30092	C	A C
	A		TCT CTTGCC GTTT TCCCAGCA		
			AGA GAACGG TAAA AGGGTCGT		
			C G _		
GAM2437	AXIN2	5'	TGCTGAGAGGAACTGGAAGAAG 17391	C G	C
	A		TCT CTT CCAGTTTCTC CAGCA		
			AGA GAA GGTCAAGGAG GTCGT		
			A _ A		
GAM2437	CDK5R2	3'	GCCAGGAGAAACTGCAG 15449	C	CA
			TTGC AGTTTCTCC GC		
			GACG TCAAAGAGG CG		
			_ AC		
GAM2437	CHRM1	3'	GCTGGGAGAAAAGCCAGATGA 96434	TC T	CAG
			TC CT GC TTTCTCCCAGC		
			AG GA CG AAAGAGGGTCG		
			TA C A_		
GAM2437	CPT1A	3'	CTGGAGCTGCTGGGAAGGA 10290	G TT	C
			TCCTT CCAGT CTCC AG		

			AGGAA GGTCG GAGG TC	
			G TC _	
GAM2437	CRP	3'	TGCTGGGAAACGGTCCAAAAGA 72084	CCTT_ A TC
			TCT GCC GTT TCCCAGCA	
			AGA TGG CAA AGGGTCGT	
			AAACC _ _	
GAM2437	CSPG4	3'	GCTAAGAGGGCAAGGAGA 10325	AGTTT CC
			TCTCCTTGCC CTC AGC	
			AGAGGAACGG GAG TCG	
			_ _ _ AA	
GAM2437	DLG5	5'	TGCTGGGAGAGCCAACAAGGAG 83825	CCA T
	G		TCTCCTTG GTT CTCCCAGCA	
			GGAGGAAC CGA GAGGGTCGT	
			AAC _	
GAM2437	DLX4	5'	GCCGGAGGCTTGAAAAGAGA 57112	CTTG TT CA
			TCTC CCAG TCTCC GC	
			AGAG GGTT GGAGG CG	
			AAAA C_ C_	
GAM2437	EDN1	3'	TGCTGGTTCTGACTGGCAAAG 10480	_ TCTC_
	GA		TCCTT GCCAGTT CCAGCA	
			AGGAA CGGTCAG GGTCGT	
			A TCCTT	
GAM2437	EPHB2	3'	GCTGAAAATGACAGGGAGA 16699	C G TCCC
			TCTCCTTG CA TTTC AGC	
			AGAGGGAC GT AAAG TCG	
			A A _ _	
GAM2437	FS	5'	GCCGGGCCCGGCAGCAAGGAG 42081	CA TCT A
			CTCCTTGC GTT CCC GC	
			GAGGAACG CGG GGG CG	
			A_ CC_ C	
GAM2437	GTF2I	3'	TGCTGGGAAATGACAGGGA 53383	C GTTTC
			TCCTTG CA TCCCAGCA	
			AGGGAC GT AGGGTCGT	
			A AA_ _	
GAM2437	GTF2I	3'	TGCTGGGAAATGACAGGGA 53385	C GTTTC
			TCCTTG CA TCCCAGCA	
			AGGGAC GT AGGGTCGT	
			A AA_ _	
GAM2437	HAS3	3'	TGCCAGGAGGAACAAAGAGA 19233	C GCCA CA
			TCTC TT GTTTCTCC GCA	

			AGAG AA CAAGGAGG CGT		
			A ____ AC		
GAM2437	MBNL	5'	GCCAGGAAATCAAGGAGG 41068	CCA	CCCA
			TCTCCTTG GTTTCT GC		
			GGAGGAAC TAAAGG CG		
			____ AC__		
GAM2437	MEST	5'	GCTGACGCCTGGCAGGGAGA 70460	TTTCTCC	
			TCTCCTTGCCAG CAGC		
			AGAGGGACGGTC GTCG		
			CGCA____		
GAM2437	NRCAM	3'	GCTGGGAAAAGAAGGA 18455	GCCAG C	
			TCCTT TTT TCCCAGC		
			AGGAA GAA AGGGTCG		
			____ A		
GAM2437	PCDHA1	3'	TGCCAAGACTTCTGCTGGCAAG 49416	T	TTC__ CCA
	GGA		TC CCTTGCCAGT TC GCA		
			AG GGAACGGTCG AG CGT		
			____ TCTTC AAC		
GAM2437	PCDHA1	3'	TGCCAAGACTTCTGCTGGCAAG 38786	T	TTC__ CCA
	GGA		TC CCTTGCCAGT TC GCA		
			AG GGAACGGTCG AG CGT		
			____ TCTTC AAC		
GAM2437	PCDHA10	3'	TGCCAAGACTTCTGCTGGCAAG 38792	T	TTC__ CCA
	GGA		TC CCTTGCCAGT TC GCA		
			AG GGAACGGTCG AG CGT		
			____ TCTTC AAC		
GAM2437	PCDHA10	3'	TGCCAAGACTTCTGCTGGCAAG 49857	T	TTC__ CCA
	GGA		TC CCTTGCCAGT TC GCA		
			AG GGAACGGTCG AG CGT		
			____ TCTTC AAC		
GAM2437	PCDHA11	3'	TGCCAAGACTTCTGCTGGCAAG 38794	T	TTC__ CCA
	GGA		TC CCTTGCCAGT TC GCA		
			AG GGAACGGTCG AG CGT		
			____ TCTTC AAC		
GAM2437	PCDHA12	3'	TGCCAAGACTTCTGCTGGCAAG 38800	T	TTC__ CCA
	GGA		TC CCTTGCCAGT TC GCA		
			AG GGAACGGTCG AG CGT		
			____ TCTTC AAC		
GAM2437	PCDHA13	3'	TGCCAAGACTTCTGCTGGCAAG 38801	T	TTC__ CCA
	GGA		TC CCTTGCCAGT TC GCA		

			AG GGAACGGTCG	AG	CGT		
			—	TCTTC	AAC		
GAM2437	PCDHA2	3'	TGCCAAGACTTCTGCTGGCAAG	38807	T	TTC__	CCA
	GGA		TC CCTTGCCAGT	TC	GCA		
			AG GGAACGGTCG	AG	CGT		
			—	TCTTC	AAC		
GAM2437	PCDHA3	3'	TGCCAAGACTTCTGCTGGCAAG	38809	T	TTC__	CCA
	GGA		TC CCTTGCCAGT	TC	GCA		
			AG GGAACGGTCG	AG	CGT		
			—	TCTTC	AAC		
GAM2437	PCDHA4	3'	TGCCAAGACTTCTGCTGGCAAG	38815	T	TTC__	CCA
	GGA		TC CCTTGCCAGT	TC	GCA		
			AG GGAACGGTCG	AG	CGT		
			—	TCTTC	AAC		
GAM2437	PCDHA5	3'	TGCCAAGACTTCTGCTGGCAAG	38817	T	TTC__	CCA
	GGA		TC CCTTGCCAGT	TC	GCA		
			AG GGAACGGTCG	AG	CGT		
			—	TCTTC	AAC		
GAM2437	PCDHA6	3'	TGCCAAGACTTCTGCTGGCAAG	38823	T	TTC__	CCA
	GGA		TC CCTTGCCAGT	TC	GCA		
			AG GGAACGGTCG	AG	CGT		
			—	TCTTC	AAC		
GAM2437	PCDHA6	3'	TGCCAAGACTTCTGCTGGCAAG	49821	T	TTC__	CCA
	GGA		TC CCTTGCCAGT	TC	GCA		
			AG GGAACGGTCG	AG	CGT		
			—	TCTTC	AAC		
GAM2437	PCDHA7	3'	TGCCAAGACTTCTGCTGGCAAG	38825	T	TTC__	CCA
	GGA		TC CCTTGCCAGT	TC	GCA		
			AG GGAACGGTCG	AG	CGT		
			—	TCTTC	AAC		
GAM2437	PCDHA8	3'	TGCCAAGACTTCTGCTGGCAAG	38831	T	TTC__	CCA
	GGA		TC CCTTGCCAGT	TC	GCA		
			AG GGAACGGTCG	AG	CGT		
			—	TCTTC	AAC		
GAM2437	PCDHA9	3'	TGCCAAGACTTCTGCTGGCAAG	49854	T	TTC__	CCA
	GGA		TC CCTTGCCAGT	TC	GCA		
			AG GGAACGGTCG	AG	CGT		
			—	TCTTC	AAC		
GAM2437	PCDHAC1	3'	TGCCAAGACTTCTGCTGGCAAG	38782	T	TTC__	CCA
	GGA		TC CCTTGCCAGT	TC	GCA		

AG GGAACGGTCG AG CGT
 _ TCTTC AAC
 GAM2437 PCDHAC2 3' TGCCAAGACTTCTGCTGGCAAG 38785 T TTC__ CCA
 GGA TC CCTTGCCAGT TC GCA
 || ||||| || |||
 AG GGAACGGTCG AG CGT
 _ TCTTC AAC
 GAM2437 PEA15 3' GCTGGAAGAAGGAAGAAG 15011 C G AGT C
 CT CTT CC TTCT CCAGC
 || ||| || |||||
 GA GAA GG AAGA GGTCG
 A _ _ A
 GAM2437 PKHD1 3' GCTGGGACAACATAAGAAGA 57715 C GCC TC
 TCT CTT AGTT TCCCAGC
 ||| ||| |||||
 AGA GAA TCAA AGGGTCG
 A _ _ C_
 GAM2437 PLCB2 3' CTGGGACATTTAGCAAGGAGG 17112 C TTTC
 TCTCCTTGC AG TCCCAG
 ||||| || |||||
 GGAGGAACG TT AGGGTC
 A TAC_
 GAM2437 PRX 3' GCTAAAATGGGCAAGGG 40897 A CTCCC
 TCCTTGCC GTTT AGC
 ||||| ||| |||
 GGGAACGG TAAA TCG
 G A____
 GAM2437 TACC1 3' CTGAGAAGAGGAGTGCAAGGAG 21871 CAG _ C
 A TCTCCTTGC TTTCT C CAG
 ||||| ||||| |||
 AGAGGAACG GGAGA G GTC
 TGA A A
 GAM2437 VCX 5' CTGGGAGAAGGAAGTGAGA 69701 _ G AGT
 TCTC CTT CC TTCTCCCAG
 ||| ||| || |||||
 AGAG GAA GG AAGAGGGTC
 T _ _
 GAM2437 ABHD2 5' GCTCTAAACTGGCAGGAGA 23795 T CTCCC
 TCTCCT GCCAGTTT AGC
 ||||| ||||| |||
 AGAGGA CGGTCAAA TCG
 _ TC____
 GAM2437 AIF1 5' TGCTGAAGGCCAGCAGGAAGA 17929 C CAGTT CC
 TCT CTTGC TCT CAGCA
 ||| |||| ||| |||||
 AGA GGACG GGA GTCGT
 A ACCC_ A_
 GAM2437 C1orf34 3' GCCGACCTGCTCAGCAAGGAGA 61312 C_ TTC CCA
 TCTCCTTGC AGT TC GC
 ||||| ||| || ||

AGAGGAACG TCG AG CG
 AC TCC C__
 GAM2437 CENTG3 3' TGCTGAGAGGACGAAGCCAAGG 50048 CCA _ _
 A TCCTTG GTTTC TCC CAGCA
 ||||| ||||| || |||||
 AGGAAC CGAAG AGG GTCGT
 _ C AGA
 GAM2437 dJ383J4.3 3' TGCTGAAAGAGACTGCAGGAGA 67499 T C CC
 TCTCCT GC AGTTTCT CAGCA
 ||||| || ||||| |||||
 AGAGGA CG TCAGAGA GTCGT
 _ _ AA
 GAM2437 DKFZP434B168 5' GGAAGAAAAACCAGCAAGAAGG 31870 C CAG__ C
 TCT CTTGC TTTCT CC
 || ||||| ||||| ||
 GGA GAACG AAAGA GG
 A ACCAA A
 GAM2437 DKFZP434F0318 3' CTGGGAGAAAAAAGAGAGGA 48753 GCCAG
 TCCTT TTTCTCCCAG
 ||||| |||||
 AGGAG AAAGAGGGTC
 AGAAA
 GAM2437 DKFZP564K0822 3' GCTGGGAAAAGACAGGAGA 95698 TGCCA C_
 TCTCCT GTTT TCCCAGC
 ||||| ||| |||||
 AGAGGA CAGA AGGGTCG
 _ AA
 GAM2437 DKFZP586M1120 3' CTGGGAAACCCAAAGGAGA 49280 GCCA TC
 TCTCCTT GTT TCCCAG
 ||||| ||| |||||
 AGAGGAA CAA AGGGTC
 ACC_ _
 GAM2437 EPB41L1 3' GAACTGGCCCAGCTAAGGAGA 71108 _
 TCTCCTT GCCAGTTT
 ||||| |||||
 AGAGGAA CGGTCAAG
 TCGACC
 GAM2437 FLJ10901 3' GCTGGAAAAAAGTGTTCATAG 37368 CT C__ CTC
 AGG TCTC TG CAGTTT CCAGC
 ||| || ||||| |||||
 GGAG AC GTCAAA GGTCG
 AT TTT AAA
 GAM2437 FLJ12568 3' TGCTGGAAGAACTAGTGAAGA 47143 C TG C C
 GA TCTC T C AGTTTCT CCAGCA
 ||| | ||||| |||||
 AGAG A G TCAAAGA GGTCGT
 A GT A A
 GAM2437 FLJ13441 3' TGCTGGGAGCTACAGCAAG 43920 CA TT
 CTTGC GT CTCCCAGCA
 ||||| || |||||

		GAACG CA GAGGGTCGT	
		A_ TC	
GAM2437	FLJ20424 3'	GGAAAATCTAGCAAGGAGA 35617	C T C
		TCTCCTTGC AG TT TCC	
		AGAGGAACG TC AA AGG	
		A T A	
GAM2437	FLJ31762 3'	TGCCAAAAACCAGCACAAGGAG 58767	__ CA CTCCCA
	A	TCTCCT TGC GTTT GCA	
		AGAGGA ACG CAAA CGT	
		AC AC AAC__	
GAM2437	GPS2 5'	GCCGGAAGCTGCGAGGAGA 16889	C CCCA
		TCTCCTTGC AGTTTCT GC	
		AGAGGAGCG TCGAAGG CG	
		_ C__	
GAM2437	KIAA0286 3'	TGCTGGBAATAAACAAAGCAG 68862	CA_ C_
		TTGC GTTT TCCCAGCA	
		GACG CAAA AGGGTCGT	
		AAA TA	
GAM2437	KIAA0603 3'	TGCTGGGTATAGGCAAGGA 29837	AGTTTCT
		TCCTTGCC CCCAGCA	
		AGGAACGG GGGTCGT	
		ATAT__	
GAM2437	KIAA0987 3'	GAGAAGGTGGTGCAGGAGA 25508	_ G
		TCTCCT TGCCA TTTCTC	
		AGAGGA GTGGT GAAGAG	
		C G	
GAM2437	KIAA1189 3'	CTGGGAGGGGCTAGAAGA 72507	C TGCC TT
		TCT CT AGT CTCCCAG	
		AGA GA TCG GAGGGTC	
		A ____ GG	
GAM2437	KIAA1609 5'	GGAAGCCCGGCAGGGAGA 74708	A_
		TCTCCTTGCC GTTTCT	
		AGAGGGACGG CGAAGG	
		CC	
GAM2437	KIAA1737 3'	CTGAGTGGCAGGGAGA 67940	G TTCTCC
		TCTCCTTGCCA T CAG	
		AGAGGGACGGT A GTC	
		G _____	
GAM2437	MGC14436 5'	GCCGGGAGAGACAGGA 52928	TGCCA A
		TCCT GTTTCTCCC GC	

			AGGA CAGAGAGGG CG		
			_____ C		
GAM2437	MGC2941	3'	GCCAGAAATGCAAGGA 44415	CA	CCCA
			TCCTTGC GTTTCT GC		
			AGGAACG TAAAGA CG		
			_____ C_____		
GAM2437	MRPS27	3'	CTGGGAGAAACCAAGGCTGA 31328	T_	CCA
			TC CCTTG GTTTCTCCCAG		
			AG GGAAC CAAAGAGGGTC		
			TC _____		
GAM2437	MRPS27	3'	CTGGGAGAAATTCAGGA 31329	TGCC	
			TCCT AGTTTCTCCCAG		
			AGGA TTAAAGAGGGTC		
			C_____		
GAM2437	MUC17	3'	TGCTGGGAGATTCTCAAATAGA 95928	CC	CC TT
			TCT TTG AG TCTCCCAGCA		
			AGA AAC TC AGAGGGTCGT		
			TA _ TT		
GAM2437	PIGPC1	3'	TGCTGAGATGGACTCCAGAAGA 42351	C	GCC_ TC C
	AGA		TCT CTT AGTT TC CAGCA		
			AGA GAA TCAG AG GTCGT		
			A GACC GT A		
GAM2437	RP4-622L5	3'	TGCTGGGGTCTGGCATAGA 39431	CT	TTTC
			TC TGCCAG TCCCAGCA		
			AG ACGGTC GGGGTCGT		
			AT T_____		
GAM2437	STX3A	3'	CTGGGAGAATAAAATGAGA 16068	C	GCCAGT
			TCTC TT TTCTCCCAG		
			AGAG AA AAGAGGGTC		
			T AAT_____		
GAM2437	TRPV5	5'	GCCAGTGTCTGCAAGGAGA 39524	C	TTT CCCA
			TCTCCTTGC AG CT GC		
			AGAGGAACG TC GA CG		
			_ TGT C_____		
GAM2437	TRPV6	5'	TGCTGGGAGACTCCCAAGGA 38464	CC	TT
			TCCTTG AG TCTCCCAGCA		
			AGGAAC TC AGAGGGTCGT		
			CC _____		
GAM2437	TUSP	5'	TGGTTCTGAAACAACAAGGAGA 40035	CCA	TC_____
			TCTCCTTG GTTTC CCA		

AGAGGAAC CAAAG GGT
 AA_ TCTT
 GAM2437 LOC115286 3' TGCTAAGATACCGGCATGGAGA 73766 T A T CCC
 TCTCC TGCC GT TCT AGCA
 ||||| ||||| || |||||
 AGAGG ACGG CA AGA TCGT
 T C T A__
 GAM2437 LOC145761 5' TGCCAAAAAGAGGCCCTGGCAG 84485 T TT CCA__
 GAGA TCTCCT GCCAG TCTC GCA
 ||||| ||||| ||||| |||||
 AGAGGA CGGTC GGAG CGT
 _ CC AAAAAC
 GAM2437 LOC146445 3' TGCTAGGAAAACTGGTGA 84685 TG C C
 T CCAGTTT TCC AGCA
 | ||||| |||||
 A GGTC AAA AGG TCGT
 GT A A
 GAM2437 LOC149721 3' TGCTGGGGACAGCAAG 80321 CA TCT
 CTTGC GTT CCCAGCA
 ||||| ||||| |||||
 GAACG CAG GGGTCGT
 A_ ____
 GAM2437 LOC151963 3' TTGAGAAAACTGGCAGGAAGA 81220 C C C
 TCT CTTGCCAGTTT TC CAG
 ||| ||||| ||||| |||||
 AGA GGACGGTCAAA AG GTT
 A A A
 GAM2437 LOC153514 5' TGCCAGGAAATTGCCAAG 81713 C C CCA
 CTTG CAGTTTCT GCA
 ||||| ||||| |||||
 GAAC GTTAAAGG CGT
 C AC__
 GAM2437 LOC153733 5' GCTGGGAACACAAGGAGA 81801 CCA TTC
 TCTCCTTG GT TCCCAGC
 ||||| ||||| |||||
 AGAGGAAC CA AGGGTCG
 A_ ____
 GAM2437 LOC154789 5' TGCTCTCAACTAGCAGAGAGA 82035 C C TCTCCC
 TCTC TTGC AGTT AGCA
 ||||| ||||| ||||| |||||
 AGAG GACG TCAA TCGT
 A A CTC__
 GAM2437 LOC222193 3' TGCTGAAAAGTGGGAAGGAGA 95845 G G CTCC
 TCTCCTT CCA TTT CAGCA
 ||||| ||||| ||||| |||||
 AGAGGAA GGT AAA GTCGT
 G G A__
 GAM2437 LOC245771 5' GCTGGAAAAAAGTGTTCATAG 94482 CT C__ CTC
 AGG TCTC TG CAGTTT CCAGC
 ||||| ||||| ||||| |||||

GGAG AC GTCAAA GGTCG
AT TTT AAA
GAM2437 LOC253482 3' TGCTAAGCTTTTGGCAAGAGA 97870 C TTT CCC
TCTC TTGCCAG CT AGCA
||||| || ||||
AGAG AACGGTT GA TCGT
_ TTC A_
GAM2437 LOC255565 3' TGCCAGAAGTTGGGCAGAGAGA 96805 C AG_ CCCA
TCTC TTGCC TTTCT GCA
||||| |||| ||
AGAG GACGG GAAGA CGT
A GTT C_
GAM2437 LOC90010 3' TGCCAGAAGTTGGGCAGAGAGA 61724 C AG_ CCCA
TCTC TTGCC TTTCT GCA
||||| |||| ||
AGAG GACGG GAAGA CGT
A GTT C_
GAM2438 MUCDHL 3' ACGGTGACCTCTGGCACCG 41913 GA_ A
CGG TGGA GTCACCGT
||| ||| |||||
GCC GTCT CAGTGGCA
ACG C
GAM2438 NPR2L 3' ACAGTGACTTCCATGTAGT 22589 GGG C
AC ATGGAAGTCAC GT
|| ||||| ||
TG TACCTTCAGTG CA
ATG A
GAM2438 PPGB 3' TGATTCCATCCCAGGAA 6126 AC G
TTC GGGATGGAA TCA
||| ||||| ||
AAG CCCTACCTT AGT
GA _
GAM2438 ZRF1 5' ACGAAAGATCCATCCCGGAA 95944 A AG AC_
TTC CGGGATGGA TC CGT
||| ||||| || ||
AAG GCCCTACCT AG GCA
_ _ AAA
GAM2438 FLJ10932 3' ACAGTGCCCTTTCCATCCGTGAA 37421 G _T C
TTCACGG ATGGAA G CAC GT
||||| ||||| | ||| ||
AAGTGCC TACCTT C GTG CA
_ T C A
GAM2438 FLJ22477 3' ACGGTGACTGTGGCCTTGAA 45664 C ATGGA
TTCA GGG AGTCACCGT
||||| ||| |||||
AAGT TCC TCAGTGGCA
_ GGTG_
GAM2438 MGC3020 3' ACGGTGACTAAAAGCCCCTGAA 44121 C ATGGA
TTCA GGG AGTCACCGT
||||| ||| |||||

AAGT CCC TCAGTGGCA
 C GAAAA
 GAM2438 LOC255565 3' ACAGTGAAGTTCGAGACCAGGAA 96799 AC GATG C
 TTC GG GAAGTCAC GT
 ||| || ||||| ||
 AAG CC CTTCAAGT CA
 GA AGAG A
 GAM2438 LOC257104 5' ACGGTGGGGGCACCCCGTGGA 99363 A GAAG
 TTCACGGG TG TCACCGT
 ||||| || |||||
 AGGTGCCC AC GGTGGCA
 C GGG_
 GAM2439 APOB 3' TTGAACTTTCACATAGCACAGA 6356 TC CTAA
 TCTGTGCT GTGAAG TCAA
 ||||| ||||| |||
 AGACACGA CACTTT AGTT
 TA CA_
 GAM2439 DKFZP727C091 3' TTGATTCTGTTCGCAAAGCACA 66795 C GCT
 GA TCTGTGCTT GTGAA AATCAA
 ||||| ||||| |||||
 AGACACGAA CGCTT TTAGTT
 A GTC
 GAM2439 FLJ20055 3' AGCTTCATCAAAACAGA 34903 GC C
 TCTGT TT GTGAAGCT
 |||| |||||
 AGACA AA TACTTCGA
 A_ C
 GAM2439 FLJ30567 3' TAGTCTCATGAAGCACAGA 59479 AG
 TCTGTGCTTCGTGA CTA
 ||||| ||||| |||
 AGACACGAAGTACT GAT
 CT
 GAM2439 GLTP 3' TTGGAATTTACGACAGCACAG 33593 _ _
 A TCTGTGCT TCGTGAAG CTAA
 ||||| ||||| |||||
 AGACACGA AGCACTTT GGTT
 C AA
 GAM2439 IPLA2(GAMMA) 3' AGCTTGCATAGCACAGA 61340 TC _
 TCTGTGCT GTG AAGCT
 ||||| ||| |||||
 AGACACGA TAC TTCGA
 _ G
 GAM2439 KIAA1016 3' GATTTTCCAGAAGCACA 93385 GT GCT
 TGTGCTTC GAA AATC
 ||||| ||| |||||
 ACACGAAG CTT TTAG
 AC _
 GAM2439 KIAA1500 3' TGATCAGCCAGGCACAGA 64813 CGTGAA A
 TCTGTGCTT GCT ATCA
 ||||| ||| |||||

			AGACACGGA	CGA TAGT	
			C_____C		
GAM2439	RAB6C	3'	ATTAGCTTCACAAGCACA	50482	C
			TGTGCTT GTGAAGCTAAT		
			ACACGAA CACTTCGATTA		
			—		
GAM2439	SLC5A6	5'	TGATCTCAGGAAGCACA	41181	G A CTA
			TGTGCTTC TGA G ATCA		
			ACACGAAG ACT C TAGT		
			G _ _ _ _		
GAM2439	TRAF2	3'	AGCTCACGAAGACAGA	41234	G A
			TCTGT CTTCGTGA GCT		
			AGACA GAAGCACT CGA		
			— —		
GAM2439	LOC147645	3'	GGCCTACCAAGCACAGA	79071	C AA
			TCTGTGCTT GTG GCT		
			AGACACGAA CAT CGG		
			C C_		
GAM2439	LOC256295	3'	TTGGCTTCCAGAAGCACAGA	98378	GT
			TCTGTGCTTC GAAGCTAA		
			AGACACGAAG CTTCGGTT		
			AC		
GAM2440	SCAMP1	3'	GCTAAATAAATATTCTCC	54500	T C
			GGA AATATT ATTTAGC		
			CCT TTATAA TAAATCG		
			C A		
GAM2440	SCAMP1	3'	GCTAAATAAATATTCTCC	54501	T C
			GGA AATATT ATTTAGC		
			CCT TTATAA TAAATCG		
			C A		
GAM2440	NX-17	3'	TGAATATCAGCCCCTAATA	40706	ATA_
			TATTAGGG ATATTCA		
			ATAATCCC TATAAGT		
			CGAC		
GAM2440	LOC161589	3'	GCTAAATGAATATTATCCCTAA	83159	
	TA		TATTAGGGATAATATTCATTTAGC		
			ATAATCCCTATTATAAGTAAATCG		
GAM2441	SCAMP1	3'	GCTAAATAAATATTCTCC	54500	T C
			GGA AATATT ATTTAGC		

			CCT TTATAA TAAATCG			
			C A			
GAM2441	SCAMP1	3'	GCTAAATAAATATTCTCC	54501	T C	
			GGA AATATT ATTTAGC			
			CCT TTATAA TAAATCG			
			C A			
GAM2441	NX-17	3'	TGAATATCAGCCCCTAATA	40706	ATA_	
			TATTAGGG ATATTCA			
			ATAATCCC TATAAGT			
			CGAC			
GAM2441	LOC161589	3'	GCTAAATGAATATTATCCCTAA	83159		
		TA	TATTAGGGATAATATTCATTTAGC			
			ATAATCCCTATTATAAGTAAATCG			
GAM2442	FGFR2	5'	CACAACCCCGGGCTCGTCGCTT	5557	AG	AA__ A
		TCTC	GA AAGCGAC TTGGG TTGTG			
			CT TTCGCTG GGCCC AACAC			
			CT CTCG C			
GAM2442	FGFR2	5'	CACAACCCCGGGCTCGTCGCTT	43632	AG	AA__ A
		TCTC	GA AAGCGAC TTGGG TTGTG			
			CT TTCGCTG GGCCC AACAC			
			CT CTCG C			
GAM2442	FGFR2	5'	CACAACCCCGGGCTCGTCGCTT	43637	AG	AA__ A
		TCTC	GA AAGCGAC TTGGG TTGTG			
			CT TTCGCTG GGCCC AACAC			
			CT CTCG C			
GAM2442	FGFR2	5'	CACAACCCCGGGCTCGTCGCTT	43641	AG	AA__ A
		TCTC	GA AAGCGAC TTGGG TTGTG			
			CT TTCGCTG GGCCC AACAC			
			CT CTCG C			
GAM2442	FGFR2	5'	CACAACCCCGGGCTCGTCGCTT	43651	AG	AA__ A
		TCTC	GA AAGCGAC TTGGG TTGTG			
			CT TTCGCTG GGCCC AACAC			
			CT CTCG C			
GAM2442	FGFR2	5'	CACAACCCCGGGCTCGTCGCTT	43664	AG	AA__ A
		TCTC	GA AAGCGAC TTGGG TTGTG			
			CT TTCGCTG GGCCC AACAC			
			CT CTCG C			
GAM2442	FGFR2	5'	CACAACCCCGGGCTCGTCGCTT	43672	AG	AA__ A
		TCTC	GA AAGCGAC TTGGG TTGTG			

CT TTCGCTG GGCCC AACAC
 CT CTCG C
 GAM2442 FGFR2 5' CACAACCCCGGGCTCGTCGCTT 43762 AG AA__ A
 TCTC GA AAGCGAC TTGGG TTGTG
 || ||||| |||| |||||
 CT TTCGCTG GGCCC AACAC
 CT CTCG C
 GAM2442 FKSG28 3' CACAGTTCTAACTGCCCTTCCT 48905 A CGA A
 C GA GAAG CA TTGGGATTGTG
 || |||| || |||||
 CT CTTC GT AATCTTGACAC
 C CC_ C
 GAM2442 KIAA1918 3' CACAATCTTCCAATGACTTCT 73536 CGACA __
 AGAAG ATTGG GATTGTG
 |||| |||| |||||
 TCTTC TAACC CTAACAC
 AG__ TT
 GAM2442 TACTILE 3' CACAAAATACACTGTGGCTTCT 20582 G AT GGA_
 TC GAAGAAGC ACA TG TTGTG
 ||||| || || |||||
 CTTCTTCG TGT AC AACAC
 G C_ ATAA
 GAM2442 LOC145989 5' CCCGACTGCCGCTTCCTC 60290 A A A
 GA GAAGCG CA TTGGG
 || ||||| || |||||
 CT CTTCGC GT AGCCC
 C C C
 GAM2442 LOC151009 3' CACAACACAGCTGCCGTTTCTT 86364 A A GGA
 C GAAGAAGCG CA TTG TTGTG
 ||||| || || |||||
 CTTCTTTGC GT GAC AACAC
 C C AC_
 GAM2442 LOC90371 5' CACAATCCCACCCCTCCCTCCTT 63156 A C CAAT
 C GAAG AG GA TGGGATTGTG
 |||| || || |||||
 CTTC TC CT ACCCTAACAC
 C C CCC_
 GAM2443 BBS4 3' ATTTGCCCAAAGGGAATCCAGA 53447 G_ G_ A
 ACA TGTCTGGA CT TTGG CAAAT
 ||||| || || |||||
 ACAAGACCT GG AACC GTTTA
 AA GA C
 GAM2443 CENTD2 3' CCAACAACTCCAGAACA 58270 C_
 TGTCTGGAG TGTTGG
 ||||| |||||
 ACAAGACCTC ACAACC
 AA
 GAM2443 HAMP 3' TCCTGCTGCCCCAGAACA 41289 A T T
 TGTCTGG GC GT GGA
 ||||| || || |||

			ACAAGACC CG CG CCT		
			C T T		
GAM2443	ITGA11	3'	TCTGCCGGCCCCCAGGACA 25213	A_	TT
			TGTTCTGG GCTG GGA		
			ACAGGACC CGGC TCT		
			CC CG		
GAM2443	KITLG	3'	ATTTGCATGGCTCCAGAA 8023	TGGA	
			TTCTGGAGCTGT CAAAT		
			AAGACCTCGGTA GTTTA		
			C_		
GAM2443	MAPK4	5'	CCTGGGCAGCTCCAGATCA 12300	T	_
			TG TCTGGAGCTGTT GG		
			AC AGACCTCGACGG CC		
			T GT		
GAM2443	MGAT2	3'	ATTTGTCCAAACAGGACA 11557	GAGCTG	
			TGTTCTG TTGGACAAAT		
			ACAGGAC AACCTGTTTA		
			A_		
GAM2443	PSPHL	5'	TTGTCATACAGCTCCAAACA 94499	C	TG
			TGTT TGGAGCTGT GACAA		
			ACAA ACCTCGACA CTGTT		
			_ TA		
GAM2443	TTC3	3'	TATTTGTCCAACAACTGTCAGA 13885	_	C
	ATA		TGTTCTGG AG TGTTGGACAAATA		
			ATAAGACT TC ACAACCTGTTTAT		
			G A		
GAM2443	FLJ14213	3'	TGATAACAGCTCCAGAA 46218	GA	
			TTCTGGAGCTGTTG CA		
			AAGACCTCGACAAT GT		
			A_		
GAM2443	H2BFQ	3'	TTTAAGAGAACTCCAGGACA 60079	_	G
			TGTTCTGGAG CT TTGGA		
			ACAGGACCTC GA AATTT		
			AA G		
GAM2443	LRG	3'	TCCATCCATGCTTCCTAGAACA 54825	_ _ _	T_
			TGTTCT GGA GC TG TGGA		
			ACAAGA CCT CG AC ACCT		
			T T T CT		
GAM2443	NMT2	3'	ATTTGTCCATGTAACAGAACA 17852	GA	TGT
			TGTTCTG GC TGACAAAT		

ACAAGAC TG ACCTGTTTA
 AA T__
 GAM2443 NYD-SP21 3' TATTTGTCCAATCTAGATTCAG 51863 G __
 AACA TGTTCTGGA CT GTTGGACAAATA
 ||||| || |||||
 ACAAGACTT GA TAACCTGTTTAT
 A TC
 GAM2443 PSPH 3' TTGTCGTACAGCTCCAAACA 17143 C TG
 TGTT TGGAGCTGT GACAA
 ||| ||||| ||||
 ACAA ACCTCGACA CTGTT
 _ TG
 GAM2443 LOC122258 3' CCACCAGCCTCCGGAACA 59820 _ T
 TGTTCTGGAG CTG TGG
 ||||| ||| |||
 ACAAGGCCTC GAC ACC
 C C
 GAM2443 LOC151826 3' ATTTGTCCAACCTAGCACA 81176 T AGCT
 TGT CTGG GTTGGACAAAT
 ||| ||| |||||
 ACA GATC CAACCTGTTTA
 C ____
 GAM2443 LOC169611 3' TCCAGTGGCAGCTCCAGAA 83663 ____
 TTCTGGAGCTGT TGGA
 ||||| |||
 AAGACCTCGACG ACCT
 GTG
 GAM2443 LOC196746 3' TCAGAGCAGCTCCAAGACA 88903 TC G_
 TGT TGGAGCTGTT GA
 ||| ||||| ||
 ACA ACCTCGACGA CT
 GA GA
 GAM2443 LOC253142 5' TTGCTAGGATGCCCCAGAATA 99230 A TG_ A
 TGTTCTGG GC TTGG CAA
 ||||| || ||| |||
 ATAAGACC CG GATC GTT
 C TAG _
 GAM2444 CDH12 3' CTTATCATTTAAAGTGGTGTA 15777 CCCAA GA
 TACACCACT GAA ATAAG
 ||||| ||| ||||
 ATGTGGTGA TTT TATTC
 AA__ AC
 GAM2444 GOCAP1 3' ATTGTTCTTGGGAGCAGTGTA 43007 CA G
 TACAC CTCCCAAGAA AAT
 |||| ||||| |||
 ATGTG GAGGGTTCTT TTA
 AC G
 GAM2444 DKFZp434N2435 5' CTTATTACTGTGGGGTGGT 98090 T AGAAG
 ACCAC CCCA AATAAG
 |||| ||| |||||

		TGGTG GGGT TTATTC	
		_ GTCA_	
GAM2444	DKFZP564I122	3' CTTATTCTTCTCCCTCATGTGT 63877	CACTCCCA
	A	TACAC AGAAGAATAAG	
		ATGTG TCTTCTTATTC	
		TACTCCC_	
GAM2444	FLJ21791	3' CTTATTTGCAGAAAGTGGTGTA 62126	CCCAAGAA
		TACACCACT GAATAAG	
		ATGTGGTGA TTTATTC	
		AGACG__	
GAM2444	HMP19	3' CTTATTCTTTGTAGGAAAATG 88860	CCAC CAA_
	TA	TACA TCC GAAGAATAAG	
		ATGT AGG TTTCTTATTC	
		AAA_ ATTG	
GAM2444	KIAA1719	3' TCTGTCTTGGGAGTGGTGTA 68742	_
		TACACCACTCCCAAGA AGA	
		ATGTGGTGAGGGTTCT TCT	
		G	
GAM2444	KIAA1853	3' TTTTCTTGAAGCAGTG 69929	CA C
		CAC CT CCAAGAAGAA	
		GTG GA GGTTCTTTT	
		AC A	
GAM2444	KIAA1877	3' CTTATTCTTCTGCCATGAGT 66748	CCA_
		ACTC AGAAGAATAAG	
		TGAG TCTTCTTATTC	
		TACCG	
GAM2444	KIAA1906	3' CTTATTCTTCTTGACTTTTGG 73571	CTCC_
		CCA CAAGAAGAATAAG	
		GGT GTTCTTCTTATTC	
		TTTCA	
GAM2444	OSBPL11	3' CTTAATTTCCCAAGAGTGGTG 43206	CCAA AA
		CACCACTC GAAG TAAG	
		GTGGTGAG CTTT ATTC	
		AACC A_	
GAM2444	YME1L1	3' TCATTCTTGATGTGGTGTA 58438	TCC _
		TACACCAC CAAGAA GA	
		ATGTGGTG GTTCTT CT	
		TA_ A	
GAM2444	ZNF262	3' CTTATTTTGTGTTGGGAGT 18723	A
		ACTCCCAAG AGAATAAG	

			TGAGGGTTT TTTTATTC		
			G		
GAM2444	LOC91960	3'	TGTGGCTTGGAACGTGGTGTA 68294	TC_	AAGA
			TACACCAC CCAAG ATA		
			ATGTGGTG GGTTC TGT		
			CAA GG_		
GAM2445	ALDH3B2	5'	TCTGGAGGCAGCATGTCCAAG 7345	CACA_	T
			CTTGGAC GCCT CCAGA		
			GAACCTG CGGA GGTCT		
			TACGA _		
GAM2445	BACE	3'	GTCTGGAGCTCACCCAAGG 25034	ACCAC	CT
			CCTTGG AGC TCCAGAC		
			GGAACC TCG AGGTCTG		
			CAC_ _		
GAM2445	BACE	3'	GTCTGGAGCTCACCCAAGG 58091	ACCAC	CT
			CCTTGG AGC TCCAGAC		
			GGAACC TCG AGGTCTG		
			CAC_ _		
GAM2445	EPHB3	3'	TGCCTGGCCTTAGGCTGTGGCC 16704	A	T_ _ A
	CAG		TTGG CCACAGCCT CCAG CA		
			GACC GGTGTCGGA GGTC GT		
			C TTCC C		
GAM2445	GSTM5	3'	GTCTAGAACTGGCATGGTTCAA 7800	CA _	C
			TTGGACCA GCC TTC AGAC		
			AACTTGGT CGG AAG TCTG		
			A_ TC A		
GAM2445	KLK3	3'	GAAGGCTGTGAGCCAAGG 9708	AC	
			CCTTGG CACAGCCTTC		
			GGAACC GTGTGCGGAAG		
			GA		
GAM2445	NEU3	3'	TGCCTGGAGTCGTCTGTCCAAG 22835	C_ A	CT A
	G		CCTTGGAC AC GC TCCAG CA		
			GGAACCTG TG TG AGGTC GT		
			TC C _ C		
GAM2445	PVR	3'	GCTAGGGGGTGTCCAAGG 22493	CACA	C A
			CCTTGGAC GCCTTC AG C		
			GGAACCTG TGGGGG TC G		
			_ A C		
GAM2445	SH3BP2	3'	TGGGAGGCTGTGACCCCAGG 13089	T AC	
			CCT GG CACAGCCTTCCA		

GGA CC GTGTCGGAGGGT
 C CA
 GAM2445 WFDC1 5' GTCTGGAAGGTCGCTGCCCAGG 41340 ACCACA
 G CCTTG GCCTTCCAGAC
 ||||| |||||
 GGGACC TGGAAGGTCTG
 CGTCGC
 GAM2445 C20orf160 3' TGAGAAACTATGGTTCAAG 55526 C CC _
 CTTGGACCA AG TTC CA
 ||||| || |||
 GAACTTGGT TC AAG GT
 A A_ A
 GAM2445 CLONE24945 3' TGCCTGGGTGTTACATGGCCCA 32255 A C__ CT A
 GGG CCTTG CCA AGC TCCAG CA
 ||||| || ||| |||
 GGGACC GGT TTG GGGTC GT
 C ACA T_ C
 GAM2445 COPS7A 3' TGTCTGGAGCATAACCCACAGG 33323 _ ACCACA CT
 CCT TGG GC TCCAGACA
 ||| || || |||||
 GGA ACC CG AGGTCTGT
 C CAATA_ _
 GAM2445 FLJ10647 5' TGCCTGGAAGGGGCCTCCTAGG 36887 T _ ACAG A
 CCT GGA CC CCTTCCAG CA
 ||| || || ||||| ||
 GGA CCT GG GGAAGGTC GT
 T CC _ _ C
 GAM2445 FLJ13544 3' GTCTGGAAGACCCAAGG 47208 ACCACAGC
 CCTTG CTTCCAGAC
 ||||| |||||
 GGAACC GAAGGTCTG
 CA_ _ _
 GAM2445 FLJ13841 5' CTGGACAGCCAGAGTCCAAGG 45548 CACA CT
 CCTTGAC GC TCCAG
 ||||| || |||
 GGAACCTG CG AGGTC
 AGAC AC
 GAM2445 FLJ20184 3' TGCCTGGCCCCACGTAGTTCAA 35199 C AGCCTT A
 GG CCTTGAC AC CCAG CA
 ||||| || ||| ||
 GGAAGTGT TG GGTC GT
 A CACCCC C
 GAM2445 FLJ20595 5' GAAGACTGAGGTCCAAGG 35863 A C
 CCTTGACC CAG CTTC
 ||||| ||| |||
 GGAACCTGG GTC GAAG
 A A
 GAM2445 GP 5' TCTGGGCTGTGATCCA 37976 C TTC
 TGGA CACAGCC CAGA
 ||| ||||| |||

ACCT GTGTCGG GTCT
A ____
GAM2445 KIAA0161 3' GTCTGGGGATGGCCTAAG 29207 A CAG TT
CTTGG CCA CC CCAGAC
||||| || |||||
GAATC GGT GG GGTCTG
C A__ __
GAM2445 KIAA0399 5' CTGGAAGGCTGTGGTGCTGA 31362 TG_
T G ACCACAGCCTTCCAG
| | |||||
A C TGGTGTCTGGAAGGTC
GT G
GAM2445 KIAA1808 3' GTCTGGGACAGTGCCAAG 87052 AC AGCC
CTTGG CAC TTCCAGAC
||||| || |||||
GAACC GTG AGGGTCTG
__ AC__
GAM2445 MYT1L 5' TGAGGAGGCTGTAGCCAAGG 67367 ACC _
CCTTGG ACAGCCTTC CA
||||| ||||| ||
GGAACC TGTCGGAGG GT
GA_ A
GAM2445 PRKWNK2 3' CTGAAGCGGTTCAAGG 92196 ACA C C
CCTTGGACC GC TTC AG
||||||| || || ||
GGAACCTGG CG AAG TC
__ _
GAM2445 RALGPS1A 3' TCTGGAAGGCCTGCTTCCAGG 28338 CCA _
CTTGGA CAG CCTTCCAGA
||||| || |||||
GGACCT GTC GGAAGGTCT
TC_ C
GAM2445 RES4-25 3' GCTTGAGCTGAGTCCAAGG 65268 CA CT C A
CCTTGGAC CAGC TC AG C
||||||| || || ||
GGAACCTG GTCG AG TC G
A_ __ T _
GAM2445 RISC 3' CTGGGGCTGTGATCAAG 41556 AC TT
CTTGG CACAGCC CCAG
||||| ||||| |||||
GAACT GTGTCGG GGTC
A_ __
GAM2445 SLC26A10 5' TGTCCGAGCCTGTGGTCAAGG 56850 G C CCA
CCTTG ACCACAG CTT GACA
||||| ||||| || |||||
GGAAC TGGTGTG CAG CTGT
_ C C__
GAM2445 UST 3' TGTTAAGAAGGCTGCAGCCAC 20356 _ ACCA CA
AGG CCT TGG CAGCCTTC GACA
||| ||| ||||| |||||

	GGA ACC GTCGGAAG TTGT C CGAC AA	
GAM2445 LOC143153 3'	CTGACAGGCTCTGGTCCAAG 76978 CTTGGACCA AGCCT CAG GAACCTGGT TCGGA GTC C CA	C TC
GAM2445 LOC143154 3'	CTGACAGGCTCTGGTCCAAG 76988 CTTGGACCA AGCCT CAG GAACCTGGT TCGGA GTC C CA	C TC
GAM2445 LOC146050 3'	GTCTGTCTCTTGTGGTCCAG 78122 TTGGACCACAG CAGAC GACCTGGTGTT GTCTG CTCT_	CCTTC
GAM2445 LOC151568 5'	TGCCTAGGGGTGCCAAGTCCAA 57497 GG CCTTGAC GC CTTC AG CA GGAACCTG CG GGGG TC GT AAC_ T A C	CACA _ C A
GAM2445 LOC151571 5'	TCTGGAAGGCCTTCGCCAGG 86627 CTTGG GCCTTCCAGA GGACC CGGAAGGTCT GCTTC_	ACCACA
GAM2445 LOC219294 3'	CTGACAGGCTCTGGTCCAAG 94593 CTTGGACCA AGCCT CAG GAACCTGGT TCGGA GTC C CA	C TC
GAM2445 LOC219295 3'	CTGACAGGCTCTGGTCCAAG 94585 CTTGGACCA AGCCT CAG GAACCTGGT TCGGA GTC C CA	C TC
GAM2445 LOC90499 5'	TGTCTGGAAGGTGAAAACCAAG 63745 G CCTTG GCCTTCCAGACA GGAACC TGAAGGTCTGT AAAAG_	ACCACA
GAM2445 LOC90750 3'	TCTGGAAATAGCACCCAGGG 64633 CCTTG GC TTCCAGA GGGACC CG AAGGTCT CA___ ATA	ACCACA C__
GAM2446 BSN 3'	GTTCATATAACAGTGGC 14389 GCCACTGTTT ATGGGC 	CC

		CGGTGACAAA TACTTG		
		TA		
GAM2446 NPR2L	3'	CCCAGGCTGGAATACAGTGGC 22594	—	—
		GCCACTGT TTCCA TGGG		
		CGGTGACA AAGGT ACCC		
		T CGG		
GAM2446 TESK1	5'	ACCCGGGCCCCAGCCAGCCGGC 21884	A_	TTTCCA A
		GCC CTG TGGGCCCG GT		
		CGG GAC ACCCGGGC CA		
		CC CG_ C		
GAM2446 ABCC13	3'	CTCAGGAAAGACAGTGGC 57810	—	A
		GCCACTGTT TCC TGGG		
		CGGTGACAG AGG ACTC		
		AA _		
GAM2446 FLJ20573	3'	ACTCACATTGAATAGAAATAGT 64623	C	GGGCCC_
	G	CACTGTTTC AT GAGT		
		GTGATAAAG TA CTCA		
		A AGTTACA		
GAM2446 KCNJ9	3'	ACTCAACCATCAATGGAAACAG 18363	A	— GCCC
	GGC	GCC CTGTTTCCA TGG GAGT		
		CGG GACAAAGGT ACC CTCA		
		_ AACT AA_		
GAM2446 KIAA0478	3'	CCCAGACTGGAACACAGTGGC 30175	—	—
		GCCACTGT TTCCA TGGG		
		CGGTGACA AAGGT ACCC		
		C CAG		
GAM2446 KIAA1303	3'	ACCCGGGCCCACCAGGCCACGG 66598	ACT	CCA A
	C	GCC GTTT TGGGCCCG GT		
		CGG CGGA ACCCGGGC CA		
		CAC CC_ C		
GAM2446 OS4	3'	ACTCACCTCTGGTAACAGTGGC 20378	T T	CCC
		GCCACTGTT CCA GGG GAGT		
		CGGTGACAA GGT TCC CTCA		
		T C A_		
GAM2446 LOC132671	3'	GTGCGTGGAACAGCTGC 59841	CA	G
		GC CTGTTTCCATG GC		
		CG GACAAAGGTGC TG		
		TC G		
GAM2446 LOC150005	3'	CTTCCTCCCACAGAAACAGTGG 85962	CA	CCC
	T	GCCACTGTTTC TGGG GAG		

TGGTGACAAAG ACCC TTC
 AC TCC
 GAM2446 LOC254454 3' CCCAGTGGAACAAAGGC 98144 AC _
 GCC TGTTTCCA TGGG
 ||| ||||| |||
 CGG ACAAAGGT ACCC
 AA G
 GAM2446 LOC256789 5' CTCGGGAAGAAGCAGTGGC 99307 CATGGG
 GCCACTGTTTC CCGAG
 ||||| |||||
 CGGTGACGAAG GGGCTC
 AA____
 GAM2447 CDH12 3' CTTATCATTTAAAGTGGTGTA 15777 CCCAA GA
 TACACCACT GAA ATAAG
 ||||| ||| |||||
 ATGTGGTGA TTT TATTC
 AA____ AC
 GAM2447 GOCAP1 3' ATTGTTCTTGGGAGCAGTGTA 43007 CA G
 TACAC CTCCCAAGAA AAT
 |||| ||||| |||
 ATGTG GAGGGTTCTT TTA
 AC G
 GAM2447 DKFZp434N2435 5' CTTATTACTGTGGGGTGGT 98090 T AGAAG
 ACCAC CCCA AATAAG
 |||| ||| |||||
 TGGTG GGGT TTATTC
 _ GTCA_
 GAM2447 DKFZP564I122 3' CTTATTCTTCTCCCTCATGTGT 63877 CACTCCCA
 A TACAC AGAAGAATAAG
 |||| |||||
 ATGTG TCTTCTTATTC
 TACTCCC_
 GAM2447 FLJ21791 3' CTTATTTGCAGAAAGTGGTGTA 62126 CCCAAGAA
 TACACCACT GAATAAG
 ||||| |||||
 ATGTGGTGA TTTATTC
 AGACG____
 GAM2447 HMP19 3' CTTATTCTTTGTTAGGAAAATG 88860 CCAC CAA_
 TA TACA TCC GAAGAATAAG
 ||| ||| |||||
 ATGT AGG TTTCTTATTC
 AAA_ ATTG
 GAM2447 KIAA1719 3' TCTGTCTTGGGAGTGGTGTA 68742 _
 TACACCACTCCCAAGA AGA
 ||||| |||||
 ATGTGGTGAGGGTTCT TCT
 G
 GAM2447 KIAA1853 3' TTTTCTTGGAAGCAGTG 69929 CA C
 CAC CT CCAAGAAGAA
 ||| || |||||

	GTG GA GGTTCTTTTT	
	AC A	
GAM2447 KIAA1877	3' CTTATTCTTCTGCCATGAGT 66748	CCA__
	ACTC AGAAGAATAAG	
	TGAG TCTTCTTATTC	
	TACCG	
GAM2447 KIAA1906	3' CTTATTCTTCTTGACTTTTGG 73571	CTCC_
	CCA CAAGAAGAATAAG	
	GGT GTTCTTCTTATTC	
	TTTCA	
GAM2447 OSBPL11	3' CTTAATTTCCCAAGAGTGGTG 43206	CCAA AA
	CACCACTC GAAG TAAG	
	GTGGTGAG CTTT ATTC	
	AACC A_	
GAM2447 YME1L1	3' TCATTCTTGATGTGGTGTA 58438	TCC _
	TACACCAC CAAGAA GA	
	ATGTGGTG GTTCTT CT	
	TA_ A	
GAM2447 ZNF262	3' CTTATTTTGTGGGAGT 18723	A
	ACTCCCAAG AGAATAAG	
	TGAGGGTTT TTTTATTC	
	G	
GAM2447 LOC91960	3' TGTGGCTTGGAACGTGGTGTA 68294	TC_ AAGA
	TACACCAC CCAAG ATA	
	ATGTGGTG GGTC TGT	
	CAA GG_	
GAM2448 GNA11	3' CGTCGTGGCCTGGATCCTCTG 76588	A T T
	TAGAGGATCCA GCT ACG ACG	
	GTCTCCTAGGT CGG TGC TGC	
	C _ _	
GAM2448 KIAA0150	3' GCGCACAGGCCGGCTGGATCCT 71882	A TAC__ A
	AGGATCCA GCT GT CGC	
	TCCTAGGT CGG CA GCG	
	_ CCGGA C	
GAM2448 KIAA1695	3' ACGCATTGACTTGGATCT 47830	C ____
	GGATCCAAG TTA CGT	
	TCTAGGTTC AGT GCA	
	_ TAC	
GAM2448 LOC152274	3' CGAAGCCTGGTCCTCTA 81339	T A A
	TAGAGGA CCA GCTT CG	

		ATCTCCT GGT CGAA GC	
		— C —	
GAM2448	LOC93626	3' CGTCGTGGCCTGGATCCTCTG 73129	A T T
		TAGAGGATCCA GCT ACG ACG	
		GTCTCCTAGGT CGG TGC TGC	
		C — —	
GAM2449	BBS4	3' ATTTGCCCAAAGGGAATCCAGA 53447	G_ G_ A
	ACA	TGTTCTGGA CT TTGG CAAAT	
		ACAAGACCT GG AACC GTTTA	
		AA GA C	
GAM2449	CENTD2	3' CCAACAAACTCCAGAACA 31539	C_
		TGTTCTGGAG TGTTGG	
		ACAAGACCTC ACAACC	
		AA	
GAM2449	HAMP	3' TCCTGCTGCCCCAGAACA 41289	A T T
		TGTTCTGG GC GT GGA	
		ACAAGACC CG CG CCT	
		C T T	
GAM2449	ITGA11	3' TCTGCCGGCCCCCAGGACA 25213	A_ TT
		TGTTCTGG GCTG GGA	
		ACAGGACC CGGC TCT	
		CC CG	
GAM2449	KITLG	3' ATTTGCATGGCTCCAGAA 8023	TGGA
		TTCTGGAGCTGT CAAAT	
		AAGACCTCGGTA GTTTA	
		C_	
GAM2449	MAPK4	5' CCTGGGCGAGCTCCAGATCA 12300	T _
		TG TCTGGAGCTGTT GG	
		AC AGACCTCGACGG CC	
		T GT	
GAM2449	MGAT2	3' ATTTGTCCAAACAGGACA 11557	GAGCTG
		TGTTCTG TTGGACAAAT	
		ACAGGAC AACCTGTTTA	
		A_	
GAM2449	PSPHL	5' TTGTCATACAGCTCCAAACA 94499	C TG
		TGTT TGGAGCTGT GACAA	
		ACAA ACCTCGACA CTGTT	
		— TA	
GAM2449	TTC3	3' TATTTGTCCAACAACCTGTCAGA 13885	_ C
	ATA	TGTTCTGG AG TGTTGGACAAATA	

		ATAAGACT TC ACAACCTGTTTAT	
		G A	
GAM2449	FLJ14213	3' TGATAACAGCTCCAGAA 46218	GA
		TTCTGGAGCTGTTG CA	
		AAGACCTCGACAAT GT	
		A_	
GAM2449	H2BFQ	3' TTTAAGAGAACTCCAGGACA 60079	_ G
		TGTTCTGGAG CT TTGGA	
		ACAGGACCTC GA AATTT	
		AA G	
GAM2449	LRG	3' TCCATCCATGCTTCCTAGAACA 54825	_ _ _ T_
		TGTTCT GGA GC TG TGGA	
		ACAAGA CCT CG AC ACCT	
		T T T CT	
GAM2449	NMT2	3' ATTTGTCCATGTAACAGAACA 17852	GA TGT
		TGTTCTG GC TGGACAAAT	
		ACAAGAC TG ACCTGTTTA	
		AA T_	
GAM2449	NYD-SP21	3' TATTTGTCCAATCTAGATTCAG 51863	G _
	AACA	TGTTCTGGA CT GTTGGACAAATA	
		ACAAGACTT GA TAACCTGTTTAT	
		A TC	
GAM2449	PSPH	3' TTGTCGTACAGCTCCAAACA 17143	C TG
		TGTT TGGAGCTGT GACAA	
		ACAA ACCTCGACA CTGTT	
		_ TG	
GAM2449	LOC122258	3' CCACCAGCCTCCGGAACA 59820	_ T
		TGTTCTGGAG CTG TGG	
		ACAAGGCCTC GAC ACC	
		C C	
GAM2449	LOC151826	3' ATTTGTCCAACCTAGCACA 81176	T AGCT
		TGT CTGG GTTGGACAAAT	
		ACA GATC CAACCTGTTTA	
		C _	
GAM2449	LOC169611	3' TCCAGTGGCAGCTCCAGAA 83663	_
		TTCTGGAGCTGT TGGA	
		AAGACCTCGACG ACCT	
		GTG	
GAM2449	LOC196746	3' TCAGAGCAGCTCCAAGACA 88903	TC G_
		TGT TGGAGCTGTT GA	

		ACA ACCTCGACGA CT	
		GA GA	
GAM2449	LOC204119 5'	TGCCACAACCTCAGAACAA 92343	G C T A
		TGTTCTG AG TGT GG CA	
		ACAAGAC TC ACA CC GT	
		_ A _ _	
GAM2449	LOC253142 5'	TTGCTAGGATGCCCCAGAATA 99230	A TG_ A
		TGTTCTGG GC TTGG CAA	
		ATAAGACC CG GATC GTT	
		C TAG _	
GAM2450	ABCD2 5'	ATGAGGGGCCTGGGAGGGA 18965	A_ G
		TCCCTCCCA CCCT GT	
		AGGGAGGGT GGGA TA	
		CCG G	
GAM2450	ADSS 3'	TTTGGTGGGGCTGGGAGGGG 72235	A G
		TCCCTCCCA CCCTG TGAG	
		GGGGAGGGT GGGG GTTT	
		C G	
GAM2450	AES 3'	CAGGGAGGTTGGGAGGGG 8522	___
		TCCCTCCCAA CCCTG	
		GGGGAGGGT GGGAC	
		GGA	
GAM2450	ALDOB 3'	CAGTGGTAGGTTGGGAAGGA 68650	C _ G
		TCC TCCCAACC CTG TG	
		AGG AGGGTTGG GGT AC	
		A AT G	
GAM2450	AMH 5'	CTCTATCACTGGGGAGGGA 6652	AACCC _
		TCCCTCCC TGGT GAG	
		AGGGAGGG ACTA CTC	
		GTC_ T	
GAM2450	ANKRD3 3'	CTCACCAGTCTTGAGGGA 40562	CC CC
		TCCCTC AA CTGGTGAG	
		AGGGAG TT GACCACTC	
		_ CT	
GAM2450	ARHGAP6 3'	CCATGGGAGTGGGAGGGA 8611	A_ _
		TCCCTCCCA CCC TGG	
		AGGGAGGGT GGG ACC	
		GA T	
GAM2450	AVPR1A 5'	CAATAGGGCGGGAGGGA 7374	AA G
		TCCCTCCC CCCTG TG	

			AGGGAGGG GGGAT AC			
			C_ A			
GAM2450	B3GNT3	3'	CTCAGAAGGTTGGGGGGA 27303	T	C	GG
			TCCC CCAACC T TGAG			
			AGGG GGGTTGG A ACTC			
			_ _ AG			
GAM2450	BASP1	3'	CAATGGGAGTTGGGAGTGA 76493	C	_	GG
			TC CTCCCAAC CCT TG			
			AG GAGGGTTG GGG AC			
			T A TA			
GAM2450	BAZ2A	5'	CTCACAGTTTGGGAGG 26508	CC	G	
			CCTCCCAA CTG TGAG			
			GGAGGGTT GAC ACTC			
			T_ _			
GAM2450	BCL11B	3'	CTCATTAGGTTGGAAGG 43484	C	C	
			CCT CCAACC TGGTGAG			
			GGA GGTTGG ATTACTC			
			A _			
GAM2450	CACNG6	3'	CCGGGTGCGGTTGGGGGAGA 49946	C	_____	
			TC CTCCCAACC CTGG			
			AG GGGGGTTGG GGCC			
			A CGTG			
GAM2450	CNTN2	3'	CTCACTCCTGCCTGGGAGGGG 18660	ACCCT_		
			TCCCTCCCA GGTGAG			
			GGGGAGGGT TCACTC			
			CCGTCC			
GAM2450	COL9A1	5'	CTCACCGGGGGCAGGAGGGA 10252	CAA		
			TCCCTCC CCCTGGTGAG			
			AGGGAGG GGGGCCACTC			
			ACG			
GAM2450	DHCR24	3'	TTCATTAGTTGAAAGGGA 29305	CC	CC	
			TCCCT CAAC TGGTGAG			
			AGGGA GTTG ATTACTT			
			AA _			
GAM2450	EPB49	3'	CGGCGGGTTGGGAGGGG 10527	T	G	
			TCCCTCCAACCC G TG			
			GGGGAGGGTTGGG C GC			
			_ G			
GAM2450	FCMD	3'	CTCACAGTAGGTTGAAAGAG 23035	C_	_	
			CTC CAACCCTG GTGAG			

			GAG GTTGGGAT CACTC		
			AAA GA		
GAM2450	FLRT2	3'	CTCATCAGGGTAAGAGG 25996	CCA	
			CCTC ACCCTGGTGAG		
			GGAG TGGGACTACTC		
			AA_		
GAM2450	GGT1	3'	CTCACCAGGACCAGGAAGGG 26420	_ CAAC	
			CCCT CC CCTGGTGAG		
			GGGA GG GGACCACTC		
			A ACCA		
GAM2450	GGT1	3'	CTCACCAGGACCAGGAAGGG 26436	_ CAAC	
			CCCT CC CCTGGTGAG		
			GGGA GG GGACCACTC		
			A ACCA		
GAM2450	GGT1	3'	CTCACCAGGACCAGGAAGGG 19158	_ CAAC	
			CCCT CC CCTGGTGAG		
			GGGA GG GGACCACTC		
			A ACCA		
GAM2450	GPR17	3'	TGGTGGGGACGGGGAGGGA 19182	AA_ G	
			TCCCTCCC CCCTG TG		
			AGGGAGGG GGGGT GT		
			GCA G		
GAM2450	GRIN2D	3'	CGCGTGGGTTGGGAAGGA 7735	C TG	
			TCC TCCCAACCC GTG		
			AGG AGGGTTGGG CGC		
			A TG		
GAM2450	KIAA0442	3'	CTCACACAGACTGGGGGGGA 32094	ACC _	
			TCCCTCCCA CTG GTGAG		
			AGGGGGGGT GAC CACTC		
			CA_ A		
GAM2450	LAD1	5'	CACCTGGGCTGGAAGGGG 19900	C A T	
			TCCCT CCA CCC GGTG		
			GGGA GGT GGG CCAC		
			A C T		
GAM2450	LTF	5'	CGCGGGGAGTGGGGAGGGA 11374	A _ G	
			TCCCTCCC AC CCT GTG		
			AGGGAGGG TG GGG CGC		
			G A G		
GAM2450	LYL1	5'	CTCACTTTCCCTGGGGGGGA 19950	ACCCT	
			TCCCTCCCA GGTGAG		

			AGGGGGGGT	TCACTC		
			CCCTT			
GAM2450	NDN	3'	CTCACCAGGGCTGTGGAAGG	11758	C _ A	
			CC TCC CA CCCTGGTGAG			
			GG AGG GT GGGACCACTC			
			A T C			
GAM2450	NEDD4L	3'	TTTATTAGAATTGGAAGG	31609	C CC	
			CCT CCAA CTGGTGAG			
			GGA GGTT GATTATTT			
			A AA			
GAM2450	OSCAR	5'	CTCATTTCTGGGAGGGG	56249	ACCCT	
			TCCCTCCCA GGTGAG			
			GGGGAGGGT TTA			
			CTCCT__			
GAM2450	OSCAR	5'	CTCATTTCTGGGAGGGG	56477	ACCCT	
			TCCCTCCCA GGTGAG			
			GGGGAGGGT TTA			
			CTCCT__			
GAM2450	OSCAR	5'	CTCATTTCTGGGAGGGG	56480	ACCCT	
			TCCCTCCCA GGTGAG			
			GGGGAGGGT TTA			
			CTCCT__			
GAM2450	P53AIP1	3'	CTGTGGTGATGGGAGGGA	42336	__ C	
			TCCCTCCCA ACC TGG			
			AGGGAGGGT TGG GTC			
			AG T			
GAM2450	PIP5K1A	3'	TGTTAGGGGTGGGAGGGA	14523	A GT	
			TCCCTCCCA CCCTG G			
			AGGGAGGGT GGGAT T			
			G TG			
GAM2450	POV1	3'	CTCCTTGGGTTGGAGGAGA	14636	_ C T T	
			TC CCTCC AACCC GG GAG			
			AG GGAGG TTGGG TC CTC			
			A _ T _			
GAM2450	PPP2R5D	3'	CAAGTGGGGCCGGGGAGGGA	21803	AA_ G_	
			TCCCTCCC CCCTG TG			
			AGGGAGGG GGGGT AC			
			GCC GA			
GAM2450	SERPINH2	3'	TATTGGGGTTGGGGGGGA	8787	TG	
			TCCCTCCCAACCC GTG			

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AGGGGGGGTTGGG TAT
GT
GAM2450 SLC21A2 3' CTCACCAGCCCTGGGGGGA 20083 T ACC
TCCC CCCA CTGGTGAG
||||| |||||
AGGG GGGT GACCACTC
_ CCC
GAM2450 STK19 3' CTCAGAGTGGGCCGGGAGGGG 16097 AA TGG_
TCCCTCCC CCC TGAG
||||| ||| |||
GGGGAGGG GGG ACTC
CC TGAG
GAM2450 STK19 3' CTCAGAGTGGGCCGGGAGGGG 51613 AA TGG_
TCCCTCCC CCC TGAG
||||| ||| |||
GGGGAGGG GGG ACTC
CC TGAG
GAM2450 TSN 3' TCAGCGGTTGCCAGGAAGGG 17305 _ _ _
CCCT CC CAACC CTGG
||||| ||||| |||
GGGA GG GTTGG GACT
A ACC C
GAM2450 TUFT1 3' TTCATCAGATTGGGAGAGG 39681 _ CC
CC CTCCCA CTGGTGAG
|| ||||| |||||
GG GAGGGTT GACTACTT
A A_
GAM2450 BHLHB2 3' CTCACCAGACGTCGGGGAGAGA 14764 C A_ C_
TC CTCCC AC CTGGTGAG
|| |||| || |||||
AG GAGGG TG GACCACTC
A GC CA
GAM2450 BPESC1 3' CGATGGGGTTGAGAGGGG 41771 C GG
TCCCTC CAACCCT TG
||||| ||||| ||
GGGGAG GTTGGGG GC
A TA
GAM2450 BRPF3 5' CAGCGCGGGCCGGGAGGGG 93927 AA _ G
TCCCTCCC CCC TG TG
||||| ||| |||
GGGGAGGG GGG GC AC
CC C G
GAM2450 C20orf151 3' CACCAGGGCCTGGAGAGG 90091 _ A_
CCTC CCA CCCTGGTG
||||| ||| |||||
GGAG GGT GGGACCAC
A CC
GAM2450 C20orf180 5' TGTCAGGGTTGGGGGGA 37974 T GT
TCCC CCCAACCCTG G
||||| ||||| |||

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AGGG GGGTTGGGAC T
 — TG
 GAM2450 CCT5 5' CGCCGGTTGGGGGGA 73033 T CT
 TCCC CCAACC GGTG
 ||| ||||| |||
 AGGG GGGTTGG CCGC

— —
 GAM2450 CECR6 5' CCGGGGTTGGCGGGGAGGGA 49931 —
 TCCCTCCC AACCTGG
 ||||| |||||
 AGGGAGGG TTGGGGCC
 GCGG

GAM2450 DGS-A 3' CCAGGGCAGGCTGGGAGGGA 86051 A—
 TCCCTCCCA CCCTGG
 ||||| |||||
 AGGGAGGGT GGGACC
 CGGAC

GAM2450 DKFZp761P1010 3' CATGTGGGGTTGGAGGAGA 37942 _ C _
 TC CCTCC AACCTG GTG
 || |||| ||||| |||
 AG GGAGG TTGGGGT TAC
 A _ G

GAM2450 ET(B)R-LP-2 3' CAGTAGGGGTGGGGAGGGA 17672 AA_ G
 TCCCTCCC CCCTG TG
 ||||| ||||| ||
 AGGGAGGG GGGAT AC
 GTG G

GAM2450 FLJ10057 3' CTCATGGAAGATGTTGGGAGAG 36251 C _ TG
 A TC CTCCAAC CC GTGAG
 || ||||| || |||||
 AG GAGGGTTG GG TACTC
 A TAGAA _

GAM2450 FLJ10853 3' CTCACTGGGTCAAAGGGA 37315 CCCA T
 TCCCT ACCC GGTGAG
 ||||| ||||| |||||
 AGGGA TGGG TCACTC
 AAC_ _

GAM2450 FLJ11000 3' CAGGAGGGTGGGGAGGGA 37525 A GG
 TCCCTCCC ACCCT TG
 ||||| ||||| ||
 AGGGAGGG TGGGA AC
 G GG

GAM2450 FLJ12650 3' CTCACCAGTTGGAAGG 44820 C CC
 CCT CCAAC TGGTGAG
 || |||| |||||
 GGA GGTG ACCACTC
 A _

GAM2450 FLJ20489 3' CTCACCTAACTGGGAGGGA 35711 CCCT
 TCCCTCCCAA GGTGAG
 ||||| |||||

			AGGGAGGGTT CCACTC		
			CAAT		
GAM2450	FLJ20793	3'	CATTGTAGGTTGGGAAGGG 93448	_	CT_
			CCCT CCCAACC GGTG		
			GGGA GGGTTGG TTAC		
			A ATG		
GAM2450	FLJ21313	3'	TCAGGAAAGTGGGGAGGGA 43934	A	___
			TCCCTCCC AC CCTGG		
			AGGGAGGG TG GGA CT		
			G AAA		
GAM2450	FLJ23231	3'	CTCAGAGGGTGGGGAGGGA 47605	A	GG
			TCCCTCCC ACCCT TGAG		
			AGGGAGGG TGGGA ACTC		
			G G_		
GAM2450	FLJ32915	5'	CTCACATTTTGGGAGGGA 59432	CCCTG	
			TCCCTCCCAA GTGAG		
			AGGGAGGGTT CACTC		
			TTA__		
GAM2450	FREQ	3'	CTCAAAGGCTGGGAGGGA 27370	AC	GG
			TCCCTCCCA CCT TGAG		
			AGGGAGGGT GGA ACTC		
			C_ A_		
GAM2450	GGTL4	3'	CTCACCAGGACCAGGAAGGG 55944	_	CAAC
			CCCT CC CCTGGTGAG		
			GGGA GG GGACCACTC		
			A ACCA		
GAM2450	GMPPB	3'	CCAAGGGGGTGGGAGGGA 97439	A_	_
			TCCCTCCCA CCCT GG		
			AGGGAGGGT GGGGA CC		
			GG A		
GAM2450	GTPBP1	3'	CTTCCAGGGTTAGGACAGA 16266	CC C	T
			TC TCC AACCTGG GAG		
			AG AGG TTGGGACC TTC		
			AC A _		
GAM2450	HGC6.1.1	3'	CAGTGGGAGCTGGGAGGGA 27609	AC_	G
			TCCCTCCCA CCTG TG		
			AGGGAGGGT GGGT AC		
			CGA G		
GAM2450	HOOK2	3'	CCAGATTGGTGGGGAGGGA 26158	A	___
			TCCCTCCC ACC CTGG		

	AGGGAGGG TGG GACC	
	G TTA	
GAM2450 KIAA0140 3'	CTCAGTCCTCTGGGAGGGA 28512	ACCCT _
	TCCCTCCCA GG TGAG	
	AGGGAGGGT CC ACTC	
	CT__ TG	
GAM2450 KIAA0182 3'	TACGCAGGTGGGAGGGA 72502	AC _
	TCCCTCCCA CCTG GTG	
	AGGGAGGGT GGAC CAT	
	_ G	
GAM2450 KIAA0252 3'	TGGCAGGTGTGGGAGGGA 63461	AC G
	TCCCTCCCA CCTG TG	
	AGGGAGGGT GGAC GT	
	GT G	
GAM2450 KIAA0285 3'	CTCAGAAGAACTGGGAGGGG 29683	ACC_ GG
	TCCCTCCCA CT TGAG	
	GGGGAGGGT GA ACTC	
	CAAA AG	
GAM2450 KIAA0677 3'	CACTGTAGGTGGGAGGGA 28529	A CT_
	TCCCTCCCA CC GGTG	
	AGGGAGGGT GG TCAC	
	_ ATG	
GAM2450 KIAA0789 5'	CTCACCTTCAGTTTGGGAGGG 64429	CCCT__
	CCCTCCCA GGTGAG	
	GGGAGGGTT CCACTC	
	TGACTT	
GAM2450 KIAA0843 3'	CTTTGTAGATTGGGGGGA 30802	T CC GT
	TCCC CCAA CTG GAG	
	AGGG GGGTT GAT TTC	
	_ A_ GT	
GAM2450 KIAA0853 3'	TTTATTAATGGGGAGGGA 31217	AACCC
	TCCCTCCC TGGTGAG	
	AGGGAGGG ATTATTT	
	GTA__	
GAM2450 KIAA0864 3'	CAGTGGGGGCTGGGAGGG 63938	A_ G
	CCCTCCCA CCCTG TG	
	GGGAGGGT GGGGT AC	
	CG G	
GAM2450 KIAA1018 3'	TTCATCAGCCAGGAGGGA 31059	CAACC
	TCCCTCC CTGGTGAG	

AGGGAGG GACTACTT
 ACC__
 GAM2450 KIAA1061 3' CACACGGGTTGGGAGAGG 71716 _ TG
 CC CTCCCAACCC GTG
 || ||||| ||
 GG GAGGGTTGGG CAC
 A CA
 GAM2450 KIAA1171 3' GCTCACGGGGAGAGGTATGGGA 89344 _ _ G _
 GGGA TCCCTCCCA ACC CT GTGAG C
 ||||| || || ||| |
 AGGGAGGGT TGG GG CACTC G
 A AGAG G _
 GAM2450 KIAA1190 3' CTCGGGGGATTGGGGGA 71646 T _ GG
 TCCC CCCAA CCCT TGAG
 ||| |||| ||| |||
 AGGG GGGTT GGGG GCTC
 _ A _
 GAM2450 KIAA1649 3' TGCTGGTTGGGAGTGA 67518 C CT
 TC CTCCCAACC GGTG
 || ||||| |||
 AG GAGGGTTGG TCGT
 T _
 GAM2450 KIAA1649 3' TGCTGGTTGGGAGTGA 51256 C CT
 TC CTCCCAACC GGTG
 || ||||| |||
 AG GAGGGTTGG TCGT
 T _
 GAM2450 KIAA1655 5' CTCACCTCCAGTGGGAGGGA 67182 ACCCT
 TCCCTCCCA GGTGAG
 ||||| |||||
 AGGGAGGGT CCACTC
 GACCT
 GAM2450 KIAA1750 3' CTCAGTGATAGAGTATGGGAGG 68809 _ C G_
 GA TCCCTCCCA AC CTG TGAG
 ||||| || ||| |||
 AGGGAGGGT TG GAT ACTC
 A A AGTG
 GAM2450 KIAA1944 5' CACCAGGTAGTCACTGGGCAGA 76077 C _ _ _
 GA TC CT CCA AC CCTGGTG
 || || ||| || |||||
 AG GA GGGT TG GGACCAC
 A C CAC AT
 GAM2450 KIAA1952 5' CTCTGCCGGCTGGGAGGG 73544 ACC _
 CCCTCCCA CTGGT GAG
 ||||| ||||| |||
 GGGAGGGT GGCCG CTC
 C_ T
 GAM2450 LAGY 5' CTCAGTCCAGGGAGGGA 51658 AACCC _
 TCCCTCCC TGG TGAG
 ||||| || ||| |||

AGGGAGGG ACC ACTC
 _____ TG
 GAM2450 MGC10715 3' CTTATCAGGCATGGGAGGGA 44498 AC
 TCCCTCCCA CCTGGTGAG
 ||||| |||||
 AGGGAGGGT GGA CTATTC
 AC
 GAM2450 MGC15429 3' CTCCTGGCTGGGAAGG 52211 C A CT
 CC TCCCA CC GGTGAG
 || |||| || ||||
 GG AGGGT GG TCACTC
 A C _
 GAM2450 MGC4737 5' CTCACCAGCGGAGTGGA 49640 _ CAACC
 TCC CTCC CTGGTGAG
 || ||| |||||
 AGG GAGG GACCACTC
 T C _
 GAM2450 MGC5139 5' CTTGAAAGGGTGGGGAGGGA 74571 A GG
 TCCCTCCC ACCCT TGAG
 ||||| |||| |||
 AGGGAGGG TGGGA GTTC
 G AA
 GAM2450 MLLT10 5' CCGGGTGGAGGTGGGGAGGGA 17351 A _
 TCCCTCCC ACC CTGG
 ||||| || |||
 AGGGAGGG TGG GGCC
 G AGGTG
 GAM2450 MMP24 3' CTCACCAGGGTCTGAGGGG 22918 CCA
 TCCCTC ACCCTGGTGAG
 |||| |||||
 GGGGAG TGGGACCACTC
 TC_
 GAM2450 moblak 3' CTCACCAGAATTGTCAGTGG 56396 _ CC CC
 CC CT CAA CTGGTGAG
 || || || |||||
 GG GA GTT GACCACTC
 T CT AA
 GAM2450 NIP30 3' CTCCTGATATTGGGAGG 46896 CCC
 CCTCCCA TGGTGAG
 ||||| |||||
 GGAGGGTT GTCCTC
 ATA
 GAM2450 PRO0529 3' CTCACCAGGGTGGGCAGAGA 26856 C _ A
 TC CT CCA CCCTGGTGAG
 || || || |||||
 AG GA GGGT GGGACCACTC
 A C _
 GAM2450 PTK6 5' CTCTGAGGGTTGGGAAGG 21076 C GGT
 CC TCCCAACCCT GAG
 || ||||| |||

			GG AGGGTTGGGA	CTC		
			A	GT_		
GAM2450	RAB3IL1	3'	CTCAGCCCTTGGGAGGGG	26365	CCCT	_
			TCCCTCCCAA	GG TGAG		
			GGGGAGGGTT	CC ACTC		
			C__	G		
GAM2450	RIN3	3'	TTCATTAGACGGAAGGGA	46164	C_	AACC
			TCCCT CC	CTGGTGAG		
			AGGGA GG	GATTACTT		
			AA CA__			
GAM2450	RP4-622L5	3'	CTCATTTCTTGGGAGGG	39424	CCCT	
			CCCTCCCAA	GGTGAG		
			GGGAGGGTT	TTACTC		
			CT__			
GAM2450	SCMH1	3'	CTCACCAGGAGTTTAGG	25283	CCC	_
			CCT AAC	CCTGGTGAG		
			GGA TTG	GGACCACTC		
			T__	A		
GAM2450	SERPINH1	3'	TATTGGGGTTGGGGGGGA	16375	TG	
			TCCCTCCCAACCC	GTG		
			AGGGGGGGTTGGG	TAT		
			GT			
GAM2450	SIAT4B	5'	CTCACCAGGGTGGCAGGAGA	23634	_	C A
			TC CCT CCA	CCCTGGTGAG		
			AG GGA GGT	GGGACCACTC		
			A C	_		
GAM2450	SNPH	3'	CTCTGGGGGTTGAGAGGA	28902	C	GGT
			TCCCTCC AACCT	GAG		
			AGGGAGG TTGGGG	CTC		
			_	GT_		
GAM2450	SSH-3	5'	CGCGGGGTTGAGGGA	37417	CC	G
			TCCCTC AACCTG	TG		
			AGGGAG	TTGGGGC GC		
			—	—		
GAM2450	SSH-3	5'	CGCGGGGTTGAGGGA	35790	CC	G
			TCCCTC AACCTG	TG		
			AGGGAG	TTGGGGC GC		
			—	—		
GAM2450	VIAAT	3'	CGAGGGGGTTGGGAAGGGA	55450	_	GG
			TCCCT CCCAACCT	TG		

	AGGGA GGGTTGGGG GC	
	A GA	
GAM2450 LOC114987 3'	CGGGAATGAGTTGGGAGGGG 59795	_____
	TCCCTCCCAAC CCTG	
	GGGGAGGGTTG GGGC	
	AGTAA	
GAM2450 LOC121036 3'	CAGTAGGATGGGAGGGA 74481	AC G
	TCCCTCCCA CCTG TG	
	AGGGAGGGT GGAT AC	
	A_ G	
GAM2450 LOC123346 5'	CTCTGAAAGAGTCGGGGAGGGA 76127	A_ C GGT_
	TCCCTCCC AC CT GAG	
	AGGGAGGG TG GA CTC	
	GC A AAGT	
GAM2450 LOC136306 3'	CAAAGGGGTGTGAGAGGGA 75768	C _ GG
	TCCCTC CA ACCCT TG	
	AGGGAG GT TGGGG AC	
	A G AA	
GAM2450 LOC144596 3'	CTCACCTGGAGGCAAGAGGGA 77427	___ AAC T
	TCCCTC CC CC GGTGAG	
	AGGGAG GG GG CCACTC	
	AAC A__ T	
GAM2450 LOC145497 5'	CCAGGGCTTGCTGGGAGGGA 77731	A_____
	TCCCTCCCA CCCTGG	
	AGGGAGGGT GGGACC	
	CGTTC	
GAM2450 LOC146439 5'	CTCATTCCTGGGAGGGG 78449	ACCCT
	TCCCTCCCA GGTGAG	
	GGGGAGGGT TTA CTC	
	CC_____	
GAM2450 LOC147711 3'	CTCAGCCTTTGGGAGGG 79116	CCCT _
	CCCTCCCAA GG TGAG	
	GGGAGGGTT CC ACTC	
	T__ G	
GAM2450 LOC150150 5'	CCAGTGTGGTGGGAGGGA 86009	A ____
	TCCCTCCCA CC CTGG	
	AGGGAGGGT GG GACC	
	_ TGT	
GAM2450 LOC152667 3'	CTCACTGATATTGGGAGG 81523	CCC
	CCTCCCAA TGGTGAG	

	GGAGGGTT GTCACTC	
	ATA	
GAM2450 LOC157931 3'	CTCACGGCCTGGGAGGG 87940	AC TG
	CCCTCCCA CC GTGAG	
	GGGAGGGT GG CACTC	
	CC _	
GAM2450 LOC158055 3'	CCGGCGGCTGGTGAGGGA 82580	_ A _
	TCCCTC CCA CC CTGG	
	AGGGAG GGT GG GGCC	
	T C C	
GAM2450 LOC199927 3'	CCGGAGTGGCTGGGAGGGG 91479	A _
	TCCCTCCCA CC CTGG	
	GGGGAGGGT GG GGCC	
	C TGA	
GAM2450 LOC201182 5'	CTCACTGGTTGAGATGGA 91336	C C CT
	TCC TC CAACC GGTGAG	
	AGG AG GTTGG TCACTC	
	T A _	
GAM2450 LOC219920 5'	CTCATTAGACTGGGAGG 94947	ACC
	CCTCCCA CTGGTGAG	
	GGAGGGT GATTACTC	
	CA_	
GAM2450 LOC220739 3'	TCAGGGCTTAGGGAGGGA 94529	_ _
	TCCCTCCC AA CCCTGG	
	AGGGAGGG TT GGGACT	
	A C	
GAM2450 LOC221424 3'	CCTGGGACTTGGGAGGGA 95271	_ T
	TCCCTCCCAA CCC GG	
	AGGGAGGGTT GGG CC	
	CA T	
GAM2450 LOC221718 5'	CTCACCAGCCTGAGGTAGGA 95280	CT _ ACC
	TCC CC CA CTGGTGAG	
	AGG GG GT GACCACTC	
	AT A CC_	
GAM2450 LOC253955 5'	CTCACCAGGTGCAGAGGGG 96072	CCAAC
	TCCCTC CCTGGTGAG	
	GGGGAG GGACCACTC	
	ACGT_	
GAM2450 LOC255328 3'	CTCACCAGGTGAGGAGTGA 98338	C _ AC
	TC CTCC CA CCTGGTGAG	

AG GAGG GT GGACCACTC
 T A ____
 GAM2450 LOC256973 3' CTCACGGCCTCCGGGAGGGG 98198 AAC__ TG
 TCCCTCCC CC GTGAG
 ||||| || ||||
 GGGGAGGG GG CACTC
 CCTCC ____
 GAM2450 LOC257456 3' CTCACTAGGACCAGGAAGGG 80594 _ CAAC
 CCCT CC CCTGGTGAG
 ||| || |||||
 GGGA GG GGATCACTC
 A ACCA
 GAM2450 LOC51696 3' CATTGGAGGTTGGGAAGGA 33079 C _TG
 TCC TCCCAACC C GTG
 || ||||| | |||
 AGG AGGGTTGG G TAC
 A A GT
 GAM2450 LOC91496 5' CATTAGAGGTGGAAGGGA 66808 C A _
 TCCCT CCA CC CTGGTG
 |||| ||| || |||||
 AGGGA GGT GG GATTAC
 A _ A
 GAM2450 LOC92228 5' CTCACCAGGGTGAGGG 69075 CCA
 CCCTC ACCCTGGTGAG
 |||| |||||
 GGGAG TGGGACCACTC

 GAM2450 LOC92293 3' CACACAGCTGGGGGGGA 69318 ACC _
 TCCCTCCCA CTG GTG
 ||||| ||| |||
 AGGGGGGGT GAC CAC
 C__ A
 GAM2451 HNRPA2B1 3' GGTTATCGAAATAACAATG 49188 GTA C
 CAT TTA TTCGATAACC
 || ||| |||||
 GTA AAT AAGCTATTGG
 AC_ A
 GAM2451 SEMA3E 3' TTATCAGTAGGTACATGGA 25815 _ TC
 TTCATGTAT TACT GATAA
 ||||| ||| |||||
 AGGTACATG ATGA CTATT
 G ____
 GAM2452 LDLR 3' GGGATTGGCAATTGTCCCCA 6741 A C GT
 TGGG AC ATTGCCAA CT
 ||| || ||||| ||
 ACCC TG TAACGGTT GG
 C T AG
 GAM2452 NRIP1 3' TACCAAACCTCAGGTGATTCC 60624 ACC TG A_ C
 GGA AT CC AGT TGGTA
 || || || |||||

CCT TA GG TCA ACCAT
 ____ GT AC A
 GAM2452 PSEN2 3' ACCAGACTTTGGCTCCC 25950 ACCATT _
 GGA GCAA GTCTGGT
 ||| ||| |||||
 CCCT CGGTT CAGACCA
 _____ T
 GAM2452 PSEN2 3' ACCAGACTTTGGCTCCC 6542 ACCATT _
 GGA GCAA GTCTGGT
 ||| ||| |||||
 CCCT CGGTT CAGACCA
 _____ T
 GAM2452 FLJ12604 3' ACATGGTAAATGGTTCCCA 65059 ____ A
 TGGGAACCAT TGCCA GT
 ||||| ||| ||
 ACCCTTGGTA ATGGT CA
 AA A
 GAM2452 FLJ13081 3' ACATGGCAGTGGTTCCCA 46169 A
 TGGGAACCATTGCCA GT
 ||||| ||| ||
 ACCCTTGGTGACGGT CA
 A
 GAM2452 FLJ23093 3' ACCAGACTCCTCAGGTTCC 45321 AT CCA
 GGAACC TG AGTCTGGT
 |||| || |||||
 CCTTGG AC TCAGACCA
 ____ TCC
 GAM2452 GP5 3' ACCAGACTCACGGTCTCCA 16857 GA AT CCA
 TGG ACC TG AGTCTGGT
 || || || |||||
 ACC TGG AC TCAGACCA
 TC C_ ____
 GAM2452 KIAA0286 3' ACCAGACTTACTGGCTCACCA 68855 _ A TTGCC
 TGG GA CCA AAGTCTGGT
 || || || |||||
 ACC CT GGT TTCAGACCA
 A C CA____
 GAM2452 MGC10540 3' ACCAGACTCAAAAGGACTCCA 51356 AA A GCCA
 TGGG CC TT AGTCTGGT
 ||| || || |||||
 ACCT GG AA TCAGACCA
 CA A AC____
 GAM2452 LOC157226 5' TACCGCAGGCAAAGGTTCCCA 64640 A AAGTC
 TGGGAACC TTGCC TGGTA
 ||||| ||| |||
 ACCCTTGG AACGG GCCAT
 A AC____
 GAM2453 ANGPT4 3' GTACCTTGAATGGGCT 32572 GGCA
 AGCCCAT GGGGTAC
 ||||| |||||

		TCGGGTAA TTCCATG		
		G__		
GAM2453 ASS	5'	GGCACCCCTGCCAGTCCTGCTC 55026	CC_	A
		GAGC ATTGGCAGGGGT CC		
		CTCG TGACCGTCCCCA GG		
		TCC C		
GAM2453 BAK1	3'	TACCCTTGTGAGAGCCCA 93634	A CCA	G
		TG GC TT GCAGGGGT A		
		AC CG GA TGTTCCT		
		C A_ G		
GAM2453 DNASE1L1	3'	GGTACCGATATGCCAATGGGCC 23018	A	A_____ GGTA
A		TG GCCCATTGGC GG C		
		AC CGGGTAACCG CC G		
		_ TATAG_ ATGG		
GAM2453 DUSP6	3'	ACACCAAATCATGGGCTCA 66576	T CAG	_
		TGAGCCCAT GG GG GT		
		ACTCGGGTA CT CC CA		
		_ AAA A		
GAM2453 MN1	3'	ACACTTTGCCAATTAGCTCA 11647	CC	_
		TGAGC ATTGGCAGGG GT		
		ACTCG TAACCGTTTC CA		
		AT A		
GAM2453 MPP2	3'	GCAGGGGCCAGTGGGCTCA 60520	AGGG	
		TGAGCCCATTTGGC GT		
		ACTCGGGTGACCG CG		
		GGGA		
GAM2453 SULT1A2	3'	CCCTGACCAATGGGCTCA 72672	_	
		TGAGCCCATTTGG CAGGG		
		ACTCGGGTAACC GTCCC		
		A		
GAM2453 SULT1A3	3'	CCCTGACCAATGGGCTCA 13483	_	
		TGAGCCCATTTGG CAGGG		
		ACTCGGGTAACC GTCCC		
		A		
GAM2453 TRPM2	3'	GGCACCCCTGCAGAGGCTC 13868	CATTG	A
		GAGCC GCAGGGGT CC		
		CTCGG CGTCCCCA GG		
		AGA_ C		
GAM2453 XBP1	3'	ACTTTTGCCAATGAACTC 18674	CC	
		GAG CATTGGCAGGGGT		

CTC GTAACCGTTTTCA
AA
GAM2453 BMF 3' GGTACCGGTGCCATATGGGCTC 54286 _ A_____ GGTA
A TGAGCCCAT TGGC GG C
||||||| ||| || |
ACTCGGGTA ACCG CC G
T TGG___ ATGG
GAM2453 DKFZP727M111 5' GCTTTTGCCAGTGAGCCCA 32061 A C
TG GC CATTGGCAGGGGT
|| || |||||
AC CG GTGACCGTTTTCG
C A
GAM2453 FLJ13162 5' GCACCCTCCATGGGCTCA 47185 T C _
TGAGCCCAT GG AGGG GT
||||||| || ||| ||
ACTCGGGTA CC TCCC CG
_ _ A
GAM2453 GMPPB 5' ACTTCTGCAATAAGCCCA 97429 A CC G
TG GC ATTG CAGGGGT
|| || ||| |||||
AC CG TAAC GTCTTCA
C AA _
GAM2453 KIAA0444 3' TGCCCCATGGGCTCA 63006 TGGCA
TGAGCCCAT GGGGTA
||||||| |||||
ACTCGGGTA CCCCCT

GAM2453 KIAA0963 3' GACCCACAAGGGCTCA 31033 A GCAG A
TGAGCCC TTG GGGT C
||||||| ||| ||| |
ACTCGGG AAC CCCA G
_ A___ C
GAM2453 KIAA1649 3' GCTTATGACCAATGGGCCA 67517 A _ GG
TG GCCCATTGG CA GGT
|| ||||| || |||
AC CGGGTAACC GT TCG
_ A AT
GAM2453 KIAA1649 5' GCTTATGACCAATGGGCCA 51243 A _ GG
TG GCCCATTGG CA GGT
|| ||||| || |||
AC CGGGTAACC GT TCG
_ A AT
GAM2453 KIAA1813 3' GCTTCTGCCAAGAAGTCA 70825 CCCA
TGAG TTGGCAGGGGT
||| |||||
ACTC AACCGTCTTCG
AAG_
GAM2453 KIAA1813 5' GGCTCCCCCACCACCAATGGGC 70828 CA_ TA
GCCCATTTGG GGGG CC
||||||| ||| ||

CGGGTAACC CCCC GG
ACC TC
GAM2453 MAP1LC3A 3' ACCCCTGCTGTGTGGTTCA 51679 _ T
TGAGCC CAT GGCAGGGGT
||||| ||| |||||
ACTTGG GTG TCGTCCCCA
T _

GAM2453 MGC11316 3' GGTGCATTGCCAAGGACTCA 53047 C A GG
TGAG CC TTGGCAG GTACC
|||| || ||||| ||||
ACTC GG AACCGTT CGTGG
A _ A_

GAM2453 PDE8B 5' GGCACCCCTGCCCGGCCTC 68203 C ATT A
GAG CC GGCAGGGGT CC
||| || ||||| ||
CTC GG CCGTCCCCA GG
C C_ C

GAM2453 PRO0529 3' TACTCACCAATGGGACCA 26857 AG CAG
TG CCCATTGG GGGTA
|| ||||| ||||
AC GGGTAACC CTCAT
CA A_

GAM2453 RAB17 3' CCCCTGCCTGGGCCA 42617 A TT
TG GCCCA GGCAGGGG
|| |||| |||||
AC CGGT CCGTCCCC

GAM2453 UBE2G1 3' ACTCCTGCCAAGAGCCCA 13950 A CCA
TG GC TTGGCAGGGGT
|| || |||||
AC CG AACCGTCCTCA
C AG_

GAM2453 LOC115708 3' GGTACCCCTACCCCTCA 73920 CCCATT C
TGAG GG AGGGGTACC
|||| || |||||
ACTC CC TCCCCATGG
C_ A

GAM2453 LOC150481 3' GCACCTAACAATGGGTCA 80705 G GC G
TGA CCCATTG AGG GT
||| ||||| ||| ||
ACT GGGTAAC TCC CG
_ AA A

GAM2453 LOC153196 5' GGCAGTGCCTTGCCATCGGGCC 87171 A AT _ A
CA TG GCCC TGGCAGGG GT CC
|| |||| ||||| |||
AC CGGG ACCGTTCC CA GG
C CT GT C

GAM2453 LOC153711 5' ACCTGTTAGCCGATGGGCCCA 87342 A AG_
TG GCCCATTGGC GGGT
|| ||||| |||

		AC CGGGTAGCCG TCCA		
		C ATTG		
GAM2453	LOC157860 3'	GGCACCCCCTCCTGGGCTC 87878	TT CA	A
		GAGCCCA GG GGGGT CC		
		CTCGGGT CC CCCCAGG		
		__ TC C		
GAM2453	LOC158014 5'	GTGCCACCCATGGGCTCA 82566	T CAGG	
		TGAGCCCAT GG GGTAC		
		ACTCGGGTA CC CCGTG		
		_ CA__		
GAM2453	LOC158191 3'	GCACCTAACAATGGGTCA 82677	G GC G	
		TGA CCCATTG AGG GT		
		ACT GGGTAAC TCC CG		
		_ AA A		
GAM2453	LOC203378 5'	ATCTCTGCCAACAGTCTCA 92276	CCCA	
		TGAG TTGGCAGGGGT		
		ACTC AACCGTCTCTA		
		TGAC		
GAM2453	LOC203378 3'	GGTATTTTGCCCAAAGGCTCA 92295	CATT G	
		TGAGCC GGCAGGG TACC		
		ACTCGG CCGTTTT ATGG		
		AAAC _		
GAM2453	LOC204970 3'	GGCACCCCTGCGGGCTCA 90964	ATTG A	
		TGAGCCC GCAGGGGT CC		
		ACTCGGG CGTCCCCA GG		
		__ C		
GAM2453	LOC219700 5'	GGCTTCCCTGCCATGGACTCA 94653	C T TA	
		TGAG CCAT GGCAGGGG CC		
		ACTC GGTA CCGTCCCT GG		
		A _ TC		
GAM2453	LOC256126 3'	GCCCCTGCCATAGGCCA 97015	A CAT	
		TG GCC TGGCAGGGGT		
		AC CGG ACCGTCCCCG		
		C AT_		
GAM2453	LOC51246 3'	ACCTGGGCCAATGGGCCA 33636	A AG	
		TG GCCCATTGGC GGGT		
		AC CGGGTAACCG TCCA		
		_ GG		
GAM2453	LOC90190 3'	ACTGTTACCAATGGGCTC 62421	C G	
		GAGCCCATTTGG AG GGT		

			CTCGGGTAACC TT TCA		
			A G		
GAM2454	CDO1	3'	ACATGATCCCCAGACCACAACA 10162	GA	
			TGTTGTGGTCTGGGGA ATGT		
			ACAACACCAGACCCCT TACA		
			AG		
GAM2454	SMTN	3'	ACACCCTCCCCCCCACATACAC 23651	_ TCT AA	
	A		TGTGT TGTGG GGGGAG TGT		
			ACACA ACACC CCCCTC ACA		
			T C_ CC		
GAM2454	SMTN	3'	ACACCCTCCCCCCCACATACAC 56999	_ TCT AA	
	A		TGTGT TGTGG GGGGAG TGT		
			ACACA ACACC CCCCTC ACA		
			T C_ CC		
GAM2454	SMTN	3'	ACACCCTCCCCCCCACATACAC 57001	_ TCT AA	
	A		TGTGT TGTGG GGGGAG TGT		
			ACACA ACACC CCCCTC ACA		
			T C_ CC		
GAM2454	HB-1	5'	TCCTCTGCCACACCACA 41317	T CT	
			TGTG TGTGGT GGGGA		
			ACAC ACACCG CTCCT		
			C T_		
GAM2455	APAF1	5'	TCGGGGGAAGGGCGCCACAGGC 25985	A_____ G	
			GCCTGTGGC CCCC GA		
			CGGACACCG GGGG CT		
			CGGGAA G		
GAM2455	BCL9	5'	TCACCTCCAGGATGAGCACTGC 16323	CT G_ C C A	
			GC GTG CA CC GGAG TGA		
			CG CAC GT GG CCTC ACT		
			T_ GA A A C		
GAM2455	ENO1	3'	TCATCTCCGGGGTGGCCACAGG 9279	_	
	CTA		TAGCCTGTGGC ACCCCGGAGATGA		
			ATCGGACACCG TGGGCCTCTACT		
			G		
GAM2455	HDAC4	3'	TCATCTCCGGGGGCCAGGGGCTG 21251	G AC	
			TAGCCT TGGC CCCGGAGATGA		
			GTCGGG ACCG GGGCCTCTACT		
			G _		
GAM2455	MUCDHL	3'	TCATCCCCGAGACGCAACTGCA 88648	TG CACCC_ A	
	GGCTG		TAGCCTG G CGG GATGA		

		GTCGGAC C	GCC CTACT		
		GT AACGCAGA C			
GAM2455	SEPN1	3'	CCAGGGGTGCCCCAGGCTA	66966	T _
			TAGCCTG GGCACCCC GG		
			ATCGGAC CCGTGGGG CC		
			C A		
GAM2455	TP73	3'	CATCCCCAGGCACCTCACAGGC	19470	CAC_ C A
			GCCTGTGG CC GG GATG		
			CGGACACT GG CC CTAC		
			CCAC A C		
GAM2455	FLJ10120	3'	TCATCTCCAGGACAGGCCAC	36309	AC__ C
			GTGGC CC GGAGATGA		
			CACCG GG CCTCTACT		
			GACA A		
GAM2455	FLJ10324	5'	CATCCCCGGGGCGCACAT	36497	_ A A
			GTG GC CCCCCG GATG		
			TAC CG GGGGCC CTAC		
			A C C		
GAM2455	FLJ21777	3'	CACCTCTGCCACAGGT	50835	CCCCG A
			GCCTGTGGCA GAG TG		
			TGGACACCGT CTC AC		
			_____ C		
GAM2455	KIAA0229	3'	TCTTTGAGATGCCCAGGC	94029	T CCC
			GCCTG GGCA CGGAGA		
			CGGAC CCGT GTTTCT		
			_ AGA		
GAM2455	KIAA0720	3'	CACCTTCCCAGTCCCACAGGC	62975	C CCC A
			GCCTGTGG AC GGAG TG		
			CGGACACC TG CTTC AC		
			C ACC C		
GAM2455	KIAA1036	3'	TCAGGGAAGGCGCCACAGGCTG	30497	A __ G_
			TAGCCTGTGGC CC CC GA		
			GTCGGACACCG GG GG CT		
			C AA GA		
GAM2455	KIAA1069	3'	TCATCTCCGGAGCTGATAGC	68532	CTG ACC
			GC TGGC CCGGAGATGA		
			CG GTCG GGCCTCTACT		
			ATA A__		
GAM2455	MGC16279	5'	TCATCTCCCACGGTACCACAGG	52994	C CC_
			C GCCTGTGG ACC GGAGATGA		

		CGGACACC TGG CCTCTACT	
		A CAC	
GAM2455	MGC16279 5'	TCATCTCCACGGTACCACAGG 52995	C CC_
	C	GCCTGTGG ACC GGAGATGA	
		CGGACACC TGG CCTCTACT	
		A CAC	
GAM2455	SCAMP-4 3'	TCACCCCCAGGATGCTGTTGCT 55355	CT TG C C AGA
	G	TAGC G GCA CC GG TGA	
		GTCG T CGT GG CC ACT	
		T_ GT A A CCC	
GAM2455	TRIM22 3'	TCATTTTCAATGTCACA 21388	CCCC
		TGTGGCA GGAGATGA	
		AACTGT TTTTACT	
		AAC_	
GAM2455	LOC115219 3'	CATGGATGAAGTCCACAGGC 73691	C CC GAG
		GCCTGTGG AC CG ATG	
		CGGACACC TG GT TAC	
		_ AA AGG	
GAM2455	LOC127798 5'	TCATCTCTTCTGCCTCAAGC 75987	C T CCCC
		GC TG GGCA GGAGATGA	
		CG AC CCGT TCTCTACT	
		A T CT_	
GAM2455	LOC145497 5'	CCAGGGGTACCAAGGCTA 77732	G C _
		TAGCCT TGG ACCCC GG	
		ATCGGA ACC TGGGG CC	
		_ A A	
GAM2455	LOC155063 5'	CCAGGAATGCCACAGGCTG 87645	CC _
		TAGCCTGTGGCA CC GG	
		GTCGGACACCGT GG CC	
		AA A	
GAM2455	LOC196483 5'	TCATCTCTCACGGTACCACAGG 61027	C CC_
	C	GCCTGTGG ACC GGAGATGA	
		CGGACACC TGG TCTCTACT	
		A CAC	
GAM2455	LOC196500 3'	TCACCTCCACCTTCACAGGC 89087	CACCCC A
		GCCTGTGG GGAG TGA	
		CGGACACT CCTC ACT	
		TCCA_ C	
GAM2455	LOC199988 5'	CATCCCCAGGCACCTCACAGGC 91499	CAC_ C A
		GCCTGTGG CC GG GATG	

	CGGACACT GG CC CTAC	
	CCAC A C	
GAM2455 LOC200170 3'	TCATCTCCGGGGTGGCCACAGG 89996	—
C	GCCTGTGGC ACCCCGGAGATGA	
	CGGACACCG TGGGGCCTCTACT	
	G	
GAM2455 LOC202024 5'	TCATCTCCCACGGCACCACAGG 90614	CA CC_
C	GCCTGTGG CC GGAGATGA	
	CGGACACC GG CCTCTACT	
	AC CAC	
GAM2455 LOC220662 3'	CACCTCCAGGGTTCAGAG 92808	G C C A
	CT TGG ACCC GGAG TG	
	GA ACT TGGG CCTC AC	
	G _ A C	
GAM2455 LOC220930 5'	TCAGAGCTAAGGTATCCACAGG 94752	C_ CC AGA
C	GCCTGTGG ACC GG TGA	
	CGGACACC TGG TC ACT	
	TA AA GAG	
GAM2455 LOC221749 3'	CATTCCAGGTGCCACAGGC 93648	CC A
	GCCTGTGGCACC GGAG TG	
	CGGACACCGTGG CCTT AC	
	A_ _	
GAM2455 LOC253782 3'	TCATTATATAATGCCACAGGC 97404	CCCCGGA
	GCCTGTGGCA GATGA	
	CGGACACCGT TTACT	
	AATATA_	
GAM2455 LOC254003 5'	CATCCCCACCCGCTCACAGGC 98027	_ ACCCC A
	GCCTGTG GC GG GATG	
	CGGACAC CG CC CTAC	
	T CCCAC _	
GAM2455 LOC255332 3'	TCATCTCCAGAACTATCAGGAC 97949	_ _ CACCCC
TA	TAG CCTG TGG GGAGATGA	
	ATC GGAC ATC CCTCTACT	
	A T AAGA_	
GAM2455 LOC255995 3'	TCATCTGAACAGAAGTGCACAG 98750	G CCCGG_
GCTA	TAGCCTGTG CAC AGATGA	
	ATCGGACAC GTG TCTACT	
	_ AAGACAAG	
GAM2455 LOC256072 3'	TCATCTCCGGGGTGGCCACAGG 96158	_
CTA	TAGCCTGTGGC ACCCCGGAGATGA	

ATCGGACACCG TGGGGCCTCTACT
 G
 GAM2456 ENO1 3' ACACAGACCCCTCCCCTCGTGT 9277 GG__
 CA TGACACGAGGGGAGGGGTCTGTGT
 |||||
 ACTGTGCTCCCCTCCCCAGACACA

 GAM2456 ESR1 3' ACACAGACCCCTTTGCATTC 5507 GG__
 GAG GAGGGGTCTGTGT
 ||| |||||
 CTT TTCCCCAGACACA
 ACGT
 GAM2456 STAT6 3' ACTCCATCCCCCGTATCA 13446 C A _
 TGA ACG GGGGA GGGGT
 ||| ||| |||||
 ACT TGC CCCCT CCTCA
 A C A
 GAM2456 FBXO27 3' ACCATCCCCTCCCCTC 74996 TC T
 GAGGGGAGGGG TG GT
 ||||| |||
 CTCCCCTCCCC AC CA
 T _ _
 GAM2456 KIAA1259 5' ACACAGACCCCTTTAGATGCT 50796 _ CGA A
 CA TGA CA GGGG GGGGTCTGTGT
 ||| || |||||
 ACT GT TTTC CCCCAGACACA
 C AGA _
 GAM2456 KIAA1297 5' CACAGACCTGCTCGGTCA 72630 A GGGAG
 TGAC CGAG GGGTCTGTG
 |||| ||| |||||
 ACTG GCTC TCCAGACAC
 _ G _ _
 GAM2456 LOC150157 5' ACAGTCCTCCCCCTGCATCA 86017 CA G A T
 TGA C AGGGG GGGG CTGT
 ||| | |||| ||| ||||
 ACT G TCCCC CTCC GACA
 AC _ _ T
 GAM2456 LOC151808 5' ACACAGACCCCGTTGCTC 86684 G A
 GAG GG GGGGTCTGTGT
 ||| || |||||
 CTC TT CCCCAGACACA
 G G
 GAM2456 LOC196890 5' ACAGTCCTCCCCCTGCATCA 91220 CA G A T
 TGA C AGGGG GGGG CTGT
 ||| | |||| ||| ||||
 ACT G TCCCC CTCC GACA
 AC _ _ T
 GAM2456 LOC256072 3' ACACAGACCCCTCCCCTCGTGT 96156
 CA TGACACGAGGGGAGGGGTCTGTGT
 |||||

ACTGTGCTCCCCTCCCCAGACACA

GAM2457 BIKE 3' TACCATTGGACCAACAGAAACC 34608 GC_ A_ A
TCA TGAGGTTTC TGG TAGT GGTA

||||||| ||| |||||
ACTCCAAAG ACC GTTA CCAT
ACA AG _

GAM2457 LOC221641 5' ACCTACTACCCTGACCCCT 95339 TT CT A
AGG TCG GG TAGTAGGT

||| ||| || |||||
TCC AGT CC ATCATCCA
CC _ C

GAM2457 LOC256158 5' TACCCACTATCCAGTGGCTGC 99513 T_ A
GT TCGCTGGATAGT GGTA

|| ||||| |||||
CG GGTGACCTATCA CCAT
TC C

GAM2458 ADAM8 3' GCCACACCTGCCCTGCT 8476 C__ A
AGCAG CGG GTGTGGC

||||| ||| |||||
TCGTC GTC CACACCG
CCC _

GAM2458 AGRN 3' GCCAGCCCCAGGCTGCTG 79587 _ A G
CAGCAGCC GG GT TGGC

||||||| || |||
GTCGTCCG CC CG ACCG
A C _

GAM2458 ATP2C1 3' GCCATATTTTCAGCTACTG 27662 C C
CAG AGC GGAGTGTGGC

||| ||| |||||
GTC TCG CTTTATACCG
A A

GAM2458 CD97 3' GCCACTGGTCCTGCTGCTG 55305 C G_
CAGCAGC GGA T GTGGC

||||||| ||| | |||||
GTCGTCCG CCT G CACCG
T G T

GAM2458 DUOX2 3' GCCTGTCCCTCCCTGGCTGCTG 26867 _ TG_
CAGCAGCC GGAG T GGC

||||||| |||| | |||
GTCGTCCG CCTC G CCG
TC CT T

GAM2458 FAFL4 5' GCCAGGCGCCGGCCGGCTG 16744 A_ A G
CAGC GCCGG GT TGGC

||| ||||| || |||
GTCG CGGCC CG ACCG
GC G G

GAM2458 FANCC 3' GCCCACTGTCTTGCTGT 71043 C _
GCAGC GGA GTGTGGC

||||| ||| |||||

			TGTCG TCT CACACCG		
			T GT		
GAM2458	HIRA	3'	GCCACACTCTCGCCGCTG 13906	A C	
			CAGC GC GGAGTGTGGC		
			GTCG CG TCTCACACCG		
			C C		
GAM2458	MAPK8IP1	3'	GCCAGGACAGCTGGCTGCTG 19580	AG	___
			CAGCAGCCGG TGT GGC		
			GTCGTCGGTC ACA CCG		
			G_ GGA		
GAM2458	MECP2	3'	CCACACATTTCACTGTCTG 18393	_ CC	_
			CAG CAG GGA GTGTGG		
			GTC GTC TTT CACACC		
			T AC A		
GAM2458	MYO1D	3'	GCCACACTCCGAGTCCTG 72248	CA	_
			CAG GC CGGAGTGTGGC		
			GTC TG GCCTCACACCG		
			C_ A		
GAM2458	PEX6	3'	GCTCCTCCTCAGGCTGCTG 6085	___	TGT
			CAGCAGCC GGAG GGC		
			GTCGTCGG CCTC TCG		
			ACT C__		
GAM2458	POLR2E	3'	GCCACACCTGGTGTCTG 60596	CA_	A
			CAG GCCGG GTGTGGC		
			GTC TGGTC CACACCG		
			TTG _		
GAM2458	RENT1	3'	GCCCCATCCCGGCTGTTG 12814	AG	T
			CAGCAGCCGG TG GGC		
			GTTGTCCGCC AC CCG		
			CT C		
GAM2458	RNMT	3'	GCCACACCTGCAGGCGCTG 15053	A	___ A
			CAGC GCC GG GTGTGGC		
			GTCG CGG TC CACACCG		
			_ ACG _		
GAM2458	RPL30	5'	GCCATCTTAGCGGCTGCTG 8272	___	T
			CAGCAGCCG GAG GTGGC		
			GTCGTCGGC TTC TACCG		
			GA _		
GAM2458	TBL1X	5'	GCCACAAGTTGCGCTGCT 20135	_	AG
			AGCAGC CGG TGTGGC		

TCGTCG GTT ACACCG
C GA

GAM2458 ALLC 5' CCTAATTTTCAGGCTGCTG 37979 _ GT
CAGCAGCC GGAGT GG
||||||| ||| ||
GTCGTCGG CTTTA CC
A AT

GAM2458 C22orf23 3' CCCCATGGCTGGCTGCTG 51769 A_ T
CAGCAGCCGG GTG GG
||||||| ||| ||
GTCGTCGGTC TAC CC
GG C

GAM2458 COLEC12 3' CCACAGTTTTGGCCTCTG 56100 CA _
CAG GCCGGAG TGTGG
||| ||||| |||||
GTC CGGTTTT ACACC
TC G

GAM2458 DJ37E16.5 5' GCCGGCGGCCCGGCCGGCTG 40097 A_ A_ G
CAGC GCCGG GT TGGC
||| ||||| || |||||
GTCG CGGCC CG GCCG
GC GG _

GAM2458 DKFZP564O0423 3' GCCACATTGGTGCTGTTG 93352 CGG
CAGCAGC AGTGTGGC
||||||| |||||
GTTGTCG TTACACCG
TGG

GAM2458 DKFZP586J1624 3' GCCGAGTCTCCGACTGTCTG 32046 _ C TG_
CAG CAG CGGAG TGGC
||| ||| ||||| |||||
GTC GTC GCCTC GCCG
T A TGA

GAM2458 ESPL1 5' GCCCACTCCGCCTTGCT 25439 _ C
AGCA G CGGAGTGTGGC
||| | |||||
TCGT C GCCTCACACCG
T C

GAM2458 FBXO26 5' GCCAGGACTCTGGCTACTG 46628 C G_
CAG AGCCGGAGT TGGC
||| ||||| ||||| |||||
GTC TCGGTCTCA ACCG
A GG

GAM2458 FLJ00026 3' GCCACCCAGGACTGACTG 65619 _ _ _ AGT
CAG CAG CC GG GTGGC
||| ||| || ||| |||||
GTC GTC GG CC CACCG
A A A _

GAM2458 FLJ14525 3' GCCATGACATCAGCATGCTG 52482 _ C GA _
CAGCA GC G GT GTGGC
||||| || | || |||||

		GTCGT CG C CA TACCG		
		A A TA G		
GAM2458	FLJ20979	5' CGCCACACCCCAGCGCGCT	44385	A_ C A ____
		AGC GC GG GTGTGGC G		
		TCG CG CC CACACCG C		
		CG A C ____		
GAM2458	FLJ21438	5' GCCACACTCTCTGAACTG	62194	__ CC
		CAG CAG GGAGTGTGGC		
		GTC GTC TCTCACACCG		
		AA ____		
GAM2458	FLJ22283	5' GCCACATGCCCTGGCTGC	50902	_ A_
		GCAGCC GG GTGTGGC		
		CGTCGG CC TACACCG		
		T CG		
GAM2458	ITGB5	3' GCCATGTACCTGGCTGCT	60216	A ____
		AGCAGCCGG GTG TGGC		
		TCGTCGGTC CAC ACCG		
		_ TGT		
GAM2458	KIAA0643	3' GCCACACAAGTCTTGGCTG	45976	-- ____
		CAGCCG GA GTGTGGC		
		GTCGGT CT CACACCG		
		T GAA		
GAM2458	KIAA1582	5' GCCACAGGCTCCAGCTCTG	65990	C C ____
		CAG AGC GGAGT GTGGC		
		GTC TCG CCTCG CACCG		
		_ A GA		
GAM2458	KIAA1719	3' GCCTCAGGTCTGGCTGCTG	68731	G_ T
		CAGCAGCCGGA TG GGC		
		GTCGTCGGTCT AC CCG		
		GG T		
GAM2458	KIAA1737	3' GCCAATACCTGGCTGCTG	67943	A _
		CAGCAGCCGG GTGT GGC		
		GTCGTCGGTC CATA CCG		
		_ A		
GAM2458	KIAA1879	5' GCCACAGTGCTGCGGCTGCT	73941	G ____
		AGCAGCCG AGT GTGGC		
		TCGTCGGC TCG CACCG		
		G TGA		
GAM2458	LMOD1	3' GCCACACTATTTGAGTTG	25102	_ _
		CAGC CGG AGTGTGGC		

GTTG GTT TCACACCG
 A TA
 GAM2458 MGC2647 3' GCCACAGGCTGTGGCTGCT 74078 G ____
 AGCAGCCG AGT GTGGC
 ||||| || ||||
 TCGTCGGT TCG CACCG
 G GA
 GAM2458 PEPP2 3' GCCACACTCCTGTCAGCT 39202 A_ C
 AGC GC GGAGTGTGGC
 || || |||||
 TCG TG CCTCACACCG
 AC T
 GAM2458 RPS6KB2 3' CGCCACACCCGCGCTCAACTG 15534 C__ _ A ____
 CAG AGC CGG GTGTGGC G
 || || || ||||| |
 GTC TCG GCC CACACCG C
 AAC C C ____
 GAM2458 SCYA21 3' GCCCACTCTTTCTCCTG 12978 C CC
 CAG AG GGAGTGTGGC
 || || |||||
 GTC TC TCTCACACCG
 C TT
 GAM2458 SELB 3' GCCCAGTCCAGGCTGCTG 62593 _ G T
 CAGCAGCC GGA TG GGC
 ||||| || || ||
 GTCGTCGG CCT AC CCG
 A G _
 GAM2458 SID6-306 5' GCCATGAGCGCGCTGCTG 23577 _ GAG
 CAGCAGC CG TGTGGC
 ||||| || ||||
 GTCGTCG GC GTACCG
 C GA_
 GAM2458 TRIM16 5' GCCATCGCATCTGGCTGC 22373 _ _
 GCAGCCGGA GTG TGGC
 ||||| || ||||
 CGTCGGTCT CGC ACCG
 A T
 GAM2458 XYLT1 5' GCCACAAGTTAGGGCTGCTG 78414 G_ G_
 CAGCAGCC GA TGTGGC
 ||||| || ||||
 GTCGTCGG TT ACACCG
 GA GA
 GAM2458 LOC115110 3' GCCGGTCTCAGGCTGCTG 72178 G TG
 CAGCAGCC GAG TGGC
 ||||| || ||||
 GTCGTCGG CTC GCCG
 A TG
 GAM2458 LOC115648 3' GCCACATGCTTCCAGTGCT 60023 G C ____
 AGCA C GGA GTGTGGC
 ||| | || |||||

	TCGT G CCT TACACCG	
	_ A TCG	
GAM2458 LOC116437 5'	GCCACACTGCCGCTGCTG 74326	C _
	CAGCAGC GG AGTGTGGC	
	GTCGTGCG CC TCACACCG	
	_ G	
GAM2458 LOC130576 5'	GCCACACTTCTGCCTGCT 75459	_ C
	AGCAG C GGAGTGTGGC	
	TCGTC G CTTCACACCG	
	C T	
GAM2458 LOC130951 5'	GCCCCAGGGCCGGGCTGCTG 57942	_ AG__ T
	CAGCAGCC GG TG GGC	
	GTCGTGCG CC GC CCG	
	G GGGA _	
GAM2458 LOC136120 3'	GCCATCAACCTGGCTGCTG 76707	AG _
	CAGCAGCCGG TG TGGC	
	GTCGTGCGTC AC ACCG	
	CA T	
GAM2458 LOC144486 5'	GCCACCGACGCCGTTGCTG 84005	A _
	CAGCAGCCGG GT GTGGC	
	GTCGTTGGCC CA CACCG	
	G GC	
GAM2458 LOC145845 3'	GCCATCTCTTCCTGGCTGC 84547	_ T__
	GCAGCC GGAG GTGGC	
	CGTCGG CCTT TACCG	
	T CTC	
GAM2458 LOC146988 5'	GCCACCTCTGCGGCTGCT 84959	G T_
	AGCAGCCG AG GTGGC	
	TCGTGCGC TC CACCG	
	G TC	
GAM2458 LOC147160 5'	GCCTCCTTCAGGCTGCTG 85078	_ TGT
	CAGCAGCC GGAG GGC	
	GTCGTGCG CTTC CCG	
	A CT_	
GAM2458 LOC152897 5'	GCCCCATCCTGGCTGCTG 81607	AG T
	CAGCAGCCGG TG GGC	
	GTCGTGCGTC AC CCG	
	CT C	
GAM2458 LOC154790 5'	CGCCACACCCACGAGGCGGTGC 82039	_ _ _ A _
TG	CAGCA GCC GG GTGTGGC G	

GTCGT CGG CC CACACCG C
 GG AGCA _ _
 GAM2458 LOC159121 5' GCCACAGTGCTCACTGCTG 88387 CCG _
 CAGCAG GAGT GTGGC
 ||||| ||| |||||
 GTCGTC CTCG CACCG
 A_ TGA
 GAM2458 LOC200471 5' GCCAGGCTGCTGGCTGCTG 91636 _ G
 CAGCAGCCGG AGT TGGC
 ||||| ||| |||||
 GTCGTCGGTC TCG ACCG
 G G
 GAM2458 LOC200731 3' GCTGGTTCCAGGCTGCTG 91698 _ TGT
 CAGCAGCC GGAG GGC
 ||||| ||| |||
 GTCGTCGG CCTT TCG
 AC GG_
 GAM2458 LOC205143 5' GCCAGGCGGCCGGCTACCTG 92350 C_ A_ G
 CAG AGCCGG GT TGGC
 || ||||| || |||||
 GTC TCGGCC CG ACCG
 CA GG G
 GAM2458 LOC221271 3' GCCACACTCGGGTACCTG 93519 CA G
 CAG GCC GAGTGTGGC
 ||| ||| |||||
 GTC TGG CTCACACCG
 CA G
 GAM2458 LOC253148 3' GCCATCCAGGCCGGCTGCT 98666 AG _
 AGCAGCCGG TG TGGC
 ||||| || |||||
 TCGTCGGCC AC ACCG
 GG CT
 GAM2458 LOC256639 5' GCCACAACCTGCTAGCTG 97957 _ C AG
 CAGC AGC GG TGTGGC
 |||| ||| || |||||
 GTCG TCG TC ACACCG
 A T A_
 GAM2458 LOC256905 5' GCCACAGCTCTGGCTCCTG 98660 C _
 CAG AGCCGGAG TGTGGC
 ||| ||||| |||||
 GTC TCGGTCTC ACACCG
 C G
 GAM2458 LOC51011 5' GCATTTCCCGGCTGGCTG 32641 _ _
 CAGC AGCCGG AGTGT
 |||| ||||| |||||
 GTCG TCGGCC TTACG
 G CCT
 GAM2458 LOC51236 3' GCCACACTTCCTTCCTG 33622 C CC
 CAG AG GGAGTGTGGC
 ||| || |||||

GTC TT CTTACACCG
 C CC
 GAM2458 LOC90342 5' GCCACAGCGGAGGACTGGCTG 63011 _ _ GGA_
 CAGC AG CC G TGTGGC
 ||| || | ||||
 GTCG TC GG C ACACCG
 G A AGG G
 GAM2459 SEL1L 3' TAAGCAAACTTTCCTCCCA 18606 A_ TT_
 TG AGG GTTTTGCTTA
 || || |||||
 AC TCC CAAAACGAAT
 CC TTT
 GAM2459 DKFZp434B0417 3' TAAGCAAAAATACCTGGTAA 26308 TGAA TG_
 TTACCA GGT TTTTGCTTA
 |||| | |||||
 AATGGT CCA AAAACGAAT
 _ TAA
 GAM2459 KIAA1169 5' AAGCAAAACAACGTTTTTGGT 35874 T G
 ACCA GAA GTTGTTTTGCTT
 ||| || |||||
 TGGT TTT CAACAAAACGAA
 _ G
 GAM2459 LOC158819 3' AAGCAACCTGATGGTAA 88260 GA
 TTACCAT AGGTTGTTT
 |||| | |||||
 AATGGTA TCCAACGAA
 G_
 GAM2459 LOC200301 5' AAGCACAGGCCTTCACAGTGA 90126 CA GTTT
 TTAC TGAAGTT TGCTT
 ||| |||| | ||||
 AGTG ACTTCCGG ACGAA
 AC AC_
 GAM2459 LOC204285 3' AAGCACCAGTGACCTTCACAGG 91007 A_ TG T_
 CC TGAAGGT TT TGCTT
 || |||| | ||||
 GG ACTTCCA GA ACGAA
 AC GT CC
 GAM2460 ADAM17 3' TCCAGCCTGGGTGACAGAGTGA 41847 TG
 GA TCT CTCTGTCACCCAGGCTGGA
 || |||||
 AGA GAGACAGTGGGTCCGACCT
 GT
 GAM2460 ADAM17 3' TCCAGCCTGGGTGACAGAGTGA 41848 TG
 GA TCT CTCTGTCACCCAGGCTGGA
 || |||||
 AGA GAGACAGTGGGTCCGACCT
 GT
 GAM2460 ADAT1 3' TCCAGCCTGGGTGATAGAGCAA 24919
 GA TCTTGCTCTGTCACCCAGGCTGGA
 |||||

AGAACGAGATAGTGGGTCCGACCT

GAM2460 ADCY2 3' CCTGGGCAACATAGCAAGA 65646 C CA
TCTTGCT TGT CCCAGG
||||| ||| |||||
AGAACGA ACA GGGTCC
T AC

GAM2460 ADCY2 3' TCCAGCCTGGGTGACAGAGCGA 65655
GA TCTTGCTCTGTCACCCAGGCTGGA
|||||||
AGAGCGAGACAGTGGGTCCGACCT

GAM2460 AICDA 3' TCCAGCCTGGGCGACAAGAGCA 40699 _ A
AGA TCTTGCTCT GTC CCCAGGCTGGA
||||| ||| |||||
AGAACGAGA CAG GGGTCCGACCT
A C

GAM2460 AK1 3' TCCAGCCTGGGTGACAGAGCAA 6641
GA TCTTGCTCTGTCACCCAGGCTGGA
|||||||
AGAACGAGACAGTGGGTCCGACCT

GAM2460 ALDH3A2 3' TCAGCTTGGGCAACAGAGCAAG 69803 CA
A TCTTGCTCTGT CCCAGGCTGG
||||| |||||
AGAACGAGACA GGGTTCGACT
AC

GAM2460 ALPP 3' CCTGGGCGACAGAGCGAGA 69415 A
TCTTGCTCTGTC CCCAGG
||||| |||||
AGAGCGAGACAG GGGTCC
C

GAM2460 ANKH 3' TCCAGCCTGAGCAACAGAGCAA 55073 CACC
TTGCTCTGT CAGGCTGGA
||||| |||||
AACGAGACA GTCCGACCT
ACGA

GAM2460 ANKH 3' TCCAGCCTGGGTGACAAGAGCA 55075 _
A TTGCTCT GTCACCCAGGCTGGA
||||| |||||
AACGAGA CAGTGGGTCCGACCT
A

GAM2460 APAF1 3' TCCAGCCTGGGTGACATAGCAA 25984 C
GA TCTTGCT TGTACCCAGGCTGGA
||||| |||||
AGAACGA ACAGTGGGTCCGACCT
T

GAM2460 APOL1 3' TCCAGCCTGGGTGACAGAGCGA 14745
GA TCTTGCTCTGTCACCCAGGCTGGA
|||||||

AGAGCGAGACAGTGGGTCCGACCT

GAM2460 ARSD GA	3'	TCCAGCCTGGGCCACATAGCAA 9800	C	CA
		TCTTGCT TGT CCCAGGCTGGA		
		AGAACGA ACA GGGTCCGACCT		
		T CC		
GAM2460 ATM GA	3'	TCCAGCCTGGGAGACAGAGCGA 5303	A	
		TCTTGCTCTGTC CCCAGGCTGGA		
		AGAGCGAGACAG GGGTCCGACCT		
		A		
GAM2460 ATM A	3'	TCCAGCCTGGGTGACAAGAGCG 5304	_	
		TTGCTCT GTCACCCAGGCTGGA		
		AGCGAGA CAGTGGGTCCGACCT		
		A		
GAM2460 B3GAT1	3'	CCAGCCTGATGCCAGAACAA 55052	C	T CC
		TTG TCTG CA CAGGCTGG		
		AAC AGAC GT GTCCGACC		
		A C A_		
GAM2460 BCAS1 GA	3'	TCCACCCTGGGCGACAGAGCAA 14715	A	C
		TCTTGCTCTGTC CCCAGG TGGA		
		AGAACGAGACAG GGGTCC ACCT		
		C C		
GAM2460 BPHL GA	3'	TCCAACCTGGGCAACAGAGTAA 16336	CA	C
		TCTTGCTCTGT CCCAGG TGGA		
		AGAATGAGACA GGGTCC ACCT		
		AC A		
GAM2460 BRCA1 GA	5'	TCCAGCCTGGGCGACAGAGCGA 24576	A	
		TCTTGCTCTGTC CCCAGGCTGGA		
		AGAGCGAGACAG GGGTCCGACCT		
		C		
GAM2460 BRCA1	3'	TCCAGCCTGGGTGACAGTGAGA 24577	TG	CT
		TCT CT GTCACCCAGGCTGGA		
		AGA GA CAGTGGGTCCGACCT		
		GT _		
GAM2460 BRCA1	3'	TCCAGCCTGGGTGACAGTGAGA 24578	TG	CT
		TCT CT GTCACCCAGGCTGGA		
		AGA GA CAGTGGGTCCGACCT		
		GT _		
GAM2460 BRCA1	3'	TCCAGCCTGGGTGACAGTGAGA 24579	TG	CT
		TCT CT GTCACCCAGGCTGGA		

			AGA GA CAGTGGGTCCGACCT		
			GT _		
GAM2460	BRCA1	3'	TCCAGCCTGGGTGACAGTGAGA 24580	TG CT	
			TCT CT GTCACCCAGGCTGGA		
			AGA GA CAGTGGGTCCGACCT		
			GT _		
GAM2460	C1orf1	3'	TCCAGCCTAGGCGACAGAGTGA 8683	TG A C	
	GA		TCT CTCTGTC CC AGGCTGGA		
			AGA GAGACAG GG TCCGACCT		
			GT C A		
GAM2460	CA12	3'	CCTGGGTGACAGAGCGAGA 8688		
			TCTTGCTCTGTCACCCAGG		
			AGAGCGAGACAGTGGGTCC		
GAM2460	CARKL	3'	TCCAGCCTGGGTGACAGAGCAA 26109		
	GA		TCTTGCTCTGTCACCCAGGCTGGA		
			AGAACGAGACAGTGGGTCCGACCT		
GAM2460	CASP6	3'	TCCAGCCTGGGCAACGAGTGA 8735	TG T CA	
			T CTC GT CCCAGGCTGGA		
			A GAG CA GGGTCCGACCT		
			GT _ AC		
GAM2460	CASP8	3'	TTGGGTGACAGAGCAAGA 8771		
			TCTTGCTCTGTCACCCAG		
			AGAACGAGACAGTGGGTT		
GAM2460	CASP8	3'	TTGGGTGACAGAGCAAGA 54088		
			TCTTGCTCTGTCACCCAG		
			AGAACGAGACAGTGGGTT		
GAM2460	CBFA2T2	3'	AGCCTGGGCAACAGAGCAA 18700	CA	
			TTGCTCTGT CCCAGGCT		
			AACGAGACA GGGTCCGA		
			AC		
GAM2460	CD28	3'	TCCAGCCTGGGCGACAGAGTGA 21558	TG A	
	GA		TCT CTCTGTC CCCAGGCTGGA		
			AGA GAGACAG GGGTCCGACCT		
			GT C		
GAM2460	CD68	3'	TCCAGCCTGGGCGACAGAGCCA 60508	T A	
	GA		TCT GCTCTGTC CCCAGGCTGGA		

			AGA CGAGACAG GGGTCCGACCT	
			C C	
GAM2460	CEACAM5	3'	TCCAGTCTGGCAACAGAGCAAG 16425	CAC
	A		TCTTGCTCTGT CCAGGCTGGA	
			AGAACGAGACA GGTCTGACCT	
			AC_	
GAM2460	CENPB	3'	TCCAGCCTAGGCCCCCTGCAAG 70119	TCTGTCA C
	G		TCTTGC CC AGGCTGGA	
			GGAACG GG TCCGACCT	
			TCCCCC_ A	
GAM2460	CHST6	3'	CAGTGAGTGGCAGAGCAAGA 41497	C AG
			TCTTGCTCTGTAC C GCTG	
			AGAACGAGACGGTG G TGAC	
			A _	
GAM2460	COPA	3'	TCCAGCCTGGGTGACAGAGCAA 16480	
	GA		TCTTGCTCTGTACCCAGGCTGGA	
			AGAACGAGACAGTGGGTCCGACCT	
GAM2460	CPM	3'	TCCAGCTTGGGCAACAGAGTAA 60411	CA
	GA		TCTTGCTCTGT CCCAGGCTGGA	
			AGAATGAGACA GGGTTCGACCT	
			AC	
GAM2460	CPT2	3'	CCTGGGCGACAGAGCGAGA 5424	A
			TCTTGCTCTGTC CCCAGG	
			AGAGCGAGACAG GGGTCC	
			C	
GAM2460	CTSS	3'	TCCAGCCTGGATGACAGAGTGG 15821	TG C
			T CTCTGTCA CCAGGCTGGA	
			G GAGACAGT GGTCCGACCT	
			GT A	
GAM2460	CUBN	3'	TCCAGCCTGGGCGAGACGGCAA 8425	CTG A
	GA		TCTTGCT TC CCCAGGCTGGA	
			AGAACGG AG GGTCCGACCT	
			CAG C	
GAM2460	CYB561	3'	TCCAGCCTGAATAACAGTGGC 10352	C CACC_
	A		TGCT TGT CAGGCTGGA	
			ACGG GCA GTCCGACCT	
			T CAATAA	
GAM2460	CYP1A2	3'	CCTGAGTGACAGAGCAAGA 69657	C
			TCTTGCTCTGTAC CAGG	

AGAACGAGACAGTG GTCC

A

GAM2460 CYP4F3 3' TCCAGCCTGGGTGAAAGAGCTA 8015 T G
GA TCT GCTCT TCACCCAGGCTGGA

||||| ||||| |||||

AGA CGAGA AGTGGGTCCGACCT

T A

GAM2460 DBT 3' TCCAGCCTGGGCGACAGAGCAA 10379 A
GA TCTTGCTCTGTC CCCAGGCTGGA

||||| ||||| |||||

AGAACGAGACAG GGGTCCGACCT

C

GAM2460 DBT 3' TCCAGCCTGGGTGGCAGAGCAA 10381
TTGCTCTGTCACCCAGGCTGGA
||||| ||||| |||||
AACGAGACGGTGGGTCCGACCT

GAM2460 DCLRE1C 3' TCCAGCCTGGGCAACAAGAGCA 42823 _ CA
A TTGCTCT GT CCCAGGCTGGA

||||| || |||||

AACGAGA CA GGGTCCGACCT

A AC

GAM2460 DCLRE1C 3' TCTGGGTGACAGAGCAAGA 42825
TCTTGCTCTGTCACCCAGG
||||| ||||| |||||
AGAACGAGACAGTGGGTCT

GAM2460 DDOST 3' TCCAGCCTGGGCAACAGTGTTA 19067 _ T CA
AG CTTG C CTGT CCCAGGCTGGA

|||| | |||| |||||

GAAT G GACA GGGTCCGACCT

T T AC

GAM2460 DFFA 3' TCCAGCCTGGGCAACAGAGCGA 16598 CA
GA TCTTGCTCTGT CCCAGGCTGGA

||||| ||||| |||||

AGAGCGAGACA GGGTCCGACCT

AC

GAM2460 DGKI 5' TCCAGCCTGGGCGACAAAGCAA 17529 C A
GA TCTTGCT TGTC CCCAGGCTGGA

||||| |||| |||||

AGAACGA ACAG GGGTCCGACCT

A C

GAM2460 DMC1 3' TCCAGCCTAGGTGACAGAGTGA 23947 TG C
GA TCT CTCTGTCACC AGGCTGGA

||| ||||| |||||

AGA GAGACAGTGG TCCGACCT

GT A

GAM2460 DSC1 3' TCCAGCCTGGGCAACAAGAGCG 44607 _ CA
A TTGCTCT GT CCCAGGCTGGA

||||| || |||||

			AGCGAGA CA GGGTCCGACCT	
			A AC	
GAM2460	DSC1	3'	TCCAGCCTGGGCAACAAGAGCG 18242	_ CA
	A		TTGCTCT GT CCCAGGCTGGA	
			AGCGAGA CA GGGTCCGACCT	
			A AC	
GAM2460	DVL3	3'	TCCAGCCTGGGTGACAGAGTGA 16651	TG
	GA		TCT CTCTGTCACCCAGGCTGGA	
			AGA GAGACAGTGGGTCCGACCT	
			GT	
GAM2460	EGFL4	3'	TCCAACCTGGGTGACAGAGCGA 62475	C
	GA		TCTTGCTCTGTCACCCAGG TGGA	
			AGAGCGAGACAGTGGGTCC ACCT	
			A	
GAM2460	EGFL5	3'	TCCAGCCTGGGCGACAGAGCAA 87921	A
	GA		TCTTGCTCTGTC CCCAGGCTGGA	
			AGAACGAGACAG GGGTCCGACCT	
			C	
GAM2460	ENPP3	3'	TCCAGAGCCTGGGTGACAGAGC 73331	—
	AAGA		TCTTGCTCTGTCACCCAGGCT GGA	
			AGAACGAGACAGTGGGTCCGA CCT	
			GA	
GAM2460	F2R	3'	TCCAGCCTGGGCAACAGAGCAA 10573	CA
	GA		TCTTGCTCTGT CCCAGGCTGGA	
			AGAACGAGACA GGGTCCGACCT	
			AC	
GAM2460	F2RL3	3'	CCAGCCTGGGCGAAAGAG 15507	G A
			CTCT TC CCCAGGCTGG	
			GAGA AG GGGTCCGACC	
			A C	
GAM2460	F2RL3	3'	TCCAGCCTGGGCAACAGAGCAA 15527	CA
	GA		TCTTGCTCTGT CCCAGGCTGGA	
			AGAACGAGACA GGGTCCGACCT	
			AC	
GAM2460	FANCC	3'	TCCAGCCTGGGCAACAGAGCGA 71049	CA
	GA		TCTTGCTCTGT CCCAGGCTGGA	
			AGAGCGAGACA GGGTCCGACCT	
			AC	
GAM2460	FCAR	3'	TCCAGCCTGGGTGACAGAACGA 56582	C
	GA		TCTTG TCTGTCACCCAGGCTGGA	

			AGAGC AGACAGTGGGTCCGACCT		
			A		
GAM2460	FCAR	3'	TCCAGCCTGGGTGACAGAACGA 56583	C	
	GA		TCTTG TCTGTCACCCAGGCTGGA		
			AGAGC AGACAGTGGGTCCGACCT		
			A		
GAM2460	FCMD	3'	CCTGGGCGATAGAGCAAGA 23034	A	
			TCTTGCTCTGTC CCCAGG		
			AGAACGAGATAG GGGTCC		
			C		
GAM2460	FGF2	3'	TCCAGCCTAGGCAACAGAGTGA 10622	TG	CA C
	GA		TCT CTCTGT CC AGGCTGGA		
			AGA GAGACA GG TCCGACCT		
			GT AC A		
GAM2460	FGFR1	3'	TCCAGCCTGGGTGACAGAGTGA 7023	TG	
	G		CT CTCTGTCACCCAGGCTGGA		
			GA GAGACAGTGGGTCCGACCT		
			GT		
GAM2460	FGFR2	3'	TCCAGCCTTGCGACAGAGCGA 43777	A	C
	GA		TCTTGCTCTGTC CC AGGCTGGA		
			AGAGCGAGACAG GG TCCGACCT		
			C T		
GAM2460	FLRT2	5'	TCCAGCCTAAGCAACAGAGCAA 26004		CACCC
	GA		TCTTGCTCTGT AGGCTGGA		
			AGAACGAGACA TCCGACCT		
			ACGAA		
GAM2460	FUT6	3'	TCCAACCTGGACGACAGAGCAA 5644	AC	C
	GA		TCTTGCTCTGTC CCAGG TGGA		
			AGAACGAGACAG GGTCC ACCT		
			CA A		
GAM2460	GALNT7	3'	TCCAACCTGGGTGACAGAGTGA 55090	TG	C
	GA		TCT CTCTGTCACCCAGG TGGA		
			AGA GAGACAGTGGGTCC ACCT		
			GT A		
GAM2460	GAMT	3'	CCTGGGCTACAGAGCAAGA 5672	CA	
			TCTTGCTCTGT CCCAGG		
			AGAACGAGACA GGGTCC		
			TC		
GAM2460	GAS7	3'	TCCAGCTTGGGTGACAGAGCAA 20859		
	GA		TCTTGCTCTGTCACCCAGGCTGGA		

AGAACGAGACAGTGGGTTCGACCT

GAM2460 GGCX 3' CCTGGGCAACAGAGCAAGA 7703 CA
TCTTGCTCTGT CCCAGG
||||||| |||||
AGAACGAGACA GGGTCC
AC

GAM2460 GP2 3' TCCAGCCTGGGCAACAGAGCAA 9483 CA
GA TCTTGCTCTGT CCCAGGCTGGA
||||||| |||||||
AGAACGAGACA GGGTCCGACCT
AC

GAM2460 GRAF 3' TCCAGCCTGGGTGACAGAGCCA 31248 T
GA TCT GCTCTGTCACCCAGGCTGGA
||| |||||||||||||
AGA CGAGACAGTGGGTCCGACCT
C

GAM2460 GRM3 3' TCCAGAATATGGAAACAGAGCA 7747 CAC GG__
A TTGCTCTGT CCA CTGGA
||||||| ||| |||||
AACGAGACA GGT GACCT
AA_ ATAA

GAM2460 GRM6 3' TCCAGCCTGGGTGACAGAGCGA 7772
GA TCTTGCTCTGTCACCCAGGCTGGA
|||||||||||||||
AGAGCGAGACAGTGGGTCCGACCT

GAM2460 GTF2F1 3' TCCAGCCTGGGTGACAGAATGA 10893 GC
TT TCTGTCACCCAGGCTGGA
|| |||||||||||||
AG AGACAGTGGGTCCGACCT
TA

GAM2460 GTF2F1 3' TCCAGCCTGGGTGACAGTGAGA 10894 TG CT
TCT CT GTCACCCAGGCTGGA
||| || |||||||||||||
AGA GA CAGTGGGTCCGACCT
GT __

GAM2460 HIP1 3' TCCAGCCTGAGTGACAGAGCGA 19264 C
GA TCTTGCTCTGTCAC CAGGCTGGA
||||||||| |||||||
AGAGCGAGACAGTG GTCCGACCT
A

GAM2460 HIP1 3' TCCAGCCTGGGCAACAAGAGCA 19266 _ CA
A TTGCTCT GT CCCAGGCTGGA
||||||| || |||||||||
AACGAGA CA GGGTCCGACCT
A AC

GAM2460 HLA-E 3' TCCAGCCTGGGTGACAGGGTGA 92677 TG
T CTCTGTCACCCAGGCTGGA
| |||||||||||||

			A GGGACAGTGGGTCCGACCT	
			GT	
GAM2460	HRH1	3'	TCCAGCCTGGGCAACAGAGCAA 7828	CA
	GA		TCTTGCTCTGT CCCAGGCTGGA	
			AGAACGAGACA GGGTCCGACCT	
			AC	
GAM2460	ICA1	3'	TCCAGCCTGGGCGACAGAAGT 18313	_ A
			GCT CTGTC CCCAGGCTGGA	
			TGA GACAG GGGTCCGACCT	
			A C	
GAM2460	IFIT4	3'	TCCAGCCTGGGCAACAGAGCAA 71497	CA
	GA		TCTTGCTCTGT CCCAGGCTGGA	
			AGAACGAGACA GGGTCCGACCT	
			AC	
GAM2460	IL10	3'	TCCAGCCTGGGTGACAGAGCAA 6929	
	GA		TCTTGCTCTGTCACCCAGGCTGGA	
			AGAACGAGACAGTGGGTCCGACCT	
GAM2460	IL13RA1	3'	TCTAGCCTGGGTGACAGAGCAA 9576	
	GA		TCTTGCTCTGTCACCCAGGCTGGA	
			AGAACGAGACAGTGGGTCCGATCT	
GAM2460	IL17R	3'	CCTGGATGACAGAGCGAGA 27552	C
			TCTTGCTCTGTCA CCAGG	
			AGAGCGAGACAGT GGTCC	
			A	
GAM2460	IL1R1	3'	TCTAGCCTGGCAACAGAGCAAG 7925	CAC
	A		TCTTGCTCTGT CCAGGCTGGA	
			AGAACGAGACA GGTCCGATCT	
			AC_	
GAM2460	IL2RA	3'	TCCAGCCTGGGCAACAGAGCAA 6453	CA
	GA		TCTTGCTCTGT CCCAGGCTGGA	
			AGAACGAGACA GGGTCCGACCT	
			AC	
GAM2460	IL6R	3'	TCCAGCCTGGGGTGACAGAGCA 6916	_
	AG		CTTGCTCTGTCACCC AGGCTGGA	
			GAACGAGACAGTGGG TCCGACCT	
			G	
GAM2460	IRAK1	3'	TCCAGCCTGGGTGACAGAGCAA 9618	
	GA		TCTTGCTCTGTCACCCAGGCTGGA	

AGAACGAGACAGTGGGTCCGACCT

GAM2460 IRAK4	3'	TCCAGCCTGGGTGACAGAGTGA 61847	TG
GA		TCT CTCTGTCACCCAGGCTGGA	
		AGA GAGACAGTGGGTCCGACCT	
		GT	
GAM2460 ITGAL	3'	TCCAGCCTGGGCAACACAGCGA 11050	C CA
GA		TCTTGCT TGT CCCAGGCTGGA	
		AGAGCGA ACA GGGTCCGACCT	
		C AC	
GAM2460 KAI1	3'	TCCAGCCTGGGGGACAGAAAGA 11129	GC A
		TCTT TCTGTC CCCAGGCTGGA	
		AGAA AGACAG GGGTCCGACCT	
		— G	
GAM2460 KCNA7	3'	TCCAGCCTGGGCAACAGAGGGA 49905	G CA
G		CTT CTCTGT CCCAGGCTGGA	
		GAG GAGACA GGGTCCGACCT	
		G AC	
GAM2460 KCNA7	3'	TCCAGCCTGGGCAGCAGAGCAA 49907	CA
		TTGCTCTGT CCCAGGCTGGA	
		AACGAGACG GGGTCCGACCT	
		AC	
GAM2460 KCNJ5	3'	TCCAGCCTGGGCGACAGAGCGA 7978	A
GA		TCTTGCTCTGTC CCCAGGCTGGA	
		AGAGCGAGACAG GGGTCCGACCT	
		C	
GAM2460 KCNK3	3'	TCCAGCCTGGGTGACAGGGCAA 11178	
GA		TCTTGCTCTGTCACCCAGGCTGGA	
		AGAACGGGACAGTGGGTCCGACCT	
GAM2460 KIF1B	3'	TCCAGCCTGGGTGACAGAGCAA 31271	
GA		TCTTGCTCTGTCACCCAGGCTGGA	
		AGAACGAGACAGTGGGTCCGACCT	
GAM2460 KIF3B	3'	TCCAGCCTGGGTGACAGAGTGA 17810	TG
GA		TCT CTCTGTCACCCAGGCTGGA	
		AGA GAGACAGTGGGTCCGACCT	
		GT	
GAM2460 KLRG1	3'	TCCAGCCTGGGAGATAGAGCAA 20557	A
GA		TCTTGCTCTGTC CCCAGGCTGGA	

			AGAACGAGATAG GGGTCCGACCT	
			A	
GAM2460	KNSL1	3'	TCCAGCCTGGGCAACAGAGCAA 16949	CA
	GA		TCTTGCTCTGT CCCAGGCTGGA	
			AGAACGAGACA GGGTCCGACCT	
			AC	
GAM2460	LAMC2	3'	TCCAGCCTGGGGAACAGAGCAA 19909	CA
	GA		TCTTGCTCTGT CCCAGGCTGGA	
			AGAACGAGACA GGGTCCGACCT	
			AG	
GAM2460	LDLR	3'	CCTGGGCGACAGAGCGAGA 6733	A
			TCTTGCTCTGTC CCCAGG	
			AGAGCGAGACAG GGGTCC	
			C	
GAM2460	LDLR	3'	TCCAGCCTGGGCAACAGATGAA 6744	GC CA
	GA		TCTT TCTGT CCCAGGCTGGA	
			AGAA AGACA GGGTCCGACCT	
			GT AC	
GAM2460	LDLR	3'	TCCAGCCTGGGCAACATAGTAA 6745	C CA
	GA		TCTTGCT TGT CCCAGGCTGGA	
			AGAATGA ACA GGGTCCGACCT	
			T AC	
GAM2460	LPIN1	3'	TCCAGCCTGGGTGACAGAGTAA 67992	
	GA		TCTTGCTCTGTCACCCAGGCTGGA	
			AGAATGAGACAGTGGGTCCGACCT	
GAM2460	LRRC2	3'	TCCAGCCTGGGTGACAGAGCCA 44760	T
	GA		TCT GCTCTGTCACCCAGGCTGGA	
			AGA CGAGACAGTGGGTCCGACCT	
			C	
GAM2460	LRRC2	3'	TCCAGCCTGGGTGACAGAGTGA 44761	TG
	GA		TCT CTCTGTCACCCAGGCTGGA	
			AGA GAGACAGTGGGTCCGACCT	
			GT	
GAM2460	LRRC2	3'	TCCAGCCTGGGCAACAGAGTGA 44759	TG CA
	GA		TCT CTCTGT CCCAGGCTGGA	
			AGA GAGACA GGGTCCGACCT	
			GT AC	
GAM2460	LUZP1	3'	TCCAGCCTGGGCAACAAGAGTG 54405	TG _ CA
	A		T CTCT GT CCCAGGCTGGA	

			A GAGA CA GGGTCCGACCT	
			GT A AC	
GAM2460 LY94	3'	CCTGGGCGACAGAGCGAGA	17897	A
		TCTTGCTCTGTC CCCAGG		
		AGAGCGAGACAG GGGTCC		
		C		
GAM2460 MAFF	3'	TCCAGCCTGGGCAACATAGCAA	25584	C CA
		TTGCT TGT CCCAGGCTGGA		
		AACGA ACA GGGTCCGACCT		
		T AC		
GAM2460 MDM4	3'	TCCAGCCTGGGTGACAGCGCGA	11514	T
GA		TCTTGC CTGTCACCCAGGCTGGA		
		AGAGCG GACAGTGGGTCCGACCT		
		C		
GAM2460 MEN1	5'	TCCAGCCTGGGCGAAAGAGAAA	5960	G G A
GA		TCTT CTCT TC CCCAGGCTGGA		
		AGAA GAGA AG GGGTCCGACCT		
		A A C		
GAM2460 MOG	3'	CCGGAGTGACAGAGTAAGA	11671	_ A
		TCTTGCTCTGTAC CC GG		
		AGAATGAGACAGTG GG CC		
		A _		
GAM2460 MSH3	3'	TCCAGCTTGGGCAACAGAGCAA	11693	CA
GA		TCTTGCTCTGT CCCAGGCTGGA		
		AGAACGAGACA GGGTTCGACCT		
		AC		
GAM2460 MTMR8	3'	TCCAGCCTGAGCAACAGAGCGA	31917	CACC
GA		TCTTGCTCTGT CAGGCTGGA		
		AGAGCGAGACA GTCCGACCT		
		ACGA		
GAM2460 MTMR8	3'	TCCAGCCTGGGCGAAAGGGCAA	31918	G A
GA		TCTTGCTCT TC CCCAGGCTGGA		
		AGAACGGGA AG GGGTCCGACCT		
		A C		
GAM2460 MYH11	3'	TCCAGCCTGGGCAACAGAG	43447	CA
		CTCTGT CCCAGGCTGGA		
		GAGACA GGGTCCGACCT		
		AC		
GAM2460 MYH11	3'	TCCAGCCTGGGCAACAGAG	11744	CA
		CTCTGT CCCAGGCTGGA		

			GAGACA GGGTCCGACCT		
			AC		
GAM2460 MYH11	3'	TCCAGCCTGGGCAACGTAGTAA 11748		C	CA
		TTGCT TGT CCCAGGCTGGA			
		AATGA GCA GGGTCCGACCT			
		T AC			
GAM2460 MYH11	3'	TCCAGCCTGGGCAACGTAGTAA 11749		C	CA
		TTGCT TGT CCCAGGCTGGA			
		AATGA GCA GGGTCCGACCT			
		T AC			
GAM2460 MYO1B	3'	TCCAGCCCGGGTGACAATACAA 25247		CTC	A
GA		TCTTG TGTCACCC GGCTGGA			
		AGAAC ACAGTGGG CCGACCT			
		ATA C			
GAM2460 MYO1C	3'	TCCAGCCTGGGCAACAGAGCGA 61870		CA	
GA		TCTTGCTCTGT CCCAGGCTGGA			
		AGAGCGAGACA GGGTCCGACCT			
		AC			
GAM2460 NCOA6	5'	TCCAGCCCAGGCAACAGAGCGT 26849		T	CA CA
GA		TC TGCTCTGT CC GGCTGGA			
		AG GCGAGACA GG CCGACCT			
		T AC AC			
GAM2460 NFKBIL2	3'	TCCAGCCTGGGCGACAGACCGA 26455		C	A
GA		TCTTG TCTGTC CCCAGGCTGGA			
		AGAGC AGACAG GGGTCCGACCT			
		C C			
GAM2460 NKX3A	3'	TCCAGCCTGGGCAACGAGCAAG 21617		T	CA
A		TCTTGCTC GT CCCAGGCTGGA			
		AGAACGAG CA GGGTCCGACCT			
		_ AC			
GAM2460 NPHP1	3'	TCCAGCCTAGGCAACAAGAGTG 63150		TG _	CA C
A		T CTCT GT CC AGGCTGGA			
		A GAGA CA GG TCCGACCT			
		GT A AC A			
GAM2460 NPHS1	3'	TCCAGCCTGGGCGACAGAGCGA 17374		A	
GA		TCTTGCTCTGTC CCCAGGCTGGA			
		AGAGCGAGACAG GGGTCCGACCT			
		C			
GAM2460 NT5C2	3'	TCCAGCCTGGGCAACAAGAACA 25269		C _	CA
A		TTG TCT GT CCCAGGCTGGA			

			AAC AGA CA GGGTCCGACCT		
			A A AC		
GAM2460	NUP62	3'	TCCAGCCTAGGCAACAGAG 25652	CA C	
			CTCTGT CC AGGCTGGA		
			GAGACA GG TCCGACCT		
			AC A		
GAM2460	OGG1	5'	TCCAGCCTAGGCGACAGAGTGA 34160	TG A C	
	GA		TCT CTCTGTC CC AGGCTGGA		
			AGA GAGACAG GG TCCGACCT		
			GT C A		
GAM2460	OPA3	3'	CTAGCCTGGGCAACAGAGCAAG 47843	CA	
	A		TCTTGCTCTGT CCCAGGCTGG		
			AGAACGAGACA GGGTCCGATC		
			AC		
GAM2460	OPA3	3'	TCCAGCCCGGGTGACAGAGCAA 47848	A	
	GA		TCTTGCTCTGTCACCC GGCTGGA		
			AGAACGAGACAGTGGG CCGACCT		
			C		
GAM2460	OPTN	3'	TCCAGCCTGGGTGACAGAGGGA 42053	G	
	GA		TCTT CTCTGTCACCCAGGCTGGA		
			AGAG GAGACAGTGGGTCCGACCT		
			G		
GAM2460	OTX1	5'	TCACCTAAACAACCGAGCAAGA 28058	T CACCC C	
			TCTTGCTC GT AGG TGG		
			AGAACGAG CA TCC ACT		
			C ACAA _		
GAM2460	P53AIP1	3'	TCCAGCCTGGGCGACAGAGAGA 42340	TG A	
	GA		TCT CTCTGTC CCCAGGCTGGA		
			AGA GAGACAG GGGTCCGACCT		
			GA C		
GAM2460	PA2G4	3'	TCCAGCCTGGGTGACAGAATGA 71831	GC	
	GA		TCTT TCTGTCACCCAGGCTGGA		
			AGAG AGACAGTGGGTCCGACCT		
			TA		
GAM2460	PAICS	3'	TCCAACCTGGGCAGCAGAGCAA 22268	CA C	
	GA		TCTTGCTCTGT CCCAGG TGGA		
			AGAACGAGACG GGGTCC ACCT		
			AC A		
GAM2460	PCDH11X	3'	TCCAGCCTGGGTGACAGAGCAA 28017		
	GA		TCTTGCTCTGTCACCCAGGCTGGA		

AGAACGAGACAGTGGGTCCGACCT

GAM2460 PCDH11Y 3' TCCAGCCTGGGTGACAGAGCAA 53169
GA TCTTGCTCTGTCACCCAGGCTGGA
|||||
AGAACGAGACAGTGGGTCCGACCT

GAM2460 PCDHB9 3' TCCAGCCTGGGCAATAAGAGCA 39452 GTCA_
A TTGCTCT CCCAGGCTGGA
||||| |||||
AACGAGA GGGTCCGACCT
ATAAC

GAM2460 PDE4C 3' CCTGGGCAACATAGCAAGA 8101 C CA
TCTTGCT TGT CCCAGG
||||| ||| |||||
AGAACGA ACA GGGTCC
T AC

GAM2460 PDE4C 3' TCCAGCCTGGGCAACACAGCAA 8107 C CA
GA TCTTGCT TGT CCCAGGCTGGA
||||| ||| |||||
AGAACGA ACA GGGTCCGACCT
C AC

GAM2460 PDE4C 3' TCCAGCCTGGGGCTGACAGAGC 8108 ____
AAGA TCTTGCTCTGTCA CCCAGGCTGGA
||||| |||||
AGAACGAGACAGT GGGTCCGACCT
CG

GAM2460 PHKB 3' CCTGGGTGACAGAGCGAGA 6097
TCTTGCTCTGTCACCCAGG
|||||
AGAGCGAGACAGTGGGTCC

GAM2460 PIK3CG 3' TCCAGCCTGGATAACAGAGCGA 12125 CAC
GA TCTTGCTCTGT CCAGGCTGGA
||||| |||||
AGAGCGAGACA GGTCCGACCT
ATA

GAM2460 PLA2G2D 3' TCCAGCCTGGGCAACAGAGTGA 25723 TG CA
T CTCTGT CCCAGGCTGGA
| ||||| |||||
A GAGACA GGGTCCGACCT
GT AC

GAM2460 POLH 3' TCCAGCCTGGGCAACAGAGCGA 22484 CA
GA TCTTGCTCTGT CCCAGGCTGGA
||||| |||||
AGAGCGAGACA GGGTCCGACCT
AC

GAM2460 POLH 3' TCCAGCCTGGGCAACAGAGCGA 22485 CA
GA TCTTGCTCTGT CCCAGGCTGGA
||||| |||||

			AGAGCGAGACA GGGTCCGACCT	
			AC	
GAM2460	POLK	3'	CCAGCCTGAAGAGCGAGA 33100	GTCACC
			TCTTGCTCT CAGGCTGG	
			AGAGCGAGA GTCCGACC	
			A_____	
GAM2460	PPP1R12B	3'	TCCAGCCTGGGTGACAGAGCAA 50366	
	GA		TCTTGCTCTGTCACCCAGGCTGGA	
			AGAACGAGACAGTGGGTCCGACCT	
GAM2460	PRKY	3'	TCCAGCCTGGGTGACAGAGTGA 12384	TG
	GA		TCT CTCTGTCACCCAGGCTGGA	
			AGA GAGACAGTGGGTCCGACCT	
			GT	
GAM2460	PRKY	3'	TCCAGGCTGGACGACAGAGCAA 12385	AC G
	GA		TCTTGCTCTGTC CCAG CTGGA	
			AGAACGAGACAG GGTC GACCT	
			CA G	
GAM2460	PSMB2	3'	TCCAGCCTGGCTGACAGAGCAA 12479	C
	GA		TCTTGCTCTGTCA CCAGGCTGGA	
			AGAACGAGACAGT GGTCCGACCT	
			C	
GAM2460	PSMB9	3'	TCCAGCCTGGGCGACAAAGCGA 12510	C A
	GA		TCTTGCT TGTC CCCAGGCTGGA	
			AGAGCGA ACAG GGGTCCGACCT	
			A C	
GAM2460	PSMD5	3'	CCTGGGCAACACAGCAAGA 18557	C CA
			TCTTGCT TGT CCCAGG	
			AGAACGA ACA GGGTCC	
			C AC	
GAM2460	PTGIS	3'	TCCAGCCTGGGCGACAGAGCAA 8229	A
	GA		TCTTGCTCTGTC CCCAGGCTGGA	
			AGAACGAGACAG GGGTCCGACCT	
			C	
GAM2460	RABIF	3'	TCCAGCCTGGGCAACAGAGTGA 12730	TG CA
	GA		TCT CTCTGT CCCAGGCTGGA	
			AGA GAGACA GGGTCCGACCT	
			GT AC	
GAM2460	RAD1	3'	TCCAGCCTAGGCAATAAGAGCA 12648	GTCA_ C
	A		TTGCTCT CC AGGCTGGA	

			AACGAGA GG TCCGACCT		
			ATAAC A		
GAM2460	RBBP5	3'	TCCAGCCTAGGTGACAGAATGA 18579	GC	C
	GA		TCTT TCTGTCACC AGGCTGGA		
			AGAG AGACAGTGG TCCGACCT		
			TA A		
GAM2460	RBL1	3'	TCCAGCCTGGGCAACAAGAGTA 12790	_ CA	
	A		TTGCTCT GT CCCAGGCTGGA		
			AATGAGA CA GGGTCCGACCT		
			A AC		
GAM2460	RBM3	3'	TCCAGCCTGGGCAACAGCGAGA 71013	CT CA	
			TCTTGCT GT CCCAGGCTGGA		
			AGAGCGA CA GGGTCCGACCT		
			_ AC		
GAM2460	RFC2	3'	TCCAGCCTGGGCGACAGAG 12847	A	
			CTCTGTC CCCAGGCTGGA		
			GAGACAG GGGTCCGACCT		
			C		
GAM2460	ROCK2	3'	TCCAGCCTGGGCAGCTGAACAA 66625	C T CA	
	GA		TCTTG TC GT CCCAGGCTGGA		
			AGAAC AG CG GGGTCCGACCT		
			A T AC		
GAM2460	SCAP2	3'	TCCAGCCTGGGCGACAGAGTGA 15427	TG A	
	GA		TCT CTCTGTC CCCAGGCTGGA		
			AGA GAGACAG GGGTCCGACCT		
			GT C		
GAM2460	SFRS2IP	5'	TCCAGCCTGGGTGACAGAGTGA 17547	TG	
	GA		TCT CTCTGTCACCCAGGCTGGA		
			AGA GAGACAGTGGGTCCGACCT		
			GT		
GAM2460	SIGLEC11	3'	TCCAGCCTGGGCAACAGAGTGA 54657	TG CA	
	GA		TCT CTCTGT CCCAGGCTGGA		
			AGA GAGACA GGGTCCGACCT		
			GT AC		
GAM2460	SIGLEC6	3'	CCTGGGCAACAGAGCGAGA 60606	CA	
			TCTTGCTCTGT CCCAGG		
			AGAGCGAGACA GGGTCC		
			AC		
GAM2460	SIM2	3'	TCCAGCCTGGGTAACAGAGTGA 18624	TG C	
	GA		TCT CTCTGT ACCCAGGCTGGA		

			AGA GAGACA TGGGTCCGACCT		
			GT A		
GAM2460	SLC14A1	3'	TCCAACCTGGGTGACAAGAGTG 32415	TG _	C
	A		T CTCT GTCACCCAGG TGGA		
			A GAGA CAGTGGGTCC ACCT		
			GT A A		
GAM2460	SLC17A5	3'	TCCAGCCTGGGCGATGGAGCGA 25835		A
	GA		TCTTGCTCTGTC CCCAGGCTGGA		
			AGAGCGAGGTAG GGGTCCGACCT		
			C		
GAM2460	SLC26A4	3'	TCCAGCCTGGGCGACAGAGCAA 6530		A
	GA		TCTTGCTCTGTC CCCAGGCTGGA		
			AGAACGAGACAG GGGTCCGACCT		
			C		
GAM2460	SLC28A2	3'	TCCAGCCTGGGTGACAGAGCGA 16154		
	GA		TCTTGCTCTGTCACCCAGGCTGGA		
			AGAGCGAGACAGTGGGTCCGACCT		
GAM2460	SLC2A6	3'	TCCAGCCTGGGCAACGAGAGT 34576	_ CA	
			GCTCT GT CCCAGGCTGGA		
			TGAGA CA GGGTCCGACCT		
			G AC		
GAM2460	SLC31A1	3'	TCCAGCCTGGGTGACAAGAGTG 10279	TG _	
	A		T CTCT GTCACCCAGGCTGGA		
			A GAGA CAGTGGGTCCGACCT		
			GT A		
GAM2460	SMG1	3'	TCCAGCCTGGGCAACAGAGCTA 31352	T CA	
	GA		TCT GCTCTGT CCCAGGCTGGA		
			AGA CGAGACA GGGTCCGACCT		
			T AC		
GAM2460	SRGAP1	5'	TCCAGCCTGGGCAACAGAGCGA 72721		CA
	GA		TCTTGCTCTGT CCCAGGCTGGA		
			AGAGCGAGACA GGGTCCGACCT		
			AC		
GAM2460	STAC	3'	CCTGGGTGACAGAGCAGGA 13425		
			TCTTGCTCTGTCACCCAGG		
			AGGACGAGACAGTGGGTCC		
GAM2460	STK38	5'	TCCAGCCTGGGCAACAAGAGCG 24401	_ CA	
	A		TTGCTCT GT CCCAGGCTGGA		

			AGCGAGA CA GGGTCCGACCT		
			A AC		
GAM2460	SULT1A3	3'	CAGCCTGGATGACAAGCAAGA 13482	C	C
			TCTTGCT TGTCA CCAGGCTG		
			AGAACGA ACAGT GGTCCGAC		
			_ A		
GAM2460	SULT2A1	3'	TCCAGCCTGGGTGACAGAGCGA 72232		
	GA		TCTTGCTCTGTCACCCAGGCTGGA		
			AGAGCGAGACAGTGGGTCCGACCT		
GAM2460	TADA2L	3'	TCCAGCCTGGGCAACAAAGTGA 56765	TG	C CA
	GA		TCT CT TGT CCCAGGCTGGA		
			AGA GA ACA GGTCCGACCT		
			GT A AC		
GAM2460	TBX1	3'	TCCAGCCTGGGTGACAGAGTGA 55541	TG	
	GA		TCT CTCTGTCACCCAGGCTGGA		
			AGA GAGACAGTGGGTCCGACCT		
			GT		
GAM2460	TBX6	3'	TCCAGCCTAGGCAACACGAGCA 55818	_	CA C
	A		TTGCTC TGT CC AGGCTGGA		
			AACGAG ACA GG TCCGACCT		
			C AC A		
GAM2460	TCTA	3'	TCCAGCCTGGGCAACAGAGCAA 42503		CA
	GA		TCTTGCTCTGT CCCAGGCTGGA		
			AGAACGAGACA GGTCCGACCT		
			AC		
GAM2460	TEM7	3'	TCCAGCCTGGGTGACAGAGCGA 40269		
	GA		TCTTGCTCTGTCACCCAGGCTGGA		
			AGAGCGAGACAGTGGGTCCGACCT		
GAM2460	TEM7	3'	TCCAGCCTGGGTGACAGAGTGA 40270	TG	
	GA		TCT CTCTGTCACCCAGGCTGGA		
			AGA GAGACAGTGGGTCCGACCT		
			GT		
GAM2460	TMPRSS4	3'	CCAAAGTCAGACACAGAGCAAG 39587	CACCCA	_
	A		TCTTGCTCTGT GGCT GG		
			AGAACGAGACA CTGA CC		
			CAGA_ AA		
GAM2460	TNFRSF1B	3'	TCCAGCCTGAGCAACAGAGTGA 8402	TG	CACC
	GA		TCT CTCTGT CAGGCTGGA		

			AGA GAGACA GTCCGACCT	
			GT ACGA	
GAM2460	TNFRSF1B	3'	TCCAGCCTGGGCGACAGAGCGA 8403	A
	GA		TCTTGCTCTGTC CCCAGGCTGGA	
			AGAGCGAGACAG GGGTCCGACCT	
			C	
GAM2460	TNFSF10	3'	TCCAGCCTGGGCGACAGAGCGAG 15094	AC
	A		TCTTGCTCTGTC CCAGGCTGGA	
			AGAGCGAGACAG GGTCCGACCT	
			C_	
GAM2460	TNFSF15	3'	TCCAGCCTGGGTAACAAGAGCA 18871	_ C
	A		TTGCTCT GT ACCCAGGCTGGA	
			AACGAGA CA TGGGTCCGACCT	
			A A	
GAM2460	TPMT	3'	CCAGCCTGGGCAACAGAGCAAG 6307	CA
	A		TCTTGCTCTGT CCCAGGCTGG	
			AGAACGAGACA GGGTCCGACC	
			AC	
GAM2460	TRIM14	3'	TCCAGCCTGGGGACAGAGCAAG 29517	A
	A		TCTTGCTCTGTC CCCAGGCTGGA	
			AGAACGAGACAG GGGTCCGACCT	
			-	
GAM2460	TSNAX	3'	TCCAGCCTGGGTAACAGAGCAA 21160	C
	GA		TCTTGCTCTGT ACCCAGGCTGGA	
			AGAACGAGACA TGGGTCCGACCT	
			A	
GAM2460	UBE2B	3'	TCCAGCCTGGGTGACAGAGCAA 13939	
			TTGCTCTGTCACCCAGGCTGGA	
			AACGAGACAGTGGGTCCGACCT	
GAM2460	UBE2G2	3'	TCCAGCCTGGGCAACAGAGCGA 65495	CA
	GA		TCTTGCTCTGT CCCAGGCTGGA	
			AGAGCGAGACA GGGTCCGACCT	
			AC	
GAM2460	UBE2G2	3'	TCCAGCCTGGGCAACAGAGTGA 65496	TG CA
	GA		TCT CTCTGT CCCAGGCTGGA	
			AGA GAGACA GGGTCCGACCT	
			GT AC	
GAM2460	UC28	3'	TCCAGCCTGGGCAACAGGAGTA 41591	_ CA
	A		TTGCTC TGT CCCAGGCTGGA	

			AATGAG ACA GGGTCCGACCT	
			G AC	
GAM2460	USP14	3'	TCCAGCCTGGGTGACAGAGAGA 18940	TG
			TCT CTCTGTCACCCAGGCTGGA	
			AGA GAGACAGTGGGTCCGACCT	
			—	
GAM2460	VHL	3'	CCAGCCTGGGAAACAAGAG 6841	_ CA
			CTCT GT CCCAGGCTGG	
			GAGA CA GGGTCCGACC	
			A AA	
GAM2460	VHL	3'	TCCAGCCTGGGGGACAGAGCAA 6876	A
	GA		TCTTGCTCTGTC CCCAGGCTGGA	
			AGAACGAGACAG GGGTCCGACCT	
			G	
GAM2460	VHL	3'	TCCAGCCTGTGTGACAGAGCAA 6878	C
			TTGCTCTGTCAC CAGGCTGGA	
			AACGAGACAGTG GTCCGACCT	
			T	
GAM2460	VPS41	3'	TCCAGCCTGGGCAACAAGAGCA 27698	_ CA
	A		TTGCTCT GT CCCAGGCTGGA	
			AACGAGA CA GGGTCCGACCT	
			A AC	
GAM2460	WIG1	3'	TCCAGCCTGGGTGACAGAGCGA 96105	
	GA		TCTTGCTCTGTCACCCAGGCTGGA	
			AGAGCGAGACAGTGGGTCCGACCT	
GAM2460	XT3	3'	TCCAGTCTGGGCGACAGAGCAA 39918	A
	GA		TCTTGCTCTGTC CCCAGGCTGGA	
			AGAACGAGACAG GGGTCTGACCT	
			C	
GAM2460	ZNF264	3'	TCCAGCCTGGGCAACAGAGCGA 14232	CA
	GA		TCTTGCTCTGT CCCAGGCTGGA	
			AGAGCGAGACA GGGTCCGACCT	
			AC	
GAM2460	ZNF264	3'	TCCAGCCTGGGCAGCAGAGCGA 14233	CA
	GA		TCTTGCTCTGT CCCAGGCTGGA	
			AGAGCGAGACG GGGTCCGACCT	
			AC	
GAM2460	ZNF36	3'	TCCAGCCTGGGTGACTAGCAA 95588	CT
			TTGCT GTCACCCAGGCTGGA	

			AACGA CAGTGGGTCCGACCT	
			T_	
GAM2460	ZNF74	3'	CAGCCTGGGTGACAAAGCAAGA 14258	C
			TCTTGCT TGTCACCCAGGCTG	
			AGAACGA ACAGTGGGTCCGAC	
			A	
GAM2460	ZNF91	3'	CCTGGGCGACAGAGCGAGA 14280	A
			TCTTGCTCTGTC CCCAGG	
			AGAGCGAGACAG GGGTCC	
			C	
GAM2460	ADAR3	5'	CCAGCCCAGTGGGAGCAAG 38632	GT CCA
			CTTGCTCT CAC GGCTGG	
			GAACGAGG GTG CCGACC	
			_ AC_	
GAM2460	AF020591	3'	TCCAGCCTGGGCAACAGAGCAA 27916	CA
			GA TCTTGCTCTGT CCCAGGCTGGA	
			AGAACGAGACA GGGTCCGACCT	
			AC	
GAM2460	ALTE	3'	TCCAGCCTGGGCGACAAGAGCG 61007	_ A
			AGA TCTTGCTCT GTC CCCAGGCTGGA	
			AGAGCGAGA CAG GGGTCCGACCT	
			A C	
GAM2460	AP1GBP1	3'	TCTGAGCGACAGAGCAAGA 24356	ACC
			TCTTGCTCTGTC CAGG	
			AGAACGAGACAG GTCT	
			CGA	
GAM2460	AP4S1	3'	TCCAATCTGGCAACAGAGCGAG 23965	CAC GC
			A TCTTGCTCTGT CCAG TGGA	
			AGAGCGAGACA GGTC ACCT	
			AC_ TA	
GAM2460	APOF	3'	TCCAGCCTGGGTGACAGAGCGA 9696	
			GA TCTTGCTCTGTCACCCAGGCTGGA	
			AGAGCGAGACAGTGGGTCCGACCT	
GAM2460	APXL2	3'	TCCAGCCTGGGCGACAGAGCAA 75686	A
			GA TCTTGCTCTGTC CCCAGGCTGGA	
			AGAACGAGACAG GGGTCCGACCT	
			C	
GAM2460	ARNTL2	3'	CCAGCCTGGGCGACAGAGCGAG 39843	A
			A TCTTGCTCTGTC CCCAGGCTGG	

			AGAGCGAGACAG GGGTCCGACC		
			C		
GAM2460	ASAH1	3'	CCTGGGCAACAGAGCGAGA 64315	CA	
			TCTTGCTCTGT CCCAGG		
			AGAGCGAGACA GGGTCC		
			AC		
GAM2460	ATP1B4	3'	TCCAGCCTGGGTGACAGAGTGA 24852	TG	
	GA		TCT CTCTGTCACCCAGGCTGGA		
			AGA GAGACAGTGGGTCCGACCT		
			GT		
GAM2460	BANP	3'	TCCAGACTGTGCGACAGAGCGA 66805	ACC G	
	GA		TCTTGCTCTGTC CAG CTGGA		
			AGAGCGAGACAG GTC GACCT		
			CGT A		
GAM2460	BIRC1	3'	TCCAGCCTGGGCAACAGAGCAA 16995	CA	
	GA		TCTTGCTCTGT CCCAGGCTGGA		
			AGAACGAGACA GGGTCCGACCT		
			AC		
GAM2460	BIVM	3'	TCCAGCCTGGGCAACAGGGCAA 35160	CA	
	GA		TCTTGCTCTGT CCCAGGCTGGA		
			AGAACGGGACA GGGTCCGACCT		
			AC		
GAM2460	BLOV1	3'	TCCAGCCTGGGCAACAAGAGCG 76799	_ CA	
	A		TTGCTCT GT CCCAGGCTGGA		
			AGCGAGA CA GGGTCCGACCT		
			A AC		
GAM2460	BLOV1	3'	TCCAGCCTGGGCGACAGAGCAA 76800	A	
	GA		TCTTGCTCTGTC CCCAGGCTGGA		
			AGAACGAGACAG GGGTCCGACCT		
			C		
GAM2460	BTN3A2	3'	TCCAGCCTGGGAGACAGAGCGA 23880	A	
	GA		TCTTGCTCTGTC CCCAGGCTGGA		
			AGAGCGAGACAG GGGTCCGACCT		
			A		
GAM2460	C12orf2	3'	TCCAGCCTGGGTAACAGAGTGA 83688	TG C	
	GA		TCT CTCTGT ACCCAGGCTGGA		
			AGA GAGACA TGGGTCCGACCT		
			GT A		
GAM2460	C13orf1	3'	TCCAGCCTAGGCAACAGAGTGA 40372	TG CA C	
	GA		TCT CTCTGT CC AGGCTGGA		

		AGA GAGACA GG TCCGACCT		
		GT AC A		
GAM2460	C1orf33	3' TCCAGCCTGGGCAACAGAGTAA 32988	CA	
		TTGCTCTGT CCCAGGCTGGA		
		AATGAGACA GGGTCCGACCT		
		AC		
GAM2460	C1orf34	3' CCTGGGCGACAGAGCGAGA 61304	A	
		TCTTGCTCTGTC CCCAGG		
		AGAGCGAGACAG GGGTCC		
		C		
GAM2460	C1QTNF2	3' TCCAGCCTGGGCAACAGAGTGA 49977	TG	CA
	GA	TCT CTCTGT CCCAGGCTGGA		
		AGA GAGACA GGGTCCGACCT		
		GT AC		
GAM2460	C20orf106	3' TCCAGCCCAGGTGACAGAGTGA 55914	TG	CA
	GA	TCT CTCTGTCACC GGCTGGA		
		AGA GAGACAGTGG CCGACCT		
		GT AC		
GAM2460	C20orf108	3' TCCAGCCTGGGCGACAGAGGGA 55883	G	A
	GA	TCTT CTCTGTC CCCAGGCTGGA		
		AGAG GAGACAG GGGTCCGACCT		
		G C		
GAM2460	C20orf12	3' TCCAGCCTGGGCAACAAGAGCA 36851	_	CA
	A	TTGCTCT GT CCCAGGCTGGA		
		AACGAGA CA GGGTCCGACCT		
		A AC		
GAM2460	C20orf142	3' TCCAGCCTGAGCGACAGAGTGA 75289	TG	ACC
	GA	TCT CTCTGTC CAGGCTGGA		
		AGA GAGACAG GTCCGACCT		
		GT CGA		
GAM2460	C20orf172	3' TCCAGCCTGAGCGACAGAGTGA 46768	TG	ACC
	GA	TCT CTCTGTC CAGGCTGGA		
		AGA GAGACAG GTCCGACCT		
		GT CGA		
GAM2460	C20orf177	3' TCCAGCCTGGGCAACAAGAGGG 62841	G	_ CA
	A	TT CTCT GT CCCAGGCTGGA		
		AG GAGA CA GGGTCCGACCT		
		G A AC		
GAM2460	C20orf183	3' TCCAGGCTGGGCGACAGAGCGA 48537	A	G
	GA	TCTTGCTCTGTC CCCAG CTGGA		

AGAGCGAGACAG GGGTC GACCT
 C G
 GAM2460 C20orf29 3' TCCAGCCTGGGCAACAGAGTGA 37712 TG CA
 GA TCT CTCTGT CCCAGGCTGGA
 ||| ||||| |||||
 AGA GAGACA GGGTCCGACCT
 GT AC
 GAM2460 C21orf108 3' TCCAGCCTAGGTGACAGAGCAA 90121 C
 GA TCTTGCTCTGTCACC AGGCTGGA
 |||||
 AGAACGAGACAGTGG TCCGACCT
 A
 GAM2460 C22orf19 3' TCTGGACAACAGAGCAAGA 14831 CAC
 TCTTGCTCTGT CCAGG
 |||||
 AGAACGAGACA GGTCT
 ACA
 GAM2460 C22orf20 3' TCCAGCCTGGGCAACATGAGTG 48200 TG _ CA
 A T CTC TGT CCCAGGCTGGA
 | ||| |||||
 A GAG ACA GGGTCCGACCT
 GT T AC
 GAM2460 C3IP1 3' TCCAGCCTAGATGATTGGAAAG 41580 GC T CCC
 A TCTT TC GTCA AGGCTGGA
 ||| || |||||
 AGAA GG TAGT TCCGACCT
 A_ T AGA
 GAM2460 C6orf29 3' TCCAACCTGGGTGACAGA 52460 C
 TCTGTCACCCAGG TGGA
 |||||
 AGACAGTGGGTCC ACCT
 A
 GAM2460 CAMKK2 5' TCCAGCCTGGGCAACACAGAGA 22630 TG CA__
 GA TCT CTCTGT CCCAGGCTGGA
 ||| ||||| |||||
 AGA GAGACA GGGTCCGACCT
 _ CAAC
 GAM2460 CAMKK2 5' TCCAGCGTGGGCGACAGAGCGA 22631 A G
 GA TCTTGCTCTGTC CCCA GCTGGA
 ||||| ||| |||||
 AGAGCGAGACAG GGGT CGACCT
 C G
 GAM2460 CBCIP2 3' TCCAGCCTGGGCGACAGAGCCA 52661 T A
 GA TCT GCTCTGTC CCCAGGCTGGA
 ||| ||||| |||||
 AGA CGAGACAG GGGTCCGACCT
 C C
 GAM2460 CCR6 3' TCCAGCCTGGGTGACAGAGCGA 49408
 GA TCTTGCTCTGTCACCCAGGCTGGA
 |||||

AGAGCGAGACAGTGGGTCCGACCT

GAM2460	CDT1	3'	TCCAGCCTGGGTGACAGAGCGA 78166		
	GA		TCTTGCTCTGTCACCCAGGCTGGA		
			AGAGCGAGACAGTGGGTCCGACCT		
GAM2460	CENTA2	3'	TCCAGCCTGGGTGACAGAGCGA 37868		
	GA		TCTTGCTCTGTCACCCAGGCTGGA		
			AGAGCGAGACAGTGGGTCCGACCT		
GAM2460	cerk	3'	TCCAGCCTGGGCAACAGAGGGA 43169	G	CA
	GA		TCTT CTCTGT CCCAGGCTGGA		
			AGAG GAGACA GGGTCCGACCT		
			G AC		
GAM2460	CG012	5'	TCCAGCCCAGGTGACAGAGGGA 84166	G	CA
	GA		TCTT CTCTGTCACC GGCTGGA		
			AGAG GAGACAGTGG CCGACCT		
			G AC		
GAM2460	CG012	3'	TCCAGCCTCGCCGACAAAGCGA 84167	C	ACCC
	GA		TCTTGCT TGTC AGGCTGGA		
			AGAGCGA ACAG TCCGACCT		
			A CCGC		
GAM2460	CG012	5'	TCCAGCCTGGGCAACAGAACGA 84168	C	CA
	GA		TCTTG TCTGT CCCAGGCTGGA		
			AGAGC AGACA GGGTCCGACCT		
			A AC		
GAM2460	CGI-203	3'	TCCAGCCTGGGTGACAGAGTGA 40277	TG	
	GA		TCT CTCTGTCACCCAGGCTGGA		
			AGA GAGACAGTGGGTCCGACCT		
			GT		
GAM2460	CNNM1	3'	CCTAGGCAACAGAGCGAGA 40117	CA	C
			TCTTGCTCTGT CC AGG		
			AGAGCGAGACA GG TCC		
			AC A		
GAM2460	COE2	3'	TCCAGCCTGGGTGACAGAGACA 64911	_	
	G		TTG CTCTGTCACCCAGGCTGGA		
			GAC GAGACAGTGGGTCCGACCT		
			A		
GAM2460	CPR2	3'	TCCAGCCTGGGCGACAGAGTGA 48839	TG	A
	GA		TCT CTCTGTC CCCAGGCTGGA		

			AGA GAGACAG GGGTCCGACCT		
			GT C		
GAM2460	CPR2	3'	TCCAGCCTGGGTAACAGAGCAA 48840	C	
	GA		TCTTGCTCTGT ACCCAGGCTGGA		
			AGAACGAGACA TGGGTCCGACCT		
			A		
GAM2460	CRTAM	3'	TCCAGCCTGGGCGACAGAGGGA 39476	G	A
	GA		TCTT CTCTGTC CCCAGGCTGGA		
			AGAG GAGACAG GGGTCCGACCT		
			G C		
GAM2460	D21S2056E	3'	TCCAGCCTGGGCAACGAGAG 14872	_	CA
			CTCT GT CCCAGGCTGGA		
			GAGA CA GGGTCCGACCT		
			G AC		
GAM2460	DARS	3'	TCCAGTGTGGATGACAGAGCGA 9051	C	G
	GA		TCTTGCTCTGTCA CCA GCTGGA		
			AGAGCGAGACAGT GGT TGACCT		
			A G		
GAM2460	DDX34	3'	TCCAGCCTGGTTGACAGAGCAA 28678		C
	GA		TCTTGCTCTGTCA CCAGGCTGGA		
			AGAACGAGACAGT GGTCCGACCT		
			T		
GAM2460	DEGS	3'	TCCACCCTGGGCAACAGAGCAA 14805	CA	C
	GA		TCTTGCTCTGT CCCAGG TGGA		
			AGAACGAGACA GGGTCC ACCT		
			AC C		
GAM2460	DEGS	3'	TCCACCCTGGGCAACAGAGCAA 59270	CA	C
	GA		TCTTGCTCTGT CCCAGG TGGA		
			AGAACGAGACA GGGTCC ACCT		
			AC C		
GAM2460	DIS3	3'	TCCAGCCTGGGTGACAGAACAA 30922		C
	GA		TCTTG TCTGTCACCCAGGCTGGA		
			AGAAC AGACAGTGGGTCCGACCT		
			A		
GAM2460	dJ383J4.3	3'	TCCAGCCTGGGCAACAAAGTGA 67498	TG	C CA
	GA		TCT CT TGT CCCAGGCTGGA		
			AGA GA ACA GGGTCCGACCT		
			GT A AC		
GAM2460	DKFZP434A0131	3'	TCCAGCCTGGGTGACAGAGCAA 39154		
	GA		TCTTGCTCTGTCACCCAGGCTGGA		

AGAACGAGACAGTGGGTCCGACCT

GAM2460	DKFZP434B168 3'	TCCAGCCTGGGCGACAGAGCGA 31872	A
	GA	TCTTGCTCTGTC CCCAGGCTGGA	
		AGAGCGAGACAG GGGTCCGACCT	
		C	
GAM2460	DKFZP434C171 3'	TCCAGCCCGGGTGACAGAGCAA 32199	A
	GA	TCTTGCTCTGTCACCC GGCTGGA	
		AGAACGAGACAGTGGG CCGACCT	
		C	
GAM2460	DKFZp434E0519 3'	TCTGGGCAACACAGCAAGA 51001	C CA
		TCTTGCT TGT CCCAGG	
		AGAACGA ACA GGGTCT	
		C AC	
GAM2460	DKFZp434E169 3'	CCTGGGCGACAGAGCGAGA 51076	A
		TCTTGCTCTGTC CCCAGG	
		AGAGCGAGACAG GGGTCC	
		C	
GAM2460	DKFZp434E2220 5'	TCCAGCCTGGGCGACAGGGTGA 34720	TG A
	GA	TCT CTCTGTC CCCAGGCTGGA	
		AGA GGGACAG GGGTCCGACCT	
		GT C	
GAM2460	DKFZP434F1735 3'	TCCAGCCTGGGCAGTATAGCAA 32117	___ TCA
	GA	TCTTGCT CTG CCCAGGCTGGA	
		AGAACGA GAC GGGTCCGACCT	
		TAT ___	
GAM2460	DKFZp434G171 3'	TCCAGCCTGGGCAACAAGAGGG 80248	G _ CA
	A	TT CTCT GT CCCAGGCTGGA	
		AG GAGA CA GGGTCCGACCT	
		G A AC	
GAM2460	DKFZP434I1735 3'	TCCAGCCTGGGCGACAGAGTGA 89173	TG A
	GA	TCT CTCTGTC CCCAGGCTGGA	
		AGA GAGACAG GGGTCCGACCT	
		GT C	
GAM2460	DKFZP434N1511 3'	TCCAGCCTGGGCAACAGAGCAA 93063	CA
	GA	TCTTGCTCTGT CCCAGGCTGGA	
		AGAACGAGACA GGGTCCGACCT	
		AC	
GAM2460	DKFZP434N161 3'	CCTGGGCAACACAGCAAGA 79214	C CA
		TCTTGCT TGT CCCAGG	

		AGAACGA ACA GGGTCC		
		C AC		
GAM2460	DKFZp547C176 3'	TCCAGCCTGGCGACAGAGCAAG 67806	AC	
	A	TCTTGCTCTGTC CCAGGCTGGA		
		AGAACGAGACAG GGTCCGACCT		
		C_		
GAM2460	DKFZp547G183 3'	TCCAGCCTGGGCGACAAGAGCA 38650	_ A	
	A	TTGCTCT GTC CCCAGGCTGGA		
		AACGAGA CAG GGTCCGACCT		
		A C		
GAM2460	DKFZP564A022 3'	TCCAGCCTGGGCAACAGAGTGA 48975	TG CA	
	GA	TCT CTCTGT CCCAGGCTGGA		
		AGA GAGACA GGTCCGACCT		
		GT AC		
GAM2460	DKFZP564B1023 3'	TCCAGCCTGGACAACAGATTGA 49368	GC CAC	
	GA	TCTT TCTGT CCAGGCTGGA		
		AGAG AGACA GGTCCGACCT		
		TT ACA		
GAM2460	DKFZP564B1023 3'	TCCAGCCTGGGCAACAAGAGTG 49369	TG _ CA	
	A	T CTCT GT CCCAGGCTGGA		
		A GAGA CA GGTCCGACCT		
		GT A AC		
GAM2460	DKFZp564K142 3'	TCCAGCCTGGCAACAGAGCGAG 50437	CAC	
	A	TCTTGCTCTGT CCAGGCTGGA		
		AGAGCGAGACA GGTCCGACCT		
		AC_		
GAM2460	DKFZP564M182 3'	TCCAGCCTGATGACAGAGCAAG 78642	CC	
	A	TCTTGCTCTGTCA CAGGCTGGA		
		AGAACGAGACAGT GTCCGACCT		
		A_		
GAM2460	DKFZP564M182 3'	TCCAGCCTGGGCAACAGAGAGA 78643	TG CA	
	GA	TCT CTCTGT CCCAGGCTGGA		
		AGA GAGACA GGTCCGACCT		
		GA AC		
GAM2460	DKFZP564M182 3'	TCCAGCCTGGGCGGCAGAGCAA 78645	A	
		TTGCTCTGTC CCCAGGCTGGA		
		AACGAGACGG GGTCCGACCT		
		C		
GAM2460	DKFZp566H0824 3'	TCCAGCCTGGGCAACAGAGCAA 34492	CA	
	GG	TCTTGCTCTGT CCCAGGCTGGA		

			GGAACGAGACA GGGTCCGACCT		
			AC		
GAM2460	DKFZp566H0824	5'	TCCAGCCTGGGCGACAGAGCGA 34493		A
	GA		TCTTGCTCTGTC CCCAGGCTGGA		
			AGAGCGAGACAG GGGTCCGACCT		
			C		
GAM2460	DKFZP586D2223	3'	TCAGCCTGGGTGACAGAGCAAG 38296		
	A		TCTTGCTCTGTCACCCAGGCTGG		
			AGAACGAGACAGTGGGTCCGACT		
GAM2460	DKFZP586M1120	3'	TCCAGCCTGGGCAACAGAGTGA 49286	TG	CA
			T CTCTGT CCCAGGCTGGA		
			A GAGACA GGGTCCGACCT		
			GT AC		
GAM2460	DKFZp727G131	3'	TCCAGCCTGGGCAACAGCGTGA 59698	TG T	CA
	GA		TCT C CTGT CCCAGGCTGGA		
			AGA G GACA GGGTCCGACCT		
			GT C AC		
GAM2460	DRF1	3'	TCCAGCCTGGGCGATAGAGCTA 47757	T	A
	GA		TCT GCTCTGTC CCCAGGCTGGA		
			AGA CGAGATAG GGGTCCGACCT		
			T C		
GAM2460	DRF1	3'	TCCAGCCTGGGTGACAGAGCGA 47758		
	GA		TCTTGCTCTGTCACCCAGGCTGGA		
			AGAGCGAGACAGTGGGTCCGACCT		
GAM2460	DSCR6	3'	TCCAGCCTGGGCAACAAGAGCG 39076	_	CA
	A		TTGCTCT GT CCCAGGCTGGA		
			AGCGAGA CA GGGTCCGACCT		
			A AC		
GAM2460	EIF2S1	3'	TCGAGCCTGGGTGACAGGGCAA 15848		G
	GA		TCTTGCTCTGTCACCCAGGCT GA		
			AGAACGGGACAGTGGGTCCGA CT		
			G		
GAM2460	ET	3'	TCCAGCCTGGATGACAAGAGTG 44474	TG _	C
	A		T CTCT GTCA CCAGGCTGGA		
			A GAGA CAGT GGTCCGACCT		
			GT A A		
GAM2460	FADS1	3'	TCCAGCCTGGGCGACAGAGCAA 26386		A
	GA		TCTTGCTCTGTC CCCAGGCTGGA		

			AGAACGAGACAG GGGTCCGACCT	
			C	
GAM2460	FADS1	3'	TCCAGCCTGGGGTGATAGAACA 26387	C _
	AGA		TCTTG TCTGTCACCC AGGCTGGA	
			AGAAC AGATAGTGGG TCCGACCT	
			A G	
GAM2460	FBXO26	3'	TCCAGCCTGGGTGAGAAAGCAA 46631	CTG
	GA		TCTTGCT TCACCCAGGCTGGA	
			AGAACGA AGTGGGTCCGACCT	
			AAG	
GAM2460	FBXO27	3'	TCCAGCCTGGGCAACACAGCGA 75014	C CA
	GA		TCTTGCT TGT CCCAGGCTGGA	
			AGAGCGA ACA GGGTCCGACCT	
			C AC	
GAM2460	FBXO27	3'	TCCAGCCTGGGTGACAGAGCGA 75015	
	GA		TCTTGCTCTGTCACCCAGGCTGGA	
			AGAGCGAGACAGTGGGTCCGACCT	
GAM2460	FBXO6	3'	TCCAGCCTGGGTGACAGAGCGA 37997	
	GA		TCTTGCTCTGTCACCCAGGCTGGA	
			AGAGCGAGACAGTGGGTCCGACCT	
GAM2460	FBXO9	3'	CCTGGACAACATAGCAAGA 54244	C CAC
			TCTTGCT TGT CCAGG	
			AGAACGA ACA GGTCC	
			T ACA	
GAM2460	FBXO9	3'	TCCAGCCTGAGCAACACAGTGA 54255	TG C CACC
	GA		TCT CT TGT CAGGCTGGA	
			AGA GA ACA GTCCGACCT	
			GT C ACGA	
GAM2460	FKBP14	3'	TCCAGCCTGGGTGACAGAGCAA 36070	
	GA		TCTTGCTCTGTCACCCAGGCTGGA	
			AGAACGAGACAGTGGGTCCGACCT	
GAM2460	FKSG17	3'	TCCAGCCTGGGTGACAGAGTGA 50159	TG
	GA		TCT CTCTGTCACCCAGGCTGGA	
			AGA GAGACAGTGGGTCCGACCT	
			GT	
GAM2460	FKSG43	5'	TCCAGCCTGGGTGACAGAGCAA 50163	
	GA		TCTTGCTCTGTCACCCAGGCTGGA	

AGAACGAGACAGTGGGTCCGACCT

GAM2460 FKSG44 5' TCCAGCCTGGGCGACAGAGCGA 49963 A
GA TCTTGCTCTGTC CCCAGGCTGGA
||||||| |||||
AGAGCGAGACAG GGGTCCGACCT
C

GAM2460 FKSG83 3' TCCAGCCTGGGAGACAGCAAGA 50146 CT A
TCTTGCT GTC CCCAGGCTGGA
||||| || |||||
AGAACGA CAG GGGTCCGACCT
— A

GAM2460 FLJ00060 3' TCCAGCCTGGGCGATAGAGCAA 61755 A
GA TCTTGCTCTGTC CCCAGGCTGGA
||||||| |||||
AGAACGAGATAG GGGTCCGACCT
C

GAM2460 FLJ10008 3' TCCAGCCTGGGCGACACAGCAA 36193 C A
GA TCTTGCT TGTC CCCAGGCTGGA
||||| ||| |||||
AGAACGA ACAG GGGTCCGACCT
C C

GAM2460 FLJ10043 3' TCCAGCCTGGGTGACAGAGCGA 36237
GA TCTTGCTCTGTCACCCAGGCTGGA
|||||||
AGAGCGAGACAGTGGGTCCGACCT

GAM2460 FLJ10058 3' TCCAGCCTGGGCAACACAGTGA 36264 TG C CA
GA TCT CT TGT CCCAGGCTGGA
||| || |||||
AGA GA ACA GGGTCCGACCT
GT C AC

GAM2460 FLJ10139 3' TCCAGCCTGGGTGACAAAGTAA 36317 C
GA TCTTGCT TGTCACCCAGGCTGGA
||||| |||||
AGAATGA ACAGTGGGTCCGACCT
A

GAM2460 FLJ10159 3' CCATTTGGGAACAGAGCAAGA 36335 CA C
TCTTGCTCTGT CCCAGG TGG
||||||| ||||| |||
AGAACGAGACA GGGTTT ACC
A_ _

GAM2460 FLJ10244 3' TCCAGCCTGGGCAAAAAGAGCA 36407 GTCA_
A TTGCTCT CCCAGGCTGGA
||||| |||||
AACGAGA GGGTCCGACCT
AAAAC

GAM2460 FLJ10314 3' CCAGCCTGCACAACAAGA 36486 CTC CACC
TCTTG TGT CAGGCTGG
||||| ||| |||||

			AGAAC ACA GTCCGACC		
			A_ C_		
GAM2460	FLJ10460	3'	TCCAACCTGGGTGATGGAGCAA 36623		C
	GA		TCTTGCTCTGTCACCCAGG TGGA		
			AGAACGAGGTAGTGGGTCC ACCT		
			A		
GAM2460	FLJ10520	3'	TCCAGCCTCGGTGACAGAGCAA 36710		C
	GA		TCTTGCTCTGTCACC AGGCTGGA		
			AGAACGAGACAGTGG TCCGACCT		
			C		
GAM2460	FLJ10547	3'	TCCAGCCTGGGCTACAGAGCGA 36779		CA
	GA		TCTTGCTCTGT CCCAGGCTGGA		
			AGAGCGAGACA GGGTCCGACCT		
			TC		
GAM2460	FLJ10597	3'	CCAGCCTGGGCTGACAGG 36835		_
			TCTGTCA CCCAGGCTGG		
			GGACAGT GGGTCCGACC		
			C		
GAM2460	FLJ10650	3'	TCCAGCCTGGGCGACAGAATGA 36903	GC	A
	GA		TCTT TCTGTC CCCAGGCTGGA		
			AGAG AGACAG GGGTCCGACCT		
			TA C		
GAM2460	FLJ10704	3'	TCCAGCCTGGACGACAGAGTGA 36984	TG	AC
	GA		TCT CTCTGTC CCAGGCTGGA		
			AGA GAGACAG GGTCCGACCT		
			GT CA		
GAM2460	FLJ10803	3'	TCCAGCCTGGGCAACAGAGCAA 37209		CA
	GA		TCTTGCTCTGT CCCAGGCTGGA		
			AGAACGAGACA GGGTCCGACCT		
			AC		
GAM2460	FLJ10826	3'	TCCAGCCTGGGCAACAAGAGTG 37250	TG	_ CA
	A		T CTCT GT CCCAGGCTGGA		
			A GAGA CA GGGTCCGACCT		
			GT A AC		
GAM2460	FLJ10830	3'	TCCAGCCTGGGCGACAGAACGA 37267	C	A
	GA		TCTTG TCTGTC CCCAGGCTGGA		
			AGAGC AGACAG GGGTCCGACCT		
			A C		
GAM2460	FLJ10936	3'	TCCAGCCTGGGCAACAGAGGGA 37450	G	CA
	GA		TCTT CTCTGT CCCAGGCTGGA		

		AGAG GAGACA GGGTCCGACCT	
		G AC	
GAM2460	FLJ10989	3' TCCAGCCTGGGTGACAAAGCAA 37507	C
	GA	TCTTGCT TGT CACCCAGGCTGGA	
		AGAACGA ACAGTGGGTCCGACCT	
		A	
GAM2460	FLJ11016	3' CCTGGGCAACACAGCAAGA 37540	C CA
		TCTTGCT TGT CCCAGG	
		AGAACGA ACA GGGTCC	
		C AC	
GAM2460	FLJ11036	3' TCCAGCCTGGGCGACAGAGCAA 37556	A
	GA	TCTTGCTCTGTC CCCAGGCTGGA	
		AGAACGAGACAG GGGTCCGACCT	
		C	
GAM2460	FLJ11106	3' TCCAGCCTGGGTGACAGATCCA 37626	TGC
	GA	TCT TCTGTCACCCAGGCTGGA	
		AGA AGACAGTGGGTCCGACCT	
		CCT	
GAM2460	FLJ11126	3' TCCAGCCTGGGTAACAGAGCGA 37655	C
	GA	TCTTGCTCTGT ACCCAGGCTGGA	
		AGAGCGAGACA TGGGTCCGACCT	
		A	
GAM2460	FLJ11151	3' TCCAGCCTGGGCAACAGAGCAA 68482	CA
	GA	TCTTGCTCTGT CCCAGGCTGGA	
		AGAACGAGACA GGGTCCGACCT	
		AC	
GAM2460	FLJ11301	3' TCCAGCCTGGGCGACAGAGTGA 37810	TG A
	GA	TCT CTCTGTC CCCAGGCTGGA	
		AGA GAGACAG GGGTCCGACCT	
		GT C	
GAM2460	FLJ11577	3' TCCAGCCTGGGCAACAAGAGTG 47960	TG _ CA
	AGA	TCT CTCT GT CCCAGGCTGGA	
		AGA GAGA CA GGGTCCGACCT	
		GT A AC	
GAM2460	FLJ11700	3' TCCAGCCTGGGCAACAGAACAA 46567	C CA
	GA	TCTTG TCTGT CCCAGGCTGGA	
		AGAAC AGACA GGGTCCGACCT	
		A AC	
GAM2460	FLJ11710	5' TCCAGCCTGGGCAACAGAGCAA 46252	CA
	GA	TCTTGCTCTGT CCCAGGCTGGA	

			AGAACGAGACA GGGTCCGACCT	
			AC	
GAM2460	FLJ11722	3'	TCCAGCCTGGCAACAGAGCAAG 47008	CAC
	G		TCTTGCTCTGT CCAGGCTGGA	
			GGAACGAGACA GGTCCGACCT	
			AC_	
GAM2460	FLJ11722	3'	TCCAGCCTGGCCACAGAGCGAG 47009	CAC
	A		TCTTGCTCTGT CCAGGCTGGA	
			AGAGCGAGACA GGTCCGACCT	
			CC_	
GAM2460	FLJ11726	3'	TCCAGCCTGGGCGACAGAGCAG 47031	A
	GA		TCTTGCTCTGTC CCCAGGCTGGA	
			AGGACGAGACAG GGGTCCGACCT	
			C	
GAM2460	FLJ11800	3'	TCCAGCCTGGGCAACAGAG 47042	CA
			CTCTGT CCCAGGCTGGA	
			GAGACA GGGTCCGACCT	
			AC	
GAM2460	FLJ11827	3'	CCTGGGCAACATAGCAAGA 47681	C CA
			TCTTGCT TGT CCCAGG	
			AGAACGA ACA GGGTCC	
			T AC	
GAM2460	FLJ11996	3'	TCCAACCTGGGCAACAGAGTAA 47069	CA C
	GA		TCTTGCTCTGT CCCAGG TGGA	
			AGAATGAGACA GGGTCC ACCT	
			AC A	
GAM2460	FLJ11996	3'	TCCAGCTTGGGTGACAGAGCAA 47070	
	GA		TCTTGCTCTGTCACCCAGGCTGGA	
			AGAACGAGACAGTGGGTTCGACCT	
GAM2460	FLJ12078	3'	CCAGCCTGGGTGGCAGAG 47078	
			CTCTGTCACCCAGGCTGG	
			GAGACGGTGGGTCCGACC	
GAM2460	FLJ12190	3'	TCCAGCCTGGGCAACAGAGCAA 47573	CA
			TTGCTCTGT CCCAGGCTGGA	
			AACGAGACA GGGTCCGACCT	
			AC	
GAM2460	FLJ12294	3'	TCCAGCCTGGGTGACAGAGAGA 47721	TG
	GA		TCT CTCTGTCACCCAGGCTGGA	

AGA GAGACAGTGGGTCCGACCT
GA

GAM2460 FLJ12298 3' TCCAGCCTGGGCAACAGAGCGA 50600 CA
GA TCTTGCTCTGT CCCAGGCTGGA
||||||| |||||
AGAGCGAGACA GGGTCCGACCT
AC

GAM2460 FLJ12331 3' TCCAGCCTGAGCTACAGAGCAA 47114 CACC
GA TCTTGCTCTGT CAGGCTGGA
||||||| |||||
AGAACGAGACA GTCCGACCT
TCGA

GAM2460 FLJ12363 3' TCCAGCCTGGGCAACAAGAGAG 50643 TG _ CA
A TCT CTCT GT CCCAGGCTGGA
||| ||| || |||||
AGA GAGA CA GGGTCCGACCT
_ A AC

GAM2460 FLJ12586 3' TCCAGCCTGGGTGACAGAGCGA 45212
GA TCTTGCTCTGTCACCCAGGCTGGA
|||||||
AGAGCGAGACAGTGGGTCCGACCT

GAM2460 FLJ12592 3' CCAGCCTGGGTGACCGAGT 50649 T
GCTC GTCACCCAGGCTGG
||| |||||
TGAG CAGTGGGTCCGACC
C

GAM2460 FLJ12618 3' TCCAGCCTGGGTGACAGAGCAA 46508
GA TCTTGCTCTGTCACCCAGGCTGGA
|||||||
AGAACGAGACAGTGGGTCCGACCT

GAM2460 FLJ12618 3' TCCAGGCTGGATGATAGAGCAA 46509 C G
GA TCTTGCTCTGTCA CCAG CTGGA
||||||| ||| |||
AGAACGAGATAGT GGTC GACCT
A G

GAM2460 FLJ12666 3' TCCAGCCTGGGCAACAAAACGA 45072 CTC CA
GA TCTTG TGT CCCAGGCTGGA
|||| ||| |||||
AGAGC ACA GGGTCCGACCT
AAA AC

GAM2460 FLJ12671 3' TCCAGCCTGGGTGACAAGAGTG 49112 TG _
AGA TCT CTCT GTCACCCAGGCTGGA
||| ||| |||||
AGA GAGA CAGTGGGTCCGACCT
GT A

GAM2460 FLJ12687 3' TCCAGCCTGGGTGACAGAGTGA 46759 TG
GA TCT CTCTGTCACCCAGGCTGGA
||| |||||

			AGA GAGACAGTGGGTCCGACCT		
			GT		
GAM2460	FLJ12847	3'	TCCAGCCTGGGCAACAGAGTAA 45080	CA	
			TTGCTCTGT CCCAGGCTGGA		
			AATGAGACA GGGTCCGACCT		
			AC		
GAM2460	FLJ12921	3'	TCCAGCCTGGGCGACGGAGCGA 46400	A	
	GA		TCTTGCTCTGTC CCCAGGCTGGA		
			AGAGCGAGGCAG GGGTCCGACCT		
			C		
GAM2460	FLJ12949	3'	TCCAGCCTGGGCAACAAAGCAA 43727	C CA	
	GA		TCTTGCT TGT CCCAGGCTGGA		
			AGAACGA ACA GGGTCCGACCT		
			A AC		
GAM2460	FLJ13117	3'	TCCAGCCTGGGAGACAGAGCAA 43811	A	
	GA		TCTTGCTCTGTC CCCAGGCTGGA		
			AGAACGAGACAG GGGTCCGACCT		
			A		
GAM2460	FLJ13193	3'	TCCAGCCTGGCGACAGAGCGAG 50736	AC	
	A		TCTTGCTCTGTC CCAGGCTGGA		
			AGAGCGAGACAG GGTCCGACCT		
			C_		
GAM2460	FLJ13241	3'	TCCAGCCTGGGTGGCAGAGCCA 47656	T	
	GA		TCT GCTCTGTCACCCAGGCTGGA		
			AGA CGAGACGGTGGGTCCGACCT		
			C		
GAM2460	FLJ13352	3'	CGGCCTGGGCAACAGAGCAAGA 45052	CA TG	
			TCTTGCTCTGT CCCAGGC G		
			AGAACGAGACA GGGTCCG C		
			AC GT		
GAM2460	FLJ13448	3'	TCCAGCCTGGGCAACAGAGGGA 47885	G CA	
	GA		TCTT CTCTGT CCCAGGCTGGA		
			AGAG GAGACA GGGTCCGACCT		
			G AC		
GAM2460	FLJ13456	3'	CCAGCCTGGACAACGGAGT 66539	CAC	
			GCTCTGT CCAGGCTGG		
			TGAGGCA GGTCCGACC		
			ACA		
GAM2460	FLJ13456	3'	TCCAGCCTGGGTGACAGAGTAA 66564		
	GA		TCTTGCTCTGTCACCCAGGCTGGA		

AGAATGAGACAGTGGGTCCGACCT

GAM2460 FLJ13544 3' TCCAGCCTGGATGACAGAGTGA 47210 TG C
GA TCT CTCTGTCA CCAGGCTGGA

||| ||||| |||||

AGA GAGACAGT GGTCCGACCT

GT A

GAM2460 FLJ13621 3' TCCAGCCTGGGCGACAGAGCGA 47226 A
GA TCTTGCTCTGTC CCCAGGCTGGA

||||||| |||||

AGAGCGAGACAG GGTCCGACCT

C

GAM2460 FLJ13659 3' TCCAGCCTGGGCAACAAGAGTG 48036 TG _ CA
G T CTCT GT CCCAGGCTGGA

| ||| || |||||

G GAGA CA GGTCCGACCT

GT A AC

GAM2460 FLJ13769 3' TCCAGCCTGGGTGACAGAGCGA 47264
GA TCTTGCTCTGTCACCCAGGCTGGA

||||||| |||||

AGAGCGAGACAGTGGGTCCGACCT

GAM2460 FLJ13848 3' TCCAGCCTAGGCGACAGAGTGA 45831 TG A C
GA TCT CTCTGTC CC AGGCTGGA

||| ||||| || |||||

AGA GAGACAG GG TCCGACCT

GT C A

GAM2460 FLJ13952 3' TCCAGCCTGGGCAACAAGAGTG 46021 TG _ CA
A T CTCT GT CCCAGGCTGGA

| ||| || |||||

A GAGA CA GGTCCGACCT

GT A AC

GAM2460 FLJ14011 3' TCCAGTCTGGGCAACAGAGCAA 42320 CA
GA TCTTGCTCTGT CCCAGGCTGGA

||||||| |||||

AGAACGAGACA GGTCTGACCT

AC

GAM2460 FLJ14100 3' TCCAGCCTGGGCGACAAAGCAA 47340 C A
GA TCTTGCT TGTC CCCAGGCTGGA

||||| ||| |||||

AGAACGA ACAG GGTCCGACCT

A C

GAM2460 FLJ14117 3' TCCAGCCTGGGCAACAGACA 43234 C CA
TG TCTGT CCCAGGCTGGA

|| |||| |||||

AC AGACA GGTCCGACCT

_ AC

GAM2460 FLJ14117 3' TCCAGCTTGGGCAACAGAGCAA 43235 CA
GA TCTTGCTCTGT CCCAGGCTGGA

||||||| |||||

AGAACGAGACA GGGTTCGACCT
 AC
 GAM2460 FLJ14251 3' TCCAGCCTGGGTAACAGAGCGA 46491 C
 GA TCTTGCTCTGT ACCCAGGCTGGA
 ||||| |||||
 AGAGCGAGACA TGGGTCCGACCT
 A
 GAM2460 FLJ14326 3' TCCAGCTTGGGCAACGAGCAA 50785 T CA
 TTGCTC GT CCCAGGCTGGA
 |||| || |||||
 AACGAG CA GGGTTCGACCT
 _ AC
 GAM2460 FLJ14327 3' TCCAGCCTGGACAACAGAGCTA 46688 T CAC
 GA TCT GCTCTGT CCAGGCTGGA
 || ||||| |||||
 AGA CGAGACA GGTCCGACCT
 T ACA
 GAM2460 FLJ14345 3' TCCAGCCTGGGCAACAAGAGTG 45662 TG _ CA
 A T CTCT GT CCCAGGCTGGA
 | |||| |||||
 A GAGA CA GGGTCCGACCT
 GT A AC
 GAM2460 FLJ14346 3' CCTGGGCAACATAGCAAGA 47362 C CA
 TCTTGCT TGT CCCAGG
 ||||| || |||||
 AGAACGA ACA GGGTCC
 T AC
 GAM2460 FLJ14346 3' TCCAGCCTGGGCAACAGAGCAA 47372 CA
 GA TCTTGCTCTGT CCCAGGCTGGA
 ||||| |||||
 AGAACGAGACA GGGTCCGACCT
 AC
 GAM2460 FLJ14346 3' TCCAGCCTGGGGGACAGAGCGA 47373 A
 GA TCTTGCTCTGTC CCCAGGCTGGA
 ||||| |||||
 AGAGCGAGACAG GGGTCCGACCT
 G
 GAM2460 FLJ14397 3' TCCAGCCTGGGCAACAAGGGCA 52334 _ CA
 A TTGCTCT GT CCCAGGCTGGA
 ||||| || |||||
 AACGGGA CA GGGTCCGACCT
 A AC
 GAM2460 FLJ14397 3' TCCAGCCTGGGTGACAGAGCAA 52335
 GA TCTTGCTCTGTCACCCAGGCTGGA
 ||||| |||||
 AGAACGAGACAGTGGGTCCGACCT
 GAM2460 FLJ14466 3' TCCAGCCTGGGCAACAACAGTG 52432 TG C_ CA
 A T CT TGT CCCAGGCTGGA
 | || |||||

		A GA ACA GGGTCCGACCT	
		GT CA AC	
GAM2460	FLJ14490	3' TCCAGCCTGGGCAACAGAGCAA 52448	CA
	GA	TCTTGCTCTGT CCCAGGCTGGA	
		AGAACGAGACA GGGTCCGACCT	
		AC	
GAM2460	FLJ14621	3' TCCAGCCTGGGCAACAGAGCAA 52541	CA
		TTGCTCTGT CCCAGGCTGGA	
		AACGAGACA GGGTCCGACCT	
		AC	
GAM2460	FLJ14641	3' TCCAGCTGGAGTGACAGAGC 52568	_ G
		GCTCTGTCAC CCAG CTGGA	
		CGAGACAGTG GGTC GACCT	
		A _	
GAM2460	FLJ14888	3' CCTGGGCAACATAGCAAGA 52747	C CA
		TCTTGCT TGT CCCAGG	
		AGAACGA ACA GGGTCC	
		T AC	
GAM2460	FLJ20004	3' TCCAGCCTGGGCAACAGAGGGA 97012	G CA
	GA	TCTT CTCTGT CCCAGGCTGGA	
		AGAG GAGACA GGGTCCGACCT	
		G AC	
GAM2460	FLJ20004	3' TCCAGCCTAGGCAACAAGAGTG 34765	TG _ CA C
	A	T CTCT GT CC AGGCTGGA	
		A GAGA CA GG TCCGACCT	
		GT A AC A	
GAM2460	FLJ20004	3' TCCAGCCTGGCAACAGAGCAAG 34766	CAC
	A	TCTTGCTCTGT CCAGGCTGGA	
		AGAACGAGACA GGTCCGACCT	
		AC_	
GAM2460	FLJ20004	3' TCCAGCCTGGGTGACAGAGTGA 34768	TG
	GA	TCT CTCTGTCACCCAGGCTGGA	
		AGA GAGACAGTGGGTCCGACCT	
		GT	
GAM2460	FLJ20013	3' TCCAGCCTCGGTGACAGAGCAA 34803	C
	GA	TCTTGCTCTGTCACC AGGCTGGA	
		AGAACGAGACAGTGG TCCGACCT	
		C	
GAM2460	FLJ20019	3' TCCAGCCTAGGTGACAGGGCAA 34816	C
	GA	TCTTGCTCTGTCACC AGGCTGGA	

			AGAACGGGACAGTGG TCCGACCT		
			A		
GAM2460	FLJ20045	3'	CCAGCCTGGGTGAGAAGAG 34879	G_	
			CTCT TCACCCAGGCTGG		
			GAGA AGTGGGTCCGACC		
			AG		
GAM2460	FLJ20069	3'	TCCAGCCTGGGGGACAGAGCAA 34957	A	
			GA TCTTGCTCTGTC CCCAGGCTGGA		
			AGAACGAGACAG GGGTCCGACCT		
			G		
GAM2460	FLJ20084	3'	TCCAGCCTGGGCAACAGAGCGA 34999	CA	
			GA TCTTGCTCTGT CCCAGGCTGGA		
			AGAGCGAGACA GGGTCCGACCT		
			AC		
GAM2460	FLJ20170	3'	TCCAGCCTGGGTGACAGAGTGA 35166	TG	
			GA TCT CTCTGTCACCCAGGCTGGA		
			AGA GAGACAGTGGGTCCGACCT		
			GT		
GAM2460	FLJ20211	3'	TCCAGCCTGGGCAACAGAGTGA 35266	TG CA	
			GA TCT CTCTGT CCCAGGCTGGA		
			AGA GAGACA GGGTCCGACCT		
			GT AC		
GAM2460	FLJ20211	3'	TCCAGCCTGGGCGACAGAGTGA 35267	TG A	
			GA TCT CTCTGTC CCCAGGCTGGA		
			AGA GAGACAG GGGTCCGACCT		
			GT C		
GAM2460	FLJ20241	3'	TCCAGCCTGGACAACAGAGCGA 35291	CAC	
			GA TCTTGCTCTGT CCAGGCTGGA		
			AGAGCGAGACA GGTCCGACCT		
			ACA		
GAM2460	FLJ20280	3'	TCCAGCCTGGGTGACAGAGCGA 35334		
			GA TCTTGCTCTGTCACCCAGGCTGGA		
			AGAGCGAGACAGTGGGTCCGACCT		
GAM2460	FLJ20306	3'	CCAGCCTGGACGACTGAGT 35388	T AC	
			GCTC GTC CCAGGCTGG		
			TGAG CAG GGTCCGACC		
			T CA		
GAM2460	FLJ20306	3'	TCCAGCCTGGCGACAGAGCAAG 35400	AC	
			A TCTTGCTCTGTC CCAGGCTGGA		

AGAACGAGACAG GGTCCGACCT
 C_
 GAM2460 FLJ20340 3' TCCAGCCTGGTGACAGAGCGAG 35460 C
 A TCTTGCTCTGTCACC AGGCTGGA
 |||||
 AGAGCGAGACAGTGG TCCGACCT
 —
 GAM2460 FLJ20456 3' TCCAGCCTGGGTAACAGAGCTA 35666 T C
 GA TCT GCTCTGT ACCCAGGCTGGA
 ||| ||||| |||||
 AGA CGAGACA TGGGTCCGACCT
 T A
 GAM2460 FLJ20546 3' TCCAGCCTGGGCAACGAGCGA 35814 T CA
 TTGCTC GT CCCAGGCTGGA
 ||||| || |||||
 AGCGAG CA GGGTCCGACCT
 — AC
 GAM2460 FLJ20671 3' TCCAGCCTGGGTGACAGAGCGA 35945
 GA TCTTGCTCTGTCACCCAGGCTGGA
 |||||
 AGAGCGAGACAGTGGGTCCGACCT
 GAM2460 FLJ20694 3' TCCAGCCTGGCGACAGAGCAAG 35979 AC
 A TCTTGCTCTGTC CCAGGCTGGA
 ||||| |||||
 AGAACGAGACAG GGTCCGACCT
 C_
 GAM2460 FLJ20700 3' TCCAGCCTGGGCGACACAGCGA 36020 C A
 GA TCTTGCT TGTC CCCAGGCTGGA
 ||||| ||| |||||
 AGAGCGA ACAG GGGTCCGACCT
 C C
 GAM2460 FLJ20802 3' TCCAGCCTGGGCGACAGAGCGA 36114 A
 GA TCTTGCTCTGTC CCCAGGCTGGA
 ||||| |||||
 AGAGCGAGACAG GGGTCCGACCT
 C
 GAM2460 FLJ20825 3' TCCAGCCTGGGCAACAAGAGCG 36149 — CA
 A TTGCTCT GT CCCAGGCTGGA
 ||||| || |||||
 AGCGAGA CA GGGTCCGACCT
 A AC
 GAM2460 FLJ20972 3' TCCAGCCTGGGCAACAAGAGAA 47389 G — CA
 GA TCTT CTCT GT CCCAGGCTGGA
 ||| ||| || |||||
 AGAA GAGA CA GGGTCCGACCT
 — A AC
 GAM2460 FLJ21144 3' TCCAGCCTGGGCAACAGAGTGA 43194 TG CA
 GA TCT CTCTGT CCCAGGCTGGA
 ||| ||||| |||||

			AGA GAGACA GGGTCCGACCT	
			GT AC	
GAM2460	FLJ21240	3'	TCCAGCCTGGGCAAAAAGAGCA 46269	GTCA_
	A		TTGCTCT CCCAGGCTGGA	
			AACGAGA GGGTCCGACCT	
			AAAAC	
GAM2460	FLJ21369	3'	TCCAGCCTGGGTGACAGAGCAA 46056	
	GA		TCTTGCTCTGTCACCCAGGCTGGA	
			AGAACGAGACAGTGGGTCCGACCT	
GAM2460	FLJ21551	3'	CCTGGGTGACAGAGCGAGA 46036	
			TCTTGCTCTGTCACCCAGG	
			AGAGCGAGACAGTGGGTCC	
GAM2460	FLJ21687	3'	TCCAGCCTGGGTGACAGAGCGA 46304	
	GA		TCTTGCTCTGTCACCCAGGCTGGA	
			AGAGCGAGACAGTGGGTCCGACCT	
GAM2460	FLJ21870	3'	TCCAGCCTGGGCAACGGAG 43750	CA
			CTCTGT CCCAGGCTGGA	
			GAGGCA GGGTCCGACCT	
			AC	
GAM2460	FLJ22009	3'	TCCAGCTTGGGCGACAGAGCGA 60921	A
	GA		TCTTGCTCTGTC CCCAGGCTGGA	
			AGAGCGAGACAG GGGTTCGACCT	
			C	
GAM2460	FLJ22054	3'	TCCAGCCTGGGCAACAGAGCAA 96053	CA
	GA		TCTTGCTCTGT CCCAGGCTGGA	
			AGAACGAGACA GGGTCCGACCT	
			AC	
GAM2460	FLJ22167	3'	TTGGGTGGCAGAGCAAGA 44883	
			TCTTGCTCTGTCACCCAG	
			AGAACGAGACGGTGGGTT	
GAM2460	FLJ22316	3'	TCCAGCCTGGGCAACAGAGCCA 47619	T CA
	GG		TCT GCTCTGT CCCAGGCTGGA	
			GGA CGAGACA GGGTCCGACCT	
			C AC	
GAM2460	FLJ22415	3'	TCCAGCCTGGGTGACAAAGCAA 93121	C
	GA		TCTTGCT TGTACCCAGGCTGGA	

AGAACGA ACAGTGGGTCCGACCT
 A
 GAM2460 FLJ22474 3' TCCAGCCTGGGCAACAGAGTGA 45618 TG CA
 GA TCT CTCTGT CCCAGGCTGGA
 ||| ||||| |||||
 AGA GAGACA GGGTCCGACCT
 GT AC
 GAM2460 FLJ22644 3' TCCAGCCTGGGCTACAGAGCGA 47703 CA
 GA TCTTGCTCTGT CCCAGGCTGGA
 ||||| |||||
 AGAGCGAGACA GGGTCCGACCT
 TC
 GAM2460 FLJ22814 3' TCCAACCTGGGTGACGAGTGAG 46731 TG T C
 A TCT CTC GTCACCCAGG TGGA
 ||| || ||||| |||
 AGA GAG CAGTGGGTCC ACCT
 GT _ A
 GAM2460 FLJ22814 3' TCCAGCCTGGGTGACAGAGGGA 46732 G
 TT CTCTGTCACCCAGGCTGGA
 || |||||
 AG GAGACAGTGGGTCCGACCT
 G
 GAM2460 FLJ23022 3' TCCAGCCTGGGCGACAAGAGCA 47500 _ A
 A TTGCTCT GTC CCCAGGCTGGA
 ||||| || |||||
 AACGAGA CAG GGGTCCGACCT
 A C
 GAM2460 FLJ23040 3' TCCAGCCTGGGCAATAGAGCAA 47992 CA
 GA TCTTGCTCTGT CCCAGGCTGGA
 ||||| |||||
 AGAACGAGATA GGGTCCGACCT
 AC
 GAM2460 FLJ23042 3' TCCAGCCTGGGCAACAAGAGTG 47949 TG _ CA
 A T CTCT GT CCCAGGCTGGA
 | |||| || |||||
 A GAGA CA GGGTCCGACCT
 GT A AC
 GAM2460 FLJ23120 3' TCCAGCCTGGGTGACGGAGAAA 86330 G
 GA TCTT CTCTGTCACCCAGGCTGGA
 |||| |||||
 AGAA GAGGCAGTGGGTCCGACCT
 A
 GAM2460 FLJ23185 3' TCCAGCCTTGCGCAACAAAGCAA 47522 C CA C
 GA TCTTGCT TGT CC AGGCTGGA
 ||||| || |||||
 AGAACGA ACA GG TCCGACCT
 A AC T
 GAM2460 FLJ23209 3' CCTGGGCAACATAGCAAGA 46586 C CA
 TCTTGCT TGT CCCAGG
 ||||| || |||||

AGAACGA ACA GGGTCC
 T AC
 GAM2460 FLJ23229 3' TCCAGCCTGGACAACAGAGCAA 47532 CAC
 GA TCTTGCTCTGT CCAGGCTGGA
 ||||| |||||
 AGAACGAGACA GGTCCGACCT
 ACA
 GAM2460 FLJ23360 3' TCCAGCCCGGGTGACAGAGCGA 43835 A
 GA TCTTGCTCTGTCACCC GGCTGGA
 ||||| |||||
 AGAGCGAGACAGTGGG CCGACCT
 C
 GAM2460 FLJ23447 3' CTGGGCAACAGAGCAAGA 46132 CA
 TCTTGCTCTGT CCCAG
 ||||| |||||
 AGAACGAGACA GGGTC
 AC
 GAM2460 FLJ23499 3' CCTGGGCAACATAGCAAGA 43132 C CA
 TCTTGCT TGT CCCAGG
 ||||| |||||
 AGAACGA ACA GGGTCC
 T AC
 GAM2460 FLJ23499 3' CCTGGGTGACAGAGCGAGA 43133
 TCTTGCTCTGTCACCCAGG
 ||||| |||||
 AGAGCGAGACAGTGGGTCC
 GAM2460 FLJ23499 3' TCCAGCCTGGGCGACAAGAGCG 43140 _ A
 A TTGCTCT GTC CCCAGGCTGGA
 ||||| |||||
 AGCGAGA CAG GGTCCGACCT
 A C
 GAM2460 FLJ23537 3' TCCAGCCTGGGCAACAAGAGGA 88922 G _ CA
 A TT CTCT GT CCCAGGCTGGA
 || ||||| |||||
 AA GAGA CA GGTCCGACCT
 G A AC
 GAM2460 FLJ23556 3' TCCAGCCTGGGCGACTGTGAGA 46455 TG TCT A
 TCT C GTC CCCAGGCTGGA
 || | |||||
 AGA G CAG GGTCCGACCT
 GT T_ C
 GAM2460 FLJ23878 3' TCCAGCCTGGGTGACAGGGCGA 59373
 GA TCTTGCTCTGTCACCCAGGCTGGA
 ||||| |||||
 AGAGCGGGACAGTGGGTCCGACCT
 GAM2460 FLJ25006 3' TCCAGCCTGAGCAACAGAGTGA 58789 TG CACC
 GA TCT CTCTGT CAGGCTGGA
 || ||||| |||||

			AGA GAGACA GTCCGACCT		
			GT ACGA		
GAM2460	FLJ25012	3'	TCCAATCTGGGTGACAGAATAA 58713	C	GC
		GA	TCTTG TCTGTCACCCAG TGGA		
			AGAAT AGACAGTGGGTC ACCT		
			A TA		
GAM2460	FLJ30092	3'	TCCAGCCTGGGCAACAGAGTGA 59342	TG	CA
		G	CT CTCTGT CCCAGGCTGGA		
			GA GAGACA GGGTCCGACCT		
			GT AC		
GAM2460	FLJ30681	3'	TCCAGCCTAGGCAACAGAGGGA 93440	G	CA C
		GA	TCTT CTCTGT CC AGGCTGGA		
			AGAG GAGACA GG TCCGACCT		
			G AC A		
GAM2460	FLJ31168	3'	TCCAGCCTGGGCGACAGAGCGA 59186		A
		GA	TCTTGCTCTGTC CCCAGGCTGGA		
			AGAGCGAGACAG GGGTCCGACCT		
			C		
GAM2460	FLJ31455	3'	TCCAGCCTGGGCGACAGAGCCA 59291	T	A
		GA	TCT GCTCTGTC CCCAGGCTGGA		
			AGA CGAGACAG GGGTCCGACCT		
			C C		
GAM2460	FLJ31455	3'	TCCAGCCTGGGTGACAGAGCAA 59292		
		GA	TCTTGCTCTGTCACCCAGGCTGGA		
			AGAACGAGACAGTGGGTCCGACCT		
GAM2460	FLJ31952	3'	TCCAGCCTGGGCAACAGAGTGA 59050	TG	CA
		GA	TCT CTCTGT CCCAGGCTGGA		
			AGA GAGACA GGGTCCGACCT		
			GT AC		
GAM2460	FLJ32499	5'	TCCAGTGACCGACAGAGCAAGA 58782		ACCCAG
			TCTTGCTCTGTC GCTGGA		
			AGAACGAGACAG TGACCT		
			CCAG__		
GAM2460	FLJ32915	5'	TCCAGCCTGGGCGACAAGAGCG 59437	_	A
		AGA	TCTTGCTCT GTC CCCAGGCTGGA		
			AGAGCGAGA CAG GGGTCCGACCT		
			A C		
GAM2460	FRSB	3'	TCCAGCCTGGGTGACAGAGTGA 20293	TG	
		GA	TCT CTCTGTCACCCAGGCTGGA		

			AGA GAGACAGTGGGTCCGACCT		
			GT		
GAM2460	FUSIP1	3'	TCCAGCCTGGGCAACAGAGTGA 55043	TG	CA
	GA		TCT CTCTGT CCCAGGCTGGA		
			AGA GAGACA GGGTCCGACCT		
			GT AC		
GAM2460	GALNT6	3'	CCAGCCTGAGCAACAAGAGCGA 24244	_	CACC
			TTGCTCT GT CAGGCTGG		
			AGCGAGA CA GTCCGACC		
			A ACGA		
GAM2460	GALNT6	3'	TCCAGCCTGGGCAACAGGTAAG 24252	T	CA
	A		TCTTGC CTGT CCCAGGCTGGA		
			AGAATG GACA GGGTCCGACCT		
			_ AC		
GAM2460	GCN2	3'	CCAGCCTGAGCAACAAAGCAAG 63437	C	CACC
	A		TCTTGCT TGT CAGGCTGG		
			AGAACGA ACA GTCCGACC		
			A ACGA		
GAM2460	GCN2	3'	TCCAGTCTGGGACAACAGAGCA 63440	CA_	
	AGA		TCTTGCTCTGT CCCAGGCTGGA		
			AGAACGAGACA GGGTCTGACCT		
			ACA		
GAM2460	GLTP	3'	TCCAGCCTGGGCAACAAGAGCG 33588	_	CA
	A		TTGCTCT GT CCCAGGCTGGA		
			AGCGAGA CA GGGTCCGACCT		
			A AC		
GAM2460	GNB4	3'	TCCAGCCTAGGCGACAGAGTGA 41570	TG	A C
	GA		TCT CTCTGTC CC AGGCTGGA		
			AGA GAGACAG GG TCCGACCT		
			GT C A		
GAM2460	GP5	3'	CCTGGGCGACAGAGCGAGA 16872	A	
			TCTTGCTCTGTC CCCAGG		
			AGAGCGAGACAG GGGTCC		
			C		
GAM2460	GTPBP5	3'	TCCAGCCTGAGCGACAGAGCAA 65981		ACC
	GA		TCTTGCTCTGTC CAGGCTGGA		
			AGAACGAGACAG GTCCGACCT		
			CGA		
GAM2460	GTPBP5	3'	TCCAGCCTGAGTGACAGAGCGA 65982		C
	GA		TCTTGCTCTGTAC CAGGCTGGA		

			AGAGCGAGACAGTG GTCCGACCT		
			A		
GAM2460	HCGIX	3'	TCCAGCCTGGGTGACAGCAAGA 20715	CT	
			TCTTGCT GTCACCCAGGCTGGA		
			AGAACGA CAGTGGGTCCGACCT		
			—		
GAM2460	HEI10	3'	TCCAGCCTGGGCAACAGAGTGA 41299	TG	CA
	GA		TCT CTCTGT CCCAGGCTGGA		
			AGA GAGACA GGGTCCGACCT		
			GT AC		
GAM2460	HES2	3'	TCCAGGCTGGGCGACAGAGCGA 39378	A	G
	GA		TCTTGCTCTGTC CCCAG CTGGA		
			AGAGCGAGACAG GGGTC GACCT		
			C G		
GAM2460	HIC	3'	TCCAGCCTGGGCAACAGAGCGA 68052	CA	
	GA		TCTTGCTCTGT CCCAGGCTGGA		
			AGAGCGAGACA GGGTCCGACCT		
			AC		
GAM2460	HIG2	3'	CCAGCCTGGGCCACAGTGCAAG 26198	T	CA
	A		TCTTGC CTGT CCCAGGCTGG		
			AGAACG GACA GGGTCCGACC		
			T CC		
GAM2460	HRH4	3'	CCAGCCTGGCAACAGAGCAAGA 41530	CAC	
			TCTTGCTCTGT CCAGGCTGG		
			AGAACGAGACA GGTCCGACC		
			AC_		
GAM2460	HSC3	3'	TCCAGCTTGGGTGACAAAGTAA 59734	C	
	GA		TCTTGCT TGTCACCCAGGCTGGA		
			AGAATGA ACAGTGGGTTCGACCT		
			A		
GAM2460	HSD17B7	3'	TCCAGCCTGGGTGACAGCGAGA 33484	CT	
			TCTTGCT GTCACCCAGGCTGGA		
			AGAGCGA CAGTGGGTCCGACCT		
			—		
GAM2460	HSH2	3'	TCCAGCCTGGATGACAGAGTGA 52744	TG	C
	GA		TCT CTCTGTCA CCAGGCTGGA		
			AGA GAGACAGT GGTCCGACCT		
			GT A		
GAM2460	HSMPP8	3'	TCCAGCCTGAGTGACAGAATGA 95141	GC	C
	GA		TCTT TCTGTCAC CAGGCTGGA		

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AGAG AGACAGTG GTCCGACCT
TA    A
GAM2460 HSPC043 3' TCCAGCCTGGGTGACAGTGAG 68353 TG CT
CT CT GTCACCCAGGCTGGA
|| || |||||
GA GA CAGTGGGTCCGACCT
GT __
GAM2460 HSU79252 5' TCCAGCCTGGGTGACAGAGTGA 26143 TG
GA TCT CTCTGTCACCCAGGCTGGA
||| |||||
AGA GAGACAGTGGGTCCGACCT
GT
GAM2460 ICAM4 3' TCCAGCCTGGGGGACAGAGCAC 42597 T A
GA TC TGCTCTGTC CCCAGGCTGGA
|| ||||| |||||
AG ACGAGACAG GGGTCCGACCT
C G
GAM2460 ICAM4 3' TCCAGCCTGGGGGACAGAGCAC 42598 T A
GA TC TGCTCTGTC CCCAGGCTGGA
|| ||||| |||||
AG ACGAGACAG GGGTCCGACCT
C G
GAM2460 IL-23R 3' TCCAGCCTGGGCAACAAGAGCA 59133 _ CA
A TTGCTCT GT CCCAGGCTGGA
||||| || |||||
AACGAGA CA GGGTCCGACCT
A AC
GAM2460 IL10RB 3' TCCAGCCTGGGTGACAAAGTGA 7129 TG C
GA TCT CT TGTCACCCAGGCTGGA
||| || |||||
AGA GA ACAGTGGGTCCGACCT
GT A
GAM2460 IMAGE:4907098 3' TCCAGCCTGGGCGACAGAGCAA 57758 A
GA TCTTGCTCTGTC CCCAGGCTGGA
||||||| |||||
AGAACGAGACAG GGGTCCGACCT
C
GAM2460 ITGB5 3' CCAGCCTGGCCAGACAAGA 60214 C TCAC
TCTTG TCTG CCAGGCTGG
|||| ||| |||||
AGAAC AGAC GGTCCGACC
_ C__
GAM2460 JDD1 3' CCAGCCTGGGTGATGGAG 63913
CTCTGTCACCCAGGCTGG
|||||||
GAGGTAGTGGGTCCGACC
GAM2460 KBRAS2 3' TCCAGCCTGGTCAACAGAGCAA 34628 CAC
GA TCTTGCTCTGT CCAGGCTGGA
||||||| |||||

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			AGAACGAGACA	GGTCCGACCT		
			ACT			
GAM2460	KCNH6	3'	TCCAGCCTGGGTGACAGAGTGA	48576	TG	
	GA		TCT CTCTGTCACCCAGGCTGGA			
			AGA GAGACAGTGGGTCCGACCT			
			GT			
GAM2460	KIAA0042	3'	TCCAGTCTGAGCAACAGAACGA	30239	C	CACC
	GA		TCTTG TCTGT CAGGCTGGA			
			AGAGC AGACA GTCTGACCT			
			A ACGA			
GAM2460	KIAA0057	3'	TCCAGCCTGGACAACAAGAGCG	25424	_	CAC
	A		TTGCTCT GT CCAGGCTGGA			
			AGCGAGA CA GGTCCGACCT			
			A ACA			
GAM2460	KIAA0184	3'	TCCAGCCTGGGTGACAGCACGA	65815	CT	
	GA		TCTTG CTGTCACCCAGGCTGGA			
			AGAGC GACAGTGGGTCCGACCT			
			AC			
GAM2460	KIAA0186	3'	TCCAGCCTGGGTGACAAAGTGA	41119	TG	C
	GA		TCT CT TGTCACCCAGGCTGGA			
			AGA GA ACAGTGGGTCCGACCT			
			GT A			
GAM2460	KIAA0226	3'	TCCAGCCTGGGTGACAGAGTGA	64264	TG	
	GA		TCT CTCTGTCACCCAGGCTGGA			
			AGA GAGACAGTGGGTCCGACCT			
			GT			
GAM2460	KIAA0355	3'	TCCAGCCTGGGTGACAGAGTGA	28710	TG	
	GA		TCT CTCTGTCACCCAGGCTGGA			
			AGA GAGACAGTGGGTCCGACCT			
			GT			
GAM2460	KIAA0391	3'	CCTGGGTGACAGAGCGAGA	28606		
			TCTTGCTCTGTCACCCAGG			
			AGAGCGAGACAGTGGGTCC			
GAM2460	KIAA0391	3'	TCCAGCCTAGGTGACAGAGTGA	28621	TG	C
	GA		TCT CTCTGTCACC AGGCTGGA			
			AGA GAGACAGTGG TCCGACCT			
			GT A			
GAM2460	KIAA0408	3'	TCCAGCCTGGGTGACAGAGTGA	28802	TG	
	GA		TCT CTCTGTCACCCAGGCTGGA			

		AGA GAGACAGTGGGTCCGACCT	
		GT	
GAM2460	KIAA0409	3' TCCAGCCTGGCTGTGAGCCAAG 31682	_ TGT C
	A	TCTTG CTC CA CCAGGCTGGA	
		AGAAC GAG GT GGTCCGACCT	
		C T__ C	
GAM2460	KIAA0419	3' TCCAGTCGGGTTAACAGAGCAA 28863	C_ A
	GA	TCTTGCTCTGT ACCC GGCTGGA	
		AGAACGAGACA TGGG CTGACCT	
		AT _	
GAM2460	KIAA0420	3' CCTGGGTGACAAAGCAAGA 64086	C
		TCTTGCT TGTCACCCAGG	
		AGAACGA ACAGTGGGTCC	
		A	
GAM2460	KIAA0427	3' CCAGCCTGGGAACACAGA 29375	CA_
		TCTGT CCCAGGCTGG	
		AGACA GGGTCCGACC	
		CAA	
GAM2460	KIAA0431	3' TCCAACCTGGGTAACAGGGCAA 31554	C C
	GA	TCTTGCTCTGT ACCCAGG TGGA	
		AGAACGGGACA TGGGTCC ACCT	
		A A	
GAM2460	KIAA0445	5' TCCAGCCTGTGTGACAGAGCAA 28642	C
	GA	TCTTGCTCTGTCTAC CAGGCTGGA	
		AGAACGAGACAGTG GTCCGACCT	
		T	
GAM2460	KIAA0446	5' TCCAGCCTGGGCGACAGAGCGA 69460	A
	GA	TCTTGCTCTGTC CCCAGGCTGGA	
		AGAGCGAGACAG GGGTCCGACCT	
		C	
GAM2460	KIAA0447	3' TCCAGCCTGGGCAACAGGGCAA 72129	CA
	GA	TCTTGCTCTGT CCCAGGCTGGA	
		AGAACGGGACA GGGTCCGACCT	
		AC	
GAM2460	KIAA0451	5' TCAGCCTGGGCAACAGAGCAAG 29781	CA
	A	TCTTGCTCTGT CCCAGGCTGG	
		AGAACGAGACA GGGTCCGACT	
		AC	
GAM2460	KIAA0472	3' TCCAGCCTGGGCAACAGAGCGA 72367	CA
	GA	TCTTGCTCTGT CCCAGGCTGGA	

			AGAGCGAGACA GGGTCCGACCT		
			AC		
GAM2460	KIAA0472	3'	TCCAGCCTGGGCAGCAGAGCAA 72368	CA	
	GA		TCTTGCTCTGT CCCAGGCTGGA		
			AGAACGAGACG GGGTCCGACCT		
			AC		
GAM2460	KIAA0472	3'	TCCAGCCTGGGCGACAGAGTGA 72369	TG	A
	GA		TCT CTCTGTC CCCAGGCTGGA		
			AGA GAGACAG GGGTCCGACCT		
			GT C		
GAM2460	KIAA0475	3'	TCCAGCCTGGGAGACAGAGCGA 30130	A	
	GA		TCTTGCTCTGTC CCCAGGCTGGA		
			AGAGCGAGACAG GGGTCCGACCT		
			A		
GAM2460	KIAA0514	3'	TCCAGCCTGGATGACGGAGCCA 28755	T	C
	GA		TCT GCTCTGTCA CCAGGCTGGA		
			AGA CGAGGCAGT GGTCCGACCT		
			C A		
GAM2460	KIAA0547	3'	TCCAGCCTGGCAACAGAGCAAG 29600	CAC	
	A		TCTTGCTCTGT CCAGGCTGGA		
			AGAACGAGACA GGTCCGACCT		
			AC_		
GAM2460	KIAA0557	3'	TCCAGCCTGGTGATAGAACGAG 78576	C	C
	A		TCTTG TCTGTCACC AGGCTGGA		
			AGAGC AGATAGTGG TCCGACCT		
			A _		
GAM2460	KIAA0563	3'	TCCAGCCTGGGCGACAGAGCAA 29890	A	
	GA		TCTTGCTCTGTC CCCAGGCTGGA		
			AGAACGAGACAG GGGTCCGACCT		
			C		
GAM2460	KIAA0565	3'	TCCAACCTGGGCGACAGAGCAA 67441	A	C
	GA		TCTTGCTCTGTC CCCAGG TGGA		
			AGAACGAGACAG GGGTCC ACCT		
			C A		
GAM2460	KIAA0635	3'	TCCAGCCTGGGTGACAGAGTAA 28422		
			TTGCTCTGTCACCCAGGCTGGA		
			AATGAGACAGTGGGTCCGACCT		
GAM2460	KIAA0643	3'	TCCAGCCTGGGTGACAGAGTGA 45980	TG	
	GA		TCT CTCTGTCACCCAGGCTGGA		

		AGA GAGACAGTGGGTCCGACCT		
		GT		
GAM2460	KIAA0673	5' TCCAGGACCCCGCAGAGCAA 62948	CACCCA	___
		TTGCTCTGT GG CTGGA		
		AACGAGACG CC GACCT		
		CC___ AG		
GAM2460	KIAA0694	3' TCCAGCCTGGGCAACAGAGTGA 72974	TG	CA
	GA	TCT CTCTGT CCCAGGCTGGA		
		AGA GAGACA GGGTCCGACCT		
		GT AC		
GAM2460	KIAA0752	3' TCCAGCCTGGGCAACGAGCGA 67635	T	CA
		TTGCTC GT CCCAGGCTGGA		
		AGCGAG CA GGGTCCGACCT		
		_ AC		
GAM2460	KIAA0794	3' TCCAGCCTGGGCGACAAAGCGA 81238	C	A
		TTGCT TGTC CCCAGGCTGGA		
		AGCGA ACAG GGGTCCGACCT		
		A C		
GAM2460	KIAA0798	3' TCCAGCCTGGGCAACAAGAGCG 28455	_	CA
	A	TTGCTCT GT CCCAGGCTGGA		
		AGCGAGA CA GGGTCCGACCT		
		A AC		
GAM2460	KIAA0831	3' TCCAGCCTGGGCAACAAGAGCG 30655	_	CA
	AGG	TCTTGCTCT GT CCCAGGCTGGA		
		GGAGCGAGA CA GGGTCCGACCT		
		A AC		
GAM2460	KIAA0853	3' TCCAACCTAGGTGACAGAGCAA 31215	C	C
	GA	TCTTGCTCTGTCACC AGG TGGA		
		AGAACGAGACAGTGG TCC ACCT		
		A A		
GAM2460	KIAA0872	3' TCCAGCCTGGGTGACAGAGTGA 30762	TG	
	GA	TCT CTCTGTCACCCAGGCTGGA		
		AGA GAGACAGTGGGTCCGACCT		
		GT		
GAM2460	KIAA0876	3' TCCAGCCTGGGCAACAGAGCGA 65319	CA	
	GA	TCTTGCTCTGT CCCAGGCTGGA		
		AGAGCGAGACA GGGTCCGACCT		
		AC		
GAM2460	KIAA0884	3' TCCAACCTGGGTAACAGAGTGA 70758	TG	C C
	GA	TCT CTCTGT ACCCAGG TGGA		


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          AGA GAGACA TGGGTCC ACCT
          GT  A  A
GAM2460 KIAA0889 3' TCCAGCCTGGGTGACAGACTAA 31785    C
          GA          TCTTG TCTGTCACCCAGGCTGGA
                   ||||| |||||
          AGAAT AGACAGTGGGTCCGACCT
          C
GAM2460 KIAA0889 3' TCCAGCCTGGGTGACAGAGTGA 31786    TG
          GA          TCT CTCTGTCACCCAGGCTGGA
                   ||| |||||
          AGA GAGACAGTGGGTCCGACCT
          GT
GAM2460 KIAA0889 5' TCCAGCCTGGGTGACATATCAA 31787    CTC
          GA          TCTTG TGTACCCAGGCTGGA
                   ||||| |||||
          AGAAC ACAGTGGGTCCGACCT
          TAT
GAM2460 KIAA0892 3' TCCAGCCTGGGTGACGGTGAGA 71572    TG CT
          TCT CT GTCACCCAGGCTGGA
          ||| || |||||
          AGA GG CAGTGGGTCCGACCT
          GT _
GAM2460 KIAA0894 3' TCCAGCCTGGGTGACAGAGCGA 30342
          GA          TCTTGCTCTGTCACCCAGGCTGGA
                   |||||
          AGAGCGAGACAGTGGGTCCGACCT

GAM2460 KIAA0907 3' TCCAGCCTGGGCAATAGAGCAA 30882    CA
          GA          TCTTGCTCTGT CCCAGGCTGGA
                   ||||| |||||
          AGAACGAGATA GGGTCCGACCT
          AC
GAM2460 KIAA0912 3' TCCAGCCTGGGTGACAGAGTGA 65045    TG
          GG          TCT CTCTGTCACCCAGGCTGGA
                   ||| |||||
          GGA GAGACAGTGGGTCCGACCT
          GT
GAM2460 KIAA0924 3' TCCAGCCTGGGCAACAGAGCGA 30376    CA
          GA          TCTTGCTCTGT CCCAGGCTGGA
                   ||||| |||||
          AGAGCGAGACA GGGTCCGACCT
          AC
GAM2460 KIAA0961 3' TCCAGCCTGGGCAACAAGAGCA 30410    _ CA
          A          TTGCTCT GT CCCAGGCTGGA
                   ||||| || |||||
          AACGAGA CA GGGTCCGACCT
          A AC
GAM2460 KIAA0981 3' TCCAGCCTGGGCAACAGAGCAA 62093    CA
          GA          TCTTGCTCTGT CCCAGGCTGGA
                   ||||| |||||

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AGAACGAGACA GGGTCCGACCT
 AC
 GAM2460 KIAA1001 3' TCCAGCCTGGGTGATGGAGCAA 31012
 GA TCTTGCTCTGTCACCCAGGCTGGA
 |||||
 AGAACGAGGTAGTGGGTCCGACCT

GAM2460 KIAA1017 3' TCTGGGTGACAGAGAAAGA 24270 G
 TCTT CTCTGTCACCCAGG
 ||| |||||
 AGAA GAGACAGTGGGTCT
 A

GAM2460 KIAA1030 3' TCCAGCCTGGGTGACAGAG 94985
 CTCTGTCACCCAGGCTGGA
 |||||
 GAGACAGTGGGTCCGACCT

GAM2460 KIAA1032 3' TCCAGCCTGGGCAACAGAACAA 66733 C CA
 TTG TCTGT CCCAGGCTGGA
 ||| ||| |||||
 AAC AGACA GGGTCCGACCT
 A AC

GAM2460 KIAA1056 3' CCTGGGTGACAGAGCCAGA 30314 T
 TCT GCTCTGTCACCCAGG
 ||| |||||
 AGA CGAGACAGTGGGTCC
 C

GAM2460 KIAA1086 3' TCCAGCCTGGGCAACAGAAGAA 71289 GC CA
 GA TCTT TCTGT CCCAGGCTGGA
 ||| ||| |||||
 AGAA AGACA GGGTCCGACCT
 GA AC

GAM2460 KIAA1086 3' TCCAGCCTGGGTTACAGAGCGA 71290 C
 GA TCTTGCTCTGT ACCCAGGCTGGA
 ||||| |||||
 AGAGCGAGACA TGGGTCCGACCT
 T

GAM2460 KIAA1130 3' CCTGGGCAACATAGCAAGA 63085 C CA
 TCTTGCT TGT CCCAGG
 ||||| ||| |||||
 AGAACGA ACA GGGTCC
 T AC

GAM2460 KIAA1130 3' CCTGGGTGACAGAGCGAGA 63086
 TCTTGCTCTGTCACCCAGG
 |||||
 AGAGCGAGACAGTGGGTCC

GAM2460 KIAA1143 3' CCAGCCTGGGCGACAAAGCAA 69234 C A
 TTGCT TGTC CCCAGGCTGG
 |||| ||| |||||

			AACGA ACAG GGGTCCGACC		
			A C		
GAM2460	KIAA1143	3'	TCCAGCCTGGGCAACAGAGTAA 69251	CA	
	GA		TCTTGCTCTGT CCCAGGCTGGA		
			AGAATGAGACA GGGTCCGACCT		
			AC		
GAM2460	KIAA1164	3'	TCCAGCCTGGGTGACAGAGGGA 70051	G	
	GA		TCTT CTCTGTCACCCAGGCTGGA		
			AGAG GAGACAGTGGGTCCGACCT		
			G		
GAM2460	KIAA1191	3'	TCCAGCCTGGGCGACAGAACGA 40336	C A	
	GA		TCTTG TCTGTC CCCAGGCTGGA		
			AGAGC AGACAG GGGTCCGACCT		
			A C		
GAM2460	KIAA1228	3'	TCCAGCCTGGGCAACAGAGTGA 65678	TG CA	
	GA		TCT CTCTGT CCCAGGCTGGA		
			AGA GAGACA GGGTCCGACCT		
			GT AC		
GAM2460	KIAA1253	3'	TCTAGCCTGGGCAACAGAGTAA 93550	CA	
	GA		TCTTGCTCTGT CCCAGGCTGGA		
			AGAATGAGACA GGGTCCGATCT		
			AC		
GAM2460	KIAA1257	3'	TCCAGCCTGGGCAGCAGAGCAA 63419	CA	
	GA		TCTTGCTCTGT CCCAGGCTGGA		
			AGAACGAGACG GGGTCCGACCT		
			AC		
GAM2460	KIAA1271	3'	TCCAACCTGGGTGAGAGAGCGA 70145	G C	
	GA		TCTTGCTCT TCACCCAGG TGGA		
			AGAGCGAGA AGTGGGTCC ACCT		
			G A		
GAM2460	KIAA1271	3'	TCCAGCCTGGGCGACAGAGTGG 70146	TG A	
			T CTCTGTC CCCAGGCTGGA		
			G GAGACAG GGGTCCGACCT		
			GT C		
GAM2460	KIAA1277	3'	TCCAGCCTGGACAACAGAGCAA 65086	CAC	
	GA		TCTTGCTCTGT CCAGGCTGGA		
			AGAACGAGACA GGTCCGACCT		
			ACA		
GAM2460	KIAA1328	3'	TCCAGCCTGGGTGACAGAGCAA 62334		
	GA		TCTTGCTCTGTCACCCAGGCTGGA		

AGAACGAGACAGTGGGTCCGACCT

GAM2460 KIAA1340 3' TCCAGCCTGGGCGACAGTGCAA 69699 T A
GA TCTTGC CTGTC CCCAGGCTGGA

||||| |||| |||||||||
AGAACG GACAG GGGTCCGACCT
T C

GAM2460 KIAA1348 3' TCCAGCCTGGGCAACAAGAGTG 69129 TG _ CA
A T CTCT GT CCCAGGCTGGA

| |||| || |||||||||
A GAGA CA GGGTCCGACCT
GT A AC

GAM2460 KIAA1404 3' TCCAGTCTGGGCGACAGGAGCA 62694 _ A
AGA TCTTGCTC TGTC CCCAGGCTGGA

|||||| |||| |||||||||
AGAACGAG ACAG GGGTCTGACCT
G C

GAM2460 KIAA1423 3' TCCAGCCTGGGTGTCAGAGCGA 62398 T
GA TCTTGCTCTG CACCCAGGCTGGA

|||||| |||||||||
AGAGCGAGAC GTGGGTCCGACCT
T

GAM2460 KIAA1456 5' CCAGCCTGGGTGACTGAG 67540 T
CTC GTCACCCAGGCTGG

||| |||||||||
GAG CAGTGGGTCCGACC
T

GAM2460 KIAA1456 3' CCTGGGCAACATAGCAAGA 67546 C CA
TCTTGCT TGT CCCAGG

|||||| ||| |||||
AGAACGA ACA GGGTCC
T AC

GAM2460 KIAA1456 3' CCTGGGCAACATAGCAAGA 67547 C CA
TCTTGCT TGT CCCAGG

|||||| ||| |||||
AGAACGA ACA GGGTCC
T AC

GAM2460 KIAA1486 3' TCCAGCCTGGGTGACAGAGCGA 67979
GA TCTTGCTCTGTCACCCAGGCTGGA

|||||||||||||||||
AGAGCGAGACAGTGGGTCCGACCT

GAM2460 KIAA1497 5' TCCAGCCTGGGCGACAGAGCGA 68132 A
GA TCTTGCTCTGTC CCCAGGCTGGA

|||||||| |||||||||
AGAGCGAGACAG GGGTCCGACCT
C

GAM2460 KIAA1503 3' TCCAGCCTGGGCGACAGAGTGA 68900 TG A
T CTCTGTC CCCAGGCTGGA

| |||||| |||||||||

A GAGACAG GGGTCCGACCT
 GT C
 GAM2460 KIAA1508 3' TCCAGCCTGGGTGACAGAGCGA 62564
 GA TCTTGCTCTGTCACCCAGGCTGGA
 |||||
 AGAGCGAGACAGTGGGTCCGACCT

GAM2460 KIAA1554 3' TCCAACCTGGGTGACAGAGTGA 96862 TG C
 GA TCT CTCTGTCACCCAGG TGGA
 || |||||
 AGA GAGACAGTGGGTCC ACCT
 GT A

GAM2460 KIAA1559 3' TCCAGCCTGGGTAACAGAGCAA 73461 C
 GA TCTTGCTCTGT ACCCAGGCTGGA
 ||||| |||||
 AGAACGAGACA TGGGTCCGACCT
 A

GAM2460 KIAA1559 3' TCCAGCCTGGGTGACAGAGTGA 73462 TG
 GA TCT CTCTGTCACCCAGGCTGGA
 || |||||
 AGA GAGACAGTGGGTCCGACCT
 GT

GAM2460 KIAA1586 5' CCTGGGCAACAGAGCAAGA 93938 CA
 TCTTGCTCTGT CCCAGG
 ||||| |||||
 AGAACGAGACA GGGTCC
 AC

GAM2460 KIAA1586 5' TCCAGCTTGGGTGACAGAGCGA 93941
 GA TCTTGCTCTGTCACCCAGGCTGGA
 |||||
 AGAGCGAGACAGTGGGTTCGACCT

GAM2460 KIAA1614 3' TCCAGCCTGGGCAACAAGAGCA 70669 _ CA
 A TTGCTCT GT CCCAGGCTGGA
 ||||| || |||||
 AACGAGA CA GGGTCCGACCT
 A AC

GAM2460 KIAA1630 3' TCCAGCCTGGGTGACAGAGCAA 38657
 GA TCTTGCTCTGTCACCCAGGCTGGA
 |||||
 AGAACGAGACAGTGGGTCCGACCT

GAM2460 KIAA1641 3' TCCAGCCTGAGCAACAGAGTGA 81022 TG CACC
 T CTCTGT CAGGCTGGA
 | ||||| |||||
 A GAGACA GTCCGACCT
 GT ACGA

GAM2460 KIAA1644 3' TCCAGCCTGGGCAACAGAGTGA 86223 TG CA
 GA TCT CTCTGT CCCAGGCTGGA
 || ||||| |||||

		AGA GAGACA GGGTCCGACCT	
		GT AC	
GAM2460	KIAA1674	3' TCCAGCCTGGGCGACAGAGCGA 69348	A
	GA	TCTTGCTCTGTC CCCAGGCTGGA	
		AGAGCGAGACAG GGGTCCGACCT	
		C	
GAM2460	KIAA1715	3' TCCAGCCTGGGCAACAAGAGTG 68691	TG _ CA
	A	T CTCT GT CCCAGGCTGGA	
		A GAGA CA GGGTCCGACCT	
		GT A AC	
GAM2460	KIAA1724	3' TCCAGCCAGAGTGACAGAGCAA 67622	CCA
	GA	TCTTGCTCTGTCAC GGCTGGA	
		AGAACGAGACAGTG CCGACCT	
		AGA	
GAM2460	KIAA1727	3' TCCAGCCTGGATGACAGAGTGA 64765	TG C
	GA	TCT CTCTGTCA CCAGGCTGGA	
		AGA GAGACAGT GGTCCGACCT	
		GT A	
GAM2460	KIAA1771	3' TCCAGCCTGGACAACAGAGTAA 79868	CAC
		TTGCTCTGT CCAGGCTGGA	
		AATGAGACA GGTCCGACCT	
		ACA	
GAM2460	KIAA1786	3' CCAGCCCGGGTGACAGAGCGAG 66630	A
	A	TCTTGCTCTGTCACCC GGCTGG	
		AGAGCGAGACAGTGGG CCGACC	
		C	
GAM2460	KIAA1829	3' TCCAGCCTGGGCAACAAGAGCG 62656	_ CA
	A	TTGCTCT GT CCCAGGCTGGA	
		AGCGAGA CA GGGTCCGACCT	
		A AC	
GAM2460	KIAA1841	3' CTAGCCTGGGTGACAGAGCAAG 80851	
	A	TCTTGCTCTGTCACCCAGGCTGG	
		AGAACGAGACAGTGGGTCCGATC	
GAM2460	KIAA1871	3' TCCAGCCTGGGCAACAAGTGCG 61911	T _ CA
	A	TTGC CT GT CCCAGGCTGGA	
		AGCG GA CA GGGTCCGACCT	
		T A AC	
GAM2460	KIAA1872	3' TCCAGCCTGGGAGACAGAGCAA 63620	A
	GA	TCTTGCTCTGTC CCCAGGCTGGA	

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          AGAACGAGACAG GGGTCCGACCT
            A
GAM2460 KIAA1872 3' TCCAGCCTGGGCAACAAGAGCA 63622 _ CA
            A
            TTGCTCT GT CCCAGGCTGGA
            ||||| || |||||
            AACGAGA CA GGGTCCGACCT
            A AC
GAM2460 KIAA1872 3' TCCAGCCTGGGCGACAGAGCAA 63623 A
            GA
            TCTTGCTCTGTC CCCAGGCTGGA
            ||||| |||||
            AGAACGAGACAG GGGTCCGACCT
            C
GAM2460 KIAA1879 3' TCCAGCCTGGGAGACAGAGCAA 73946 A
            GA
            TCTTGCTCTGTC CCCAGGCTGGA
            ||||| |||||
            AGAACGAGACAG GGGTCCGACCT
            A
GAM2460 KIAA1948 3' TCCAGCCTGGGTGACAGACCGA 83306 C
            GA
            TCTTG TCTGTCACCCAGGCTGGA
            |||| |||||
            AGAGC AGACAGTGGGTCCGACCT
            C
GAM2460 KIAA1948 5' TCCAGCCTGGGTGACAGAGTGA 83307 TG
            GA
            TCT CTCTGTCACCCAGGCTGGA
            || |||||
            AGA GAGACAGTGGGTCCGACCT
            GT
GAM2460 KIAA1951 3' TCCAGCCTGGGCGACAGAGTGA 74165 TG A
            GA
            TCT CTCTGTC CCCAGGCTGGA
            || |||||
            AGA GAGACAG GGGTCCGACCT
            GT C
GAM2460 KIAA1951 3' TCCAGTCTGGGCAACAGTGCAA 74166 T CA
            GA
            TCTTGCTGT CCCAGGCTGGA
            |||| || |||||
            AGAACG GACA GGGTCTGACCT
            T AC
GAM2460 KIAA1954 3' TCCAGCCTGAGCAACAGAGCAA 78231 CACC
            GA
            TCTTGCTCTGT CAGGCTGGA
            ||||| |||||
            AGAACGAGACA GTCCGACCT
            ACGA
GAM2460 KIAA1958 3' TCCAGCCTGGGCAACAAAGCTA 82792 T C CA
            GA
            TCT GCT TGT CCCAGGCTGGA
            || || || |||||
            AGA CGA ACA GGGTCCGACCT
            T A AC
GAM2460 KR18 3' TCCAGCCTGGGCAACAAGAACA 53897 C _ CA
            A
            TTG TCT GT CCCAGGCTGGA
            || || || |||||

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			AAC AGA CA GGGTCCGACCT	
			A A AC	
GAM2460	LANO	3'	TCCAGCCCCGGGTGACAGAGCGA 37163	A
	GA		TCTTGCTCTGTCACCC GGCTGGA	
			AGAGCGAGACAGTGGG CCGACCT	
			C	
GAM2460	LIAS	3'	TCCAGCCTGGGTGACAAGAGCA 71170	_
	A		TTGCTCT GTCACCCAGGCTGGA	
			AACGAGA CAGTGGGTCCGACCT	
			A	
GAM2460	LIM	3'	TCCAGCCTGGGTGACAGAGTGA 22334	TG
	GA		TCT CTCTGTCACCCAGGCTGGA	
			AGA GAGACAGTGGGTCCGACCT	
			GT	
GAM2460	LIM	3'	TCCAGCCTGGTGACAGAGCAAG 22335	C
	A		TCTTGCTCTGTCACC AGGCTGGA	
			AGAACGAGACAGTGG TCCGACCT	
			-	
GAM2460	LIN-28	3'	TCCAGCCTGGTTACAGAGCGAG 45471	CAC
	A		TCTTGCTCTGT CCAGGCTGGA	
			AGAGCGAGACA GGTCCGACCT	
			TT_	
GAM2460	LRG	3'	TCTAGCCTGGGCGACAGAGCAA 54826	A
	GA		TCTTGCTCTGTC CCCAGGCTGGA	
			AGAACGAGACAG GGTCCGATCT	
			C	
GAM2460	LRRFIP1	3'	TCCAGCCTGGACAACAAGAGCG 17617	_ CAC
	A		TTGCTCT GT CCAGGCTGGA	
			AGCGAGA CA GGTCCGACCT	
			A ACA	
GAM2460	LSR68	3'	TCCAGCCTGGGCGACAGAATGA 38559	GC A
	GA		TCTT TCTGTC CCCAGGCTGGA	
			AGAG AGACAG GGTCCGACCT	
			TA C	
GAM2460	MACF1	3'	TCCAGCCTGGGCAACAGACAGA 53434	TG A_____
	GTGAG		CT CTCTGTC CCCAGGCTGGA	
			GA GAGACAG GGTCCGACCT	
			GT ACAAC	
GAM2460	MAWBP	3'	TCCAGCCTGGGCAACAGAGTAA 42388	CA
	GA		TCTTGCTCTGT CCCAGGCTGGA	

			AGAATGAGACA GGGTCCGACCT	
			AC	
GAM2460	MCAM	3'	TCCAGCCTGGGCAACACAGCGA 22466	C CA
	GA		TCTTGCT TGT CCCAGGCTGGA	
			AGAGCGA ACA GGGTCCGACCT	
			C AC	
GAM2460	MESDC2	3'	TCCAGCCTGGATGACGGG 72923	C
			TCTGTCA CCAGGCTGGA	
			GGGCAGT GGTCCGACCT	
			A	
GAM2460	METL	3'	TCCAGCCTGGGCAAAATAGCGA 37841	CTGTCA
	GA		TCTTGCT CCCAGGCTGGA	
			AGAGCGA GGGTCCGACCT	
			TAAAC	
GAM2460	MGC10200	3'	TCCAGTCTGGGCAACAGAGCGA 59649	CA
	GA		TCTTGCTCTGT CCCAGGCTGGA	
			AGAGCGAGACA GGGTCTGACCT	
			AC	
GAM2460	MGC10765	3'	TCCAGCCTAGGCGACAGAGCGA 44567	A C
	GA		TCTTGCTCTGTC CC AGGCTGGA	
			AGAGCGAGACAG GG TCCGACCT	
			C A	
GAM2460	MGC10814	3'	TCCAGCCTGGGCAACAAGAGCA 52026	_ CA
	AGA		TCTTGCTCT GT CCCAGGCTGGA	
			AGAACGAGA CA GGGTCCGACCT	
			A AC	
GAM2460	MGC10814	5'	TCCAGCCTGGGCAACAGAGTGA 52027	TG CA
	GG		TCT CTCTGT CCCAGGCTGGA	
			GGA GAGACA GGGTCCGACCT	
			GT AC	
GAM2460	MGC11352	3'	TCCAGCCTGGGCTCAAAAAAGA 65438	GCTC TCA
			TCTT TG CCCAGGCTGGA	
			AGAA AC GGGTCCGACCT	
			AAA_ TC_	
GAM2460	MGC11386	3'	TCCAGCCTGGGCAACAGAGCGA 53072	CA
	GA		TCTTGCTCTGT CCCAGGCTGGA	
			AGAGCGAGACA GGGTCCGACCT	
			AC	
GAM2460	MGC12972	3'	CCTGGGCAACATAGCAAGA 52052	C CA
			TCTTGCT TGT CCCAGG	

			AGAACGA ACA GGGTCC		
			T AC		
GAM2460	MGC13008	3'	TCCAGCCTGGGCAACAGAATGA 52059	GC	CA
	GA		TCTT TCTGT CCCAGGCTGGA		
			AGAG AGACA GGGTCCGACCT		
			TA AC		
GAM2460	MGC13017	3'	TCCAGCCTAGGCAATAAGAGCA 55579	GTCA_	C
	A		TTGCTCT CC AGGCTGGA		
			AACGAGA GG TCCGACCT		
			ATAAC A		
GAM2460	MGC13053	3'	TCCAGCCTGGGCGACAGAGTGA 52114	TG	A
	GA		TCT CTCTGTC CCCAGGCTGGA		
			AGA GAGACAG GGGTCCGACCT		
			GT C		
GAM2460	MGC13053	3'	TCCAGCCTGGGCGACAGCAAGA 52115	CT	A
			TCTTGCT GTC CCCAGGCTGGA		
			AGAACGA CAG GGGTCCGACCT		
			_ C		
GAM2460	MGC14126	3'	TCCAGCCTGGGCGATGAGCAA 52943	T	A
			TTGCTC GTC CCCAGGCTGGA		
			AACGAG TAG GGGTCCGACCT		
			_ C		
GAM2460	MGC14407	3'	TCCAGCCTGGGTGACAGAGCAA 52977		
	GA		TCTTGCTCTGTCACCCAGGCTGGA		
			AGAACGAGACAGTGGGTCCGACCT		
GAM2460	MGC14436	3'	TCCAGCCTGGGTGACAGAACGA 52931	C	
	GA		TCTTG TCTGTCACCCAGGCTGGA		
			AGAGC AGACAGTGGGTCCGACCT		
			A		
GAM2460	MGC14799	3'	TCCAGCCTGGGTGACAGTGAGA 51332	TG	CT
			TCT CT GTCACCCAGGCTGGA		
			AGA GA CAGTGGGTCCGACCT		
			GT _		
GAM2460	MGC15631	3'	CCTGGGTGACACAGCAAGA 52228	C	
			TCTTGCT TGTCACCCAGG		
			AGAACGA ACAGTGGGTCC		
			C		
GAM2460	MGC15631	3'	TCCAGCCTGTGCAACAGAGCCA 52235	T	CACC
	GA		TCT GCTCTGT CAGGCTGGA		

			AGA CGAGACA GTCCGACCT		
			C ACGT		
GAM2460	MGC16037	3'	TCCAGCCTGGACAACAGAGTGG 52894	TG	CAC
	GA		TCT CTCTGT CCAGGCTGGA		
			AGG GAGACA GGTCCGACCT		
			GT ACA		
GAM2460	MGC16175	3'	TCCAGCCTGGGCAATAGAGCAA 52279		CA
	GA		TCTTGCTCTGT CCCAGGCTGGA		
			AGAACGAGATA GGGTCCGACCT		
			AC		
GAM2460	MGC16332	3'	TCCAGCCTGGTCAACAAAGCAA 57545	C	CAC
	GA		TCTTGCT TGT CCAGGCTGGA		
			AGAACGA ACA GGTCCGACCT		
			A ACT		
GAM2460	MGC16703	3'	TCCAGCCTGGGCAACAGAGCGA 73498		CA
	GA		TCTTGCTCTGT CCCAGGCTGGA		
			AGAGCGAGACA GGGTCCGACCT		
			AC		
GAM2460	MGC20235	3'	TCCAGCCTGGGCAAAAGAGCAA 59563		GTCA
			TTGCTCT CCCAGGCTGGA		
			AACGAGA GGGTCCGACCT		
			AAAC		
GAM2460	MGC23244	3'	TCCAGCCTGGGCGACAGAGTGA 58838	TG	A
	GA		TCT CTCTGTC CCCAGGCTGGA		
			AGA GAGACAG GGGTCCGACCT		
			GT C		
GAM2460	MGC2562	3'	TCCAGCCTGACGACAAAGCGAG 51449	C	ACC
	A		TCTTGCT TGTC CAGGCTGGA		
			AGAGCGA ACAG GTCCGACCT		
			A CA_		
GAM2460	MGC2562	3'	TCCAGCCTGGAAGACCAAACGA 51450	CTCT	AC
	GA		TCTTG GTC CCAGGCTGGA		
			AGAGC CAG GGTCCGACCT		
			AAAC AA		
GAM2460	MGC2562	3'	TCCAGCCTGGGCGACAGAGCAA 51452		A
			TTGCTCTGTC CCCAGGCTGGA		
			AACGAGACAG GGGTCCGACCT		
			C		
GAM2460	MGC26641	3'	TCCAGCCTGGGCAATAGGGCAA 59326		CA
	GA		TCTTGCTCTGT CCCAGGCTGGA		

			AGAACGGGATA GGGTCCGACCT	
			AC	
GAM2460	MGC26877	5'	CCAGCCTGGGTGACAGAGCGAG 58890	
	A		TCTTGCTCTGTCACCCAGGCTGG	
			AGAGCGAGACAGTGGGTCCGACC	
GAM2460	MGC29762	3'	TCCAGCCTGGGCAACAAGAGCA 59149	_ CA
	A		TTGCTCT GT CCCAGGCTGGA	
			AACGAGA CA GGGTCCGACCT	
			A AC	
GAM2460	MGC29891	3'	TCCAGCCTGGGCAACAGAGCCA 58871	T CA
	GA		TCT GCTCTGT CCCAGGCTGGA	
			AGA CGAGACA GGGTCCGACCT	
			C AC	
GAM2460	MGC29891	3'	TCCAGGCTTGAGTGACAGAGCA 58873	C _
	AGA		TCTTGCTCTGTAC CAGGC TGGA	
			AGAACGAGACAGTG GTTCG ACCT	
			A G	
GAM2460	MGC29937	3'	TCCAGCCTGGGCAACAAGAGTG 58734	TG _ CA
	A		T CTCT GT CCCAGGCTGGA	
			A GAGA CA GGGTCCGACCT	
			GT A AC	
GAM2460	MGC3101	5'	TCCAGCCTGGGTGACAGAGCGA 44105	
	GA		TCTTGCTCTGTCACCCAGGCTGGA	
			AGAGCGAGACAGTGGGTCCGACCT	
GAM2460	MGC3207	3'	TCCAGCCTGGGCAACAGAGCGA 63242	CA
	GA		TCTTGCTCTGT CCCAGGCTGGA	
			AGAGCGAGACA GGGTCCGACCT	
			AC	
GAM2460	MGC4248	3'	TCCAGCCTGGGTGACTGAG 51319	T
			CTC GTCACCCAGGCTGGA	
			GAG CAGTGGGTCCGACCT	
			T	
GAM2460	MGC4368	3'	CCTGGGCAACACAGCAAGA 44725	C CA
			TCTTGCT TGT CCCAGG	
			AGAACGA ACA GGGTCC	
			C AC	
GAM2460	MGC4562	3'	TCCAGCCTGGGCAACAGAGCGA 56743	CA
	GA		TCTTGCTCTGT CCCAGGCTGGA	

			AGAGCGAGACA GGGTCCGACCT		
			AC		
GAM2460	MGC4663	3'	TCCAGCCTGGGCAACAGAGCCA 44791	T	CA
	GA		TCT GCTCTGT CCCAGGCTGGA		
			AGA CGAGACA GGGTCCGACCT		
			C AC		
GAM2460	MGC4771	3'	TCCAGCCTGGGCAACAGAGTGA 52006	TG	CA
	GA		TCT CTCTGT CCCAGGCTGGA		
			AGA GAGACA GGGTCCGACCT		
			GT AC		
GAM2460	MGC4840	3'	TCCAGCCTGGCTGACAGAGCGA 72029		C
	GA		TCTTGCTCTGTCA CCAGGCTGGA		
			AGAGCGAGACAGT GGTCCGACCT		
			C		
GAM2460	MGC5384	3'	TCCAGCCTGGGCGACAGAGTGA 49094	TG	A
	GA		TCT CTCTGTC CCCAGGCTGGA		
			AGA GAGACAG GGGTCCGACCT		
			GT C		
GAM2460	MGC5457	3'	TCCAGCCTGGGTGACAGAGCGA 51943		
	GA		TCTTGCTCTGT CACCCAGGCTGGA		
			AGAGCGAGACAGTGGGTCCGACCT		
GAM2460	MKRN4	3'	CCAGCCTGGGTGACAGAGCGAG 48455		
	A		TCTTGCTCTGT CACCCAGGCTGG		
			AGAGCGAGACAGTGGGTCCGACC		
GAM2460	MOST2	5'	TCCAGCCTGGGCACCACAGCAA 40072	C	TCA
	GA		TCTTGCT TG CCCAGGCTGGA		
			AGAACGA AC GGGTCCGACCT		
			C CAC		
GAM2460	MRPL48	5'	TCCAGCCTGCGCAACAGAGCGA 32662		CACC
	GA		TCTTGCTCTGT CAGGCTGGA		
			AGAGCGAGACA GTCCGACCT		
			ACGC		
GAM2460	MRPS10	3'	TCCAGCCTGGCGACAGAGCGAG 36822		AC
	A		TCTTGCTCTGTC CCAGGCTGGA		
			AGAGCGAGACAG GGTCCGACCT		
			C_		
GAM2460	MRPS18B	3'	TCCAGCCTGGGTGACAGCTAGA 26755	TGCT	
			TCT CTGTCACCCAGGCTGGA		

			AGA GACAGTGGGTCCGACCT	
			TC__	
GAM2460	My015	3'	TCCAGCCTGGGAGACAGAGCAA 67235	A
	GA		TCTTGCTCTGTC CCCAGGCTGGA	
			AGAACGAGACAG GGGTCCGACCT	
			A	
GAM2460	N4BP2	3'	TCAGCCTGGGTGACAGAGCAAG 36943	
	A		TCTTGCTCTGTCACCCAGGCTGG	
			AGAACGAGACAGTGGGTCCGACT	
GAM2460	NDUFC2	3'	TCCAGCCTGGGTGACAAAGGAG 17038	G C
	A		TCTT CT TGTCACCCAGGCTGGA	
			AGAG GA ACAGTGGGTCCGACCT	
			_ A	
GAM2460	NMNAT	3'	TCCAGCCTGGCGACAGAGCAAG 43292	AC
	A		TCTTGCTCTGTC CCAGGCTGGA	
			AGAACGAGACAG GGTCCGACCT	
			C_	
GAM2460	NMNAT	3'	TCCAGCCTGGGCAAAAAGCAA 43294	CTGTCA
			TTGCT CCCAGGCTGGA	
			AACGA GGGTCCGACCT	
			AAAAAC	
GAM2460	NMNAT	3'	TCCAGCCTGGGTGACAGAGCGA 43295	
	GA		TCTTGCTCTGTCACCCAGGCTGGA	
			AGAGCGAGACAGTGGGTCCGACCT	
GAM2460	NMT2	3'	TCCAGCCTGGGTGACAGAGCGT 17859	T
	GA		TC TGCTCTGTCACCCAGGCTGGA	
			AG GCGAGACAGTGGGTCCGACCT	
			T	
GAM2460	NPTXR	3'	TCCAGCCTGGGCAACAGAGCAA 55218	CA
	GA		TCTTGCTCTGT CCCAGGCTGGA	
			AGAACGAGACA GGGTCCGACCT	
			AC	
GAM2460	Nup43	3'	TCCAGCCTGGGCAAAAGAGCAA 45356	GTCA
			TTGCTCT CCCAGGCTGGA	
			AACGAGA GGGTCCGACCT	
			AAAC	
GAM2460	NY-BR-1	3'	TCCAGCCTAGGTGACAGAGTGA 54853	TG C
	GA		TCT CTCTGTCACC AGGCTGGA	

			AGA GAGACAGTGG TCCGACCT	
			GT A	
GAM2460	OR51E2	3'	TCCAGCCTGGGCAACGGAGCAA 48521	CA
	GA		TCTTGCTCTGT CCCAGGCTGGA	
			AGAACGAGGCA GGGTCCGACCT	
			AC	
GAM2460	ORC6L	3'	TCCAGCCTGGGTGACAGAGCGA 27494	
	GA		TCTTGCTCTGTCACCCAGGCTGGA	
			AGAGCGAGACAGTGGGTCCGACCT	
GAM2460	ORC6L	3'	TCCAGCCTGGGTGACAGAGCGA 27495	
	GA		TCTTGCTCTGTCACCCAGGCTGGA	
			AGAGCGAGACAGTGGGTCCGACCT	
GAM2460	PAFAH2	3'	TCCAGCCTGGGTGACAGAGCAA 6508	
	GA		TCTTGCTCTGTCACCCAGGCTGGA	
			AGAACGAGACAGTGGGTCCGACCT	
GAM2460	PB1	3'	TCCAGCCTGGGCAACAAGAGCG 36880	_ CA
	A		TTGCTCT GT CCCAGGCTGGA	
			AGCGAGA CA GGGTCCGACCT	
			A AC	
GAM2460	PB1	3'	TCCAGCCTGGGCAACAGAGTGA 36881	TG CA
	G		CT CTCTGT CCCAGGCTGGA	
			GA GAGACA GGGTCCGACCT	
			GT AC	
GAM2460	PDCD7	3'	TCCAGCCTGGGAGACAGAGCAA 72611	A
	GA		TCTTGCTCTGTC CCCAGGCTGGA	
			AGAACGAGACAG GGGTCCGACCT	
			A	
GAM2460	phorbolin-1	3'	TCCAGCCTGGGCGACAGTACCA 90213	TGCT A
	GA		TCT CTGTC CCCAGGCTGGA	
			AGA GACAG GGGTCCGACCT	
			CCAT C	
GAM2460	PIWIL2	3'	TCCAGCCTGTTGACAAAGCAAG 36547	C CC
	A		TCTTGCT TGTCA CAGGCTGGA	
			AGAACGA ACAGT GTCCGACCT	
			A T_	
GAM2460	POFUT1	3'	TCCAGCCTGGGCAACAGAGCGA 70984	CA
	GA		TCTTGCTCTGT CCCAGGCTGGA	

AGAGCGAGACA GGGTCCGACCT
 AC
 GAM2460 POLYDOM 3' TCCAGCCTGGGCAATGGAGAGA 44690 TG CA
 TCT CTCTGT CCCAGGCTGGA
 ||| ||||| |||||
 AGA GAGGTA GGGTCCGACCT
 — AC
 GAM2460 PP591 5' TCCAGCCTGGGTGACAGAG 48150
 CTCTGTCACCCAGGCTGGA
 |||||
 GAGACAGTGGGTCCGACCT

 GAM2460 PRDM14 3' CCTGGGTGACAGAACCAGA 44705 TGC
 TCT TCTGTCACCCAGG
 ||| |||||
 AGA AGACAGTGGGTCC
 CCA
 GAM2460 PRIC285 3' TCCAGCCTGGGTGACAGAGCGA 62120
 GA TCTTGCTCTGTCACCCAGGCTGGA
 |||||
 AGAGCGAGACAGTGGGTCCGACCT

 GAM2460 PRO0038 3' TCCAGCCTGGGTGACAGACCGA 26931 C
 GA TCTTG TCTGTCACCCAGGCTGGA
 |||||
 AGAGC AGACAGTGGGTCCGACCT
 C
 GAM2460 PRO0478 5' TCCAGCCTAGGCAACAAGAGCG 27035 — CA C
 A TTGCTCT GT CC AGGCTGGA
 ||||| || |||||
 AGCGAGA CA GG TCCGACCT
 A AC A
 GAM2460 PRO0478 5' TCCAGCCTGGACAACAGAGTGA 27036 TG CAC
 GA TCT CTCTGT CCAGGCTGGA
 ||| ||||| |||||
 AGA GAGACA GGTCCGACCT
 GT ACA
 GAM2460 PRO0478 3' TCCAGCCTGGCAACAGAGCGAG 27037 CAC
 A TCTTGCTCTGT CCAGGCTGGA
 ||||| |||||
 AGAGCGAGACA GGTCCGACCT
 AC_
 GAM2460 PRO0478 3' TCCAGCCTGGGGGACAGAGCAA 27038 A
 GG TCTTGCTCTGTC CCCAGGCTGGA
 ||||| |||||
 GGAACGAGACAG GGGTCCGACCT
 G
 GAM2460 PRO1048 5' TCCAGCCTGGGTGACAGAGCGA 38119
 GA TCTTGCTCTGTCACCCAGGCTGGA
 |||||

AGAGCGAGACAGTGGGTCCGACCT

GAM2460 PRO1386 3' TCCAGCCTGGGCAACAGAGTGA 49218 TG CA
GA TCT CTCTGT CCCAGGCTGGA

||| ||||| |||||
AGA GAGACA GGGTCCGACCT
GT AC

GAM2460 PRO1496 3' TCCAACCTGGGTGACAGACCGA 38368 C C
GA TCTTG TCTGTCACCCAGG TGGA

||||| |||||
AGAGC AGACAGTGGGTCC ACCT
C A

GAM2460 PRO1942 5' TCCAGCCTGGACAACAGAAAGA 38384 GC CAC
GA TCTT TCTGT CCAGGCTGGA

||| ||||| |||||
AGAG AGACA GGTCCGACCT
AA ACA

GAM2460 PRO2859 3' TCCAGCCTGGGGAGACAGAGCG 38214 A_
AGA TCTTGCTCTGTC CCCAGGCTGGA

||||| |||||
AGAGCGAGACAG GGGTCCGACCT
AG

GAM2460 PROL2 3' TCCAGCCTGGGTAACAGACGC 23323 _ C
GC TCTGT ACCCAGGCTGGA

|| ||||| |||||
CG AGACA TGGGTCCGACCT
C A

GAM2460 PRPF4 3' CCTGTGTGACAGAGCAAGA 17465 C
TCTTGCTCTGTAC CAGG

||||| |||||
AGAACGAGACAGTG GTCC
T

GAM2460 PSR 3' TCCAGCCTGGGTGACAGACCGA 65794 C
GA TCTTG TCTGTCACCCAGGCTGGA

||||| |||||
AGAGC AGACAGTGGGTCCGACCT
C

GAM2460 PTD012 3' CCAGCTTGGGCAACATAGCAAG 26736 C CA
A TCTTGCT TGT CCCAGGCTGG

||||| ||| |||||
AGAACGA ACA GGGTTCGACC
T AC

GAM2460 PTK6 3' TCCAGCCTGGGCGACAGAGCGA 21082 A
GA TCTTGCTCTGTC CCCAGGCTGGA

||||| |||||
AGAGCGAGACAG GGGTCCGACCT
C

GAM2460 PTRF 3' TCCAGCCTGGGTGACAGAGTGA 64245 TG
GA TCT CTCTGTCACCCAGGCTGGA

||| |||||

			AGA GAGACAGTGGGTCCGACCT		
			GT		
GAM2460	RAB4B	5'	TCCAGCCTGGGCAACGAAAAG 32904	GC T CA	
			CTT TC GT CCCAGGCTGGA		
			GAA AG CA GGGTCCGACCT		
			A_ _ AC		
GAM2460	Rabip4R	3'	TCCAACCTGGGTGACAGAGCAA 36279		C
	GA		TCTTGCTCTGTCACCCAGG TGGA		
			AGAACGAGACAGTGGGTCC ACCT		
			A		
GAM2460	RAP140	3'	CCAGGTGGTGACAGAGCAGA 31511	T CAGG	
			TCT GCTCTGTCACC CTGG		
			AGA CGAGACAGTGG GACC		
			_ TG_		
GAM2460	RHOBTB3	3'	TCCAGCCTGGGTGACAAGAGCG 30432		_
	A		TTGCTCT GTCACCCAGGCTGGA		
			AGCGAGA CAGTGGGTCCGACCT		
			A		
GAM2460	RNO2	5'	TCCAGCCTAGACAACAGGGCAA 53941		CACCC
	GG		TCTTGCTCTGT AGGCTGGA		
			GGAACGGGACA TCCGACCT		
			ACAGA		
GAM2460	RNO2	5'	TCCAGCCTGGGCAACAAGAGCG 53942	_ CA	
	A		TTGCTCT GT CCCAGGCTGGA		
			AGCGAGA CA GGGTCCGACCT		
			A AC		
GAM2460	Rpo1-2	3'	TCCAGCCTGGGCGACAGAATGA 39225	GC A	
	GA		TCTT TCTGTC CCCAGGCTGGA		
			AGAG AGACAG GGGTCCGACCT		
			TA C		
GAM2460	Rpo1-2	3'	TCCAGCCTGGGTGACAGAGCAG 39226		
	GA		TCTTGCTCTGTCACCCAGGCTGGA		
			AGGACGAGACAGTGGGTCCGACCT		
GAM2460	RRP4	3'	TCCAGCCTGGGTGACAGAGCGA 27363		
	GA		TCTTGCTCTGTCACCCAGGCTGGA		
			AGAGCGAGACAGTGGGTCCGACCT		
GAM2460	SAC2	3'	TCCAGCCTGGGGGACAGAGCAA 30728		A
	GA		TCTTGCTCTGTC CCCAGGCTGGA		

			AGAACGAGACAG GGGTCCGACCT		
			G		
GAM2460	SAMHD1	3'	TCCAGCCTGGGTGACAGAGTGA 61991	TG	
	GA		TCT CTCTGTCACCCAGGCTGGA		
			AGA GAGACAGTGGGTCCGACCT		
			GT		
GAM2460	SC65	3'	TCCAGCCTGGGCGACAGAGCGA 22302	A	
	GA		TCTTGCTCTGTC CCCAGGCTGGA		
			AGAGCGAGACAG GGGTCCGACCT		
			C		
GAM2460	SC65	3'	TCCAGCCTGGGCGACAGAGTGA 22303	TG	A
	GA		TCT CTCTGTC CCCAGGCTGGA		
			AGA GAGACAG GGGTCCGACCT		
			GT C		
GAM2460	SCAND2	3'	TCCAGCCTGGGCGACAGAGTGA 54423	TG	A
	GA		TCT CTCTGTC CCCAGGCTGGA		
			AGA GAGACAG GGGTCCGACCT		
			GT C		
GAM2460	SCAND2	3'	TCCAGCCTGGGCGACAGAGTGA 54424	TG	A
	GA		TCT CTCTGTC CCCAGGCTGGA		
			AGA GAGACAG GGGTCCGACCT		
			GT C		
GAM2460	SCIN	3'	TCCAGCCTGGGCAACAGAG 53605	CA	
			CTCTGT CCCAGGCTGGA		
			GAGACA GGGTCCGACCT		
			AC		
GAM2460	SCYA5	3'	TCCAGCCTGGGCGACAGAGCGA 12971	A	
	GA		TCTTGCTCTGTC CCCAGGCTGGA		
			AGAGCGAGACAG GGGTCCGACCT		
			C		
GAM2460	SCYA5	3'	TCCAGCCTGGGTGACAAAGTGA 12972	TG	C
	GA		TCT CT TGTCACCCAGGCTGGA		
			AGA GA ACAGTGGGTCCGACCT		
			GT A		
GAM2460	SEMA3E	3'	CCTGGGCGACAGAGCGAGA 25806	A	
			TCTTGCTCTGTC CCCAGG		
			AGAGCGAGACAG GGGTCC		
			C		
GAM2460	SLC7A11	3'	TCCAGCCTGGGTGACAAAGTCA 27532	T	C
	GA		TCT GCT TGTCACCCAGGCTGGA		

			AGA TGA ACAGTGGGTCCGACCT		
			C A		
GAM2460	SMA3	3'	TCCAGCCTGGGTGACAGAGC 23262		
			GCTCTGTCACCCAGGCTGGA		
			CGAGACAGTGGGTCCGACCT		
GAM2460	SMAP-5	3'	TCCAGCCTGGGTGACAGGGTGA 48662	TG	
	GA		TCT CTCTGTCACCCAGGCTGGA		
			AGA GGGACAGTGGGTCCGACCT		
			GT		
GAM2460	SMCR5	3'	TCTGGGCGACAGAGCAAGA 59251		A
			TCTTGCTCTGTC CCCAGG		
			AGAACGAGACAG GGGTCT		
			C		
GAM2460	SNAPC1	3'	TCCAGCCTGGGCAACAGAGTGA 13279	TG	CA
	GA		TCT CTCTGT CCCAGGCTGGA		
			AGA GAGACA GGGTCCGACCT		
			GT AC		
GAM2460	SPRY4	3'	TCCAGCCTGGGTGACAGAGCAA 49032		
	GA		TCTTGCTCTGTCACCCAGGCTGGA		
			AGAACGAGACAGTGGGTCCGACCT		
GAM2460	SPRY4	3'	TCCAGCCTGGGTGACAGAGTGA 49033	TG	
	GA		TCT CTCTGTCACCCAGGCTGGA		
			AGA GAGACAGTGGGTCCGACCT		
			GT		
GAM2460	SPTLC2	3'	CCTGGGCAACACAGCAAGA 17989		C CA
			TCTTGCT TGT CCCAGG		
			AGAACGA ACA GGGTCC		
			C AC		
GAM2460	SPTLC2	3'	TCCAGCCTGGGTGACAGAGTGA 18001	TG	
	GA		TCT CTCTGTCACCCAGGCTGGA		
			AGA GAGACAGTGGGTCCGACCT		
			GT		
GAM2460	SPTLC2	3'	TCTAGCCTGGGTGACAGAGCAA 18004		
			TTGCTCTGTCACCCAGGCTGGA		
			AACGAGACAGTGGGTCCGATCT		
GAM2460	SYT12	3'	CCAGCCTGAGCAATGGCAGGA 96376		C_ CACC
			TCTTGCT TGT CAGGCTGG		

			AGGACGG ACG GTCCGACC	
			TA A___	
GAM2460	TA-LRRP	3'	CCAGCCTGGGTGACAGAGCAAG 31712	
	A		TCTTGCTCTGTCACCCAGGCTGG	
			AGAACGAGACAGTGGGTCCGACC	
GAM2460	TADA3L	3'	TCCAGCCTGGGCAACAAGAGTG 22047	TG _ CA
	A		T CTCT GT CCCAGGCTGGA	
			A GAGA CA GGGTCCGACCT	
			GT A AC	
GAM2460	THEA	3'	TCCAGCCCAGGCAATAGAGTAA 66896	CA CA
	GA		TCTTGCTCTGT CC GGCTGGA	
			AGAATGAGATA GG CCGACCT	
			AC AC	
GAM2460	THEA	3'	TCCAGCCTGGGTGACAGAGTGA 66898	TG
			T CTCTGTCACCCAGGCTGGA	
			A GAGACAGTGGGTCCGACCT	
			GT	
GAM2460	TMG4	3'	TCCAGCCTGGGCGACAGAGCAA 44217	A
	GA		TCTTGCTCTGTC CCCAGGCTGGA	
			AGAACGAGACAG GGGTCCGACCT	
			C	
GAM2460	TOMM70A	3'	TCCAGCCTGGGCAATATAGCAA 29739	C CA
	GA		TCTTGCT TGT CCCAGGCTGGA	
			AGAACGA ATA GGGTCCGACCT	
			T AC	
GAM2460	TRIAD3	3'	TCCAGCCTGAGCAACAAAAGCA 96139	C_ CACC
	A		TTGCT TGT CAGGCTGGA	
			AACGA ACA GTCCGACCT	
			AA ACGA	
GAM2460	TSGA2	3'	TCCAGCCTGGGTGGCAGAGCGA 55956	
	GA		TCTTGCTCTGTCACCCAGGCTGGA	
			AGAGCGAGACGGTGGGTCCGACCT	
GAM2460	UBCE7IP5	3'	CCAGCCTGGGCGACGGAGT 30844	A
			GCTCTGTC CCCAGGCTGG	
			TGAGGCAG GGGTCCGACC	
			C	
GAM2460	USP24	3'	CCAGCCTGAGAGGAGTCAAGA 92791	_ G ACC
			TCTTG CTCT TC CAGGCTGG	

			AGAAC GAGG AG GTCCGACC		
			T _ A_		
GAM2460	UST	3'	TCCAGCCTGGGTGACAGAGTGA 20354	TG	
	GA		TCT CTCTGTCACCCAGGCTGGA		
			AGA GAGACAGTGGGTCCGACCT		
			GT		
GAM2460	VPS4B	3'	TCCAGCCTGGGCGACTGAATAA 18025	C T A	
			TTG TC GTC CCCAGGCTGGA		
			AAT AG CAG GGGTCCGACCT		
			A T C		
GAM2460	WBSCR21	3'	TCCAGCCTAGGCAACAGAGCAA 49306	CA C	
	GA		TCTTGCTCTGT CC AGGCTGGA		
			AGAACGAGACA GG TCCGACCT		
			AC A		
GAM2460	WBSCR23	3'	TCCAGCCTGGGCGACAAAAGTGA 47443	TG C A	
	GA		TCT CT TGTC CCCAGGCTGGA		
			AGA GA ACAG GGGTCCGACCT		
			GT A C		
GAM2460	WBSCR23	3'	TCCAGCCTGGGCGACAGAGCAA 47444	A	
	GA		TCTTGCTCTGTC CCCAGGCTGGA		
			AGAACGAGACAG GGGTCCGACCT		
			C		
GAM2460	WBSCR23	5'	TCCAGCCTGGGCGACAGAGCCA 47445	T A	
	GA		TCT GCTCTGTC CCCAGGCTGGA		
			AGA CGAGACAG GGGTCCGACCT		
			C C		
GAM2460	WBSCR23	3'	TCCAGCCTGGGTGATAGAGCAA 47446		
	GA		TCTTGCTCTGTCACCCAGGCTGGA		
			AGAACGAGATAGTGGGTCCGACCT		
GAM2460	WIRE	3'	TCCAGCCTGGGCGACAGAGCCA 78907	T A	
	GA		TCT GCTCTGTC CCCAGGCTGGA		
			AGA CGAGACAG GGGTCCGACCT		
			C C		
GAM2460	WSB1	3'	TCCAACCTGGACAACAGAGCGA 56978	CAC C	
	GA		TCTTGCTCTGT CCAGG TGGA		
			AGAGCGAGACA GGTCC ACCT		
			ACA A		
GAM2460	WSB1	3'	TCCAACCTGGACAACAGAGCGA 56979	CAC C	
	GA		TCTTGCTCTGT CCAGG TGGA		

AGAGCGAGACA GGTCC ACCT
 ACA A
 GAM2460 YME1L1 3' TCCAGCCTGGGCAACAGAGCAA 58439 CA
 GA TCTTGCTCTGT CCCAGGCTGGA
 ||||| |||||
 AGAACGAGACA GGGTCCGACCT
 AC
 GAM2460 YME1L1 3' TCCAGCCTGGGTGACAGAGTGA 58440 TG
 GA TCT CTCTGTCACCCAGGCTGGA
 || |||||
 AGA GAGACAGTGGGTCCGACCT
 GT
 GAM2460 ZAK 3' CCTGGGCAAGAGAACAAGA 34103 _ GTCA
 TCTTG CTCT CCCAGG
 |||| |||
 AGAAC GAGA GGGTCC
 AA AC_
 GAM2460 ZAK 3' TCCAGCCTGGATGACAGAGTGA 34109 TG C
 GA TCT CTCTGTCA CCAGGCTGGA
 || |||||
 AGA GAGACAGT GGTCCGACCT
 GT A
 GAM2460 ZFP106 3' TCCAGCCTGGGCGACAAGAGTG 42741 TG _ A
 A T CTCT GTC CCCAGGCTGGA
 | |||| |||||
 A GAGA CAG GGGTCCGACCT
 GT A C
 GAM2460 ZNF197 3' TCCAGCCTGGGCAACAAGAGCG 23760 _ CA
 A TTGCTCT GT CCCAGGCTGGA
 ||||| || |||||
 AGCGAGA CA GGGTCCGACCT
 A AC
 GAM2460 ZNF271 3' TCCAGCCTGGGCAACAGAGTGA 96968 TG CA
 GA TCT CTCTGT CCCAGGCTGGA
 || ||||| |||||
 AGA GAGACA GGGTCCGACCT
 GT AC
 GAM2460 ZNF271 3' TCCAGTCTGGGCAACAGAGCAA 96969 CA
 GA TCTTGCTCTGT CCCAGGCTGGA
 ||||| |||||
 AGAACGAGACA GGGTCTGACCT
 AC
 GAM2460 ZNF297B 5' CCAGCCTGGGTAAAAGAG 26652 GTC
 CTCT ACCCAGGCTGG
 |||| |||||
 GAGA TGGGTCCGACC
 AAA
 GAM2460 ZNF297B 5' TCCAGCCTGGGCAACAAGAGCA 26674 _ CA
 A TTGCTCT GT CCCAGGCTGGA
 ||||| || |||||

			AACGAGA CA GGGTCCGACCT		
			A AC		
GAM2460	ZNF297B	5'	TCCAGCCTGGGCAACAGAGCAA 26675	CA	
	GA		TCTTGCTCTGT CCCAGGCTGGA		
			AGAACGAGACA GGGTCCGACCT		
			AC		
GAM2460	ZNF333	3'	TCCAGCCTGGGCAACAGAGTGA 51595	TG	CA
			T CTCTGT CCCAGGCTGGA		
			A GAGACA GGGTCCGACCT		
			GT AC		
GAM2460	ZNF339	3'	TCCAGCCTGGGCAACAGAGTGG 41398	TG	CA
			T CTCTGT CCCAGGCTGGA		
			G GAGACA GGGTCCGACCT		
			GT AC		
GAM2460	LOC112687	3'	TCCAGCCTGGGCAACAGAGTGG 73243	TG	CA
	GA		TCT CTCTGT CCCAGGCTGGA		
			AGG GAGACA GGGTCCGACCT		
			GT AC		
GAM2460	LOC112868	3'	TCCAGCCTGACCCAGAGCAGA 73271	T	TCACC
			TCT GCTCTG CAGGCTGGA		
			AGA CGAGAC GTCCGACCT		
			_ CCCA_		
GAM2460	LOC113201	3'	TCCAGCTTGGGCACCAGAGCAA 57357		TCA
	GA		TCTTGCTCTG CCCAGGCTGGA		
			AGAACGAGAC GGGTTCGACCT		
			CAC		
GAM2460	LOC113523	3'	TCCAGCCTGGGCGACAGGGCAA 73434		A
	GA		TCTTGCTCTGTC CCCAGGCTGGA		
			AGAACGGGACAG GGGTCCGACCT		
			C		
GAM2460	LOC114987	3'	TCCAGCCTGGGCAACAAGAGCG 59800	_	CA
	A		TTGCTCT GT CCCAGGCTGGA		
			AGCGAGA CA GGGTCCGACCT		
			A AC		
GAM2460	LOC115129	3'	TCCAGCCTGAGCGACAGAGTAA 73629		ACC
	GA		TCTTGCTCTGTC CAGGCTGGA		
			AGAATGAGACAG GTCCGACCT		
			CGA		
GAM2460	LOC115196	3'	TCCAGCCTGGGAGACAGAGCGA 73661		A
	GA		TCTTGCTCTGTC CCCAGGCTGGA		

		AGAGCGAGACAG GGGTCCGACCT		
		A		
GAM2460	LOC115273 3'	TCCAGCCTGGGCAACAGAGTGA 73754	TG	CA
	GA	TCT CTCTGT CCCAGGCTGGA		
		AGA GAGACA GGGTCCGACCT		
		GT AC		
GAM2460	LOC116143 3'	TCCAGCCTGGGCAACTGAGCAA 74194	T	CA
	GA	TCTTGCTC GT CCCAGGCTGGA		
		AGAACGAG CA GGGTCCGACCT		
		T AC		
GAM2460	LOC116236 3'	TCCAGCCTGGGCGACAGAGTAA 74248		A
	GA	TCTTGCTCTGTC CCCAGGCTGGA		
		AGAATGAGACAG GGGTCCGACCT		
		C		
GAM2460	LOC116349 3'	TCCAGCCTGGGCAACAGAGCGA 74281		CA
	GG	TCTTGCTCTGT CCCAGGCTGGA		
		GGAGCGAGACA GGGTCCGACCT		
		AC		
GAM2460	LOC119504 5'	TCCAGCCTGGGCAACAAGAGGG 74449	G	_ CA
	A	TT CTCT GT CCCAGGCTGGA		
		AG GAGA CA GGGTCCGACCT		
		G A AC		
GAM2460	LOC120406 3'	TCCAGCCTGGGTGACAGAGCGA 76066		
	GA	TCTTGCTCTGTCACCCAGGCTGGA		
		AGAGCGAGACAGTGGGTCCGACCT		
GAM2460	LOC122704 3'	TCCAACCTGGGCGACAGGGCGA 74611	A	C
	GA	TCTTGCTCTGTC CCCAGG TGGA		
		AGAGCGGGACAG GGGTCC ACCT		
		C A		
GAM2460	LOC126282 3'	TCCAGCCTGGGTGACAGAGCAA 74967		
	GA	TCTTGCTCTGTCACCCAGGCTGGA		
		AGAACGAGACAGTGGGTCCGACCT		
GAM2460	LOC126669 3'	TCCAGCCTGAGTGACAGAGTGA 75951	TG	C
	GA	TCT CTCTGTAC CAGGCTGGA		
		AGA GAGACAGTG GTCCGACCT		
		GT A		
GAM2460	LOC127262 3'	TCCAGCCCGGGCGACAGAGCGA 76605	A	A
	GA	TCTTGCTCTGTC CCC GGCTGGA		

		AGAGCGAGACAG GGG CCGACCT		
		C C		
GAM2460	LOC127428 3'	TCCAGCCTGGGCAACAGAGTGA 75163	TG	CA
	GA	TCT CTCTGT CCCAGGCTGGA		
		AGA GAGACA GGGTCCGACCT		
		GT AC		
GAM2460	LOC128272 5'	CCAGGTGGGTGGCAGAGCAA 75240	GG	
		TTGCTCTGTCACCCA CTGG		
		AACGAGACGGTGGGT GACC		
		G_		
GAM2460	LOC129880 3'	TCCAGCTTGGGCAACAGAGCAA 75409	CA	
	GA	TCTTGCTCTGT CCCAGGCTGGA		
		AGAACGAGACA GGGTTCGACCT		
		AC		
GAM2460	LOC130026 3'	TCCAGCCTAGGCAACAGAGCAA 57441	CA C	
	GA	TCTTGCTCTGT CC AGGCTGGA		
		AGAACGAGACA GG TCCGACCT		
		AC A		
GAM2460	LOC130535 3'	TCCAGCCTGGGCAACAAGAATG 76655	TTG C CA	
	A	TC CT TGT CCCAGGCTGGA		
		AG GA ACA GGGTCCGACCT		
		TAA _ AC		
GAM2460	LOC130535 3'	TCCAGCCTGGGTGACAGAGCAA 76656		
	GA	TCTTGCTCTGTCACCCAGGCTGGA		
		AGAACGAGACAGTGGGTCCGACCT		
GAM2460	LOC131744 3'	TCCAGCCTGGGTGACAGAGTGA 76392	TG	
		T CTCTGTCACCCAGGCTGGA		
		A GAGACAGTGGGTCCGACCT		
		GT		
GAM2460	LOC131965 3'	TCCAGCCTGGGCGACAGAGTGA 75528	TG A	
	GA	TCT CTCTGTC CCCAGGCTGGA		
		AGA GAGACAG GGGTCCGACCT		
		GT C		
GAM2460	LOC133926 3'	TCCAGCCTGGGCGACAGAGCGA 75634	A	
	GA	TCTTGCTCTGTC CCCAGGCTGGA		
		AGAGCGAGACAG GGGTCCGACCT		
		C		
GAM2460	LOC134147 3'	TCCAGCCTGGACAACAGAGGGA 57967	G CAC	
	GA	TCTT CTCTGT CCAGGCTGGA		

		AGAG GAGACA GGTCCGACCT	
		G ACA	
GAM2460	LOC134265 3'	TCCAGCCTAAGCAAATAGCAAG 75657	C__ CACCC
	A	TCTTGCT TGT AGGCTGGA	
		AGAACGA ACG TCCGACCT	
		TAA AA__	
GAM2460	LOC135154 3'	TCCAGCCTGGGCAACAAGAGCG 75736	_ CA
	A	TTGCTCT GT CCCAGGCTGGA	
		AGCGAGA CA GGGTCCGACCT	
		A AC	
GAM2460	LOC135818 3'	TCCAGCCTGGGCAATAGGGTAA 75749	CA
	GA	TCTTGCTCTGT CCCAGGCTGGA	
		AGAATGGGATA GGGTCCGACCT	
		AC	
GAM2460	LOC137362 3'	TCCAGCCTGGGCAACAAGAGCA 75788	_ CA
	A	TTGCTCT GT CCCAGGCTGGA	
		AACGAGA CA GGGTCCGACCT	
		A AC	
GAM2460	LOC138389 3'	TCCAGCCTGGGCAACAAGAGTG 76744	TG _ CA
	A	T CTCT GT CCCAGGCTGGA	
		A GAGA CA GGGTCCGACCT	
		GT A AC	
GAM2460	LOC139422 3'	CCTGGGTGACAGAGCGAGA 76346	
		TCTTGCTCTGTCACCCAGG	
		AGAGCGAGACAGTGGGTCC	
GAM2460	LOC142927 3'	CCTGGGTGACAGAACGAGA 76944	C
		TCTTG TCTGTCACCCAGG	
		AGAGC AGACAGTGGGTCC	
		A	
GAM2460	LOC142937 3'	TCCAGCCTGGGCCACAGAACGA 57447	C CA
	GA	TCTTG TCTGT CCCAGGCTGGA	
		AGAGC AGACA GGGTCCGACCT	
		A CC	
GAM2460	LOC142948 3'	TCCAGCCTGGGTGACAGAGCGA 83780	
	GG	TCTTGCTCTGTCACCCAGGCTGGA	
		GGAGCGAGACAGTGGGTCCGACCT	
GAM2460	LOC143196 3'	TCCAGCTTGGCAACAGAGCGAG 83805	CAC
	A	TCTTGCTCTGT CCAGGCTGGA	

AGAGCGAGACA GGTTCGACCT
 AC_
 GAM2460 LOC143310 3' CCAGCCTGGGTGACAGAGCGAG 77040
 A TCTTGCTCTGTCACCCAGGCTGG
 |||||
 AGAGCGAGACAGTGGGTCCGACC

 GAM2460 LOC143465 3' CCAGCCTGGGTGACGGAGT 83870
 GCTCTGTCACCCAGGCTGG
 |||||
 TGAGGCAGTGGGTCCGACC

 GAM2460 LOC143888 3' TCCAGCCTGGGTGACAGAGTGA 77175 TG
 GA TCT CTCTGTCACCCAGGCTGGA
 ||| |||||
 AGA GAGACAGTGGGTCCGACCT
 GT
 GAM2460 LOC143943 3' TCCAGCCTGGGTGACAGAGCGA 83921
 GA TCTTGCTCTGTCACCCAGGCTGGA
 |||||
 AGAGCGAGACAGTGGGTCCGACCT

 GAM2460 LOC144289 3' TCCAGCCTGGGTGACAGAGTGA 83962 TG
 GA TCT CTCTGTCACCCAGGCTGGA
 ||| |||||
 AGA GAGACAGTGGGTCCGACCT
 GT
 GAM2460 LOC144308 5' TCCAGCCTGGGTGACAGAGCAA 83986
 TTGCTCTGTCACCCAGGCTGGA
 |||||
 AACGAGACAGTGGGTCCGACCT

 GAM2460 LOC144465 3' TCCAGCCTGGGCAACAAGAGCA 77351 _ CA
 A TTGCTCT GT CCCAGGCTGGA
 ||||| || |||||
 AACGAGA CA GGGTCCGACCT
 A AC
 GAM2460 LOC144465 3' TCCAGCCTGGGCAACAAGAGTG 77352 TG _ CA
 A T CTCT GT CCCAGGCTGGA
 | |||| || |||||
 A GAGA CA GGGTCCGACCT
 GT A AC
 GAM2460 LOC144519 5' TCCAGCCTGGGCGACAGAGTGA 77380 TG A
 GA TCT CTCTGTC CCCAGGCTGGA
 ||| ||||| |||||
 AGA GAGACAG GGGTCCGACCT
 GT C
 GAM2460 LOC144524 3' TCCAGCCTGGGTGACAGAGTGG 84067 TG
 GA TCT CTCTGTCACCCAGGCTGGA
 ||| ||||| |||||

		AGG GAGACAGTGGGTCCGACCT		
		GT		
GAM2460	LOC144563 3'	TCCAGCTTGGGCAACAGAGTAA 77405	CA	
	GA	TCTTGCTCTGT CCCAGGCTGGA		
		AGAATGAGACA GGGTTCGACCT		
		AC		
GAM2460	LOC144583 3'	TCCAGCCCGAGTGACAGAATGA 77422	GC	CCA
	GG	TCTT TCTGTAC GGCTGGA		
		GGAG AGACAGTG CCGACCT		
		TA AGC		
GAM2460	LOC144845 3'	TCCAGCCCGGGCGACAGAGCAA 57464	A	A
	GA	TCTTGCTCTGTC CCC GGCTGGA		
		AGAACGAGACAG GGG CCGACCT		
		C C		
GAM2460	LOC145216 3'	CCAGCCTAGCGACAGAGCAAGA 84219	ACCC	
		TCTTGCTCTGTC AGGCTGG		
		AGAACGAGACAG TCCGACC		
		CGA_		
GAM2460	LOC145231 3'	TCCAGCCTGAACAACATAACAA 84259	CTC	CACC
	GA	TCTTG TGT CAGGCTGGA		
		AGAAC ACA GTCCGACCT		
		AAT ACAA		
GAM2460	LOC145231 3'	TCCAGCCTGGGTGACAGTGTGA 84260	TG	T
		T C CTGTCACCCAGGCTGGA		
		A G GACAGTGGGTCCGACCT		
		GT T		
GAM2460	LOC145299 3'	CCTGGGCGACAGAGCGAGA 84275	A	
		TCTTGCTCTGTC CCCAGG		
		AGAGCGAGACAG GGGTCC		
		C		
GAM2460	LOC145333 3'	TCCAGCCTGGGCGACAGAGCGA 84304	A	
	GA	TCTTGCTCTGTC CCCAGGCTGGA		
		AGAGCGAGACAG GGGTCCGACCT		
		C		
GAM2460	LOC145387 3'	TCCAGCCTGGGCGACAGAGAGA 84344	TG	A
	GA	TCT CTCTGTC CCCAGGCTGGA		
		AGA GAGACAG GGGTCCGACCT		
		GA C		
GAM2460	LOC145438 3'	TCCAGCCTGGGCGACAGAGCGA 84316	A	
	GA	TCTTGCTCTGTC CCCAGGCTGGA		

		AGAGCGAGACAG GGGTCCGACCT	
		C	
GAM2460	LOC145482 3'	TCCAGCCTGGGCGACAAGAGTG 77747	TG _ A
	A	T CTCT GTC CCCAGGCTGGA	
		A GAGA CAG GGGTCCGACCT	
		GT A C	
GAM2460	LOC145483 3'	TCCAGCCTGGGCGAGCAGAGCAA 77759	CA
		TTGCTCTGT CCCAGGCTGGA	
		AACGAGACG GGGTCCGACCT	
		AC	
GAM2460	LOC145608 5'	TCCAGCCTGGGTGACAGAGCAA 84386	
	GA	TCTTGCTCTGTCACCCAGGCTGGA	
		AGAACGAGACAGTGGGTCCGACCT	
GAM2460	LOC145609 3'	TCCAGCCTGGGTGACAGAGCAA 84370	
	GA	TCTTGCTCTGTCACCCAGGCTGGA	
		AGAACGAGACAGTGGGTCCGACCT	
GAM2460	LOC145663 3'	TCCAGCCTGGGCGACAGAGCTA 84430	T A
	GA	TCT GCTCTGTC CCCAGGCTGGA	
		AGA CGAGACAG GGGTCCGACCT	
		T C	
GAM2460	LOC145757 3'	TCCAGCCTAGGTGACAGAGCGA 77942	C
	GA	TCTTGCTCTGTCACC AGGCTGGA	
		AGAGCGAGACAGTGG TCCGACCT	
		A	
GAM2460	LOC145820 3'	TCCAGCCTGGGCGACAGAGCAA 77980	A
	GA	TCTTGCTCTGTC CCCAGGCTGGA	
		AGAACGAGACAG GGGTCCGACCT	
		C	
GAM2460	LOC145945 5'	TCCAGCCTGAGCAACAGAGCAA 84571	CACC
	GA	TCTTGCTCTGT CAGGCTGGA	
		AGAACGAGACA GTCCGACCT	
		ACGA	
GAM2460	LOC146059 3'	TCCAGTCTGGGTAACAGAGCGA 78090	C
	GA	TCTTGCTCTGT ACCCAGGCTGGA	
		AGAGCGAGACA TGGGTCTGACCT	
		A	
GAM2460	LOC146229 3'	TCCAGCCTGGGCGACAGAGCGA 78317	A
	GA	TCTTGCTCTGTC CCCAGGCTGGA	

		AGAGCGAGACAG GGGTCCGACCT	
		C	
GAM2460	LOC146540 3'	TCCAGCCTGGGCTACAAAGCAG 78530	C CA
	GA	TCTTGCT TGT CCCAGGCTGGA	
		AGGACGA ACA GGGTCCGACCT	
		A TC	
GAM2460	LOC146713 3'	TCCAGCCTGGGCAACAGAGCAA 84740	CA
		TTGCTCTGT CCCAGGCTGGA	
		AACGAGACA GGGTCCGACCT	
		AC	
GAM2460	LOC146713 3'	TCCAGCCTGGTCAACAGAGCAA 84741	CAC
	GA	TCTTGCTCTGT CCAGGCTGGA	
		AGAACGAGACA GGTCCGACCT	
		ACT	
GAM2460	LOC146728 5'	TCCAGACTGGACAACAGAGCAA 84773	CAC G
		TTGCTCTGT CCAG CTGGA	
		AACGAGACA GGTC GACCT	
		ACA A	
GAM2460	LOC146756 3'	TCCAGCCTGGGCGACAGAGCGA 84813	A
	GA	TCTTGCTCTGTC CCCAGGCTGGA	
		AGAGCGAGACAG GGGTCCGACCT	
		C	
GAM2460	LOC146839 5'	TCCAGCCTGGGCAACATAGCAA 84854	C CA
	G	CTTGCT TGT CCCAGGCTGGA	
		GAACGA ACA GGGTCCGACCT	
		T AC	
GAM2460	LOC146895 3'	TCCAGCCTGGGTGACAAGAGCA 84875	—
	AGA	TCTTGCTCT GTCACCCAGGCTGGA	
		AGAACGAGA CAGTGGGTCCGACCT	
		A	
GAM2460	LOC146901 3'	CAGCCTAGACAACAGAGCAAGA 84894	CACCC
		TCTTGCTCTGT AGGCTG	
		AGAACGAGACA TCCGAC	
		ACAGA	
GAM2460	LOC146923 3'	TCCAGCCTGGGCGACAGAGTGA 78804	TG A
	GA	TCT CTCTGTC CCCAGGCTGGA	
		AGA GAGACAG GGGTCCGACCT	
		GT C	
GAM2460	LOC146958 3'	TCCAGCCTGGGTGACACAGCGA 84946	C
	GA	TCTTGCT TGTCACCCAGGCTGGA	

		AGAGCGA ACAGTGGGTCCGACCT		
		C		
GAM2460	LOC146958 3'	TCCAGCCTGGGTGACAGAGCGA 84948		
	GA	TCTTGCTCTGTCACCCAGGCTGGA		
		AGAGCGAGACAGTGGGTCCGACCT		
GAM2460	LOC147071 3'	TCCAGCCTGGGCGACAGAGCAA 73373		A
	GA	TCTTGCTCTGTC CCCAGGCTGGA		
		AGAACGAGACAG GGGTCCGACCT		
		C		
GAM2460	LOC147180 5'	TCCAGCCCAGGTGACAGAGTGA 85105	TG	A
		T CTCTGTCACCC GGCTGGA		
		A GAGACAGTGGG CCGACCT		
		GT C		
GAM2460	LOC147599 3'	TCCAGCCTGGGCAACAGAGAGA 85166	TG	CA
		TCT CTCTGT CCCAGGCTGGA		
		AGA GAGACA GGGTCCGACCT		
		— AC		
GAM2460	LOC147622 3'	TCCAGCCTGGGTGACAGAGCTA 85172	T	
	GA	TCT GCTCTGTCACCCAGGCTGGA		
		AGA CGAGACAGTGGGTCCGACCT		
		T		
GAM2460	LOC147649 3'	CCTGGGCGACAGAGCGAGA 79060		A
		TCTTGCTCTGTC CCCAGG		
		AGAGCGAGACAG GGGTCC		
		C		
GAM2460	LOC147664 3'	TCCAGCCTGGGCAACGAGAG 79049	—	CA
		CTCT GT CCCAGGCTGGA		
		GAGA CA GGGTCCGACCT		
		G AC		
GAM2460	LOC147669 3'	TCCAGCCTGGGTGACAAGGGAA 85186	G TC	
	GA	TCTT C TGTCACCCAGGCTGGA		
		AGAA G ACAGTGGGTCCGACCT		
		G GA		
GAM2460	LOC147727 5'	TCCAGTCTGGGCGACAGAGCGA 79140		A
	GA	TCTTGCTCTGTC CCCAGGCTGGA		
		AGAGCGAGACAG GGGTCTGACCT		
		C		
GAM2460	LOC147837 3'	CCAGCCTGGGCGACAGAGCCAG 79204	T	A
	A	TCT GCTCTGTC CCCAGGCTGG		

		AGA CGAGACAG GGGTCCGACC	
		C C	
GAM2460	LOC147837 3'	TCCAGCCTGGGCAGCAAGAGCA 79210	_ CA
	A	TTGCTCT GT CCCAGGCTGGA	
		AACGAGA CG GGGTCCGACCT	
		A AC	
GAM2460	LOC147990 3'	TCCAGCCTGGGCAACAGAGCAA 85236	CA
		TTGCTCTGT CCCAGGCTGGA	
		AACGAGACA GGGTCCGACCT	
		AC	
GAM2460	LOC148166 3'	TCCAGCCTAGGCGACGGGGCAA 79424	A C
	GA	TCTTGCTCTGTC CC AGGCTGGA	
		AGAACGGGGCAG GG TCCGACCT	
		C A	
GAM2460	LOC148206 3'	TCCAGCCTGGGCCACAAGGCAA 79466	TC CA
	GA	TCTTGC TGT CCCAGGCTGGA	
		AGAACG ACA GGGTCCGACCT	
		GA CC	
GAM2460	LOC148397 3'	CCAGCCTGGGCAACAAGAGTAA 79566	_ CA
		TTGCTCT GT CCCAGGCTGG	
		AATGAGA CA GGGTCCGACC	
		A AC	
GAM2460	LOC148534 3'	TCCAGCCTGGGCGACAGAGCAA 79640	A
	GA	TCTTGCTCTGTC CCCAGGCTGGA	
		AGAACGAGACAG GGGTCCGACCT	
		C	
GAM2460	LOC148758 5'	TCCAGCCTGGGCAACAAGAGCA 79727	_ CA
	A	TTGCTCT GT CCCAGGCTGGA	
		AACGAGA CA GGGTCCGACCT	
		A AC	
GAM2460	LOC148809 3'	TCCAGCCTGGGCGACAGAGCAA 79762	A
	GA	TCTTGCTCTGTC CCCAGGCTGGA	
		AGAACGAGACAG GGGTCCGACCT	
		C	
GAM2460	LOC148809 5'	TCCAGCCTGGGTGACAGAGCAA 79763	
	GA	TCTTGCTCTGTCACCCAGGCTGGA	
		AGAACGAGACAGTGGGTCCGACCT	
GAM2460	LOC148936 3'	TCCAGGTTGGGCAACAGAGCAA 85459	CA G
	GA	TCTTGCTCTGT CCCAG CTGGA	

		AGAACGAGACA GGGTT GACCT	
		AC G	
GAM2460	LOC149073 3'	TCCAGCCTGGGCAACAGTGTGA 85487	TG T CA
	GA	TCT C CTGT CCCAGGCTGGA	
		AGA G GACA GGGTCCGACCT	
		GT T AC	
GAM2460	LOC149113 5'	CCAGCCTGGGCTACAAGAG 79905	_ CA
		CTCT GT CCCAGGCTGG	
		GAGA CA GGGTCCGACC	
		A TC	
GAM2460	LOC149157 5'	TCCAGCCTGGTCCAGAGAGAAA 79943	G GTCAC
	GA	TCTT CTCT CCAGGCTGGA	
		AGAA GAGA GGTCCGACCT	
		A GACCT	
GAM2460	LOC149175 3'	TCCAGCCTGGGCGACAGAGCGA 79957	A
	GA	TCTTGCTCTGTC CCCAGGCTGGA	
		AGAGCGAGACAG GGGTCCGACCT	
		C	
GAM2460	LOC149194 5'	TCCAGCCTGGGCAACAAGAGCA 79991	_ CA
	A	TTGCTCT GT CCCAGGCTGGA	
		AACGAGA CA GGGTCCGACCT	
		A AC	
GAM2460	LOC149271 3'	TCCAGCCTGGGCAACAAGAGTG 80012	TG _ CA
	A	T CTCT GT CCCAGGCTGGA	
		A GAGA CA GGGTCCGACCT	
		GT A AC	
GAM2460	LOC149460 3'	CCTGGATGACAGAGCAAGA 85609	C
		TCTTGCTCTGTCA CCAGG	
		AGAACGAGACAGT GGTCC	
		A	
GAM2460	LOC149464 3'	CCAGCCTGGGCAACAAGAG 85588	_ CA
		CTCT GT CCCAGGCTGG	
		GAGA CA GGGTCCGACC	
		A AC	
GAM2460	LOC149464 5'	TCAGCTTGGGTGACAGAGCCAG 85599	T
	A	TCT GCTCTGTACCCAGGCTGG	
		AGA CGAGACAGTGGGTTCGACT	
		C	
GAM2460	LOC149579 5'	TCCAGCCTGTGTGACAGAGCAA 71695	C
	GA	TCTTGCTCTGTAC CAGGCTGGA	

		AGAACGAGACAGTG GTCCGACCT		
		T		
GAM2460	LOC149628 3'	TCCAGCCTGGGTGACAGAGCGA 80281		
	GA	TCTTGCTCTGTCACCCAGGCTGGA		
		AGAGCGAGACAGTGGGTCCGACCT		
GAM2460	LOC149672 5'	TCCAGCCTGGGCAACAGAGTGA 80339	TG	CA
	GA	TCT CTCTGT CCCAGGCTGGA		
		AGA GAGACA GGGTCCGACCT		
		GT AC		
GAM2460	LOC149705 3'	TCCAGCCTGGGTGACGAGTGA 85787	TG	T
		T CTC GTCACCCAGGCTGGA		
		A GAG CAGTGGGTCCGACCT		
		GT _		
GAM2460	LOC149711 3'	TCCAGCCTGGGTGACAGAGTGA 85856	TG	
	GA	TCT CTCTGTCACCCAGGCTGGA		
		AGA GAGACAGTGGGTCCGACCT		
		GT		
GAM2460	LOC149912 3'	TCCAGCCTGGGCGACAGTGACA 85883	CT_	A
		TG CTGTC CCCAGGCTGGA		
		AC GACAG GGGTCCGACCT		
		AGT C		
GAM2460	LOC150095 3'	TCCAGCCTGGGCAACAGAGCGA 85996		CA
	GA	TCTTGCTCTGT CCCAGGCTGGA		
		AGAGCGAGACA GGGTCCGACCT		
		AC		
GAM2460	LOC150139 3'	TCCAGCCTGGGTGACAGAGAGA 80413	TG	
		TCT CTCTGTCACCCAGGCTGGA		
		AGA GAGACAGTGGGTCCGACCT		
		—		
GAM2460	LOC150142 5'	CCAGCCTGGGCAACAAAGTAAG 80404	C	CA
	A	TCTTGCT TGT CCCAGGCTGG		
		AGAATGA ACA GGGTCCGACC		
		A AC		
GAM2460	LOC150185 3'	TCCAGCCTGGGTGACAGAGCGA 86070		
	GA	TCTTGCTCTGTCACCCAGGCTGGA		
		AGAGCGAGACAGTGGGTCCGACCT		
GAM2460	LOC150244 3'	TCCAGCCTGGGCGACAGAGCGA 80552		A
	GA	TCTTGCTCTGTC CCCAGGCTGGA		

		AGAGCGAGACAG GGGTCCGACCT	
		C	
GAM2460	LOC150245 3'	TCCAGCCTGGGTGACAGAATAA 86119	C
	GA	TCTTG TCTGTCACCCAGGCTGGA	
		AGAAT AGACAGTGGGTCCGACCT	
		A	
GAM2460	LOC150299 3'	TCCAGCCTGGCGACAGAGCAAG 86170	AC
	A	TCTTGCTCTGTC CCAGGCTGGA	
		AGAACGAGACAG GGTCCGACCT	
		C_	
GAM2460	LOC150319 3'	TCCAGCCTGGGCAACAAGAGCG 80477	_ CA
	A	TTGCTCT GT CCCAGGCTGGA	
		AGCGAGA CA GGGTCCGACCT	
		A AC	
GAM2460	LOC150358 3'	TCCAGCCTGGGCGACAGAGCGA 86101	A
	GA	TCTTGCTCTGTC CCCAGGCTGGA	
		AGAGCGAGACAG GGGTCCGACCT	
		C	
GAM2460	LOC150481 3'	TCCAGCCTGGTGACAGAGCAAG 80714	C
	A	TCTTGCTCTGTCACC AGGCTGGA	
		AGAACGAGACAGTGG TCCGACCT	
		-	
GAM2460	LOC150577 3'	TCCAGCCTGGATGACAGAGTGA 86260	TG C
		T CTCTGTCA CCAGGCTGGA	
		A GAGACAGT GGTCCGACCT	
		GT A	
GAM2460	LOC150622 3'	TCCAGCCTGGGCAACAAGAGCA 80769	_ CA
	A	TTGCTCT GT CCCAGGCTGGA	
		AACGAGA CA GGGTCCGACCT	
		A AC	
GAM2460	LOC150998 3'	CAGCCTGGGTGACAGAGCAAGA 86356	
		TCTTGCTCTGTCACCCAGGCTG	
		AGAACGAGACAGTGGGTCCGAC	
GAM2460	LOC151196 3'	TCCAGCCTGGGCAACACAGCAA 86456	C CA
	GA	TCTTGCT TGT CCCAGGCTGGA	
		AGAACGA ACA GGGTCCGACCT	
		C AC	
GAM2460	LOC151248 5'	CCTGGGCGACAGAGCGAGA 80992	A
		TCTTGCTCTGTC CCCAGG	

		AGAGCGAGACAG GGGTCC		
		C		
GAM2460	LOC151248 3'	TCCAGCCCAGGTAACAGAGTGA 80998	TG	C CA
	GA	TCT CTCTGT ACC GGCTGGA		
		AGA GAGACA TGG CCGACCT		
		GT A AC		
GAM2460	LOC151248 3'	TCCAGCCTGGTGACAGAGCGAG 80999		C
	A	TCTTGCTCTGTCACC AGGCTGGA		
		AGAGCGAGACAGTGG TCCGACCT		
		—		
GAM2460	LOC151429 3'	TCCAGCCTGGGCGACAGAGCAA 86549		A
	GA	TCTTGCTCTGTC CCCAGGCTGGA		
		AGAACGAGACAG GGGTCCGACCT		
		C		
GAM2460	LOC151429 3'	TCCAGCCTGGGTGACAGAGCAA 86550		
	GA	TCTTGCTCTGTCACCCAGGCTGGA		
		AGAACGAGACAGTGGGTCCGACCT		
GAM2460	LOC151438 3'	CCTGGGCAACACAGCAAGA 86555	C	CA
		TCTTGCT TGT CCCAGG		
		AGAACGA ACA GGGTCC		
		C AC		
GAM2460	LOC151446 3'	TCTGAACAACAGAGCAAGA 86575		CACC
		TCTTGCTCTGT CAGG		
		AGAACGAGACA GTCT		
		ACAA		
GAM2460	LOC151556 3'	TCCAGCCTGAGCAACAGAGCAA 81085		CACC
	GA	TCTTGCTCTGT CAGGCTGGA		
		AGAACGAGACA GTCCGACCT		
		ACGA		
GAM2460	LOC151602 3'	TCCAGCTTGGGTGACAGAGCGA 81114		
	GA	TCTTGCTCTGTCACCCAGGCTGGA		
		AGAGCGAGACAGTGGGTTCGACCT		
GAM2460	LOC151632 3'	TCCAGCCTGGGCAACAGAGTAA 86651		CA
	GA	TCTTGCTCTGT CCCAGGCTGGA		
		AGAATGAGACA GGGTCCGACCT		
		AC		
GAM2460	LOC151720 3'	TCCAGCCTGGGCGACAGAGCGA 81158		A
	GA	TCTTGCTCTGTC CCCAGGCTGGA		

		AGAGCGAGACAG GGGTCCGACCT		
		C		
GAM2460	LOC151904 3'	TCCAGCCTGGGCAACAGAGCGA 81210	CA	
	GA	TCTTGCTCTGT CCCAGGCTGGA		
		AGAGCGAGACA GGGTCCGACCT		
		AC		
GAM2460	LOC152002 3'	TCCAGCCTGGACGACAGAGTGA 81268	TG	AC
	GA	TCT CTCTGTC CCAGGCTGGA		
		AGA GAGACAG GGTCCGACCT		
		GT CA		
GAM2460	LOC152263 3'	TCCAGCCAGGATGACAGAGCAA 86860	C	A
	GA	TCTTGCTCTGTCA CC GGCTGGA		
		AGAACGAGACAGT GG CCGACCT		
		A A		
GAM2460	LOC152271 3'	TCCAGCCTGGGCAACAGAGTAA 81365	CA	
	GA	TCTTGCTCTGT CCCAGGCTGGA		
		AGAATGAGACA GGGTCCGACCT		
		AC		
GAM2460	LOC152283 3'	TCCAGCCTGGGCAACAAGAGTG 86875	TG	_ CA
	AGA	TCT CTCT GT CCCAGGCTGGA		
		AGA GAGA CA GGGTCCGACCT		
		GT A AC		
GAM2460	LOC152313 3'	TCCAGCCTGGGTGACAGAGCGA 86853		
	GA	TCTTGCTCTGTCACCCAGGCTGGA		
		AGAGCGAGACAGTGGGTCCGACCT		
GAM2460	LOC152316 3'	TCCAGCCTAGGCAACAGAGCGA 86794	CA	C
	GA	TCTTGCTCTGT CC AGGCTGGA		
		AGAGCGAGACA GG TCCGACCT		
		AC A		
GAM2460	LOC152317 3'	TCCAGCCTGAGTGACAGAACAA 86838	C	C
	GG	TCTTG TCTGTCAC CAGGCTGGA		
		GGAAC AGACAGTG GTCCGACCT		
		A A		
GAM2460	LOC152426 3'	TCCAGCCTGGGCGACAGAGTGA 86902	TG	A
	GA	TCT CTCTGTC CCCAGGCTGGA		
		AGA GAGACAG GGGTCCGACCT		
		GT C		
GAM2460	LOC152445 3'	TCCAGCCTGAGTGAGGAAGCAA 86965	_ G	C
		TTGCT CT TCAC CAGGCTGGA		

		AACGA GG AGTG GTCCGACCT	
		A _ A	
GAM2460	LOC152453 5'	CCAGACTGCAGAGCAAGA 81468	TCACC G
		TCTTGCTCTG CAG CTGG	
		AGAACGAGAC GTC GACC	
		_____ A	
GAM2460	LOC152453 3'	TCCAGCCTGGGCAACAAGAGCG 81480	_ CA
	A	TTGCTCT GT CCCAGGCTGGA	
		AGCGAGA CA GGGTCCGACCT	
		A AC	
GAM2460	LOC152453 3'	TCCAGCTTGGGTGACAGAGCGA 81481	
	GA	TCTTGCTCTGTCACCCAGGCTGGA	
		AGAGCGAGACAGTGGGTTCGACCT	
GAM2460	LOC152627 5'	TCCAGCCTGGATAAAAGAGCAA 81515	GTCAC
	GA	TCTTGCTCT CCAGGCTGGA	
		AGAACGAGA GGTCCGACCT	
		AAATA	
GAM2460	LOC152804 3'	TCCAGCCTGGGCAACAGAGCGA 87088	CA
	GG	TCTTGCTCTGT CCCAGGCTGGA	
		GGAGCGAGACA GGGTCCGACCT	
		AC	
GAM2460	LOC152860 3'	CCAGCCTGGGCAGCAAGA 81577	CTGTCA
		TCTTGCT CCCAGGCTGG	
		AGAACGA GGGTCCGACC	
		C_____	
GAM2460	LOC153077 3'	TCCAGCCTGGGCTACAGAGCAA 87133	CA
	GA	TCTTGCTCTGT CCCAGGCTGGA	
		AGAACGAGACA GGGTCCGACCT	
		TC	
GAM2460	LOC153146 3'	TCCAGCCTGGGTGACAGAGGGA 87148	G
	GA	TCTT CTCTGTCACCCAGGCTGGA	
		AGAG GAGACAGTGGGTCCGACCT	
		G	
GAM2460	LOC153338 3'	TCCAGCCTGGGTGACAGAGCAA 87198	
	GA	TCTTGCTCTGTCACCCAGGCTGGA	
		AGAACGAGACAGTGGGTCCGACCT	
GAM2460	LOC153579 3'	CCAGCCTGGGCCCGCAGA 81767	CA_
		TCTGT CCCAGGCTGG	

		AGACG GGGTCCGACC		
		CCC		
GAM2460	LOC153579 3'	TCCAGCCTGGGCGACAGAGCGA 81774	A	
	GA	TCTTGCTCTGTC CCCAGGCTGGA		
		AGAGCGAGACAG GGGTCCGACCT		
		C		
GAM2460	LOC153682 3'	TCCAGCCTGAGCGACAGAGCAA 87276	ACC	
	GA	TCTTGCTCTGTC CAGGCTGGA		
		AGAACGAGACAG GTCCGACCT		
		CGA		
GAM2460	LOC153688 3'	TCCAGCCTGGGCGACAGAGGGA 87333	G	A
	GA	TCTT CTCTGTC CCCAGGCTGGA		
		AGAG GAGACAG GGGTCCGACCT		
		G C		
GAM2460	LOC154089 3'	TCTGGGTGACAGAGCAAGA 81945		
		TCTTGCTCTGTCACCCAGG		
		AGAACGAGACAGTGGGTCT		
GAM2460	LOC154403 5'	CCAGCCTGGGCTACAAGAG 81971	_	CA
		CTCT GT CCCAGGCTGG		
		GAGA CA GGGTCCGACC		
		A TC		
GAM2460	LOC154739 5'	TCCAGCCTGGGCAACAGGTGAG 87443	TG T	CA
	A	TCT C CTGT CCCAGGCTGGA		
		AGA G GACA GGGTCCGACCT		
		GT _ AC		
GAM2460	LOC154739 3'	TCCAGCCTGGGTGACAGAGTGA 87444	TG	
	GA	TCT CTCTGTCACCCAGGCTGGA		
		AGA GAGACAGTGGGTCCGACCT		
		GT		
GAM2460	LOC154791 3'	TCCAGCCTGGGCAACAAGAGCA 82056	_	CA
	A	TTGCTCT GT CCCAGGCTGGA		
		AACGAGA CA GGGTCCGACCT		
		A AC		
GAM2460	LOC154877 3'	TCCAGCCTAGGTGATAGAGCAA 87576	C	
	GA	TCTTGCTCTGTCACC AGGCTGGA		
		AGAACGAGATAGTGG TCCGACCT		
		A		
GAM2460	LOC155006 3'	TCCAGCCTGGGCGGCAGAGCAA 82176	A	
	GA	TCTTGCTCTGTC CCCAGGCTGGA		

		AGAACGAGACGG GGGTCCGACCT	
		C	
GAM2460	LOC155054 3'	TCCAGCCTGGGTGACAGAGCAA 82206	
	GA	TCTTGCTCTGTCACCCAGGCTGGA	
		AGAACGAGACAGTGGGTCCGACCT	
GAM2460	LOC155072 3'	TCCAACCTGGGTGACAGAGCGA 87672	C
		TTGCTCTGTCACCCAGG TGGA	
		AGCGAGACAGTGGGTCC ACCT	
		A	
GAM2460	LOC155072 3'	TCCAGCCTGGGTGACTGAGCGA 87673	T
	GA	TCTTGCTC GTCACCCAGGCTGGA	
		AGAGCGAG CAGTGGGTCCGACCT	
		T	
GAM2460	LOC155376 3'	TCCAGCCTGGGTGACAAAGCAA 82251	C
	GA	TCTTGCT TGTCACCCAGGCTGGA	
		AGAACGA ACAGTGGGTCCGACCT	
		A	
GAM2460	LOC157247 5'	CCTGGGCAACATAGCAAGA 82294	C CA
		TCTTGCT TGT CCCAGG	
		AGAACGA ACA GGGTCC	
		T AC	
GAM2460	LOC157381 3'	CTGGATGACAGAGAAAGA 87733	G C
		TCTT CTCTGTCA CCAG	
		AGAA GAGACAGT GGTC	
		A A	
GAM2460	LOC157464 5'	TCCAGCCTGGGCAACGGGCGAG 87752	T CA
	A	TCTTGC CTGT CCCAGGCTGGA	
		AGAGCG GGCA GGGTCCGACCT	
		- AC	
GAM2460	LOC157562 5'	CCAGCTTGGATAAGAAAGCAAG 87772	CTGTCAC
	A	TCTTGCT CCAGGCTGG	
		AGAACGA GGTTCGACC	
		AAGAATA	
GAM2460	LOC157562 5'	TCCAGCCTGGGCAACATAGTGA 87776	TG C CA
	GA	TCT CT TGT CCCAGGCTGGA	
		AGA GA ACA GGGTCCGACCT	
		GT T AC	
GAM2460	LOC157657 3'	TCCAGCCTGGACAACACAGTGA 82437	TG C CAC
	GA	TCT CT TGT CCAGGCTGGA	

		AGA GA ACA GGTCCGACCT		
		GT C ACA		
GAM2460	LOC157737 3'	TCCAGCCTGGGCAACAGAGAGA 87846	TG	CA
	GA	TCT CTCTGT CCCAGGCTGGA		
		AGA GAGACA GGGTCCGACCT		
		GA AC		
GAM2460	LOC157983 3'	TCCAGCCTGGCGACAGAGCAAG 82544		AC
		CTTGCTCTGTC CCAGGCTGGA		
		GAACGAGACAG GGTCCGACCT		
		C_		
GAM2460	LOC158088 3'	TCCAGCCTGGCGACAGAGCAAG 87978		AC
	A	TCTTGCTCTGTC CCAGGCTGGA		
		AGAACGAGACAG GGTCCGACCT		
		C_		
GAM2460	LOC158160 3'	TCCAGCCTGGGTGACAGCGAGA 73476		CT
		TCTTGCT GTCACCCAGGCTGGA		
		AGAGCGA CAGTGGGTCCGACCT		
		—		
GAM2460	LOC158187 3'	TCCAGCCTGGGTGACAGAGCAA 87998		
	GA	TCTTGCTCTGTCACCCAGGCTGGA		
		AGAACGAGACAGTGGGTCCGACCT		
GAM2460	LOC158191 3'	TCCAGCCTGGCGACAGAGCTAG 82682	T	AC
	A	TCT GCTCTGTC CCAGGCTGGA		
		AGA CGAGACAG GGTCCGACCT		
		T C_		
GAM2460	LOC158235 3'	TCCAGCCTGGGCAACACAGAGA 88008	TG	CA__
	GA	TCT CTCTGT CCCAGGCTGGA		
		AGA GAGACA GGGTCCGACCT		
		— CAAC		
GAM2460	LOC158292 5'	TCCAGCCTGGGCAACAGAGCAA 88056		CA
	GA	TCTTGCTCTGT CCCAGGCTGGA		
		AGAACGAGACA GGGTCCGACCT		
		AC		
GAM2460	LOC158292 5'	TCCAGCCTGGGCGACAGAGCGA 88057		A
	GA	TCTTGCTCTGTC CCCAGGCTGGA		
		AGAGCGAGACAG GGGTCCGACCT		
		C		
GAM2460	LOC158337 3'	TCCAGCCTGGGTGACAGAGCGA 88112		
	GA	TCTTGCTCTGTCACCCAGGCTGGA		

AGAGCGAGACAGTGGGTCCGACCT

GAM2460 LOC158677 5' TCCAGCCTGGGTGACAGAGCAA 88252
GA TCTTGCTCTGTCACCCAGGCTGGA
|||||||
AGAACGAGACAGTGGGTCCGACCT

GAM2460 LOC158819 3' TCCAGCCTGGGTGACAGAGCGA 88286
GA TCTTGCTCTGTCACCCAGGCTGGA
|||||||
AGAGCGAGACAGTGGGTCCGACCT

GAM2460 LOC158987 3' TCCAGCCTGGGCAACAGAGGGA 88334 G CA
G CTT CTCTGT CCCAGGCTGGA
||| |||||
GAG GAGACA GGGTCCGACCT
G AC

GAM2460 LOC158987 3' TCCAGCCTGGGCAACATAGTGA 88335 TG C CA
GA TCT CT TGT CCCAGGCTGGA
||| ||| |||||
AGA GA ACA GGGTCCGACCT
GT T AC

GAM2460 LOC158987 3' TCCAGCCTGGGTGACAGAGCGA 88337
GA TCTTGCTCTGTCACCCAGGCTGGA
|||||||
AGAGCGAGACAGTGGGTCCGACCT

GAM2460 LOC159036 3' TCCAGCCTGGGCGACAGAGTGA 88351 TG A
GG TCT CTCTGTC CCCAGGCTGGA
||| ||||| |||||
GGA GAGACAG GGGTCCGACCT
GT C

GAM2460 LOC159053 3' TCCAGCCTGGGCAACAGTGAGA 88377 TG CT CA
TCT CT GT CCCAGGCTGGA
||| || |||||
AGA GA CA GGGTCCGACCT
GT _ AC

GAM2460 LOC159110 3' CCAGCCTGGGCAACAGAACAGG 82986 C CA
A TCTTG TCTGT CCCAGGCTGG
|||| ||||| |||||
AGGAC AGACA GGGTCCGACC
A AC

GAM2460 LOC159116 3' CCAGCCTGGGCAACAGAACAGG 82969 C CA
A TCTTG TCTGT CCCAGGCTGG
|||| ||||| |||||
AGGAC AGACA GGGTCCGACC
A AC

GAM2460 LOC161823 3' TCCAGCCTGGGCAACAGAGTGA 83176 TG CA
T CTCTGT CCCAGGCTGGA
| ||||| |||||

		A GAGACA GGGTCCGACCT	
		GT AC	
GAM2460	LOC162962 3'	TCCAGCCTGGGTGACAGCGAGA 83260	CT
		TCTTGCT GTCACCCAGGCTGGA	
		AGAGCGA CAGTGGGTCCGACCT	
		—	
GAM2460	LOC166042 5'	AGCAAGTGCAGAGCAAGA 83504	T CCAG
		TCTTGCTCTG CAC GCT	
		AGAACGAGAC GTG CGA	
		— AA —	
GAM2460	LOC170395 3'	TCCAGCCTGGGCAACAAGAGCA 76878	_ CA
	A	TTGCTCT GT CCCAGGCTGGA	
		AACGAGA CA GGGTCCGACCT	
		A AC	
GAM2460	LOC196047 5'	TCCAGCCTGGGTGACAGAGCGA 91167	
	GA	TCTTGCTCTGTCACCCAGGCTGGA	
		AGAGCGAGACAGTGGGTCCGACCT	
GAM2460	LOC196529 3'	TCTAGCCTGGGTGACAAGAGCA 89142	_
	AGA	TCTTGCTCT GTCACCCAGGCTGGA	
		AGAACGAGA CAGTGGGTCCGATCT	
		A	
GAM2460	LOC196540 3'	TCCAGCCTGGGTGACAGAGTGA 91208	TG
	GA	TCT CTCTGTCACCCAGGCTGGA	
		AGA GAGACAGTGGGTCCGACCT	
		GT	
GAM2460	LOC197196 3'	TCCAGCCTGGGCGACAAGAGCG 91306	_ A
	A	TTGCTCT GTC CCCAGGCTGGA	
		AGCGAGA CAG GGGTCCGACCT	
		A C	
GAM2460	LOC197201 3'	TCCAGCCTGGGCAACACAGCAA 89288	C CA
	GA	TCTTGCT TGT CCCAGGCTGGA	
		AGAACGA ACA GGGTCCGACCT	
		C AC	
GAM2460	LOC197362 3'	TCCAGCCTGGGTGACAGAGTGA 91312	TG
	GA	TCT CTCTGTCACCCAGGCTGGA	
		AGA GAGACAGTGGGTCCGACCT	
		GT	
GAM2460	LOC199858 3'	TCCAGCCTGGGCGACAGAGCGA 89803	A
	GA	TCTTGCTCTGTC CCCAGGCTGGA	

		AGAGCGAGACAG GGGTCCGACCT	
		C	
GAM2460	LOC199923 3'	TCCAGCCTGGACGACAGAGCAA 89874	AC
	GA	TCTTGCTCTGTC CCAGGCTGGA	
		AGAACGAGACAG GGTCCGACCT	
		CA	
GAM2460	LOC199923 3'	TCCAGCCTGGGCAACTGAGCAA 89876	T CA
		TTGCTC GT CCCAGGCTGGA	
		AACGAG CA GGGTCCGACCT	
		T AC	
GAM2460	LOC200014 3'	TCCAGCCTGGGCGACAGAGCAA 89948	A
	GA	TCTTGCTCTGTC CCCAGGCTGGA	
		AGAACGAGACAG GGGTCCGACCT	
		C	
GAM2460	LOC200251 3'	TCCAGCCTAGGCAACAAGAGCA 90067	_ CA C
	A	TTGCTCT GT CC AGGCTGGA	
		AACGAGA CA GG TCCGACCT	
		A AC A	
GAM2460	LOC200316 3'	TCCAGTTTGAGCAACAGATCAA 90194	C CACC
	GA	TCTTG TCTGT CAGGCTGGA	
		AGAAC AGACA GTTTGACCT	
		T ACGA	
GAM2460	LOC200317 3'	TCCAGCCTGGGCAACAAGAGTG 90229	TG _ CA
	A	T CTCT GT CCCAGGCTGGA	
		A GAGA CA GGGTCCGACCT	
		GT A AC	
GAM2460	LOC200728 3'	TCCATCCTGGGTGACAGAGCAA 91687	C
	GA	TCTTGCTCTGTCACCCAGG TGGA	
		AGAACGAGACAGTGGGTCC ACCT	
		T	
GAM2460	LOC200853 3'	TCCAGCCTGGGAGACAGAGCGA 90335	A
		TTGCTCTGTC CCCAGGCTGGA	
		AGCGAGACAG GGGTCCGACCT	
		A	
GAM2460	LOC200904 3'	TCTAGCCTGGGCAACAGAGTAA 91785	CA
	GA	TCTTGCTCTGT CCCAGGCTGGA	
		AGAATGAGACA GGGTCCGATCT	
		AC	
GAM2460	LOC200918 3'	TCCAGCCTGGGCGACAAGAGTG 90370	TG _ A
	A	T CTCT GTC CCCAGGCTGGA	

		A GAGA CAG GGGTCCGACCT		
		GT A C		
GAM2460	LOC200940 3'	TCCAGCCTGGGCGACAGAGTGA 90396	TG	A
	GA	TCT CTCTGTC CCCAGGCTGGA		
		AGA GAGACAG GGGTCCGACCT		
		GT C		
GAM2460	LOC201173 3'	TCCAGCCTGGGCGACAGAGCAA 88694		A
	GA	TCTTGCTCTGTC CCCAGGCTGGA		
		AGAACGAGACAG GGGTCCGACCT		
		C		
GAM2460	LOC201182 5'	TCCAGCCTGGTCAACAGAGCAA 91338		CAC
	GA	TCTTGCTCTGT CCAGGCTGGA		
		AGAACGAGACA GGTCCGACCT		
		ACT		
GAM2460	LOC201220 3'	TCCAGCCTGGGTGACAGAGCAA 88727		
	GA	TCTTGCTCTGTCACCCAGGCTGGA		
		AGAACGAGACAGTGGGTCCGACCT		
GAM2460	LOC201252 3'	TCTAGCCTGAGTGACAGAGCAG 89555		C
		TTGCTCTGTCAC CAGGCTGGA		
		GACGAGACAGTG GTCCGATCT		
		A		
GAM2460	LOC201264 3'	CTGGGCGACAGAGCCAGA 91348	T	A
		TCT GCTCTGTC CCCAG		
		AGA CGAGACAG GGGTC		
		C C		
GAM2460	LOC201564 3'	TCCAGCCTGGGCAACAAGAGCA 81277		_ CA
	A	TTGCTCT GT CCCAGGCTGGA		
		AACGAGA CA GGGTCCGACCT		
		A AC		
GAM2460	LOC201685 3'	TCAAGCCTGGACAACAGGGCAA 91846		CAC G
	GA	TCTTGCTCTGT CCAGGCT GA		
		AGAACGGGACA GGTCCGA CT		
		ACA A		
GAM2460	LOC201689 3'	TCCAGCCTGGGTGACAGGGTGA 67736	TG	
	GA	TCT CTCTGTCACCCAGGCTGGA		
		AGA GGGACAGTGGGTCCGACCT		
		GT		
GAM2460	LOC201705 3'	TCCAGCCTGGGTGACAGAGTCA 91856	T	
	GA	TCT GCTCTGTCACCCAGGCTGGA		

		AGA TGAGACAGTGGGTCCGACCT		
		C		
GAM2460	LOC201868 5'	CCAGCCTGGGCTACAAGAG	90518	_ CA
		CTCT GT CCCAGGCTGG		
		GAGA CA GGGTCCGACC		
		A TC		
GAM2460	LOC201895 3'	TCCAGCCTAAGCAATAGAGCGA	90548	CACCC
	GA	TCTTGCTCTGT AGGCTGGA		
		AGAGCGAGATA TCCGACCT		
		ACGAA		
GAM2460	LOC201911 3'	TCCAGCCTGGGCAACAAGAGCA	91870	_ CA
	A	TTGCTCT GT CCCAGGCTGGA		
		AACGAGA CA GGGTCCGACCT		
		A AC		
GAM2460	LOC201931 3'	TCCAGCCTGGGCGACAGAGCGA	90569	A
	GA	TCTTGCTCTGTC CCCAGGCTGGA		
		AGAGCGAGACAG GGGTCCGACCT		
		C		
GAM2460	LOC202020 3'	TCCAGCCCGGGCGACAGAGTGA	90603	TG A A
	GA	TCT CTCTGTC CCC GGCTGGA		
		AGA GAGACAG GGG CCGACCT		
		GT C C		
GAM2460	LOC202781 3'	TCCAGCCTGGACGATATAGCCA	91975	T C AC
	GA	TCT GCT TGTC CCAGGCTGGA		
		AGA CGA ATAG GGTCCGACCT		
		C T CA		
GAM2460	LOC202781 3'	TCCAGCCTGGGCGACAGAGCGA	91976	A
	GA	TCTTGCTCTGTC CCCAGGCTGGA		
		AGAGCGAGACAG GGGTCCGACCT		
		C		
GAM2460	LOC202868 3'	TCCAACCTGGGTGACAGAGCGA	92009	C
		TTGCTCTGTCACCCAGG TGGA		
		AGCGAGACAGTGGGTCC ACCT		
		A		
GAM2460	LOC202868 3'	TCCAGCCTGGGTGACAGAGCGA	92010	
	GA	TCTTGCTCTGTCACCCAGGCTGGA		
		AGAGCGAGACAGTGGGTCCGACCT		
GAM2460	LOC203025 3'	TCCAGCCTGGGCAACAAGAGCA	90750	_ CA
	A	TTGCTCT GT CCCAGGCTGGA		

		AACGAGA CA GGGTCCGACCT		
		A AC		
GAM2460	LOC203083 3'	TCCAGCCTGGGCAACAGAGTAA 92095	CA	
	GA	TCTTGCTCTGT CCCAGGCTGGA		
		AGAATGAGACA GGGTCCGACCT		
		AC		
GAM2460	LOC203276 3'	TCCAGCCTGGGCAACAGAGTGA 92130	TG	CA
	GA	TCT CTCTGT CCCAGGCTGGA		
		AGA GAGACA GGGTCCGACCT		
		GT AC		
GAM2460	LOC203276 3'	TCCAGCCTGGGTGACACAGTGA 92131	TG	C
	GA	TCT CT TGTCACCCAGGCTGGA		
		AGA GA ACAGTGGGTCCGACCT		
		GT C		
GAM2460	LOC203289 3'	TCCAGCCTGGCGACAGAGCAAG 90871		AC
		CTTGCTCTGTC CCAGGCTGGA		
		GAACGAGACAG GGTCCGACCT		
		C_		
GAM2460	LOC203305 3'	TCCAGCCTGGGCAACAGAGTGA 92183	TG	CA
	GA	TCT CTCTGT CCCAGGCTGGA		
		AGA GAGACA GGGTCCGACCT		
		GT AC		
GAM2460	LOC203305 3'	TCCAGCCTGGGTGACACAGTGA 92184	TG	C
	GA	TCT CT TGTCACCCAGGCTGGA		
		AGA GA ACAGTGGGTCCGACCT		
		GT C		
GAM2460	LOC203350 3'	TCCAGCCTGGATGACAGAGTGA 92250	TG	C
	GA	TCT CTCTGTCA CCAGGCTGGA		
		AGA GAGACAGT GGTCCGACCT		
		GT A		
GAM2460	LOC203378 3'	TCCAGCCTGGGCGACAGAACAA 92303	C	A
	GA	TCTTG TCTGTC CCCAGGCTGGA		
		AGAAC AGACAG GGGTCCGACCT		
		A C		
GAM2460	LOC219347 3'	TCCAGCCTGGGCAACAGAGTGA 94581	TG	CA
	GA	TCT CTCTGT CCCAGGCTGGA		
		AGA GAGACA GGGTCCGACCT		
		GT AC		
GAM2460	LOC219376 3'	CCTGGGTGACACAGCAAGA 95514	C	
		TCTTGCT TGTCACCCAGG		

		AGAACGA ACAGTGGGTCC		
		C		
GAM2460	LOC219540 3'	TCCAGCCTGGGCGACAGAGCGA 95247	A	
	GA	TCTTGCTCTGTC CCCAGGCTGGA		
		AGAGCGAGACAG GGGTCCGACCT		
		C		
GAM2460	LOC219627 3'	TCCAGCCTGGGCAACAAGCGA 93812	C CA	
		TTGCT TGT CCCAGGCTGGA		
		AGCGA ACA GGGTCCGACCT		
		_ AC		
GAM2460	LOC219627 3'	TCCAGCTGGGCGACAGAGCGAG 93813	A G	
	A	TCTTGCTCTGTC CCCAG CTGGA		
		AGAGCGAGACAG GGGTC GACCT		
		C _		
GAM2460	LOC219649 3'	TCCAGCCTAGGCAACAAGAGC 94557	_ CA C	
		GCTCT GT CC AGGCTGGA		
		CGAGA CA GG TCCGACCT		
		A AC A		
GAM2460	LOC219649 3'	TCCAGCCTGGGCGACAGAGTGA 94558	TG A	
	GA	TCT CTCTGTC CCCAGGCTGGA		
		AGA GAGACAG GGGTCCGACCT		
		GT C		
GAM2460	LOC219672 5'	TCCAGCCTGGGCAACAAGAGTG 92973	TG _ CA	
	A	T CTCT GT CCCAGGCTGGA		
		A GAGA CA GGGTCCGACCT		
		GT A AC		
GAM2460	LOC219722 5'	CCAGCCTGGGCAACAGAACAAG 94677	C CA	
	A	TCTTG TCTGT CCCAGGCTGG		
		AGAAC AGACA GGGTCCGACC		
		A AC		
GAM2460	LOC219919 3'	TCCAGCCTGGGCAACAGAGTAA 94933	CA	
	GA	TCTTGCTCTGT CCCAGGCTGGA		
		AGAATGAGACA GGGTCCGACCT		
		AC		
GAM2460	LOC220506 3'	TCCAGCCTGGGCAACAGAACAA 74521	C CA	
	GA	TCTTG TCTGT CCCAGGCTGGA		
		AGAAC AGACA GGGTCCGACCT		
		A AC		
GAM2460	LOC220549 3'	TCCAGCCTGGGTGACAGAATGA 94511	GC	
	GA	TCTT TCTGTCACCCAGGCTGGA		

		AGAG AGACAGTGGGTCCGACCT		
		TA		
GAM2460	LOC220662 3'	TCCAGCCTGGGCAACACGAGCG 92831	_	CA
	A	TTGCTC TGT CCCAGGCTGGA		
		AGCGAG ACA GGGTCCGACCT		
		C AC		
GAM2460	LOC220906 3'	TCCAGCCTGGGCAACAAGCGA 93037	C	CA
		TTGCT TGT CCCAGGCTGGA		
		AGCGA ACA GGGTCCGACCT		
		_ AC		
GAM2460	LOC220906 3'	TCCAGCTGGGCGACAGAGCGAG 93038	A	G
	A	TCTTGCTCTGTC CCCAG CTGGA		
		AGAGCGAGACAG GGGTC GACCT		
		C _		
GAM2460	LOC220992 3'	TCCAGCCTGGGCAACATAGCAA 93110	C	CA
	GA	TCTTGCT TGT CCCAGGCTGGA		
		AGAACGA ACA GGGTCCGACCT		
		T AC		
GAM2460	LOC221042 3'	TCCAGCCTGGGTGACAGAGCAA 94807		
	GA	TCTTGCTCTGTCACCCAGGCTGGA		
		AGAACGAGACAGTGGGTCCGACCT		
GAM2460	LOC221069 3'	TCCAGCCTGGGCGACAGAGCAA 94821	A	
	GA	TCTTGCTCTGTC CCCAGGCTGGA		
		AGAACGAGACAG GGGTCCGACCT		
		C		
GAM2460	LOC221271 3'	TCCAGCCTGGGCAACAGAGGGA 93530	G	CA
	GA	TCTT CTCTGT CCCAGGCTGGA		
		AGAG GAGACA GGGTCCGACCT		
		G AC		
GAM2460	LOC221271 3'	TCCAGCCTGGGCGACATCTAGA 93531	TGCTC	A
		TCT TGTC CCCAGGCTGGA		
		AGA ACAG GGGTCCGACCT		
		TCT__ C		
GAM2460	LOC221271 3'	TCCAGCCTGGGTGACAGAGCGA 93532		
	GA	TCTTGCTCTGTCACCCAGGCTGGA		
		AGAGCGAGACAGTGGGTCCGACCT		
GAM2460	LOC221288 3'	TCCAGCCTGGGCGACAGAGTGA 95263	TG	A
	GA	TCT CTCTGTC CCCAGGCTGGA		

		AGA GAGACAG GGGTCCGACCT	
		GT C	
GAM2460	LOC221337 3'	TCCAGCCTGGGCAACAAGAGTG 93738	TG _ CA
	A	T CTCT GT CCCAGGCTGGA	
		A GAGA CA GGGTCCGACCT	
		GT A AC	
GAM2460	LOC221410 3'	TCCAGCCTGGGTGACAGAGCGA 93699	
	GA	TCTTGCTCTGTCACCCAGGCTGGA	
		AGAGCGAGACAGTGGGTCCGACCT	
GAM2460	LOC221474 3'	CCTGGGTGACAGAGCGAGA 93994	
		TCTTGCTCTGTCACCCAGG	
		AGAGCGAGACAGTGGGTCC	
GAM2460	LOC221477 3'	TCCAGCCTGGGCGACAGAGCGA 93776	A
		TTGCTCTGTC CCCAGGCTGGA	
		AGCGAGACAG GGGTCCGACCT	
		C	
GAM2460	LOC221489 3'	CCAGCCTGGGTGATAAGAG 95287	_
		CTCT GTCACCCAGGCTGG	
		GAGA TAGTGGGTCCGACC	
		A	
GAM2460	LOC221490 3'	CAGCCTAGGCGACAGAGCAAGA 95299	A C
		TCTTGCTCTGTC CC AGGCTG	
		AGAACGAGACAG GG TCCGAC	
		C A	
GAM2460	LOC221543 3'	TCCAGCCTGGGCAACAAGAGTA 95387	_ CA
	AGA	TCTTGCTCT GT CCCAGGCTGGA	
		AGAATGAGA CA GGGTCCGACCT	
		A AC	
GAM2460	LOC221543 5'	TCCAGCCTGGGCGACAGAGCAA 95388	A
	GA	TCTTGCTCTGTC CCCAGGCTGGA	
		AGAACGAGACAG GGGTCCGACCT	
		C	
GAM2460	LOC221641 3'	TAGCCTGGGTGACAGAGCAAGA 95347	
		TCTTGCTCTGTCACCCAGGCTG	
		AGAACGAGACAGTGGGTCCGAT	
GAM2460	LOC221641 5'	TCCAGCCTGGGTGGCAGAGCGA 95348	
	GA	TCTTGCTCTGTCACCCAGGCTGGA	

AGAGCGAGACGGTGGGTCCGACCT

GAM2460 LOC221795 3' TCCAGCCTGGGCAACAGAGTAA 94081 CA
GA TCTTGCTCTGT CCCAGGCTGGA
||||||| |||||||
AGAATGAGACA GGGTCCGACCT
AC

GAM2460 LOC221943 5' TCCAGCCTGGGCGACAGAGCAA 95625 A
GA TCTTGCTCTGTC CCCAGGCTGGA
||||||| |||||||
AGAACGAGACAG GGGTCCGACCT
C

GAM2460 LOC221954 5' TCCAGCCTGGGCAACAGAGCGA 95651 CA
GA TCTTGCTCTGT CCCAGGCTGGA
||||||| |||||||
AGAGCGAGACA GGGTCCGACCT
AC

GAM2460 LOC221954 5' TCCAGCCTGGGTGACAGAGTAA 95652
GA TCTTGCTCTGTCACCCAGGCTGGA
|||||||
AGAATGAGACAGTGGGTCCGACCT

GAM2460 LOC221954 5' TCCAGCTTGGGCGACAGAGCAA 95653 A
GA TCTTGCTCTGTC CCCAGGCTGGA
||||||| |||||||
AGAACGAGACAG GGGTTCGACCT
C

GAM2460 LOC222008 5' TCCAGCCTGGGCTCCGCAGGA 95660 TCTGTCA
TCTTGC CCCAGGCTGGA
||||| |||||||
AGGACG GGGTCCGACCT
CCTC__

GAM2460 LOC222060 5' TCCAGCCTGGGCGACAGAGCAA 95758 A
GA TCTTGCTCTGTC CCCAGGCTGGA
||||||| |||||||
AGAACGAGACAG GGGTCCGACCT
C

GAM2460 LOC222160 3' TCCAGCCTGGGCAGCAGAGGAA 95791 G CA
GA TCTT CTCTGT CCCAGGCTGGA
||| ||||| |||||||
AGAA GAGACG GGGTCCGACCT
G AC

GAM2460 LOC222160 5' TCCAGCCTGGGCGACAGAGCAA 95792 A
GA TCTTGCTCTGTC CCCAGGCTGGA
||||||| |||||||
AGAACGAGACAG GGGTCCGACCT
C

GAM2460 LOC222256 3' TCTAGCCTGGGTGACAAAGCAA 95912 C
GA TCTTGCT TGTCACCCAGGCTGGA
||||| |||||||

		AGAACGA ACAGTGGGTCCGATCT		
		A		
GAM2460	LOC222865 3'	TCCAGCCTGAGTGACAGAGCGA 94450		C
	GA	TCTTGCTCTGTAC CAGGCTGGA		
		AGAGCGAGACAGTG GTCCGACCT		
		A		
GAM2460	LOC253039 3'	TCCAGCCTGGGCGACAGAGCAA 97867		A
	GA	TCTTGCTCTGTC CCCAGGCTGGA		
		AGAACGAGACAG GGGTCCGACCT		
		C		
GAM2460	LOC253128 3'	AGACAGGCACAGAGCAAGA 96575		CAC AGG
		TCTTGCTCTGT CC CT		
		AGAACGAGACA GG GA		
		C__ ACA		
GAM2460	LOC253532 3'	TCCAGCCTGGGTGACAAAGCAA 97740		C
	GA	TCTTGCT TGTCACCCAGGCTGGA		
		AGAACGA ACAGTGGGTCCGACCT		
		A		
GAM2460	LOC253612 5'	TCCAGCCTAGGCAACAGAGTGA 98559	TG	CA C
	GA	TCT CTCTGT CC AGGCTGGA		
		AGA GAGACA GG TCCGACCT		
		GT AC A		
GAM2460	LOC253639 3'	TCCAGCCTGGGCGACAGAGTGA 97517	TG	A
	GA	TCT CTCTGTC CCCAGGCTGGA		
		AGA GAGACAG GGGTCCGACCT		
		GT C		
GAM2460	LOC253778 5'	TCCAGCCTGGGCGACAGAGTGA 96527	TG	A
	GA	TCT CTCTGTC CCCAGGCTGGA		
		AGA GAGACAG GGGTCCGACCT		
		GT C		
GAM2460	LOC253786 3'	TCCAGCCTGGGCAATAGAGCAA 98834		CA
	GA	TCTTGCTCTGT CCCAGGCTGGA		
		AGAACGAGATA GGGTCCGACCT		
		AC		
GAM2460	LOC253832 3'	TCCAGCCTGGGCGACGAGTGA 96593	TG T A	
		T CTC GTC CCCAGGCTGGA		
		A GAG CAG GGGTCCGACCT		
		GT _ C		
GAM2460	LOC253840 5'	TCCAGCCTGGGCAACAGAGCAA 97914		CA
	GA	TCTTGCTCTGT CCCAGGCTGGA		

	AGAACGAGACA GGGTCCGACCT		
	AC		
GAM2460 LOC253906 3'	TTGGGTGACAGAGTAAGA 98302		
	TCTTGCTCTGTCACCCAG		
	AGAATGAGACAGTGGGTT		
GAM2460 LOC254041 5'	CAGCCTGGACGACAGAGCAAGA 96552	AC	
	TCTTGCTCTGTC CCAGGCTG		
	AGAACGAGACAG GGTCCGAC		
	CA		
GAM2460 LOC254100 3'	TCCAGCCTGGGCAACAGAGTGA 98160	TG	CA
GA	TCT CTCTGT CCCAGGCTGGA		
	AGA GAGACA GGGTCCGACCT		
	GT AC		
GAM2460 LOC254176 3'	TCCAGCCTGGGCAACAGAGTAA 99176	CA	
GA	TCTTGCTCTGT CCCAGGCTGGA		
	AGAATGAGACA GGGTCCGACCT		
	AC		
GAM2460 LOC254243 3'	TCCAGCCTGGGCAACAGAGTGA 99269	TG	CA
GA	TCT CTCTGT CCCAGGCTGGA		
	AGA GAGACA GGGTCCGACCT		
	GT AC		
GAM2460 LOC254243 3'	TCCAGCCTGGGTGACACAGTGA 99270	TG	C
GA	TCT CT TGTCACCCAGGCTGGA		
	AGA GA ACAGTGGGTCCGACCT		
	GT C		
GAM2460 LOC254531 5'	TCCAGCCTGGGTGACAGAGCAA 96673		
GA	TCTTGCTCTGTCACCCAGGCTGGA		
	AGAACGAGACAGTGGGTCCGACCT		
GAM2460 LOC254659 3'	TCCAGAGTGGGAAACAGAGCAA 96822	CA	GG
GA	TCTTGCTCTGT CCA CTGGA		
	AGAACGAGACA GGGT GACCT		
	AA GA		
GAM2460 LOC254756 3'	TCCAGCCTGGGCAATAGAGTAA 99212	CA	
GA	TCTTGCTCTGT CCCAGGCTGGA		
	AGAATGAGATA GGGTCCGACCT		
	AC		
GAM2460 LOC254808 3'	TCCAGCCTGGGCAACAGAGCAA 98810	CA	
GA	TCTTGCTCTGT CCCAGGCTGGA		

		AGAACGAGACA GGGTCCGACCT	
		AC	
GAM2460	LOC254875 3'	TCCAGCCTGGGTGACAAAGCAA 97785	C
	GA	TCTTGCT TGTCACCCAGGCTGGA	
		AGAACGA ACAGTGGGTCCGACCT	
		A	
GAM2460	LOC255030 5'	TCCAGCCTGGGTGACAGAGCGA 99086	
	GA	TCTTGCTCTGTACCCAGGCTGGA	
		AGAGCGAGACAGTGGGTCCGACCT	
GAM2460	LOC255042 3'	TCCAGCCTGGGCAACAAGAGCG 97056	_ CA
	A	TTGCTCT GT CCCAGGCTGGA	
		AGCGAGA CA GGGTCCGACCT	
		A AC	
GAM2460	LOC255042 3'	TCCAGCCTGGGCGACGAGCAA 97058	T A
		TTGCTC GTC CCCAGGCTGGA	
		AACGAG CAG GGGTCCGACCT	
		_ C	
GAM2460	LOC255177 3'	TCCAGCCTAGGCAACAGAGTGA 98401	TG CA C
	GA	TCT CTCTGT CC AGGCTGGA	
		AGA GAGACA GG TCCGACCT	
		GT AC A	
GAM2460	LOC255231 3'	TCCAGCCTGGGTGACAGAGTGA 97123	TG
	GA	TCT CTCTGTACCCAGGCTGGA	
		AGA GAGACAGTGGGTCCGACCT	
		GT	
GAM2460	LOC255326 3'	TCCAGCCTGGGTGACAGAGCAA 98124	
	GA	TCTTGCTCTGTACCCAGGCTGGA	
		AGAACGAGACAGTGGGTCCGACCT	
GAM2460	LOC255328 3'	TCCAGCCTGGGTGATAAGAGCA 98348	_
	AGA	TCTTGCTCT GTCACCCAGGCTGGA	
		AGAACGAGA TAGTGGGTCCGACCT	
		A	
GAM2460	LOC255463 3'	TCCAGCCTGGACAACATAGTGA 96543	TG C CAC
	GA	TCT CT TGT CCAGGCTGGA	
		AGA GA ACA GGTCCGACCT	
		GT T ACA	
GAM2460	LOC255523 3'	TCCAGCCTGGGCAACAGAGCAA 96737	CA
	GA	TCTTGCTCTGT CCCAGGCTGGA	

		AGAACGAGACA GGGTCCGACCT	
		AC	
GAM2460	LOC255652 3'	TCCAGGACTGCCACAGAGCAAG 98532	CACC G_
	A	TCTTGCTCTGT CAG CTGA	
		AGAACGAGACA GTC GACCT	
		CC__ AG	
GAM2460	LOC255671 5'	TCCAGCCTGGGCGACAGAG 99074	A
		CTCTGTC CCCAGGCTGGA	
		GAGACAG GGGTCCGACCT	
		C	
GAM2460	LOC255671 3'	TCCAGCCTGGGTAACAGAGCAA 99076	C
	GA	TCTTGCTCTGT ACCCAGGCTGGA	
		AGAACGAGACA TGGGTCCGACCT	
		A	
GAM2460	LOC255671 5'	TCCAGCCTGGGTGACAGAGTGA 99077	TG
	GA	TCT CTCTGTCACCCAGGCTGGA	
		AGA GAGACAGTGGGTCCGACCT	
		GT	
GAM2460	LOC255937 3'	TCCATCCTGGGTGACAGAGCAA 97684	C
	GA	TCTTGCTCTGTCACCCAGG TGGA	
		AGAACGAGACAGTGGGTCC ACCT	
		T	
GAM2460	LOC255971 3'	CAGCCTGGGTGACAGAGCAAGA 98308	
		TCTTGCTCTGTCACCCAGGCTG	
		AGAACGAGACAGTGGGTCCGAC	
GAM2460	LOC256207 3'	TCCAACCTGGGCGACAGAGCAA 96880	A C
	GA	TCTTGCTCTGTC CCCAGG TGGA	
		AGAACGAGACAG GGGTCC ACCT	
		C A	
GAM2460	LOC256267 3'	CCAGCCTGGAAAACAAGT 98608	C CAC
		GCT TGT CCAGGCTGG	
		TGA ACA GGTCCGACC	
		_ AAA	
GAM2460	LOC256515 3'	TCCAGCCTGGGCAACAGAGTAA 98218	CA
	GA	TCTTGCTCTGT CCCAGGCTGGA	
		AGAATGAGACA GGGTCCGACCT	
		AC	
GAM2460	LOC256520 3'	TCCAGCCTGGGCGACAGAGCCA 97670	T A
	GA	TCT GCTCTGTC CCCAGGCTGGA	

		AGA CGAGACAG GGGTCCGACCT		
		C C		
GAM2460	LOC256544 3'	TCCAGCCTGGCGACAGAGCAAG 97935	AC	
		CTTGCTCTGTC CCAGGCTGGA		
		GAACGAGACAG GGTCCGACCT		
		C_		
GAM2460	LOC256594 3'	TCCAGCCTGGGCAACAGAGTAA 98868	CA	
	GA	TCTTGCTCTGT CCCAGGCTGGA		
		AGAATGAGACA GGGTCCGACCT		
		AC		
GAM2460	LOC257282 5'	TCAAGCCTGGGCAACAGAGCAA 98136	CA	G
	GA	TCTTGCTCTGT CCCAGGCT GA		
		AGAACGAGACA GGGTCCGA CT		
		AC A		
GAM2460	LOC257354 3'	CCTGGGTGACAAAGCAAGA 96788	C	
		TCTTGCT TGTCACCCAGG		
		AGAACGA ACAGTGGGTCC		
		A		
GAM2460	LOC257397 3'	TCCAGCCTGGACAGCAGAACAA 97953	C	CAC
	GA	TCTTG TCTGT CCAGGCTGGA		
		AGAAC AGACG GGTCCGACCT		
		A ACA		
GAM2460	LOC257489 5'	CCTGCAGGAATGCCAGAGCAAG 66228	T	C_ AG T
	A	TCTTGCTCTG CA CC GC GG		
		AGAACGAGAC GT GG CG CC		
		C AA A_ T		
GAM2460	LOC257539 3'	TCCAGCCTGGGTGACAGGGTGA 99551	TG	
		T CTCTGTCACCCAGGCTGGA		
		A GGGACAGTGGGTCCGACCT		
		GT		
GAM2460	LOC257578 3'	TCCAGCCTGGGTGACAGGGTGA 99663	TG	
		T CTCTGTCACCCAGGCTGGA		
		A GGGACAGTGGGTCCGACCT		
		GT		
GAM2460	LOC257596 3'	TCCAGCCTGGGCAACAAGAGTA 99790	_	CA
	AGA	TCTTGCTCT GT CCCAGGCTGGA		
		AGAATGAGA CA GGGTCCGACCT		
		A AC		
GAM2460	LOC257596 5'	TCCAGCCTGGGCGACAGAGCAA 99791	A	
	GA	TCTTGCTCTGTC CCCAGGCTGGA		

			AGAACGAGACAG GGGTCCGACCT		
			C		
GAM2460	LOC51031	5'	CAACCTGGGTGACAGAACAAGA 32706	C	C
			TCTTG TCTGTCACCCAGG TG		
			AGAAC AGACAGTGGGTCC AC		
			A A		
GAM2460	LOC51145	3'	TCCAGCCTGGGCGACAGAGTGA 32928	TG	A
			GA TCT CTCTGTC CCCAGGCTGGA		
			AGA GAGACAG GGGTCCGACCT		
			GT C		
GAM2460	LOC51212	3'	TCCAGCCTGGGTGACAGAGCAA 33501		
			GA TCTTGCTCTGTCACCCAGGCTGGA		
			AGAACGAGACAGTGGGTCCGACCT		
GAM2460	LOC51279	3'	TCCAGCCTGCGGACAGACCAAG 33764	C	ACC
			A TCTTG TCTGTC CAGGCTGGA		
			AGAAC AGACAG GTCCGACCT		
			C GC_		
GAM2460	LOC51333	3'	TCCGGCCTGGGCAACAGAGGAA 34057	G	CA
			GA TCTT CTCTGT CCCAGGCTGGA		
			AGAA GAGACA GGGTCCGGCCT		
			G AC		
GAM2460	LOC51336	3'	TCCAGCCTGGGTGACAGCGTAA 34079	T	
			GA TCTTGC CTGTCACCCAGGCTGGA		
			AGAATG GACAGTGGGTCCGACCT		
			C		
GAM2460	LOC51652	3'	CCTGGGCAACATAGCAAGA 32700	C	CA
			TCTTGCT TGT CCCAGG		
			AGAACGA ACA GGGTCC		
			T AC		
GAM2460	LOC51759	3'	TCCAGCCTGGGCAACGAGCAA 73173	T	CA
			TTGCTC GT CCCAGGCTGGA		
			AACGAG CA GGGTCCGACCT		
			_ AC		
GAM2460	LOC57107	5'	CCAGCCTGGGCTGCTAGA 40182	T	_
			TCTG CA CCCAGGCTGG		
			AGAT GT GGGTCCGACC		
			C C		
GAM2460	LOC57118	3'	TCCAGCCTGGGTGACAGATTGA 40228	GC	
			GA TCTT TCTGTCACCCAGGCTGGA		

		AGAG AGACAGTGGGTCCGACCT		
		TT		
GAM2460	LOC63929 3'	TCCAGCCTGGGTGACTGAGCAA 42285	T	
	GA	TCTTGCTC GTCACCCAGGCTGGA		
		AGAACGAG CAGTGGGTCCGACCT		
		T		
GAM2460	LOC64167 3'	TCCAGCCTGGGTGACTGAGCGA 42543	T	
	GA	TCTTGCTC GTCACCCAGGCTGGA		
		AGAGCGAG CAGTGGGTCCGACCT		
		T		
GAM2460	LOC85479 5'	TCCAGCCTGGGCGACAGAGCAA 53571	A	
	GA	TCTTGCTCTGTC CCCAGGCTGGA		
		AGAACGAGACAG GGGTCCGACCT		
		C		
GAM2460	LOC89890 3'	TCCAGCCTGGATGACAGAGTGA 61209	TG	C
	GA	TCT CTCTGTCA CCAGGCTGGA		
		AGA GAGACAGT GGTCCGACCT		
		GT A		
GAM2460	LOC89894 5'	TCCAACCCTCGGTACAGAGCAG 61231	C	C C_
	GA	TCTTGCTCTGT ACC AGG TGGA		
		AGGACGAGACA TGG TCC ACCT		
		_ C CA		
GAM2460	LOC90038 3'	TCCAGCCTGGGCAACAGAGTGA 61813	TG	CA
	GA	TCT CTCTGT CCCAGGCTGGA		
		AGA GAGACA GGGTCCGACCT		
		GT AC		
GAM2460	LOC90038 3'	TCCAGCCTGGGTGACACAGTGA 61814	TG	C
	GA	TCT CT TGTCACCCAGGCTGGA		
		AGA GA ACAGTGGGTCCGACCT		
		GT C		
GAM2460	LOC90072 3'	TCCAGCCTGGGGAACAGAGCAA 61963	CA	
	GA	TCTTGCTCTGT CCCAGGCTGGA		
		AGAACGAGACA GGGTCCGACCT		
		AG		
GAM2460	LOC90072 5'	TCCAGCCTGGGTGACAGAACAA 61964	C	
	GA	TCTTG TCTGTCACCCAGGCTGGA		
		AGAAC AGACAGTGGGTCCGACCT		
		A		
GAM2460	LOC90072 5'	TCCAGCCTGGGTGACATATCAA 61965	CTC	
	GA	TCTTG TGTCACCCAGGCTGGA		

AGAAC ACAGTGGGTCCGACCT
 TAT
 GAM2460 LOC90092 3' TCCAGCCTGGCGACAAGAGCGA 62075 _ AC
 GA TCTTGCTCT GTC CCAGGCTGGA
 ||||| || |||||
 AGAGCGAGA CAG GGTCCGACCT
 A C_
 GAM2460 LOC90110 5' CCAGCCTGGGCAACGGAGT 62177 CA
 GCTCTGT CCCAGGCTGG
 ||||| |||||
 TGAGGCA GGGTCCGACC
 AC
 GAM2460 LOC90141 3' TCCAGCCTGGATGATAGAGCAA 62310 C
 GA TCTTGCTCTGTCA CCAGGCTGGA
 ||||| |||||
 AGAACGAGATAGT GGTCCGACCT
 A
 GAM2460 LOC90155 5' TCCAGCCTGGGCAACAAGAGTG 62368 TG _ CA
 A T CTCT GT CCCAGGCTGGA
 | ||| || |||||
 A GAGA CA GGGTCCGACCT
 GT A AC
 GAM2460 LOC90233 3' TCCAGCCCAGGCAACAGAGTGA 57197 TG CA CA
 GA TCT CTCTGT CC GGCTGGA
 || |||| || |||||
 AGA GAGACA GG CCGACCT
 GT AC AC
 GAM2460 LOC90321 3' TCCAACCTGGGTGACAGAGCGA 62938 C
 GA TCTTGCTCTGTCACCCAGG TGGA
 ||||| |||||
 AGAGCGAGACAGTGGGTCC ACCT
 A
 GAM2460 LOC90321 3' TCCAGCTTGGGTGACAGAGCGA 62939
 GA TCTTGCTCTGTCACCCAGGCTGGA
 ||||| |||||
 AGAGCGAGACAGTGGGTTCGACCT
 A
 GAM2460 LOC90393 5' TCCAGCCTGGGTGACAGAGTGA 63309 TG
 GA TCT CTCTGTCACCCAGGCTGGA
 || ||||| |||||
 AGA GAGACAGTGGGTCCGACCT
 GT
 GAM2460 LOC90573 5' TCCAGCCTGGGCGACAGAGTGA 63962 TG A
 GA TCT CTCTGTC CCCAGGCTGGA
 || |||| |||||
 AGA GAGACAG GGGTCCGACCT
 GT C
 GAM2460 LOC90591 3' TCCAGCGGCGACAGAGCAAGA 64190 A CAG
 TCTTGCTCTGTC CC GCTGGA
 ||||| || |||||

			AGAACGAGACAG GG CGACCT		
			C ____		
GAM2460	LOC90639	3'	TCCAGCCTGAGCAACAGAGCCG 64416	T	CACC
	GA		TCT GCTCTGT CAGGCTGGA		
			AGG CGAGACA GTCCGACCT		
			C ACGA		
GAM2460	LOC90784	5'	TCCAGCCTGGGCAACAGAGTGA 64700	TG	CA
	GA		TCT CTCTGT CCCAGGCTGGA		
			AGA GAGACA GGGTCCGACCT		
			GT AC		
GAM2460	LOC90785	3'	TCCAGCCTGGGTGACAGAGCGA 64720		
	GA		TCTTGCTCTGTCACCCAGGCTGGA		
			AGAGCGAGACAGTGGGTCCGACCT		
GAM2460	LOC90918	5'	TCCAGCCTAGGCAACAAGAGTG 65005	TG	_ CA C
	A		T CTCT GT CC AGGCTGGA		
			A GAGA CA GG TCCGACCT		
			GT A AC A		
GAM2460	LOC91035	3'	TCCAGCCTGGACAACAAGAGCA 65307	_	CAC
	AGA		TCTTGCTCT GT CCAGGCTGGA		
			AGAACGAGA CA GGTCCGACCT		
			A ACA		
GAM2460	LOC91056	3'	TCCAGCCTGGGCGACAGAGCAA 96410		A
	GG		TCTTGCTCTGTC CCCAGGCTGGA		
			GGAACGAGACAG GGGTCCGACCT		
			C		
GAM2460	LOC91064	3'	TCCAGCGTGGGCGACAGAGCAA 65391	A	G
	GA		TCTTGCTCTGTC CCA GCTGGA		
			AGAACGAGACAG GGGT CGACCT		
			C G		
GAM2460	LOC91250	5'	TCCAGCCTGAGTGACAGAGTGA 65921	TG	C
	GA		TCT CTCTGTAC CAGGCTGGA		
			AGA GAGACAGTG GTCCGACCT		
			GT A		
GAM2460	LOC91250	5'	TCCAGCCTGGGCAACAGAGTGA 65922	TG	CA
	GA		TCT CTCTGT CCCAGGCTGGA		
			AGA GAGACA GGGTCCGACCT		
			GT AC		
GAM2460	LOC91286	3'	TCCAGCCTGGACAACAGACAA 66062	C	CAC
			TTG TCTGT CCAGGCTGGA		

AAC AGACA GGTCCGACCT
 _ ACA
 GAM2460 LOC91380 3' TCCAGCCTGGGTGACAGAGTGA 66454 TG
 GA TCT CTCTGTCACCCAGGCTGGA
 ||| |||||
 AGA GAGACAGTGGGTCCGACCT
 GT
 GAM2460 LOC91442 3' TCCAGCCTGGGCACCAGAGCGA 66648 TCA
 GA TCTTGCTCTG CCCAGGCTGGA
 ||||| |||||
 AGAGCGAGAC GGGTCCGACCT
 CAC
 GAM2460 LOC91547 3' TCCAGCCTGGGCGACAGAGCGA 67006 A
 GA TCTTGCTCTGTC CCCAGGCTGGA
 ||||| |||||
 AGAGCGAGACAG GGGTCCGACCT
 C
 GAM2460 LOC91574 3' CTTGTGTGACAGAACAAGA 67111 C C
 TCTTG TCTGTCAC CAGG
 |||| ||||| |||
 AGAAC AGACAGTG GTTC
 A T
 GAM2460 LOC91750 3' TCCAGCCTGGGCAACAGAGTGA 67657 TG CA
 GA TCT CTCTGT CCCAGGCTGGA
 ||| |||| |||||
 AGA GAGACA GGGTCCGACCT
 GT AC
 GAM2460 LOC91812 3' TCCAGCCTGGGCAACAGAACGA 67821 C CA
 GA TCTTG TCTGT CCCAGGCTGGA
 |||| |||| |||||
 AGAGC AGACA GGGTCCGACCT
 A AC
 GAM2460 LOC91813 3' TCCAGCCTGGGCAACAGAACGA 67848 C CA
 GA TCTTG TCTGT CCCAGGCTGGA
 |||| |||| |||||
 AGAGC AGACA GGGTCCGACCT
 A AC
 GAM2460 LOC91862 3' TCCAGCCCAGGTGACAGAGCGA 54574 CA
 GA TCTTGCTCTGTCACC GGCTGGA
 ||||| |||||
 AGAGCGAGACAGTGG CCGACCT
 AC
 GAM2460 LOC91963 5' TCCAGCCTGGGCAACAGAGTGA 68327 TG CA
 T CTCTGT CCCAGGCTGGA
 | |||| |||||
 A GAGACA GGGTCCGACCT
 GT AC
 GAM2460 LOC91963 3' TTGGGTGACAGAGCAAGA 68330
 TCTTGCTCTGTCACCCAG
 |||||

AGAACGAGACAGTGGGTT

GAM2460 LOC92078 3' TCCAGCCTGGGTGACAGAGTGA 68612 TG
GA TCT CTCTGTCACCCAGGCTGGA
||| |||||
AGA GAGACAGTGGGTCCGACCT
GT

GAM2460 LOC92223 3' TCCAGCCTGGGCAACAAGAGTG 69055 TG _ CA
A T CTCT GT CCCAGGCTGGA
| |||| || |||||
A GAGA CA GGGTCCGACCT
GT A AC

GAM2460 LOC92228 3' CCAGCCTGGGCAACGGAGT 69072 CA
GCTCTGT CCCAGGCTGG
||||| |||||
TGAGGCA GGGTCCGACC
AC

GAM2460 LOC92267 3' TCCAGCCTGGGCAACAAGAGAG 69179 TG _ CA
A TCT CTCT GT CCCAGGCTGGA
||| |||| || |||||
AGA GAGA CA GGGTCCGACCT
_ A AC

GAM2460 LOC92299 3' CCTAGGTGACAGAGCGAGA 69364 C
TCTTGCTCTGTCACC AGG
||||| |||||
AGAGCGAGACAGTGG TCC
A

GAM2460 LOC92299 3' TCCAGCCTGGCGACAAAGCGAG 69373 C AC
A TCTTGCT TGTC CCAGGCTGGA
||||| |||| |||||
AGAGCGA ACAG GGTCCGACCT
A C_

GAM2460 LOC92340 3' TCCAGCCTAGTAATGGAGCAAG 69568 C CC
A TCTTGCTCTGT AC AGGCTGGA
||||| || |||||
AGAACGAGGTA TG TCCGACCT
A A_

GAM2460 LOC92360 3' TCCAGCCTGGGTGACAGAGCAA 69626
GG TCTTGCTCTGTCACCCAGGCTGGA
||||| |||||
GGAACGAGACAGTGGGTCCGACCT

GAM2460 LOC92405 3' TCTAGCCTGGGCAACAGAGCAA 69718 CA
GG TCTTGCTCTGT CCCAGGCTGGA
||||| |||||
GGAACGAGACA GGGTCCGATCT
AC

GAM2460 LOC92465 5' TCCAGCCTGGGCGACAGAGCGA 69955 A
GA TCTTGCTCTGTC CCCAGGCTGGA
||||| |||||

		AGAGCGAGACAG GGGTCCGACCT	
		C	
GAM2460	LOC92465 5'	TCCAGTCTGGGCAACAGAGCAA 69956	CA
	GA	TCTTGCTCTGT CCCAGGCTGGA	
		AGAACGAGACA GGGTCTGACCT	
		AC	
GAM2460	LOC92466 3'	CCAGCCTGGAAAACAAGT 69964 C CAC	
		GCT TGT CCAGGCTGG	
		TGA ACA GGTCCGACC	
		_ AAA	
GAM2460	LOC92482 3'	CCAGCCTGGGCAACAGAGCAAG 70019	CA
	A	TCTTGCTCTGT CCCAGGCTGG	
		AGAACGAGACA GGGTCCGACC	
		AC	
GAM2460	LOC92492 3'	TCCAGCCTGGATGACAGCGAGA 70083	CT C
		TCTTGCT GTCA CCAGGCTGGA	
		AGAGCGA CAGT GGTCCGACCT	
		_ A	
GAM2460	LOC92499 5'	CAGCCTGGACGACAGAGCAAGA 70103	AC
		TCTTGCTCTGTC CCAGGCTG	
		AGAACGAGACAG GGTCCGAC	
		CA	
GAM2460	LOC92568 3'	TCCAGCCTGGGTGACAGAGTGA 70331	TG
	GA	TCT CTCTGTCACCCAGGCTGGA	
		AGA GAGACAGTGGGTCCGACCT	
		GT	
GAM2460	LOC92573 3'	TCCAGCCTGGGTGACAGAGCGA 70379	
	GA	TCTTGCTCTGTCACCCAGGCTGGA	
		AGAGCGAGACAGTGGGTCCGACCT	
GAM2460	LOC92659 3'	TCCAGCCTGGGCGACAGAG 70610	A
		CTCTGTC CCCAGGCTGGA	
		GAGACAG GGGTCCGACCT	
		C	
GAM2460	LOC92661 5'	TCATGATGGGTGGCAGAGCAAG 70635	GGC
	A	TCTTGCTCTGTCACCCA TGG	
		AGAACGAGACGGTGGGT ACT	
		AGT	
GAM2460	LOC92973 5'	TCCAGCCTGGGCAACAGAGTGA 71594	TG CA
	GG	TCT CTCTGT CCCAGGCTGGA	

GGA GAGACA GGGTCCGACCT
 GT AC
 GAM2460 LOC93070 3' TCCAGCCTGGGCAACAGAGGGA 71815 G CA
 GA TCTT CTCTGT CCCAGGCTGGA
 |||| |||| ||||
 AGAG GAGACA GGGTCCGACCT
 G AC
 GAM2460 LOC96597 5' TCCAGCCTGGGCGACAAGAGGG 67467 G _ A
 AG CTT CTCT GTC CCCAGGCTGGA
 ||| ||| ||| ||||
 GAG GAGA CAG GGGTCCGACCT
 G A C
 GAM2461 CDH12 3' CTTATCATTTAAAGTGGTGTA 15777 CCCAA GA
 TACACCACT GAA ATAAG
 |||| ||| ||||
 ATGTGGTGA TTT TATTC
 AA_ AC
 GAM2461 GOCAP1 3' ATTGTTCTTGGGAGCAGTGTA 43007 CA G
 TACAC CTCCCAAGAA AAT
 |||| |||| ||| |||
 ATGTG GAGGGTTCTT TTA
 AC G
 GAM2461 DKFZp434N2435 5' CTTATTACTGTGGGGTGGT 98090 T AGAAG
 ACCAC CCCA AATAAG
 |||| ||| ||||
 TGGTG GGGT TTATTC
 _ GTCA_
 GAM2461 DKFZP564I122 3' CTTATTCTTCTCCCTCATGTGT 63877 CACTCCCA
 A TACAC AGAAGAATAAG
 |||| ||||
 ATGTG TCTTCTTATTC
 TACTCCC_
 GAM2461 FLJ21791 3' CTTATTTGCAGAAAGTGGTGTA 62126 CCCAAGAA
 TACACCACT GAATAAG
 |||| ||||
 ATGTGGTGA TTTATTC
 AGACG_
 GAM2461 HMP19 3' CTTATTCTTTGTTAGGAAAATG 88860 CCAC CAA_
 TA TACA TCC GAAGAATAAG
 ||| ||| ||||
 ATGT AGG TTTCTTATTC
 AAA_ ATTG
 GAM2461 KIAA1719 3' TCTGTCTTGGGAGTGGTGTA 68742 _
 TACACCACTCCCAAGA AGA
 ||||
 ATGTGGTGAGGGTTCT TCT
 G
 GAM2461 KIAA1853 3' TTTTCTTGGAAGCAGTG 69929 CA C
 CAC CT CCAAGAAGAA
 ||| ||| ||||

		GTG GA GGTTCTTTTT	
		AC A	
GAM2461 KIAA1877	3'	CTTATTCTTCTGCCATGAGT 66748	CCA__
		ACTC AGAAGAATAAG	
		TGAG TCTTCTTATTC	
		TACCG	
GAM2461 KIAA1906	3'	CTTATTCTTCTTGACTTTTGG 73571	CTCC_
		CCA CAAGAAGAATAAG	
		GGT GTTCTTCTTATTC	
		TTTCA	
GAM2461 OSBPL11	3'	CTTAATTTCCCAAGAGTGGTG 43206	CCAA AA
		CACCACTC GAAG TAAG	
		GTGGTGAG CTTT ATTC	
		AACC A_	
GAM2461 YME1L1	3'	TCATTCTTGATGTGGTGTA 58438	TCC _
		TACACCAC CAAGAA GA	
		ATGTGGTG GTTCTT CT	
		TA_ A	
GAM2461 ZNF262	3'	CTTATTTTGTGTTGGGAGT 18723	A
		ACTCCCAAG AGAATAAG	
		TGAGGGTTT TTTTATTC	
		G	
GAM2461 LOC91960	3'	TGTGGCTTGGAACGTGGTGTA 68294	TC_ AAGA
		TACACCAC CCAAG ATA	
		ATGTGGTG GGTC TGT	
		CAA GG__	
GAM2462 ADAM12	3'	TTCACTCTTCAAATGCCT 14426	_
		AGGCATTTGAAGA TGAA	
		TCCGTAAACTTCT ACTT	
		C	
GAM2462 CNTN3	3'	TTTCATTTAATTCAAATGCT 67272	GATG
		GGCATTTGAA AAATGAAA	
		TCGTAAACTT TTTACTTT	
		AA__	
GAM2462 FGA	3'	TCTGTATTCCCAAATGCCT 6702	AA AAAT
		AGGCATTTG GATG GA	
		TCCGTAAAC TTAT CT	
		CC GT__	
GAM2462 GTF2F1	3'	TTCTGGAATCTTCAGATGCCT 10896	GAAAT
		AGGCATTTGAAGAT GAA	

TCCGTAGACTTCTA CTT
 AGGT_
 GAM2462 H4FH 3' TTTCATTTTCAACCAAAGGCC 14515 AT____
 GGC TTGAAGATGAAA
 ||| |||||
 CCG AACTTTTACTTT
 GAAACC
 GAM2462 MGAT4B 5' TTTCCACTTCAGATGCCT 27342 AT
 AGGCATTTGAAG GAAA
 ||||| |||
 TCCGTAGACTTC CTTT
 AC
 GAM2462 MSN 3' CACTTGATTTTGCAAATGCC 60880 _ G A
 GGCATTTG AAGAT AA TG
 ||||| |||| ||
 CCGTAAAC TTTTA TT AC
 G G C
 GAM2462 PLEK 3' TCATTTTATCAAATCCT 12167 C AGA
 AGG ATTTGA TGAAATGA
 || ||||| |||||
 TCC TAAACT ATTTTACT
 - -
 GAM2462 PPEF1 5' TTCATTTCTTTTGAAACACCT 21781 CA_ TG AT
 AGG TT AAG GAAATGAA
 ||| || ||| |||||
 TCC AA TTC CTTTACTT
 ACA GT _
 GAM2462 RNF26 5' CAGCCCATCTTCAAAACCT 50133 CA AAA
 AGG TTTGAAGATG TG
 ||| ||||| ||
 TCC AAACCTTCTAC AC
 A_ CCG
 GAM2462 C(27)-3BETA-HSD 3' CATTGTTTTTCAAAGGCCT 48049 A TGA
 AGGC TTTGAAGA AATG
 ||||| ||||| |||
 TCCG AAACCTTTT TTAC
 G TG_
 GAM2462 DEFA3 3' TCATCTCAAATAAATGCCT 19069 A____
 AGGCATTTG AGATGA
 ||||| |||||
 TCCGTAAAT TCTACT
 AAAC
 GAM2462 DKFZP434N014 3' CAGCCCATCCCCAGATGCCT 61227 AA AAA
 AGGCATTTG GATG TG
 ||||| ||| ||
 TCCGTAGAC CTAC AC
 CC CCG
 GAM2462 DKFZP564O1664 3' TTTTCATTTCAACTGAAAATGC 48671 GA A
 TT
 AGGCATTT AG TGAAATGAAAA
 ||||| || |||||

		TTCGTAAA TC ACTTTACTTTT		
		AG A		
GAM2462	FLJ11618	3' TTCACCCCATTTCCTCAAGTGCC 42628	A	AAA
		GGCATTG AGATG TGAA		
		CCGTGAAC TTTAC ACTT		
		C CCC		
GAM2462	FLJ20360	3' TTTTCATTTTAAACAAGATGCC 92511	GAAGA	
	T	AGGCATT TGAAATGAAAA		
		TCCGTAGA ATTTTACTTTT		
		ACAA_		
GAM2462	FLJ31737	3' TTTTCATCTTCCATCAATGCCT 59352	T__	
		AGGCATT GAAGATGAAA		
		TCCGTAA CTTCTACTTT		
		CTAC		
GAM2462	FUBP1	3' TTTCACTTTCCAAATGCCT 15334	_ A	
		AGGCATTTG AAG TGAAA		
		TCCGTAAAC TTT ACTTT		
		C C		
GAM2462	KIAA0377	3' CATATCATCCCCAAGTGCC 28499	AA A	
		GGCATTG GATGA ATG		
		CCGTGAAC CTACT TAC		
		CC A		
GAM2462	KIAA0547	3' TTTCACTTCTACAAGTGCC 29604	A _	
		AGGCATTTG AGA TGAAA		
		TCCGTGAAC TCT ACTTT		
		A T		
GAM2462	KIAA0819	3' ATTCCATCTTCAAACCCC 64329	CA A	
		GG TTTGAAGATG AAT		
		CC AAATTCTAC TTA		
		CC C		
GAM2462	KIAA0993	3' TTTTCATTTCAAATAAATACCT 64825	C AAGA	
		AGG ATTTG TGAAATGAAAA		
		TCC TAAAT ACTTTACTTTT		
		A AA__		
GAM2462	KIAA1238	3' TTTTCATTTACAAATCCT 71636	C A	
		AGG ATTTG AGATGAAA		
		TCC TAAAC TTTACTTT		
		_ A		
GAM2462	KIAA1613	3' TCATTTACAAATCCAGCCT 65443	__ AAGA	
		AGGC ATTTG TGAAATGA		

TCCG TAAAC ACTTTACT
 ACC ____
 GAM2462 KIAA1677 3' TTTTCACTTTATATCTCAAATG 67668 AG_ A
 CC GGCATTTGA ATGAA TGAAAA
 ||||| ||| |||||
 CCGTAAACT TATTT ACTTTT
 CTA C
 GAM2462 MGC27277 3' TTTCATCTATCAAATACT 59364 C _
 GG ATTTGA AGATGAAA
 || ||||| |||||
 TC TAAACT TCTACTTT
 A A
 GAM2462 MRV11 3' CATCTCATTTCATAATACT 56094 GCAT A
 AG TTGAAGATGA ATG
 || ||||| |||
 TC AACTTTTACT TAC
 AAT_ C
 GAM2462 P5-1 3' TTTTCATCTCATGATGGATGCT 22891 TT AAG A
 GGCAT G ATGA ATGAAAA
 |||| | ||| |||||
 TCGTA T TACT TACTTTT
 GG AG_ C
 GAM2462 PSR 3' TTCTGCATCCTCAAATGCC 65797 A AAAT
 GGCATTTGA GATG GAA
 ||||| ||| |||
 CCGTAAACT CTAC CTT
 C GT_
 GAM2462 TACTILE 3' TCTTTCATCTCCAAACGCCT 20595 A A T
 AGGC TTTG AGATGAAA GA
 ||| ||| ||||| ||
 TCCG AAAC TCTACTTT CT
 C C _
 GAM2462 LOC122830 3' TTTCATTTCTTAAAATGCTT 74633 GAAGAT
 AGGCATTT GAAATGAAA
 ||||| |||||
 TTCGTAAA CTTTACTTT
 ATT_
 GAM2462 LOC146895 5' CAGATCATCTTACAAATGCCT 84861 _ AA
 AGGCATTTG AAGATGA TG
 ||||| ||||| ||
 TCCGTAAAC TTCTACT AC
 A AG
 GAM2462 LOC149271 5' TTTTCATTTGCAAAGCAAAGCC 80015 A AAGA _
 T AGGC TTTG TG AAATGAAAA
 ||| ||| || |||||
 TCCG AAAC AC TTTACTTTT
 _ GAA_ G
 GAM2462 LOC149386 5' TTCAAGTACACTTCAAATACCT 85566 C A AAA_
 AGG ATTTGAAG TG TGAA
 ||| ||||| || |||

TCC TAAACTTC AC ACTT
 A _ ATGA
 GAM2462 LOC200609 5' TTTCATTTCACCTTCTATCCT 91672 C TT A
 AGG AT GAAG TGAAATGAAA
 ||| || ||| |||||
 TCC TA CTTC ACTTTACTTT
 _ T_ _
 GAM2462 LOC220081 3' TCTGGCATCCACCAAATGCCT 93405 AA_ AAAT
 AGGCATTTG GATG GA
 ||||| ||| ||
 TCCGTAAAC CTAC CT
 CAC GGT_
 GAM2463 LYN 3' CCATTGCAATGAATCCCC 11404 TGCTGG
 GGGGATTC GCAATGG
 ||||| |||||
 CCCCTAAG CGTTACC
 TAA_
 GAM2463 APCL 3' CCACTCTCAGAACCCCG 20814 A CT CAA
 CGGGG TTCTG GGG TGG
 |||| |||| || ||
 GCCCC AAGAC CTC ACC
 C T_ _
 GAM2463 GFRA4 3' GCACCATCCAGAATCCCAGA 42420 G C_ _
 TC GGGATTCTG TGG GC
 || ||||| || ||
 AG CCCTAAGAC ACC CG
 A CT A_
 GAM2463 RASSF2 3' GCCATTGCCATAAGACCCCG 29100 AT GC
 GGGG TCT TGGGCAATGGC
 ||| || |||||
 CCCC AGA ACCCGTTACCG
 C_ AT
 GAM2463 LOC91875 3' GCCATGGGACAGAGTCCCC 68033 _ G_
 GGGGATTCTG CT GGC
 ||||| || |||
 CCCCTGAGAC GG CCG
 A GTA
 GAM2464 CDH12 3' CTTATCATTTAAAGTGGTGTA 15777 CCCAA GA
 TACACCACT GAA ATAAG
 ||||| || |||||
 ATGTGGTGA TTT TATTC
 AA_ AC
 GAM2464 GOCAP1 3' ATTGTTCTTGGGAGCAGTGTA 43007 CA G
 TACAC CTCCCAAGAA AAT
 |||| ||||| |||
 ATGTG GAGGGTTCTT TTA
 AC G
 GAM2464 DKFZp434N2435 5' CTTATTACTGTGGGGTGGT 98090 T AGAAG
 ACCAC CCCA AATAAG
 |||| ||| |||||

		TGGTG GGGT TTATTC	
		_ GTCA_	
GAM2464	DKFZP564I122	3' CTTATTCTTCTCCCTCATGTGT 63877	CACTCCCA
	A	TACAC AGAAGAATAAG	
		ATGTG TCTTCTTATTC	
		TACTCCC_	
GAM2464	FLJ21791	3' CTTATTTGCAGAAAGTGGTGTA 62126	CCCAAGAA
		TACACCACT GAATAAG	
		ATGTGGTGA TTTATTC	
		AGACG__	
GAM2464	HMP19	3' CTTATTCTTTGTAGGAAAATG 88860	CCAC CAA_
	TA	TACA TCC GAAGAATAAG	
		ATGT AGG TTTCTTATTC	
		AAA_ ATTG	
GAM2464	KIAA1579	3' TACTCTTAGTGGTGTA 37154	CCCAAG A
		TACACCACT AAGA TA	
		ATGTGGTGA TTCT AT	
		_____ C	
GAM2464	KIAA1719	3' TCTGTCTTGGGAGTGGTGTA 68742	_
		TACACCACTCCCAAGA AGA	
		ATGTGGTGAGGGTTCT TCT	
		G	
GAM2464	KIAA1853	3' TTTTCTTGGAAGCAGTG 69929	CA C
		CAC CT CCAAGAAGAA	
		GTG GA GGTTC TTTT	
		AC A	
GAM2464	KIAA1877	3' CTTATTCTTCTGCCATGAGT 66748	CCA_
		ACTC AGAAGAATAAG	
		TGAG TCTTCTTATTC	
		TACCG	
GAM2464	KIAA1906	3' CTTATTCTTCTTGACTTTTGG 73571	CTCC_
		CCA CAAGAAGAATAAG	
		GGT GTTCTTCTTATTC	
		TTTCA	
GAM2464	OSBPL11	3' CTTAATTTCCCAAGAGTGGTG 43206	CCAA AA
		CACCACTC GAAG TAAG	
		GTGGTGAG CTTT ATTC	
		AACC A_	
GAM2464	YME1L1	3' TCATTCTTGATGTGGTGTA 58438	TCC _
		TACACCAC CAAGAA GA	

		ATGTGGTG GTTCTT CT		
		TA_ A		
GAM2464	YME1L1	3' TCATTCTTGATGTGGTGTA 27323	TCC	_
		TACACCAC CAAGAA GA		
		ATGTGGTG GTTCTT CT		
		TA_ A		
GAM2464	ZNF262	3' CTTATTTTGTGTTGGGAGT 18723	A	
		ACTCCCAAG AGAATAAG		
		TGAGGGTTT TTTTATTC		
		G		
GAM2464	LOC91960	3' TGTGGCTTGGAACGTGGTGTA 68294	TC_	AAGA
		TACACCAC CCAAG ATA		
		ATGTGGTG GGTTCT TGT		
		CAA GG_		
GAM2465	CACNG6	5' CCTCGCTCCCGCCCTCGAGG 49947	G	CATGAT
		CCT GAGGG GAGCGAGG		
		GGA CTCCC CTCGCTCC		
		G CGCC_		
GAM2465	CCND1	3' CCCGCCCCACCCCTCCAG 54957	CA	ATGA A
		CTGGAGGG TG GCG GG		
		GACCTCCC AC CGC CC		
		C_ CC_ _		
GAM2465	CYP1A1	3' CTCTGCACACCCTCCAG 6688	CATGA	A _
		CTGGAGGG TG GC GAG		
		GACCTCCC AC CG CTC		
		_ _ _ A T		
GAM2465	EGFL4	3' CGAGCACCATGCCCTCAAG 62462	G	A AG
		CT GAGGGCATG TG CG		
		GA CTCCCGTAC AC GC		
		A C GA		
GAM2465	HOXD4	3' CCCACTCCACCCCTCCAGG 28256	CA	AT CGA
		CCTGGAGGG TG GAG GG		
		GGACCTCCC AC CTC CC		
		C_ _ AC_		
GAM2465	KCNK4	5' CCCGCCCGGCCCTCCAGG 33978	CATGA	A A
		CCTGGAGGG TG GCG GG		
		GGACCTCCC GC CGC CC		
		CG_ C _		
GAM2465	KCNK4	5' CCCGCCCGGCCCTCCAGG 33979	CATGA	A A
		CCTGGAGGG TG GCG GG		

			GGACCTCCC	GC CGC CC		
			CG__ C _			
GAM2465	LASS1	3'	CCGGCCACGCCCCCAGG	41475	A	ATGA A GA
			CCTGG GGGC	TG GC GG		
			GGACC CCG	AC CG CC		
			C C__ _ G_			
GAM2465	MBP	3'	CCCGCAATGTGCCCCAG	91351	A	G GA A
			CTGG GGGCAT	AT GCG GG		
			GACC CCGTG	TA CGC CC		
			_ _ A_ _			
GAM2465	NAV2	3'	CCTCAGCACAGACCCTCCAG	60792		CA A AGC
			CTGGAGGG	TG TG GAGG		
			GACCTCCC	AC AC CTCC		
			AG _ GA_			
GAM2465	SIRT7	3'	CTCGCTCACCAGGCCAGTC	33736	AG	A A
			GG GGC	TG TGAGCGAG		
			CT CCG	AC ACTCGCTC		
			GA G C			
GAM2465	SLC22A12	3'	CTCCCCATGTCCCTCCAGG	58687		_ AT
			CCTGGAGGG	CATG GAG		
			GGACCTCCC	GTAC CTC		
			T CC			
GAM2465	STIM1	3'	CCACCCTTCCCACCCTCTAG	60774		CA AT CGA
			CTGGAGGG	TG GAG GG		
			GATCTCCC	AC TTC CC		
			_ CC CCA			
GAM2465	TGIF	5'	CCCGCTCCTGGCCCCCTCCAG	13743		_ ATGAT A
			CTGGAGGG	C GAGCG GG		
			GACCTCCC	G CTCGC CC		
			C GTC__ _			
GAM2465	CXYorf1	3'	CCTCACTCAGCCTTTTCCCTCC	82910		CATGA__ C
	AGG		CCTGGAGGG	TGAG GAGG		
			GGACCTCCC	ACTC CTCC		
			TTTTCCG	A		
GAM2465	DKFZP434O047	5'	CCTGGAGCCACGCCCTCCGG	32121		ATGA A G__
			CTGGAGGGC	TG GC AGG		
			GGCCTCCCG	AC CG TCC		
			C__ _ AGG			
GAM2465	DKFZP586C1619	3'	CCTCCGCCCAGGCCCTCCA	62616		ATGA A _
			TGGAGGGC	TG GCG AGG		

	ACCTCCCG AC CGC TCC		
	G__ C C		
GAM2465 FLJ12547	3' CCCACTTCCGATGCCCTCCAG 47129	GAT	CGA
	CTGGAGGGCAT GAG GG		
	GACCTCCCGTA TTC CC		
	GCC AC_		
GAM2465 FLJ20085	3' CCCGCCCCCGCACCTTCCAG 35004	CA	ATGA A
	CTGGAGGG TG GCG GG		
	GACCTTCC GC CGC CC		
	AC CCC_ _		
GAM2465 FLJ23191	5' CCTCCGTCCCCGCCCTCCAGG 45007	AT_	AGC
	CCTGGAGGGC GATG GAGG		
	GGACCTCCCG CTGC CTCC		
	CCC _		
GAM2465 KIAA0040	3' CTCACCTGCCCTCCAGGT 28489	TGA	
	ACCTGGAGGGCA TGAG		
	TGGACCTCCCGT ACTC		
	CC_		
GAM2465 KIAA0415	3' CCCGCCCACCTCCCCTCCGG 94160	CATGA	A A
	CTGGAGGG TG GCG GG		
	GGCCTCCC AC CGC CC		
	CTCC_ C _		
GAM2465 KIAA0775	3' CCAGGCCCATGCCCTCCTGGT 28950	T	ATGA GA
	ACC GGAGGGCATG GC GG		
	TGG CCTCCCGTAC CG CC		
	T C__ GA		
GAM2465 KIAA1036	3' CCTCACCCATCATGCCAGCCA 30487	AG	AGC
	TGG GGCATGATG GAGG		
	ACC CCGTACTAC CTCC		
	GA CCA		
GAM2465 KIAA1545	3' CCTCACCCACATGAGCCCCCCC 61334	A _	A AGC
A	TGG GGG CATG TG GAGG		
	ACC CCC GTAC AC CTCC		
	C CGA _ CCA		
GAM2465 MDS028	3' CCTCACCCATCATGCCAGCAGG 38063	GAG	AGC
	CCTG GGCATGATG GAGG		
	GGAC CCGTACTAC CTCC		
	GA_ CCA		
GAM2465 N4BP2	3' CCTGATTCATGCCCCCA 36937	A	TGAG G
	TGG GGGCATGA C AGG		

ACC CCCGTACT G TCC
 C TA__
 GAM2465 PRKWNK2 3' CCCGCTCAGCTGAAGCCCCTCC 92195 _ ATGA_ A
 AG CTGGAGGG C TGAGCG GG
 ||||| | ||||| ||
 GACCTCCC G ACTCGC CC
 C AAGTCG _
 GAM2465 SLC26A6 3' CCTCACCCCTAGGCCGCCTCCA 43581 _ ATGATGAGC
 GGT ACCTGGAG GGC GAGG
 ||||| || ||||
 TGGACCTC CCG CTCC
 CG GATCCCCA_
 GAM2465 TU3A 3' CCTCAAGCACACGCCCTCCAG 24181 A A AGC
 G CCTGGAGGGC TG TG GAGG
 ||||| || || ||||
 GGACCTCCCG AC AC CTCC
 C C GAA
 GAM2465 LOC129303 3' CCTCACTACCCAGCCAGCCCT 75371 A__ A_ C
 TCAGGT ACCTGGAGGGC TG TGAG GAGG
 ||||| || ||||| ||||
 TGGACTTCCCG AC ACTC CTCC
 ACCG CC A
 GAM2465 LOC143969 5' CTCGCTCCCCCTCCCG 77177 T CATGAT
 CC GGAGGG GAGCGAG
 || ||||| |||||
 GG CCTCCC CTCGCTC
 C C____
 GAM2465 LOC148137 3' CCTCGCCGCCAGCCTTCCAGGT 59095 A A A
 ACCTGGAGGGC TG TG GCGAGG
 ||||| || || |||||
 TGGACCTTCCG AC GC CGCTCC
 _ C _
 GAM2465 LOC151996 5' CCGGCCCATACCCCTCCAG 86716 CATG A GA
 CTGGAGGG ATG GC GG
 ||||| || || ||
 GACCTCCC TAC CG CC
 CA_ C G_
 GAM2465 LOC165288 5' CCTACCCACGCCCTCCGGG 83374 A ATGAGCG
 CCTGGAGGGC TG AGG
 ||||| || ||||
 GGGCCTCCCG AC TCC
 C CCA____
 GAM2465 LOC195977 3' CTCACCTGCTCCTCCAGGT 88931 _ TGA
 ACCTGGAGG GCA TGAG
 ||||| || ||||
 TGGACCTCC CGT ACTC
 T CC_
 GAM2465 LOC196746 3' CCCATCTCATGCCCCAGG 88898 AG T GCGA
 CCTGG GGCATGA GA GG
 |||| ||||| || ||

GGACC CCGTACT CT CC
___ AC___
GAM2465 LOC199800 5' CCTCGCTCCACGCCCTCCAGG 91447 A AT
CCTGGAGGGC TG GAGCGAGG
||||||| || |||||
GGACCTCCCG AC CTCGCTCC
C ___
GAM2465 LOC200093 3' CCTCACTCAGCCTTTTCCCTCC 63767 CATGA___ C
AGG CCTGGAGGG TGAG GAGG
||||||| ||| ||||
GGACCTCCC ACTC CTCC
TTTTCCG A
GAM2465 LOC255975 5' CCTCAGGTCATACTCTCCAGG 97577 C GAGC
CCTGGAGGG ATGAT GAGG
||||||| |||| ||||
GGACCTCTC TACTG CTCC
A GA___
GAM2465 LOC91040 3' CCTCACTCAGCCTTTTCCCTCC 65342 CATGA___ C
AGG CCTGGAGGG TGAG GAGG
||||||| ||| ||||
GGACCTCCC ACTC CTCC
TTTTCCG A
GAM2466 ATP2B2 5' CAGCCATCACCCGGCAGC 9846 A ___
GCT CTGGGTGA GCTG
||| ||||| ||||
CGA GGCCCACT CGAC
C AC
GAM2466 BSCL2 5' GGACTACCGGCTTTACCCTCCC 51994 T_____ T___ ACTA
AGTAGCT AGCTACTGGG GAGC GG CC
||||||| |||| || ||
TCGATGACCC TTCG CC GG
TCCCAT G___ ATCA
GAM2466 IMPA2 5' AGTGTGTGCTCACCCACAGC 96944 AC _ G
GCT TGGGTGAGC TG ACT
||| ||||| || ||||
CGA ACCCACTCG GT TGA
C_ T G
GAM2466 KCNE1L 3' AGTCCAGCTTCCAGTTGC 25388 T GT
GC ACTGG GAGCTGGA
|| |||| |||||
CG TGACC TTCGACCTGA
T ___
GAM2466 KRTHA1 3' GGCAGCCAAGAACTCACCCAA 11237 AC C_____ A A
AGC GCT TGGGTGAG TGG CT CC
||| ||||| ||| || ||
CGA ACCCACTC ACC GA GG
A_ AAAGA _ C
GAM2466 MADH7 3' AGTATTGCTCACCCAGTGC 20922 T TGG
GC ACTGGGTGAGC ACT
|| ||||| |||

CG TGACCCACTCG TGA
 _ TTA
 GAM2466 RXRA 3' GTTGTTCACCCAGAGC 12922 A TG
 GCT CTGGGTGAGC GAC
 ||| ||||| |||
 CGA GACCCACTTG TTG

GAM2466 SQSTM1 3' GCTACCAGCAGCCCAGCACATA 15328 GA T ACTA
 GCT AGCTA CTGGGT GC GG C
 |||| |||| || || |
 TCGAT GACCCG CG CC G
 ACAC A A ATCA

GAM2466 TPI1 3' AGCCCAGAAGCCCAGTAACT 6294 C GAG A
 AG TACTGGGT CTGG CT
 || ||||| |||| ||
 TC ATGACCCG GACC GA
 A AA C

GAM2466 TRHDE 3' GGTATTCTACCCAGTAG 26316 CTGG
 CTACTGGGTGAG ACT
 ||||| |||
 GATGACCCACTC TGG
 TTA_

GAM2466 C11orf21 3' AGTCCAGCCCATGGAGC 27100 A GG A
 GCT CT GTG GCTGGACT
 ||| || |||||
 CGA GG TAC CGACCTGA
 _ _ C

GAM2466 CAPN6 3' CAGCATTTCACCCAGCAGC 27398 A
 GCT CTGGGTGA GCTG
 ||| ||||| |||
 CGA GACCCACT CGAC
 C TTA

GAM2466 DT1P1A10 3' AGTTTCTGGGCCCACCCTAGCA 62246 A _ A
 GC GCT CT GGGTG GCT GGACT
 ||| || |||| ||||
 CGA GA CCCAC CGG TTTGA
 C T C GTC

GAM2466 FLJ12700 3' GGCAGTCCACAGGCCTACAGCT 46657 AC GAGC A
 AGCT TGGGT TGGACT CC
 |||| |||| |||| ||
 TCGA ATCCG ACCTGA GG
 C_ GAC_ C

GAM2466 FLJ32780 3' AGTCCTCTGGTCCCACAGCT 59297 AC _ G CT
 AGCT TGGG T AG GGACT
 |||| |||| | || ||||
 TCGA ACCC G TC CCTGA
 C_ T G T_

GAM2466 HRD1 3' CCTGTCTACCCAGCAGC 70148 A _ T
 GCT CTGGGTGAG C GG
 ||| ||||| ||| ||

		CGA GACCCACTC G CC		
		C T T		
GAM2466 KIAA0356	3'	GGTCTATGGGCCACCCAGTGC 66779	T	A ____
		GC ACTGGGTG GCT GGACT		
		CG TGACCCAC CGG TCTGG		
		_ C GTA		
GAM2466 KIAA0984	3'	AGCTCACTCACCCACCAGCT 66137	AC	C GA
		AGCT TGGGTGAG TG CT		
		TCGA ACCCACTC AC GA		
		CC _ TC		
GAM2466 KIAA1598	5'	GTAGTCCAAGTGGGATATTAGC 37639	____	G GAGC
		GCTA CT GGT TGGACTAC		
		CGAT GG TCA ACCTGATG		
		TATA G ____		
GAM2466 KIAA1681	3'	AGTCCAAGTCCAGTAACT 61714	C	GTGA _
		AG TACTGG GCT GGACT		
		TC ATGACC TGA CCTGA		
		A ____ A		
GAM2466 MGC17303	3'	GGCAGTCAGATCCACCCAGTGC 58233	T	AG_ G A
	T	AGC ACTGGGTG CTG ACT CC		
		TCG TGACCCAC GAC TGA GG		
		_ CTA _ C		
GAM2466 PDE4DIP	5'	CCAGTGGTCACCCAGTAGC 28404	__	T__
		GCTACTGGGTGA GC GG		
		CGATGACCCACT TG CC		
		GG A__		
GAM2466 SLC26A10	5'	CCGGTAACCCAACAGTGGCT 56842	__	GA T__
		AGCTACT GGGT GC GG		
		TCGGTGA CCCA TG CC		
		CAA A_ G__		
GAM2466 USP2	5'	AGCCGGGACTCACCCGCAGCT 16108	AC	_ A
		AGCT TGGGTGAG CTGG CT		
		TCGA GCCCACTC GGCC GA		
		C_ AG _		
GAM2466 LOC143425	3'	CTACTCACTCAGTAGCT 89013	C	
		AGCTACTGGGTGAG TGG		
		TCGATGACTCACTC ATC		
		_		
GAM2466 LOC145828	5'	AGTCCCTCCCAGTGGCT 84537	TGAGCT	
		AGCTACTGGG GGACT		

		TCGGTGACCC	CCTGA		
		TC_____			
GAM2466	LOC151174	5'	GGCCCGGCTCACCCACAGCT	86438	ACT A
			AGCT GGGTGAGCTGG CT		
			TCGA CCCACTCGGCC GG		
			CAC C		
GAM2466	LOC158055	3'	AGGCCTCCACCCAGTGCT	82576	T AGCT A
			AGC ACTGGGTG GG CT		
			TCG TGACCCAC CC GA		
			_ CT_ G		
GAM2466	LOC158696	3'	GTAGATCCACCAATAGCT	82861	C GTGAGC _
			AGCTA TGG TGGA CTAC		
			TCGAT ACC ACCT GATG		
			A _ A		
GAM2466	LOC196027	3'	GGTTTTCACCCAGTAGTT	88940	CTG
			AGCTACTGGGTGAG GACT		
			TTGATGACCCACTT TTGG		

GAM2466	LOC200812	5'	CAGCCCATCCAGTATGCT	90301	_ A
			AGC TACTGGGTG GCTG		
			TCG ATGACCTAC CGAC		
			T C		
GAM2466	LOC253836	5'	CAGCGCTTCACCCAGTGC	99465	T _
			GC ACTGGGTGA GCTG		
			CG TGACCCACT CGAC		
			_ TCG		
GAM2466	LOC256436	3'	AGCCCAGAAGCCCAGTAACT	96247	C GAG A
			AG TACTGGGT CTGG CT		
			TC ATGACCCG GACC GA		
			A AA_ C		
GAM2466	LOC256492	5'	TCCAGCTCAGTACAGCAGC	99434	A GG_
			GCT CTG TGAGCTGGA		
			CGA GAC ACTCGACCT		
			C ATG		
GAM2466	LOC56181	3'	GTCACCTCACTCAGCAGCT	97284	A CTG
			AGCT CTGGGTGAG GAC		
			TCGA GACTCACTC CTG		
			C A_		
GAM2466	LOC92148	5'	TCTACACACCCAGTACT	68888	C AGC
			AG TACTGGGTG TGGA		

			TC ATGACCCAC ATCT		
			— AC—		
GAM2467	BACH2	3'	GCTGTCAAGCAATGGATAAACA 41787	C	GGA—
			GCTCT AGAGTTGTT ATCCA GACAGC		
			TCTCGACAA TAGGT CTGTCTG		
			A AACGAA		
GAM2467	DGCR2	3'	GCTGCCTCCTGTCTCTCCACTC 18902	TGTTTCATC	A
			T AGAGT CAGGAG CAGC		
			TCTCA GTCCTC GTCG		
			CCTCTCT_ C		
GAM2467	HHIP	5'	CTGTCCCACCTAAACAACCTC 42752	CATCCA	A
			GAGTTGTT GG GACAG		
			CTCAACAA CC CTGTC		
			ATCCA_ _		
GAM2467	HS3ST2	3'	CTGTCTCTGAAAACAACCTT 21277	CATCCA	
			AGAGTTGTT GGAGACAG		
			TTTCAACAA TCTCTGTC		
			AAG—		
GAM2467	MTCP1	5'	CTACATGGATAACAACCTCT 27241	C	GG_
			AGAGTTGTT ATCCA AG		
			TCTCAACAA TAGGT TC		
			_ ACA		
GAM2467	PCOLN3	3'	GCTGCCCTGTTGCCAAACAACCT 12414	— TC	AGA
			C GAGTTGTT CA CAGG CAGC		
			CTCAACAA GT GTCC GTCG		
			ACC T_ C_		
GAM2467	PFN2	3'	CTGTCTTCATCAACAACCCT 54885	A	C CCA
			AG GTTGTT AT GGAGACAG		
			TC CAACAA TA CTTCTGTC		
			C C _		
GAM2467	PFN2	3'	CTGTCTTCATCAACAACCCT 54886	A	C CCA
			AG GTTGTT AT GGAGACAG		
			TC CAACAA TA CTTCTGTC		
			C C _		
GAM2467	RAD52	3'	CTGTCTCAGAACCACTC 57026	T	ATCCAG
			GAGT GTTC GAGACAG		
			CTCA CAAG CTCTGTC		
			C A—		
GAM2467	TIMP3	3'	CTCCTGAGATCCTCACCTCT 6283	T TTC	_
			AGAG TG ATC CAGGAG		

		TCTC AC TAG GTCCTC	
		C TCC A	
GAM2467 AKAP11	3'	TTGTAGTCAGTTGAACAACTCT 58468	TCCA AG
		AGAGTTGTTCA GG ACAG	
		TCTCAACAAGT CT TGTT	
		TGA_ GA	
GAM2467 CHST3	3'	CGTCTCCTGGAAACGCT 16237 T CA A	
		AGT GTT TCCAGGAGAC G	
		TCG CAA AGGTCCTCTG C	
		_ _ C	
GAM2467 FLJ10511	3'	GTCCCCTAGAAAAACAACCTCT 36690	CA C A
		AGAGTTGTT TC AGG GAC	
		TCTCAACAA AG TCC CTG	
		AA A C	
GAM2467 FLJ13102	3'	GCTGTCTGCCTGAGCAACTCT 46534	TCCA _
		AGAGTTGTTCA GG AGACAGC	
		TCTCAACGAGT CC TCTGTCTG	
		_ _ G	
GAM2467 HAAO	3'	GCCATCCCTGCCAAACAACCTCT 60172	CATC A CA
		AGAGTTGTT CAGG GA GC	
		TCTCAACAA GTCC CT CG	
		ACC_ _ AC	
GAM2467 KIAA0628	3'	CTGTCTCAAAAAACAACCTTT 29528	CATCCAG
		AGAGTTGTT GAGACAG	
		TTTCAACAA CTCTGTC	
		AAAA_	
GAM2467 KIAA0843	3'	CTGAACAACCAGACAGACAACCT 30800	CA CA AGA_
CT		AGAGTTGTT TC GG CAG	
		TCTCAACAG AG CC GTC	
		AC A_ AACAA	
GAM2467 KIAA1497	5'	CTGTCCTTGTATGAGCAAC 68120	C A
		GTTGTTTCAT CAGG GACAG	
		CAACGAGTA GTTC CTGTC	
		T _	
GAM2467 KIAA1710	3'	GCTATCTCCATACATGAACAAT 63178	G CCA_ C
CT		AGA TTGTTTCAT GGAGA AGC	
		TCT AACAAAGTA CCTCT TCG	
		_ CATA A	
GAM2467 MBLL39	3'	CTGTCTCTGCAGCAACAACCTC 59259	CATCCA
		GAGTTGTT GGAGACAG	

CTCAACAA TCTCTGTC
 CGACG_
 GAM2467 MGC12972 3' CTGTCTCCTGGCGGACCAC 52053 T AT
 GT GTTC CCAGGAGACAG
 || ||| |||||
 CA CAGG GGTCCTCTGTC
 C C_
 GAM2467 MGC4308 3' CTGTCCTTTTGACAACTCT 66184 T TCC A
 AGAGTTGT CA AGG GACAG
 ||||| || ||| |||||
 TCTCAACA GT TTC CTGTC
 _ T_ _
 GAM2467 PDE7B 3' GCTGCCGAAATGAGCAACTC 38952 CCA AGA
 GAGTTGTTTCAT GG CAGC
 ||||| || |||
 CTCAACGAGTA CC GTCG
 AAG _
 GAM2467 SEC24B 3' GCTGCATTGTTGGATGACAACT 21985 T G A_
 CT AGAGTTGT CATCCAG AG CAGC
 ||||| ||||| || |||
 TCTCAACA GTAGGTT TT GTCG
 _ G AC
 GAM2467 LOC142948 3' CCGGGAGGAATGAATAACTC 83775 _ A
 GAGTTGTTCA TCC GG
 ||||| ||| ||
 CTCAATAAGT AGG CC
 AAGG G
 GAM2467 LOC145225 3' CTGTCTCCAGTTGGGCAGCTC 84266 TCCA
 T AGAGTTGTTCA GGAGACAG
 ||||| |||||
 TCTCGACGGGT CCTCTGTC
 TGAC
 GAM2467 LOC219914 5' CTGGGAGGAACGAACAACTC 94968 A_ AGGAGA
 GAGTTGTTTC TCC CAG
 ||||| ||| |||
 CTCAACAAG AGG GTC
 CA AGG_
 GAM2467 LOC219972 3' GCTGCCCTTGATGAACACTC 93278 T C AGA
 GAGT GTTCATC AGG CAGC
 ||| ||||| ||| |||
 CTCA CAAGTAG TCC GTCG
 _ T CC_
 GAM2468 SCA1 3' CCACTTACAATTCTTAAATTC 6175 GGCA_ C
 GAAT AATTGTAAG GG
 ||| ||||| ||
 CTTA TTAACATTC CC
 AATTC A
 GAM2468 KIAA0596 3' CCACTCCAGATTTGCCCCCGC 63486 AAT GTA C
 GCG GGCAAATT AG GG
 ||| ||||| |||

			CGC CCGTTTAG TC CC		
			CC_ ACC A		
GAM2468	SLC17A3	5'	CTGTAGCTGGCCATTTCGC 22790	AAATT	AA
			GCGAATGGC GT GCGG		
			CGCTTACCG CG TGTC		
			GT__ A_		
GAM2468	LOC136319	5'	CCGCTTGCTGCTGCCACCGC 75771	AA	AATT
			GCG TGGCA GTAAGCGG		
			CGC ACCGT CGTTCGCC		
			C_ CGT_		
GAM2469	A1BG	3'	AACTCCTGAGCTCAGGTGATCC 56274		G
	A		TGGATCACCTGAG TCAGGAGTT		
			ACCTAGTGGACTC AGTCCTCAA		
			G		
GAM2469	A1BG	3'	GAACTCTTGGGCTCAAGTGATC 56290	C	G
	C		GGATCAC TGAG TCAGGAGTTC		
			CCTAGTG ACTC GGTTCCTCAAG		
			A G		
GAM2469	ADAMTS4	3'	GAACTCCTGACCTCAGGTAATC 18758		C
			GAT ACCTGAGGTCAGGAGTTC		
			CTA TGGACTCCAGTCCTCAAG		
			A		
GAM2469	ADAMTS4	3'	GAACTCCTGACCTTAGGTGATC 18759		
	CA		TGGATCACCTGAGGTCAGGAGTTC		
			ACCTAGTGGATTCCAGTCCTCAAG		
GAM2469	AGL	5'	GAACTCCTGGACTCAAGCAACC 7213	ATCACC	GT
	C		GG TGAG CAGGAGTTC		
			CC ACTC GTCCTCAAG		
			CAACGA AG		
GAM2469	ALDH1B1	3'	GAACTCCTGACCTCAGGTGATC 7324		
	CA		TGGATCACCTGAGGTCAGGAGTTC		
			ACCTAGTGGACTCCAGTCCTCAAG		
GAM2469	APAF1	3'	GAACTCTTGGCCTCAAGTAATC 8586	C	C
	C		GGAT AC TGAGGTCAGGAGTTC		
			CCTA TG ACTCCGGTTCTCAAG		
			A A		
GAM2469	APAF1	3'	GAACTCTTGGCCTCAAGTAATC 25972	C	C
	C		GGAT AC TGAGGTCAGGAGTTC		

			CCTA TG ACTCCGGTTCTCAAG	
			A A	
GAM2469	APM1	3'	AACTCCTGACTTTGTGATCCA 17749	CT
			TGGATCAC GAGGTCAGGAGTT	
			ACCTAGTG TTTCAGTCCTCAA	
			—	
GAM2469	APM1	3'	GAACTCCTGGCCTAGGTGATCC 17781	G
	A		TGGATCACCT AGGTCAGGAGTTC	
			ACCTAGTGGA TCCGGTCCTCAAG	
			—	
GAM2469	AQP6	3'	TCCTGACCCCAGATGCCCA 55017	AT C A
			TGG CA CTG GGTCAGGA	
			ACC GT GAC CCAGTCCT	
			C_ A C	
GAM2469	AQP6	3'	TCCTGACCCCAGATGCCCA 9736	AT C A
			TGG CA CTG GGTCAGGA	
			ACC GT GAC CCAGTCCT	
			C_ A C	
GAM2469	ARCN1	3'	GAACTCCTGAGCTCAGGCAATC 9752	CA G
	C		GGAT CCTGAG TCAGGAGTTC	
			CCTA G GACTC AGTCCTCAAG	
			AC G	
GAM2469	ARSF	5'	GAACTCCCGACCTCAAGTGATC 65208	C A
	C		GGATCAC TGAGGTC GGAGTTC	
			CCTAGTG ACTCCAG CCTCAAG	
			A C	
GAM2469	ATP1B2	3'	GAACTCCCGACCTCAGGTGATC 9834	A
	CA		TGGATCACCTGAGGTC GGAGTTC	
			ACCTAGTG GACTCCAG CCTCAAG	
			C	
GAM2469	ATP6V1A1	3'	GAACTCCAGACCTCAGGTGATC 9868	A
	C		GGATCACCTGAGGTC GGAGTTC	
			CCTAGTG GACTCCAG CCTCAAG	
			A	
GAM2469	ATP7A	3'	AACTCCTAACCTCAGGTGATCC 5307	C
	A		TGGATCACCTGAGGT AGGAGTT	
			ACCTAGTG GACTCCA TCCTCAA	
			A	
GAM2469	AXL	3'	AACTCCTGACCTCAAGTGATCT 9895	C
			GGATCAC TGAGGTCAGGAGTT	

			TCTAGTG ACTCCAGTCCTCAA		
			A		
GAM2469	AXL	3'	AACTCCTGACCTCAAGTGATCT 41868	C	
			GGATCAC TGAGGTCAGGAGTT		
			TCTAGTG ACTCCAGTCCTCAA		
			A		
GAM2469	B4GALT5	3'	GAACTCCTGGACTCAAGCAATC 17687	CACC	GT
	C		GGAT TGAG CAGGAGTTC		
			CCTA ACTC GTCCTCAAG		
			ACGA AG		
GAM2469	C7	3'	AACTCCTGACCTCAGGTAATCC 6973	C	
			GGAT ACCTGAGGTCAGGAGTT		
			CCTA TGGACTCCAGTCCTCAA		
			A		
GAM2469	CASP10	3'	AACTCCTGGGCTCAAGCGATCC 53210	ACC	G
			GGATC TGAG TCAGGAGTT		
			CCTAG ACTC GGTCTCAA		
			CGA G		
GAM2469	CASP10	3'	AACTCCTGGGCTCAAGCGATCC 53233	ACC	G
			GGATC TGAG TCAGGAGTT		
			CCTAG ACTC GGTCTCAA		
			CGA G		
GAM2469	CBFA2T2	3'	AACCCCGGACCTCAGGTGATCC 18696		A A
			GGATCACCTGAGGTC GG GTT		
			CCTAGTGGACTCCAG CC CAA		
			G C		
GAM2469	CBFB	3'	GAACTCCTGGCATCAAGCGATC 43439	ACC	G
	C		GGATC TGA GTCAGGAGTTC		
			CCTAG ACT CGGTCCTCAAG		
			CGA A		
GAM2469	CBFB	3'	GAACTCCTGGCATCAAGCGATC 10038	ACC	G
	C		GGATC TGA GTCAGGAGTTC		
			CCTAG ACT CGGTCCTCAAG		
			CGA A		
GAM2469	CCNF	3'	GAACTCATGACCTCAAGTGATC 10074	C	G
	C		GGATCAC TGAGGTCA GAGTTC		
			CCTAGTG ACTCCAGT CTCAAG		
			A A		
GAM2469	CDH1	3'	AACTCCTGGCCTCAAGCAATCC 16395	CACC	
			GGAT TGAGGTCAGGAGTT		

			CCTA ACTCCGGTCCTCAA	
			ACGA	
GAM2469	CDH1	3'	AACTCCTGGGCTCAAGTGATCC 16396	C G
			GGATCAC TGAG TCAGGAGTT	
			CCTAGTG ACTC GGTCCTCAA	
			A G	
GAM2469	CHRN4	3'	GAACTCCTGACCTCAGATGACC 7449	A C
	CA		TGG TCA CTGAGGTCAGGAGTTC	
			ACC AGT GACTCCAGTCCTCAAG	
			C A	
GAM2469	CLECSF12	3'	GAACTCCTGACCTCAAGTGATC 77211	C
	T		GGATCAC TGAGGTCAGGAGTTC	
			TCTAGTG ACTCCAGTCCTCAAG	
			A	
GAM2469	CNP	3'	GAACTCCTGGGCTCAAGCAATC 53621	CACC G
	C		GGAT TGAG TCAGGAGTTC	
			CCTA ACTC GGTCCTCAAG	
			ACGA G	
GAM2469	COX15	3'	GAACTCCTGACCTCAGGTAATC 55284	C
	C		GGAT ACCTGAGGTCAGGAGTTC	
			CCTA TGGACTCCAGTCCTCAAG	
			A	
GAM2469	CRTAP	3'	GAACTCTTGACTTCAGATGATC 22078	C
	CA		TGGATCA CTGAGGTCAGGAGTTC	
			ACCTAGT GACTTCAGTTCTCAAG	
			A	
GAM2469	CXCL16	3'	GAACTCCTGAGTCAAGTGATCC 42167	C GG
			GGATCAC TGA TCAGGAGTTC	
			CCTAGTG ACT AGTCCTCAAG	
			A G_	
GAM2469	CYP1A2	3'	AACTCCTGACCTCAAGTGATCT 7492	C
			GGATCAC TGAGGTCAGGAGTT	
			TCTAGTG ACTCCAGTCCTCAA	
			A	
GAM2469	CYP1A2	3'	GAACTCCTGACCCCAAGTTATC 7514	C C A
	CA		TGGAT AC TG GGTCAGGAGTTC	
			ACCTA TG AC CCAGTCCTCAAG	
			T A C	
GAM2469	CYP2B6	3'	CCTGGCCTCAGGTGATCCA 7558	
			TGGATCACCTGAGGTCAGG	

ACCTAGTGGACTCCGGTCC

GAM2469 CYP2B6 3' GAACTCCTGAACTCAAGTGATT 7561 C G
CA TGGATCAC TGAG TCAGGAGTTC

||||| ||| |||||
ACTTAGTG ACTC AGTCCTCAAG
A A

GAM2469 CYP4F3 3' GAACTCCTAACCTCAGGTGATC 8007 C
CA TGGATCACCTGAGGT AGGAGTTC

||||||| |||||
ACCTAGTGGACTCCA TCCTCAAG
A

GAM2469 DFFB 3' AACTCCTGACCTCAGGTGATCC 88746
GGATCACCTGAGGTCAGGAGTT

|||||||
CCTAGTGGACTCCAGTCCTCAA

GAM2469 DFFB 3' GAACTCCTGACCTCAGGTGATC 88770
T GGATCACCTGAGGTCAGGAGTTC

|||||||
TCTAGTGGACTCCAGTCCTCAAG

GAM2469 DIAPH2 3' GAACTCCTAGCCTCAAGCAATC 23006 CACC TC
CA TGGAT TGAGG AGGAGTTC

|||| ||| |||||
ACCTA ACTCC TCCTCAAG
ACGA GA

GAM2469 DISC1 3' AACTCCTGACCTCAGGCGATCC 38494 A
A TGGATC CCTGAGGTCAGGAGTT

|||| |||||
ACCTAG GGA CTCCAGTCCTCAA
C

GAM2469 DSCR3 3' GAACTCCTAGACTCAAGTGATC 21312 C G _
C GGATCAC TGAG TC AGGAGTTC

||||| ||| || |||||
CCTAGTG ACTC AG TCCTCAAG
A _ A

GAM2469 DSCR3 3' GAACTCCTGACCTCGTGACCCA 21313 A CT
TGG TCAC GAGGTCAGGAGTTC

||| ||| |||||
ACC AGTG CTCCAGTCCTCAAG
C _

GAM2469 EPB72 3' GAACTCCTAACCTCAGGTGATC 15873 C
CA TGGATCACCTGAGGT AGGAGTTC

||||||| |||||
ACCTAGTGGACTCCA TCCTCAAG
A

GAM2469 F2RL2 3' GAACTCCTGACCTCAAGTGATC 15896 C
T GGATCAC TGAGGTCAGGAGTTC

||||| |||||

			TCTAGTG ACTCCAGTCCTCAAG		
			A		
GAM2469	F3	3'	GAATTCCTGACCTCAGTTGATC 67677	C	
	CA		TGGATCA CTGAGGTCAGGAGTTC		
			ACCTAGT GACTCCAGTCCTTAAG		
			T		
GAM2469	FABP2	3'	GAACCCCTGGCCTCAAGCAATC 5535	CACC	A
	C		GGAT TGAGGTCAGG GTTC		
			CCTA ACTCCGGTCC CAAG		
			ACGA C		
GAM2469	FCAR	3'	GAATCCTGACCTCAGGTGATC 56572		
	CA		TGGATCACCTGAGGTCAGGAGTTC		
			ACCTAGTGGACTCCAGTCCTCAAG		
GAM2469	FCAR	3'	GAATCCTGACCTCAGGTGATC 56592		
	CA		TGGATCACCTGAGGTCAGGAGTTC		
			ACCTAGTGGACTCCAGTCCTCAAG		
GAM2469	FCAR	3'	GAATCCTGACCTCAGGTGATC 56604		
	CA		TGGATCACCTGAGGTCAGGAGTTC		
			ACCTAGTGGACTCCAGTCCTCAAG		
GAM2469	FCAR	3'	GAATCCTGACCTCAGGTGATC 56616		
	CA		TGGATCACCTGAGGTCAGGAGTTC		
			ACCTAGTGGACTCCAGTCCTCAAG		
GAM2469	FCAR	3'	GAATCCCGACCTCAGGTGATC 56634		A
	CA		TGGATCACCTGAGGTC GGAGTTC		
			ACCTAGTGGACTCCAG CCTCAAG		
			C		
GAM2469	FCAR	3'	GAATCCTGACCTCAGGTGATC 10587		
	CA		TGGATCACCTGAGGTCAGGAGTTC		
			ACCTAGTGGACTCCAGTCCTCAAG		
GAM2469	G6PC	3'	GAATCCTGACCTCAAGTGATC 5660	C	
	CA		TGGATCAC TGAGGTCAGGAGTTC		
			ACCTAGTG ACTCCAGTCCTCAAG		
			A		
GAM2469	GNE	3'	GAATCCTGACCTCAGGTGATC 19669		
	C		GGATCACCTGAGGTCAGGAGTTC		

CCTAGTGGACTCCAGTCCTCAAG

GAM2469 GPR81 3' CCTGACCTCAGGTGATCC 51745
GGATCACCTGAGGTCAGG
|||||
CCTAGTGGACTCCAGTCC

GAM2469 GRAF 3' GAACTCCTGACCTCAAGTGATC 31236 C
T GGATCAC TGAGGTCAGGAGTTC
|||||
TCTAGTG ACTCCAGTCCTCAAG
A

GAM2469 HCS 3' AACTCCTGAGCTCAAGCAATCC 38956 CACC G
GGAT TGAG TCAGGAGTT
||| |||
CCTA ACTC AGTCCTCAA
ACGA G

GAM2469 HLCS 5' GAACTCCTGACCTCGTGATCCA 6412 CT
TGGATCAC GAGGTCAGGAGTTC
|||||
ACCTAGTG CTCCAGTCCTCAAG

GAM2469 IFNAR2 3' GAACTCCTGACCTCAAGTGATC 7900 C
T GGATCAC TGAGGTCAGGAGTTC
|||||
TCTAGTG ACTCCAGTCCTCAAG
A

GAM2469 IL11 3' GAACTCCTGACCTCAGGTGATC 7183
C GGATCACCTGAGGTCAGGAGTTC
|||||
CCTAGTGGACTCCAGTCCTCAAG

GAM2469 JAK3 3' GAACTCCTAACCTCAAGTGATC 5830 C C
C GGATCAC TGAGGT AGGAGTTC
|||||
CCTAGTG ACTCCA TCCTCAAG
A A

GAM2469 JRK 3' GAACTCTTGGCCTCAAGCGATC 87826 ACC
C GGATC TGAGGTCAGGAGTTC
||| |||
CCTAG ACTCCGGTTCTCAAG
CGA

GAM2469 LNK 3' GAATGTCTGACCTCAGGTGATC 19644 GA
CA TGGATCACCTGAGGTCAG GTTC
|||||
ACCTAGTGGACTCCAGTC TAAG
TG

GAM2469 LZTS1 3' AACTTGTGGCCTCAAGCAATCC 41019 CACC G
A TGGAT TGAGGTCA GAGTT
||| |||

			ACCTA ACTCCGGT TTCAA	
			ACGA G	
GAM2469	MAK	3'	AACTCCTGACCTCAGGTGATCC 20933	
	A		TGGATCACCTGAGGTCAGGAGTT	
			ACCTAGTGGACTCCAGTCCTCAA	
GAM2469	MEFV	3'	AACTCCTGACCTCAGGTGATGC 5917 G	
	A		TG ATCACCTGAGGTCAGGAGTT	
			AC TAGTGGACTCCAGTCCTCAA	
			G	
GAM2469	MEFV	3'	GAACCTCCTGACCTCAGGTGATC 5937	
	CA		TGGATCACCTGAGGTCAGGAGTTC	
			ACCTAGTGGACTCCAGTCCTCAAG	
GAM2469	MHC2TA	3'	GAACTCTTGACCTCGGGTGATC 5983	
	CA		TGGATCACCTGAGGTCAGGAGTTC	
			ACCTAGTGGGCTCCAGTTCTCAAG	
GAM2469	MICB	3'	AACTCCTGACCTCAGGTGATCT 21016	
			GGATCACCTGAGGTCAGGAGTT	
			TCTAGTGGACTCCAGTCCTCAA	
GAM2469	MLANA	3'	AACTCCTGACCTCAGGTGATCT 19752	
			GGATCACCTGAGGTCAGGAGTT	
			TCTAGTGGACTCCAGTCCTCAA	
GAM2469	MPL	3'	GAACCTCCTAACCTCGGGTGATC 19354	C
	CA		TGGATCACCTGAGGT AGGAGTTC	
			ACCTAGTGGGCTCCA TCCTCAAG	
			A	
GAM2469	MRPL49	3'	AACTCCTGACTCGAAGTGATCC 70154	CTGA
			GGATCAC GGTCAGGAGTT	
			CCTAGTG TCAGTCCTCAA	
			AAGC	
GAM2469	MYCL2	3'	CCTGACCTAGGTGATCCA 19373	G
			TGGATCACCT AGGTCAGG	
			ACCTAGTGGA TCCAGTCC	
GAM2469	NCOA6	5'	AACTCCTGACCTCAAGTGATCC 26816	C
	A		TGGATCAC TGAGGTCAGGAGTT	

			ACCTAGTG ACTCCAGTCCTCAA	
			A	
GAM2469	NCOA6	5'	GAAGTCCTGAGCTCAAGCAGTC 26835	CACC G
	CA		TGGAT TGAG TCAGGAGTTC	
			ACCTG ACTC AGTCCTCAAG	
			ACGA G	
GAM2469	NDRG3	3'	AACTCCTGACCTCAGGTGATCC 50112	
	A		TGGATCACCTGAGGTCAGGAGTT	
			ACCTAGTGGACTCCAGTCCTCAA	
GAM2469	NQO1	3'	AACTCCTGACCTCAGGTGATCC 8037	
			GGATCACCTGAGGTCAGGAGTT	
			CCTAGTGGACTCCAGTCCTCAA	
GAM2469	NT5C2	5'	CCTGACGTCAAGTGATCCA 25262	C G
			TGGATCAC TGA GTCAGG	
			ACCTAGTG ACT CAGTCC	
			A G	
GAM2469	PDE6B	3'	GAAGTCCTGACCTCAGGTGATC 6076	
			GATCACCTGAGGTCAGGAGTTC	
			CTAGTGGACTCCAGTCCTCAAG	
GAM2469	PER2	3'	GAAGTCCTGACCTCAAGCGATC 43351	ACC
	CA		TGGATC TGAGGTCAGGAGTTC	
			ACCTAG ACTCCAGTCCTCAAG	
			CGA	
GAM2469	PIK3CD	3'	GAAGTCCTGACCTCAGGTGATC 18491	
	CA		TGGATCACCTGAGGTCAGGAGTTC	
			ACCTAGTGGACTCCAGTCCTCAAG	
GAM2469	PMCHL1	3'	GAAGTCCTGACCTCGTGATCCA 49916	CT
			TGGATCAC GAGGTCAGGAGTTC	
			ACCTAGTG CTCCAGTCCTCAAG	
GAM2469	PPEF2	3'	GAAGTCCCAACCTCAGGTGATC 21775	CA
	CA		TGGATCACCTGAGGT GGAGTTC	
			ACCTAGTGGACTCCA CCTCAAG	
			AC	
GAM2469	PPID	3'	GAAGTCCTGACCTTGTGATCCA 88825	CT
			TGGATCAC GAGGTCAGGAGTTC	

ACCTAGTG TTCCAGTCCTCAAG

GAM2469 PRKR 3' AACTCCTGACCTCAAGTAATCC 12334 C C
A TGGAT AC TGAGGTCAGGAGTT
||||| || |||||||||
ACCTA TG ACTCCAGTCCTCAA
A A

GAM2469 PRKWNK3 3' AACTCCTAACCTTGTGATCC 62221 CT C
GGATCAC GAGGT AGGAGTT
||||| ||||| |||||
CCTAGTG TTCCA TCCTCAA
A

GAM2469 PTGES 3' GAACTCCTGGCCTCAAGTGATC 18060 C
CA TGGATCAC TGAGGTCAGGAGTTC
||||| |||||||||
ACCTAGTG ACTCCGGTCCTCAAG
A

GAM2469 RBBP9 3' GAACTCCTGGCCTCAAGTGATC 70690 C
CA TGGATCAC TGAGGTCAGGAGTTC
||||| |||||||||
ACCTAGTG ACTCCGGTCCTCAAG
A

GAM2469 RGS9 5' AACTCCTGGGCTCAAGCGATCC 15166 ACC G
GGATC TGAG TCAGGAGTT
||||| ||||| |||||
CCTAG ACTC GGTCTCAA
CGA G

GAM2469 RHD 3' AACTCCTGACCTCAAGTGATCT 32797 C
GGATCAC TGAGGTCAGGAGTT
||||| |||||||||
TCTAGTG ACTCCAGTCCTCAA
A

GAM2469 RHD 3' AACTCCTGACCTCAAGTGATCT 33127 C
GGATCAC TGAGGTCAGGAGTT
||||| |||||||||
TCTAGTG ACTCCAGTCCTCAA
A

GAM2469 RP2 3' GAACTCCTGACCTCAGGTGATC 23602
C GGATCACCTGAGGTCAGGAGTTC
||||| |||||||||
CCTAGTGGA CTCCAGTCCTCAAG

GAM2469 RPH3AL 3' GAACTCCTGGTCTCAAGTGATC 23733 C GT
C GGATCAC TGAG CAGGAGTTC
||||| ||||| |||||
CCTAGTG ACTC GTCCTCAAG
A TG

GAM2469 SAS 3' GAACTCCTGACCTCAGGTGATC 21100
CA TGGATCACCTGAGGTCAGGAGTTC
||||| |||||||||

ACCTAGTGGACTCCAGTCCTCAAG

GAM2469 SCML2 3' AACTCCTGACCTCAGGTGATCC 21417
GGATCACCTGAGGTCAGGAGTT
|||||
CCTAGTGGACTCCAGTCCTCAA

GAM2469 SEDL 3' AACTCCTGACCTCAGTTGATCC 28064 C
A TGGATCA CTGAGGTCAGGAGTT
|||||
ACCTAGT GACTCCAGTCCTCAA
T

GAM2469 SEDL 3' GAACTCCTGACCTCGTGATCCA 28098 CT
TGGATCAC GAGGTCAGGAGTTC
|||||
ACCTAGTG CTCCAGTCCTCAAG

GAM2469 SEPN1 3' GAACTTCTGACCTCAGGTGATC 66971
CA TGGATCACCTGAGGTCAGGAGTTC
|||||
ACCTAGTGGACTCCAGTCTTCAAG

GAM2469 SERPINB9 3' GAACTCCTGGCCTCAAGCAATC 16020 CACC
C GGAT TGAGGTCAGGAGTTC
|||
CCTA ACTCCGGTCCTCAAG
ACGA

GAM2469 SH3BP2 3' GAACTCCTGACCTCAACTGATC 13071 CC
C GGATCA TGAGGTCAGGAGTTC
|||||
CCTAGT ACTCCAGTCCTCAAG
CA

GAM2469 SH3BP2 3' GAACTCCTGACCTCAGGTGATC 13072
T GGATCACCTGAGGTCAGGAGTTC
|||||
TCTAGTGGACTCCAGTCCTCAAG

GAM2469 SHOX 3' AACTCCTGGGCTCAAGCAATCC 23510 CACC G
GGAT TGAG TCAGGAGTT
||| |||
CCTA ACTC GGTCTCAA
ACGA G

GAM2469 SHOX 3' GAACTCCTGACCTCAGGTGATC 23519
CA TGGATCACCTGAGGTCAGGAGTTC
|||||
ACCTAGTGGACTCCAGTCCTCAAG

GAM2469 SHOX 3' GAACTCCTGACCTCAGGTGATC 6574
T GGATCACCTGAGGTCAGGAGTTC
|||||

TCTAGTGGACTCCAGTCCTCAAG

GAM2469 SIL 3' AACTCCCGACCTCAGGTGATCC 13147 A
GGATCACCTGAGGTC GGAGTT
||||||| |||||
CCTAGTGGACTCCAG CCTCAA
C

GAM2469 SIL 5' TCCTGACTTCAGGTGATCCA 13164
TGGATCACCTGAGGTCAGGA
|||||||
ACCTAGTGGACTTCAGTCCT

GAM2469 SLA2 3' GAACTCCTGACCTCAGGTGATC 50889
CA TGGATCACCTGAGGTCAGGAGTTC
|||||||
ACCTAGTGGACTCCAGTCCTCAAG

GAM2469 SLC14A2 5' GAACTTCTGACGTCAAGTGATC 24117 C G
CA TGGATCAC TGA GTCAGGAGTTC
||||| ||| |||||
ACCTAGTG ACT CAGTCTTCAAG
A G

GAM2469 SLC17A5 3' GAACTCCTGGCTTCAAGCGATC 25831 ACC
C GGATC TGAGGTCAGGAGTTC
|||| |||||
CCTAG ACTTCGGTCCTCAAG
CGA

GAM2469 SLC3A2 5' GAACTCTTGGCCTCAGGTGATC 11520
C GGATCACCTGAGGTCAGGAGTTC
|||||||
CCTAGTGGACTCCGGTTCTCAAG

GAM2469 SMAC 5' GAACTCCTGGGCTCAAGTGATC 58020 C G
C GGATCAC TGAG TCAGGAGTTC
||||| ||| |||||
CCTAGTG ACTC GGTCCTCAAG
A G

GAM2469 SMAC 5' GAATTCCTGACCTCAAGTGATC 58021 C
CA TGGATCAC TGAGGTCAGGAGTTC
||||| |||||
ACCTAGTG ACTCCAGTCCTTAAG
A

GAM2469 SNX15 3' GAACTCCTGACCTCAAGTGATC 74119 C
CA TGGATCAC TGAGGTCAGGAGTTC
||||| |||||
ACCTAGTG ACTCCAGTCCTCAAG
A

GAM2469 SPN 3' AACTCCTGACCTCAGGTGATCT 13361
A TGGATCACCTGAGGTCAGGAGTT
|||||||

ATCTAGTGGACTCCAGTCCTCAA

GAM2469 SULT2B1 5' AACTCCTGACCTCAGGTGATCC 17218
A TGGATCACCTGAGGTCAGGAGTT
|||||
ACCTAGTGGACTCCAGTCCTCAA

GAM2469 TAF11 3' GAACTCCTGGGCTTAAGTGACC 20120 A C G
C GG TCAC TGAG TCAGGAGTTC
|| ||| ||| |||
CC AGTG ATTG GGTCTCAAG
C A G

GAM2469 TAT 3' AACTCCTGACCTCAGGCAATCT 6243 CA
GGAT CCTGAGGTCAGGAGTT
||| |||
TCTA GGA CTCCAGTCCTCAA
AC

GAM2469 TBXA2R 3' GAACTCCTGACCTCAGGTGATT 8357
CA TGGATCACCTGAGGTCAGGAGTTC
|||||
ACTTAGTGGACTCCAGTCCTCAAG

GAM2469 TES 3' AACTCCTGACCTCAGATGATCC 72454 C
GGATCA CTGAGGTCAGGAGTT
|||||
CCTAGT GACTCCAGTCCTCAA
A

GAM2469 TMPRSS3 3' AACCCCTGACCTCAAATGAT 51506 CC A
ATCA TGAGGTCAGG GTT
||| |||
TAGT ACTCCAGTCC CAA
AA C

GAM2469 TMPRSS3 3' AACCCCTGACCTCAAATGAT 51534 CC A
ATCA TGAGGTCAGG GTT
||| |||
TAGT ACTCCAGTCC CAA
AA C

GAM2469 TMPRSS3 3' AACCCCTGACCTCAAATGAT 44008 CC A
ATCA TGAGGTCAGG GTT
||| |||
TAGT ACTCCAGTCC CAA
AA C

GAM2469 TNFRSF10B 3' CCTGACCTCAGGTGATCCA 15222
TGGATCACCTGAGGTCAGG
|||||
ACCTAGTGGACTCCAGTCC

GAM2469 TNFRSF10B 3' GAACTCCTGACCTCAGGTGATC 15226
CA TGGATCACCTGAGGTCAGGAGTTC
|||||

ACCTAGTGGACTCCAGTCCTCAAG

GAM2469 TNFSF9 3' GAACTCCTGGACTTAGACGATC 15097 AC GT
C GGATC CTGAG CAGGAGTTC

||||| ||||| |||||
CCTAG GATTC GTCCTCAAG
CA AG

GAM2469 TP53 3' AACTCCTGGGCTCAGGCGATCC 6789 A G
A TGGATC CCTGAG TCAGGAGTT

||||| ||||| |||||
ACCTAG GGA CTC GGT CCTCAA
C G

GAM2469 TPMT 3' GAGCTCCTGACCTCAGGTGATC 6312
TA TGGATCACCTGAGGTCAGGAGTTC

|||||
ATCTAGTGGACTCCAGTCCTCGAG

GAM2469 TRAF5 3' AACTCCTGACCTCAAGTGATCT 17262 C
GGATCAC TGAGGTCAGGAGTT

||||| |||||
TCTAGTG ACTCCAGTCCTCAA
A

GAM2469 TRPM6 3' AACTCCTGACCTCAGATGATCC 35017 C
A TGGATCA CTGAGGTCAGGAGTT

||||| |||||
ACCTAGT GACTCCAGTCCTCAA
A

GAM2469 TRPV1 3' GAACTCCTGACCTCAGGTGATC 38696
C GGATCACCTGAGGTCAGGAGTTC

|||||
CCTAGTGGACTCCAGTCCTCAAG

GAM2469 TRPV1 3' GAACTCCTGACCTCAGGTGATC 55672
C GGATCACCTGAGGTCAGGAGTTC

|||||
CCTAGTGGACTCCAGTCCTCAAG

GAM2469 TRPV1 3' GAACTCCTGACCTCAGGTGATC 55712
C GGATCACCTGAGGTCAGGAGTTC

|||||
CCTAGTGGACTCCAGTCCTCAAG

GAM2469 TRPV1 3' GAACTCCTGACCTCAGGTGATC 55743
C GGATCACCTGAGGTCAGGAGTTC

|||||
CCTAGTGGACTCCAGTCCTCAAG

GAM2469 TUFT1 3' GAATTCCTGACCTCAGGTGATC 39674
CA TGGATCACCTGAGGTCAGGAGTTC

|||||

ACCTAGTGGACTCCAGTCCTTAAG

GAM2469 VENTX2 3' AACTCCTGACCCTGTGATCC 27849 CTGA
GGATCAC GGTCAGGAGTT
||||| |||||
CCTAGTG CCAGTCCTCAA
TC__

GAM2469 VHL 3' AACTCCTGACCTCAGGTGATCC 6812
GGATCACCTGAGGTCAGGAGTT
|||||
CCTAGTGGACTCCAGTCCTCAA

GAM2469 WHSC1 3' GAACTCCTGACCTCGTGATCCA 56695 CT
TGGATCAC GAGGTCAGGAGTTC
||||| |||||
ACCTAGTG CTCCAGTCCTCAAG

GAM2469 XRCC2 3' GAACTCCTGACCTCAAGTGATC 19500 C
CA TGGATCAC TGAGGTCAGGAGTTC
||||| |||||
ACCTAGTG ACTCCAGTCCTCAAG
A

GAM2469 ZNF133 5' GAACTGCTGACCTCAGGTGATC 14296 G
CA TGGATCACCTGAGGTCAG AGTTC
||||| |||||
ACCTAGTGGACTCCAGTC TCAAG
G

GAM2469 ZNF157 3' AACTCCTGACCTCAGGTGATCC 14318
A TGGATCACCTGAGGTCAGGAGTT
|||||
ACCTAGTGGACTCCAGTCCTCAA

GAM2469 ZNF264 3' AACTCCTGACCTTGTGATCC 14177 CT
GGATCAC GAGGTCAGGAGTT
||||| |||||
CCTAGTG TTCCAGTCCTCAA

GAM2469 AAK1 3' GAACTCCTGACCTCAGGTGATC 30522
C GGATCACCTGAGGTCAGGAGTTC
|||||
CCTAGTGGACTCCAGTCCTCAAG

GAM2469 AP3S2 3' GAACTCCTGGACCTCAAGTGAT 20651 C _
CTA TGGATCAC TGAGGTC AGGAGTTC
||||| ||||| |||||
ATCTAGTG ACTCCAG TCCTCAAG
A G

GAM2469 ARHF 3' GAACTCCTGACCTCGTGATCCA 39268 CT
TGGATCAC GAGGTCAGGAGTTC
||||| |||||

ACCTAGTG CTCCAGTCCTCAAG

GAM2469 ARHGAP5 5' GAACTCCCAACCTCAGGTGATC 77601 CA
C GGATCACCTGAGGT GGAGTTC

|||||
CCTAGTGGACTCCA CCTCAAG

AC

GAM2469 ASB16 3' CTGACCTCAGGTGATCCA 55982
TGGATCACCTGAGGTCAG

|||||
ACCTAGTGGACTCCAGTC

GAM2469 ASE-1 3' GAACTCCTGACCTCGTGATCCA 24979 CT
TGGATCAC GAGGTCAGGAGTTC

|||||
ACCTAGTG CTCCAGTCCTCAAG

GAM2469 ATP1B4 3' GAACTCCTGACCTCAAGTGATC 24843 C
C GGATCAC TGAGGTCAGGAGTTC

|||||
CCTAGTG ACTCCAGTCCTCAAG

A

GAM2469 BA108L7.2 3' GAACTCCTGACCTCAGGTGATC 49074
CA TGGATCACCTGAGGTCAGGAGTTC

|||||
ACCTAGTGGACTCCAGTCCTCAAG

GAM2469 C13orf1 3' AACTCCTGACCTCATGATCCA 40343 CC
TGGATCA TGAGGTCAGGAGTT

|||||
ACCTAGT ACTCCAGTCCTCAA

GAM2469 C1QTNF6 3' GAACTCCTGACTTCAGGTGACC 49992 A
CA TGG TCACCTGAGGTCAGGAGTTC

|||
ACC AGTGGACTTCAGTCCTCAAG

C

GAM2469 C20orf142 3' AACTCCTGACCGCAGGTGATCC 75266 A
A TGGATCACCTG GGTCAGGAGTT

|||||
ACCTAGTGGAC CCAGTCCTCAA

G

GAM2469 C21orf25 3' GAACTCCTGACCTCAGGTGATC 64293
CA TGGATCACCTGAGGTCAGGAGTTC

|||||
ACCTAGTGGACTCCAGTCCTCAAG

GAM2469 C3F 3' GAACTCCTGACCGCAAGTGATC 20476 C A
CA TGGATCAC TG GGTCAGGAGTTC

||||| || |||

			ACCTAGTG AC CCAGTCCTCAAG		
			A G		
GAM2469	C5orf4	5'	AACTCCTGCAGGCAATC 33421 CA AGGT		
			GAT CCTG CAGGAGTT		
			CTA GGAC GTCCTCAA		
			AC ____		
GAM2469	C6orf33	3'	GAAGTCCTGAACTCAAGTGATC 56715 C G		
	C		GGATCAC TGAG TCAGGAGTTC		
			CCTAGTG ACTC AGTCCTCAAG		
			A A		
GAM2469	C9orf14	5'	GAAGTCCTGACCTGAAGTGATG 87957 G CTG		
	CA		TG ATCAC AGGTCAGGAGTTC		
			AC TAGTG TCCAGTCCTCAAG		
			G AAG		
GAM2469	C9orf9	3'	GAAGTCCTGACCTCAACTGGTC 39019 CC		
	CA		TGGATCA TGAGGTCAGGAGTTC		
			ACCTGGT ACTCCAGTCCTCAAG		
			CA		
GAM2469	CARD6	3'	GAAGTCCCGACCTCAGGTGATC 51841 A		
	C		GGATCACCTGAGGTC GGAGTTC		
			CCTAGTGGACTCCAG CCTCAAG		
			C		
GAM2469	CDC14B	3'	GAAGTCCTGACCTCAAGTGATC 54004 C		
	T		GGATCAC TGAGGTCAGGAGTTC		
			TCTAGTG ACTCCAGTCCTCAAG		
			A		
GAM2469	CENPH	3'	GAAGTCCTGAGCTCAGGCAGTC 43565 CA G		
	CA		TGGAT CCTGAG TCAGGAGTTC		
			ACCTG GGA CTC AGTCCTCAAG		
			AC G		
GAM2469	CIP29	3'	GAAGTCCTGAGCTCAGGTGATC 51376 G		
	CA		TGGATCACCTGAG TCAGGAGTTC		
			ACCTAGTGGACTC AGTCCTCAAG		
			G		
GAM2469	COLEC12	3'	AACTTCTGGCCTCAAGTGATCC 48603 C		
	A		TGGATCAC TGAGGTCAGGAGTT		
			ACCTAGTG ACTCCGGTCTTCAA		
			A		
GAM2469	COLEC12	3'	GAAGTCCTGGCCTCAAGCAACC 48611 ATCACC		
	C		GG TGAGGTCAGGAGTTC		

			CC ACTCCGGTCCTCAAG	
			CAACGA	
GAM2469	CPSF2	3'	AACTCCCGACCTCAGGTGATCC 62252	A
			GGATCACCTGAGGTC GGAGTT	
			CCTAGTGGACTCCAG CCTCAA	
			C	
GAM2469	CPSF2	3'	AACTCCTGACCTCAAGCGATCC 62253	ACC
	A		TGGATC TGAGGTCAGGAGTT	
			ACCTAG ACTCCAGTCCTCAA	
			CGA	
GAM2469	DBR1	3'	AACTCCTGACCTCAGGCGATCC 33054	A
	A		TGGATC CCTGAGGTCAGGAGTT	
			ACCTAG GGAAGTCAGTCCTCAA	
			C	
GAM2469	DCOHM	3'	AACTCCTGGCCTCAAGTGATCC 50503	C
			GGATCAC TGAGGTCAGGAGTT	
			CCTAGTG ACTCCGGTCCTCAA	
			A	
GAM2469	DKFZp434A2417	3'	AACTCCCAACCTCAGGTGATCT 66671	CA
			GGATCACCTGAGGT GGAGTT	
			TCTAGTGGACTCCA CCTCAA	
			AC	
GAM2469	DKFZP434B044	3'	GAATCCTTACCTCAGGTGATC 49717	C
	CA		TGGATCACCTGAGGT AGGAGTTC	
			ACCTAGTGGACTCCA TCCTCAAG	
			T	
GAM2469	DKFZP434D146	3'	AACTCCTGCCCTCAAGTGATCC 32128	C T
	A		TGGATCAC TGAGG CAGGAGTT	
			ACCTAGTG ACTCC GTCCTCAA	
			A C	
GAM2469	DKFZP434J037	3'	AACTCCCGACCTCAGGTGATCC 48933	A
	A		TGGATCACCTGAGGTC GGAGTT	
			ACCTAGTGGACTCCAG CCTCAA	
			C	
GAM2469	DKFZp547H025	3'	AACTCTTGACTTCAAGTGATCC 39762	C
	A		TGGATCAC TGAGGTCAGGAGTT	
			ACCTAGTG ACTTCAGTTCTCAA	
			A	
GAM2469	DKFZP564G092	5'	GAATCCTGACCTCAAGTAATC 32159	C C
	T		GGAT AC TGAGGTCAGGAGTTC	

		TCTA TG ACTCCAGTCCTCAAG		
		A A		
GAM2469	DKFZP564K0322 3'	AACTTCTGGCCTCAAGTGATCC 50183	C	
		GGATCAC TGAGGTCAGGAGTT		
		CCTAGTG ACTCCGGTCTTCAA		
		A		
GAM2469	DKFZP564O0423 3'	AACTCCTGGCCTCAGGCGATCC 93335	A	
	A	TGGATC CCTGAGGTCAGGAGTT		
		ACCTAG GGA CTCCGGTCCTCAA		
		C		
GAM2469	DKFZP564O0523 3'	GAACCTCCTGACCTTGTGATACA 50420	G	CT
		TG ATCAC GAGGTCAGGAGTTC		
		AC TAGTG TTCCAGTCCTCAAG		
		A _		
GAM2469	DKFZP566I1024 3'	GAACCTCCTGGCCTCAAGCGATC 70649	ACC	
	C	GGATC TGAGGTCAGGAGTTC		
		CCTAG ACTCCGGTCCTCAAG		
		CGA		
GAM2469	DKFZp761O0113 5'	GAACCTCCCGGACTCGGGTGATC 37892		GT A
	CA	TGGATCACCTGAG C GGAGTTC		
		ACCTAGTGGGCTC G CCTCAAG		
		AG C		
GAM2469	DKFZp762P2111 3'	GAACCTCCTGATGTTAGGTGACC 87634	A	G
	C	GG TCACCTGA GTCAGGAGTTC		
		CC AGTGGATT TAGTCCTCAAG		
		C G		
GAM2469	DSCR6 3'	GAACCTCCTGACCTCAGGTGATC 39067		
	CA	TGGATCACCTGAGGTCAGGAGTTC		
		ACCTAGTGGACTCCAGTCCTCAAG		
GAM2469	EVI5 3'	AACTTCTGACCTCAGGTGATCC 20187		
	A	TGGATCACCTGAGGTCAGGAGTT		
		ACCTAGTGGACTCCAGTCTTCAA		
GAM2469	EVI5 3'	GAACCTCCTAACCTCAAGTGATC 20207	C	C
	CA	TGGATCAC TGAGGT AGGAGTTC		
		ACCTAGTG ACTCCA TCCTCAAG		
		A A		
GAM2469	FBP17 3'	AACTCCTGACCTCAGGTGATCC 73137		
		GGATCACCTGAGGTCAGGAGTT		

CCTAGTGGACTCCAGTCCTCAA

GAM2469 FER1L4 3' GAACCCCTGACCTCAAGTGATC 48121 C A
CA TGGATCAC TGAGGTCAGG GTTC

||||| ||||||| |||
ACCTAGTG ACTCCAGTCC CAAG
A C

GAM2469 FLB6421 3' GAACTCCTGAGCTCAAGTGATC 39644 C G
C GGATCAC TGAG TCAGGAGTTC

||||| ||| |||||||
CCTAGTG ACTC AGTCCTCAAG
A G

GAM2469 FLJ10232 3' GAACTCCTGACCTCAGGTGATC 36379
CA TGGATCACCTGAGGTCAGGAGTTC

||||| |||||||
ACCTAGTGGACTCCAGTCCTCAAG

GAM2469 FLJ10298 3' AACTCCTGACCTAGTGATCCA 36448 CTG
TGGATCAC AGGTCAGGAGTT

||||| |||||||
ACCTAGTG TCCAGTCCTCAA
A__

GAM2469 FLJ10607 3' AACTCCTGAGCTCAAGTGATCC 77618 C G
GGATCAC TGAG TCAGGAGTT

||||| ||| |||||||
CCTAGTG ACTC AGTCCTCAA
A G

GAM2469 FLJ10713 3' AACTCCTGGACTCAAGTGATC 36992 C GT
GATCAC TGAG CAGGAGTT

||||| ||| |||||||
CTAGTG ACTC GTCCTCAA
A AG

GAM2469 FLJ10901 3' GAACTCCTGACCTCAAGTGATC 37360 C
CA TGGATCAC TGAGGTCAGGAGTTC

||||| |||||||
ACCTAGTG ACTCCAGTCCTCAAG
A

GAM2469 FLJ11186 3' GAACTCCTGGCTACAAGTGATC 37725 C A
C GGATCAC TG GGTCAGGAGTTC

||||| || |||||||
CCTAGTG AC TCGGTCCTCAAG
A A

GAM2469 FLJ11193 3' AACTCCTGGGCACAAGCAATCC 37742 CAC GAG _
A TGGAT CT GTC AGGAGTT

|||| || ||| |||||||
ACCTA GA CGG TCCTCAA
AC_ ACA G

GAM2469 FLJ12363 3' AACTCCTGACCTCAGGTGATCT 50623
GGATCACCTGAGGTCAGGAGTT

||||| |||||||

TCTAGTGGACTCCAGTCCTCAA

GAM2469 FLJ12668 3' AACTCCTGACCTCAGGGGATCC 47151 A
A TGGATC CCTGAGGTCAGGAGTT

||||| ||||||||||||
ACCTAG GGACTCCAGTCCTCAA
G

GAM2469 FLJ12687 3' AACTCCTGACCTCAAGTGATCC 46737 C
A TGGATCAC TGAGGTCAGGAGTT

||||| ||||||||||||
ACCTAGTG ACTCCAGTCCTCAA
A

GAM2469 FLJ12747 3' GATTCCCGACCTCAGGTGATCC 50666 A
GGATCACCTGAGGTC GGAGTT

|||||||||| |||||
CCTAGTGGACTCCAG CCTTAG
C

GAM2469 FLJ12787 3' AACTCCTGACCTCAAGTGATCT 50685 C
A TGGATCAC TGAGGTCAGGAGTT

||||| ||||||||||||
ATCTAGTG ACTCCAGTCCTCAA
A

GAM2469 FLJ12903 3' GAACTCCTGACCTCAGGTGATC 43070
T GGATCACCTGAGGTCAGGAGTTC

|||||||||||||||||
TCTAGTGGACTCCAGTCCTCAAG

GAM2469 FLJ12975 3' GAACTCCTGACCTCATGATCC 70194 CC
GGATCA TGAGGTCAGGAGTTC

||||| ||||||||||||
CCTAGT ACTCCAGTCCTCAAG

GAM2469 FLJ13072 5' GAACTCCTGACCTCAGGTAATC 91390 C
C GGAT ACCTGAGGTCAGGAGTTC

||| |||||||||||||||
CCTA TGGACTCCAGTCCTCAAG
A

GAM2469 FLJ13102 3' GAACTCCTGACCTCAGGTGATT 46532
C GGATCACCTGAGGTCAGGAGTTC

|||||||||||||||||
CTTAGTGGACTCCAGTCCTCAAG

GAM2469 FLJ13197 3' GAACTCCTGACCTCAAGTGATC 45179 C
CA TGGATCAC TGAGGTCAGGAGTTC

||||| ||||||||||||
ACCTAGTG ACTCCAGTCCTCAAG
A

GAM2469 FLJ13305 5' GATTCCCTGACCTCAAGTGACCC 91712 A C
A TGG TCAC TGAGGTCAGGAGTT

||| ||| |||||||||||||

			ACC AGTG ACTCCAGTCCTTAG	
			C A	
GAM2469	FLJ13590	5'	GAATCCTGACCTCAAGTGATC 46206	C
		C	GGATCAC TGAGGTCAGGAGTTC	
			CCTAGTG ACTCCAGTCCTCAAG	
			A	
GAM2469	FLJ13952	3'	CCTGACGTCAGGTGATCCA 46011	G
			TGGATCACCTGA GTCAGG	
			ACCTAGTGGACT CAGTCC	
			G	
GAM2469	FLJ14351	3'	GAATCCTGAGCTCAAGCAATC 45648	CACC G
		C	GGAT TGAG TCAGGAGTTC	
			CCTA ACTC AGTCCTCAAG	
			ACGA G	
GAM2469	FLJ14950	3'	GAATCCTGACCGCAGGTAATC 52788	C A
		CA	TGGAT ACCTG GGTCAGGAGTTC	
			ACCTA TGGAC CCAGTCCTCAAG	
			A G	
GAM2469	FLJ14957	3'	GAATCCTGACCTCAGGTGATC 52818	
		CA	TGGATCACCTGAGGTCAGGAGTTC	
			ACCTAGTGGACTCCAGTCCTCAAG	
GAM2469	FLJ20034	3'	AACTCCCGACCTCAGGTGATCC 34827	A
			GGATCACCTGAGGTC GGAGTT	
			CCTAGTGGACTCCAG CCTCAA	
			C	
GAM2469	FLJ20045	3'	GAATCCTGACCTCGTGATCCA 34884	CT
			TGGATCAC GAGGTCAGGAGTTC	
			ACCTAGTG CTCCAGTCCTCAAG	
GAM2469	FLJ20344	3'	GAATCCTGACCTCAAGTGATC 35481	C
		C	GGATCAC TGAGGTCAGGAGTTC	
			CCTAGTG ACTCCAGTCCTCAAG	
			A	
GAM2469	FLJ20452	3'	GAATCCTGACCTCAGGTGATC 35648	
		CA	TGGATCACCTGAGGTCAGGAGTTC	
			ACCTAGTGGACTCCAGTCCTCAAG	
GAM2469	FLJ20507	3'	GAATCCTAACCTCAGGTTATC 35739	C C
		CA	TGGAT ACCTGAGGT AGGAGTTC	

			ACCTA TGGACTCCA TCCTCAAG		
			T A		
GAM2469	FLJ20507	3'	GAAGTCCTAACCTCAGGTTATC 60844	C	C
	CA		TGGAT ACCTGAGGT AGGAGTTC		
			ACCTA TGGACTCCA TCCTCAAG		
			T A		
GAM2469	FLJ20671	3'	GAAGTGCTGGCCTCAAGCGATC 35938	ACC	G
	CA		TGGATC TGAGGTCAG AGTTC		
			ACCTAG ACTCCGGTC TCAAG		
			CGA G		
GAM2469	FLJ20813	3'	AACTCCTGACCTCATGATCCA 36123	CC	
			TGGATCA TGAGGTCAGGAGTT		
			ACCTAGT ACTCCAGTCCTCAA		
			—		
GAM2469	FLJ21324	5'	AACTCCTGACCTCAAGTGATCT 92837	C	
			GGATCAC TGAGGTCAGGAGTT		
			TCTAGTG ACTCCAGTCCTCAA		
			A		
GAM2469	FLJ21459	3'	GAAGTCCTGACCTCAGGTGATC 44804		
	C		GGATCACCTGAGGTCAGGAGTTC		
			CCTAGTGGAAGTCCAGTCCTCAAG		
GAM2469	FLJ22002	3'	GAACCTCTGACCTCAGGTGATC 46197		GA
	CA		TGGATCACCTGAGGTCAG GTTC		
			ACCTAGTGGAAGTCCAGTC CAAG		
			TC		
GAM2469	FLJ22329	3'	GAAGTCCTGACCTCAAGTGATC 45400	C	
	T		GGATCAC TGAGGTCAGGAGTTC		
			TCTAGTG ACTCCAGTCCTCAAG		
			A		
GAM2469	FLJ22529	3'	GAAGTCCTGACCTCAAGTGATC 45943	C	
	T		GGATCAC TGAGGTCAGGAGTTC		
			TCTAGTG ACTCCAGTCCTCAAG		
			A		
GAM2469	FLJ22625	3'	AACTGCTGACTTCAGGTGATCC 45584		G
	A		TGGATCACCTGAGGTCAG AGTT		
			ACCTAGTGGAAGTTCAGTC TCAA		
			G		
GAM2469	FLJ22684	3'	AACTCCTGACCTCAGGTGATCC 47459		
			GGATCACCTGAGGTCAGGAGTT		

CCTAGTGGACTCCAGTCCTCAA

GAM2469 FLJ22794 3' GAACTCCTGACCTCGTGATCCA 93246 CT
TGGATCAC GAGGTCAGGAGTTC
||||| |||||
ACCTAGTG CTCCAGTCCTCAAG

GAM2469 FLJ23416 3' GAACTCCTGAGCTCAAGCAATC 50932 CACC G
C GGAT TGAG TCAGGAGTTC
||| ||| |||||
CCTA ACTC AGTCCTCAAG
ACGA G

GAM2469 FLJ23556 3' GAACTCCTGACCTCAGGTGA 46440
TCACCTGAGGTCAGGAGTTC
|||||
AGTGGACTCCAGTCCTCAAG

GAM2469 FLJ23563 3' CCTGACCTCAGGTGATCC 68214
GGATCACCTGAGGTCAGG
|||||
CCTAGTGGACTCCAGTCC

GAM2469 FLJ30532 3' AGCTCCTGACCTCAGATGATCT 59215 C
A TGGATCA CTGAGGTCAGGAGTT
||||| |||||
ATCTAGT GACTCCAGTCCTCGA
A

GAM2469 FLJ31101 3' GAACTCCTGACCTCATGATCCA 36161 CC
TGGATCA TGAGGTCAGGAGTTC
||||| |||||
ACCTAGT ACTCCAGTCCTCAAG

GAM2469 FLJ31153 3' GAACTCCTGACCTCAGGTGATC 58747
T GGATCACCTGAGGTCAGGAGTTC
|||||
TCTAGTGGACTCCAGTCCTCAAG

GAM2469 FLJ32865 3' AACCCTGACCTCAGGCAATCT 58792 CA A
GGAT CCTGAGGTCAGG GTT
||| ||||| |||
TCTA GGA CTCCAGTCC CAA
AC C

GAM2469 FLJ32894 3' GAACTCCTGACCTCGGGATCCA 58997 A T
TGGATC CC GAGGTCAGGAGTTC
||||| || |||||
ACCTAG GG CTCCAGTCCTCAAG

GAM2469 GAL3ST-4 3' GAACTCCTCACCTCAGGTGATC 45279 C
CA TGGATCACCTGAGGT AGGAGTTC
||||| |||||

			ACCTAGTGGACTCCA TCCTCAAG	
			C	
GAM2469	GGA2	3'	GAATCCTGACCTCAGGTGATC 57668	
	C		GGATCACCTGAGGTCAGGAGTTC	
			CCTAGTGGACTCCAGTCCTCAAG	
GAM2469	GGA2	3'	GAATCCTGACCTCAGGTGATC 31167	
	C		GGATCACCTGAGGTCAGGAGTTC	
			CCTAGTGGACTCCAGTCCTCAAG	
GAM2469	GMPPB	5'	GAATTCCTGACCTCAGGTGATC 97446	
	CA		TGGATCACCTGAGGTCAGGAGTTC	
			ACCTAGTGGACTCCAGTCCTTAAG	
GAM2469	GNG4	3'	AACTCCTGACCTCGTGATCCA 16833	CT
			TGGATCAC GAGGTCAGGAGTT	
			ACCTAGTG CTCCAGTCCTCAA	
GAM2469	H2AV	3'	AACTCCTGACCTCAGGCGATCC 57623	A
			GGATC CCTGAGGTCAGGAGTT	
			CCTAG GGA CTCCAGTCCTCAA	
			C	
GAM2469	HRH4	3'	AACTCCTGGGCTGAAACAATCC 41518	CACCTG G
			GGAT AG TCAGGAGTT	
			CCTA TC GGTCTCAA	
			ACAAAG G	
GAM2469	HRH4	3'	GAATCCTTGGCTCAAGCAATC 41538	CAC GA _
	C		GGAT CT GGTCA GGAGTTC	
			CCTA GA TCGGT CCTCAAG	
			AC_ AC T	
GAM2469	HSMPP8	3'	GAATCCTGACCTCAGGTGATC 95133	
	C		GGATCACCTGAGGTCAGGAGTTC	
			CCTAGTGGACTCCAGTCCTCAAG	
GAM2469	HSPC065	3'	GAATCCTGACCTCATGATCCA 27151	CC
			TGGATCA TGAGGTCAGGAGTTC	
			ACCTAGT ACTCCAGTCCTCAAG	
GAM2469	JAM1	3'	AACTCCTGACCTCTTGATCC 34205	CCT
			GGATCA GAGGTCAGGAGTT	

			CCTAGT CTCCAGTCCTCAA			
			T__			
GAM2469	JAM1	3'	AACTCCTGACCTCTTGATCC 58501	CCT		
			GGATCA GAGGTCAGGAGTT			
			CCTAGT CTCCAGTCCTCAA			
			T__			
GAM2469	JAM1	3'	AACTCCTGACCTCTTGATCC 58529	CCT		
			GGATCA GAGGTCAGGAGTT			
			CCTAGT CTCCAGTCCTCAA			
			T__			
GAM2469	JAM1	3'	AACTCCTGACCTCTTGATCC 58556	CCT		
			GGATCA GAGGTCAGGAGTT			
			CCTAGT CTCCAGTCCTCAA			
			T__			
GAM2469	KIAA0022	3'	AACTCCTGACCTCAAGTGATCC 30273	C		
	A		TGGATCAC TGAGGTCAGGAGTT			
			ACCTAGTG ACTCCAGTCCTCAA			
			A			
GAM2469	KIAA0063	3'	AACTCCCGACCTCAAGTGATCT 30245	C	A	
			GGATCAC TGAGGTC GGAGTT			
			TCTAGTG ACTCCAG CCTCAA			
			A C			
GAM2469	KIAA0161	3'	AACTCCTGACCTCAGGTGATCT 29183			
			GGATCACCTGAGGTCAGGAGTT			
			TCTAGTGGACTCCAGTCCTCAA			
GAM2469	KIAA0186	3'	AACTCCTGACCTCAAGTGACCC 41089	A	C	
	A		TGG TCAC TGAGGTCAGGAGTT			
			ACC AGTG ACTCCAGTCCTCAA			
			C A			
GAM2469	KIAA0186	3'	CCTGACCTCAAGTGACCCA 41104	A	C	
			TGG TCAC TGAGGTCAGG			
			ACC AGTG ACTCCAGTCC			
			C A			
GAM2469	KIAA0205	3'	GAACCTCCTGACCTCAGGTGATC 30213			
	T		GGATCACCTGAGGTCAGGAGTTC			
			TCTAGTGGACTCCAGTCCTCAAG			
GAM2469	KIAA0210	5'	GAACCTGCTGACCTCAAGTAATC 29158	C	C	G
	C		GGAT AC TGAGGTCAG AGTTC			

			CCTA TG ACTCCAGTC TCAAG	
			A A G	
GAM2469	KIAA0391	3'	AACTCCTGACCTCAGGTGATCC 28594	
	A		TGGATCACCTGAGGTCAGGAGTT	
			ACCTAGTGGACTCCAGTCCTCAA	
GAM2469	KIAA0447	3'	GAACCTCTCGGCTCAAGCAATC 72122	CAC GA _
	C		GGAT CT GGTC AGGAGTTC	
			CCTA GA TCGG TCCTCAAG	
			AC_ AC C	
GAM2469	KIAA0472	5'	GAACCTCTGACCTCAAACGATC 72351	ACC
	T		GGATC TGAGGTCAGGAGTTC	
			TCTAG ACTCCAGTCCTCAAG	
			CAA	
GAM2469	KIAA0475	3'	GACTCCTGACCCAGGTGATCC 30117	A
	A		TGGATCACCTG GGTCAGGAGTT	
			ACCTAGTGGAC CCAGTCCTCAG	
			C	
GAM2469	KIAA0513	5'	GAACCTCTGACCTCAGGTGAGC 29029	A
	CA		TGG TCACCTGAGGTCAGGAGTTC	
			ACC AGTGGACTCCAGTCCTCAAG	
			G	
GAM2469	KIAA0513	3'	GAACCTCTGACCTCAGGTGATC 29030	
	C		GGATCACCTGAGGTCAGGAGTTC	
			CCTAGTGGACTCCAGTCCTCAAG	
GAM2469	KIAA0527	3'	GAACCTCTGACCTCAAGTGATC 97497	C
	T		GGATCAC TGAGGTCAGGAGTTC	
			TCTAGTG ACTCCAGTCCTCAAG	
			A	
GAM2469	KIAA0555	3'	GAACCTCTGACCTCAAGTGATC 29549	C
	T		GGATCAC TGAGGTCAGGAGTTC	
			TCTAGTG ACTCCAGTCCTCAAG	
			A	
GAM2469	KIAA0557	3'	GAACCTCCGACCTTGTGATCCA 78561	CT A
			TGGATCAC GAGGTC GGAGTTC	
			ACCTAGTG TTCCAG CCTCAAG	
			_ C	
GAM2469	KIAA0562	3'	AACTCCTGACCTTGTGATCCA 28810	CT
			TGGATCAC GAGGTCAGGAGTT	

ACCTAGTG TTCCAGTCCTCAA

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GAM2469 KIAA0594 3' GAACTCCTGACCTTGTGATCCA 65512 CT
TGGATCAC GAGGTCAGGAGTTC
||||| |||||||||
ACCTAGTG TTCCAGTCCTCAAG

—
GAM2469 KIAA0599 3' GAACTTCTGACCTCAGGTGATC 77692
CA TGGATCACCTGAGGTCAGGAGTTC
|||||||||||||||
ACCTAGTGGACTCCAGTCTTCAAG

GAM2469 KIAA0682 3' GAACTCCCAACCTCAAGTGATC 30021 C CA
CA TGGATCAC TGAGGT GGAGTTC
||||| ||||| |||||
ACCTAGTG ACTCCA CCTCAAG
A AC

GAM2469 KIAA0682 3' GAATTCCTGACCTCAAGTGATC 30022 C
CA TGGATCAC TGAGGTCAGGAGTTC
||||| |||||||||
ACCTAGTG ACTCCAGTCCTTAAG
A

GAM2469 KIAA0720 3' GAACTCCTGACCCCAAGTGTTT 62984 T C A
C GGA CAC TG GGTCAGGAGTTC
||| ||| |||||||||
CCT GTG AC CCAGTCCTCAAG
T A C

GAM2469 KIAA0737 3' GAACTCCTGACCTCATGATCC 29808 CC
GGATCA TGAGGTCAGGAGTTC
||||| |||||||||
CCTAGT ACTCCAGTCCTCAAG

—
GAM2469 KIAA0828 3' AACTCCTGGGCTCAAGCAATCC 82106 CACC G
GGAT TGAG TCAGGAGTT
||| ||| |||||||||
CCTA ACTC GGTCCTCAA
ACGA G

GAM2469 KIAA0841 3' GAACTCCTGACCTCAAGTGATC 71895 C
T GGATCAC TGAGGTCAGGAGTTC
||||| |||||||||
TCTAGTG ACTCCAGTCCTCAAG
A

GAM2469 KIAA0889 3' GAACTCCCGACCTCAAGTGATC 31776 C A
C GGATCAC TGAGGTC GGAGTTC
||||| ||||| |||||
CCTAGTG ACTCCAG CCTCAAG
A C

GAM2469 KIAA0924 3' AACTCCTGACCTTGTGATCC 30345 CT
GGATCAC GAGGTCAGGAGTT
||||| |||||||||

CCTAGTG TTCCAGTCCTCAA

—
GAM2469 KIAA0931 3' GAACTCTTGACCTCAGGTGATC 68011
CA TGGATCACCTGAGGTCAGGAGTTC
|||||
ACCTAGTGGACTCCAGTTCTCAAG

GAM2469 KIAA0961 3' AACTCCTGACCTCAGGTGATCC 30381
A TGGATCACCTGAGGTCAGGAGTT
|||||
ACCTAGTGGACTCCAGTCCTCAA

GAM2469 KIAA1040 3' GAACTCCTGACCTCAGGTGATC 72686
T GGATCACCTGAGGTCAGGAGTTC
|||||
TCTAGTGGACTCCAGTCCTCAAG

GAM2469 KIAA1054 3' GAACTCCTGACCTCAAGTGATC 68964 C
GATCAC TGAGGTCAGGAGTTC
|||||
CTAGTG ACTCCAGTCCTCAAG
A

GAM2469 KIAA1128 3' GAACTCCTGACCTCAAGTGATC 69005 C
CA TGGATCAC TGAGGTCAGGAGTTC
|||||
ACCTAGTG ACTCCAGTCCTCAAG
A

GAM2469 KIAA1161 5' AACTCCTGACCTAGTGATGCA 82634 G CTG
TG ATCAC AGGTCAGGAGTT
|| |||||
AC TAGTG TCCAGTCCTCAA
G A__

GAM2469 KIAA1170 3' AACTCCTGACCTCAGGTGATCC 70402
GGATCACCTGAGGTCAGGAGTT
|||||
CCTAGTGGACTCCAGTCCTCAA

GAM2469 KIAA1198 3' AACTCCTGACCTCAGGTGATCT 63970
GGATCACCTGAGGTCAGGAGTT
|||||
TCTAGTGGACTCCAGTCCTCAA

GAM2469 KIAA1198 3' AACTCTTGACCTCAAATGATCC 63971 CC
A TGGATCA TGAGGTCAGGAGTT
|||||
ACCTAGT ACTCCAGTTCTCAA
AA

GAM2469 KIAA1198 3' GAACTCCTGACCTCAGGTAATC 64035 C
CA TGGAT ACCTGAGGTCAGGAGTTC
|||||

ACCTA TGGACTCCAGTCCTCAAG
 A
 GAM2469 KIAA1200 3' GAACTCCTGACCTCAGGTGATC 63037
 T GGATCACCTGAGGTCAGGAGTTC
 |||||
 TCTAGTGGACTCCAGTCCTCAAG

 GAM2469 KIAA1243 3' CTTGACCTCAAGTAACCA 74025 ATC C
 TGG AC TGAGGTCAGG
 ||| || |||||
 ACC TG ACTCCAGTTC
 AA_ A
 GAM2469 KIAA1254 3' TCCTGACCTCAAGTGATCCA 70567 C
 TGGATCAC TGAGGTCAGGA
 ||||| |||||
 ACCTAGTG ACTCCAGTCCT
 A
 GAM2469 KIAA1257 3' AACTCCCGACTTCAGGTGATCC 63382 A
 GGATCACCTGAGGTC GGAGTT
 ||||| |||||
 CCTAGTGGACTTCAG CCTCAA
 C
 GAM2469 KIAA1257 3' AACTCCTGGTCACAAGTAATCC 63383 C C A GT
 GGAT AC TG G CAGGAGTT
 ||| || || |||||
 CCTA TG AC C GTCCTCAA
 A A A TG
 GAM2469 KIAA1320 5' GAATTCCTGACCTCAAGTGATC 69840 C
 TA TGGATCAC TGAGGTCAGGAGTTC
 ||||| |||||
 ATCTAGTG ACTCCAGTCCTTAAG
 A
 GAM2469 KIAA1396 3' AACTCCTGTGCTCAAGTGACCC 63666 A C GT
 GG TCAC TGAG CAGGAGTT
 || ||| ||| |||||
 CC AGTG ACTC GTCCTCAA
 C A GT
 GAM2469 KIAA1465 3' GATCTCTTGACCTCAGGTGATC 61498 T
 CA TGGATCACCTGAGGTCAGGAG TC
 ||||| ||||| ||
 ACCTAGTGGACTCCAGTTCTC AG
 T
 GAM2469 KIAA1467 3' GAACTCCTGACCTCAGATAATC 72067 CAC
 CA TGGAT CTGAGGTCAGGAGTTC
 |||| |||||
 ACCTA GACTCCAGTCCTCAAG
 ATA
 GAM2469 KIAA1493 3' AACTCCTGACCTCAGGTGATCC 64827
 A TGGATCACCTGAGGTCAGGAGTT
 |||||

ACCTAGTGGACTCCAGTCCTCAA

GAM2469 KIAA1508 3' GAACTCCTGACCTCAGGTAATC 62550 C
CA TGGAT ACCTGAGGTCAGGAGTTC
||||| |||||||||
ACCTA TGGACTCCAGTCCTCAAG
A

GAM2469 KIAA1530 3' GAACTCCTAGCCTCAAGCGATC 68560 ACC TC
C GGATC TGAGG AGGAGTTC
||||| ||||| |||||
CCTAG ACTCC TCCTCAAG
CGA GA

GAM2469 KIAA1571 3' AACTCCTGACCTTGTGGTCCA 61609 CT
TGGATCAC GAGGTCAGGAGTT
||||||| |||||||||
ACCTGGTG TTCCAGTCCTCAA

GAM2469 KIAA1615 3' AACTCCCCGACCTCAGGTGATCC 69261 A
A TGGATCACCTGAGGTC GGAGTT
||||||| ||||| |||||
ACCTAGTGGACTCCAG CCTCAA
C

GAM2469 KIAA1617 3' GAACTCCCAACCTCAAGTGATC 93077 C CA
T GGATCAC TGAGGT GGAGTTC
||||||| ||||| |||||
TCTAGTG ACTCCA CCTCAAG
A AC

GAM2469 KIAA1649 3' GAACTCCTGGGCACAAGTGATC 51236 C AG _
C GGATCAC TG GTC AGGAGTTC
||||||| || ||| |||||
CCTAGTG AC CGG TCCTCAAG
A A_ G

GAM2469 KIAA1655 3' AACTCCTGACCTCCAGTGATCC 67167 CT
A TGGATCAC GAGGTCAGGAGTT
||||||| |||||||||
ACCTAGTG CTCCAGTCCTCAA
AC

GAM2469 KIAA1712 3' AACTCCTGACCTCAGGTGATCT 68142
GGATCACCTGAGGTCAGGAGTT
||||||| |||||||||
TCTAGTGGACTCCAGTCCTCAA

GAM2469 KIAA1737 3' GAACTCCTGACCTCAGTTGATC 67941 C
C GGATCA CTGAGGTCAGGAGTTC
||||| |||||||||
CCTAGT GACTCCAGTCCTCAAG
T

GAM2469 KIAA1755 3' AACTCCTGGGCTCAAGTGATCC 62002 C G
GGATCAC TGAG TCAGGAGTT
||||||| ||||| |||||

			CCTAGTG ACTC GGCCTCAA		
			A G		
GAM2469	KIAA1829	3'	GAACCTCCTGACTTTAGGTGATC 62643		
	CA		TGGATCACCTGAGGTCAGGAGTTC		
			ACCTAGTGGATTTCAGTCCTCAAG		
GAM2469	KIAA1922	5'	GAACCTCCTGACCTCAGGTGATC 73993		
	C		GGATCACCTGAGGTCAGGAGTTC		
			CCTAGTGGACTCCAGTCCTCAAG		
GAM2469	KIAA1962	3'	GAACCTCCTGGGCTCAAGTGATC 82801	C	G
	C		GGATCAC TGAG TCAGGAGTTC		
			CCTAGTG ACTC GGCCTCAA		
			A G		
GAM2469	KIAA1971	3'	GAACCTCCTGACCTCGTGATCCA 74679	CT	
			TGGATCAC GAGGTCAGGAGTTC		
			ACCTAGTG CTCCAGTCCTCAAG		
GAM2469	KIAA1987	5'	GAACCTTCTGACCTCAGGTGATC 89383		
	CA		TGGATCACCTGAGGTCAGGAGTTC		
			ACCTAGTGGACTCCAGTCTTCAAG		
GAM2469	KLK7	3'	GAACGCCTGACCTCAGATGATC 58389	C	A
	CA		TGGATCA CTGAGGTCAGG GTTC		
			ACCTAGT GACTCCAGTCC CAAG		
			A G		
GAM2469	KLK7	3'	GAACGCCTGACCTCAGATGATC 18543	C	A
	CA		TGGATCA CTGAGGTCAGG GTTC		
			ACCTAGT GACTCCAGTCC CAAG		
			A G		
GAM2469	LAMP3	3'	GAACCTTTGACCTCAGGTGATC 60203		
	CA		TGGATCACCTGAGGTCAGGAGTTC		
			ACCTAGTGGACTCCAGTTCTCAAG		
GAM2469	LIECG3	3'	GAACCTCCTGGGCTCAAGCGGTC 88798	ACC	G
	CA		TGGATC TGAG TCAGGAGTTC		
			ACCTGG ACTC GGCCTCAA		
			CGA G		
GAM2469	LNIR	3'	GAACCTCCTGGGCTCAAGCAATC 48871	CACC	G
	C		GGAT TGAG TCAGGAGTTC		

			CCTA	ACTC	GGTCCTCAAG		
			ACGA	G			
GAM2469	MAP-1	3'	GA	ACTCCTGACCTCAAGTGATC	42440	C	
	CA			TGGATCAC TGAGGTCAGGAGTTC			
			AC	CTAGTG ACTCCAGTCCTCAAG			
			A				
GAM2469	MCLC	3'	GA	ACTCCTGACCTCAAGTGACC	31381	A C	
	C			GG TCAC TGAGGTCAGGAGTTC			
			CC	AGTG ACTCCAGTCCTCAAG			
			C A				
GAM2469	MCM10	3'	AA	CTCCTGAGCACTAGCAATCC	38171	CAC AG _	
	A			TGGAT CTG G TCAGGAGTT			
			AC	CTA GAT C AGTCCTCAA			
			AC_	CA G			
GAM2469	MEF-2	3'	AA	CTCCTGACCTCGTGATCCA	65012	CT	
				TGGATCAC GAGGTCAGGAGTT			
			AC	CTAGTG CTCCAGTCCTCAA			
GAM2469	MGC10200	3'	GAG	CTCCTGAGCTCAAACAATC	59645	CACC G	
	CA			TGGAT TGAG TCAGGAGTTC			
			AC	CTA ACTC AGTCCTCGAG			
			ACAA	G			
GAM2469	MGC11386	3'	AA	CTCCTGGGCTCAAGCAATCC	53049	CACC G	
				GGAT TGAG TCAGGAGTT			
			CCTA	ACTC GGTCCTCAA			
			ACGA	G			
GAM2469	MGC13159	3'	GA	ACTCCTGGGATCAAGTGATC	53037	C GG	
	C			GGATCAC TGA TCAGGAGTTC			
			CCT	AGTG ACT GGTCTCAAG			
			A	AG			
GAM2469	MGC1842	3'	GA	ACCCCTGAGCTCAGGTGATC	66255	G A	
	CA			TGGATCACCTGAG TCAGG GTTC			
			AC	CTAGTG GACTC AGTCC CAAG			
			G	C			
GAM2469	MGC20235	3'	GA	ACTCCTGGGCTCAAGCGATC	59553	ACC G	
	C			GGATC TGAG TCAGGAGTTC			
			CCTAG	ACTC GGTCCTCAAG			
			CGA	G			
GAM2469	MGC21675	3'	GA	ACTCCTGACCTCAGGTGATC	54591		
	CA			TGGATCACCTGAGGTCAGGAGTTC			

ACCTAGTGGACTCCAGTCCTCAAG

GAM2469 MGC21738 3' GAACTCCTGACCTCAAGTGATC 59576 C
C GGATCAC TGAGGTCAGGAGTTC

||||| |||||||||
CCTAGTG ACTCCAGTCCTCAAG
A

GAM2469 MGC2474 3' GAACTCCTGCCCTCAGGTGATC 43957 T
CA TGGATCACCTGAGG CAGGAGTTC

||||||| |||||
ACCTAGTGGACTCC GTCCTCAAG
C

GAM2469 MKRN4 3' GAACTCCTGACCTCAGGTGATC 48462
CA TGGATCACCTGAGGTCAGGAGTTC

||||||| |||||||||
ACCTAGTGGACTCCAGTCCTCAAG

GAM2469 MLZE 5' GAACTCCTGACCTCGGGATCCA 49451 A T
TGGATC CC GAGGTCAGGAGTTC

||||| || |||||||||
ACCTAG GG CTCCAGTCCTCAAG

GAM2469 MMPL1 3' GAACTCTTGGGCTCAAGCGATC 15964 ACC G
C GGATC TGAG TCAGGAGTTC

|||| | || |||||||
CCTAG ACTC GGTTCTCAAG
CGA G

GAM2469 moblak 3' AACTCCTGACTTCAGGTGATCC 56377
GGATCACCTGAGGTCAGGAGTT

||||||| |||||||||
CCTAGTGGACTTCAGTCCTCAA

GAM2469 MRPL44 3' GAACTCCTGACCTCAGGTGATC 43597
CA TGGATCACCTGAGGTCAGGAGTTC

||||||| |||||||||
ACCTAGTGGACTCCAGTCCTCAAG

GAM2469 NFAT5 3' GAACTCCTAACCTCCAGTGATC 57788 CT C
CA TGGATCAC GAGGT AGGAGTTC

||||| || |||||||
ACCTAGTG CTCCA TCCTCAAG
AC A

GAM2469 NINJ2 3' GAACTCCTGACCTCAGGTGATC 33724
T GGATCACCTGAGGTCAGGAGTTC

||||||| |||||||||
TCTAGTGGACTCCAGTCCTCAAG

GAM2469 Nup43 3' GAACTCCTGACCACAGGTAATC 45346 C A
GAT ACCTG GGTCAGGAGTTC

||| || |||||||||

			CTA TGGAC CCAGTCCTCAAG		
			A A		
GAM2469	NXN	3'	GAACCTCTGACCTCAGGTGATC 42674		
	CA		TGGATCACCTGAGGTCAGGAGTTC		
			ACCTAGTGGACTCCAGTCCTCAAG		
GAM2469	OCT11	3'	GAACCTCTGACCTCCTGATCCA 27589	CCT	
			TGGATCA GAGGTCAGGAGTTC		
			ACCTAGT CTCCAGTCCTCAAG		
			C__		
GAM2469	PELI1	5'	AACTCCCAACCTCAAGTGATCC 40614	C	CA
			GGATCAC TGAGGT GGAGTT		
			CCTAGTG ACTCCA CCTCAA		
			A AC		
GAM2469	PELI1	5'	GAACCTCTGACCTCAAGTGATC 40639	C	
	T		GGATCAC TGAGGTCAGGAGTTC		
			TCTAGTG ACTCCAGTCCTCAAG		
			A		
GAM2469	PIG7	3'	GAACCTCTGGGCTCAAGCGATC 17969	ACC	G
	C		GGATC TGAG TCAGGAGTTC		
			CCTAG ACTC GGTCCTCAAG		
			CGA G		
GAM2469	PIP3-E	3'	AACTCCTGACCTCAGGTGATCT 67339		
			GGATCACCTGAGGTCAGGAGTT		
			TCTAGTGGACTCCAGTCCTCAA		
GAM2469	POLR2D	3'	AACTCCTGGGCTCAAGTGATCC 17837	C	G
			GGATCAC TGAG TCAGGAGTT		
			CCTAGTG ACTC GGTCCTCAA		
			A G		
GAM2469	PRO0899	5'	GAACCTCTGGGCCCAAGCAATC 38310	CAC	GA _
	C		GGAT CT GGTC AGGAGTTC		
			CCTA GA CCGG TCCTCAAG		
			AC_ AC G		
GAM2469	PRO1992	3'	GAACCTAACCTCAGGTGATCC 26904		CAG
			GGATCACCTGAGGT GAGTTC		
			CCTAGTGGACTCCA CTCAAG		
			A__		
GAM2469	PRO2955	3'	AACTCCTGACCTCAGGTGATCC 38228		
	A		TGGATCACCTGAGGTCAGGAGTT		

ACCTAGTGGACTCCAGTCCTCAA

GAM2469 PSTPIP2 3' AACTCCTGACCTCAGGTGATCC 44644
A TGGATCACCTGAGGTCAGGAGTT
|||||
ACCTAGTGGACTCCAGTCCTCAA

GAM2469 RASSF2 3' GAACTCCTGACCTCGTGATCCA 29098 CT
TGGATCAC GAGGTCAGGAGTTC
||||| |||||
ACCTAGTG CTCCAGTCCTCAAG

GAM2469 RES4-25 3' GAATTCCCGACCTCAGGTAATC 65266 C A
CA TGGAT ACCTGAGGTC GGAGTTC
|||| ||||| |||||
ACCTA TGGACTCCAG CCTTAAG
A C

GAM2469 RNF8 3' AATTCCTGACCTTAAGTGATCC 15552 C
A TGGATCAC TGAGGTCAGGAGTT
||||| |||||
ACCTAGTG ATTCCAGTCCTTAA
A

GAM2469 Rpo1-2 3' GACCCTGACCTCAAGTGATCCA 50867 C A
TGGATCAC TGAGGTCAGG GTT
||||| ||||| |||
ACCTAGTG ACTCCAGTCC CAG
A

GAM2469 Rpo1-2 3' GACCCTGACCTCAAGTGATCCA 39221 C A
TGGATCAC TGAGGTCAGG GTT
||||| ||||| |||
ACCTAGTG ACTCCAGTCC CAG
A

GAM2469 SARM 3' GAACTCCTGGGCTCAAGTGATC 31290 C G
C GGATCAC TGAG TCAGGAGTTC
||||| ||| |||||
CCTAGTG ACTC GGTCCTCAAG
A G

GAM2469 SCAMP-4 3' GAACTCCTGACCTCAAGTGATC 55347 C
CA TGGATCAC TGAGGTCAGGAGTTC
||||| |||||
ACCTAGTG ACTCCAGTCCTCAAG
A

GAM2469 SCYA22 3' AACTCCTGGGCTCAAGCGATCC 92565 ACC G
GGATC TGAG TCAGGAGTT
|||| ||| |||||
CCTAG ACTC GGTCCTCAA
CGA G

GAM2469 SCYA22 3' GAACTCCTGACCTCAAGTGATC 92593 C
CA TGGATCAC TGAGGTCAGGAGTTC
||||| |||||

			ACCTAGTG ACTCCAGTCCTCAAG		
			A		
GAM2469	SCYA22	3'	GAAGTCCTGTCCTCAGGTAATC 92594	C	T
	C		GGAT ACCTGAGG CAGGAGTTC		
			CCTA TGGACTCC GTCCTCAAG		
			A T		
GAM2469	SCYA28	3'	GAAGTTCTGATCTCAAGTGATC 39542	C	
	CA		TGGATCAC TGAGGTCAGGAGTTC		
			ACCTAGTG ACTCTAGTCTTCAAG		
			A		
GAM2469	SFXN2	3'	GAAGTCCTGACCTCAGGTGATC 74375		
	C		GGATCACCTGAGGTCAGGAGTTC		
			CCTAGTGGACTCCAGTCCTCAAG		
GAM2469	SIRPB1	3'	GAAGTCCCGACCTCAGGTGATC 21366		A
	CA		TGGATCACCTGAGGTC GGAGTTC		
			ACCTAGTGGACTCCAG CCTCAAG		
			C		
GAM2469	SLC12A8	3'	GAAGTCCTGACCTCGTGATCCA 45236		CT
			TGGATCAC GAGGTCAGGAGTTC		
			ACCTAGTG CTCCAGTCCTCAAG		
GAM2469	SLC2A10	3'	GAAGTCCTGAGCTCAAGTGATC 48551	C	G
	CA		TGGATCAC TGAG TCAGGAGTTC		
			ACCTAGTG ACTC AGTCCTCAAG		
			A G		
GAM2469	SLC6A14	3'	GAAGTCCCGACCTCAAGTGATC 24308	C	A
	T		GGATCAC TGAGGTC GGAGTTC		
			TCTAGTG ACTCCAG CCTCAAG		
			A C		
GAM2469	STAF65(gamma)	3'	AACTCCTGACCTCAAGTGATCT 30056		C
			GGATCAC TGAGGTCAGGAGTT		
			TCTAGTG ACTCCAGTCCTCAA		
			A		
GAM2469	STRBP	5'	GAAGTCCTGAACGCAAGTGATC 37818	C	AGG
	C		GGATCAC TG TCAGGAGTTC		
			CCTAGTG AC AGTCCTCAAG		
			A GCA		
GAM2469	TBCC	3'	GAAGTCCTGACCTCAGGTGATC 13603		
	CA		TGGATCACCTGAGGTCAGGAGTTC		

ACCTAGTGGACTCCAGTCCTCAAG

GAM2469	TCL6	5'	GA	ACTCCTGACCAAGTGATCCA	25905	CTGA
				TGGATCAC GGT	CAGGAGTTC	
				ACCTAGTG	CCAGTCCTCAAG	
				AA		
GAM2469	TCL6	5'	GA	ACTCCTGACCAAGTGATCCA	27757	CTGA
				TGGATCAC GGT	CAGGAGTTC	
				ACCTAGTG	CCAGTCCTCAAG	
				AA		
GAM2469	TCL6	5'	GA	ACTCCTGACCAAGTGATCCA	40473	CTGA
				TGGATCAC GGT	CAGGAGTTC	
				ACCTAGTG	CCAGTCCTCAAG	
				AA		
GAM2469	TCL6	3'	AA	CTCCTGAGCTCAAGCGATCC	40500	ACC G
				GGATC TGAG	TCAGGAGTT	
				CCTAG	ACTC AGTCCTCAA	
				CGA	G	
GAM2469	TCL6	5'	GA	ACTCCTGACCAAGTGATCCA	40509	CTGA
				TGGATCAC GGT	CAGGAGTTC	
				ACCTAGTG	CCAGTCCTCAAG	
				AA		
GAM2469	TCL6	3'	AA	CTCCTGAGCTCAAGCGATCC	40524	ACC G
				GGATC TGAG	TCAGGAGTT	
				CCTAG	ACTC AGTCCTCAA	
				CGA	G	
GAM2469	TGIF2	3'	GA	ACTCCTGACCTCGTGAGCCA	41750	A CT
				TGG TCAC	GAGGTCAGGAGTTC	
				ACC AGTG	CTCCAGTCCTCAAG	
				G		
GAM2469	TRIM16	3'	AA	CTCCTGACCTCGTGATGCA	22359	G CT
				TG ATCAC	GAGGTCAGGAGTT	
				AC TAGTG	CTCCAGTCCTCAA	
				G		
GAM2469	TRIM5 CA	3'	GA	ACCTCTGACCTCAGGTGATC	53469	GA
				TGGATCACCTGAGGTCAG	GTTC	
				ACCTAGTGGACTCCAGTC	CAAG	
				TC		
GAM2469	TRIM5 CA	3'	GA	ACCTCTGACCTCAGGTGATC	53539	GA
				TGGATCACCTGAGGTCAG	GTTC	

			ACCTAGTGGACTCCAGTC CAAG	
			TC	
GAM2469	TRIM6	3'	GAAGTCCTGACCGCAAGTGATC 55179	C A
	CA		TGGATCAC TG GGTCAGGAGTTC	
			ACCTAGTG AC CCAGTCCTCAAG	
			A G	
GAM2469	TU12B1-TY	3'	GAAGTCCTGACCTCAGATAATC 33847	CAC
	T		GGAT CTGAGGTCAGGAGTTC	
			TCTA GACTCCAGTCCTCAAG	
			ATA	
GAM2469	TU12B1-TY	3'	GAAGTCCTGACCTTGGGTAATC 33848	C TG
	CA		TGGAT ACC AGGTCAGGAGTTC	
			ACCTA TGG TCCAGTCCTCAAG	
			A GT	
GAM2469	TUCAN	3'	GAAGTCCTGGCCTCAAGTGATC 30976	C
	CA		TGGATCAC TGAGGTCAGGAGTTC	
			ACCTAGTG ACTCCGGTCCTCAAG	
			A	
GAM2469	TUSP	3'	GAAGTCCTGACCTCAGGTGATC 40025	
	C		GGATCACCTGAGGTCAGGAGTTC	
			CCTAGTGGACTCCAGTCCTCAAG	
GAM2469	UBF-fl	3'	AACTCCTGACCTCAAGTGATCC 52613	C
	A		TGGATCAC TGAGGTCAGGAGTT	
			ACCTAGTG ACTCCAGTCCTCAA	
			A	
GAM2469	VDU1	3'	AACTCCTGACCTCAGGTGATCC 31111	
	A		TGGATCACCTGAGGTCAGGAGTT	
			ACCTAGTGGACTCCAGTCCTCAA	
GAM2469	VMP	3'	GAAGTCCTGGGCTCAAGCGATC 55762	ACC G
	C		GGATC TGAG TCAGGAGTTC	
			CCTAG ACTC GGTCCTCAAG	
			CGA G	
GAM2469	VPS33A	3'	AACTCCTGACCTCAGGTGATCC 43604	
	A		TGGATCACCTGAGGTCAGGAGTT	
			ACCTAGTGGACTCCAGTCCTCAA	
GAM2469	WBSCR23	3'	AACTCCTGACCTCAGGTGATCC 47405	
	A		TGGATCACCTGAGGTCAGGAGTT	

ACCTAGTGGACTCCAGTCCTCAA

GAM2469	WIT-1	3'	GA	ACTCCTGACCCCAGATTCA	32398	ACC	A
				TGGATC TG GGT	CAGGAGTTC		
				ACTTAG	AC CCAGTCCTCAAG		
				___	C		
GAM2469	ZNF177	5'	AA	CTCCTGCTCTCAAGTGATCC	14355	C	GT
				GGATCAC TGAG	CAGGAGTT		
				CCTAGTG ACTC	GTCCTCAA		
				A	TC		
GAM2469	ZNF338	3'	GA	ACTCCTGACCTCAAGTGATC	42255	C	
	T			GGATCAC TGAGGTCAGGAGTTC			
				TCTAGTG ACTCCAGTCCTCAAG			
				A			
GAM2469	ZTL1	3'	GA	ACTCCTGACCTCAGGTGATC	44141		
	T			GGATCACCTGAGGTCAGGAGTTC			
				TCTAGTGGACTCCAGTCCTCAAG			
GAM2469	LOC112687	3'	AA	CTCCTGACCTCATGTAATCC	73214	C	C
	A			TGGAT AC TGAGGTCAGGAGTT			
				ACCTA TG ACTCCAGTCCTCAA			
				A	T		
GAM2469	LOC112817	3'	GA	ACTCCTGACCTCAGGTGATC	57325		
	CA			TGGATCACCTGAGGTCAGGAGTTC			
				ACCTAGTGGACTCCAGTCCTCAAG			
GAM2469	LOC113026	3'	CCT	GACCTCAAGTGATCC	56727	C	
				GGATCAC TGAGGTCAGG			
				CCTAGTG ACTCCAGTCC			
				A			
GAM2469	LOC113523	3'	GA	ACTCCTGACCTCACACAATC	73422	CACC	
	C			GGAT TGAGGTCAGGAGTTC			
				CCTA ACTCCAGTCCTCAAG			
				ACAC			
GAM2469	LOC115098	5'	GA	ACTCCTGGCCTCAAGCAATC	57394	CACC	
	C			GGAT TGAGGTCAGGAGTTC			
				CCTA ACTCCGGTCCTCAAG			
				ACGA			
GAM2469	LOC115219	5'	AA	CTCCTGACGTCGTGATCC	73680	CT	G
				GGATCAC GA GTCAGGAGTT			

		CCTAGTG CT CAGTCCTCAA	
		— G	
GAM2469	LOC115648 3'	GAACCTCCTGACCTCAGGTGATC 60021	
	CA	TGGATCACCTGAGGTCAGGAGTTC	
		ACCTAGTGGACTCCAGTCCTCAAG	
GAM2469	LOC119392 3'	GAACCTCCTGACCTCAGGTGATC 59813	
	CA	TGGATCACCTGAGGTCAGGAGTTC	
		ACCTAGTGGACTCCAGTCCTCAAG	
GAM2469	LOC120114 3'	AACTCCTGACCTCGTAATCCA 76031	C CT
		TGGAT AC GAGGTCAGGAGTT	
		ACCTA TG CTCCAGTCCTCAA	
		A —	
GAM2469	LOC120224 5'	GAACCTCCTGACCTCAGGTGATC 57887	
	T	GGATCACCTGAGGTCAGGAGTTC	
		TCTAGTGGACTCCAGTCCTCAAG	
GAM2469	LOC120939 3'	GAACCTCCTGACGTCAGGTGATC 76761	G
	C	GGATCACCTGA GTCAGGAGTTC	
		CCTAGTGGACT CAGTCCTCAAG	
		G	
GAM2469	LOC121504 3'	GAACCTCCTGGCCTCAAGTGATT 74545	C
	CA	TGGATCAC TGAGGTCAGGAGTTC	
		ACTTAGTG ACTCCGGTCCTCAAG	
		A	
GAM2469	LOC124216 3'	AACTCCTGACCTCGTGATCC 74730	CT
		GGATCAC GAGGTCAGGAGTT	
		CCTAGTG CTCCAGTCCTCAA	
		—	
GAM2469	LOC125194 5'	AACTCCTGGCTTCAAGTGATCC 74859	C
		GGATCAC TGAGGTCAGGAGTT	
		CCTAGTG ACTTCGGTCCTCAA	
		A	
GAM2469	LOC126364 3'	GAACCTCCTGACCTCAAGCGATC 76191	ACC
	T	GGATC TGAGGTCAGGAGTTC	
		TCTAG ACTCCAGTCCTCAAG	
		CGA	
GAM2469	LOC126661 3'	GAACCTCCTGGGCTCAACTGATC 75056	CC G
	CA	TGGATCA TGAG TCAGGAGTTC	

		ACCTAGT ACTC GGTCTCAAG	
		CA G	
GAM2469	LOC126669 3'	AACTCCTGACCTCAAATGATCC 75916	CC
	A	TGGATCA TGAGGTCAGGAGTT	
		ACCTAGT ACTCCAGTCCTCAA	
		AA	
GAM2469	LOC128077 3'	GAACCTCCTGACATAAGGTAATC 75214	C GAG
	CA	TGGAT ACCT GTCAGGAGTTC	
		ACCTA TGGA CAGTCCTCAAG	
		A ATA	
GAM2469	LOC128989 3'	GAACCTCCTGACGTGGTGATCCA 75315	TGAG
		TGGATCACG GTCAGGAGTTC	
		ACCTAGTGG CAGTCCTCAAG	
		TG__	
GAM2469	LOC130639 5'	GAACCTCCTGACCTCAAGTGATC 75479	C
	C	GGATCAC TGAGGTCAGGAGTTC	
		CCTAGTG ACTCCAGTCCTCAAG	
		A	
GAM2469	LOC130813 3'	AACTCCCAACTTCAGGTGATCC 76257	CA
		GGATCACCTGAGGT GGAGTT	
		CCTAGTGGACTTCA CCTCAA	
		AC	
GAM2469	LOC132241 5'	GAACGCCTGACCTCAAGTGATC 75561	C A
	C	GGATCAC TGAGGTCAGG GTTC	
		CCTAGTG ACTCCAGTCC CAAG	
		A G	
GAM2469	LOC135154 3'	GAACCTCCTGACCTCAGTTGATC 75730	C
	CA	TGGATCA CTGAGGTCAGGAGTTC	
		ACCTAGT GACTCCAGTCCTCAAG	
		T	
GAM2469	LOC135293 3'	AACTCCTGGGCTCAAGCAATCC 76673	CACC G
		GGAT TGAG TCAGGAGTT	
		CCTA ACTC GGTCTCAA	
		ACGA G	
GAM2469	LOC135293 3'	GAACCTCCTGACCTCAGGTGATG 76684	G
	CA	TG ATCACCTGAGGTCAGGAGTTC	
		AC TAGTGGACTCCAGTCCTCAAG	
		G	
GAM2469	LOC135818 3'	GAACCTCCTGACCTCAGGTGATC 75747	
	T	GGATCACCTGAGGTCAGGAGTTC	

TCTAGTGGACTCCAGTCCTCAAG

GAM2469 LOC139422 5' GAACTCCTGAGCTCAAGCAATC 76350 CACC G
C GGAT TGAG TCAGGAGTTC

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CCTA ACTC AGTCCTCAAG
ACGA G

GAM2469 LOC142927 5' AACTCCTGGCCTCAAGTGATCC 76937 C
GGATCAC TGAGGTCAGGAGTT

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CCTAGTG ACTCCGGTCCTCAA
A

GAM2469 LOC143916 3' AACTTCTGACCTCAGGTGATCC 77131
A TGGATCACCTGAGGTCAGGAGTT

|||||
ACCTAGTGGACTCCAGTCTTCAA

GAM2469 LOC144305 3' AACTCCTGGACCCAAGCGATCC 83965 AC GA _
GGATC CT GGTC AGGAGTT

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CCTAG GA CCAG TCCTCAA
C_ AC G

GAM2469 LOC144317 5' GAACTCCTGACCTCAGGTGATC 77294
CA TGGATCACCTGAGGTCAGGAGTTC

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ACCTAGTGGACTCCAGTCCTCAAG

GAM2469 LOC144519 3' GAACTCCTGACCTGAAGCGATC 77372 AC G_
C GGATC CT AGGTCAGGAGTTC

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CCTAG GA TCCAGTCCTCAAG
C_ AG

GAM2469 LOC144519 5' GAACTCCTGGGCTCAAGTGGTC 77373 C G
CA TGGATCAC TGAG TCAGGAGTTC

||||| ||| |||||
ACCTGGTG ACTC GGTCTCAAG
A G

GAM2469 LOC144524 5' AACTCCTGAACTCAGGTGATCC 84044 G
GGATCACCTGAG TCAGGAGTT

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CCTAGTGGACTC AGTCCTCAA
A

GAM2469 LOC144742 5' GAACTCATGGCCTCAAATGATC 77459 CC G
CA TGGATCA TGAGGTCA GAGTTC

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ACCTAGT ACTCCGGT CTCAAG
AA A

GAM2469 LOC145009 3' GAACTCCTGACCTCGTGATCCA 60974 CT
TGGATCAC GAGGTCAGGAGTTC

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ACCTAGTG CTCCAGTCCTCAAG

GAM2469 LOC145082 5' CCTAACCTAAGGTGATCCA 84185 G C
TGGATCACCT AGGT AGG
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ACCTAGTGGA TCCA TCC
A A

GAM2469 LOC145268 5' GAACTCCTAACCTCGGGTGATC 77578 C
CA TGGATCACCTGAGGT AGGAGTTC
||||||| |||||
ACCTAGTGGGCTCCA TCCTCAAG
A

GAM2469 LOC145453 5' AACTCCTGACCTCAAGGATCT 77649 ACC
GGATC TGAGGTCAGGAGTT
||| |||||
TCTAG ACTCCAGTCCTCAA
GA_

GAM2469 LOC145725 3' GAACTCCTGGGCTCAAGTGATC 77882 C G
C GGATCAC TGAG TCAGGAGTTC
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CCTAGTG ACTC GGTCTCAAG
A G

GAM2469 LOC145732 3' GAACTCCTGGGCTCAAGTGATC 77894 C G
C GGATCAC TGAG TCAGGAGTTC
||||| ||| |||||
CCTAGTG ACTC GGTCTCAAG
A G

GAM2469 LOC145813 5' GAACTCCTGGGCTCAAGCGATC 84508 ACC G
C GGATC TGAG TCAGGAGTTC
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CCTAG ACTC GGTCTCAAG
CGA G

GAM2469 LOC145873 5' GAACTCCTGAACTCAAGTAATC 78011 C C G
CA TGGAT AC TGAG TCAGGAGTTC
|||| || ||| |||||
ACCTA TG ACTC AGTCCTCAAG
A A A

GAM2469 LOC146050 3' AACTCCCGACCTCAGGTGATCT 78094 A
GGATCACCTGAGGTC GGAGTT
||||||| |||||
TCTAGTGGA CTCCAG CCTCAA
C

GAM2469 LOC146108 3' AACTCCTGGCTTCAAGCAATCC 78145 CACC
GGAT TGAGGTCAGGAGTT
||| |||||
CCTA ACTTCGGTCCTCAA
ACGA

GAM2469 LOC146229 3' AACTCCTGACCTCAAGTGATCC 78237 C
A TGGATCAC TGAGGTCAGGAGTT
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		ACCTAGTG ACTCCAGTCCTCAA	
		A	
GAM2469	LOC146229 3'	AACTCCTGACCTCAGGTGATCC 78238	
	A	TGGATCACCTGAGGTCAGGAGTT	
		ACCTAGTGGACTCCAGTCCTCAA	
GAM2469	LOC146229 3'	AACTCCTGACTTCAAATGATCC 78239	CC
	A	TGGATCA TGAGGTCAGGAGTT	
		ACCTAGT ACTTCAGTCCTCAA	
		AA	
GAM2469	LOC146336 3'	GAACTCTTGGGCTCAAGTGATC 78372	C G
	C	GGATCAC TGAG TCAGGAGTTC	
		CCTAGTG ACTC GGTTCTCAAG	
		A G	
GAM2469	LOC146346 5'	GAACTCCTGACCACATGTGGTC 78396	C A
	CA	TGGATCAC TG GGTCAGGAGTTC	
		ACCTGGTG AC CCAGTCCTCAAG	
		T A	
GAM2469	LOC146894 3'	GAACTCCTGACCTCAAATGAGC 59861	A CC
	C	GG TCA TGAGGTCAGGAGTTC	
		CC AGT ACTCCAGTCCTCAAG	
		G AA	
GAM2469	LOC146901 3'	GAACTCCTGACCTCAGGTGATC 84900	
	CA	TGGATCACCTGAGGTCAGGAGTTC	
		ACCTAGTGGACTCCAGTCCTCAAG	
GAM2469	LOC146909 3'	GAACTCCTGACCTCAGGTGATC 78771	
	C	GGATCACCTGAGGTCAGGAGTTC	
		CCTAGTGGACTCCAGTCCTCAAG	
GAM2469	LOC146952 5'	AACTCCTGACCTCAGATGATCT 84918	C
	A	TGGATCA CTGAGGTCAGGAGTT	
		ATCTAGT GACTCCAGTCCTCAA	
		A	
GAM2469	LOC147054 3'	GAACTCCCGATCTCAGGTGATC 85006	A
	C	GGATCACCTGAGGTC GGAGTTC	
		CCTAGTGGACTCTAG CCTCAAG	
		C	
GAM2469	LOC147276 3'	GAACTCCTGACCTCAAGTGATC 78961	C
	CA	TGGATCAC TGAGGTCAGGAGTTC	

ACCTAGTG ACTCCAGTCCTCAAG
 A
 GAM2469 LOC147817 3' AACTCCTGACCTTATAATCC 79161 CACC
 GGAT TGAGGTCAGGAGTT
 ||| |||||
 CCTA ATTCCAGTCCTCAA
 AT__
 GAM2469 LOC147817 3' AACTCCTGGCTTCAAGTGATCC 79162 C
 GGATCAC TGAGGTCAGGAGTT
 ||||| |||||
 CCTAGTG ACTTCGGTCCTCAA
 A
 GAM2469 LOC147841 3' GAACTCCTGACCTCAGGTGATC 79227
 CA TGGATCACCTGAGGTCAGGAGTTC
 |||||
 ACCTAGTGGACTCCAGTCCTCAAG

 GAM2469 LOC147935 3' AACTCCTGGGCTCAAGTGATCC 85202 C G
 GGATCAC TGAG TCAGGAGTT
 ||||| ||| |||||
 CCTAGTG ACTC GGTCTCAA
 A G
 GAM2469 LOC147990 3' GAACTCCTGGGCTCAAGCGATC 85222 ACC G
 C GGATC TGAG TCAGGAGTTC
 |||| ||| |||||
 CCTAG ACTC GGTCTCAAG
 CGA G
 GAM2469 LOC148195 3' GAACTCCTGACCTCAGGTGAGC 85282 A
 C GG TCACCTGAGGTCAGGAGTTC
 || |||||
 CC AGTGGACTCCAGTCCTCAAG
 G
 GAM2469 LOC148645 5' GAACTCCTGGGCCCAAGTGATC 85334 C A _
 C GGATCAC TG GGTC AGGAGTTC
 ||||| || ||| |||||
 CCTAGTG AC CCGG TCCTCAAG
 A _ G
 GAM2469 LOC148709 3' AACTCCCGACCTTAGGTGATGC 79685 G A
 A TG ATCACCTGAGGTC GGAGTT
 || ||||| |||||
 AC TAGTGGATTCCAG CCTCAA
 G C
 GAM2469 LOC148918 5' GAACTCCTGACCTCAGGTGATC 79827
 CA TGGATCACCTGAGGTCAGGAGTTC
 |||||
 ACCTAGTGGACTCCAGTCCTCAAG

 GAM2469 LOC149478 3' GAACTCCTGACTTCATGTGATC 80169 C
 C GGATCAC TGAGGTCAGGAGTTC
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		CCTAGTG ACTTCAGTCCTCAAG	
		T	
GAM2469	LOC149577 3'	ACTCCTGACCTCAAGTGATCCA 85663	C
		TGGATCAC TGAGGTCAGGAGT	
		ACCTAGTG ACTCCAGTCCTCA	
		A	
GAM2469	LOC149577 3'	GAACCTCCTGACCTCAAGTGATC 85675	C
	CA	TGGATCAC TGAGGTCAGGAGTTC	
		ACCTAGTG ACTCCAGTCCTCAAG	
		A	
GAM2469	LOC149692 3'	GAACCTCCTGACCTCAGGTGATC 85734	
	CA	TGGATCACCTGAGGTCAGGAGTTC	
		ACCTAGTGGACTCCAGTCCTCAAG	
GAM2469	LOC149711 3'	AACTCCTGACCTCAGGTGATCC 85829	
	A	TGGATCACCTGAGGTCAGGAGTT	
		ACCTAGTGGACTCCAGTCCTCAA	
GAM2469	LOC150054 5'	GAACCTTATGACCTCAGGTGATC 85972	G
	C	GGATCACCTGAGGTCA GAGTTC	
		CCTAGTGGACTCCAGT TTCAAG	
		A	
GAM2469	LOC150225 3'	AACTCCTGACCTCAGATGATTC 86174	C
	A	TGGATCA CTGAGGTCAGGAGTT	
		ACTTAGT GACTCCAGTCCTCAA	
		A	
GAM2469	LOC150282 5'	GAACCTCCTGACCTCAGGTGATC 80543	
	CA	TGGATCACCTGAGGTCAGGAGTTC	
		ACCTAGTGGACTCCAGTCCTCAAG	
GAM2469	LOC150290 3'	AACTCCTGGCCTCAAGCAATCC 80581	CACC
		GGAT TGAGGTCAGGAGTT	
		CCTA ACTCCGGTCCTCAA	
		ACGA	
GAM2469	LOC150397 3'	GAACCCCTGACCTCAGGTGATC 80662	A
	C	GGATCACCTGAGGTCAGG GTTC	
		CCTAGTGGACTCCAGTCC CAAG	
		C	
GAM2469	LOC150407 3'	AACTCCTGGGCTCAAGTAATCC 80634	C C G
		GGAT AC TGAG TCAGGAGTT	

		CCTA TG ACTC GGCCTCAA	
		A A G	
GAM2469	LOC150587 3'	AACTCCTGGGCTCAAGCAATCC 86238	CACC G
		GGAT TGAG TCAGGAGTT	
		CCTA ACTC GGCCTCAA	
		ACGA G	
GAM2469	LOC150587 3'	AACTCCTGGGCTCAAGCGATCC 86239	ACC G
		GGATC TGAG TCAGGAGTT	
		CCTAG ACTC GGCCTCAA	
		CGA G	
GAM2469	LOC150960 3'	AATTCCTGACCTCAGGTGATCC 80859	
	A	TGGATCACCTGAGGTCAGGAGTT	
		ACCTAGTGGACTCCAGTCCTTAA	
GAM2469	LOC151201 3'	GAACCTCCTGGTTTCAAGCGATC 86476	ACC GT
	C	GGATC TGAG CAGGAGTTC	
		CCTAG ACTT GTCCTCAAG	
		CGA TG	
GAM2469	LOC151701 3'	GAACCTCCTGACCTCAGATGATC 86671	C
	T	GGATCA CTGAGGTCAGGAGTTC	
		TCTAGT GACTCCAGTCCTCAAG	
		A	
GAM2469	LOC151826 3'	GAACCTCCTGACATCAGGTGATC 81181	G
	CA	TGGATCACCTGA GTCAGGAGTTC	
		ACCTAGTGGACT CAGTCCTCAAG	
		A	
GAM2469	LOC152137 3'	GAACCCCTGACCTCAAGTGATC 81316	C A
	CA	TGGATCAC TGAGGTCAGG GTTC	
		ACCTAGTG ACTCCAGTCC CAAG	
		A C	
GAM2469	LOC152343 3'	GAACCTCCTGTGCTCAAGTGATC 81426	C GT
	C	GGATCAC TGAG CAGGAGTTC	
		CCTAGTG ACTC GTCCTCAAG	
		A GT	
GAM2469	LOC152794 5'	GAACCTCCTGACCTCAGGTGATC 81558	
	C	GGATCACCTGAGGTCAGGAGTTC	
		CCTAGTGGACTCCAGTCCTCAAG	
GAM2469	LOC153077 3'	GAACCTCCTGACCTCAGGTGATC 87125	
	CA	TGGATCACCTGAGGTCAGGAGTTC	

ACCTAGTGGACTCCAGTCCTCAAG

GAM2469	LOC153443	3'	AACTCCTGGGCTCAAGTGATCC	81686	C	G
			GGATCAC TGAG TCAGGAGTT			
			CCTAGTG ACTC GGTCCTCAA			
			A G			
GAM2469	LOC153606	5'	GAACCTCCTGACTGCAGGTGATC	87256	A	
	C		GGATCACCTG GGTCAGGAGTTC			
			CCTAGTGGAC TCAGTCCTCAAG			
			G			
GAM2469	LOC153688	3'	GAACCTCCCAACCTCAGGTGATC	87311	CA	
	C		GGATCACCTGAGGT GGAGTTC			
			CCTAGTGGACTCCA CCTCAAG			
			AC			
GAM2469	LOC153688	3'	GAACCTCCTGGGCTCAAGCGATC	87312	ACC	G
	CA		TGGATC TGAG TCAGGAGTTC			
			ACCTAG ACTC GGTCCTCAAG			
			CGA G			
GAM2469	LOC153811	3'	AACTCCTGACCTCAAATGATCC	81816	CC	
	A		TGGATCA TGAGGTCAGGAGTT			
			ACCTAGT ACTCCAGTCCTCAA			
			AA			
GAM2469	LOC153883	5'	GAACCTCCTGACCTCAAGTGATC	81894	C	
	CA		TGGATCAC TGAGGTCAGGAGTTC			
			ACCTAGTG ACTCCAGTCCTCAAG			
			A			
GAM2469	LOC154007	3'	GAACCTCCTGGGCTCAGATGATC	81927	C	G
	C		GGATCA CTGAG TCAGGAGTTC			
			CCTAGT GACTC GGTCCTCAAG			
			A G			
GAM2469	LOC154726	3'	AACTCCTGGGCTCAGATGATCC	82003	C	G
	A		TGGATCA CTGAG TCAGGAGTT			
			ACCTAGT GACTC GGTCCTCAA			
			A G			
GAM2469	LOC154877	3'	AACTCCTGGGCTCAAGTGATCC	87512	C	G
			GGATCAC TGAG TCAGGAGTT			
			CCTAGTG ACTC GGTCCTCAA			
			A G			
GAM2469	LOC154877	3'	GAACCTCCCGACCTCAGGTGATC	87547	A	
	TA		TGGATCACCTGAGGTC GGAGTTC			

		ATCTAGTGGACTCCAG CCTCAAG	
		C	
GAM2469	LOC154877 5'	GAACCTCCTAGGCTCAAGTGATC 87548	C G _
	C	GGATCAC TGAG TC AGGAGTTC	
		CCTAGTG ACTC GG TCCTCAAG	
		A _ A	
GAM2469	LOC154877 3'	GAACCTCCTGACCTTACGTGATC 87549	C
	CA	TGGATCAC TGAGGTCAGGAGTTC	
		ACCTAGTG ATTCCAGTCCTCAAG	
		C	
GAM2469	LOC154930 3'	GAACCTCCTGACTTGAAATGATC 82090	CCTG
	CA	TGGATCA AGGTCAGGAGTTC	
		ACCTAGT TTCAGTCCTCAAG	
		AAAG	
GAM2469	LOC157247 5'	GAACCTCCTGACCTCAGGTGATC 82296	
	CA	TGGATCACCTGAGGTCAGGAGTTC	
		ACCTAGTGGACTCCAGTCCTCAAG	
GAM2469	LOC157623 3'	AACTCCTGGGCTCAAGTGATCC 82405	C G
		GGATCAC TGAG TCAGGAGTT	
		CCTAGTG ACTC GGTCCTCAA	
		A G	
GAM2469	LOC157867 5'	AACTCCTGGCTTCAAGCAATCC 87871	CACC
		GGAT TGAGGTCAGGAGTT	
		CCTA ACTTCGGTCCTCAA	
		ACGA	
GAM2469	LOC158310 5'	GAACCTCCTGACCTTAAGTGATC 88081	C
	CA	TGGATCAC TGAGGTCAGGAGTTC	
		ACCTAGTG ATTCCAGTCCTCAAG	
		A	
GAM2469	LOC158476 3'	GAACCTCCTGACCCCAGGTGATC 88193	A
	C	GGATCACCTG GGTCAGGAGTTC	
		CCTAGTGGAC CCAGTCCTCAAG	
		C	
GAM2469	LOC158865 5'	GAACCTCCTGACCTCAAGTGAT 88307	C
		ATCAC TGAGGTCAGGAGTTC	
		TAGTG ACTCCAGTCCTCAAG	
		A	
GAM2469	LOC160646 3'	GAACCTCCTGACCTTCAGGTGAT 83111	_
	CCA	TGGATCACCTGA GGTCAGGAGTTC	

		ACCTAGTGGACT CCAGTCCTCAAG	
		T	
GAM2469	LOC162427 3'	AACTCCTGACCTCAAGTGAGCT 83217	A C
		GG TCAC TGAGGTCAGGAGTT	
		TC AGTG ACTCCAGTCCTCAA	
		G A	
GAM2469	LOC162461 5'	GAACCTCCTAGGCTCAAGTGATC 83238	C G _
	C	GGATCAC TGAG TC AGGAGTTC	
		CCTAGTG ACTC GG TCCTCAAG	
		A _ A	
GAM2469	LOC169611 3'	AACTCCTGACCTCAGGTGATCC 83627	
	A	TGGATCACCTGAGGTCAGGAGTT	
		ACCTAGTGGACTCCAGTCCTCAA	
GAM2469	LOC169611 3'	GAACCTCCTGACCTTAGGTGATC 83648	
	C	GGATCACCTGAGGTCAGGAGTTC	
		CCTAGTGGATTCCAGTCCTCAAG	
GAM2469	LOC196047 5'	AACTCCTGACCTCAGGTGATCC 91133	
	A	TGGATCACCTGAGGTCAGGAGTT	
		ACCTAGTGGACTCCAGTCCTCAA	
GAM2469	LOC196529 3'	GAACCTCCTGATCTCAGGCAATC 89132	CA
	CA	TGGAT CCTGAGGTCAGGAGTTC	
		ACCTA GGACTCTAGTCCTCAAG	
		AC	
GAM2469	LOC196957 3'	GAACCTCCTGGGCTCAAGTGATC 89187	C G
	C	GGATCAC TGAG TCAGGAGTTC	
		CCTAGTG ACTC GGTCCTCAAG	
		A G	
GAM2469	LOC196961 3'	GAACCTCCTGGGCTCAAGTGATC 89201	C G
	C	GGATCAC TGAG TCAGGAGTTC	
		CCTAGTG ACTC GGTCCTCAAG	
		A G	
GAM2469	LOC197138 3'	GAACCTCCTGGGCTCAAGTGATC 89250	C G
	C	GGATCAC TGAG TCAGGAGTTC	
		CCTAGTG ACTC GGTCCTCAAG	
		A G	
GAM2469	LOC197358 3'	AACTCCTGACCTCAAGTGATCC 89403	C
	A	TGGATCAC TGAGGTCAGGAGTT	

		ACCTAGTG ACTCCAGTCCTCAA	
		A	
GAM2469	LOC197358 3'	GAACCTCCTGACCTCAGGTGATC 89431	
	CA	TGGATCACCTGAGGTCAGGAGTTC	
		ACCTAGTGGACTCCAGTCCTCAAG	
GAM2469	LOC199725 5'	GAACCTCCTGACCTCGTGATC 91418	CT
		GATCAC GAGGTCAGGAGTTC	
		CTAGTG CTCCAGTCCTCAAG	
GAM2469	LOC199786 3'	AACTCCTGGACTCAAGCAATCC 89729	CACC GT
		GGAT TGAG CAGGAGTT	
		CCTA ACTC GTCCTCAA	
		ACGA AG	
GAM2469	LOC199786 3'	GAACCTCCTGACCTCATGATCC 89752	CC
		GGATCA TGAGGTCAGGAGTTC	
		CCTAGT ACTCCAGTCCTCAAG	
GAM2469	LOC199906 3'	AACTCCTGACCTCAGGCGATCC 89838	A
		GGATC CCTGAGGTCAGGAGTT	
		CCTAG GGACTCCAGTCCTCAA	
		C	
GAM2469	LOC200014 3'	GAACCTCCTGACCTCATGATCCA 89934	CC
		TGGATCA TGAGGTCAGGAGTTC	
		ACCTAGT ACTCCAGTCCTCAAG	
GAM2469	LOC200314 3'	GAACCTCCTGACCTCAGGTGATC 91599	
	CA	TGGATCACCTGAGGTCAGGAGTTC	
		ACCTAGTGGACTCCAGTCCTCAAG	
GAM2469	LOC200316 3'	GAACCTCCTGACCTCAGGTGATC 90180	
	T	GGATCACCTGAGGTCAGGAGTTC	
		TCTAGTGGACTCCAGTCCTCAAG	
GAM2469	LOC200339 3'	GAACCTCCTGGCCTCAAGCGATC 91615	ACC
	CA	TGGATC TGAGGTCAGGAGTTC	
		ACCTAG ACTCCGGTCCTCAAG	
		CGA	
GAM2469	LOC200407 3'	AACTCCTGACCTCAGGTGATCC 91621	
	A	TGGATCACCTGAGGTCAGGAGTT	

ACCTAGTGGACTCCAGTCCTCAA

GAM2469 LOC201164 3' AACTCCTGACCTCAAGTGATCC 89480 C
A TGGATCAC TGAGGTCAGGAGTT

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ACCTAGTG ACTCCAGTCCTCAA
A

GAM2469 LOC201411 3' GAACTCCAGACCTCAGGTGATC 63641 A
TA TGGATCACCTGAGGTC GGAGTTC

||||||||||| |||||
ATCTAGTGGACTCCAG CCTCAAG
A

GAM2469 LOC201510 3' AACTCCTGGTCTCAAGTGATCC 89627 C GT
GGATCAC TGAG CAGGAGTT

||||| ||| |||||||
CCTAGTG ACTC GTCCTCAA
A TG

GAM2469 LOC201626 3' GAACTCCTGACCTCAGGTGATC 90432
CA TGGATCACCTGAGGTCAGGAGTTC

|||||||||||
ACCTAGTGGACTCCAGTCCTCAAG

GAM2469 LOC201627 3' AACTCCCGACCTCAGGTGATCC 90442 A
GGATCACCTGAGGTC GGAGTT

||||||||||| |||||
CCTAGTGGACTCCAG CCTCAA
C

GAM2469 LOC203197 3' ACTCCTGACCTCAGGTGATCCA 90799
TGGATCACCTGAGGTCAGGAGT

|||||||||||
ACCTAGTGGACTCCAGTCCTCA

GAM2469 LOC203197 3' GAACTCCTGACCTCAGGTGATC 90811
CA TGGATCACCTGAGGTCAGGAGTTC

|||||||||||
ACCTAGTGGACTCCAGTCCTCAAG

GAM2469 LOC203378 3' AACTCCTCCACTCAGGTGATCC 92267 GTC
A TGGATCACCTGAG AGGAGTT

||||||||| |||||
ACCTAGTGGACTC TCCTCAA
ACC

GAM2469 LOC204804 3' GAACTCCTGGCCTCAGGTGATC 91042
CA TGGATCACCTGAGGTCAGGAGTTC

|||||||||||
ACCTAGTGGACTCCGGTCCTCAAG

GAM2469 LOC219529 5' AACTCCTGAGCCCAGGTGATCC 94560 A _
GGATCACCTG GG TCAGGAGTT

||||||| || |||||||

		CCTAGTGGAC CC AGTCCTCAA		
		_ G		
GAM2469	LOC219673 5'	AACGCCTGACCTCAAGTAATCC 94603	C C	A
	A	TGGAT AC TGAGGTCAGG GTT		
		ACCTA TG ACTCCAGTCC CAA		
		A A G		
GAM2469	LOC219673 5'	GAACCTCCTGGGCTCAAGTGATC 94624	C G	
	C	GGATCAC TGAG TCAGGAGTTC		
		CCTAGTG ACTC GGTCCTCAAG		
		A G		
GAM2469	LOC220074 3'	AACTCCTGACCTCAGGTGATCT 59949		
		GGATCACCTGAGGTCAGGAGTT		
		TCTAGTGGACTCCAGTCCTCAA		
GAM2469	LOC220074 3'	GAACCTCCTGACCTCAGGTGATC 59977		
	C	GGATCACCTGAGGTCAGGAGTTC		
		CCTAGTGGACTCCAGTCCTCAAG		
GAM2469	LOC220662 3'	GAACCTCCTGGACTCAAGCAATC 92818	CACC	GT
	C	GGAT TGAG CAGGAGTTC		
		CCTA ACTC GTCCTCAAG		
		ACGA AG		
GAM2469	LOC221060 3'	GAACCTCCTGACCTCAGGTGATC 94831		
	C	GGATCACCTGAGGTCAGGAGTTC		
		CCTAGTGGACTCCAGTCCTCAAG		
GAM2469	LOC221964 3'	GAACCTCCTGACCTCAGGTGATC 95605		
	CA	TGGATCACCTGAGGTCAGGAGTTC		
		ACCTAGTGGACTCCAGTCCTCAAG		
GAM2469	LOC222031 3'	GAACCTCCTGACCTCAGGTGATC 95680		
	CA	TGGATCACCTGAGGTCAGGAGTTC		
		ACCTAGTGGACTCCAGTCCTCAAG		
GAM2469	LOC222068 3'	GACTCCTGACCTCAGTTGATCC 94275	C	
	A	TGGATCA CTGAGGTCAGGAGTT		
		ACCTAGT GACTCCAGTCCTCAG		
		T		
GAM2469	LOC222070 5'	GAACCTCCTGGCCTCAAGTGACC 95814	A C	
	C	GG TCAC TGAGGTCAGGAGTTC		

		CC AGTG ACTCCGGTCCTCAAG	
		C A	
GAM2469	LOC245771 5'	GAACCTCCTGACCTCAAGTGATC 94473	C
	CA	TGGATCAC TGAGGTCAGGAGTTC	
		ACCTAGTG ACTCCAGTCCTCAAG	
		A	
GAM2469	LOC253805 3'	GAACCTCCTGACCTCAGATGATT 98174	C
	CA	TGGATCA CTGAGGTCAGGAGTTC	
		ACTTAGT GACTCCAGTCCTCAAG	
		A	
GAM2469	LOC253981 3'	GAACCTCCTGACCTCAGGCGATC 97536	A
	TA	TGGATC CCTGAGGTCAGGAGTTC	
		ATCTAG GGA CTCCAGTCCTCAAG	
		C	
GAM2469	LOC254268 3'	AACTCCTGACCTCAAGTGATCC 97133	C
		GGATCAC TGAGGTCAGGAGTT	
		CCTAGTG ACTCCAGTCCTCAA	
		A	
GAM2469	LOC254351 5'	AGCTCCTGACCTCGGGTGATCC 96681	
	A	TGGATCACCTGAGGTCAGGAGTT	
		ACCTAGTGGGCTCCAGTCCTCGA	
GAM2469	LOC254532 5'	AACTCCTGACCTCAAGTGATCC 98441	C
	A	TGGATCAC TGAGGTCAGGAGTT	
		ACCTAGTG ACTCCAGTCCTCAA	
		A	
GAM2469	LOC254655 3'	GAACCTCCTGACCTCAGGTGATC 97219	
	CA	TGGATCACCTGAGGTCAGGAGTTC	
		ACCTAGTGGACTCCAGTCCTCAAG	
GAM2469	LOC254672 3'	GAACCTCCTGACCCTGTGATCCA 96294	CTGA
		TGGATCAC GGT CAGGAGTTC	
		ACCTAGTG CCAGTCCTCAAG	
		TC__	
GAM2469	LOC254778 3'	AACTCCTGGGTTCAAGAGATCC 97825	ACC G
	A	TGGATC TGAG TCAGGAGTT	
		ACCTAG ACTT GGT CCTCAA	
		AGA G	
GAM2469	LOC255065 5'	AACTCCTGACCTCAAGTAATCC 98367	C C
	A	TGGAT AC TGAGGTCAGGAGTT	

		ACCTA TG ACTCCAGTCCTCAA		
		A A		
GAM2469	LOC255065 5'	CCTGACCTCAAGTAATCCA	98370	C C
		TGGAT AC TGAGGTCAGG		
		ACCTA TG ACTCCAGTCC		
		A A		
GAM2469	LOC255458 5'	AACTCCTGGGCTCAAGCGATCC	98930	ACC G
		GGATC TGAG TCAGGAGTT		
		CCTAG ACTC GGTCCTCAA		
		CGA G		
GAM2469	LOC255497 3'	AACTCCTGACCTCAGGTG	98978	
		CACCTGAGGTCAGGAGTT		
		GTGGACTCCAGTCCTCAA		
GAM2469	LOC255707 3'	TCTTGAAGTCAAGTGATCCA	98733	C G
		TGGATCAC TGAG TCAGGA		
		ACCTAGTG ACTC AGTTCT		
		A A		
GAM2469	LOC256306 3'	GAACACCTGACCTCAAATGATC	98514	CC A
	C	GGATCA TGAGGTCAGG GTTC		
		CCTAGT ACTCCAGTCC CAAG		
		AA A		
GAM2469	LOC256364 5'	AACTCCTGGCCTCAGGTGACCC	96440	A
		GG TCACCTGAGGTCAGGAGTT		
		CC AGTGGACTCCGGTCCTCAA		
		C		
GAM2469	LOC257127 5'	GAACCTCCTGACCTCAGGTGATC	98496	
	C	GGATCACCTGAGGTCAGGAGTTC		
		CCTAGTGGACTCCAGTCCTCAAG		
GAM2469	LOC257465 3'	GAACCTCCTGACCTTGGTGATCC	82495	T
	A	TGGATCACC GAGGTCAGGAGTTC		
		ACCTAGTGG TTCCAGTCCTCAAG		
GAM2469	LOC51008 5'	GAACCTCCCGACCTCAGGTGATC	32532	A
	CA	TGGATCACCTGAGGTC GGAGTTC		
		ACCTAGTGGACTCCAG CCTCAAG		
		C		
GAM2469	LOC51193 3'	AACTCCTGGACTCAAGCAATCC	33352	CACC GT
		GGAT TGAG CAGGAGTT		

			CCTA	ACTC	GTCCTCAA		
			ACGA	AG			
GAM2469	LOC51200	3'	AACTCCCAACCTCAGGTGATCT	33430		CA	
			GGATCACCTGAGGT	GGAGTT			
			TCTAGTGGACTCCA	CCTCAA			
			AC				
GAM2469	LOC51219	5'	GAACTCCCGACCTCAGGTGATC	33544		A	
		T	GGATCACCTGAGGTC	GGAGTTC			
			TCTAGTGGACTCCAG	CCTCAAG			
			C				
GAM2469	LOC57107	3'	GAACTCCTGACCTCAGGTGATC	40187			
		C	GGATCACCTGAGGTCAGGAGTTC				
			CCTAGTGGACTCCAGTCCTCAAG				
GAM2469	LOC57146	3'	AACTCCTGACCTCAGGTGCTCC	40285	T		
		A	TGGA CACCTGAGGTCAGGAGTT				
			ACCT GTGGACTCCAGTCCTCAA				
			C				
GAM2469	LOC89231	3'	GAACTCCTGGACTCAAGCAATC	94298	CACC	GT	
		C	GGAT TGAG CAGGAGTTC				
			CCTA ACTC GTCCTCAAG				
			ACGA AG				
GAM2469	LOC89932	3'	GAACTCCCGACCTCAGGTAATC	61459	C	A	
		C	GGAT ACCTGAGGTC GGAGTTC				
			CCTA TGGACTCCAG CCTCAAG				
			A C				
GAM2469	LOC90072	3'	GAACTCCCGACCTCAAGTGATC	61958	C	A	
		C	GGATCAC TGAGGTC GGAGTTC				
			CCTAGTG ACTCCAG CCTCAAG				
			A C				
GAM2469	LOC90110	5'	GAACTTCTGACCTCAAGTGGTC	62178	C		
		CA	TGGATCAC TGAGGTCAGGAGTTC				
			ACCTGGTG ACTCCAGTCTTCAAG				
			A				
GAM2469	LOC90288	3'	GAACTACTGACCTCAGCTGATC	62788	C	G	
		CA	TGGATCA CTGAGGTCAG AGTTC				
			ACCTAGT GACTCCAGTC TCAAG				
			C A				
GAM2469	LOC90408	5'	GAACTCCTGACTTCAAGTGATC	63344	C		
		CA	TGGATCAC TGAGGTCAGGAGTTC				

		ACCTAGTG ACTTCAGTCCTCAAG	
		A	
GAM2469	LOC90459 3'	GAACTCCTGACCTCAAGTGATT 63555	C
	T	GGATCAC TGAGGTCAGGAGTTC	
		TTTAGTG ACTCCAGTCCTCAAG	
		A	
GAM2469	LOC90591 3'	GAACTCCTGACCTCAGGTGATC 64166	
	CA	TGGATCACCTGAGGTCAGGAGTTC	
		ACCTAGTGGACTCCAGTCCTCAAG	
GAM2469	LOC90591 3'	GAACTCCTGACCTGAAGTGATC 64167	CTG
	CA	TGGATCAC AGGTCAGGAGTTC	
		ACCTAGTG TCCAGTCCTCAAG	
		AAG	
GAM2469	LOC91115 3'	AACTCCTGACCTCAGATGGTCC 65532	C
	A	TGGATCA CTGAGGTCAGGAGTT	
		ACCTGGT GACTCCAGTCCTCAA	
		A	
GAM2469	LOC91547 3'	GAACTCCTGGGCTCAAGTGATC 67002	C G
	C	GGATCAC TGAG TCAGGAGTTC	
		CCTAGTG ACTC GGTCCTCAAG	
		A G	
GAM2469	LOC91561 5'	GAACTCCTGACCTCAGGTGATC 67043	
	T	GGATCACCTGAGGTCAGGAGTTC	
		TCTAGTGGACTCCAGTCCTCAAG	
GAM2469	LOC92267 3'	AACTCCTGACCTCAAGTGATCC 69159	C
		GGATCAC TGAGGTCAGGAGTT	
		CCTAGTG ACTCCAGTCCTCAA	
		A	
GAM2469	LOC92303 3'	GAATTCCAGACCTCAGGTGATC 69391	A
	CA	TGGATCACCTGAGGTC GGAGTTC	
		ACCTAGTGGACTCCAG CCTTAAG	
		A	
GAM2469	LOC92697 5'	GAACTCCCAACCTCAGGTGATC 70810	CA
	C	GGATCACCTGAGGT GGAGTTC	
		CCTAGTGGACTCCA CCTCAAG	
		AC	
GAM2469	LOC92841 3'	GAACTCCTGACCTCAAGTGATC 71252	C
	C	GGATCAC TGAGGTCAGGAGTTC	

CCTAGTG ACTCCAGTCCTCAAG
 A
 GAM2469 LOC92876 5' GACTCCTGACCTCAGGTGATCC 71349
 A TGGATCACCTGAGGTCAGGAGTT
 |||||
 ACCTAGTGGACTCCAGTCCTCAG

 GAM2469 LOC93408 5' AACTCCTGGCCTCAAGTGATCC 57281 C
 GGATCAC TGAGGTCAGGAGTT
 ||||| |||||
 CCTAGTG ACTCCGGTCCTCAA
 A
 GAM2470 BCL2L2 5' CTCCCAGCTCCTGCACC 15759 GT CCCA
 GGTGCAGG GGCT GGAG
 ||||| ||| |||
 CCACGTCC TCGA CCTC
 _ C_
 GAM2470 BLTR2 5' CTCCTGGAACCTAGCACC 39519 A GGCTC
 GGTGC GGGT CCAGGAG
 ||||| ||| |||||
 CCACG TCCA GGTCTC
 A A_
 GAM2470 BNC 3' CCTCCCCTCAGCCCTGCACC 9941 GGCTCCCA
 GGTGCAGGGT GGAGG
 ||||| |||||
 CCACGTCCCG CCTCC
 ACTCC_
 GAM2470 C6 5' CCTCCTGGGAGATTTTGGACC 96121 G GG
 GGT CAGGGT CTCCCAGGAGG
 ||| ||||| |||||
 CCA GTTTTA GAGGGTCCTCC
 G _
 GAM2470 CACNG3 5' CCCCCGAGCCTGCACC 22565 GGGT CA A
 GGTGCA GGCTCC GG G
 ||||| ||||| |||
 CCACGT CCGAGG CC C
 _ CC _
 GAM2470 CAPN1 3' CTCCTACCACACCACACC 19008 CA _ CTCCC
 GGTG GG GTGG AGGAG
 |||| || |||| |||||
 CCAC CC CACC TCCTC
 A_ A A_
 GAM2470 DRG2 3' CTCCCAGCCCCCTGCACTG 9130 T CCCA
 CGGTGCAGGG GGCT GGAG
 ||||| ||||| |||||
 GTCACGTCCC CCGA CCTC
 _ C_
 GAM2470 GPC1 3' CCCAGCTCCCTGCACCG 10857 T CCCA A
 CGGTGCAGGG GGCT GG G
 ||||| ||||| |||

GCCACGTCCC TCGA CC C
 _ _ _ C
 GAM2470 KCNA7 3' CCTCCTGTTTACCCCACATC 49895 CA CTCC
 GGTG GGGTGG CAGGAGG
 ||| ||||| |||||
 CTAC CCCATT GTCCTCC
 AC T__
 GAM2470 KCNJ5 5' CCTGAGCCCCCCTGCACCG 7971 T CC
 CGGTGCAGGG GGCTC AGG
 ||||| ||||| |||
 GCCACGTCCC CCGAG TCC
 C _
 GAM2470 LGMN 3' CCTCCTGGGGAGCCCCCGCTCC 20032 T A T _
 GG GC GGG GGCTCCC AGGAGG
 || || || ||||| |||||
 CC CG CCC CCGAGGG TCCTCC
 T _ _ G
 GAM2470 NLGN2 5' CCTCCCGGGAGCTGGTGGACC 89531 G GGG A
 GGT CA TGGCTCCC GGAGG
 ||| || ||||| |||||
 CCA GT GTCGAGGG CCTCC
 G G__ C
 GAM2470 OLFM1 3' CCTCCTGGAAGCCAAGGGCCC 27343 T AGGG C
 GG GC TGGCT CCAGGAGG
 || || ||||| |||||
 CC CG ACCGA GGTCCTCC
 _ GGA_ A
 GAM2470 RUNX3 3' CTCCCGACCCCTGCACC 16364 TGGC CCA
 GGTGCAGGG TC GGAG
 ||||| || |||||
 CCACGTCCC AG CCTC
 C__ C__
 GAM2470 SIAT8E 3' CCTCCTGGCCTGGCCCCACCG 60551 GCA T C__
 CGGT GGG GGCT CCAGGAGG
 ||| || ||||| |||||
 GCCA CCC CCGG GGTCCTCC
 _ _ TCC
 GAM2470 STIM1 5' CCCGCAGCCACCCTGCCCG 60776 T CCCA A
 CGG GCAGGGTGGCT GG G
 ||| ||||| |||
 GCC CGTCCCACCGA CC C
 _ CG__ _
 GAM2470 TK2 3' CCTCCTGAGAGCTGTTCCCCAC 17247 CA TG C
 CG CGGTG GGG GCTC CAGGAGG
 |||| || ||||| |||||
 GCCAC CTT CGAG GTCCTCC
 CC GT A
 GAM2470 ARHF 3' CCTCATCACAGCCACCCCCACC 39263 CA CCCAG
 GGTG GGGTGGCT GAGG
 ||| ||||| |||

CCAC CCCACCGA CTCC
 C_ CACTA
 GAM2470 ATP6V1B1 3' CCTCCCTCGCCACCCCAACC 9877 GCA TCCCA
 GGT GGGTGGC GGAGG
 ||| ||||| |||||
 CCA CCCACCG CCTCC
 AC_ CTC_
 GAM2470 BRD2 3' CCCCTAGACCACCCTGCCCC 18793 T C CC A
 GG GCAGGGTGG TC AGG GG
 || ||||| || ||| ||
 CC CGTCCCACC AG TCC CC
 C _ A_ _
 GAM2470 DKFZP434J193 3' CCCAGGCCACCCCCACC 71559 CA CCCA A
 GGTG GGGTGGCT GG G
 ||| ||||| |||
 CCAC CCCACCGG CC C
 C_ A_ _
 GAM2470 DKFZP434N1511 5' CCTCAGGAGCCACCCTGCAC 93057 CAG
 GTGCAGGGTGGCTCC GAGG
 ||||| |||||
 CACGTCCCACCGAGG CTCC
 A_
 GAM2470 DKFZp761G2113 3' CCTCCTGCCCACCCTGCCCC 70464 T CTCC
 GG GCAGGGTGG CAGGAGG
 || ||||| |||||
 CC CGTCCCACC GTCCTCC
 C C_
 GAM2470 EPB41L1 3' CCCCTTCCCCACCCACACC 71106 CA CTCCC A
 GGTG GGGTGG AGG GG
 ||| ||||| ||| ||
 CCAC CCCACC TCC CC
 AC CCCT_ _
 GAM2470 FLJ20320 3' TTTGGGAGCCACCCACACC 35429 CA
 GGTG GGGTGGCTCCAGG
 ||| ||||| |||||
 CCAC CCCACCGAGGGTTT
 AC
 GAM2470 FLJ22056 3' CTCCTGGACCGCCTGCAC 42832 G CTC
 GTGCAGG TGG CCAGGAG
 ||||| ||| |||||
 CACGTCC GCC GGTCTC
 _ A_
 GAM2470 FLJ23375 5' CCCCCAGGAGGCCGCACCCTGC 46947 _ TC A A
 GCC GGTGCAGGGT GGC CC GG GG
 ||||| ||| || |||
 CCGCGTCCCA CCG GG CC CC
 CG GA A C
 GAM2470 FLJ32934 3' CCTCCTGGACAATACCTGCTCC 58881 T GTGGCTC
 G CGG GCAGG CCAGGAGG
 ||| ||||| |||||

GCC CGTCC GGTCTCC
 T ATAACA_
 GAM2470 KIAA0161 3' CCTGAGCCACCCACC 29198 CA CC
 GGTG GGGTGGCTC AGG
 ||| ||||| ||
 CCAC CCCACCGAG TCC

 GAM2470 KIAA0222 5' CTCCTGGGAGCAGGCAC 28395 AGGGTG
 GTGC GCTCCCAGGAG
 ||| |||||
 CACG CGAGGGTCCTC
 GA____
 GAM2470 KIAA0731 5' CCCCCAGAACTCTGCTCC 67478 T GC CCA A
 GG GCAGGGTG TC GG GG
 || ||||| || ||
 CC CGTCTCAC AG CC CC
 T A_ AC_ _
 GAM2470 KIAA0884 3' CCTTTATAGCTACCCACACCG 70752 CA CCCA
 CGGTG GGGTGGCT GGAGG
 |||| ||||| ||||
 GCCAC CCCATCGA TTTCC
 AC TA____
 GAM2470 KIAA1025 3' CCTCCCGGGAGCCACTGTGACC 64675 G G A
 GGT CA GGTGGCTCCC GGAGG
 ||| || ||||| ||||
 CCA GT TCACCGAGGG CCTCC
 _ G C
 GAM2470 KIAA1691 3' GGCAGAGCCACCCACATC 94133 CA _____
 GGTG GGGTGGCTC CC
 |||| ||||| ||
 CTAC CCCACCGAG GG
 AC AC____
 GAM2470 MGC14386 5' CCTCCATTCTGGCCACCCTGCT 54326 T CCCA_
 CC GG GCAGGGTGGCT GGAGG
 || ||||| ||||
 CC CGTCCCACCGG CCTCC
 T TCTTA
 GAM2470 MGC4737 5' CTCCTGGAAACGCTGCCCCG 49641 T G GGCTC
 CGG GCAG GT CCAGGAG
 ||| ||| || |||||
 GCC CGTC CA GGTCTC
 _ G AA____
 GAM2470 PIB5PA 5' CCTCCTGGCCTAAGCCCCGCC 66651 T A GGCTC
 GG GC GGT CCAGGAG
 || || ||| |||||
 CC CG CCCG GGTCTCC
 _ C AATCC
 GAM2470 PYY 3' CTCCTGGGAGATCTGCCAACC 16040 _ GTGG
 GGT GCAGG CTCCCAGGAGG
 || |||| |||||

CCA CGTCT GAGGGTCCTCC
AC A__

GAM2470 SAST 5' CCTCCAGGAGCGCCTTCACC 63660 C G CA
GGTG AGGGTG CTCC GGAGG
||||| ||| |||
CCAC TTCCGC GAGG CCTCC
_ _ AC

GAM2470 SERF2 5' CCTCCACCCCCACCCTGCC 20489 T CTCCCA
GG GCAGGGTGG GGAGG
|| ||||| |||
CC CGTCCCACC CCTCC
_ CCCA__

GAM2470 SLC26A1 3' CTCCTGGGGACCCACAGC 42127 GCA GGC
GT GGGT TCCCAGGAG
|| ||| |||||
CG CCCA GGGGTCCTC
ACA _

GAM2470 SSB-4 3' CCTCCTGGAATCCTGCCACC 55962 _ GGCTC
GGTG CAGGGT CCAGGAGG
||||| |||||
CCAC GTCCTA GGTCCTCC
C AA__

GAM2470 TOR2A 3' CCTCCCCTCCACCCACACC 56184 CA CTCCCA
GGTG GGGTGG GGAGG
||||| |||
CCAC CCCACC CCTCC
AC TCC__

GAM2470 LOC115574 3' CCTCCCAGGAGCCCTTGCCAC 73850 _AG T CA
C GGTG C GG GGCTCC GGAGG
|||| | ||||| |||
CCAC G TC CCGAGG CCTCC
C GT _ AC

GAM2470 LOC125268 3' CTCCCAGCCCCTGCAC 76576 TG CCCA
GTGCAGGG GCT GGAG
||||| ||| |||
CACGTCCC CGA CCTC
_ C__

GAM2470 LOC126695 3' CCCCTATTGCCACCCTAACC 75956 GC TCCC A
GGT AGGGTGGC AGG GG
|| ||||| ||| ||
CCA TCCCACCG TCC CC
A_ TTA_ _

GAM2470 LOC128989 5' GGCAGAGCCGCCCTGCACC 75320 _____
GGTGCAGGGTGGCTC CC
||||||| ||
CCACGTCCCGCCGAG GG
AC__

GAM2470 LOC143392 3' CTCCCAGACCCCTGCATC 83853 TGG CCCA
GGTGCAGGG CT GGAG
||||| || |||

	CTACGTCCC GA CCTC		
	CA_ C__		
GAM2470 LOC146909 3'	CCTGTAGCCACCTGCACC 78767	G	CC
	GGTGCAGG TGGCT CAGG		
	CCACGTCC ACCGA GTCC		
	_ T_		
GAM2470 LOC147160 5'	CCTGCAGCCACCCTGCCCG 85070	T	CC
	CGG GCAGGGTGGCT CAGG		
	GCC CGTCCCACCGA GTCC		
	_ C_		
GAM2470 LOC150378 3'	CCCCTGGAATTGTCTGCACC 80556	G TG CTC	A
	GGTGCAG G G CCAGG GG		
	CCACGTC T T GGTCC CC		
	_ GT AA_ _		
GAM2470 LOC152756 3'	CCTCCTGGGTCATGCCATCCTA 87055	C	T__
	CACC GGTG AGGGTGGC CCCAGGAGG		
	CCAC TCCTACCG GGGTCCTCC		
	A TACT		
GAM2470 LOC200316 3'	CCTCCCCTCCATCCTGCACC 90175		CTCCCA
	GGTGCAGGGTGG GGAGG		
	CCACGTCCTACC CCTCC		
	TCC__		
GAM2470 LOC204970 3'	CCTCCTGGGCTGGACCCACACT 90960	CA	GGCT
	G CGGTG GGGT CCCAGGAGG		
	GTCAC CCCA GGGTCCTCC		
	A_ GGTC		
GAM2470 LOC205095 3'	CCTCCCGGGCCCCCCTCACC 92382	C T	CCA
	GGTG AGGG GGCTC GGAGG		
	CCAC TCCC CCGGG CCTCC		
	_ C C_		
GAM2470 LOC219918 5'	CCATCTGAGCCCCCTGCACC 93170	T	CC GA
	GGTGCAGGG GGCTC AG GG		
	CCACGTCCC CCGAG TC CC		
	_ _ TA		
GAM2470 LOC220071 5'	CCATCTGAGCCCCCTGCACC 95080	T	CC GA
	GGTGCAGGG GGCTC AG GG		
	CCACGTCCC CCGAG TC CC		
	_ _ TA		
GAM2470 LOC222662 3'	CCTCCCGGGAGCCAAATATCAC 94412	CAGGG	A
	GTG TGGCTCCC GGAGG		

CAC ACCGAGGG CCTCC
TATAA C
GAM2470 LOC51008 3' CTCCCAGCCCCCGCAGCC 32531 _ A T CCCA
GG TGC GGG GGCT GGAG
|| ||| ||| |||
CC ACG CCC CCGA CCTC
G _ _ C__
GAM2471 BCL2L2 5' CTCCCAGCTCCTGCACC 15759 GT CCCA
GGTGCAGG GGCT GGAG
||||||| ||| |||
CCACGTCC TCGA CCTC
_ C__
GAM2471 BLTR2 5' CTCCTGGAACCTAGCACC 39519 A GGCTC
GGTGC GGGT CCAGGAG
||||| ||| |||||
CCACG TCCA GGTCTC
A A__
GAM2471 BNC 3' CCTCCCCTCAGCCCTGCACC 9941 GGCTCCCA
GGTGCAGGGT GGAGG
||||||| |||
CCACGTCCCG CCTCC
ACTCC__
GAM2471 C6 5' CCTCCTGGGAGATTTTGGACC 96121 G GG
GGT CAGGGT CTCCCAGGAGG
||| ||||| |||||
CCA GTTTTA GAGGGTCCTCC
G _
GAM2471 CACNG3 5' CCCCCGGAGCCTGCACC 22565 GGGT CA A
GGTGCA GGCTCC GG G
||||| ||||| |||
CCACGT CCGAGG CC C
_ CC _
GAM2471 CAPN1 3' CTCCTACCACACCACACC 19008 CA _ CTCCC
GGTG GG GTGG AGGAG
|||| || ||| |||||
CCAC CC CACC TCCTC
A_ A A__
GAM2471 DRG2 3' CTCCCAGCCCCCTGCACTG 9130 T CCCA
CGGTGCAGGG GGCT GGAG
||||||| ||| |||
GTCACGTCCC CCGA CCTC
_ C__
GAM2471 GPC1 3' CCCAGCTCCCTGCACCG 10857 T CCCA A
CGGTGCAGGG GGCT GG G
||||||| ||| |||
GCCACGTCCC TCGA CC C
_ _ C
GAM2471 KCNA7 3' CCTCCTGTTTACCCACATC 49895 CA CTCC
GGTG GGGTGG CAGGAGG
||| ||||| |||||

CTAC CCCATT GTCCTCC
 AC T___
 GAM2471 KCNJ5 5' CCTGAGCCCCCCTGCACCG 7971 T CC
 CCGTGCAGGG GGCTC AGG
 ||||| |||| ||
 GCCACGTCCC CCGAG TCC
 C ___
 GAM2471 LGMN 3' CCTCCTGGGGAGCCCCCGCTCC 20032 T A T _
 GG GC GGG GGCTCCC AGGAGG
 || || || ||||| |||||
 CC CG CCC CCGAGGG TCCTCC
 T _ _ G
 GAM2471 NLGN2 5' CCTCCCGGGAGCTGGTGGACC 89531 G GGG A
 GGT CA TGGCTCCC GGAGG
 ||| || ||||| |||||
 CCA GT GTCGAGGG CCTCC
 G G_ C
 GAM2471 OLFM1 3' CCTCCTGGAAGCCAAGGGCCC 27343 T AGGG C
 GG GC TGGCT CCAGGAGG
 || || ||||| |||||
 CC CG ACCGA GGTCCTCC
 _ GGA_ A
 GAM2471 RUNX3 3' CTCCCGACCCCTGCACC 16364 TGGC CCA
 GGTGCAGGG TC GGAG
 ||||| || ||||
 CCACGTCCC AG CCTC
 C_ C_
 GAM2471 SIAT8E 3' CCTCCTGGCCTGGCCCCCACC 60551 GCA T C_
 CCGT GGG GGCT CCAGGAGG
 |||| |||| |||||
 GCCA CCC CCGG GGTCCTCC
 _ _ TCC
 GAM2471 STIM1 5' CCCGCAGCCACCCTGCCCCG 60776 T CCCA A
 CGG GCAGGGTGGCT GG G
 || ||||| || ||
 GCC CGTCCCACCGA CC C
 CG_ _
 GAM2471 TK2 3' CCTCCTGAGAGCTGTTCCCCAC 17247 CA TG C
 CG CCGTG GGG GCTC CAGGAGG
 |||| || ||||| |||||
 GCCAC CTT CGAG GTCCTCC
 CC GT A
 GAM2471 ARHF 3' CCTCATCACAGCCACCCCAACC 39263 CA CCCAG
 GGTG GGGTGGCT GAGG
 |||| ||||| ||||
 CCAC CCCACCGA CTCC
 C_ CACTA
 GAM2471 ATP6V1B1 3' CCTCCCTCGCCACCCCAACC 9877 GCA TCCCA
 GGT GGGTGGC GGAGG
 || ||||| ||||

CCA CCCACCG CCTCC
 AC_ CTC_
 GAM2471 BRD2 3' CCCCTAGACCACCCTGCCCC 18793 T C CC A
 GG GCAGGGTGG TC AGG GG
 || ||||| || ||| ||
 CC CGTCCCACC AG TCC CC
 C _ A_ _
 GAM2471 DKFZP434J193 3' CCCAGGCCACCCCCACC 71559 CA CCCA A
 GGTG GGGTGGCT GG G
 ||| ||||| ||
 CCAC CCCACCGG CC C
 C_ A_ _
 GAM2471 DKFZP434N1511 5' CCTCAGGAGCCACCCTGCAC 93057 CAG
 GTGCAGGGTGGCTCC GAGG
 ||||| ||||| ||||
 CACGTCCCACCGAGG CTCC
 A_
 GAM2471 DKFZp761G2113 3' CCTCCTGCCCACCCTGCCCC 70464 T CTCC
 GG GCAGGGTGG CAGGAGG
 || ||||| |||||
 CC CGTCCCACC GTCCTCC
 C C_
 GAM2471 EPB41L1 3' CCCCTTCCCCACCCCACACC 71106 CA CTCCC A
 GGTG GGGTGG AGG GG
 ||| |||| ||| ||
 CCAC CCCACC TCC CC
 AC CCCT_ _
 GAM2471 FLJ20320 3' TTTGGGAGCCACCCCACACC 35429 CA
 GGTG GGGTGGCTCCAGG
 ||| ||||| |||||
 CCAC CCCACCGAGGGTTT
 AC
 GAM2471 FLJ22056 3' CTCCTGGACCGCCTGCAC 42832 G CTC
 GTGCAGG TGG CCAGGAG
 ||||| || |||||
 CACGTCC GCC GGTCCCTC
 _ A_
 GAM2471 FLJ23375 5' CCCCCAGGAGGCCGACCCCTGC 46947 _ TC A A
 GCC GGTGCAGGGT GGC CC GG GG
 ||||| || ||| ||
 CCGCGTCCCA CCG GG CC CC
 CG GA A C
 GAM2471 FLJ32934 3' CCTCCTGGACAATACCTGCTCC 58881 T GTGGCTC
 G CGG GCAGG CCAGGAGG
 || |||| |||||
 GCC CGTCC GGTCCCTCC
 T ATAACA_
 GAM2471 KIAA0161 3' CCTGAGCCACCCCACC 29198 CA CC
 GGTG GGGTGGCTC AGG
 ||| ||||| |||

CCAC CCCACCGAG TCC

GAM2471 KIAA0222 5' CTCCTGGGAGCAGGCAC 28395 AGGGTG
GTGC GCTCCCAGGAG
|||| ||||||||
CACG CGAGGGTCCTC
GA____

GAM2471 KIAA0731 5' CCCCCAGAACTCTGCTCC 67478 T GC CCA A
GG GCAGGGTG TC GG GG
|| |||||| || ||||
CC CGTCTCAC AG CC CC
T A_ AC_ _

GAM2471 KIAA0884 3' CCTTTATAGCTACCCACACCG 70752 CA CCCA
CGGTG GGGTGGCT GGAGG
|||| |||||| ||||
GCCAC CCCATCGA TTTCC
AC TA_

GAM2471 KIAA1025 3' CCTCCCGGGAGCCACTGTGACC 64675 G G A
GGT CA GGTGGCTCCC GGAGG
||| || |||||| ||||
CCA GT TCACCGAGGG CCTCC
_ G C

GAM2471 KIAA1691 3' GGCAGAGCCACCCACATC 94133 CA _____
GGTG GGGTGGCTC CC
|||| |||||| ||
CTAC CCCACCGAG GG
AC AC_

GAM2471 MGC14386 5' CCTCCATTCTGGCCACCCTGCT 54326 T CCCA_
CC GG GCAGGGTGGCT GGAGG
|| |||||| ||||
CC CGTCCCACCGG CCTCC
T TCTTA

GAM2471 MGC4737 5' CTCCTGGAAACGCTGCCCCG 49641 T G GGCTC
CGG GCAG GT CCAGGAG
||| ||| || |||||
GCC CGTC CA GGTCTC
_ G AA_

GAM2471 PIB5PA 5' CCTCCTGGCCTAAGCCCCGCC 66651 T A GGCTC
GG GC GGT CCAGGAG
|| |||| |||||
CC CG CCG GGTCTCC
_ C AATCC

GAM2471 PYY 3' CTCCTGGGAGATCTGCCAACC 16040 _ GTGG
GGT GCAG CTCCCAGGAGG
|| |||| |||||||
CCA CGTCT GAGGGTCCTCC
AC A_

GAM2471 SAST 5' CCTCCAGGAGCGCCTTCACC 63660 C G CA
GGTG AGGGTG CTCC GGAGG
|||| |||| ||||

CCAC TTCCGC GAGG CCTCC
 _ _ AC
 GAM2471 SERF2 5' CCTCCACCCCCACCCTGCCC 20489 T CTCCCA
 GG GCAGGGTGG GGAGG
 || ||||| ||||
 CC CGTCCCACC CCTCC
 _ CCCA_
 GAM2471 SLC26A1 3' CTCCTGGGGACCCACAGC 42127 GCA GGC
 GT GGGT TCCCAGGAG
 || ||| |||||
 CG CCCA GGGGTCCTC
 ACA _
 GAM2471 SSB-4 3' CCTCCTGGAAATCCTGCCACC 55962 _ GGCTC
 GGTG CAGGGT CCAGGAGG
 ||| ||||| |||||
 CCAC GTCCTA GGTCCTCC
 C AA_
 GAM2471 TOR2A 3' CCTCCCCTCCACCCACACC 56184 CA CTCCCA
 GGTG GGGTGG GGAGG
 ||| ||||| ||||
 CCAC CCCACC CCTCC
 AC TCC_
 GAM2471 LOC115574 3' CCTCCCAGGAGCCCTTGCCAC 73850 _AG T CA
 C GGTG C GG GGCTCC GGAGG
 |||| | || ||||| ||||
 CCAC G TC CCGAGG CCTCC
 C GT _ AC
 GAM2471 LOC125268 3' CTCCCAGCCCCTGCAC 76576 TG CCCA
 GTGCAGGG GCT GGAG
 ||||| ||| |||
 CACGTCCC CGA CCTC
 _ C_
 GAM2471 LOC126695 3' CCCCTATTGCCACCCTAACC 75956 GC TCCC A
 GGT AGGGTGGC AGG GG
 ||| ||||| ||| ||
 CCA TCCCACCG TCC CC
 A_ TTA_ _
 GAM2471 LOC128989 5' GGCAGAGCCGCCCTGCACC 75320 _____
 GGTGCAGGGTGGCTC CC
 ||||| ||||| ||
 CCACGTCCCGCCGAG GG
 AC_
 GAM2471 LOC143392 3' CTCCCAGACCCCTGCATC 83853 TGG CCCA
 GGTGCAGGG CT GGAG
 ||||| || |||
 CTACGTCCC GA CCTC
 CA_ C_
 GAM2471 LOC146909 3' CCTGTAGCCACCTGCACC 78767 G CC
 GGTGCAGG TGGCT CAGG
 ||||| ||||| |||

CCACGTCC ACCGA GTCC
 _ T_
 GAM2471 LOC147160 5' CCTGCAGCCACCCTGCCCCG 85070 T CC
 CGG GCAGGGTGGCT CAGG
 ||| ||||| |||
 GCC CGTCCCACCGA GTCC
 _ C_
 GAM2471 LOC150378 3' CCCCTGGAATTGTCTGCACC 80556 G TG CTC A
 GGTGCAG G G CCAGG GG
 ||||| | | |||||
 CCACGTC T T GGTCC CC
 _ GT AA _
 GAM2471 LOC152756 3' CCTCCTGGGTCATGCCATCCTA 87055 C T____
 CACC GGTG AGGGTGGC CCCAGGAGG
 ||| ||||| |||||
 CCAC TCCTACCG GGGTCCTCC
 A TACT
 GAM2471 LOC200316 3' CCTCCCCTCCATCCTGCACC 90175 CTCCCA
 GGTGCAGGGTGG GGAGG
 ||||| |||||
 CCACGTCCTACC CCTCC
 TCC____
 GAM2471 LOC204970 3' CCTCCTGGGCTGGACCCACACT 90960 CA GGCT
 G CGGTG GGGT CCCAGGAGG
 |||| ||| |||||
 GTCAC CCCA GGGTCCTCC
 A_ GGTC
 GAM2471 LOC205095 3' CCTCCCGGGCCCCCCTCACC 92382 C T CCA
 GGTG AGGG GGCTC GGAGG
 |||| ||| ||||| |||||
 CCAC TCCC CCGGG CCTCC
 _ C C_
 GAM2471 LOC219918 5' CCATCTGAGCCCCCTGCACC 93170 T CC GA
 GGTGCAGGG GGCTC AG GG
 ||||| ||||| || ||
 CCACGTCCC CCGAG TC CC
 _ TA
 GAM2471 LOC220071 5' CCATCTGAGCCCCCTGCACC 95080 T CC GA
 GGTGCAGGG GGCTC AG GG
 ||||| ||||| || ||
 CCACGTCCC CCGAG TC CC
 _ TA
 GAM2471 LOC222662 3' CCTCCCGGGAGCCAAATATCAC 94412 CAGGG A
 GTG TGGCTCCC GGAGG
 || ||||| |||||
 CAC ACCGAGGG CCTCC
 TATAA C
 GAM2471 LOC51008 3' CTCCCAGCCCCCGCAGCC 32531 _ A T CCCA
 GG TGC GGG GGCT GGAG
 || ||| ||| |||||

				CC ACG CCC CCGA CCTC			
				G _ _ C__			
GAM2472	DLEC1	3'	CATCTGGCCCTCCCTTG	24716	A	A	C
			CAAGG AGGGC GG GTG				
			GTTCC TCCCG TC TAC				
			C G _				
GAM2472	DLEC1	3'	CATCTGGCCCTCCCTTG	24728	A	A	C
			CAAGG AGGGC GG GTG				
			GTTCC TCCCG TC TAC				
			C G _				
GAM2472	PIP5K1A	3'	TATCCCACCCTGCCTTGATA	14520	A	CA	C
			TATCAAGG AGGG GG GTG				
			ATAGTTCC TCCC CC TAT				
			G A_ C				
GAM2472	SOX11	3'	ACCCACCCCCCTTG GTA	13308	AA	CA	C
			TATCAAGG GGG GG GT				
			ATGGTTCC CCC CC CA				
			CC A_ _				
GAM2472	CHL1	3'	TGTTACCTTTCCTCAATA	22768	CA		CA
			TAT AGGAAGGG GGCG				
			ATA TCCTTTCC TTGT				
			AC A_				
GAM2472	EPB41L1	3'	CATTCTGCCCTTCCCTGA	71104	A		C
			TCA GGAAGGGCAGG GTG				
			AGT CCTTCCCGTCT TAC				
			C _				
GAM2472	FLJ00060	3'	CATACCCCCTGCCCTCCTCTGA	61741	_	A	CGTG
			TCA AGGA GGGCAGG ATG				
			AGT TCCT CCCGTCC TAC				
			C _ CCCA				
GAM2472	FLJ10898	5'	CACCACAGCCCTTTCTCAATA	60126	CA		AGGC
			TAT AGGAAGGGC GTG				
			ATA TCTTTCCCG CAC				
			AC ACAC				
GAM2472	FLJ22557	3'	ATCATCCCATCCTTAATA	45581	C	A	CAGGC
			TAT AAGGA GGG GTGAT				
			ATA TTCCT CCC TACTA				
			A A _				
GAM2472	KIAA0574	3'	CATCCCCTGCCCTCCCCTGA	69808	A	A	CGT
			TCA GG AGGGCAGG GATG				

AGT CC TCCCGTCC CTAC
 C C C__
 GAM2472 KIAA0632 3' CACCTCAGAAACCCTTCCTTGA 32071 CA__ C
 TCAAGGAAGGG GG GTG
 ||||| ||||
 AGTTCCTTCCC CT CAC
 AAAGA C
 GAM2472 KIAA1045 3' CATCACATGTCCTTCC 71599 GGC
 GGAAGGGCA GTGATG
 ||||| ||||
 CCTTCCTGT CACTAC
 A__
 GAM2472 KIAA1354 5' CAGTGA CTGCCTTCCTTGATA 61572 A G _
 TATCAAGG AGGGCAG CG TG
 ||||| ||||| || ||
 ATAGTTCC TTCCGTC GT AC
 C A G
 GAM2472 MGC20460 5' CACCGCCTCCTACCCTTCTT 54901 C__ _
 AGGAAGGG AGGCG TG
 ||||| |||| ||
 TTCTTCCC TCCGC AC
 ATCC C
 GAM2472 LOC158476 3' CACGCCCGCCCCCCCCATTGA 88186 _ AA_ A
 TCAA GG GGGC GGC GTG
 ||| || ||| |||||
 AGTT CC CCG CCGCAC
 A CCC C
 GAM2472 LOC90459 3' CACACCCGCCTAATTTTGT 63550 A_ A C
 CAAGGA GGGC GG GTG
 ||||| ||| || |||
 GTTTT TCCG CC CAC
 AA C A
 GAM2473 ABCC3 3' CCCAGCTGCTGCGCACGGC 39613 G _ CAA
 GT GTG GCAGCAGC GG
 || ||| ||||| ||
 CG CAC CGTCGTCG CC
 G G AC_
 GAM2473 ARF3 3' CCCTGGCTGCTAAGCCCT 9774 T _ A
 GG GGC AGCAGCCA GG
 || ||| ||||| ||
 TC CCG TCGTCGGT CC
 _ AA C
 GAM2473 CBFA2T2 3' CCTTGGCTGCTGCCCGC 18709 TG
 GTGG GCAGCAGCCAAGG
 ||| ||||| |||||
 CGCC CGTCGTCGGTTCC
 _
 GAM2473 DUOX2 3' CCCTGGCTGCTGCTTCCA 26864 T A
 TGG GGCAGCAGCCA GG
 ||| ||||| ||| ||

			ACC TCGTCGTCGGT CC		
			T C		
GAM2473	E2F2	5'	CCCTGGCAGTGCCACCAC 15838	G A A	
			GTGGTGGCA C GCCA GG		
			CACCACCGT G CGGT CC		
			_ A C		
GAM2473	EFNA1	3'	CCTGGGAACCACTCCCACCACA 16663	C CAG_ A	
			TGTGGTGG AG CC AGG		
			ACACCACC TC GG TCC		
			C ACCAA G		
GAM2473	EPHB4	3'	CCCAGCTGCTGCCTTCATA 16707	T CAA	
			TGTGG GGCAGCAGC GG		
			ATACT CCGTCGTCG CC		
			T AC_		
GAM2473	FMR2	5'	CCCCGGCTGCCGCGCCGC 10687	G A AA	
			GTGGTG C GCAGCC GG		
			CGCCGC G CGTCGG CC		
			_ C CC		
GAM2473	FTHL17	5'	GCCTCAGCTGCTGCCCTCGCTA 49940	CA _	
			CCGCA TGTGGT GGCAGCAGC AGG C		
			ACGCCA CCGTCGTCG TCC G		
			TCGCTC AC _		
GAM2473	FXD2	3'	CCTCGGCGGTGCCACCCA 9845	T GCA A	
			TG GGTGGCA GCC AGG		
			AC CCACCGT CGG TCC		
			_ GG_ C		
GAM2473	GARP	3'	CCTTGGCTGCTGAGCCA 19777	GG	
			TGGT CAGCAGCCAAGG		
			ACCG GTCGTCGGTTCC		
			A_		
GAM2473	GAS7	3'	CCCGGGCCGCCACCACA 20845	CA A AA	
			TGTGGTGG GC GCC GG		
			ACACCACC CG CGG CC		
			_ C GC		
GAM2473	GSBS	3'	CCTTGGCTGATGATACCA 92731	G G	
			TGGTG CA CAGCCAAGG		
			ACCAT GT GTCGGTTCC		
			A A		
GAM2473	HHLA1	5'	GCCTTAAGTATGATGATCCAC 20337	G CC _	
			CACA TGTGGTGG CA CAG AAGG C		

ACACCACC GT GTC TTCC G
 TTACA A AA ____
 GAM2473 HLA-DQA1 3' CCTTGGCATTGCCACCCA 98031 T CA
 TG GGTGGCAG GCCAAGG
 || ||||| |||||
 AC CCACCGTT CGGTTCC
 _ A_
 GAM2473 HR 3' CTCCGTTTCTACCACCGCA 37910 C C CA
 TGTGGTGG AG AGC AG
 ||||| || ||| ||
 ACGCCACC TC TTG TC
 A T CC
 GAM2473 IL1F5 3' CCTCTCTCTCTGCCACCCA 25376 T C CCA_
 TG GGTGGCAG AG AGG
 || ||||| || |||
 AC CCACCGTC TC TCC
 _ _ TCTC
 GAM2473 ITPKB 3' CCTTGGGGCTTGCCACCCA 11063 T _ AG
 TG GGTGGCA GC CCAAGG
 || ||||| || |||||
 AC CCACCGT CG GGTTC
 _ T G_
 GAM2473 KCNA7 3' CCTCCTGTTTACCCACACA 49894 T C_ CCA
 TGTGG GG AGCAG AGG
 |||| || |||| |||
 ACACC CC TTGTC TCC
 _ AT C_
 GAM2473 L1CAM 3' CCTTCGGTACCCACCACA 43988 CAGCA _
 TGTGGTGG GCC AAGG
 ||||| || |||||
 ACACCACC TGG TTCC
 CA__ C
 GAM2473 LTBP1 3' CCTTGGCTACTGTTTTTC 7120 T_ C
 GG GGCAG AGCCAAGG
 || |||| |||||
 CT TTGTC TCGGTTCC
 TT A
 GAM2473 MAPT 5' CCTTCTGCCGCCGCCACCACA 34176 A A C_
 TGTGGTGGC GC GC AAGG
 ||||| || || |||
 ACACCACCG CG CG TTCC
 C C TC
 GAM2473 MARS 3' CCTTGGTCAGCCACCTCA 96564 T AGCA
 TG GGTGGC GCCAAGG
 || |||| |||||
 AC CCACCG TGGTTCC
 T AC_
 GAM2473 MSR1 3' CCTCAGTTCTCTGCCACCCA 11703 T C_ CA
 TG GGTGGCAG AGC AGG
 || ||||| || |||

			AC CCACCGTC TTG TCC		
			— TC AC		
GAM2473	NFE2L1	5'	CCTTGGCCTTGGCTCCACA 13628	T	AGCA
			TGTGG GGC GCCAAGG		
			ACACC TCG CGGTTCC		
			— GTTC		
GAM2473	NORE1	3'	CCCAGGCTGTGCCCCACCACA 49524	CA_	AA
			TGTGGTGG GCAGCC GG		
			ACACCACC TGTCGG CC		
			CCG AC		
GAM2473	OAS3	3'	CCCTGGCTGCTGCCACACAC 21650	—	A
			GTG GTGGCAGCAGCCA GG		
			CAC CACCGTCGTCGGT CC		
			A C		
GAM2473	OGDH	3'	CCTCGCTGTGCCACCAC 92747	G	CA
			GTGGTGGCA CAGC AGG		
			CACCACCGT GTCG TCC		
			— C_		
GAM2473	PCDHB4	3'	CCTCTTGTGACCACCACA 38941	CA	CCA
			TGTGGTGG GCAG AGG		
			ACACCACC TGTT TCC		
			AG C_		
GAM2473	PFKL	5'	CCTCAGCTGCTGCCTGCCA 12057	—	CA
			TGGT GGCAGCAGC AGG		
			ACCG CCGTCGTCG TCC		
			T AC		
GAM2473	PIM2	3'	CCTCCTACTACCACCACA 60652	C C	CCA
			TGTGGTGG AG AG AGG		
			ACACCACC TC TC TCC		
			A A C_		
GAM2473	PLA2G4B	3'	CCCTGGCTGCTGAGTTGCA 18692	GG GG	A
			TGT T CAGCAGCCA GG		
			ACG G GTCGTCGGT CC		
			TT A_ C		
GAM2473	PTPRA	5'	CCCCGGCCGCTGCCGCCAT 55950	A	AA
			GTGGTGGCAGC GCC GG		
			TACCGCCGTCG CGG CC		
			C CC		
GAM2473	RAG1	3'	CCTTCTTCTTTCCACCACA 6544	C_ C	CC
			TGTGGTGG AG AG AAGG		

ACACCACC TC TC TTCC
 TT T ____
 GAM2473 RNPEPL1 3' CCTATGGTGACCGCCACA 37215 CAGCA _
 TGTGGTGG GCCA AGG
 ||||| ||| ||
 ACACCGCC TGGT TCC
 AG__ A
 GAM2473 SCAP1 3' CCTACTTCTGCCACCCCA 14946 T C CCA
 TG GGTGGCAG AG AGG
 || ||||| || ||
 AC CCACCGTC TC TCC
 C T A__
 GAM2473 SLC12A7 3' CCTTGGCTGGATTTACCCA 22738 T CAG
 TG GGTGG CAGCCAAGG
 || ||| |||||
 AC CCATT GTCGGTTCC
 _ TAG
 GAM2473 SLC25A1 3' CCTCGGCCTGGCTTCACCGCA 21117 C A__ A
 TGTGGTGG AGC GCC AGG
 ||||| || ||| ||
 ACGCCACT TCG CGG TCC
 _ GTC C
 GAM2473 SLN 3' CCTGATCTGTCTCACCACA 13236 CA CCA
 TGTGGTGG GCAG AGG
 ||||| ||| ||
 ACACCACT TGTC TCC
 C_ TAG
 GAM2473 SQSTM1 3' CCTTGGCTGCTCACTGT 15327 TG GC
 G GTG AGCAGCCAAGG
 | ||| |||||
 T CAC TCGTCGGTTCC
 GT _
 GAM2473 STAT6 3' CCCAGGTGTACCCACCACA 13450 CA G AA
 TGTGGTGG GCA CC GG
 ||||| ||| || ||
 ACACCACC TGT GG CC
 CA _ AC
 GAM2473 SUFU 3' CCCTGGGCTGCCACCA 32933 AG A
 TGGTGGCAGC CCA GG
 ||||| ||| ||
 ACCACCGTCG GGT CC
 _ C
 GAM2473 TGFA 3' CCTGGTAAGCTGCCACACA 13706 G A_ A
 TGTG TGGCAGC GCCA GG
 ||| ||||| ||| ||
 ACAC ACCGTCG TGGT CC
 _ AA _
 GAM2473 TRIM14 3' CCTCTCTGCTGCCAGCACA 29509 G CCA
 TGTG TGGCAGCAG AGG
 ||| ||||| |||

		ACAC ACCGTCGTC TCC	
		G TC_	
GAM2473 TSN	5'	CCTTGGCCGCCCTTGCTACA 17299	TG CA A
		TGTGG G GC GCCAAGG	
		ACATC T CG CGGTTCC	
		GT CC C	
GAM2473 WHSC1	3'	CCTCAGCGTTACCGCCACA 24661	C A CA
		TGTGGTGG AGC GC AGG	
		ACACCGCC TTG CG TCC	
		A _ AC	
GAM2473 WHSC1	3'	CCTCAGCGTTACCGCCACA 24662	C A CA
		TGTGGTGG AGC GC AGG	
		ACACCGCC TTG CG TCC	
		A _ AC	
GAM2473 WHSC1	3'	CCTCAGCGTTACCGCCACA 24663	C A CA
		TGTGGTGG AGC GC AGG	
		ACACCGCC TTG CG TCC	
		A _ AC	
GAM2473 WHSC1	3'	CCTCAGCGTTACCGCCACA 24664	C A CA
		TGTGGTGG AGC GC AGG	
		ACACCGCC TTG CG TCC	
		A _ AC	
GAM2473 ZNF289	3'	CCTTCTGTCCTGCCCCACACA 65927	T _ CC
		TGTGG GGCAG CAG AAGG	
		ACACC CCGTC GTC TTCC	
		C CT _	
GAM2473 ALDH5A1	3'	CCCTGGCTCCCCACCACA 8414	CAGC A
		TGTGGTGG AGCCA GG	
		ACACCACC TCGGT CC	
		CC_ C	
GAM2473 ASB13	3'	CCCAGGTGCAGGCCACCAC 45544	A_ G AA
		GTGGTGGC GCA CC GG	
		CACCACCG CGT GG CC	
		GA _ AC	
GAM2473 BCAN	3'	CCCTGCGCTCCCGCCACCACA 41968	AGC _ A
		TGTGGTGGC AGC CA GG	
		ACACCACCG TCG GT CC	
		CCC C C	
GAM2473 BCL2L1	3'	CCTTCTCTGCTCCACCACA 57592	C CC
		TGTGGTGG AGCAG AAGG	

ACACCACC TCGTC TTCC
 _ TC
 GAM2473 C20orf173 5' GCCTCAACTGCTCCTCCTGCCA 55916 _____ CCA ____
 CCACA TGTGGTGGCA GCAG AGG C
 ||||| ||| ||| |
 ACACCACCGT CGTC TCC G
 CCTCCT AAC ____
 GAM2473 C21orf7 3' CCTTGTCTACCTATCACCACA 39747 GC C_ C_
 TGTGGTG AG AG CAAGG
 ||||| || || ||||
 ACACCAC TC TC GTTCC
 TA CA TT
 GAM2473 CSEN 3' CCTCAGGAGAGCATCACCACCA 26458 CA__ AG_ A_
 CA TGTGGTGG GC CC AGG
 ||||| || || |||
 ACACCACC CG GG TCC
 ACTA AGA AC
 GAM2473 CX46.6 3' CCCTGGCTTGGTCACCAC 40312 AGC A
 GTGGTGGC AGCCA GG
 ||||| ||||| ||
 CACCACTG TCGGT CC
 GT_ C
 GAM2473 DKFZP564L2423 3' CCTCCTGCTGCCACCAC 63021 CCA
 GTGGTGGCAGCAG AGG
 ||||| ||||| |||
 CACCACCGTCGTC TCC
 C_
 GAM2473 DKFZP564O0423 3' CCTCAGCCCCTCTGCCACCAC 93347 CA__ CA
 GTGGTGGCAG GC AGG
 ||||| || |||
 CACCACCGTC CG TCC
 TCCC AC
 GAM2473 DKFZP566J091 3' CCTTAAGTCTGCCCTTCCA 48862 T__ CC
 TGG GGCAGCAG AAGG
 || ||||| ||||
 ACC CCGTCGTC TTCC
 TTC AA
 GAM2473 FBXO24 3' CCCTGGCCGTGTGTCCCCA 25148 T _ A A
 TGG GGCA GC GCCA GG
 || |||| || |||| ||
 ACC CTGT TG CGGT CC
 C G C C
 GAM2473 FLJ10539 3' CCCTGCGTAAACTATCACCAC 36761 GC CA__ _ A
 A TGTGGTG AG GC CA GG
 ||||| || || || ||
 ACACCAC TC TG GT CC
 TA AAAA C C
 GAM2473 FLJ10851 3' CCCTGGCTGCTGCTCGCC 37313 _ A
 GGTG GCAGCAGCCA GG
 |||| ||||| ||

			CCGC CGTCGTCGGT CC			
			T C			
GAM2473	FLJ10900	3'	CCCTGGCTGCTTTACACA 66205	G C	A	
			TGTG TGG AGCAGCCA GG			
			ACAC ATT TCGTCGGT CC			
			— — C			
GAM2473	FLJ12783	3'	CCTTGACTACCCATCATA 49485	CAGC	C	
			TGTGGTGG AG CAAGG			
			ATACTACC TC GTTCC			
			CA__ A			
GAM2473	FLJ14810	5'	CCCCGGCTGCTGGCCCG 52699	T GG	AA	
			TG GGT CAGCAGCC GG			
			GC CCG GTCGTCGG CC			
			— — CC			
GAM2473	FLJ20297	5'	CCTATGGCCTCCACCACA 36077	C CA	_	
			TGTGGTGG AG GCCA AGG			
			ACACCACC TC CGGT TCC			
			— — A			
GAM2473	FLJ20432	5'	CCTCTAGCTGCCACCA 35620	_ CCA		
			TGGTGGCAGC AG AGG			
			ACCACCGTCG TC TCC			
			A _			
GAM2473	FLJ20716	3'	CCTTGGCAGATTGCCACCCCA 36039	T	CA_	
			TG GGTGGCAG GCCAAGG			
			AC CCACCGTT CGGTTCC			
			C AGA			
GAM2473	FLJ22479	3'	CCCTGGCTGCTGGCTACCG 46605	_	A	
			TGGTGGC AGCAGCCA GG			
			GCCATCG TCGTCGGT CC			
			G C			
GAM2473	FLJ22795	3'	CCTTGGCTGAATAGCACA 47633	G GCAG		
			TGTG TG CAGCCAAGG			
			ACAC AT GTCGGTTCC			
			G AA_			
GAM2473	FLJ23093	3'	CCTCAGTGTAGCCACCAC 45323	A G CA		
			GTGGTGGC GCA C AGG			
			CACCACCG TGT G TCC			
			A _ AC			
GAM2473	GPR9	3'	CCTTAGCTGCCAAGCCCCA 9485	T A_	C	
			TGG GGC GCAGC AAGG			

		ACC CCG CGTCG TTCC	
		_ AAC A	
GAM2473 HBP1	3'	CCTCTAGTAACCACCACA 25319	CA _ CCA
		TGTGGTGG GC AG AGG	
		ACACCACC TG TC TCC	
		AA A _	
GAM2473 HEYL	3'	CCTTGGGCCACACCATCACA 28125	CA__ AG
		TGTGGTGG GC CCAAGG	
		ACACTACC CG GGTTC	
		ACAC _	
GAM2473 HIF3A	3'	CCTCAGCTGTCTGCCACCA 42654	_ CA
		TGGTGGCAG CAGC AGG	
		ACCACCGTC GTCG TCC	
		T AC	
GAM2473 HSPC065	3'	CTAGGCAGCCACCACCACA 27149	CA A A
		TGTGGTGG GC GCC AG	
		ACACCACC CG CGG TC	
		AC A A	
GAM2473 IL22R	3'	CCTTGGCTGTCAATCCCA 41470	T CA_
		TGG GG GCAGCCAAGG	
		ACC CT TGTCGGTTCC	
		_ AAC	
GAM2473 KCNS1	5'	CCCGGGAGGTGCCACCACA 11192	G AG AA
		TGTGGTGGCA C CC GG	
		ACACCACCGT G GG CC	
		_ GA GC	
GAM2473 KIAA0215	5'	CCTCAGCCGCCGCCGCCGC 29081	A A CA
		GTGGTGGC GC GC AGG	
		CGCCGCCG CG CG TCC	
		C C AC	
GAM2473 KIAA0229	3'	CCTGGGCCTGCCACCAC 94025	CA A
		GTGGTGGCAG GCC AGG	
		CACCACCGTC CGG TCC	
		_ G	
GAM2473 KIAA0255	5'	CCTCGGCTGCTGCCTTCGC 29132	T A
		GTGG GGCAGCAGCC AGG	
		CGCT CCGTCGTCGG TCC	
		T C	
GAM2473 KIAA0280	5'	CCTCAGCCGCCGCCGCCGC 93294	A A CA
		GTGGTGGC GC GC AGG	

		CGCCGCCG CG CG TCC		
		C C AC		
GAM2473	KIAA0370	3' CCTTGGCTTCTCCCACCGCA 73583	C C	
		TGTGGTGG AG AGCCAAGG		
		ACGCCACC TC TCGGTTCC		
		C T		
GAM2473	KIAA0397	3' CCTCGCTCCTGCCACCCCA 62348	T C CA	
		TG GGTGGCAG AGC AGG		
		AC CCACCGTC TCG TCC		
		C C C_		
GAM2473	KIAA0700	3' CCTGGGGCTCAGCCCCACCACA 72518	CA _ A_	
		TGTGGTGG GC AGCC AGG		
		ACACCACC CG TCGG TCC		
		C_ AC GG		
GAM2473	KIAA0841	3' CCCTGGCTGCTGTTTCCCA 71892	T TG A	
		TG GG GCAGCAGCCA GG		
		AC CC TGTCGTCGGT CC		
		_ TT C		
GAM2473	KIAA0953	3' CTTTGACTGTTGCCACCACA 67326	C	
		TGTGGTGGCAGCAG CAAGG		
		ACACCACCGTTGTC GTTTC		
		A		
GAM2473	KIAA0970	3' CCATAACTGCTGCCACCAC 30617	CCAA	
		GTGGTGGCAGCAG GG		
		CACCACCGTCGTC CC		
		AATA		
GAM2473	KIAA1130	3' CCTAGCTCCTGACAACCACCAC 63084	___ C CA	
A		TGTGGTGG CAG AGC AGG		
		ACACCACC GTC TCG TCC		
		AACA C A_		
GAM2473	KIAA1297	3' CCTAGCTCCTGCTGCCCCACA 72635	T CCA_	
		TGTGG GGCAGCAG AGG		
		ACACC CCGTCGTC TCC		
		C CTCGA		
GAM2473	KIAA1377	5' CCTCAGCTGCCATCGCCGCTAC 67758	A_ CA	
A		TGTGGTGGC GCAGC AGG		
		ACATCGCCG CGTCG TCC		
		CTAC AC		
GAM2473	KIAA1576	5' CCAGCGCCGCAGCCACCGCA 66491	A A CAA	
		TGTGGTGGC GC GC GG		

ACGCCACCG CG CG CC
 A C CGA
 GAM2473 KIAA1607 3' CCCTGGCCAGCATCACCACA 64536 CA A_ A
 TGTGGTGG GC GCCA GG
 ||||| || ||||
 ACACCACT CG CGGT CC
 A_ AC C
 GAM2473 KIAA1691 3' CCCTGGCCCATTGCCACCCA 94126 T _ CA_ A
 TG GGTGG CAG GCCA GG
 || |||| || ||||
 AC CCACC GTT CGGT CC
 _ C ACC C
 GAM2473 KIAA1735 3' CCCTGGCTGCTTCACTCA 89003 T C A
 G GGTGG AGCAGCCA GG
 | |||| ||||| ||
 A TCACT TCGTCGGT CC
 C _ C
 GAM2473 KIAA1881 3' CCTCCAGCTGCCCACCACA 97084 CA CA_
 TGTGGTGG GCAGC AGG
 ||||| |||| ||
 ACACCACC CGTCG TCC
 _ ACC
 GAM2473 KLF12 3' CCTTAAAGGTCACCTACCACA 33278 CAGCA _
 TGTGGTGG GCC AAGG
 ||||| || ||||
 ACACCATC TGG TTCC
 CAC_ AAA
 GAM2473 KRT6IRS 3' CCTTGGCTGTGGTCCCCCA 54228 T T A
 TG GG GGC GCAGCCAAGG
 || || || |||||
 AC CC CTG TGTCGGTTCC
 _ C G
 GAM2473 MAP3K3 5' CCTTAGCCACCGCCGCGCCAT 11537 A A_ C
 GTGGTGGC GC GC AAGG
 ||||| || ||||
 TACCGCCG CG CG TTCC
 C CCAC A
 GAM2473 MGC10981 3' CCTAGCTGGATCTACTACA 51985 CAG CA
 TGTGGTGG CAGC AGG
 ||||| |||| ||
 ACATCATC GTCG TCC
 TAG A_
 GAM2473 MGC15548 5' CCCTGGACTTCCGCGCCACA 52222 AGC _ A
 TGTGGTGGC AG CCA GG
 ||||| || ||||
 ACACCGCCG TC GGT CC
 CCT A C
 GAM2473 MSC 3' CCGAGGCTGCACTACCACA 76838 CA AA
 TGTGGTGG GCAGCC GG
 ||||| |||| ||

		ACACCATC CGTCGG CC	
		A_ AG	
GAM2473 MTCH1	3'	CCCTGGCACGTGGCCACCAT 27563	A A_ A
		GTGGTGGC GC GCCA GG	
		TACCACCG TG CGGT CC	
		G CA C	
GAM2473 NAF1	3'	CCTTGCTGAAGCCATCACA 21341	AG C
		TGTGGTGGC CAGC AAGG	
		ACACTACCG GTCG TTCC	
		AA _	
GAM2473 NIR3	3'	CCTTAGTCCCACTCCCACCACA 66825	C CA_ C
		TGTGGTGG AG GC AAGG	
		ACACCACC TC TG TTCC	
		C ACCC A	
GAM2473 NLI-IF	3'	CCATGGGCGCGCCGACACA 41342	A AG A
		TGTGGTGGC GC CCA GG	
		ACACCGCCG CG GGT CC	
		C _ A	
GAM2473 NPEPL1	5'	CCTCGGCCGCCCCACTTCA 45422	T CA A A
		TG GGTGG GC GCC AGG	
		AC TCACC CG CGG TCC	
		T _ C C	
GAM2473 NRM	3'	CCCTGGCTGCTTCATGCCA 99716	GC_ A
		TGGTG AGCAGCCA GG	
		ACCGT TCGTCGGT CC	
		ACT C	
GAM2473 P5326	3'	CCTTGGCTACTTTGACAT 49550	GT C C
		GTG GG AG AGCCAAGG	
		TAC TT TC TCGGTTCC	
		AG _ A	
GAM2473 phospho1	3'	CCTCGGCTGCCTCCCCAC 83244	T CA A
		GTGG GG GCAGCC AGG	
		CACC CC CGTCGG TCC	
		C TC C	
GAM2473 PORIMIN	5'	CCTCGGCTGGGAGCCACG 54703	TG AG_ A
		TGTGG GC CAGCC AGG	
		GCACC CG GTCGG TCC	
		_ AGG C	
GAM2473 PP1628	5'	CCTGGGACCTGCCACCTCA 48076	T CAG A
		TG GGTGGCAG CC AGG	

AC CCACCGTC GG TCC
 T CA_ G
 GAM2473 PPM1A 5' CCCCGGCTGCCGCGCCGC 41005 A AA
 GTGGTGGC GCAGCC GG
 ||||| ||||| ||
 CGCCGCCG CGTCGG CC
 C CC
 GAM2473 PRAM-1 3' CCACAGCAGTTGCCACCCA 69911 T A CAA
 TG GGTGGCAGC GC GG
 || ||||| || ||
 AC CCACCGTTG CG CC
 _ A ACA
 GAM2473 PTPRU 3' CCCTGGCCTGGGGCACCCA 20322 T G AG _ A
 TG GGTG C CAG CCA GG
 || |||| | || || ||
 AC CCAC G GTC GGT CC
 _ _ GG C C
 GAM2473 RAI16 3' CCTGGCACTGCCGCCACA 43046 CA A
 TGTGGTGGCAG GCCA GG
 ||||| |||| ||
 ACACCGCCGTC CGGT CC
 A_ _
 GAM2473 RAI17 3' CCTTGGCTGCCAGCCTACC 92904 _ A_
 GGT GGC GCAGCCAAGG
 ||| || ||||| ||
 CCA CCG CGTCGGTTCC
 T AC
 GAM2473 SCMH1 3' GCCCTGGCTCATACTGCCCCCA 25284 _ C_ A _
 CCACA TGTGGT GGCAG AGCCA GG C
 ||||| |||| ||||| || |
 ACACCA CCGTC TCGGT CC G
 CCC ATAC C _
 GAM2473 SCYA21 3' CCCTGGAGCAGCCACCCCA 12976 T A AG A
 TG GGTGGC GC CCA GG
 || ||||| || || ||
 AC CCACCG CG GGT CC
 C A A_ C
 GAM2473 SDC3 3' CCTTGGCTGCCAGAGCA 28473 GG GCA
 TGT TGGCA GCCAAGG
 || |||| |||||
 ACG ACCGT CGGTTCC
 AG _
 GAM2473 SDCCAG3 3' GCCTCAGCCAGTTCTTGGCCAC 22802 _ A_ CA _
 CACA TGTGGTGGC AGC GC AGG C
 ||||| || || || |
 ACACCACCG TTG CG TCC G
 GTTC AC AC _
 GAM2473 SEPT3 3' CCTTGGCTACTGTAGAAGCA 39402 GGTG C
 TGT GCAG AGCCAAGG
 || |||| |||||

ACG TGTC TCGGTTCC
 AAGA A
 GAM2473 SHANK3 3' CCTCACTGCCACTGCCACCCCA 66103 T ____ CCA
 TG GGTGGCA GCAG AGG
 || ||||| ||| |||
 AC CCACCGT CGTC TCC
 C CAC AC_
 GAM2473 SMARCF1 5' CCTCGGCCGCGCCGCGCCGC 21186 A A A
 GTGGTGGC GC GCC AGG
 ||||| || ||| |||
 CGCCGCCG CG CGG TCC
 C C C
 GAM2473 STRIN 5' CCTCGGCCGCTGCCGCTGT 33230 TG A A
 G GTGGCAGC GCC AGG
 | ||||| ||| |||
 T CGCCGTCG CGG TCC
 GT C C
 GAM2473 TBC1D2 3' CCTTGCTGGCAGACCCA 37928 T G_ AG
 TG GGT GC CAGCCAAGG
 || ||| || |||||
 AC CCA CG GTCGGTTCC
 _ GA _
 GAM2473 TERE1 5' CCCCAGACCTTGCCGCCACA 26167 CAG AA
 TGTGGTGGCAG CC GG
 ||||| || ||
 ACACGCGGTT GG CC
 CCA CC
 GAM2473 TIGD5 3' CCTGGGGTGGCCCACCGCA 52768 CA A A_
 TGTGGTGG GC GCC AGG
 ||||| || ||| |||
 ACGCCACC CG TGG TCC
 _ G GG
 GAM2473 TRIM38 3' CCTTGGTTTAACCAGCACA 22054 G CAGC
 TGTG TGG AGCCAAGG
 ||| ||| |||||
 ACAC ACC TTGGTTCC
 G AAT_
 GAM2473 TU3A 3' CCTGTGTGTGCTGCCAGCACA 24182 G GC _
 TGTG TGGCAGCA CA AGG
 ||| ||||| || |||
 ACAC ACCGTCGT GT TCC
 G GT G
 GAM2473 VPS39 3' CCTGGCTGCCACCACCACA 63498 CA A
 TGTGGTGG GCAGCCA GG
 ||||| ||||| ||
 ACACCACC CGTCGGT CC
 AC _
 GAM2473 XPO5 3' CCTTCTTGCACTGCCACCTCA 92873 T CA C_
 TG GGTGGCAG GC AAGG
 || ||||| || |||

			AC CCACCGTC CG TTCC		
			T A_ TTC		
GAM2473	ZAK	5'	CCCCGGCTGCTGCTCACGC 34101	GT	AA
			GTG GGCAGCAGCC GG		
			CGC TCGTCGTCGG CC		
			AC CC		
GAM2473	ZAK	5'	CCCCGGCTGCTGCTCACGC 34102	GT	AA
			GTG GGCAGCAGCC GG		
			CGC TCGTCGTCGG CC		
			AC CC		
GAM2473	ZDHC7	5'	CCTCGGCCGCTGCAGTCGC 35319	TG	A A
			GTGG GCAGC GCC AGG		
			CGCT CGTCG CGG TCC		
			GA C C		
GAM2473	ZNF297	3'	CCCGGGTGATCTCCACCACA 19570	C CA_	AA
			TGTGGTGG AG GCC GG		
			ACACCACC TC TGG CC		
			C TAG GC		
GAM2473	LOC115207	3'	CCCTGGCTGCTGCCCTCCCA 57397	T T_	A
			TG GG GGCAGCAGCCA GG		
			AC CC CCGTCGTCGGT CC		
			_ TC C		
GAM2473	LOC115574	3'	CCTTTAGCGGCCTGCCACCACA 73852	CA	_____
			TGTGGTGGCAG GCC AAGG		
			ACACCACCGTC CGG TTCC		
			_ CGAT		
GAM2473	LOC127281	3'	CCTTGGCTACCACACGCG 75135	_	CAGC
			TGTG GTGG AGCCAAGG		
			GCGC CACC TCGGTTCC		
			A A_		
GAM2473	LOC131377	5'	CCTTGGCACCGCCACCGCA 76778	AGCA	
			TGTGGTGGC GCCAAGG		
			ACGCCACCG CGGTTCC		
			CCA_		
GAM2473	LOC139770	5'	CCTCGGCTGCTGCCCGGCA 75904	GGT	A
			TGT GGCAGCAGCC AGG		
			ACG CCGTCGTCGG TCC		
			GC_ C		
GAM2473	LOC142779	3'	CCTAGCTGCTGCTGGTA 76904	G	CA
			TG TGGCAGCAGC AGG		

AT GTCGTCGTCG TCC
 G A_
 GAM2473 LOC145125 3' CCTTAGCAACACTGCTCACCAC 77546 _ CA_ C
 A TGTGGTG GCAG GC AAGG
 ||||| ||| || ||||
 ACACCAC CGTC CG TTCC
 T ACAA A
 GAM2473 LOC145717 3' CCTTGGCTGAATAGCACA 67373 G GCAG
 TGTG TG CAGCCAAGG
 ||| || |||||
 ACAC AT GTCGGTTCC
 G AA_
 GAM2473 LOC147976 3' CCTCAGGCGCATGTCACCACA 79288 _ A A_
 TGTGGTGGCA GC GCC AGG
 ||||| || ||| |||
 ACACCACTGT CG CGG TCC
 A _ AC
 GAM2473 LOC148479 3' CCTCAGCTGCTGCCTGACC 79611 _ CA
 GGT GGCAGCAGC AGG
 ||| ||||| |||
 CCA CCGTCGTCG TCC
 GT AC
 GAM2473 LOC149302 5' CCTTGGCTGTTTATCCCA 80040 T TGGC
 TG GG AGCAGCCAAGG
 || || |||||
 AC CC TTGTCGGTTCC
 _ TAT_
 GAM2473 LOC149606 3' CCTTGGCACCAGCACCACCAC 80259 CA A_
 GTGGTGG GC GCCAAGG
 ||||| || |||||
 CACCACC CG CGGTTCC
 A_ ACCA
 GAM2473 LOC151361 5' CCTTAGCTTCCCCACCATA 86502 CAGC C
 TGTGGTGG AGC AAGG
 ||||| || |||
 ATACCACC TCG TTCC
 CCT_ A
 GAM2473 LOC152925 3' CCTGTAAGTGCTGCCACCAC 81618 GCCA_
 GTGGTGGCAGCA AGG
 ||||| |||
 CACCACCGTCGT TCC
 GAATG
 GAM2473 LOC154881 3' CCTTGGCTGCTATCTCAT 82070 T GC
 GTGG G AGCAGCCAAGG
 ||| | |||||
 TACT C TCGTCGGTTCC
 _ TA
 GAM2473 LOC157931 3' CCCTGGCAAGCCACCACA 87937 AGCA A
 TGTGGTGGC GCCA GG
 ||||| ||| ||

	ACACCACCG CGGT CC	
	AA__ C	
GAM2473 LOC158337 3'	CCTTGACCACTGAGTTATCACA 88108	AG C__
	TGTGGTGGC CAG CAAGG	
	ACACTATTG GTC GTTCC	
	A_ ACCA	
GAM2473 LOC163759 5'	CCTCTTCTCCTGCCACCCA 88417 T	C CCA
	TG GGTGGCAG AG AGG	
	AC CCACCGTC TC TCC	
	_ C TTC	
GAM2473 LOC196955 5'	CCCAGTAGCTGGCCACCAC 77864	_ A CAA
	GTGGTGGC AGC GC GG	
	CACCACCG TCG TG CC	
	G A AC_	
GAM2473 LOC197131 3'	CCTGCTGCTATCACCACA 89233	GC CA
	TGTGGTG AGCAGC AGG	
	ACACCAC TCGTCG TCC	
	TA _	
GAM2473 LOC197342 3'	CCTCAGGGCAGTCCCCACCACA 89358	CA A A__
	TGTGGTGG GC GCC AGG	
	ACACCACC TG CGG TCC	
	CC A GAC	
GAM2473 LOC200093 3'	CCTCCTCTGCCGCCACCGCA 63769	A CCA
	TGTGGTGGC GCAG AGG	
	ACGCCACCG CGTC TCC	
	C TCC	
GAM2473 LOC200853 3'	CCCTGTGTTTTTCCACCACA 90325	C C _ A
	TGTGGTGG AG AGC CA GG	
	ACACCACC TT TTG GT CC	
	_ T T C	
GAM2473 LOC202284 5'	CCCCGGCTGTGATGCCACC 91932	_ AA
	GGTGGCA GCAGCC GG	
	CCACCGT TGTCGG CC	
	AG CC	
GAM2473 LOC202915 3'	CCTTGGCTGCACGGACCCCA 92016	T CA__
	TGG GG GCAGCCAAGG	
	ACC CC CGTCGGTTCC	
	_ AGGCA	
GAM2473 LOC219653 3'	CCTTTCTCTCCCACCACA 92914	C C CC
	TGTGGTGG AG AG AAGG	

		ACACCACC TC TC TTCC		
		C _ T_		
GAM2473	LOC220537 3'	CCTTGGCTGAATAGCACA 92422	G GCAG	
		TGTG TG CAGCCAAGG		
		ACAC AT GTCGGTTCC		
		G AA_		
GAM2473	LOC221466 5'	CCCTGGCTGCTCCGACA 95312	G C A	
		TG TGG AGCAGCCA GG		
		AC GCC TCGTCGGT CC		
		A _ C		
GAM2473	LOC253980 3'	CCTTCCTGACATCACCACA 96771	CAG CC	
		TGTGGTGG CAG AAGG		
		ACACCACT GTC TTCC		
		ACA C_		
GAM2473	LOC254755 5'	CCTGGCACTGCCGCCACA 99213	CA A	
		TGTGGTGGCAG GCCA GG		
		ACACCGCCGTC CGGT CC		
		A_ _		
GAM2473	LOC254826 3'	CCTCGACTCTGCTACCAC 99049	C CCA	
		GTGGTGGCAG AG AGG		
		CACCATCGTC TC TCC		
		_ AGC		
GAM2473	LOC255313 5'	CCTCGGCCGTAGCCACCTCA 97942	T A A A	
		TG GGTGGC GC GCC AGG		
		AC CCACCG TG CGG TCC		
		T A C C		
GAM2473	LOC256416 3'	CCCTGACTGCTTGCCTCATA 96057	T _ C A	
		TGTGG GGCA GCAG CA GG		
		ATACT CCGT CGTC GT CC		
		_ T A C		
GAM2473	LOC256416 3'	CCTGCTGGACCTGCCACCCA 96058	T _ CA	
		TG GGTGGCAG CAGC AGG		
		AC CCACCGTC GTCG TCC		
		_ CAG _		
GAM2473	LOC51619 3'	CCTGGCCCCCTCACCACA 32568	GC CA A	
		TGTGGTG AG GCCA GG		
		ACACCAC TC CGGT CC		
		_ CC _		
GAM2473	LOC51673 3'	CCCTGACTGCTTGCCTCATA 96205	T _ C A	
		TGTGG GGCA GCAG CA GG		

ATACT CCGT CGTC GT CC
 _ T A C
 GAM2473 LOC51673 3' CCTGCTGGACCTGCCACCCA 96206 T ____ CA
 TG GGTGGCAG CAGC AGG
 || ||||| ||| ||
 AC CCACCGTC GTCG TCC
 _ CAG _
 GAM2473 LOC58525 5' GCCTTGGCCAAGAAGTTGCCAC 79344 A_____
 CAC GTGGTGGCAGC GCCAAGG C
 ||||| |||| |
 CACCACCGTTG CGGTTCC G
 AAGAAC _
 GAM2473 LOC64116 5' CCTCGGCTACGCTGCCACT 42459 _ A
 GGTGGCAGC AGCC AGG
 ||||| ||| ||
 TCACCGTCG TCGG TCC
 CA C
 GAM2473 LOC90529 3' CCCTGGCTGCTTCCCCAC 63860 T C A
 GTGG GG AGCAGCCA GG
 ||| || ||||| ||
 CACC CC TCGTCGGT CC
 _ T C
 GAM2473 LOC91040 3' CCCTGGGCTGCCACCA 65340 AG A
 TGGTGGCAGC CCA GG
 ||||| ||| ||
 ACCACCGTCG GGT CC
 _ C
 GAM2473 LOC91040 3' CCTCCTCTGCCGCCACCGCA 65343 A CCA
 TGTGGTGGC GCAG AGG
 ||||| ||| ||
 ACGCCACCG CGTC TCC
 C TCC
 GAM2473 LOC91373 3' CTTGTGGATCCACCACA 66412 CAG GC
 TGTGGTGG CA CAAGG
 ||||| || ||||
 ACACCACC GT GTTCC
 TAG _
 GAM2473 LOC92293 3' CTTCAACTGTCACCACA 69321 CAGCC
 TGTGGTGGCAG AAGG
 ||||| ||| ||
 ACACCACTGTC TTCC
 AAC_
 GAM2473 LOC93259 5' CTTGACCCCGTAGCCACCAC 72283 A AGC_
 GTGGTGGC GC CAAGG
 ||||| || ||||
 CACCACCG TG GTTCC
 A CCCC
 GAM2473 LOC96597 3' CCCTGGCTGCTGTTTTCC 67452 T_ A
 GG GGCAGCAGCCA GG
 || ||||| ||| ||

		CC TTGTCGTCGGT CC		
		TT C		
GAM2474 BCAT1	5'	AGGTGGGCAGGAGCCAGTGA 66783		CAC TG
		TCGCTGGCTCC TT TCT		
		AGTGACCGAGG GG GGA		
		AC_ GT		
GAM2474 FAAH	3'	AGAAGGAGAAGCCAGTGA 97235		CCCA TG
		TCGCTGGCT CTT TCT		
		AGTGACCGA GAG AGA		
		A__ GA		
GAM2474 FADD	5'	AGACCTGGCCAGGGCCAGCGA 15121		CCA TT
		TCGCTGGCTC CT GTCT		
		AGCGACCGGG GG CAGA		
		ACC TC		
GAM2474 FCMD	3'	ACATAAGTGGAACCAAAGA 23021	GC C	_
		TC TGG TCCCACTT TGT		
		AG ACC AGGGTGAA ACA		
		AA A T		
GAM2474 FOXD2	5'	AGAACCCTGGGAGCCAGGA 16783	G	CTTTG
		TC CTGGCTCCCA TCT		
		AG GACCGAGGGT AGA		
		_ CCCA_		
GAM2474 GNGT2	3'	AGACCCCCAGGGAGCCAGTGA 49809		ACTTT
		TCGCTGGCTCCC GTCT		
		AGTGACCGAGGG CAGA		
		ACCCC		
GAM2474 GRIA3	5'	GGGGTGTAAGAGCCAGCGA 24646		C__
		TCGCTGGCTC CACTTT		
		AGCGACCGAG GTGGGG		
		AAT		
GAM2474 GRIA3	5'	GGGGTGTAAGAGCCAGCGA 24647		C__
		TCGCTGGCTC CACTTT		
		AGCGACCGAG GTGGGG		
		AAT		
GAM2474 IFNAR2	3'	ACAGGGAAGAGCCATCGA 7893	C	CCA
		TCG TGGCTC CTTTGT		
		AGC ACCGAG GGGACA		
		T AA_		
GAM2474 MDFI	5'	GCACCCGGGAGCCAGCGG 19981		ACTT
		TCGCTGGCTCCC TGT		

			GGCGACCGAGGG	ACG		
			CCC_			
GAM2474	OAS1	3'	AGACAAAGCTCCTCAGTGA	34146	CTCCCA	
			TCGCTGG	CTTTGTCT		
			AGTGA	CT	GAAACAGA	
			CCTC_			
GAM2474	PLAB	5'	AGACAAGGAGAGCCAGGA	66426	G	CCA
			TC	CTGGCTC	CTTTGTCT	
			AG	GACCGAG	GGAACAGA	
			_	A_		
GAM2474	RLN2	3'	AGACAAAGTGAAGCCGC	18583	T	CC
			GC	GGCT	CACTTTGTCT	
			CG	CCGA	GTGAAACAGA	
			_	A_		
GAM2474	SDS	3'	AAGGTCGGCAGCCAGCGA	23377	_	C
			TCGCTGGCT	CC	ACTTT	
			AGCGACCGA	GG	TGGAA	
			C	C		
GAM2474	SEPN1	3'	GGA	CTGCGGGAGCCAGCG	66975	ACTTT
			CGCTGGCTCCC	GTCT		
			GCGACCGAGGG	CAGG		
			CGT_			
GAM2474	SLC2A1	3'	GGGCCTGTGGGAGCCTGC	22517	T	TTT
			GC	GGCTCCCAC	GTCT	
			CG	CCGAGGGTG	CGGG	
			T	TC_		
GAM2474	SLC9A3R2	3'	AGACAGAGAGAGAGCGAGCGA	62098	G	CCA
			TCGCT	GCTC	CTTTGTCT	
			AGCGA	CGAG	GAGACAGA	
			G	AGA		
GAM2474	TUFT1	3'	AGGCCTGGTGAGAGCCAGTGA	39668	C	TT
			TCGCTGGCTC	CACT	GTCT	
			AGTGACCGAG	GTGG	CGGA	
			A	TC		
GAM2474	C20orf32	5'	AGACAAAGTGAGACGTCAG	40138	_	C
			CTGGC	TC	CACTTTGTCT	
			GA	CTG	AG	GTGAAACAGA
			C	A		
GAM2474	DKFZP564I052	3'	AGACAAAGTTTTTAACCAATGA	67277	C	CTCCC
			TCG	TGG	ACTTTGTCT	

		AGT ACC TGAAACAGA		
		A AATTT		
GAM2474	DKFZP727M111	5' AGACAAGCTGGAGCCAG	32052	CAC
		CTGGCTCC TTTGTCT		
		GACCGAGG GAACAGA		
		TC_		
GAM2474	DREV1	3' AGACAAAGCAATAGTCACGA	32617	C CCCA
		TCG TGGCT CTTTGTCT		
		AGC ACTGA GAAACAGA		
		_ TAAC		
GAM2474	FLJ11588	5' GGGGCGGAAGCCGAGCGA	45123	_ C A
		TCGCT GGCT CC CTTT		
		AGCGA CCGA GG GGGG		
		G A C		
GAM2474	FLJ12089	3' AGATCTGGGAGCCAGC	44948	CTTT
		GCTGGCTCCCA GTCT		
		CGACCGAGGGT TAGA		
		C__		
GAM2474	FLJ12221	5' GGGCGCGGGAGCCGGCGA	63221	ACTT
		TCGCTGGCTCCC TGTCT		
		AGCGGCCGAGGG GCGGG		
		C__		
GAM2474	FLJ21596	3' ACAAATGGAGTGTAAAGCGG	46112	G__ CAC
		TCGCT GCTCC TTTGT		
		GGCGA TGAGG AAACA		
		ATG TA_		
GAM2474	HIC2	3' AGTCGTGTGCAGGAGCCAGC	65858	_ TT T
		GCTGGCTCC CAC TG CT		
		CGACCGAGG GTG GC GA		
		AC T_ T		
GAM2474	KCNH8	3' AGAGTGTGAGGAGCCAGGGA	58904	G _ TTTG
		TC CTGGCTCC CAC TCT		
		AG GACCGAGG GTG AGA		
		G A TG__		
GAM2474	KIAA0523	5' AGGTGCCAGGAGCCAGGA	68355	G ____
		TC CTGGCTCC CACTT		
		AG GACCGAGG GTGGA		
		_ ACC		
GAM2474	KIAA0876	3' GGGCGACAGGAGCCAGCGG	65318	CACT
		TCGCTGGCTCC TTGTCT		

GGCGACCGAGG AGCGGG
AC__
GAM2474 KIAA1483 3' AGACAAAACAGGAGCCAG 70430 CAC
CTGGCTCC TTTGTCT
||||| |||||
GACCGAGG AACAGA
ACA
GAM2474 KIAA1822 3' AGCCGGGGTGGGAACCAGGA 68178 G C T
TC CTGG TCCCACTTTG CT
|| ||| ||||||| ||
AG GACC AGGGTGGGGC GA
_ A C
GAM2474 LENG9 3' AGACAAAGCAGGAGCGTGC 75022 TG CA
GC GCTCC CTTTGTCT
|| ||| |||||||
CG CGAGG GAAACAGA
TG AC
GAM2474 MGC1842 3' AGACAAAGCCTTTGGCCAAGA 66244 GC CCCA_
TC TGGCT CTTTGTCT
|| ||| |||||||
AG ACCGG GAAACAGA
A_ TTTCC
GAM2474 p25 3' AGACATGCGGGAGCCAGGA 23822 G ACTT
TC CTGGCTCCC TGTCT
|| ||||||| |||||
AG GACCGAGGG ACAGA
_ CGT_
GAM2474 PRO0132 5' AGGCCTAGGAGCTAGCGA 26936 CACTTT
TCGCTGGCTCC GTCT
||||||||| |||
AGCGATCGAGG CGGA
ATC__
GAM2474 RANBP1 5' AGGCCGCGGAGCCAGCGA 12762 CACTTT
TCGCTGGCTCC GTCT
||||||||| |||
AGCGACCGAGG CGGA
CGC__
GAM2474 SDCCAG3 3' AGACATTGTCATAAAAGCCAGT 22800 CCC__ TT
GA TCGCTGGCT AC TGTCT
||||||| || |||||
AGTGACCGA TG ACAGA
AAATAC TT
GAM2474 LOC134701 5' AGAGGGGCGGAGAGGCAGCGA 75694 G _ A G
TCGCTG CTC CC CTTT TCT
||||| ||| || ||||| |||
AGCGAC GAG GG GGGG AGA
G A C _
GAM2474 LOC145694 5' AGGCGGCGGCAGCCAGCGA 84439 C A TT
TCGCTGGCT CC CT GTCT
||||||| || || |||||

AGCGACCGA GG GG CGGA
 C C ____
 GAM2474 LOC145826 5' GGGTGCAGGAGCCAGGGA 84530 G ____
 TC CTGGCTCC CACTT
 || ||||| ||||
 AG GACCGAGG GTGGG
 G AC
 GAM2474 LOC149773 3' AGACAAAGTGGTTGGCGA 80289 TG CTC
 TCGC G CCACTTTGTCT
 ||| | |||||
 AGCG T GGTGAAACAGA
 GT ____
 GAM2474 LOC151963 5' AAAGCCTGGGAGCCTGCGA 81214 T ____
 TCGC GGCTCCCA CTTT
 ||| ||||| |||
 AGCG CCGAGGGT GAAA
 T CC
 GAM2474 LOC152441 5' AGACAAAATGGGACCAG 86914 C C
 CTGG TCCCA TTTGTCT
 ||| ||| |||||
 GACC AGGGT AAACAGA
 _ A
 GAM2474 LOC158943 5' AGGCCGCGGAGCCAGCGA 61149 CACTTT
 TCGCTGGCTCC GTCT
 ||||| |||
 AGCGACCGAGG CGGA
 CGC ____
 GAM2474 LOC206973 5' AGATCTGGCACGGGGGCCAGCG 91110 A__ TT
 A TCGCTGGCTCCC CT GTCT
 ||||| || |||
 AGCGACCGGGGG GG TAGA
 CAC TC
 GAM2474 LOC221399 5' AGACAGTGTGTGAGCCAGC 95482 C_ TT
 GCTGGCTC CACT GTCT
 ||||| ||| |||
 CGACCGAG GTGA CAGA
 TT ____
 GAM2474 LOC58525 3' GGGCGCCGGGAGCCAGC 79349 ACTT
 GCTGGCTCCC TGTCT
 ||||| |||
 CGACCGAGGG GCGGG
 CC ____
 GAM2475 SLC1A1 3' AAGCTGTCACTCACAAAA 16055 _
 TTTTGTGA TGACAGCTT
 ||||| |||||
 AAAACACT ACTGTCGAA
 C
 GAM2475 C5orf6 3' CTGAAGCTGCCACCACAA 33952 A A GG
 TTGTG TG CAGCTT CGG
 |||| || ||||| |||

		AACAC AC GTCGAA GTC	
		C C _	
GAM2475	FLJ20281 5'	CCACGGACCCCATCACAAA 92621	ACAG _
		TTTTGTGATG CT TGG	
		AAAACACTAC GG ACC	
		CCCA C	
GAM2475	KIAA0255 3'	ACCCGTGCATGTCATCACAAA 29127	_ TTG
		TTTGTGATGACA GC GCGGGT	
		AAACACTACTGT CG TGCCCA	
		A _	
GAM2475	MGC3047 3'	CCTGCCACCATCACAA 51347	ACAGCT
		TTGTGATG TGGCGGG	
		AACACTAC ACCGTCC	
		C _	
GAM2475	LOC197131 3'	ACCTGCTGCTATCACCACAAA 89231	A C TT
		TTTGTG TGA AGC GCGGGT	
		AAACAC ACT TCG TCGTCCA	
		C A _	
GAM2475	LOC221550 5'	CCAATACTGGCCATCACAAA 93744	A_ C_
		TTTTGTGATG CAG TTGG	
		AAAACACTAC GTC AACC	
		CG AT	
GAM2475	LOC257495 5'	CCAATACTGGCCATCACAAA 99571	A_ C_
		TTTTGTGATG CAG TTGG	
		AAAACACTAC GTC AACC	
		CG AT	
GAM2475	LOC257576 5'	CCAATACTGGCCATCACAAA 99708	A_ C_
		TTTTGTGATG CAG TTGG	
		AAAACACTAC GTC AACC	
		CG AT	
GAM2476	CDH12 3'	CTTATCATTTAAAGTGGTGTA 15777	CCCAA GA
		TACACCACT GAA ATAAG	
		ATGTGGTGA TTT TATTC	
		AA_ AC	
GAM2476	GOCAP1 3'	ATTGTTCTTGGGAGCAGTGTA 43007	CA G
		TACAC CTCCCAAGAA AAT	
		ATGTG GAGGGTTCTT TTA	
		AC G	
GAM2476	DKFZp434N2435 5'	CTTATTACTGTGGGGTGGT 98090	T AGAAG
		ACCAC CCCA AATAAG	

		TGGTG GGGT TTATTC	
		_ GTCA_	
GAM2476	DKFZP564I122	3' CTTATTCTTCTCCCTCATGTGT 63877	CACTCCCA
	A	TACAC AGAAGAATAAG	
		ATGTG TCTTCTTATTC	
		TACTCCC_	
GAM2476	FLJ21791	3' CTTATTTGCAGAAAGTGGTGTA 62126	CCCAAGAA
		TACACCACT GAATAAG	
		ATGTGGTGA TTTATTC	
		AGACG__	
GAM2476	HMP19	3' CTTATTCTTTGTTAGGAAAATG 88860	CCAC CAA_
	TA	TACA TCC GAAGAATAAG	
		ATGT AGG TTTCTTATTC	
		AAA_ ATTG	
GAM2476	KIAA1579	3' TACTCTTAGTGGTGTA 37154	CCCAAG A
		TACACCACT AAGA TA	
		ATGTGGTGA TTCT AT	
		_____ C	
GAM2476	KIAA1719	3' TCTGTCTTGGGAGTGGTGTA 68742	_
		TACACCACTCCCAAGA AGA	
		ATGTGGTGAGGGTTCT TCT	
		G	
GAM2476	KIAA1853	3' TTTTCTTGAAGCAGTG 69929	CA C
		CAC CT CCAAGAAGAA	
		GTG GA GGTTC TTTT	
		AC A	
GAM2476	KIAA1877	3' CTTATTCTTCTGCCATGAGT 66748	CCA_
		ACTC AGAAGAATAAG	
		TGAG TCTTCTTATTC	
		TACCG	
GAM2476	KIAA1906	3' CTTATTCTTCTTGACTTTTGG 73571	CTCC_
		CCA CAAGAAGAATAAG	
		GGT GTTCTTCTTATTC	
		TTTCA	
GAM2476	OSBPL11	3' CTTAATTTCCCAAGAGTGGTG 43206	CCAA AA
		CACCACTC GAAG TAAG	
		GTGGTGAG CTTT ATTC	
		AACC A_	
GAM2476	YME1L1	3' TCATTCTTGATGTGGTGTA 58438	TCC _
		TACACCAC CAAGAA GA	

			ATGTGGTG GTTCTT CT		
			TA_ A		
GAM2476	YME1L1	3'	TCATTCTTGATGTGGTGTA 27323	TCC	_
			TACACCAC CAAGAA GA		
			ATGTGGTG GTTCTT CT		
			TA_ A		
GAM2476	ZNF262	3'	CTTATTTTGTGGGAGT 18723	A	
			ACTCCCAAG AGAATAAG		
			TGAGGGTTT TTTTATTC		
			G		
GAM2476	LOC91960	3'	TGTGGCTTGAACGTGGTGTA 68294	TC_	AAGA
			TACACCAC CCAAG ATA		
			ATGTGGTG GGTTT TGT		
			CAA GG_		
GAM2477	A1BG	3'	GGGTCTCACTGTGTTGCCCA 56294	AC	A A
			TG CAACATGG GA ACCC		
			AC GTTGTGTC CT TGGG		
			CC A C		
GAM2477	ACADSB	3'	TGGGGTTTTACCATATTGCCCA 9649	AC	C A
	GG		CCTG CAA ATGG GAAACCCCA		
			GGAC GTT TACC TTTTGGGGT		
			CC A A		
GAM2477	ADAMTS4	3'	GGGGTTTCACCATGTTGGCCAG 18767	A	A
	G		CCTG CCAACATGG GAAACCCC		
			GGAC GGTGTACC CTTTGGGG		
			C A		
GAM2477	ADAMTS4	3'	GGGTTTCACCATGTTGGCCAGG 18769	A	A
			CCTG CCAACATGG GAAACCC		
			GGAC GGTGTACC CTTTGGG		
			C A		
GAM2477	AIM1	3'	TGGGGTTTCATCACGTTGCCCA 93472	AC	A GA
	GG		CCTG CAAC TG GAAACCCCA		
			GGAC GTTG AC CTTTGGGGT		
			CC C TA		
GAM2477	APAF1	3'	GGGGTTTCACCATGTTGGCCGG 8590	A	A
	G		CCTG CCAACATGG GAAACCCC		
			GGGC GGTGTACC CTTTGGGG		
			C A		
GAM2477	APAF1	3'	GGGGTTTCACCATGTTGGCCGG 25977	A	A
	G		CCTG CCAACATGG GAAACCCC		

			GGGC GGTGTACC CTTTGGGG		
			C A		
GAM2477	APM1	3'	GGGGTTTCACCACATTCGTCAG 17785	C CA A	
	G		CCTGAC AA TGG GAAACCCC		
			GGACTG TT ACC CTTTGGGG		
			C AC A		
GAM2477	APM1	3'	TGGGGTTTCGTCATGTTGGCCA 17797	A GA	
	GG		CCTG CCAACATG GAAACCCCA		
			GGAC GGTGTAC CTTTGGGGT		
			C TG		
GAM2477	APOL1	3'	TGGGGTTTCACCATGTTGGCCA 14747	A A	
	GG		CCTG CCAACATGG GAAACCCCA		
			GGAC GGTGTACC CTTTGGGGT		
			C A		
GAM2477	APPL	3'	GGGGTTTCACCGTGTTAGCCAG 24951	ACC A	
	G		CCTG AACATGG GAAACCCC		
			GGAC TTGTGCC CTTTGGGG		
			CGA A		
GAM2477	AQP6	3'	TGGGGTTTCATCATATTGGTCA 9737	C GA	
	GG		CCTGACCAA ATG GAAACCCCA		
			GGACTGGTT TAC CTTTGGGGT		
			A TA		
GAM2477	AQP6	3'	TGGGGTTTCATCATATTGGTCA 55019	C GA	
	GG		CCTGACCAA ATG GAAACCCCA		
			GGACTGGTT TAC CTTTGGGGT		
			A TA		
GAM2477	ARCN1	3'	GGGGTTTCACCGTGTTGCCAG 9756	AC A	
	G		CCTG CAACATGG GAAACCCC		
			GGAC GTTGTGCC CTTTGGGG		
			CC A		
GAM2477	ARSF	5'	GGCTCTCACCATGTTGACCAGG 65210	AC A AAC	
			CCTG CAACATGG GA CC		
			GGAC GTTGTACC CT GG		
			CA A CTC		
GAM2477	ATM	3'	TGGGGTTTCACCATATTGCCCA 57150	AC C A	
	GG		CCTG CAA ATGG GAAACCCCA		
			GGAC GTT TACC CTTTGGGGT		
			CC A A		
GAM2477	ATP1B2	3'	GGGGTTTCTCCTTGTTGGTCAG 9838	T	
	G		CCTGACCAACA GGAGAAACCCC		

			GGACTGGTTGT CCTCTTTGGGG		
			T		
GAM2477	ATP6V1A1	3'	GGGGTTTCACCATATTGGTCAG 9871	C	A
	G		CCTGACCAA ATGG GAAACCCC		
			GGACTGGTT TACC CTTTGGGG		
			A A		
GAM2477	ATP8A2	3'	GGACTCCCAGCCGTGGTCAGG 95155	ACA_	A AA
			CCTGACCA TGG GA CC		
			GGACTGGT ACC CT GG		
			GCCG _ CA		
GAM2477	ATP8B2	3'	GTTTCACCATGTTGGCCAGG 65848	A	A
			CCTG CCAACATGG GAAAC		
			GGAC GGTGTACC CTTTG		
			C A		
GAM2477	AXL	3'	GGGTTTCACCATGTTGGCCAGG 9908	A	A
			CCTG CCAACATGG GAAACCC		
			GGAC GGTGTACC CTTTGGG		
			C A		
GAM2477	AXL	3'	GGGTTTCACCATGTTGGCCAGG 41890	A	A
			CCTG CCAACATGG GAAACCC		
			GGAC GGTGTACC CTTTGGG		
			C A		
GAM2477	BRIP1	3'	TGGGGTTTCACCATGTTGGCCA 50215	A	A
	GG		CCTG CCAACATGG GAAACCCCA		
			GGAC GGTGTACC CTTTGGGGT		
			C A		
GAM2477	C14orf1	3'	GGGGTTTCACTCTGTCACCCAG 24171	ACCA	T A
	G		CCTG ACA GG GAAACCCC		
			GGAC TGT TC CTTTGGGG		
			CCAC C A		
GAM2477	C14orf1	3'	TGGGGTCTTACTATGTTGTCCA 24173	AC	A A
	GG		CCTG CAACATGG GA ACCCCA		
			GGAC GTTGTATC TT TGGGGT		
			CT A C		
GAM2477	CAMLG	3'	GGGTTTCTCCATGTTGGTCAGG 10004		
			CCTGACCAACATGGAGAAACCC		
			GGACTGGTTGTACCTCTTTGGG		
GAM2477	CBFA2T2	3'	GGGGTTTCTCCTTGTTGGTCAG 18714	T	
	G		CCTGACCAACA GGAGAAACCCC		

GGACTGGTTGT CCTCTTTGGGG

T

GAM2477 CCNF 3' GGGATTTACCATGTTGGCCAG 10081 A A C
G CCTG CCAACATGG GAAA CCC

|||| ||||||| ||| |||

GGAC GGTTGTACC CTTT GGG

C A A

GAM2477 CDC6 3' GGGTTTTACCATGTTGGCCAGG 8824 A A
CCTG CCAACATGG GAAACCC

|||| ||||||| ||||||

GGAC GGTTGTACC TTTTGGG

C A

GAM2477 CDH1 3' TGGGGTCTTGCTATGTTGCCCA 16410 AC AG A
TG CAACATGG A ACCCCA

|| ||||||| | |||||

AC GTTGTATC T TGGGGT

CC GT C

GAM2477 CDH17 3' GGGGTTTCGCCATTTGGCCAGG 15785 A C A
CCTG CCAA ATGG GAAACCCC

|||| ||| ||| |||||||

GGAC GGTT TACC CTTTGGGG

C _ G

GAM2477 CIAS1 5' GTTTGGCCATGTTGGCCAGG 18102 A AG
CCTG CCAACATGG AAAC

|||| ||||||| |||

GGAC GGTTGTACC TTTG

C GT

GAM2477 CLECSF11 5' TGGGGTTTCACTATGTTGGCCA 56150 A A
GG CCTG CCAACATGG GAAACCCCA

|||| ||||||| |||||||

GGAC GGTTGTATC CTTTGGGGT

C A

GAM2477 CLECSF12 3' GGGTTTCTCCATGTTCGGTCAGG 77215 A
CCTGACC ACATGGAGAAACCC

||||| |||||||||

GGACTGG TGTACCTCTTTGGG

C

GAM2477 CLECSF12 3' GGGTTTTGCCATGTTGACCA 77216 AC AG
TG CAACATGG AAACCC

|| ||||||| |||||

AC GTTGTACC TTTGGG

CA GT

GAM2477 CNGA1 5' TGGGATTTACCATGTTGGCCA 60246 A A C
TG CCAACATGG GAAA CCA

|| ||||||| ||| |||

AC GGTTGTACC CTTT GGGT

C A A

GAM2477 CNN2 3' TGGGGTTTCCCCATGTTGGCCA 16466 A A
GG CCTG CCAACATGG GAAACCCCA

|||| ||||||| |||||||

			GGAC GGTGTACC CTTTGGGGT		
			C C		
GAM2477	CR1	3'	GGGGTTTCACCATGTTAGCCAG 6946	ACC	A
	G		CCTG AACATGG GAAACCCC		
			GGAC TTGTACC CTTTGGGG		
			CGA A		
GAM2477	CRTAP	3'	GGGGTTTTGCCATGTTGGCCAG 22084	A	AG
	G		CCTG CCAACATGG AAACCCC		
			GGAC GGTGTACC TTTGGGG		
			C GT		
GAM2477	CTF1	3'	GGTTTCGCCATGTTGCCCAGG 9018	AC	A
			CCTG CAACATGG GAAACC		
			GGAC GTTGTACC CTTTGG		
			CC G		
GAM2477	CXCL16	3'	GGGGTTTCACCATGTTGACCAG 42174	AC	A
	G		CCTG CAACATGG GAAACCCC		
			GGAC GTTGTACC CTTTGGGG		
			CA A		
GAM2477	CYP1A2	3'	GGGTTTCACCATGTTGGTCAG 7520		A
			CTGACCAACATGG GAAACCC		
			GA CTGGTTGTACC CTTTGGG		
			A		
GAM2477	CYP1A2	3'	GGTTTCACTGTGTTGGCCAGG 7521	A	A
			CCTG CCAACATGG GAAACC		
			GGAC GGTGTGTC CTTTGG		
			C A		
GAM2477	CYP1A2	3'	TGGGGTTTCACCATGTTGGCCA 7531	A	A
	GG		CCTG CCAACATGG GAAACCCCA		
			GGAC GGTGTACC CTTTGGGGT		
			C A		
GAM2477	CYP2B6	3'	GGGACATGTTGGCCAGG 7563	A	GAGAAA
			CCTG CCAACATG CCC		
			GGAC GGTGTAC GGG		
			C A_____		
GAM2477	CYP2B6	3'	TGGGGTTTCACTGTGTAGGCCA 7573	A A	A
	GG		CCTG CC ACATGG GAAACCCCA		
			GGAC GG TGTGTC CTTTGGGGT		
			C A A		
GAM2477	DFFB	3'	GGGGTTTCACCATGTTGGCCAG 88777	A	A
	G		CCTG CCAACATGG GAAACCCC		

			GGAC GGTGTACC CTTTGGGG			
			C A			
GAM2477	DFFB	3'	GGGGTTTCACCATGTTGGTCAG 88779	A		
	G		CCTGACCAACATGG GAAACCCC			
			GGACTGGTTGTACC CTTTGGGG			
			A			
GAM2477	DHFR	3'	TGGGGTTTCACCATGTTGGTCA 7660	A		
	GG		CCTGACCAACATGG GAAACCCCA			
			GGACTGGTTGTACC CTTTGGGGT			
			A			
GAM2477	DISC1	3'	GGGCTTCACCATGTTGGCTAGG 38511	A	A	A
			CCTG CCAACATGG GAA CCC			
			GGAT GGTGTACC CTT GGG			
			C A C			
GAM2477	DSC3	3'	GGGGTTTCACTGTGTTAGCCAG 10444	ACC		A
	G		CCTG AACATGG GAAACCCC			
			GGAC TTGTGTC CTTTGGGG			
			CGA A			
GAM2477	DSC3	3'	GGGGTTTCACTGTGTTAGCCAG 44630	ACC		A
	G		CCTG AACATGG GAAACCCC			
			GGAC TTGTGTC CTTTGGGG			
			CGA A			
GAM2477	DSCR3	3'	GGGTCTCCCTATGTTGCCCAGG 21320	AC		A A
			CCTG CAACATGG GA ACCC			
			GGAC GTTGTATC CT TGGG			
			CC C C			
GAM2477	EHD2	3'	GGGGTTTCACCATGTTGGCCAG 28226	A		A
	G		CCTG CCAACATGG GAAACCCC			
			GGAC GGTGTACC CTTTGGGG			
			C A			
GAM2477	EIF2S3	3'	GGGGTTTCAGCATGTTGGCTAG 9210	A		GA
	G		CCTG CCAACATG GAAACCCC			
			GGAT GGTGTAC CTTTGGGG			
			C GA			
GAM2477	ENC1	3'	TGGGGTTTGGTTGTGCTGATAG 14653	AC	A	TG AG
	G		CCTG CA CA G AAACCCCA			
			GGAT GT GT T TTTGGGGT			
			A_ C GT GG			
GAM2477	EPB72	3'	GGGGTTTCACCATGTTGGCCAG 15879	A		A
	G		CCTG CCAACATGG GAAACCCC			

			GGAC GGTGTACC CTTTGGGG		
			C A		
GAM2477	F2RL2	3'	GGGGTTTCACCATGTTGACCAG 15899	AC	A
	G		CCTG CAACATGG GAAACCCC		
			GGAC GTTGTACC CTTTGGGG		
			CA A		
GAM2477	F2RL3	3'	GGAGTTTCACCATGTTGGCCAG 15523	A	A C
	G		CCTG CCAACATGG GAAAC CC		
			GGAC GGTGTACC CTTTG GG		
			C A A		
GAM2477	F3	3'	TGGGGTTTCACCATCTTGGCCA 67684	A C	A
	GG		CCTG CCAA ATGG GAAACCCCA		
			GGAC GGTT TACC CTTTGGGGT		
			C C A		
GAM2477	FANCF	3'	GGGGTTTCACCATGCTGGCCAG 42983	A A	A
	G		CCTG CCA CATGG GAAACCCC		
			GGAC GGT GTACC CTTTGGGG		
			C C A		
GAM2477	FCAR	3'	TGGGGTTTCACTGTGTTGGCCA 10596	A	A
	GG		CCTG CCAACATGG GAAACCCCA		
			GGAC GGTGTGTC CTTTGGGGT		
			C A		
GAM2477	FCAR	3'	TGGGGTTTCACTGTGTTGGCCA 56599	A	A
	GG		CCTG CCAACATGG GAAACCCCA		
			GGAC GGTGTGTC CTTTGGGGT		
			C A		
GAM2477	FCAR	3'	TGGGGTTTCACTGTGTTGGCCA 56611	A	A
	GG		CCTG CCAACATGG GAAACCCCA		
			GGAC GGTGTGTC CTTTGGGGT		
			C A		
GAM2477	FCAR	3'	TGGGGTTTCACTGTGTTGGCCA 56623	A	A
	GG		CCTG CCAACATGG GAAACCCCA		
			GGAC GGTGTGTC CTTTGGGGT		
			C A		
GAM2477	FCAR	3'	GGGTTTCACCATGTTGGCCAGG 56639	A	A
			CCTG CCAACATGG GAAACCC		
			GGAC GGTGTACC CTTTGGG		
			C A		
GAM2477	FCAR	3'	TGGGGTTTCACTGTGTTGGCCA 56586	A	A
	GG		CCTG CCAACATGG GAAACCCCA		

			GGAC GGTTGTGTC CTTTGGGGT			
			C A			
GAM2477	FEZ1	3'	TGGGAGTTTCACCATGTTGGCC 42876	A	A	—
	AGG		CCTG CCAACATGG GAAAC CCCA			
			GGAC GGTTGTACC CTTTG GGGT			
			C A A			
GAM2477	FGF5	3'	GGGGTTTCACCATGTTGGTCAG 16762		A	
	G		CCTGACCAACATGG GAAACCCC			
			GGA CTGGTTGTACC CTTTGGGG			
			A			
GAM2477	FGF5	3'	GGGGTTTCACCATGTTGGTCAG 53664		A	
	G		CCTGACCAACATGG GAAACCCC			
			GGA CTGGTTGTACC CTTTGGGG			
			A			
GAM2477	FUT1	3'	GGGGTTTCATCGTGTTAACCAG 5603	ACC	GA	
	G		CCTG AACATG GAAACCCC			
			GGAC TTGTGC CTTTGGGG			
			CAA TA			
GAM2477	FUT1	3'	GGGTTTCACCATGTTGGCCGGG 5605	A	A	
			CCTG CCAACATGG GAAACCC			
			GGGC GGTTGTACC CTTTGGG			
			C A			
GAM2477	G6PC	3'	GGGTCTCACTATGTTGCCCAGG 5662	AC	A A	
			CCTG CAACATGG GA ACCC			
			GGAC GTTGTATC CT TGGG			
			CC A C			
GAM2477	G6PC	3'	TGGGATTTTCATCATGTTGGCCA 5667	A	GA C	
	GG		CCTG CCAACATG GAAA CCCA			
			GGAC GGTTGTAC CTTT GGGT			
			C TA A			
GAM2477	GHR	3'	GGGGTTTCACCATGTTGGCCAG 5705	A	A	
	G		CCTG CCAACATGG GAAACCCC			
			GGAC GGTTGTACC CTTTGGGG			
			C A			
GAM2477	GM2A	3'	TGGGGTTTCACCATGTTGGCCA 68391	A	A	
	GG		CCTG CCAACATGG GAAACCCCA			
			GGAC GGTTGTACC CTTTGGGGT			
			C A			
GAM2477	GNE	3'	GGGTTTCACCATGTTGGCCAGG 19676	A	A	
			CCTG CCAACATGG GAAACCC			

			GGAC GGTGTACC CTTTGGG		
			C A		
GAM2477	GPR4	3'	GGGTCTCACTGTGTTGCCCAGG 60580	AC	A A
			CCTG CAACATGG GA ACCC		
			GGAC GTTGTGTC CT TGGG		
			CC A C		
GAM2477	GPR81	3'	GGGGTTTCATTGTGTTAGCCGG 51754	ACC	TG A
	G		CCTG AACA G GAAACCCC		
			GGGC TTGT T CTTTGGGG		
			CGA GT A		
GAM2477	GPR81	3'	GGGTTTTGCCATGTTGGCCAGG 51755	A	AG
			CCTG CCAACATGG AAACCC		
			GGAC GGTGTACC TTTGGG		
			C GT		
GAM2477	GRM6	3'	GGTCTCACTATGTTGCCCAGG 7769	AC	A A
			CCTG CAACATGG GA ACC		
			GGAC GTTGTATC CT TGG		
			CC A C		
GAM2477	GRM7	5'	GGGTTTCACCATGTTGGCCAGG 7788	A	A
			CCTG CCAACATGG GAAACCC		
			GGAC GGTGTACC CTTTGGG		
			C A		
GAM2477	HCS	3'	GGGTTTCTCCATGCTGGACAGG 38988	A A	
			CCTG CCA CATGGAGAAACCC		
			GGAC GGT GTACCTCTTTGGG		
			A C		
GAM2477	HCS	3'	TGGTGTTCACCATGTTGGCCA 38996	A	A C
	G		CTG CCAACATGG GAAAC CCA		
			GAC GGTGTACC CTTTG GGT		
			C A T		
GAM2477	HMG20A	3'	TGAGGTCTTGCTGTGTTGCCCA 37071	AC	AG A C
	GG		CCTG CAACATGG A ACC CA		
			GGAC GTTGTGTC T TGG GT		
			CC GT C A		
GAM2477	HTR1D	3'	GGGGTTTCATCATGTTGGCCAG 7846	A	GA
	G		CCTG CCAACATG GAAACCCC		
			GGAC GGTGTAC CTTTGGGG		
			C TA		
GAM2477	HTR1E	5'	GGGATTTACCATGTTGGCCA 7863	A	A C
			TG CCAACATGG GAAA CCC		

			AC GGTGTACC CTTT GGG		
			C A A		
GAM2477	HUNK	3'	TGGGGTTTCGCCATGTTGCTCA 28196	C	A
	GG		CCTGA CAACATGG GAAACCCCA		
			GGACT GTTGTACC CTTTGGGGT		
			C G		
GAM2477	HYAL4	5'	TGGGGTTTCACCGTGTGGCCA 25373	A	A
	G		CTG CCAACATGG GAAACCCCA		
			GAC GGTGTGCC CTTTGGGGT		
			C A		
GAM2477	IFNAR2	3'	GGATTTTACCATGTTGGCCAGG 7903	A	A C
			CCTG CCAACATGG GAAA CC		
			GGAC GGTGTACC TTTT GG		
			C A A		
GAM2477	IGF1	3'	GGGGTTTACCATGTTGGCCAG 7078	A	A
	G		CCTG CCAACATGG GAAACCCC		
			GGAC GGTGTACC TTTTGGGG		
			C A		
GAM2477	IL11	3'	GGGTTTCACCATGTTGGCCAGG 7193	A	A
			CCTG CCAACATGG GAAACCC		
			GGAC GGTGTACC CTTTGGG		
			C A		
GAM2477	INMT	3'	TGGGGTTTCACCGTGTAGCCA 23231	ACC	A
	GG		CCTG AACATGG GAAACCCCA		
			GGAC TTGTGCC CTTTGGGGT		
			CGA A		
GAM2477	JRK	3'	GGGTCTCACTGTGTTGCCAGG 87832	AC	A A
			CCTG CAACATGG GA ACCC		
			GGAC GTTGTGTC CT TGGG		
			CC A C		
GAM2477	JRK	3'	TGAGGTTATGGGTGTTGGTAGG 87839	A	GGAGA C
			CCTG CCAACAT AACC CA		
			GGAT GGTGTG TTGG GT		
			_ GGTA_ A		
GAM2477	KLRD1	3'	GGTCTTGCTATGTTGCCAGG 24709	AC	AG A
			CCTG CAACATGG A ACC		
			GGAC GTTGTATC T TGG		
			CC GT C		
GAM2477	KLRD1	3'	GGTCTTGCTATGTTGCCAGG 11214	AC	AG A
			CCTG CAACATGG A ACC		

			GGAC GTTGTATC T TGG			
			CC GT C			
GAM2477	LLGL1	3'	TGGGGTTTCACCATGTTAGCCA 67425	ACC	A	
	GG		CCTG AACATGG GAAACCCCA			
			GGAC TTGTACC CTTTGGGGT			
			CGA A			
GAM2477	LNK	3'	GGGTTTCACCATGTTGGCCAGG 19649	A	A	
			CCTG CCAACATGG GAAACCC			
			GGAC GGTGTACC CTTTGGG			
			C A			
GAM2477	LNK	3'	TGGAGTTTCTCTTGTCAACCGG 19654	ACCA	T	C
	G		CCTG ACA GGAGAAAC CCA			
			GGGC TGT TCTCTTG GGT			
			CAAC _ A			
GAM2477	LTB4R	5'	GGGGTTTCACCATGTTGGCCAG 7470	A	A	
	G		CCTG CCAACATGG GAAACCCC			
			GGAC GGTGTACC CTTTGGGG			
			C A			
GAM2477	MAK	3'	GGGTTTCACCATGTTGGTCAGG 20950		A	
			CCTGACCAACATGG GAAACCC			
			GGA CTGGTGTACC CTTTGGG			
			A			
GAM2477	MEF2A	5'	TGGAGTTTCACCATGTTGGCCA 20003	A	A	C
	GG		CCTG CCAACATGG GAAAC CCA			
			GGAC GGTGTACC CTTTG GGT			
			C A A			
GAM2477	MEFV	3'	GGGGTTTCACCATGTTAGCCAG 5942	ACC	A	
	G		CCTG AACATGG GAAACCCC			
			GGAC TTGTACC CTTTGGGG			
			CGA A			
GAM2477	MEFV	3'	TGAGGTTTCATCATGTTGGCCA 5955	A	GA	C
	GG		CCTG CCAACATG GAAACC CA			
			GGAC GGTGTAC CTTTGG GT			
			C TA A			
GAM2477	MHC2TA	3'	GGGTCTCACTATGTTGCCAGG 5989	AC	A	A
			CCTG CAACATGG GA ACCC			
			GGAC GTTGTATC CT TGGG			
			CC A C			
GAM2477	MLANA	3'	GGGGTTTCTCCATGTTGGTCAG 19766			
	G		CCTGACCAACATGGAGAAACCCC			

GGACTGGTTGTACCTCTTTGGGG

GAM2477	MPL	3'	GGGTTTTGCCATGTTGCCCAGG 19356	AC	AG
			CCTG CAACATGG AAACCC		
			GGAC GTTGTACC TTTGGG		
			CC GT		
GAM2477	MRPL49	3'	TGGGGTTTCACCATGTTGGCCA 70176	A	A
	GG		CCTG CCAACATGG GAAACCCCA		
			GGAC GGTGTACC CTTTGGGGT		
			C A		
GAM2477	MYCL2	3'	TGGGGTTTCACCACATTGGCCA 19383	A	CA A
	GG		CCTG CCAA TGG GAAACCCCA		
			GGAC GGTT ACC CTTTGGGGT		
			C AC A		
GAM2477	NCOA6	5'	GGGGTTTCGCCATGTTGCCCAG 26840	AC	A
	G		CCTG CAACATGG GAAACCCC		
			GGAC GTTGTACC CTTTGGGG		
			CC G		
GAM2477	NCOA6	5'	TGGGGTTTCATCATGTTGGCCA 26851	A	GA
	GG		CCTG CCAACATG GAAACCCCA		
			GGAC GGTGTAC CTTTGGGGT		
			C TA		
GAM2477	NCOA6IP	3'	GGTCCCACCATGTTGCCCAGG 46157	AC	AGAA
			CCTG CAACATGG ACC		
			GGAC GTTGTACC TGG		
			CC ACCC		
GAM2477	NDRG3	3'	TGGAGTTTCACCATGTTGGCCA 50129	A	A C
	GG		CCTG CCAACATGG GAAAC CCA		
			GGAC GGTGTACC CTTTG GGT		
			C A A		
GAM2477	NPR2L	3'	GGGTTTCCCTATGTTGCCCAGG 22596	AC	A
			CCTG CAACATGG GAAACCC		
			GGAC GTTGTATC CTTTGGG		
			CC C		
GAM2477	NQO1	3'	GGCGTTTCACCATGTTGGCCAG 8051	A	A C
	G		CCTG CCAACATGG GAAAC CC		
			GGAC GGTGTACC CTTTG GG		
			C A C		
GAM2477	ORC1L	3'	GGGCTTCACCATGTTGCCAAG 15984	GAC	A A
			CT CAACATGG GAA CCC		

			GA GTTGTACC CTT GGG		
			ACC A C		
GAM2477	PCDHA9	3'	TGGGGTTTCACCGTGTAGTCA 26629	C	A
	GG		CCTGAC AACATGG GAAACCCCA		
			GGA CTG TTGTGCC CTTTGGGGT		
			A A		
GAM2477	PCDHA9	3'	TGGGGTTTCATCATGTTGGCCA 26630	A	GA
	GG		CCTG CCAACATG GAAACCCCA		
			GGAC GGTGTAC CTTTGGGGT		
			C TA		
GAM2477	PCDHB11	3'	GGGGTTTCACCACGTTGGCCGG 38928	A	A A
	G		CCTG CCAAC TGG GAAACCCC		
			GGG C GGTG ACC CTTTGGGG		
			C C A		
GAM2477	PDE6B	3'	TGGGGTTTCACCATATTGGGCA 6081	A	C A
	GG		CCTG CCAA ATGG GAAACCCCA		
			GGAC GGT TACC CTTTGGGGT		
			G A A		
GAM2477	PER2	3'	GGGTTTCACCATGTTGGCCAGG 43357	A	A
			CCTG CCAACATGG GAAACCC		
			GGAC GGTGTACC CTTTGGG		
			C A		
GAM2477	PER2	3'	TGGAGTTTCTTTTGGCCAGG 43363	AC	CAT C
			CCTG CAA GGAGAAAC CCA		
			GGAC GTT TTTCTTTG GGT		
			CC _ A		
GAM2477	PIK3C2B	3'	GGGGTTTCACCATGTTGGCCAG 12106	A	A
	G		CCTG CCAACATGG GAAACCCC		
			GGAC GGTGTACC CTTTGGGG		
			C A		
GAM2477	POU2AF1	3'	GGGGTTTCACCATGTTGGCCAG 21747	A	A
	G		CCTG CCAACATGG GAAACCCC		
			GGAC GGTGTACC CTTTGGGG		
			C A		
GAM2477	PPEF2	3'	GGGTTTCTCCATGTTGGTCAGG 21777		
			CCTGACCAACATGGAGAAACCC		
			GGA CTG GTGTACCTCTTTGGG		
GAM2477	PPID	3'	TGGGGTTTCACCATATTGGTCA 88832	C	A
			TGACCAA ATGG GAAACCCCA		

			ACTGGTT TACC CTTTGGGGT		
			A A		
GAM2477	PPP1R12B	3'	TGGGGTTTTGCCATGTTGCCCA 50399	AC	AG
	GG		CCTG CAACATGG AAACCCCA		
			GGAC GTTGTACC TTTGGGGT		
			CC GT		
GAM2477	PRKR	3'	GGGTTTCACCATGTTGGCCAGG 12351	A	A
			CCTG CCAACATGG GAAACCC		
			GGAC GGTGTACC CTTTGGG		
			C A		
GAM2477	PRKWNK3	3'	TGGGGTTTCACTATGTTGGCCA 62243	A	A
	G		CTG CCAACATGG GAAACCCCA		
			GAC GGTGTATC CTTTGGGGT		
			C A		
GAM2477	PSMD9	3'	GGGTCTCCCTGTGTTGACCAGG 12527	AC	A A
			CCTG CAACATGG GA ACCC		
			GGAC GTTGTGTC CT TGGG		
			CA C C		
GAM2477	PTGIS	3'	GGGGTTTCCCATGTTGGTCAG 8219		A
	G		CCTGACCAACATGG GAAACCC		
			GGA CTGGTTGTACC CTTTGGGG		
			C		
GAM2477	PVR	3'	GGTTTCCCTGTGTTGCCCAGG 22495	AC	A
			CCTG CAACATGG GAAACC		
			GGAC GTTGTGTC CTTTGG		
			CC C		
GAM2477	RAB36	3'	TGGGGTTTCTCCATGTTGGTCA 18186		
	GG		CCTGACCAACATGGAGAAACCCCA		
			GGA CTGGTTGTACCTCTTTGGGGT		
GAM2477	RABL2A	3'	GGGGTTTCACCATGTTGCCCAG 26411	AC	A
	G		CCTG CAACATGG GAAACCC		
			GGAC GTTGTACC CTTTGGGG		
			CC A		
GAM2477	RABL2B	3'	GGGGTTTCACCATGTTGCCCAG 23982	AC	A
	G		CCTG CAACATGG GAAACCC		
			GGAC GTTGTACC CTTTGGGG		
			CC A		
GAM2477	RBBP9	3'	GGGTTTCACCATGTTGGCCAGG 70695	A	A
			CCTG CCAACATGG GAAACCC		

			GGAC GGTTGTACC CTTTGGG		
			C A		
GAM2477	RHD	3'	GGGTTTCACCATGTTGGCTAGG 32831	A	A
			CCTG CCAACATGG GAAACCC		
			GGAT GGTTGTACC CTTTGGG		
			C A		
GAM2477	RHD	3'	TGGGGTTTCACCATGTTGGCCA 32842	A	A
	GG		CCTG CCAACATGG GAAACCCCA		
			GGAC GGTTGTACC CTTTGGGGT		
			C A		
GAM2477	RHD	3'	GGGTTTCACCATGTTGGCTAGG 33145	A	A
			CCTG CCAACATGG GAAACCC		
			GGAT GGTTGTACC CTTTGGG		
			C A		
GAM2477	RHD	3'	TGGGGTTTCACCATGTTGGCCA 33152	A	A
	GG		CCTG CCAACATGG GAAACCCCA		
			GGAC GGTTGTACC CTTTGGGGT		
			C A		
GAM2477	RNMT	3'	TGGGAGTATATTGGTCAGG 15059	C	GGAGAA _
			CCTGACCAA AT AC CCCA		
			GGACTGGTT TA TG GGGT		
			A A		
GAM2477	RP2	3'	TGGGGTTTTTCCACGTTGGTCA 23608	A	
	GG		CCTGACCAAC TGGAGAAACCCCA		
			GGACTGGTTG ACCTTTTGGGGT		
			C		
GAM2477	RPH3AL	3'	TGGGGTTTCTCCATGTTGGCCA 23745	A	
	GG		CCTG CCAACATGGAGAAACCCCA		
			GGAC GGTTGTACCTCTTGGGGT		
			C		
GAM2477	RPP30	3'	GGGGTTTCACCGTGTTAGCCAG 22203	ACC	A
	G		CCTG AACATGG GAAACCCC		
			GGAC TTGTGCC CTTTGGGG		
			CGA A		
GAM2477	SCML2	3'	TGGGGTTTCTCCATGTTGGTCA 21434		
	GG		CCTGACCAACATGGAGAAACCCCA		
			GGACTGGTTGTACCTCTTGGGGT		
GAM2477	SCNN1G	3'	GGATCTCACTATGTTGCCCAGG 8302	AC	A AAC
			CCTG CAACATGG GA CC		

			GGAC GTTGTATC CT GG		
			CC A CTA		
GAM2477	SEDL	3'	GGGTTTCACCATATTGGTCAGG 28103	C	A
			CCTGACCAA ATGG GAAACCC		
			GGA CTGGTT TACC CTTTGGG		
			A A		
GAM2477	SEDL	3'	GGGTTTCACCATATTGGTCAGG 28104	C	A
			CCTGACCAA ATGG GAAACCC		
			GGA CTGGTT TACC CTTTGGG		
			A A		
GAM2477	SEPN1	3'	TGGGGTTTCACCATATTGGTCA 66984	C	A
	GG		CCTGACCAA ATGG GAAACCCCA		
			GGA CTGGTT TACC CTTTGGGGT		
			A A		
GAM2477	SERPINB9	3'	GGGGTTTCACCGTGTAGCCAG 16025	ACC	A
	G		CCTG AACATGG GAAACCC		
			GGAC TTGTGCC CTTTGGGG		
			CGA A		
GAM2477	SFTPA2	3'	GGTCTCTGTGGCAGG 23630	A	ACA AA
			CCTG CCA TGGAGA CC		
			GGAC GGT GTCTCT GG		
			— — — —		
GAM2477	SH3BP2	3'	GGGATTTTATCATGTTGGCCAG 13080	A	A C
	G		CCTG CCAACATGG GAAA CCC		
			GGAC GGTGTACT TTTT GGG		
			C A A		
GAM2477	SH3BP2	3'	GGGGTTTCACCATGTTGGCCAG 13081	A	A
	G		CCTG CCAACATGG GAAACCC		
			GGAC GGTGTACC CTTTGGGG		
			C A		
GAM2477	SHOX	3'	TGGGGTTTGACCATGTTGGCCA 23524	A	AG
	GG		CCTG CCAACATGG AAACCCCA		
			GGAC GGTGTACC TTTGGGGT		
			C AG		
GAM2477	SIL	5'	GGGGTTTCACCATGTTGGTCGG 13159	A	
	G		CCTGACCAACATGG GAAACCC		
			GGGCTGGTTGTACC CTTTGGGG		
			A		
GAM2477	SIL	3'	GGTTTCTCCATGTTGGTCAGG 13160		
			CCTGACCAACATGGAGAAACC		

GGACTGGTTGTACCTCTTTGG

GAM2477	SLA2	3'	TGGGGTTTCACCACATTGGCCA 50897	A	CA	A
	GG		CCTG CCAA TGG GAAACCCCA			
			GGAC GGTT ACC CTTTGGGGT			
			C AC A			
GAM2477	SLC14A2	5'	GGGGTTTCACCACATTGGCCAG 24122	A	CA	A
	G		CCTG CCAA TGG GAAACCCC			
			GGAC GGTT ACC CTTTGGGG			
			C AC A			
GAM2477	SLC15A1	3'	TGGGGTTTCACCATGTTAACCA 18650	ACC		A
	GG		CCTG AACATGG GAAACCCCA			
			GGAC TTGTACC CTTTGGGGT			
			CAA A			
GAM2477	SLC3A2	5'	TGGGGTCTCACTGTGTTGCCCA 11528	AC		A A
	G		CTG CAACATGG GA ACCCCA			
			GAC GTTGTGTC CT TGGGGT			
			CC A C			
GAM2477	SMAC	5'	TGGGGTTTCACCATGTTGGTCA 58031			A
	GG		CCTGACCAACATGG GAAACCCCA			
			GGACTGGTTGTACC CTTTGGGGT			
			A			
GAM2477	SNX15	3'	GGGGTTACACCATGTTGGCCAG 74127	A		AGA
	G		CCTG CCAACATGG AACCCC			
			GGAC GGTTGTACC TTGGGG			
			C ACA			
GAM2477	SPN	3'	TGGGGTTTCACCATGTTGGCTA 13383	A		A
	GG		CCTG CCAACATGG GAAACCCCA			
			GGAT GGTTGTACC CTTTGGGGT			
			C A			
GAM2477	SULT1C1	3'	GGGTCTTGCTATGTTGCCAGG 8321	AC		AG A
			CCTG CAACATGG A ACCC			
			GGAC GTTGTATC T TGGG			
			CC GT C			
GAM2477	SULT2B1	5'	GGGGTTTCACCATGTTGGCCAG 17223	A		A
	G		CCTG CCAACATGG GAAACCCC			
			GGAC GGTTGTACC CTTTGGGG			
			C A			
GAM2477	TAF7L	3'	TGGGGTCTTGTTATGTTGCCCA 46515	AC		A A
	GG		CCTG CAACATGG GA ACCCCA			

			GGAC GTTGTATT TT TGGGGT		
			CC G C		
GAM2477	TAPBP	3'	GGGGTTTCACCATGTTGGCCAG 13572	A	A
	G		CCTG CCAACATGG GAAACCCC		
			GGAC GGTGTACC CTTTGGGG		
			C A		
GAM2477	TAPBP	3'	GGGGTTTCACCGTGTAGCCAG 13575	ACC	A
	G		CCTG AACATGG GAAACCCC		
			GGAC TTGTGCC CTTTGGGG		
			CGA A		
GAM2477	TAPBP	3'	GGGGTTTCACCGTGTAGCCAG 13576	ACC	A
	G		CCTG AACATGG GAAACCCC		
			GGAC TTGTGCC CTTTGGGG		
			CGA A		
GAM2477	TBXA2R	3'	GGGGTTTCACCGTGTGGCCAG 8361	A	A
	G		CCTG CCAACATGG GAAACCCC		
			GGAC GGTGTGCC CTTTGGGG		
			C A		
GAM2477	TERF1	3'	GGGGTTTCACCATGCTGGTCAG 34395	A	A
	G		CCTGACCA CATGG GAAACCCC		
			GGACTGGT GTACC CTTTGGGG		
			C A		
GAM2477	TERF1	3'	GTTTCTCTCTGTTGCCAGG 34401	AC	T
			CCTG CAACA GGAGAAAC		
			GGAC GTTGT TCTCTTG		
			CC C		
GAM2477	TERF2	3'	GGGGTTTCACCGTGTAGCCAG 20158	ACC	A
	G		CCTG AACATGG GAAACCCC		
			GGAC TTGTGCC CTTTGGGG		
			CGA A		
GAM2477	TIM3	3'	GGGTTTCACCATGTTGGCCAG 52358	A	A
			CTG CCAACATGG GAAACCC		
			GAC GGTGTACC CTTTGGG		
			C A		
GAM2477	TPRSS3	3'	GGGTTTCACCATGTTGGCCAGG 51520	A	A
			CCTG CCAACATGG GAAACCC		
			GGAC GGTGTACC CTTTGGG		
			C A		
GAM2477	TPRSS3	3'	GGGTTTCACCATGTTGGCCAGG 51547	A	A
			CCTG CCAACATGG GAAACCC		

			GGAC GGTGTACC CTTTGGG		
			C A		
GAM2477	TMPRSS3	3'	GGGTTTCACCATGTTGGCCAGG 44030	A	A
			CCTG CCAACATGG GAAACCC		
			GGAC GGTGTACC CTTTGGG		
			C A		
GAM2477	TNFAIP2	3'	GGGTCTTGCTGTGTTGCCAGG 21925	AC	AG A
			CCTG CAACATGG A ACCC		
			GGAC GTTGTGTC T TGGG		
			CC GT C		
GAM2477	TNFRSF10B	3'	GGGGTTTCACCATGTTGGTCAG 15229		A
	G		CCTGACCAACATGG GAAACCC		
			GGA CTGGTTGTACC CTTTGGG		
			A		
GAM2477	TP53BP2	5'	GTTTCATCATGTTGGCCAGG 19467	A	GA
			CCTG CCAACATG GAAAC		
			GGAC GGTGTAC CTTTG		
			C TA		
GAM2477	TPMT	3'	GGGGTTTCACCATGTTGGTCAG 6316		A
	G		CCTGACCAACATGG GAAACCC		
			GGA CTGGTTGTACC CTTTGGG		
			A		
GAM2477	TRAF5	3'	GGAGTTTTGCCATGTTGGCCA 17278	A	AG C
			TG CCAACATGG AAAC CC		
			AC GGTGTACC TTTG GG		
			C GT A		
GAM2477	TRPM6	3'	TGGGGTTTCACCATGTTGGCCA 35038	A	A
	GG		CCTG CCAACATGG GAAACCCA		
			GGAC GGTGTACC CTTTGGGT		
			C A		
GAM2477	TRPV1	3'	GGGGTTTCACCATGTTGGCCAG 38701	A	A
	G		CCTG CCAACATGG GAAACCC		
			GGAC GGTGTACC CTTTGGG		
			C A		
GAM2477	TRPV1	3'	TGGGGTTTCGCCATGTTGGCCA 38708	A	A
	GG		CCTG CCAACATGG GAAACCCA		
			GGAC GGTGTACC CTTTGGGT		
			C G		
GAM2477	TRPV1	3'	GGGGTTTCACCATGTTGGCCAG 55682	A	A
	G		CCTG CCAACATGG GAAACCC		

				GGAC GGTGTACC CTTTGGGG		
				C A		
GAM2477	TRPV1	3'	TGGGGTTTCGCCATGTTGGCCA	55693	A	A
	GG		CCTG CCAACATGG GAAACCCCA			
			GGAC GGTGTACC CTTTGGGGT			
			C G			
GAM2477	TRPV1	3'	GGGGTTTCACCATGTTGGCCAG	55717	A	A
	G		CCTG CCAACATGG GAAACCCC			
			GGAC GGTGTACC CTTTGGGG			
			C A			
GAM2477	TRPV1	3'	TGGGGTTTCGCCATGTTGGCCA	55724	A	A
	GG		CCTG CCAACATGG GAAACCCCA			
			GGAC GGTGTACC CTTTGGGGT			
			C G			
GAM2477	TRPV1	3'	GGGGTTTCACCATGTTGGCCAG	55748	A	A
	G		CCTG CCAACATGG GAAACCCC			
			GGAC GGTGTACC CTTTGGGG			
			C A			
GAM2477	TRPV1	3'	TGGGGTTTCGCCATGTTGGCCA	55755	A	A
	GG		CCTG CCAACATGG GAAACCCCA			
			GGAC GGTGTACC CTTTGGGGT			
			C G			
GAM2477	TUFT1	3'	TGGGGTTTCACCATACTGGCTA	39679	A	AC A
	GG		CCTG CCA ATGG GAAACCCCA			
			GGAT GGT TACC CTTTGGGGT			
			C CA A			
GAM2477	VENTX2	3'	TGGGGTTTCACCATGTTAGCCA	27870	ACC	A
	GG		CCTG AACATGG GAAACCCCA			
			GGAC TTGTACC CTTTGGGGT			
			CGA A			
GAM2477	VHL	3'	GGGGTTTCACCATGTTGTCCAG	6870	AC	A
	G		CCTG CAACATGG GAAACCCC			
			GGAC GTTGTACC CTTTGGGG			
			CT A			
GAM2477	VHL	3'	GTTTCGCCATGTTGGCCAGG	6873	A	A
			CCTG CCAACATGG GAAAC			
			GGAC GGTGTACC CTTTG			
			C G			
GAM2477	WBSCR5	3'	TGGGGTTTTAAATGATTG	27115	_	GGA
			CAA CAT GAAACCCCA			

			GTT GTA TTTTGGGGT			
			A AA_			
GAM2477	WBSCR5	3'	TGGGGTTTTAAATGATTG 42116	_	GGA	
			CAA CAT GAAACCCCA			
			GTT GTA TTTTGGGGT			
			A AA_			
GAM2477	WBSCR5	3'	TGGGGTTTTAAATGATTG 51631	_	GGA	
			CAA CAT GAAACCCCA			
			GTT GTA TTTTGGGGT			
			A AA_			
GAM2477	WDR1	3'	GGAATTCTGTGTTGAACAG 34406	AC	AAA	
			CTG CAACATGGAG CC			
			GAC GTTGTGTCTT GG			
			AA AA_			
GAM2477	WDR1	3'	GGAATTCTGTGTTGAACAG 18849	AC	AAA	
			CTG CAACATGGAG CC			
			GAC GTTGTGTCTT GG			
			AA AA_			
GAM2477	WHSC1	5'	TTTCGCCATGTTGCCCAGG 30586	AC	A	
			CCTG CAACATGG GAAA			
			GGAC GTTGTACC CTTT			
			CC G			
GAM2477	WHSC1	5'	TTTCGCCATGTTGCCCAGG 24694	AC	A	
			CCTG CAACATGG GAAA			
			GGAC GTTGTACC CTTT			
			CC G			
GAM2477	WHSC1	5'	TTTCGCCATGTTGCCCAGG 56673	AC	A	
			CCTG CAACATGG GAAA			
			GGAC GTTGTACC CTTT			
			CC G			
GAM2477	WHSC1	5'	TTTCGCCATGTTGCCCAGG 56684	AC	A	
			CCTG CAACATGG GAAA			
			GGAC GTTGTACC CTTT			
			CC G			
GAM2477	XRCC2	3'	GGGGTTTCACCATGTTGGCCAG 19507	A	A	
	G		CCTG CCAACATGG GAAACCCC			
			GGAC GGTTGTACC CTTTGGGG			
			C A			
GAM2477	ZNF157	3'	GGGTTTCACCATGTTGGCCAGG 14335	A	A	
			CCTG CCAACATGG GAAACCC			

			GGAC GGTTGTACC CTTTGGG		
			C A		
GAM2477	ZNF264	3'	GGGGTTTCACCATCTTGCCAG 14218	A	C A
	G		CCTG CCAA ATGG GAAACCCC		
			GGAC GGTT TACC CTTTGGGG		
			C C A		
GAM2477	ZNF264	3'	GGGGTTTCACCATGTTGCTCAG 14219	C	A
	G		CCTGA CAACATGG GAAACCCC		
			GGA CT GTTGTACC CTTTGGGG		
			C A		
GAM2477	AAK1	3'	TGGGGTTTCTCCATGTTGGTCA 30529		
	GG		CCTGACCAACATGGAGAAACCCCA		
			GGA CT GTTGTACCTCTTTGGGGT		
GAM2477	ANAPC11	5'	GGAGTTTCGTCATGTTGGCCAG 33634	A	GA C
	G		CCTG CCAACATG GAAAC CC		
			GGAC GGTTGTAC CTTTG GG		
			C TG A		
GAM2477	ANKT	3'	GGGTCTCACTGTGTTGCCCAGG 33458	AC	A A
			CCTG CAACATGG GA ACCC		
			GGAC GTTGTGTC CT TGGG		
			CC A C		
GAM2477	AP3S2	3'	GGGTTTCACCATGTTGGCCAGG 20655	A	A
			CCTG CCAACATGG GAAACCC		
			GGAC GGTTGTACC CTTTGGG		
			C A		
GAM2477	ARHF	3'	GGGTTTCACCATGTTGGCCAGG 39274	A	A
			CCTG CCAACATGG GAAACCC		
			GGAC GGTTGTACC CTTTGGG		
			C A		
GAM2477	ARHGAP5	5'	TGGGGTTTCTCCATGTTGGTC 77609		
			GACCAACATGGAGAAACCCCA		
			CTGGTTGTACCTCTTTGGGGT		
GAM2477	ASB16	3'	GGGTCTCTCTCTGTGGCCCAGG 70490	A_	A T A
			CCTG CCA CA GGAGA ACCC		
			GGAC GGT GT TCTCT TGGG		
			CC _ C C		
GAM2477	ASB16	3'	GGGGTCTCGCCATGTTGGCCAG 55985	A	A A
	G		CCTG CCAACATGG GA ACCC		

			GGAC GGTGTACC CT TGGGG		
			C G C		
GAM2477 ASE-1	3'	GGGGTTTCACCATATTGGCCAG 24985	A C A		
G		CCTG CCAA ATGG GAAACCCC			
		GGAC GGT TACC CTTTGGGG			
		C A A			
GAM2477 ASE-1	3'	TGGGGTTTCACCACGTTAGCCA 24998	ACC A A		
GG		CCTG AAC TGG GAAACCCCA			
		GGAC TTG ACC CTTTGGGGT			
		CGA C A			
GAM2477 ATP1B4	3'	GGGTTTCACCATGTTGGCCAGG 24849	A A		
		CCTG CCAACATGG GAAACCC			
		GGAC GGTGTACC CTTTGGG			
		C A			
GAM2477 BA108L7.2	3'	GGGGTTTCACCATGTTGGCCAG 49079	A A		
G		CCTG CCAACATGG GAAACCCC			
		GGAC GGTGTACC CTTTGGGG			
		C A			
GAM2477 BAG5	3'	TTTCACCATGATGGTCAGG 18045	A A		
		CCTGACCA CATGG GAAA			
		GGACTGGT GTACC CTTT			
		A A			
GAM2477 BNIP-S	3'	GGGGTTTCACCATGTTGGCCAG 57093	A A		
G		CCTG CCAACATGG GAAACCCC			
		GGAC GGTGTACC CTTTGGGG			
		C A			
GAM2477 BNIP-S	3'	GGGATCTCCATGGCTCAGG 57105	CCAA AAC		
		CCTGA CATGGAGA CCC			
		GGACT GTACCTCT GGG			
		CG_ A_			
GAM2477 C11orf17	3'	GGGGTTTAACCATGTTGGCCAG 40584	A AG		
G		CCTG CCAACATGG AAACCCC			
		GGAC GGTGTACC TTTGGGG			
		C AA			
GAM2477 C11orf9	3'	TGGGGTTTGCCTGTTACGCCAG 26121	ACC_ T AG		
		CTG AACA GG AAACCCCA			
		GAC TTGT CC TTTGGGGT			
		CGCA _ G_			
GAM2477 C13orf1	3'	TGGGGTTTCACCATGTTGTCCA 40373	AC A		
GG		CCTG CAACATGG GAAACCCCA			

			GGAC GTTGTACC CTTTGGGGT		
			CT A		
GAM2477	C1orf24	3'	TGGGTTTTCACCATGTTGGCCA 54799	A	A C
	GG		CCTG CCAACATGG GAAA CCA		
			GGAC GGTGTACC CTTT GGGT		
			C A T		
GAM2477	C1orf34	3'	GGGTCTTGCTATGTTGGTCAGG 61317		AG A
			CCTGACCAACATGG A ACCC		
			GGA CTGGTTGTATC T TGGG		
			GT C		
GAM2477	C1QTNF6	3'	TGGGGTTTCACCATATTGGCCA 49998	A	C A
	GG		CCTG CCAA ATGG GAAACCCCA		
			GGAC GGTT TACC CTTTGGGGT		
			C A A		
GAM2477	C20orf142	3'	TGGGGTTTCTCCATGTTGGTCA 75290		
	GG		CCTGACCAACATGGAGAAACCCCA		
			GGA CTGGTTGTACCTCTTTGGGGT		
GAM2477	C21orf25	3'	TGGAGTCTCACCATGTTGGTCA 64305		A A C
	GG		CCTGACCAACATGG GA AC CCA		
			GGA CTGGTTGTACC CT TG GGT		
			A C A		
GAM2477	C6orf5	3'	GGGTTTTGCCATGTTGTCCAGG 31999	AC	AG
			CCTG CAACATGG AAACCC		
			GGAC GTTGTACC TTTGGG		
			CT GT		
GAM2477	CARD6	3'	GGGTTTCTCCATGTTGGTCAGG 51846		
			CCTGACCAACATGGAGAAACCC		
			GGA CTGGTTGTACCTCTTTGGG		
GAM2477	CCRN4L	3'	GGGGTTTCACCGTGTAGCCAG 25072	ACC	A
	G		CCTG AACATGG GAAACCC		
			GGAC TTGTGCC CTTTGGGG		
			CGA A		
GAM2477	CDC14B	3'	GGGTTTCACCATGTTGGCCAGG 54010	A	A
			CCTG CCAACATGG GAAACCC		
			GGAC GGTGTACC CTTTGGG		
			C A		
GAM2477	CENPH	3'	GGGGTTTCACCGTGTGCCCAG 43569	AC	A
	G		CCTG CAACATGG GAAACCC		

			GGAC GTTGTGCC CTTTGGGG		
			CC A		
GAM2477	CGRP-RCP	3'	TTTTCTCTGCTGGCAGG 27896	A A T	
			CCTG CCA CA GGAGAA		
			GGAC GGT GT TCTTTT		
			_ C C		
GAM2477	CHRA1	3'	GGGGTTCACCATGTTGGCCAGG 34337	A A A	
			CCTG CCAACATGG GAA CCCC		
			GGAC GGTGTACC CTT GGGG		
			C A _		
GAM2477	CIP29	3'	GGGGTTTCACCATGTTGCCCAG 51380	AC A	
	G		CCTG CAACATGG GAAACCCC		
			GGAC GTTGTACC CTTTGGGG		
			CC A		
GAM2477	COLEC12	3'	GGGTCTTGCTATGTTGCCCAGG 48615	AC AG A	
			CCTG CAACATGG A ACCC		
			GGAC GTTGTATC T TGGG		
			CC GT C		
GAM2477	CPSF2	3'	GGGGTTTCTCCATGTTGGTTAG 62274		
	G		CCTGACCAACATGGAGAAACCCC		
			GGATTGGTTGTACCTCTTTGGGG		
GAM2477	CPSF2	3'	GGGTTTCACCATGTTGGCCAGG 62277	A A	
			CCTG CCAACATGG GAAACCC		
			GGAC GGTGTACC CTTTGGG		
			C A		
GAM2477	DBR1	3'	GGGTTTCACCGTGTGGCCAGG 33070	A A	
			CCTG CCAACATGG GAAACCC		
			GGAC GGTGTGCC CTTTGGG		
			C A		
GAM2477	DCO1	3'	TGGGGTTTCGCCATGTTGGCCG 50539	A A	
	G		CTG CCAACATGG GAAACCCA		
			GGC GGTGTACC CTTTGGGGT		
			C G		
GAM2477	DKFZp434A2417	3'	GGGGTTTCTCCATGTTGGTAAG 66681	G	
	G		CCT ACCAACATGGAGAAACCCC		
			GGA TGGTTGTACCTCTTTGGGG		
			A		
GAM2477	DKFZp434B044	3'	TGGGGTTTCATTATGTTGGCCA 49725	A A	
	GG		CCTG CCAACATGG GAAACCCA		

		GGAC GGTTGTATT CTTTGGGGT			
		C A			
GAM2477	DKFZP434B1727 5'	GGATTTCTCCATGTGGCCTGG 50478	TGA	A	C
		CC CCA CATGGAGAAA CC			
		GG GGT GTACCTCTTT GG			
		TCC _ A			
GAM2477	DKFZP434C212 3'	GGGGTTTCACCATGTTGGCCAG 69494	A	A	
	G	CCTG CCAACATGG GAAACCCC			
		GGAC GGTTGTACC CTTTGGGG			
		C A			
GAM2477	DKFZP434D146 3'	GGGTTTCATCATGTTGGCCAGG 32138	A	GA	
		CCTG CCAACATG GAAACCC			
		GGAC GGTTGTAC CTTTGGG			
		C TA			
GAM2477	DKFZP434F0318 3'	GGGTTTCGCCATGTTGGCCAGG 48763	A	A	
		CCTG CCAACATGG GAAACCC			
		GGAC GGTTGTACC CTTTGGG			
		C G			
GAM2477	DKFZp434F1719 3'	TGGGATTTGCCATGTTGGCCA 51018	A	A	C
	GG	CCTG CCAACATGG GAAA CCCA			
		GGAC GGTTGTACC CTTT GGGT			
		C G A			
GAM2477	DKFZP434J037 3'	GGGTTTCTCCATGTTGGTCAGG 48953			
		CCTGACCAACATGGAGAAACCC			
		GGA CTGGTTGTACCTCTTTGGG			
GAM2477	DKFZp547H025 3'	TGAGGTTTCACCATGTTGGCCA 39780	A	A	C
	GG	CCTG CCAACATGG GAAACC CA			
		GGAC GGTTGTACC CTTTGG GT			
		C A A			
GAM2477	DKFZP564G092 5'	GGATTTACCATGTTGGCCAGG 32165	A	A	C
		CCTG CCAACATGG GAAA CC			
		GGAC GGTTGTACC CTTT GG			
		C A A			
GAM2477	DKFZP564O0423 3'	TGGGGTCTCACTATGTTGCCCA 93361	AC	A	A
	GG	CCTG CAACATGG GA ACCCCA			
		GGAC GTTGTATC CT TGGGGT			
		CC A C			
GAM2477	DKFZP564O0523 3'	TGGGTTTTCACCATATTGGTCA 50425	C	A	C
	GG	CCTGACCAA ATGG GAAA CCCA			

			GGACTGGTT TACC CTTT GGGT			
			A A T			
GAM2477	DKFZP566I1024	3'	GGGTCTTTCTCTGTTGCCAGG 70650	AC	T	A
			CCTG CAACA GGAGA ACCC			
			GGAC GTTGT TCTTT TGGG			
			CC C C			
GAM2477	DKFZp761J139	5'	TGGGGTTTGACCATGTTGGCCA 51116	A		AG
	GG		CCTG CCAACATGG AAACCCCA			
			GGAC GGTGTACC TTTGGGGT			
			C AG			
GAM2477	DKFZp761O0113	5'	GGGGTTTCTCCATGTTGGTCAG 37896			
	G		CCTGACCAACATGGAGAAACCCC			
			GGACTGGTTGTACCTCTTTGGGG			
GAM2477	DKFZp762P2111	3'	GGGTTTCATCATGTTGTCCAG 87638	AC		GA
			CTG CAACATG GAAACCC			
			GAC GTTGTA CTTTGGG			
			CT TA			
GAM2477	DRIM	3'	GGATTTGCGCATGTTGGCCAGG 27954	A	A	C
			CCTG CCAACATGG GAAA CC			
			GGAC GGTGTACC CTTT GG			
			C G A			
GAM2477	DSCR6	3'	GGTTTCACCATGTTGGTCAGG 39072		A	
			CCTGACCAACATGG GAAACC			
			GGACTGGTTGTACC CTTTGG			
			A			
GAM2477	EREG	3'	GGGGTTTCACCATGTTGGCCAG 9311	A		A
	G		CCTG CCAACATGG GAAACCCC			
			GGAC GGTGTACC CTTTGGGG			
			C A			
GAM2477	ERO1L	3'	GGTTTGCTGTGTTGCCCA 28161	AC		AG
			TG CAACATGG AAACC			
			AC GTGTGTC TTTGG			
			CC GT			
GAM2477	EVI5	3'	TGGGGTTTCGCTATGTTGGCCA 20221	A		A
	GG		CCTG CCAACATGG GAAACCCCA			
			GGAC GGTGTATC CTTTGGGGT			
			C G			
GAM2477	FBP17	3'	GGGTTTCACCGTGTTGGTCAGG 73153		A	
			CCTGACCAACATGG GAAACCC			

			GGACTGGTTGTGCC CTTTGGG		
			A		
GAM2477	FER1L4	3'	GGGTTTCACCATGTTGTCCAGG 48128	AC	A
			CCTG CAACATGG GAAACCC		
			GGAC GTTGTACC CTTTGGG		
			CT A		
GAM2477	FKBP9	3'	GGGGTTTCACCGTGTGGCCAG 95718	A	A
	G		CCTG CCAACATGG GAAACCCC		
			GGAC GGTGTGCC CTTTGGGG		
			C A		
GAM2477	FLJ10232	5'	TGGGGTTTTGCTATGTTGCCCA 36387	AC	AG
	GG		CCTG CAACATGG AAACCCCA		
			GGAC GTTGTATC TTTGGGGT		
			CC GT		
GAM2477	FLJ10276	3'	GGGCTTCTTCATGTCAG 36426	CAAC	A
			CTGAC ATGGAGAA CCC		
			GACTG TACTTCTT GGG		
			— C		
GAM2477	FLJ10297	3'	GGGCTTCACTGTGTTGCCAGG 36441	AC	A A
			CCTG CAACATGG GAA CCC		
			GGAC GTTGTGTC CTT GGG		
			CC A C		
GAM2477	FLJ10298	3'	GGGGTTTCACCATGTTGGTCAG 36460		A
	G		CCTGACCAACATGG GAAACCCC		
			GGACTGGTTGTACC CTTTGGGG		
			A		
GAM2477	FLJ10346	5'	GGGTTTCACCATGTTGACCAGG 36527	AC	A
			CCTG CAACATGG GAAACCC		
			GGAC GTTGTACC CTTTGGG		
			CA A		
GAM2477	FLJ10535	3'	GGGGTTTCATTATGTTGGCCAG 36752	A	A
	G		CCTG CCAACATGG GAAACCCC		
			GGAC GGTGTATT CTTTGGGG		
			C A		
GAM2477	FLJ10535	3'	TGGGGTTTCACCATGTTGGCCA 36759	A	A
	GG		CCTG CCAACATGG GAAACCCCA		
			GGAC GGTGTACC CTTTGGGGT		
			C A		
GAM2477	FLJ10560	3'	GGGGTTTCACCGTGTAGTCAG 36797	C	A
	G		CCTGAC AACATGG GAAACCCC		

			GGACTG TTGTGCC CTTTGGGG		
			A A		
GAM2477	FLJ10607	3'	GGAGTCTATGTTGCCCAGG 77639 AC	GAAA C	
			CCTG CAACATGGA C CC		
			GGAC GTTGTATCT G GG		
			CC ____ A		
GAM2477	FLJ10713	3'	TGGGGTTTCACCATGTTGGCCA 37011 A	A	
			GG CCTG CCAACATGG GAAACCCCA		
			GGAC GGTGTACC CTTTGGGGT		
			C A		
GAM2477	FLJ10901	3'	TGGGGTTTCATCATGTTGGCCA 37376 A	GA	
			GG CCTG CCAACATG GAAACCCCA		
			GGAC GGTGTAC CTTTGGGGT		
			C TA		
GAM2477	FLJ10922	3'	GGGGTTTTGTCTCATTGCCCAG 37406 AC	CAT GA	
			G CCTG CAA G GAAACCCC		
			GGAC GTT C TTTTGGGG		
			CC ACT TG		
GAM2477	FLJ10956	3'	GGGGTTTCACCATGTTGGCCAG 37471 A	A	
			G CCTG CCAACATGG GAAACCCC		
			GGAC GGTGTACC CTTTGGGG		
			C A		
GAM2477	FLJ11186	3'	TGGGGTTTCGTCATGTTGGCCA 37731 A	GA	
			G CTG CCAACATG GAAACCCCA		
			GAC GGTGTAC CTTTGGGGT		
			C TG		
GAM2477	FLJ11800	3'	TGAGGTCTCGCCATGTTGCTCA 47043 C	A A C	
			G CTGA CAACATGG GA ACC CA		
			GACT GTTGTACC CT TGG GT		
			C G C A		
GAM2477	FLJ12363	3'	TGGGGTTTCACCATGTTGGCCA 50646 A	A	
			GG CCTG CCAACATGG GAAACCCCA		
			GGAC GGTGTACC CTTTGGGGT		
			C A		
GAM2477	FLJ12610	3'	GGCTTTGCCATGTTGCCCAGG 45860 AC	AG A	
			CCTG CAACATGG AA CC		
			GGAC GTTGTACC TT GG		
			CC GT C		
GAM2477	FLJ12668	3'	TGAGGTTTCACCTTGTTGGTCA 47164 T	A C	
			GG CCTGACCAACA GG GAAACC CA		

			GGACTGGTTGT CC CTTTGG GT		
			T A A		
GAM2477	FLJ12687	3'	GGGTTTCACCATGTTGGCCAGG 46754	A	A
			CCTG CCAACATGG GAAACCC		
			GGAC GGTGTACC CTTTGGG		
			C A		
GAM2477	FLJ12747	3'	GGGTATCTCCATGTTGGTCAGG 50669		A
			CCTGACCAACATGGAGA ACCC		
			GGACTGGTTGTACCTCT TGGG		
			A		
GAM2477	FLJ12888	3'	GTTTTGCTATGTTGCCAG 46893	AC	AG
			CTG CAACATGG AAAC		
			GAC GTTGATC TTTG		
			CC GT		
GAM2477	FLJ12903	3'	GGATTTCTCCATGTTGGTCAGG 43074		C
			CCTGACCAACATGGAGAAA CC		
			GGACTGGTTGTACCTCTTT GG		
			A		
GAM2477	FLJ12960	3'	TGGGGTTTCACCGTATGAGCCA 45308	ACCAAC	A
			GG CCTG ATGG GAAACCCCA		
			GGAC TGCC CTTTGGGGT		
			CGAGTA A		
GAM2477	FLJ12973	3'	TGGGGTTTCATCATGTTGGCCA 46646	A	GA
			GG CCTG CCAACATG GAAACCCCA		
			GGAC GGTGTAC CTTTGGGGT		
			C TA		
GAM2477	FLJ12975	3'	GGGGTTTCGCCTTGTTGCCAG 70195	AC	T A
			G CCTG CAACA GG GAAACCCC		
			GGAC GTTGT CC CTTTGGGG		
			CC T G		
GAM2477	FLJ13072	5'	GGGTTTCACCATGTTGGACAGG 91394	A	A
			CCTG CCAACATGG GAAACCC		
			GGAC GGTGTACC CTTTGGG		
			A A		
GAM2477	FLJ13188	3'	GTTTTGCTGTGTTGGTCAGG 42195		AG
			CCTGACCAACATGG AAAC		
			GGACTGGTTGTGTC TTTG		
			GT		
GAM2477	FLJ13197	3'	GTTTCACCATGTTGGCCAGG 45186	A	A
			CCTG CCAACATGG GAAAC		

			GGAC GGTTGTACC CTTTG		
			C A		
GAM2477	FLJ13305	5'	TGGGGTTTCACCATGTTGGCCA 91718	A	A
	G		CTG CCAACATGG GAAACCCCA		
			GAC GGTTGTACC CTTTGGGGT		
			C A		
GAM2477	FLJ14442	3'	TGGGGTTTTACCATGTTGGTCA 52392		A
	GG		CCTGACCAACATGG GAAACCCCA		
			GGACTGGTTGTACC TTTTGGGGT		
			A		
GAM2477	FLJ14950	3'	GGGTTTCACCATGTTGGCCAGG 52795	A	A
			CCTG CCAACATGG GAAACCC		
			GGAC GGTTGTACC CTTTGGG		
			C A		
GAM2477	FLJ14957	3'	GGGGTTTCACCATGTTGGTCAG 52825		A
	G		CCTGACCAACATGG GAAACCCC		
			GGACTGGTTGTACC CTTTGGGG		
			A		
GAM2477	FLJ20034	3'	TGGGGTCTCTCCATGTTGGTCA 34857		A
	GG		CCTGACCAACATGGAGA ACCCCA		
			GGACTGGTTGTACCTCT TGGGGT		
			C		
GAM2477	FLJ20045	3'	TGGGGATTACCATGTTGGTCA 34897	A	A
	GG		CCTGACCAACATGG GAA CCCCA		
			GGACTGGTTGTACC CTT GGGGT		
			A A		
GAM2477	FLJ20079	3'	GGGTTTCTCCATGTTGGTTAGG 34972		
			CCTGACCAACATGGAGAAACCC		
			GGATTGGTTGTACCTCTTTGGG		
GAM2477	FLJ20147	3'	GGGTCTTGCTGTGTTGCCAGG 35135	AC	AG A
			CCTG CAACATGG A ACCC		
			GGAC GTTGTGTC T TGGG		
			CC GT C		
GAM2477	FLJ20344	3'	GGGTTTCACCATGTTGGCCAG 35484	A	A
			CTG CCAACATGG GAAACCC		
			GAC GGTTGTACC CTTTGGG		
			C A		
GAM2477	FLJ20452	3'	TGAGGTTTCTCCATGTTGGTCA 35654		C
	GG		CCTGACCAACATGGAGAAACC CA		

			GGACTGGTTGTACCTCTTTGG GT		
			A		
GAM2477	FLJ20507	3'	GGGTTTCACCATGTTGGCCAGG 35748	A	A
			CCTG CCAACATGG GAAACCC		
			GGAC GGTGTACC CTTTGGG		
			C A		
GAM2477	FLJ20507	3'	GGGTTTCACCATGTTGGCCAGG 60852	A	A
			CCTG CCAACATGG GAAACCC		
			GGAC GGTGTACC CTTTGGG		
			C A		
GAM2477	FLJ20897	5'	GGGGTTTCAACGTGTTGGCCAG 51476	A	GA
	G		CCTG CCAACATG GAAACCCC		
			GGAC GGTGTGC CTTTGGGG		
			C AA		
GAM2477	FLJ21302	3'	GGGTTTCACCATGTTGGCCAGG 43511	A	A
			CCTG CCAACATGG GAAACCC		
			GGAC GGTGTACC CTTTGGG		
			C A		
GAM2477	FLJ21324	5'	TGGGGTTTCACCATGTTGGCCA 92862	A	A
			TG CCAACATGG GAAACCCCA		
			AC GGTGTACC CTTTGGGGT		
			C A		
GAM2477	FLJ21459	3'	GGGTGTTACCATGTTGGCCAGG 44809	A	A A
			CCTG CCAACATGG GA ACCC		
			GGAC GGTGTACC TT TGGG		
			C A G		
GAM2477	FLJ21603	3'	TGGGGTTTCACCCTGTTAGCCA 45783	ACC	T A
	GG		CCTG AACA GG GAAACCCCA		
			GGAC TTGT CC CTTTGGGGT		
			CGA C A		
GAM2477	FLJ21777	3'	GGTCTCTCCATGTTGCCTAGG 50846	AC	A
			CCTG CAACATGGAGA ACC		
			GGAT GTTGTACCTCT TGG		
			CC C		
GAM2477	FLJ22316	5'	TGAGGTCTTGCTATGTTGCCCA 47620	AC	AG A C
	GG		CCTG CAACATGG A ACC CA		
			GGAC GTTGTATC T TGG GT		
			CC GT C A		
GAM2477	FLJ22329	3'	GGGGTTTCACCATGTTGGCCAG 45405	A	A
			CTG CCAACATGG GAAACCCC		

			GAC GGTTGTACC CTTTGGGG		
			C A		
GAM2477	FLJ22479	3'	GGGTTGTGTTGGTTA 46607	GGAGA	C
			TGACCAACAT AACC C		
			ATTGGTTGTG TTGG G		
			_____ A		
GAM2477	FLJ22529	3'	GGGTTTCATCATGTTGGCCAGG 45949	A	GA
			CCTG CCAACATG GAAACCC		
			GGAC GGTTGTAC CTTTGGG		
			C TA		
GAM2477	FLJ22684	3'	GGGTTTCACCATGTTGGCCA 47471	A	A
			TG CCAACATGG GAAACCC		
			AC GGTTGTACC CTTTGGG		
			C A		
GAM2477	FLJ22794	3'	GGGTTTCACCATGTTGGTCAGG 93251		A
			CCTGACCAACATGG GAAACCC		
			GGACTGTTGTACC CTTTGGG		
			A		
GAM2477	FLJ22800	3'	TGGGGGTTTTCCATATTGCCCA 45994	AC C	A
			GG CCTG CAA ATGGAGAA CCCCCA		
			GGAC GTT TACCTTTT GGGGT		
			CC A G		
GAM2477	FLJ22969	3'	GGGTTTCACCATGTTGCCCAGG 69214	AC	A
			CCTG CAACATGG GAAACCC		
			GGAC GTTGTACC CTTTGGG		
			CC A		
GAM2477	FLJ23024	3'	GGGGTTTCACCATGTTGGCCAG 46844	A	A
			G CCTG CCAACATGG GAAACCCC		
			GGAC GGTTGTACC CTTTGGGG		
			C A		
GAM2477	FLJ23392	3'	GGGGTTTCACCGTGTTAGTCAG 45897	C	A
			G CCTGAC AACATGG GAAACCCC		
			GGACTG TTGTGCC CTTTGGGG		
			A A		
GAM2477	FLJ23392	3'	GGGTTTCACCATGTTGGCCAGG 45899	A	A
			CCTG CCAACATGG GAAACCC		
			GGAC GGTTGTACC CTTTGGG		
			C A		
GAM2477	FLJ23519	3'	TGGGGTTTCACCGTGTTAGCCA 50965	ACC	A
			G CTG AACATGG GAAACCCCA		

			GAC TTGTGCC CTTTGGGGT			
			CGA A			
GAM2477	FLJ23556	3'	GGGCTTCACCATGTTGGCCAGG 46447	A	A	A
			CCTG CCAACATGG GAA CCC			
			GGAC GGTTGTACC CTT GGG			
			C A C			
GAM2477	FLJ23556	3'	GGGGTTTCACCGTGTAGCCAG 46449	ACC	A	
	G		CCTG AACATGG GAAACCCC			
			GGAC TTGTGCC CTTTGGGG			
			CGA A			
GAM2477	FLJ25416	5'	TGGGGTTTCACCATGTTGGCCA 59458	A	A	
	GG		CCTG CCAACATGG GAAACCCCA			
			GGAC GGTTGTACC CTTTGGGGT			
			C A			
GAM2477	FLJ30532	3'	GGATTTCACTATGTTGGCCAGG 59223	A	A	C
			CCTG CCAACATGG GAAA CC			
			GGAC GGTTGTATC CTTT GG			
			C A A			
GAM2477	FLJ31101	3'	GGGGATTTCACCATGTTGGCCA 36166	A	A	_
	GG		CCTG CCAACATGG GAAA CCCC			
			GGAC GGTTGTACC CTTT GGGG			
			C A A			
GAM2477	FLJ31153	3'	TGGGGTTTCACCATGCTGGCCA 58757	A	A	A
	GG		CCTG CCA CATGG GAAACCCCA			
			GGAC GGT GTACC CTTTGGGGT			
			C C A			
GAM2477	FLJ32499	3'	GGGTCTCGCTGTGTTGCCCAGG 58779	AC	A	A
			CCTG CAACATGG GA ACCC			
			GGAC GTTGTGTC CT TGGG			
			CC G C			
GAM2477	FLJ32865	3'	GGGGTTTCTCCGTGTTGGTCAG 58816			
	G		CCTGACCAACATGGAGAAACCCC			
			GGA CTGGTTGTGCCTCTTTGGGG			
GAM2477	FLJ32894	3'	TGGGATTTCACCTGTGTTGGCCA 59002	A	A	C
			TG CCAACATGG GAAA CCCA			
			AC GGTTGTGTC CTTT GGGT			
			C A A			
GAM2477	GGA2	3'	GGATTTCAACCATGTTGGCCAGG 57673	A	A	C
			CCTG CCAACATGG GAAA CC			

			GGAC GGTTGTACC CTTT GG		
			C A A		
GAM2477	GGA2	3'	GGATTTCACCATGTTGGCCAGG 31169	A	A C
			CCTG CCAACATGG GAAA CC		
			GGAC GGTTGTACC CTTT GG		
			C A A		
GAM2477	GNG4	3'	GGGGTTTCACCATGTTGGTCAG 16850		A
	G		CCTGACCAACATGG GAAACCCC		
			GGA CTGGTTGTACC CTTTGGGG		
			A		
GAM2477	GOLGA3	3'	TGGGGTTTCACCATGTTGGCCA 20899	A	A
	GG		CCTG CCAACATGG GAAACCCCA		
			GGAC GGTTGTACC CTTTGGGGT		
			C A		
GAM2477	GREB1	3'	GGGGTTTCACCATGTTAGCCAG 28574	ACC	A
	G		CCTG AACATGG GAAACCCC		
			GGAC TTGTACC CTTTGGGG		
			CGA A		
GAM2477	GREB1	3'	TGGGGTTTCGCCAGGTTGGCCA 28582	A	A A
	GG		CCTG CCAAC TGG GAAACCCCA		
			GGAC GGTTG ACC CTTTGGGGT		
			C G G		
GAM2477	GRWD	3'	GGGGTTTCACCATGTTGGCCAG 49786	A	A
	G		CCTG CCAACATGG GAAACCCC		
			GGAC GGTTGTACC CTTTGGGG		
			C A		
GAM2477	GTPBG3	3'	GGTTTCACCATGTTGACCAGG 51903	AC	A
			CCTG CAACATGG GAAACC		
			GGAC GTTGTACC CTTTGG		
			CA A		
GAM2477	H2AV	3'	TGGGGTTTCACCATGTTGGCCA 57638	A	A
	G		CTG CCAACATGG GAAACCCCA		
			GAC GGTTGTACC CTTTGGGGT		
			C A		
GAM2477	HARS2	3'	GGGGTTTTACCATGTTAGCCAG 55867	ACC	A
	G		CCTG AACATGG GAAACCCC		
			GGAC TTGTACC TTTTGGGG		
			CGA A		
GAM2477	HCA4	3'	GGGGTTTTGCCATGTTGGCCAG 78042	A	AG
	G		CCTG CCAACATGG AAACCCC		

			GGAC GGTTGTACC TTTGGGG		
			C GT		
GAM2477	HNRPAB	5'	GGAGCTTGGCTGTTGGTCGG 49208	TG_	AAA
			CTGACCAACA GAG CC		
			GGCTGGTTGT TTC GG		
			CGG GA_		
GAM2477	HRH4	3'	GGGTATTGCCGTGTTGGCCAG 41544	A	AG A
			CTG CCAACATGG A ACCC		
			GAC GGTTGTGCC T TGGG		
			C GT A		
GAM2477	HRH4	3'	TGAGGTTTTGCCATTTTGGTCA 41552	C	AG C
	GG		CCTGACCAA ATGG AAACC CA		
			GGACTGGTT TACC TTTGG GT		
			T GT A		
GAM2477	HSMPP8	3'	TGGGGTTTATCCATGTTGGTCA 95143		G
	GG		CCTGACCAACATGGA AAACCCCA		
			GGACTGGTTGTACCT TTTGGGGT		
			A		
GAM2477	HSNOV1	3'	TGGGGTTTCACCATGTTGCCCA 34442	AC	A
	GG		CCTG CAACATGG GAAACCCCA		
			GGAC GTTGTACC CTTTGGGGT		
			CC A		
GAM2477	HSNOV1	3'	TGGGGTTTCGCCATGTTGCCCA 34443	AC	A
	GG		CCTG CAACATGG GAAACCCCA		
			GGAC GTTGTACC CTTTGGGGT		
			CC G		
GAM2477	HSPC065	3'	TGGGGTTTCACCATGTTGGCCA 27167	A	A
	GG		CCTG CCAACATGG GAAACCCCA		
			GGAC GGTTGTACC CTTTGGGGT		
			C A		
GAM2477	HSPC065	3'	TGGGGTTTCACGATGTTGGCCA 27168	A	_GA
	GG		CCTG CCAACAT G GAAACCCCA		
			GGAC GGTTGTA C CTTTGGGGT		
			C GA_		
GAM2477	HSPC232	3'	TGGGGTTTCACCATGTTGGCCAG 33659	A	A A
	G		CCTG CCAACATGG GAA CCCCCA		
			GGAC GGTTGTACC CTT GGGGT		
			C A _		
GAM2477	HT002	3'	GGGTTTCACCGTGTGGCCAGG 26798	A	A
			CCTG CCAACATGG GAAACCC		

			GGAC GGTGTGCC CTTTGGG		
			C A		
GAM2477	ICK	3'	GGGGTTTCACTGTGTTAGCCAG 30597	ACC	A
	G		CCTG AACATGG GAAACCCC		
			GGAC TTGTGTC CTTTGGGG		
			CGA A		
GAM2477	IKKE	3'	TGGGGTTTCCCCAGGGCAG 26596	A AACA	A
			CTG CC TGG GAAACCCCA		
			GAC GG ACC CTTTGGGGT		
			_ G _ C		
GAM2477	IMPACT	3'	GGGTCTTTCTATGTTGCCCAGG 38008	AC	A
			CCTG CAACATGGAGA ACCC		
			GGAC GTTGTATCTTT TGGG		
			CC C		
GAM2477	ITGA10	3'	GGGTTTCTCTGGTGGAAATCAG 60089	_ ACAT	
			CTGA CCA GGAGAAACCC		
			GA CT GGT TCTCTTTGGG		
			AA GG _		
GAM2477	JAM1	3'	GGGTTTCACCATGTTGGTCGGG 58521		A
			CCTGACCAACATGG GAAACCC		
			GGGCTGGTTGTACC CTTTGGG		
			A		
GAM2477	JAM1	3'	GGGTTTCACCATGTTGGTCGGG 58549		A
			CCTGACCAACATGG GAAACCC		
			GGGCTGGTTGTACC CTTTGGG		
			A		
GAM2477	JAM1	3'	GGGTTTCACCATGTTGGTCGGG 58578		A
			CCTGACCAACATGG GAAACCC		
			GGGCTGGTTGTACC CTTTGGG		
			A		
GAM2477	JAM1	3'	GGGTTTCACCATGTTGGTCGGG 34235		A
			CCTGACCAACATGG GAAACCC		
			GGGCTGGTTGTACC CTTTGGG		
			A		
GAM2477	KIAA0014	3'	GGGGTTTTGCAGGCCAGG 28543	A AACA	GA
			CCTG CC TG GAAACCCC		
			GGAC GG AC TTTTGGGG		
			C _ G _		
GAM2477	KIAA0063	3'	TGGGGTTTCTCCATGTTGGTCA 30264		
	GG		CCTGACCAACATGGAGAAACCCCA		

GGACTGGTTGTACCTCTTTGGGGT

GAM2477	KIAA0087	3'	TGGGGTTTCACCATCTTGGCCA	29349	A	C	A
			GG				
			CCTG CCAA ATGG GAAACCCCA				
			GGAC GGTT TACC CTTTGGGGT				
			C C A				
GAM2477	KIAA0161	3'	GGGGTTTCACCATGTTGGCCAG	29205	A		A
			G				
			CCTG CCAACATGG GAAACCCC				
			GGAC GGTTGTACC CTTTGGGG				
			C A				
GAM2477	KIAA0186	3'	GTTTTACCATGTTGGCCAGG	41115	A		A
			CCTG CCAACATGG GAAAC				
			GGAC GGTTGTACC TTTTG				
			C A				
GAM2477	KIAA0186	3'	TGGGGTTTCACCATGTTGGCCA	41124	A		A
			GG				
			CCTG CCAACATGG GAAACCCCA				
			GGAC GGTTGTACC CTTTGGGGT				
			C A				
GAM2477	KIAA0205	3'	TGGGGTTTCACCATGTTGGCCA	30220	A		A
			GG				
			CCTG CCAACATGG GAAACCCCA				
			GGAC GGTTGTACC CTTTGGGGT				
			C A				
GAM2477	KIAA0210	5'	GGAGTTTCACCATGTTGGCCAG	29167	A	A	C
			G				
			CCTG CCAACATGG GAAAC CC				
			GGAC GGTTGTACC CTTTG GG				
			C A A				
GAM2477	KIAA0210	5'	GGGGTTTCACTATATTGGCCAG	29169	A	C	A
			G				
			CCTG CCAA ATGG GAAACCCC				
			GGAC GGTT TATC CTTTGGGG				
			C A A				
GAM2477	KIAA0426	3'	GGGGTTTCACCATGTTGGCCAG	28929	A		A
			G				
			CCTG CCAACATGG GAAACCCC				
			GGAC GGTTGTACC CTTTGGGG				
			C A				
GAM2477	KIAA0459	3'	GGGGTTTCACCATGTTAGCCAG	61656	ACC		A
			G				
			CCTG AACATGG GAAACCCC				
			GGAC TTGTACC CTTTGGGG				
			CGA A				
GAM2477	KIAA0475	3'	GGGTTTCACCATGTTGGCCAGG	30123	A		A
			CCTG CCAACATGG GAAACCC				

			GGAC GGTTGTACC CTTTGGG		
			C A		
GAM2477	KIAA0478	3'	GGGTCTCGCCATGTTGCCAGG 30181	AC	A A
			CCTG CAACATGG GA ACCC		
			GGAC GTTGTACC CT TGGG		
			CC G C		
GAM2477	KIAA0495	3'	TGGGATTTACCATGTTGGCCA 63277	A	A C
			GG CCTG CCAACATGG GAAA CCA		
			GGAC GGTTGTACC CTTT GGGT		
			C A A		
GAM2477	KIAA0513	5'	GGGTTTCGCCATGTTGGCCAGG 29045	A	A
			CCTG CCAACATGG GAAACCC		
			GGAC GGTTGTACC CTTTGGG		
			C G		
GAM2477	KIAA0513	3'	TGGGGTTTCACCATGCTGGCCA 29054	A A	A
			GG CCTG CCA CATGG GAAACCCCA		
			GGAC GGT GTACC CTTTGGGGT		
			C C A		
GAM2477	KIAA0527	3'	TGGAGTTTCACCATGTTGGCCA 97502	A	A C
			GG CCTG CCAACATGG GAAAC CCA		
			GGAC GGTTGTACC CTTTG GGT		
			C A A		
GAM2477	KIAA0555	3'	GGGTTTCACTATGCTGGTCAGG 29552	A	A
			CCTGACCA CATGG GAAACCC		
			GGA CTGGT GTATC CTTTGGG		
			C A		
GAM2477	KIAA0557	3'	TGGGGTTTCTCCATGTTGGTCA 78579		
			GG CCTGACCAACATGGAGAAACCCCA		
			GGA CTGGTTGTACCTCTTTGGGGT		
GAM2477	KIAA0561	3'	GGGGTTTCACCATGTTGGTCAG 66484		A
			G CCTGACCAACATGG GAAACCC		
			GGA CTGGTTGTACC CTTTGGGG		
			A		
GAM2477	KIAA0562	3'	GGGGTTTCACCATATTGGCCAG 28828	A C	A
			G CCTG CCAA ATGG GAAACCC		
			GGAC GGTT TACC CTTTGGGG		
			C A A		
GAM2477	KIAA0563	5'	GGAGTTTCGCCATGTTGGTCAG 29885	A	C
			G CCTGACCAACATGG GAAAC CC		

			GGACTGGTTGTACC CTTTG GG		
			G A		
GAM2477	KIAA0594	3'	TGGGGTTTCAGCATATTGGCCA 65521	A C	GA
			GG CCTG CCAA ATG GAAACCCCA		
			GGAC GGTT TAC CTTTGGGGT		
			C A GA		
GAM2477	KIAA0599	3'	GGGGTTTCGCCGTGTTGACCAG 77695	AC	A
			G CCTG CAACATGG GAAACCCC		
			GGAC GTTGTGCC CTTTGGGG		
			CA G		
GAM2477	KIAA0682	3'	GGGGTTTCACCATGTGGGCCAG 30026	A A	A
			G CCTG CC ACATGG GAAACCCC		
			GGAC GG TGTACC CTTTGGGG		
			C G A		
GAM2477	KIAA0720	3'	GGCATTTCACCATATTGGTCAG 62987	C A	CC
			G CCTGACCAA ATGG GAAA CC		
			GGACTGGTT TACC CTTT GG		
			A A AC		
GAM2477	KIAA0737	3'	GGGTTTCACCATGTTGGCCAGG 29814	A	A
			CCTG CCAACATGG GAAACCC		
			GGAC GGTTGTACC CTTTGGG		
			C A		
GAM2477	KIAA0798	3'	GGGGTTTCACTGTGTTGGCCAG 28452	A	A
			G CCTG CCAACATGG GAAACCCC		
			GGAC GGTTGTGTC CTTTGGGG		
			C A		
GAM2477	KIAA0828	3'	GGGTTTCACTATGTTGCCCAGG 82118	AC	A
			CCTG CAACATGG GAAACCC		
			GGAC GTTGTATC CTTTGGG		
			CC A		
GAM2477	KIAA0831	5'	GGGGTTTCACCATGTTGGCCAG 30645	A	A
			G CCTG CCAACATGG GAAACCCC		
			GGAC GGTTGTACC CTTTGGGG		
			C A		
GAM2477	KIAA0831	3'	GGGGTTTTCACCATGTTGGCCA 30647	A	A_
			GG CCTG CCAACATGG GAAACCCC		
			GGAC GGTTGTACC TTTTGGGG		
			C AC		
GAM2477	KIAA0841	3'	GGAGCTTTACCATGTTGGTCAG 71898	A	ACC
			G CCTGACCAACATGG GAA CC		

			GGACTGGTTGTACC TTT GG		
			A CGA		
GAM2477	KIAA0841	3'	GGGGTTTCATCATGTTGGCCAG 71900	A	GA
			CTG CCAACATG GAAACCCC		
			GAC GGTTGTAC CTTTGGGG		
			C TA		
GAM2477	KIAA0861	3'	GGGGTTTCCCCGTGTTAGCCAG 90354	ACC	A
	G		CCTG AACATGG GAAACCCC		
			GGAC TTGTGCC CTTTGGGG		
			CGA C		
GAM2477	KIAA0884	3'	TGAGGTTTCACCATGTTGCCCA 70760	AC	A C
	GG		CCTG CAACATGG GAAACC CA		
			GGAC GTTGTACC CTTTGG GT		
			CC A A		
GAM2477	KIAA0889	3'	GGGGTTTCACCGTGTGGCCGG 31781	A	A
	G		CCTG CCAACATGG GAAACCCC		
			GGGC GGTTGTGCC CTTTGGGG		
			C A		
GAM2477	KIAA0924	3'	GGTCTTGCTATGTTGCCCAGG 30369	AC	AG A
			CCTG CAACATGG A ACC		
			GGAC GTTGTATC T TGG		
			CC GT C		
GAM2477	KIAA0924	3'	TGGGGTTTCACCATATTGGCCA 30378	A C	A
	GG		CCTG CCAA ATGG GAAACCCCA		
			GGAC GGTT TACC CTTTGGGGT		
			C A A		
GAM2477	KIAA0931	3'	GGGGTTTCACCATGTTGGCCAG 68015	A	A
	G		CCTG CCAACATGG GAAACCCC		
			GGAC GGTTGTACC CTTTGGGG		
			C A		
GAM2477	KIAA0961	3'	TGGGGTTTCACCATGTTGGCCA 30415	A	A
	GG		CCTG CCAACATGG GAAACCCCA		
			GGAC GGTTGTACC CTTTGGGGT		
			C A		
GAM2477	KIAA1010	3'	TGGGGTCTTGCTATGTTGCCCA 72545	AC	AG A
	GG		CCTG CAACATGG A ACCCA		
			GGAC GTTGTATC T TGGGGT		
			CC GT C		
GAM2477	KIAA1026	3'	TTTACCATGTTGGCCAGG 71746	A	A
			CCTG CCAACATGG GAAA		

			GGAC GGTGTACC CTTT		
			C A		
GAM2477	KIAA1028	3'	TGGGGTTTCACCCTATTGGTCA 93595	CAT	A
		GG	CCTGACCAA GG GAAACCCCA		
			GGACTGGTT CC CTTTGGGGT		
			ATC A		
GAM2477	KIAA1054	3'	TGGGGTTTCACCGTGTGGTCA 68974	A	
		GG	CCTGACCAACATGG GAAACCCCA		
			GGACTGGTTGTGCC CTTTGGGGT		
			A		
GAM2477	KIAA1115	5'	GGGTTTCGCCATGTTGCCAGG 30695	AC	A
			CCTG CAACATGG GAAACCC		
			GGAC GTTGTACC CTTTGGG		
			CC G		
GAM2477	KIAA1128	3'	TTTACCTTGTGGTCAGG 69015	T	A
			CCTGACCAACA GG GAAA		
			GGACTGGTTGT CC CTTT		
			T A		
GAM2477	KIAA1143	3'	GGGGTTTCACTTTGTTAGCCAG 69245	ACC	T A
		G	CCTG AACA GG GAAACCCC		
			GGAC TTGT TC CTTTGGGG		
			CGA T A		
GAM2477	KIAA1161	5'	TGGGGTTTACCATGTTGGCCAG 82653	A	AG
		G	CCTG CCAACATGG AAACCCCA		
			GGAC GGTGTACC TTTGGGGT		
			C A_		
GAM2477	KIAA1185	3'	GGGGTTTCACCATTTTGACCAG 63291	AC	C A
		G	CCTG CAA ATGG GAAACCCC		
			GGAC GTT TACC CTTTGGGG		
			CA T A		
GAM2477	KIAA1193	3'	TGGGGTTTCTCCTTATTGCCCA 68278	AC	CAT
		GG	CCTG CAA GGAGAAACCCCA		
			GGAC GTT CCTCTTGGGGT		
			CC ATT		
GAM2477	KIAA1198	3'	GGGGTTTCACCATGTTGGCCAG 64048	A	A
		G	CCTG CCAACATGG GAAACCCC		
			GGAC GGTGTACC CTTTGGGG		
			C A		
GAM2477	KIAA1198	3'	GGGGTTTCACCATGTTGGCCAG 64049	A	A
		G	CCTG CCAACATGG GAAACCCC		

			GGAC GGTGTACC CTTTGGGG		
			C A		
GAM2477	KIAA1198	3'	GGGGTTTCACCGTGTAGCCAG 64051	ACC	A
		G	CCTG AACATGG GAAACCCC		
			GGAC TTGTGCC CTTTGGGG		
			CGA A		
GAM2477	KIAA1198	3'	GTTTCACCATGTTGACCAGG 64059	AC	A
			CCTG CAACATGG GAAAC		
			GGAC GTTGTACC CTTTG		
			CA A		
GAM2477	KIAA1198	3'	TGGGGTTTCACCATGTTGACCA 64071	AC	A
		GG	CCTG CAACATGG GAAACCCCA		
			GGAC GTTGTACC CTTTGGGGT		
			CA A		
GAM2477	KIAA1198	3'	TGGGGTTTCTCCATGTTGGTCA 64072		
		GG	CCTGACCAACATGGAGAAACCCCA		
			GGACTGGTTGTACCTCTTTGGGGT		
GAM2477	KIAA1200	3'	GGGGTTTCACCATGTTGGCCAG 63040	A	A
		G	CCTG CCAACATGG GAAACCCC		
			GGAC GGTGTACC CTTTGGGG		
			C A		
GAM2477	KIAA1209	3'	GGGGTTTCATCATGTTGGCCAG 61406	A	GA
		G	CCTG CCAACATG GAAACCCC		
			GGAC GGTGTAC CTTTGGGG		
			C TA		
GAM2477	KIAA1210	3'	GGGGTTTCACCATGTTGGCCAG 98077	A	A
		G	CCTG CCAACATGG GAAACCCC		
			GGAC GGTGTACC CTTTGGGG		
			C A		
GAM2477	KIAA1254	3'	TGGGGTTTCACCATGTTGGCCA 70569	A	A
		GG	CCTG CCAACATGG GAAACCCCA		
			GGAC GGTGTACC CTTTGGGGT		
			C A		
GAM2477	KIAA1257	3'	GGTCTTGCTATGTTGCCAGG 63408	AC	AG A
			CCTG CAACATGG A ACC		
			GGAC GTTGTATC T TGG		
			CC GT C		
GAM2477	KIAA1257	3'	GGTTTCTCCATTTTGGTCAGG 63409	C	
			CCTGACCAA ATGGAGAAACC		

			GGACTGGTT TACCTCTTTGG		
			T		
GAM2477	KIAA1257	3'	TGGGGTTTCACAATTTTGGCCA 63425	A	C GGA
		GG	CCTG CCAA AT GAAACCCCA		
			GGAC GGTT TA CTTTGGGGT		
			C T ACA		
GAM2477	KIAA1320	5'	ATGGGATTTCAATTCACCATGT 69832	A	A_____ C ____
		TGGCCAGG	CCTG CCAACATGG GAAA CCCA T		
			GGAC GGTTGTACC CTTT GGGT A		
			C ACTTAA A ____		
GAM2477	KIAA1373	3'	TGGGGTTTTACCCTGTTGGCCA 71515	A	T A
		GG	CCTG CCAACA GG GAAACCCCA		
			GGAC GGTTGT CC TTTTGGGGT		
			C C A		
GAM2477	KIAA1456	3'	GGGGTTTCACCGTGTTAGCCAG 67564	ACC	A
		G	CCTG AACATGG GAAACCCC		
			GGAC TTGTGCC CTTTGGGG		
			CGA A		
GAM2477	KIAA1465	3'	GGGGTTTCACCATGTTGGCCAG 61505	A	A
		G	CCTG CCAACATGG GAAACCCC		
			GGAC GGTTGTACC CTTTGGGG		
			C A		
GAM2477	KIAA1467	3'	GGGGTTTCACCATGTTGGCCAG 72072	A	A
		G	CCTG CCAACATGG GAAACCCC		
			GGAC GGTTGTACC CTTTGGGG		
			C A		
GAM2477	KIAA1473	3'	GGGTTTTGCCATGTTGGCCAGG 71212	A	AG
			CCTG CCAACATGG AAACCC		
			GGAC GGTTGTACC TTTGGG		
			C GT		
GAM2477	KIAA1493	3'	TGGGGTTTCACCTTGTTGGTCA 64846	T	A
			TGACCAACA GG GAAACCCCA		
			ACTGGTTGT CC CTTTGGGGT		
			T A		
GAM2477	KIAA1497	5'	GGGTTTCACCATGTTGGTCA 68125	A	
			TGACCAACATGG GAAACCC		
			ACTGGTTGTACC CTTTGGG		
			A		
GAM2477	KIAA1508	3'	GGTTTCACCATGTTGGTCAGG 62559	A	
			CCTGACCAACATGG GAAACC		

		GGACTGGTTGTACC CTTTGG		
		A		
GAM2477	KIAA1617	3' GGGTTTCACCATGTTGGTCAGG 93080	A	
		CCTGACCAACATGG GAAACCC		
		GGACTGGTTGTACC CTTTGGG		
		A		
GAM2477	KIAA1644	3' GGATCCCACATTGGTCAG 86222	CA	A AA
		CTGACCAA TGG GA CC		
		GA CTGGTT ACC CT GG		
		AC _ A_		
GAM2477	KIAA1655	3' GGTTTCACCATGTTGGCCAGG 67196	A	A
		CCTG CCAACATGG GAAACC		
		GGAC GGTTGTACC CTTTGG		
		C A		
GAM2477	KIAA1668	3' GGGGTTTCACCGTGTTAACCAG 67075	ACC	A
	G	CCTG AACATGG GAAACCCC		
		GGAC TTGTGCC CTTTGGGG		
		CAA A		
GAM2477	KIAA1712	3' GGGTTTCTCCGTGTTGGTCAGG 68163		
		CCTGACCAACATGGAGAAACCC		
		GGACTGGTTGTGCCTCTTTGGG		
GAM2477	KIAA1727	3' TGGGATCTCACTATGTTGCTCA 64766	C	A AAC
	GG	CCTGA CAACATGG GA CCCA		
		GGACT GTTGTATC CT GGGT		
		C A CTA		
GAM2477	KIAA1737	3' TGGGGTTTTACCGTGTTGGCCA 67950	A	A
	GG	CCTG CCAACATGG GAAACCCCA		
		GGAC GGTTGTGCC TTTTGGGGT		
		C A		
GAM2477	KIAA1755	3' TGGGGTCTTGCTATGTTGCCCA 62024	AC	AG A
	GG	CCTG CAACATGG A ACCCA		
		GGAC GTTGTATC T TGGGGT		
		CC GT C		
GAM2477	KIAA1784	3' GGGGTTTCACCATGTTGCTCAG 65752	C	A
	G	CCTGA CAACATGG GAAACCCC		
		GGACT GTTGTACC CTTTGGGG		
		C A		
GAM2477	KIAA1829	3' GGGGTTTCACCACATTGGTCAG 62652	CA	A
	G	CCTGACCAA TGG GAAACCCC		

			GGACTGGTT ACC CTTTGGGG		
			AC A		
GAM2477	KIAA1829	3'	TGGGGTTTCGCGAGTTGCCAG 62660	AC	A GA
		G	CCTG CAAC TG GAAACCCCA		
			GGAC GTTG GC CTTTGGGGT		
			CC A G_		
GAM2477	KIAA1856	3'	TGGAATTTTGTGTTGGCA 94231	A	TGGA CC
			TG CCAACA GAAA CCA		
			AC GGTGT TTTT GGT		
			_ TTG_ AA		
GAM2477	KIAA1871	3'	TGAGGTCTCACTATGTTGCCA 61913	AC	A A C
		GG	CCTG CAACATGG GA ACC CA		
			GGAC GTTGTATC CT TGG GT		
			CC A C A		
GAM2477	KIAA1922	5'	TGGGGTTTCGCCATATTGATCA 74009	C C	A
		GG	CCTGA CAA ATGG GAAACCCCA		
			GGACT GTT TACC CTTTGGGGT		
			A A G		
GAM2477	KIAA1962	3'	TGGAGTCTCACTATGTTGCCA 82802	AC	A A C
		G	CTG CAACATGG GA AC CCA		
			GAC GTTGTATC CT TG GGT		
			CC A C A		
GAM2477	KIAA1971	3'	GGTTTCGCTATGTTGGCCAGG 74688	A	A
			CCTG CCAACATGG GAAACC		
			GGAC GGTGTATC CTTTGG		
			C G		
GAM2477	KIAA1975	5'	TGGGGTTTCACCATGTTAACCA 74433	ACC	A
		GG	CCTG AACATGG GAAACCCCA		
			GGAC TTGTACC CTTTGGGGT		
			CAA A		
GAM2477	KLHL6	3'	TGGAGTTCTTCATGTCTGTCA 56177	CA	A C
			TGAC ACATGGAGAA C CCA		
			ACTG TGTACTTCTT G GGT		
			TC _ A		
GAM2477	KLK7	3'	GGGTTTCACCATGTTGGCCAG 58393	A	A
			CTG CCAACATGG GAAACCC		
			GAC GGTGTACC CTTTGGG		
			C A		
GAM2477	KLK7	3'	GGGTTTCACCATGTTGGCCAG 18547	A	A
			CTG CCAACATGG GAAACCC		

			GAC GGTTGTACC CTTTGGG		
			C A		
GAM2477	LAMP3	3'	GGGGTTTCACCATGTTGGCCAG 60207	A	A
			CTG CCAACATGG GAAACCCC		
			GAC GGTTGTACC CTTTGGGG		
			C A		
GAM2477	LANCL2	3'	TGGGGTTTCTTCCATATTG 38623	C	_
			CAA ATGGA GAAACCCCA		
			GTT TACCT CTTTGGGGT		
			A T		
GAM2477	LIPI	5'	GGGTCTTATTTATGTTGCTCA 80383	C	GAA_
			TGA CAACATGGA ACCC		
			ACT GTTGTATTT TGGG		
			C ATTC		
GAM2477	LNIR	3'	TGGAGTCTCACTATGTTGCTCA 48875	C	A A C
	GG		CCTGA CAACATGG GA AC CCA		
			GGACT GTTGTATC CT TG GGT		
			C A C A		
GAM2477	LY75	3'	TGGGGTTTCACCATGTTGGCCA 11401	A	A
	GG		CCTG CCAACATGG GAAACCCCA		
			GGAC GGTTGTACC CTTTGGGGT		
			C A		
GAM2477	MACF1	3'	GGGTTTCTGCGCGGTGCAGG 53431	_	AACA G
			CCTG ACC TG AGAAACCC		
			GGAC TGG GC TCTTTGGG		
			G C__ G		
GAM2477	MACF1	3'	GGGTTTCTGCGCGGTGCAGG 24906	_	AACA G
			CCTG ACC TG AGAAACCC		
			GGAC TGG GC TCTTTGGG		
			G C__ G		
GAM2477	MAP-1	3'	GGGGTTTCACCATGTTGGCCAG 42446	A	A
	G		CCTG CCAACATGG GAAACCCC		
			GGAC GGTTGTACC CTTTGGGG		
			C A		
GAM2477	MCLC	3'	TGGGGTTTCACCATGTTGGTCA 31388		A
	GG		CCTGACCAACATGG GAAACCCCA		
			GGACTGGTTGTACC CTTTGGGGT		
			A		
GAM2477	MCM10	3'	TGGGGTTTTGCCATGTTGCTCA 38181	C	AG
	GG		CCTGA CAACATGG AAACCCCA		

			GGACT GTTGTACC TTTGGGGT			
			C GT			
GAM2477	MEF-2	3'	GGGTTTCACCATGTTGGTCAGG 65026	A		
			CCTGACCAACATGG GAAACCC			
			GGACTGGTTGTACC CTTTGGG			
			A			
GAM2477	MGC12518	3'	TGAGGGTTTCACCATGTTGGCC 64782	A	A	_
	AGG		CCTG CCAACATGG GAAACCC CA			
			GGAC GGTGTACC CTTTGGG GT			
			C A A			
GAM2477	MGC13159	3'	GGGTCTTCTATGTTGCCCAGG 53038	AC	AA	
			CCTG CAACATGGAG ACCC			
			GGAC GTTGTATCTT TGGG			
			CC C_			
GAM2477	MGC13204	3'	GGTTTCTCCATGTTGGCCAGG 49630	A		
			CCTG CCAACATGGAGAAACC			
			GGAC GGTGTACCTCTTTGG			
			C			
GAM2477	MGC15563	3'	TGGGATCTCACCATGTTGCCCA 52864	AC	A AAC	
	GG		CCTG CAACATGG GA CCCA			
			GGAC GTTGTACC CT GGGT			
			CC A CTA			
GAM2477	MGC1842	3'	GGCTTCGCCATGTTGGCCAGG 66258	A	A A	
			CCTG CCAACATGG GAA CC			
			GGAC GGTGTACC CTT GG			
			C G C			
GAM2477	MGC21675	3'	TGGGGTTTCACCATGTTGGTCA 54600	A		
	GG		CCTGACCAACATGG GAAACCCCA			
			GGACTGGTTGTACC CTTTGGGGT			
			A			
GAM2477	MGC2474	3'	TGGGGTTCCCACTATGTTGATC 43969	C	AGA_	
	AGG		CCTGA CAACATGG AACCCCA			
			GGACT GTTGTATC TTGGGGT			
			A ACCC			
GAM2477	MGC2474	3'	TGGGGTTTCACCATGTTGGCTA 43970	A	A	
	GG		CCTG CCAACATGG GAAACCCCA			
			GGAT GGTGTACC CTTTGGGGT			
			C A			
GAM2477	MGC2615	3'	GGATTTTCATCATGTTGCCCAGG 44323	AC	GA C	
			CCTG CAACATG GAAA CC			

			GGAC GTTGTAC CTTT GG		
			CC TA A		
GAM2477	MGC2654	3'	GGTCCCCTTCAGTTGGTCA 44351	A	AA_
			TGACCAAC TGGAG ACC		
			ACTGGTTG ACTTC TGG		
			_ CCC		
GAM2477	MGC33182	3'	GGGTTTCTCCATCCCTGG 76097	AC_	
			CCA ATGGAGAAACCC		
			GGT TACCTCTTTGGG		
			CCC		
GAM2477	MGC3329	3'	GGTGGCTGTTGGTCAGG 44248	TGGA	AA
			CCTGACCAACA G ACC		
			GGA CTGGTTGT C TGG		
			____ GG		
GAM2477	MGC4638	3'	GGTTTCAACATGTTGGCCAGG 49742	A	GA
			CCTG CCAACATG GAAACC		
			GGAC GGTGTAC CTTTGG		
			C AA		
GAM2477	MGC4677	5'	GGGCCTTTGCTTGGTCAGG 54615	_ T_	AGAAAC
			CCTGACCAA CA GG CCC		
			GGA CTGGTT GT CC GGG		
			C TT _____		
GAM2477	MGC4766	5'	GGGGTTTCACCGTGTAGCCAG 49561	ACC	A
	G		CCTG AACATGG GAAACCCC		
			GGAC TTGTGCC CTTTGGGG		
			CGA A		
GAM2477	MGC5149	3'	TGGGGTTTCACCACATTGGCCA 72763	A	CA A
	GG		CCTG CCAA TGG GAAACCCCA		
			GGAC GGTT ACC CTTTGGGGT		
			C AC A		
GAM2477	MKRN4	3'	GGGGTTTCACCATATTGGTCAG 48470	C	A
	G		CCTGACCAA ATGG GAAACCCC		
			GGA CTGGTT TACC CTTTGGGG		
			A A		
GAM2477	moblak	3'	TTTCACCATGTTGGCCAGG 56416	A	A
			CCTG CCAACATGG GAAA		
			GGAC GGTGTACC CTTT		
			C A		
GAM2477	MRPL20	3'	GGGTTCCGCCATGTTGGTCAGG 36206		AGA
			CCTGACCAACATGG AACCC		

			GGACTGGTTGTACC TTGGG		
			GCC		
GAM2477	MRPS27	3'	TGGGGTTTCACCATGTTGGTCA 31336	A	
	GG		CCTGACCAACATGG GAAACCCCA		
			GGACTGGTTGTACC CTTTGGGGT		
			A		
GAM2477	MtFMT	3'	TGGGGTTTCACCATGTTGGTCA 58340	A	
	GG		CCTGACCAACATGG GAAACCCCA		
			GGACTGGTTGTACC CTTTGGGGT		
			A		
GAM2477	MYO5C	3'	GGTTTCACCATGTTGGCCAGG 38725	A	A
			CCTG CCAACATGG GAAACC		
			GGAC GGTGTACC CTTTGG		
			C A		
GAM2477	NDP52	3'	GGGTTTCACTATGTTGGCCAGG 20674	A	A
			CCTG CCAACATGG GAAACCC		
			GGAC GGTGTATC CTTTGGG		
			C A		
GAM2477	NDUFC2	3'	GGGGTTTCACCATGTTGGCCA 17033	A	A
			TG CCAACATGG GAAACCC		
			AC GGTGTACC CTTTGGGG		
			C A		
GAM2477	NFAT5	3'	TGGGGTTTGTCCATGTTGGCCA 57795	A	AG
	GG		CCTG CCAACATGG AAACCCCA		
			GGAC GGTGTACC TTTGGGGT		
			C GT		
GAM2477	NINJ2	3'	GGGGTTTCTCCATGTTGGTCAG 33729		
	G		CCTGACCAACATGGAGAAACCCC		
			GGACTGGTTGTACCTCTTTGGGG		
GAM2477	Nup43	3'	GGGTTTCACCATGTTGGCCAGG 45351	A	A
			CCTG CCAACATGG GAAACCC		
			GGAC GGTGTACC CTTTGGG		
			C A		
GAM2477	Nup43	3'	TGGGGTTTCACTGTGTTGGCCA 45360	A	A
	GG		CCTG CCAACATGG GAAACCCCA		
			GGAC GGTGTGTC CTTTGGGGT		
			C A		
GAM2477	NXN	3'	TGGGGTTTCACCATGTTGGCTA 42685	A	A
	GG		CCTG CCAACATGG GAAACCCCA		

			GGAT GGTTGTACC CTTTGGGGT		
			C A		
GAM2477	OCT11	3'	TGGGGTTTCACCATGTTGGTCA 27595	A	
	GG		CCTGACCAACATGG GAAACCCCA		
			GGACTGGTTGTACC CTTTGGGGT		
			A		
GAM2477	OR51E2	3'	GTTTCACCATGTTGGCCAGG 48519	A	A
			CCTG CCAACATGG GAAAC		
			GGAC GGTTGTACC CTTTG		
			C A		
GAM2477	OSBPL2	3'	GGGTTTTCACCATGTTGGTCAG 29904	A	C
	G		CCTGACCAACATGG GAAA CCC		
			GGACTGGTTGTACC CTTT GGG		
			A T		
GAM2477	OSBPL2	3'	GGGTTTTCACCATGTTGGTCAG 58490	A	C
	G		CCTGACCAACATGG GAAA CCC		
			GGACTGGTTGTACC CTTT GGG		
			A T		
GAM2477	PASK	5'	GGGGTTTCTCCATGTTGGTCAG 31417		
	G		CCTGACCAACATGGAGAAACCCC		
			GGACTGGTTGTACCTCTTTGGGG		
GAM2477	PC326	5'	CTTCGTGGTGATTGGTCAG 38026		
			CTGACCAA CATGGAG		
			GA CTGGTT GTGCTTC		
			AGTG		
GAM2477	PELI1	5'	TGGGGTTTTCACCATGTTGGCCA 40663	A	A
	GG		CCTG CCAACATGG GAAACCCCA		
			GGAC GGTTGTACC CTTTGGGGT		
			C A		
GAM2477	PELI1	5'	GGGGTTTTCACCATGTTGCCCAG 40645	AC	A
	G		CCTG CAACATGG GAAACCCC		
			GGAC GTTGTACC CTTTGGGG		
			CC A		
GAM2477	PELI1	5'	GGTTTATCCATGTTGGTCAGG 40646		G
			CCTGACCAACATGGA AAACC		
			GGACTGGTTGTACCT TTTGG		
			A		
GAM2477	PIG7	3'	TGGGGTCTTACTATGTTGCCCA 17972	AC	A A
	GG		CCTG CAACATGG GA ACCCCA		

			GGAC GTTGTATC TT TGGGGT		
			CC A C		
GAM2477	PIP3-E	3'	GGGGTTTACCATGTTGCCCAGG 67354	AC	AG
			CCTG CAACATGG AAACCCC		
			GGAC GTTGTACC TTTGGGG		
			CC A_		
GAM2477	PLCL1	3'	GGTCATTTCTTCAGTCAG 21715	CAACA	CC_
			CTGAC TGGAGAAA CC		
			GA CTG ACTTCTTT GG		
			_____ ACT		
GAM2477	POLR2D	3'	TGGGGTTTTACTATGCTGTCCA 17846	AC A	A
	G		CTG CA CATGG GAAACCCCA		
			GAC GT GTATC TTTTGGGGT		
			CT C A		
GAM2477	PRO0365	5'	GGGGTTTCACTATGTTGGCCAG 26990	A	A
	G		CCTG CCAACATGG GAAACCCC		
			GGAC GGTTGTATC CTTTGGGG		
			C A		
GAM2477	PRO0365	5'	GGTTTTGCCATGTTGGCCAGG 26991	A	AG
			CCTG CCAACATGG AAACC		
			GGAC GGTTGTACC TTTGG		
			C GT		
GAM2477	PRO0899	5'	TGGGGACACCATGTTGCCCAGG 38315	AC	AGAAA
			CCTG CAACATGG CCCCCA		
			GGAC GTTGTACC GGGGT		
			CC ACA_		
GAM2477	PRO1992	3'	TGGGGTTTTACCATGTGGCCAG 26914	A A	A
	G		CCTG CCA CATGG GAAACCCCA		
			GGAC GGT GTACC TTTTGGGGT		
			C _ A		
GAM2477	PRO2955	3'	GGGTTTTACCATGTTGGTCAGG 38242		A
			CCTGACCAACATGG GAAACCC		
			GGA CTG GTTGTACC TTTTGGG		
			A		
GAM2477	PSTPIP2	3'	GGGTTTTACCATGTTGGTCAGG 44659		A
			CCTGACCAACATGG GAAACCC		
			GGA CTG GTTGTACC TTTTGGG		
			A		
GAM2477	RAB21	3'	GGGGTTTCACCAGGTTAGCCAG 31094	ACC A	A
	G		CCTG AAC TGG GAAACCCC		

			GGAC TTG ACC CTTTGGGG		
			CGA G A		
GAM2477	RAB33B	3'	GGGGTCTTGCTATGTTGTCCAG 49330	AC	AG A
	G		CCTG CAACATGG A ACCCC		
			GGAC GTTGTATC T TGGGG		
			CT GT C		
GAM2477	RAB33B	3'	TGGGGTTTCACCATGTTGGCCA 49338	A	A
	GG		CCTG CCAACATGG GAAACCCCA		
			GGAC GGTGTACC CTTTGGGGT		
			C A		
GAM2477	RAI	5'	GGGTTCTTACCATGTTGGCCAG 22856	A	_ GA
	G		CCTG CCAACATGG A AACCC		
			GGAC GGTGTACC T TTGGG		
			C A TC		
GAM2477	RASSF2	3'	TGGGGTTTCACCATCTTGGCCA 29114	A C	A
	GG		CCTG CCAA ATGG GAAACCCCA		
			GGAC GGTT TACC CTTTGGGGT		
			C C A		
GAM2477	RES4-25	3'	GGGGTTTCTCCATGTTGGTCAG 65271		
	G		CCTGACCAACATGGAGAAACCCC		
			GGA CTG GTTGTACCTCTTTGGGG		
GAM2477	RHOBTB2	3'	TGGGGGCGGCCATGTTGTCCAG 61606	AC	AGAAA
	G		CCTG CAACATGG CCCC		
			GGAC GTTGTACC GGGGT		
			CT GGCG_		
GAM2477	RNF8	3'	GGGTTTCACCATGTTGGCCAGG 15571	A	A
			CCTG CCAACATGG GAAACCC		
			GGAC GGTGTACC CTTTGGG		
			C A		
GAM2477	RNO2	5'	TGGGGTGTACCATGTTGGCCA 53944	A	A A
	GG		CCTG CCAACATGG GA ACCCCA		
			GGAC GGTGTACC CT TGGGGT		
			C A G		
GAM2477	SARM	3'	GGTCTTGCTATGTTGCCAGG 31299	AC	AG A
			CCTG CAACATGG A ACC		
			GGAC GTTGTATC T TGG		
			CC GT C		
GAM2477	SC4MOL	3'	TGGGGTTTCTCGATGTTGGCCA 23107	A	G
	GG		CCTG CCAACAT GAGAAACCCCA		

			GGAC GGTTGTA CTCTTTGGGGT		
			C G		
GAM2477	SCAMP-4	3'	TGGGGTTTCACCATGTTGGCCA 55357	A	A
	GG		CCTG CCAACATGG GAAACCCCA		
			GGAC GGTTGTACC CTTTGGGGT		
			C A		
GAM2477	SCYA16	3'	GGGATTCTACCATGTTGCCCAG 17174	AC	_ A
	G		CCTG CAACATGG AGAA CCC		
			GGAC GTTGTACC TCTT GGG		
			CC A A		
GAM2477	SCYA22	3'	GGCTTCACCATGTTGGCCAGG 92600	A	A A
			CCTG CCAACATGG GAA CC		
			GGAC GGTTGTACC CTT GG		
			C A C		
GAM2477	SCYA22	3'	GGGGTTTTGCCATGTTACCCAG 92601	ACC	AG
	G		CCTG AACATGG AAACCCC		
			GGAC TTGTACC TTTGGGG		
			CCA GT		
GAM2477	SERF1B	3'	TGGGGTTTCACCATGTTGGCCA 43708	A	A
	GG		CCTG CCAACATGG GAAACCCCA		
			GGAC GGTTGTACC CTTTGGGGT		
			C A		
GAM2477	SFXN2	3'	GGGGTTTCACCATGCTGGCCAG 74380	A A	A
			CTG CCA CATGG GAAACCCC		
			GAC GGT GTACC CTTTGGGG		
			C C A		
GAM2477	SIRPB1	3'	TGGGGTTTCTCCATGTTGATCA 21371	C	
	G		CTGA CAACATGGAGAAACCCCA		
			GACT GTTGTACCTCTTTGGGGT		
			A		
GAM2477	SLC12A8	3'	GGGTTTCACCATGTTGGCCAGG 45242	A	A
			CCTG CCAACATGG GAAACCC		
			GGAC GGTTGTACC CTTTGGG		
			C A		
GAM2477	SLC16A4	3'	GGGGTTTCACCATGTTAGCCAG 17455	ACC	A
	G		CCTG AACATGG GAAACCCC		
			GGAC TTGTACC CTTTGGGG		
			CGA A		
GAM2477	SLC19A3	3'	TGGGGTTTCACAATGTTGGCCA 48254	A	GGA
	GG		CCTG CCAACAT GAAACCCCA		

			GGAC GGTGTGA CTTTGGGGT		
			C ACA		
GAM2477	SLC2A10	3'	TGGGGTTTCACTGTGTTGGCCA 48560	A	A
	GG		CCTG CCAACATGG GAAACCCCA		
			GGAC GGTGTGTC CTTTGGGGT		
			C A		
GAM2477	SLC6A14	3'	GTTTCCCCATGTTGGCCAGG 24312	A	A
			CCTG CCAACATGG GAAAC		
			GGAC GGTGTACC CTTTG		
			C C		
GAM2477	STAF65(gamma)	3'	TGAGGTTTCACCGTGTGGCCA 30075	A	A C
	GG		CCTG CCAACATGG GAAACC CA		
			GGAC GGTGTGCC CTTTGG GT		
			C A A		
GAM2477	STRBP	5'	GGGGTTTTGCCATGTTGACCTG 37820	TGAC	AG
	G		CC CAACATGG AAACCCC		
			GG GTGTACC TTTGGGG		
			TCCA GT		
GAM2477	SUN1	3'	GGGTTTCACTGTGTTGGCCAGG 47916	A	A
			CCTG CCAACATGG GAAACCC		
			GGAC GGTGTGTC CTTTGGG		
			C A		
GAM2477	SYT13	3'	TGGGGTTTCACCATGTTGGCCA 95109	A	A
	GG		CCTG CCAACATGG GAAACCCCA		
			GGAC GGTGTACC CTTTGGGGT		
			C A		
GAM2477	TADA3L	3'	GGGGTTTCACCGTGTTAGCCAG 56811	ACC	A
	G		CCTG AACATGG GAAACCCC		
			GGAC TTGTGCC CTTTGGGG		
			CGA A		
GAM2477	TCL6	5'	GGTTTCACCATGTTGGCCAGG 27766	A	A
			CCTG CCAACATGG GAAACC		
			GGAC GGTGTACC CTTTGG		
			C A		
GAM2477	TCL6	5'	GGTTTCACCATGTTGGCCAGG 25914	A	A
			CCTG CCAACATGG GAAACC		
			GGAC GGTGTACC CTTTGG		
			C A		
GAM2477	TCL6	5'	GGTTTCACCATGTTGGCCAGG 40489	A	A
			CCTG CCAACATGG GAAACC		

			GGAC GGTGTACC CTTTGG		
			C A		
GAM2477	TCL6	5'	GGTTTCACCATGTTGGCCAGG 40516	A	A
			CCTG CCAACATGG GAAACC		
			GGAC GGTGTACC CTTTGG		
			C A		
GAM2477	TERA	3'	GGGGTTTCACCACGTTGGCCAG 41420	A	A A
	G		CCTG CCAAC TGG GAAACCCC		
			GGAC GGTG ACC CTTTGGGG		
			C C A		
GAM2477	TGIF2	3'	GGGGTTTCACCATCTTGGCCAG 41755	A	C A
	G		CCTG CCAA ATGG GAAACCCC		
			GGAC GGT TACC CTTTGGGG		
			C C A		
GAM2477	THEA	3'	TGGGGTTTCACTGTGTTGGCCA 66902	A	A
	GG		CCTG CCAACATGG GAAACCCCA		
			GGAC GGTGTGTC CTTTGGGGT		
			C A		
GAM2477	TNFRSF19L	3'	GGGATTCTCTGTATCATCAG 52837	CCAAC	A
			CTGA ATGGAGAA CCC		
			GACT TGTCTCTT GGG		
			ACTA_ A		
GAM2477	TRIM16	3'	TGGGGTTTCACCATGTTGGCCA 22382	A	A
	GG		CCTG CCAACATGG GAAACCCCA		
			GGAC GGTGTACC CTTTGGGGT		
			C A		
GAM2477	TRIM4	3'	TTTTCTATCCAGTCAGG 53412	CAAC	
			CCTGAC ATGGAGAAA		
			GGA CTG TATCTTTT		
			ACC_		
GAM2477	TRIM5	3'	GGGGTTTCCCATGTTGGTTAG 53473		A
	G		CCTGACCAACATGG GAAACCCC		
			GGATTGGTTGTACC CTTTGGGG		
			C		
GAM2477	TRIM5	3'	GGGGTTTCCCATGTTGGTTAG 53541		A
	G		CCTGACCAACATGG GAAACCCC		
			GGATTGGTTGTACC CTTTGGGG		
			C		
GAM2477	TRIM6	3'	GGGTTTCACCGTGTGGCCAGG 55184	A	A
			CCTG CCAACATGG GAAACCC		

			GGAC GGTGTGCC CTTTGGG		
			C A		
GAM2477	TU12B1-TY 3'	GGGGTTTCACCATGTTGGCCAG 33856	A A		
	G	CCTG CCAACATGG GAAACCCC			
		GGAC GGTGTACC CTTTGGGG			
		C A			
GAM2477	TU12B1-TY 3'	TGGGGTTTCACCATGTTGGCCA 33864	A A		
	GG	CCTG CCAACATGG GAAACCCCA			
		GGAC GGTGTACC CTTTGGGGT			
		C A			
GAM2477	TU12B1-TY 3'	TGGGGTTTCTCCATGGTGGTCA 33865	A		
	GG	CCTGACCA CATGGAGAAACCCCA			
		GGACTGGT GTACCTCTTGGGGT			
		G			
GAM2477	TUCAN 3'	GTTTTGCTATGTTGGCCAGG 30987	A AG		
		CCTG CCAACATGG AAAC			
		GGAC GGTGTATC TTTG			
		C GT			
GAM2477	TUSP 3'	TGGGGTTTTGCCATGTTGGCCA 40034	A AG		
	GG	CCTG CCAACATGG AAACCCCA			
		GGAC GGTGTACC TTTGGGGT			
		C GT			
GAM2477	UBCE7IP5 3'	GGTCTTGCTATGTTGTCCAG 30849	AC AG A		
		CTG CAACATGG A ACC			
		GAC GTTGTATC T TGG			
		CT GT C			
GAM2477	UBF-fl 3'	TGGGGTTTCACCATGCTGGCCA 52637	A A A		
	GG	CCTG CCA CATGG GAAACCCCA			
		GGAC GGT GTACC CTTTGGGGT			
		C C A			
GAM2477	UBF-fl 3'	TGGGGTTTTACCATGTTGGCCA 52638	A A		
	GG	CCTG CCAACATGG GAAACCCCA			
		GGAC GGTGTACC TTTTGGGGT			
		C A			
GAM2477	VDU1 3'	TGGGGTTTCACCATGTTGGCCA 31131	A A		
	GG	CCTG CCAACATGG GAAACCCCA			
		GGAC GGTGTACC CTTTGGGGT			
		C A			
GAM2477	VPS33A 3'	TGGTGTTCACCATGTTGGCCA 43618	A A C		
	GG	CCTG CCAACATGG GAAAC CCA			

		GGAC GGTTGTACC CTTTG GGT		
		C A T		
GAM2477	WBSCR20A 5'	GGTTTCTCCTATCAGGGTCGG 50573	AACAT_	
		CTGACC GGAGAAACC		
		GGCTGG CCTCTTTGG		
		GACTAT		
GAM2477	WBSCR23 3'	GGGGTTTCACCATGTTGGCCAG 47440	A A	
	G	CCTG CCAACATGG GAAACCCC		
		GGAC GGTTGTACC CTTTGGGG		
		C A		
GAM2477	ZAK 3'	TGAGGTTTTTAAAGTGTGGTCA 56950	A GG_ C	
	GG	CCTGACCA CAT AGAAACC CA		
		GGA CTGGT GTG TTTTGG GT		
		_ AAA A		
GAM2477	ZNF17 3'	GGGGTCTTACCATGTTGGCCAG 83273	A A A	
	G	CCTG CCAACATGG GA ACCCC		
		GGAC GGTTGTACC TT TGGGG		
		C A C		
GAM2477	ZNF221 3'	GGGGTTTCACCGTGTTAGCCAG 26270	ACC A	
	G	CCTG AACATGG GAAACCCC		
		GGAC TTGTGCC CTTTGGGG		
		CGA A		
GAM2477	LOC112687 3'	TGGGGTTTGCCATGTAGGCCAG 73245	A A AG	
	G	CCTG CC ACATGG AAACCCCA		
		GGAC GG TGTACC TTTGGGGT		
		C A G_		
GAM2477	LOC112817 3'	TGGGGTTTCACCGTGTGCGCA 57335	A A	
	GG	CCTG CCAACATGG GAAACCCCA		
		GGAC GGTTGTGCC CTTTGGGGT		
		C A		
GAM2477	LOC115219 5'	GGGGTTTCATCATGTTGGCCAG 73701	A GA	
	G	CCTG CCAACATG GAAACCCC		
		GGAC GGTTGTAC CTTTGGGG		
		C TA		
GAM2477	LOC115648 3'	GGGGTTTCACCATGTTGGCTAA 60028	GA_ A	
	G	CT CCAACATGG GAAACCCC		
		GA GGTTGTACC CTTTGGGG		
		ATC A		
GAM2477	LOC116411 5'	GGGGTTTCGCTGTGTTGGCCGG 74302	A A	
	G	CCTG CCAACATGG GAAACCCC		

		GGGC GGTGTGTC CTTTGGGG		
		C G		
GAM2477	LOC120114 3'	TGGGGTTTCACCATGTTGGCCA 76055	A	A
	GG	CCTG CCAACATGG GAAACCCCA		
		GGAC GGTGTACC CTTTGGGGT		
		C A		
GAM2477	LOC121504 3'	GGGGTTTCACCATGTTGGCCAG 74551	A	A
	G	CCTG CCAACATGG GAAACCCC		
		GGAC GGTGTACC CTTTGGGG		
		C A		
GAM2477	LOC124216 3'	GGTTTCACCATGTTGGCCAGG 74738	A	A
		CCTG CCAACATGG GAAACC		
		GGAC GGTGTACC CTTTGG		
		C A		
GAM2477	LOC126364 3'	TGGGGTTTCGCCATGTTGGCCA 76202	A	A
	GG	CCTG CCAACATGG GAAACCCCA		
		GGAC GGTGTACC CTTTGGGGT		
		C G		
GAM2477	LOC126661 3'	TGGGGTTTCACCATGTTGGCCA 75067	A	A
	G	CTG CCAACATGG GAAACCCCA		
		GAC GGTGTACC CTTTGGGGT		
		C A		
GAM2477	LOC126669 3'	GTCTCGCTGTGTTGCCAGG 75945	AC	A A
		CCTG CAACATGG GA AC		
		GGAC GTTGTGTC CT TG		
		CC G C		
GAM2477	LOC128077 3'	GGGGTTTCACCATGTTAGCCAG 75223	ACC	A
	G	CCTG AACATGG GAAACCCC		
		GGAC TTGTACC CTTTGGGG		
		CGA A		
GAM2477	LOC128077 3'	GGGTTTCACCATGTTGGCCAGG 75225	A	A
		CCTG CCAACATGG GAAACCC		
		GGAC GGTGTACC CTTTGGG		
		C A		
GAM2477	LOC128989 3'	GGGGTTTCACCATGTTGGTCAG 75322		A
	G	CCTGACCAACATGG GAAACCCC		
		GGA CTGTTGTACC CTTTGGGG		
		A		
GAM2477	LOC129880 3'	GGGGTTTCGCTGTGTTGGCCGG 75407	A	A
	G	CCTG CCAACATGG GAAACCCC		

GGGC GGTGTGTC CTTTGGGG
C G
GAM2477 LOC130612 3' GGGTTTCTCCAGGCTCAG 75471 _ AACAA
CTGA CC TGGAGAAACCC
||||| || |||||
GACT GG ACCTCTTTGGG
C ____
GAM2477 LOC130813 3' GGGTCTCACTATGTTGACCAGG 76278 AC A A
CCTG CAACATGG GA ACCC
||||| ||||| || |||||
GGAC GTTGTATC CT TGGG
CA A C
GAM2477 LOC130813 3' TGGGGTTTCTCCATGTTGGTCA 76283
GG CCTGACCAACATGGAGAAACCCCA
|||||
GGACTGGTTGTACCTCTTTGGGGT

GAM2477 LOC132625 3' TGGGGTTTCACCATGTTGGCCA 76446 A A
GG CCTG CCAACATGG GAAACCCCA
||||| |||||
GGAC GGTGTACC CTTTGGGGT
C A
GAM2477 LOC133686 3' TGGGGATTACCATGTTGGTCA 75623 A A
GG CCTGACCAACATGG GAA CCCCCA
||||| || |||||
GGACTGGTTGTACC CTT GGGGT
A A
GAM2477 LOC135293 3' GGCATTTACCATGTTGGCCAG 76688 A A CC
G CCTG CCAACATGG GAAA CC
||||| ||||| || |||||
GGAC GGTGTACC CTTT GG
C A AC
GAM2477 LOC135818 3' TGGGGTTTCTCATATTGGTCAG 75754 C G
G CCTGACCAA ATG AGAAACCCCA
||||| || |||||
GGACTGGTT TAC TCTTTGGGGT
A _
GAM2477 LOC142820 5' GGAGTTTGGCCATGTTGTCCAG 76917 AC AG C
G CCTG CAACATGG AAAC CC
||||| ||||| || |||||
GGAC GTTGTACC TTTG GG
CT GT A
GAM2477 LOC142927 3' TGGGGTCTGATTGTTGGTCA 76955 TGG AA
TGACCAACA AGA CCCCCA
||||| || |||||
ACTGGTTGT TCT GGGGT
TAG _
GAM2477 LOC143187 3' TGGAGTTTACCATGTTGGCCA 59766 A A C
GG CCTG CCAACATGG GAAAC CCA
||||| ||||| ||||| |||||

		GGAC GGTTGTACC CTTTG GGT		
		C A A		
GAM2477	LOC143916 3'	TGGGGTTTCACCTTGTGGCCA 77148	A	T A
	GG	CCTG CCAACA GG GAAACCCCA		
		GGAC GGTTGT CC CTTTGGGGT		
		C T A		
GAM2477	LOC144308 5'	GGTTTCTCTGCTCTGGCTAAG 83984	GA_	ACA
		CT CCA TGGAGAAACC		
		GA GGT GTCTCTTTGG		
		ATC CTC		
GAM2477	LOC144317 5'	TGGGGTTTCTCCATGTTGGTCG 77300		
	GG	CCTGACCAACATGGAGAAACCCCA		
		GGGCTGGTTGTACCTCTTTGGGGT		
GAM2477	LOC144519 5'	GGGGTTTTGCCATGTTGCCAG 77378	AC	AG
	G	CCTG CAACATGG AAACCCC		
		GGAC GTTGTACC TTTGGGG		
		CC GT		
GAM2477	LOC144667 3'	TGGGGTCTCCCTATGTTGCCCA 84091	AC	A A
	GG	CCTG CAACATGG GA ACCCCA		
		GGAC GTTGTATC CT TGGGGT		
		CC C C		
GAM2477	LOC144742 5'	GGTTTTCACCATGTTGGCCAGG 77464	A	A C
		CCTG CCAACATGG GAAA CC		
		GGAC GGTTGTACC CTTT GG		
		C A T		
GAM2477	LOC144871 3'	TGGGGTTTCACTGTGTTAGCCA 84131	ACC	A
	GG	CCTG AACATGG GAAACCCCA		
		GGAC TTGTGTC CTTTGGGGT		
		CGA A		
GAM2477	LOC145082 5'	GGTTTGGCCATGTTGCCAGG 84193	AC	AG
		CCTG CAACATGG AAACC		
		GGAC GTTGTACC TTTGG		
		CC GT		
GAM2477	LOC145268 5'	GTTTCACCATGTTGGCCAGG 77585	A	A
		CCTG CCAACATGG GAAAC		
		GGAC GGTTGTACC CTTTG		
		C A		
GAM2477	LOC145453 5'	TGGGGTTTTGTCATGTTGGCCA 77673	A	GA
	G	CTG CCAACATG GAAACCCCA		

		GAC GGTTGTAC TTTTGGGGT			
		C TG			
GAM2477	LOC145453 3'	TTTTCTACATGGTCAGG 77677	ACA		
		CCTGACCA TGGAGAA			
		GGA CTGGT ATCTTTT			
		AC_			
GAM2477	LOC145622 3'	GGGGTTTCACCACGTTGGCCAG 77819	A A A		
	G	CCTG CCAAC TGG GAAACCCC			
		GGAC GGTTG ACC CTTTGGGG			
		C C A			
GAM2477	LOC145761 5'	GGATTCCATGTTAACAGG 84481	ACC AAA		
		CCTG AACATGGAG CC			
		GGAC TTGTACCTT GG			
		AA_ A_			
GAM2477	LOC145980 3'	TGGGGTTTCTTTTATTACTCAG 84582	CCAACAT		
		CTGA GGAGAAACCCCA			
		GACT TTTCTTTGGGGT			
		CATTAT_			
GAM2477	LOC146050 3'	TGGGGTTTCACCATGTTGGCCA 78127	A A		
	GG	CCTG CCAACATGG GAAACCCCA			
		GGAC GGTTGTACC CTTTGGGGT			
		C A			
GAM2477	LOC146050 3'	TGGGGTTTCTCCATGTTGGGCA 78128	A		
	GG	CCTG CCAACATGGAGAAACCCCA			
		GGAC GGTTGTACCTCTTTGGGGT			
		G			
GAM2477	LOC146229 3'	GGGGTTTCACCATGTTGGCCAG 78295	A A		
	G	CCTG CCAACATGG GAAACCCC			
		GGAC GGTTGTACC CTTTGGGG			
		C A			
GAM2477	LOC146229 3'	GGGGTTTCACCATGTTGGCCAG 78296	A A		
	G	CCTG CCAACATGG GAAACCCC			
		GGAC GGTTGTACC CTTTGGGG			
		C A			
GAM2477	LOC146346 5'	GGATTTCATCATGTTGGCCA 78399	A GA C		
		TG CCAACATG GAAA CC			
		AC GGTTGTAC CTTT GG			
		C TA A			
GAM2477	LOC146346 5'	GGGGTTTCACCGTGTGTCCAG 78400	AC A		
	G	CCTG CAACATGG GAAACCCC			

		GGAC GTTGTGCC CTTTGGGG		
		CT A		
GAM2477	LOC146603 5'	GGGGTTTCACCGTGTTAGCCAG 78600	ACC	A
	G	CCTG AACATGG GAAACCCC		
		GGAC TTGTGCC CTTTGGGG		
		CGA A		
GAM2477	LOC146756 3'	GGGGTTTTGATCAGTGAGG 84811	G CAACA	A_
		CCT AC TGG GAAACCCC		
		GGA TG ACT TTTTGGGG		
		G ____ AG		
GAM2477	LOC146784 5'	TGGGGTTTCACCATGTTGGCCA 78721	A	A
	GG	CCTG CCAACATGG GAAACCCCA		
		GGAC GGTTGTACC CTTTGGGGT		
		C A		
GAM2477	LOC146839 3'	GGGGTTTCACCGTGTTAGCCAG 84844	ACC	A
	G	CCTG AACATGG GAAACCCC		
		GGAC TTGTGCC CTTTGGGG		
		CGA A		
GAM2477	LOC146894 3'	TGGGGTTTCACCATGTTGGCCA 59869	A	A
	GG	CCTG CCAACATGG GAAACCCCA		
		GGAC GGTTGTACC CTTTGGGGT		
		C A		
GAM2477	LOC146901 3'	GGGGTTTCACCATGTTGGCCAG 84908	A	A
	G	CCTG CCAACATGG GAAACCCC		
		GGAC GGTTGTACC CTTTGGGG		
		C A		
GAM2477	LOC146909 3'	TGGGGTTTCACCGTGTTAGCCA 78789	ACC	A
	GG	CCTG AACATGG GAAACCCCA		
		GGAC TTGTGCC CTTTGGGGT		
		CGA A		
GAM2477	LOC147054 3'	TGGGGTTTCTCCATGTTGGTCA 85012		
	GG	CCTGACCAACATGGAGAAACCCCA		
		GGA CTGGTTGTACCTCTTTGGGGT		
GAM2477	LOC147071 5'	GGAGTTTCACCATGTTGGTTAG 73368	A	C
	G	CCTGACCAACATGG GAAAC CC		
		GGATTGGTTGTACC CTTTG GG		
		A A		
GAM2477	LOC147166 3'	TGGGGTTTCACCATGTTGGCCA 78898	A	A
	GG	CCTG CCAACATGG GAAACCCCA		

		GGAC GGTGTACC CTTTGGGGT			
		C A			
GAM2477	LOC147229 3'	TGGGGTTTTGTGCTGGGCAGG 78928	A A	GGA	
		CCTG CCA CAT GAAACCCCA			
		GGAC GGT GTG TTTTGGGGT			
		G C _			
GAM2477	LOC147276 3'	GGGGCTTCTCCATGTTGGTCAG 78968		A	
	G	CCTGACCAACATGGAGAA CCCC			
		GGA CTGTTGTACCTCTT GGGG			
		C			
GAM2477	LOC147429 3'	TGGGGTTTCACCATGTTAGTCA 79002	C A		
	GG	CCTGAC AACATGG GAAACCCCA			
		GGA CTG TTGTACC CTTTGGGGT			
		A A			
GAM2477	LOC147694 3'	GGGGTTTCACCGTGTTAGCCAG 79101	ACC A		
	G	CCTG AACATGG GAAACCCC			
		GGAC TTGTGCC CTTTGGGG			
		CGA A			
GAM2477	LOC147817 3'	GGGCTTCACCATGTTGGCAAGG 79186	GA A A		
		CCT CCAACATGG GAA CCC			
		GGA GGTGTACC CTT GGG			
		AC A C			
GAM2477	LOC147841 3'	TGGAGTTTCACCATGGTGGTCA 79233	A A C		
	GG	CCTGACCA CATGG GAAAC CCA			
		GGA CTGGT GTACC CTTTG GGT			
		G A A			
GAM2477	LOC147990 3'	GGGGTTTCAGCATATTGACCAG 85228	AC C GA		
	G	CCTG CAA ATG GAAACCCC			
		GGAC GTT TAC CTTTGGGG			
		CA A GA			
GAM2477	LOC148189 5'	GGGGTTTCACCATGTTGACCAG 79452	AC A		
	G	CCTG CAACATGG GAAACCCC			
		GGAC GTTGTACC CTTTGGGG			
		CA A			
GAM2477	LOC148195 3'	GGTTTCACCACATTGGTCAGG 85287	CA A		
		CCTGACCAA TGG GAAACC			
		GGA CTGGT ACC CTTTGG			
		AC A			
GAM2477	LOC148198 3'	GGGTTTTGCCATGTTGGCCAGG 71227	A AG		
		CCTG CCAACATGG AAACCC			

		GGAC GGTGTGACC TTTGGG		
		C GT		
GAM2477	LOC148645 5'	GGGTCTCACTGTGTTGGCCAGG 85338	A	A A
		CCTG CCAACATGG GA ACCC		
		GGAC GGTGTGTC CT TGGG		
		C A C		
GAM2477	LOC148709 3'	GGGTTTCTCCATGTTGGTCAGG 79696		
		CCTGACCAACATGGAGAAACCC		
		GGA CTGTTGTACCTCTTTGGG		
GAM2477	LOC148759 3'	TGGAATGCTGACCATGTTGATG 85377	GAC	__ AAACC
	AGG	CCT CAACATGG AG CCA		
		GGA GTTGTACC TC GGT		
		GTA AG GTAA_		
GAM2477	LOC148887 5'	GGGTTTCACCATGTTGGTCAGG 85408		A
		CCTGACCAACATGG GAAACCC		
		GGA CTGTTGTACC CTTTGGG		
		A		
GAM2477	LOC149171 5'	TGGGGTTTCTCCATGTTGGTCA 79971		
	GG	CCTGACCAACATGGAGAAACCCCA		
		GGA CTGTTGTACCTCTTTGGGGT		
GAM2477	LOC149276 5'	GGTTTCTCCCATCTGGTCAG 85539	ACAT	
		CTGACCA GGAGAAACC		
		GACTGGT CCTCTTTGG		
		CTAC		
GAM2477	LOC149478 3'	GGGGTTTCACCATGTTGGCCAG 80174	A	A
	G	CCTG CCAACATGG GAAACCCC		
		GGAC GGTGTACC CTTTGGGG		
		C A		
GAM2477	LOC149577 3'	TGGGGTTTTGCCATGTTGGCCA 85684	A	AG
	G	CTG CCAACATGG AAACCCCA		
		GAC GGTGTACC TTTGGGGT		
		C GT		
GAM2477	LOC149692 3'	GGGTTTCACCATGTTGGCCAGG 85741	A	A
		CCTG CCAACATGG GAAACCC		
		GGAC GGTGTACC CTTTGGG		
		C A		
GAM2477	LOC149692 3'	TTTCACCATGTTGACCAGG 85748	AC	A
		CCTG CAACATGG GAAA		

		GGAC GTTGTACC CTTT		
		CA A		
GAM2477	LOC149703 5'	GGGGTTTTGCCATGTTGGCCAG 85823	A	AG
	G	CCTG CCAACATGG AAACCCC		
		GGAC GGTGTACC TTTGGGG		
		C GT		
GAM2477	LOC149711 3'	TGGGGTTTTACCATGTTGGCCA 85859	A	A
		TG CCAACATGG GAAACCCCA		
		AC GGTGTACC TTTTGGGGT		
		C A		
GAM2477	LOC150054 5'	TGGGGTTTCCCATGTTGGCCAG 85979	A	A
	G	CCTG CCAACATGG GAAACCCCA		
		GGAC GGTGTACC CTTTGGGGT		
		C -		
GAM2477	LOC150166 5'	TGGGGTTTCACCATGTTGTCCA 86045	AC	A
	GG	CCTG CAACATGG GAAACCCCA		
		GGAC GTTGTACC CTTTGGGGT		
		CT A		
GAM2477	LOC150282 5'	TGGCGTTTCACCATGTTGGCCA 80547	A	A C
	GG	CCTG CCAACATGG GAAAC CCA		
		GGAC GGTGTACC CTTTG GGT		
		C A C		
GAM2477	LOC150696 3'	GGGGTTTTGCCATGTTGCCAG 59162	AC	AG
	G	CCTG CAACATGG AAACCCC		
		GGAC GTTGTACC TTTGGGG		
		CC GT		
GAM2477	LOC151050 5'	GTTTCACCATGTTGGCCA 80920	A	A
		TG CCAACATGG GAAAC		
		AC GGTGTACC CTTTG		
		C A		
GAM2477	LOC151057 3'	GGGGTTTCACCATGTTGGCCAG 86391	A	A
	G	CCTG CCAACATGG GAAACCCC		
		GGAC GGTGTACC CTTTGGGG		
		C A		
GAM2477	LOC151201 3'	GGGGTTTCACCATGTTGGCTAG 86479	A	A
	G	CCTG CCAACATGG GAAACCCC		
		GGAT GGTGTACC CTTTGGGG		
		C A		
GAM2477	LOC151475 5'	GGTTTCACCATGTTGGCCAGG 86599	A	A
		CCTG CCAACATGG GAAACC		

		GGAC GGTGTACC CTTTGG		
		C A		
GAM2477	LOC151701 3'	GGGGTTTCACCATGTTGGCCAG 86677	A	A
	G	CCTG CCAACATGG GAAACCCC		
		GGAC GGTGTACC CTTTGGGG		
		C A		
GAM2477	LOC151826 3'	GGGTTTCACCGTGTGGCGAG 81183	GA	A
		CT CCAACATGG GAAACCC		
		GA GGTGTGCC CTTTGGG		
		GC A		
GAM2477	LOC151877 3'	TGGGGTCTTGCTGTGTTGCCCA 86701	AC	AG A
	GG	CCTG CAACATGG A ACCCCA		
		GGAC GTTGTGTC T TGGGGT		
		CC GT C		
GAM2477	LOC152137 3'	GGGTTTCACCATGTTGGCCAGG 81322	A	A
		CCTG CCAACATGG GAAACCC		
		GGAC GGTGTACC CTTTGGG		
		C A		
GAM2477	LOC152719 5'	GGGGTTTCACCATGTTGGTCAG 87035		A
	G	CCTGACCAACATGG GAAACCCC		
		GGA CTG GTTGTACC CTTTGGGG		
		A		
GAM2477	LOC152794 5'	TGGGGTTTCATCATGTTGGCCA 81566	A	GA
	GG	CCTG CCAACATG GAAACCCCA		
		GGAC GGTGTAC CTTTGGGGT		
		C TA		
GAM2477	LOC152851 3'	GGATTTCACATGTTGGTCAGG 81594		A C
		CCTGACCAACATGG GAAA CC		
		GGA CTG GTTGTATC CTTT GG		
		A A		
GAM2477	LOC153077 3'	TGGGGCTTCACCATGTTGGCCA 87135	A	A A
	GG	CCTG CCAACATGG GAA CCCC		
		GGAC GGTGTACC CTT GGGGT		
		C A C		
GAM2477	LOC153606 5'	GGGTTTCACCATGTTGGCCAGG 87259	A	A
		CCTG CCAACATGG GAAACCC		
		GGAC GGTGTACC CTTTGGG		
		C A		
GAM2477	LOC153688 3'	GGATTTCATCGTGTGCCCAGG 87322	AC	GA C
		CCTG CAACATG GAAA CC		

		GGAC GTTGTGC CTTT GG			
		CC TA A			
GAM2477	LOC153688 3'	GGGCTCCCCATGTTGCCAGG 87325	AC	A	AAC
		CCTG CAACATGG GA CCC			
		GGAC GTTGTACC CT GGG			
		CC C C__			
GAM2477	LOC153688 3'	GGGTTTCACCATGTTGGCCGGG 87327	A	A	
		CCTG CCAACATGG GAAACCC			
		GGGC GGTGTACC CTTTGGG			
		C A			
GAM2477	LOC153811 3'	TTCTCCATGTTGCCAGG 81856	AC		
		CCTG CAACATGGAGAA			
		GGAC GTTGTACCTCTT			
		CC			
GAM2477	LOC153883 5'	TGGGGTTTTACCATGTTGTCCA 81897	AC	A	
	GG	CCTG CAACATGG GAAACCCCA			
		GGAC GTTGTACC TTTTGGGGT			
		CT A			
GAM2477	LOC154282 5'	TGGTGTTCACCATGTTGGCCA 87415	A	A	C
	GG	CCTG CCAACATGG GAAAC CCA			
		GGAC GGTGTACC CTTTG GGT			
		C A T			
GAM2477	LOC154789 3'	GGTCCCTTTTTTGTTCATCAG 82032	CC	T_	A_
	G	CCTGA AACA GGAG AACC			
		GGA CT TTGT TTTC TTGG			
		AC TT CC			
GAM2477	LOC154877 3'	GGATCTCACTATGTTGCCAGG 87559	AC	A	AAC
		CCTG CAACATGG GA CC			
		GGAC GTTGTATC CT GG			
		CC A CTA			
GAM2477	LOC154877 3'	GGGGTTTCACCATGTTGCCAG 87564	AC	A	
	G	CCTG CAACATGG GAAACCCC			
		GGAC GTTGTACC CTTTGGGG			
		CC A			
GAM2477	LOC154877 3'	GGGTCTCACCATGTTGGCTAGG 87566	A	A	A
		CCTG CCAACATGG GA ACCC			
		GGAT GGTGTACC CT TGGG			
		C A C			
GAM2477	LOC154877 5'	TGGGGTTTTGCCATGTTGGCCA 87584	A	AG	
	GG	CCTG CCAACATGG AAACCCCA			

		GGAC GGTTGTACC TTTGGGGT			
		C GT			
GAM2477	LOC154930 3'	GGATTTTACTGTGTTGGCCAGG 82094	A	A	C
		CCTG CCAACATGG GAAA CC			
		GGAC GGTTGTGTC TTTT GG			
		C A A			
GAM2477	LOC157247 5'	GGGGTTTCACCAGTGTGGCCA 82303	A	_	A
	G	CTG CCAACA TGG GAAACCCC			
		GAC GGTTGT ACC CTTTGGGG			
		C G A			
GAM2477	LOC157506 3'	GGGGTTTCACCATGTTGGTCAG 82371		A	
	G	CCTGACCAACATGG GAAACCCC			
		GGACTGGTTGTACC CTTTGGGG			
		A			
GAM2477	LOC157798 5'	GGGGTTTCACCTTGTGGCCAG 87863	A	T	A
	G	CCTG CCAACA GG GAAACCCC			
		GGAC GGTTGT CC CTTTGGGG			
		C T A			
GAM2477	LOC158014 5'	TGGGGTCTCGCTATGTTGACCA 82571	AC	A	A
	GG	CCTG CAACATGG GA ACCCCA			
		GGAC GTTGTATC CT TGGGGT			
		CA G C			
GAM2477	LOC158476 3'	GGGTTTCACCATGTTGGTCAGG 88200		A	
		CCTGACCAACATGG GAAACCC			
		GGACTGGTTGTACC CTTTGGG			
		A			
GAM2477	LOC158668 3'	TGGGGTTTCACCATGCTGGTCA 69909	A	A	
	GG	CCTGACCA CATGG GAAACCCCA			
		GGACTGGT GTACC CTTTGGGGT			
		C A			
GAM2477	LOC159121 3'	GGTGGCCATGTTGCCAGG 88388	AC	AGAA	
		CCTG CAACATGG ACC			
		GGAC GTTGTACC TGG			
		C_ GG_			
GAM2477	LOC160646 3'	TGGGGCTTCACCATGTTGGCCA 83126	A	A	A
	GG	CCTG CCAACATGG GAA CCCCCA			
		GGAC GGTTGTACC CTT GGGGT			
		C A C			
GAM2477	LOC161829 3'	TGGGGTTTCACCATGTTGGCCA 83196	A	A	
	GG	CCTG CCAACATGG GAAACCCCA			

		GGAC GGTGTACC CTTTGGGGT		
		C A		
GAM2477	LOC162427 3'	TGGGGTTTCACCATGTTGGCCA 83234	A	A
	GG	CCTG CCAACATGG GAAACCCCA		
		GGAC GGTGTACC CTTTGGGGT		
		C A		
GAM2477	LOC169611 3'	GGATTTCACCATGTTGGCCAGG 83653	A	A C
		CCTG CCAACATGG GAAA CC		
		GGAC GGTGTACC CTTT GG		
		C A A		
GAM2477	LOC169611 3'	GGGGTTTCACCACGTTGGCCAG 83655	A	A A
	G	CCTG CCAAC TGG GAAACCCC		
		GGAC GGTG ACC CTTTGGGG		
		C C A		
GAM2477	LOC170082 5'	TGGGGTTTCACCATGTTAGCCA 83451	ACC	A
	GG	CCTG AACATGG GAAACCCCA		
		GGAC TTGTACC CTTTGGGGT		
		CGA A		
GAM2477	LOC196264 3'	GGGGTTTCACCATTTTGGCCAG 88989	A	C A
	G	CCTG CCAA ATGG GAAACCCC		
		GGAC GGTT TACC CTTTGGGG		
		C T A		
GAM2477	LOC196411 3'	TGGGGTTTCACTATGTTGGCCA 89051	A	A
	GG	CCTG CCAACATGG GAAACCCCA		
		GGAC GGTGTATC CTTTGGGGT		
		C A		
GAM2477	LOC196529 3'	GTTTCCCCACGTTGGTCAG 89140	A	A
		CTGACCAAC TGG GAAAC		
		GACTGGTTG ACC CTTTG		
		C C		
GAM2477	LOC197259 5'	GGGGTTTCCCTCAGGTAGG 89301	A	AACAT A
		CCTG CC GG GAAACCCC		
		GGAT GG CC CTTTGGGG		
		_ ACT_ _		
GAM2477	LOC197358 3'	GGGGTTTCATCATGTTGGCCAG 89439	A	GA
	G	CCTG CCAACATG GAAACCCC		
		GGAC GGTGTAC CTTTGGGG		
		C TA		
GAM2477	LOC197358 3'	TGGGGTTTCACCATGTTGATCA 89449	C	A
	GG	CCTGA CAACATGG GAAACCCCA		

		GGACT GTTGTACC CTTTGGGGT		
		A A		
GAM2477	LOC199725 5'	GGGATTTACCATGTTGGTCAG 91423	A	C
	G	CCTGACCAACATGG GAAA CCC		
		GGACTGGTTGTACC CTTT GGG		
		A A		
GAM2477	LOC199786 3'	GGTTTCACCATGTTGGTCAGG 89762	A	
		CCTGACCAACATGG GAAACC		
		GGACTGGTTGTACC CTTTGG		
		A		
GAM2477	LOC199786 3'	TGGGGTTTCACCATGTTGGCCA 89771	A	A
	GG	CCTG CCAACATGG GAAACCCCA		
		GGAC GGTTGTACC CTTTGGGGT		
		C A		
GAM2477	LOC199906 3'	GGGTTTCATCATGTTGGCCTGG 89857	TGA	GA
		CC CCAACATG GAAACCC		
		GG GGTTGTAC CTTTGGG		
		TCC TA		
GAM2477	LOC200014 3'	GGTGTTCACCATGTTGGTCAG 89942	A	C
	G	CCTGACCAACATGG GAAAC CC		
		GGACTGGTTGTACC CTTTG GG		
		A T		
GAM2477	LOC200169 5'	GGAGTTTCACCATGTTGGCCA 91559	A	A C
		TG CCAACATGG GAAAC CC		
		AC GGTTGTACC CTTTG GG		
		C A A		
GAM2477	LOC200268 3'	TGGGATTTGCCATGTTGCCCA 90088	AC	AG C
	GG	CCTG CAACATGG AAA CCA		
		GGAC GTTGTACC TTT GGGT		
		CC GT A		
GAM2477	LOC200301 5'	GGGGTTTCACCGTGTTAGCCAG 90147	ACC	A
		CTG AACATGG GAAACCCC		
		GAC TTGTGCC CTTTGGGG		
		CGA A		
GAM2477	LOC200310 3'	GGGGTTTCACCATGTTGGTCAG 66331	A	
	G	CCTGACCAACATGG GAAACCCC		
		GGACTGGTTGTACC CTTTGGGG		
		A		
GAM2477	LOC200314 3'	TGGGGTTTCACCACGTTGGCCA 91607	A	A A
	G	CTG CCAAC TGG GAAACCCCA		

		GAC GGTTG ACC CTTTGGGGT		
		C C A		
GAM2477	LOC200316 5'	GGGGTTTCTCCATGTTGGTCAG 90187		
	G	CCTGACCAACATGGAGAAACCCC		
		GGA CTGGTTGTACCTCTTTGGGG		
GAM2477	LOC200316 3'	GGGTTTCACCATGTTGGCCAGG 90188	A	A
		CCTG CCAACATGG GAAACCC		
		GGAC GGTTGTACC CTTTGGG		
		C A		
GAM2477	LOC200339 3'	GGGATTTTCCCTTGTGTCAG 91617	T_	A
	G	CCTGACCAACA GGAGAA CCC		
		GGA CTGGTTGT CCTTTT GGG		
		TC A		
GAM2477	LOC200407 3'	GGGTTTGGCCATGTTGACCAGG 91630	AC	AG
		CCTG CAACATGG AAACCC		
		GGAC GTTGTACC TTTGGG		
		CA GT		
GAM2477	LOC200860 3'	GGGGTTTCTCCATGTTAGTCAG 91754	C	
	G	CCTGAC AACATGGAGAAACCCC		
		GGA CTG TTGTACCTCTTTGGGG		
		A		
GAM2477	LOC201164 3'	GGGTTTCACCATGTTGGTTAGG 89499	A	
		CCTGACCAACATGG GAAACCC		
		GGATTGGTTGTACC CTTTGGG		
		A		
GAM2477	LOC201173 5'	GGAGTTTCACCATGTTGGTCAG 88689	A	C
	G	CCTGACCAACATGG GAAAC CC		
		GGA CTGGTTGTACC CTTTG GG		
		A A		
GAM2477	LOC201220 5'	TGGAGTTTCACCATGTTGGTCA 88729	A	C
	GG	CCTGACCAACATGG GAAAC CCA		
		GGA CTGGTTGTACC CTTTG GGT		
		A A		
GAM2477	LOC201294 3'	GGGGTTTCACCATGTTGGCCAG 89591	A	A
	G	CCTG CCAACATGG GAAACCCC		
		GGAC GGTTGTACC CTTTGGGG		
		C A		
GAM2477	LOC201411 3'	GGGTTTCACCATGTTGGTCAGG 63646	A	
		CCTGACCAACATGG GAAACCC		

		GGACTGGTTGTACC CTTTGGG			
		A			
GAM2477	LOC201626 3'	TGGGGTTTCGCCACGTTGGCCA 90440	A	A	A
	GG	CCTG CCAAC TGG GAAACCCCA			
		GGAC GGTG ACC CTTTGGGGT			
		C C G			
GAM2477	LOC201627 3'	TGGGGTTTCTCCATGTTGGTCA 90465			
	GG	CCTGACCAACATGGAGAAACCCCA			
		GGACTGGTTGTACCTCTTTGGGGT			
GAM2477	LOC201696 3'	GGTTTCTCCATGTTGACAGG 63824	ACC		
		CCTG AACATGGAGAAACC			
		GGAC TTGTACCTCTTTGG			
		AGC			
GAM2477	LOC202460 5'	TGGGGTTTCACCATGTAGGCCA 90682	A	A	A
	GG	CCTG CC ACATGG GAAACCCCA			
		GGAC GG TGTACC CTTTGGGGT			
		C A A			
GAM2477	LOC202460 5'	TGGGGTTTCCAGTTACAACCAG 90683	ACC__	A	GA
		CTG AAC TGGA AACCCCA			
		GAC TTG ACCT TTGGGGT			
		CAACA _ _			
GAM2477	LOC203197 3'	TGGGGTTTCGCCATGTTGGCCA 90821	A		A
		TG CCAACATGG GAAACCCCA			
		AC GGTTGTACC CTTTGGGGT			
		C G			
GAM2477	LOC203339 3'	TGGGGTTTCACCATGTTTGCCA 92219	ACC		A
	GG	CCTG AACATGG GAAACCCCA			
		GGAC TTGTACC CTTTGGGGT			
		CGT A			
GAM2477	LOC203350 3'	GGGGTTTCACCGTGTTGGCCAG 92243	A		A
	G	CCTG CCAACATGG GAAACCCC			
		GGAC GGTTGTGCC CTTTGGGG			
		C A			
GAM2477	LOC203369 3'	TGGGGTTTCACTGTGTTAGCTA 90893	ACC		A
	GG	CCTG AACATGG GAAACCCCA			
		GGAT TTGTGTC CTTTGGGGT			
		CGA A			
GAM2477	LOC203378 3'	TGGGATTTTACCACATTGGTCA 92308	CA	A	C
	GG	CCTGACCAA TGG GAAA CCCA			

		GGACTGGTT ACC TTTT GGGT		
		AC A A		
GAM2477	LOC219445 5'	GGGGTTTCACCGTGTTAGCCAG 93210	ACC	A
	G	CCTG AACATGG GAAACCCC		
		GGAC TTGTGCC CTTTGGGG		
		CGA A		
GAM2477	LOC219673 5'	GGGGTTTCACCATGTTGGCCAG 94628	A	A
	G	CCTG CCAACATGG GAAACCCC		
		GGAC GGTGTACC CTTTGGGG		
		C A		
GAM2477	LOC219731 5'	GGGTTTCTCCATTTTGGCCAG 94710	A	C
		CTG CCAA ATGGAGAAACCC		
		GAC GGTT TACCTCTTTGGG		
		C T		
GAM2477	LOC219731 5'	GTTTCGTCATGTTGCCAGG 94714	AC	GA
		CCTG CAACATG GAAAC		
		GGAC GTTGTAC CTTTG		
		CC TG		
GAM2477	LOC219731 5'	TCTTGCTATGTTGTCCAGG 94717	AC	—
		CCTG CAACATGG AGA		
		GGAC GTTGTATC TCT		
		CT GT		
GAM2477	LOC219735 3'	GGGGTTTCACCGTGTTAGCCAG 94731	ACC	A
	G	CCTG AACATGG GAAACCCC		
		GGAC TTGTGCC CTTTGGGG		
		CGA A		
GAM2477	LOC219894 3'	TGGGGTTTCACCGTGTTAGCCA 94911	ACC	A
	GG	CCTG AACATGG GAAACCCCA		
		GGAC TTGTGCC CTTTGGGGT		
		CGA A		
GAM2477	LOC220064 3'	TGGGGTTTTGCCTTGTTGGCCA 95070	A	T AG
	GG	CCTG CCAACA GG AAACCCCA		
		GGAC GGTTGT CC TTTGGGGT		
		C T GT		
GAM2477	LOC220074 3'	GGGGTTTCACCATGTTAGCCAG 59987	ACC	A
	G	CCTG AACATGG GAAACCCC		
		GGAC TTGTACC CTTTGGGG		
		CGA A		
GAM2477	LOC220074 3'	GGTTTCGCCATGTTGGCCAGG 59990	A	A
		CCTG CCAACATGG GAAACC		

		GGAC GGTTGTACC CTTTGG		
		C G		
GAM2477	LOC220074 3'	TGGGGTTTCGCCATGTTGGCCA 60001	A	A
	GG	CCTG CCAACATGG GAAACCCCA		
		GGAC GGTTGTACC CTTTGGGGT		
		C G		
GAM2477	LOC220662 3'	GGGTCTCACTATGTTGCCAGG 92826	AC	A A
		CCTG CAACATGG GA ACCC		
		GGAC GTTGTATC CT TGGG		
		CC A C		
GAM2477	LOC220662 3'	GGGTTTTGCCATGTTGGCCAGG 92827	A	AG
		CCTG CCAACATGG AAACCC		
		GGAC GGTTGTACC TTTGGG		
		C GT		
GAM2477	LOC221296 3'	GGGGTTTCACCATGCTGGCCAG 93613	A A	A
	G	CCTG CCA CATGG GAAACCCC		
		GGAC GGT GTACC CTTTGGGG		
		C C A		
GAM2477	LOC221477 3'	GGAGTCTCCGTGATGCCAGG 93774	AC A	AA
		CCTG CA CATGGAGA CC		
		GGAC GT GTGCCTCT GG		
		C_ A GA		
GAM2477	LOC221584 5'	GGGTTCTATTGATGGTTAGG 95471	A TGG	A
		CCTGACCA CA AG AACCC		
		GGATTGGT GT TC TTGGG		
		A TA_ C		
GAM2477	LOC221663 5'	GGTTTCACTATGTTGCCAGG 95467	AC	A
		CCTG CAACATGG GAAACC		
		GGAC GTTGTATC CTTTGG		
		CC A		
GAM2477	LOC221964 3'	GGGTTTTGCCGTGTTGGCCAGG 95608	A	AG
		CCTG CCAACATGG AAACCC		
		GGAC GGTTGTGCC TTTGGG		
		C GT		
GAM2477	LOC222031 3'	GGTTTCAACATGTTGGCCAGG 95683	A	GA
		CCTG CCAACATG GAAACC		
		GGAC GGTTGTAC CTTTGG		
		C AA		
GAM2477	LOC222068 3'	TGGGGTTTACCATGTTGGCCA 94281	A	A
	GG	CCTG CCAACATGG GAAACCCCA		

		GGAC GGTTGTACC TTTTGGGGT			
		C A			
GAM2477	LOC222070 5'	GGTGTTCACCATGTTGGCCAG 95819	A	A	C
	G	CCTG CCAACATGG GAAAC CC			
		GGAC GGTTGTACC CTTTG GG			
		C A T			
GAM2477	LOC222224 5'	GGGTTTCACCATGTTGGCCAGG 95875	A	A	
		CCTG CCAACATGG GAAACCC			
		GGAC GGTTGTACC CTTTGGG			
		C A			
GAM2477	LOC245771 5'	TGGGGTTTCATCATGTTGGCCA 94491	A	GA	
	GG	CCTG CCAACATG GAAACCCCA			
		GGAC GGTTGTAC CTTTGGGGT			
		C TA			
GAM2477	LOC253142 3'	TGGAATTTCTCCATTCCCTGG 99228	AC__	CC	
		CCA ATGGAGAAA CCA			
		GGT TACCTCTTT GGT			
		CCCT AA			
GAM2477	LOC253612 5'	GTTTTGCCATGTTGGCCAGG 98557	A	AG	
		CCTG CCAACATGG AAAC			
		GGAC GGTTGTACC TTTG			
		C GT			
GAM2477	LOC253664 3'	TGGGGTTTCCCCATGTTGGCCA 96476	A	A	
	GG	CCTG CCAACATGG GAAACCCCA			
		GGAC GGTTGTACC CTTTGGGGT			
		C C			
GAM2477	LOC253666 3'	GGGGTTTCACCATGTTGCGCCAG 96763	ACC	A	
	G	CCTG AACATGG GAAACCCC			
		GGAC TTGTACC CTTTGGGG			
		CGC A			
GAM2477	LOC253836 5'	GGGATCTGCCTGGTCAGG 99466	ACAT _	AAC	
		CCTGACCA GG AGA CCC			
		GGA CTGGT CC TCT GGG			
		___ G A__			
GAM2477	LOC253981 3'	GGGGTATCACTATATTGGTCAG 97538	C	A A	
	G	CCTGACCAA ATGG GA ACCCC			
		GGA CTGGT TATC CT TGGGG			
		A A A			
GAM2477	LOC254018 5'	TGGGGTTTCGCCATGTTAGCCA 98744	ACC	A	
	GG	CCTG AACATGG GAAACCCCA			

		GGAC TTGTACC CTTTGGGGT		
		CGA G		
GAM2477	LOC254100 5'	TGGGGTTTCCCTTTCGGCGCAG 98161	A_	AACAT A
	G	CCTG CC GG GAAACCCCA		
		GGAC GG CC CTTTGGGGT		
		GC CTTT_ _		
GAM2477	LOC254100 3'	TGGGGTTTCGTCATGTTGCCCA 98162	AC	GA
	GG	CCTG CAACATG GAAACCCCA		
		GGAC GTTGTAC CTTTGGGGT		
		CC TG		
GAM2477	LOC254268 3'	TGGGGTTTCACCATGTTGGCCA 97147	A	A
	GG	CCTG CCAACATGG GAAACCCCA		
		GGAC GGTGTACC CTTTGGGGT		
		C A		
GAM2477	LOC254295 5'	GGGGTTTCACCGTGTTAGCCAG 97893	ACC	A
	G	CCTG AACATGG GAAACCCC		
		GGAC TTGTGCC CTTTGGGG		
		CGA A		
GAM2477	LOC254351 5'	GGGGTTTCTCCGTGTTGGTCGG 96693		
	G	CCTGACCAACATGGAGAAACCCC		
		GGGCTGGTTGTGCCTCTTTGGGG		
GAM2477	LOC254532 5'	GGGTTTCTCCATGTTGCCCA 98457	AC	
		TG CAACATGGAGAAACCC		
		AC GTTGTACCTCTTTGGG		
		CC		
GAM2477	LOC254655 3'	GGGGTTTCACCATGTTGGCCAG 97222	A	A
	G	CCTG CCAACATGG GAAACCCC		
		GGAC GGTGTACC CTTTGGGG		
		C A		
GAM2477	LOC254778 3'	GGATTTTGCTGTGTTGCCAG 97836	AC	AG C
		CTG CAACATGG AAA CC		
		GAC GTTGTGTC TTT GG		
		CC GT A		
GAM2477	LOC255308 3'	GGGGTTTCGGCATGTTGGCCAG 96177	A	GA
	G	CCTG CCAACATG GAAACCCC		
		GGAC GGTGTAC CTTTGGGG		
		C GG		
GAM2477	LOC255465 3'	GGGTTTCACCATGTTGGCCAGG 99120	A	A
		CCTG CCAACATGG GAAACCC		

		GGAC GGTTGTACC CTTTGGG		
		C A		
GAM2477	LOC255497 3'	GGGGTTTCACCATGTTGGCCAG 98989	A	A
	G	CCTG CCAACATGG GAAACCCC		
		GGAC GGTTGTACC CTTTGGGG		
		C A		
GAM2477	LOC255927 5'	GGGGTTTCACCATCTTGGCCAG 97712	A	C A
	G	CCTG CCAA ATGG GAAACCCC		
		GGAC GGTT TACC CTTTGGGG		
		C C A		
GAM2477	LOC256221 3'	GGGGTTTCACCGTGTTAGCCAG 96916	ACC	A
	G	CCTG AACATGG GAAACCCC		
		GGAC TTGTGCC CTTTGGGG		
		CGA A		
GAM2477	LOC256306 3'	GGGGTTTCACCATGTTGGCCAG 98519	A	A
	G	CCTG CCAACATGG GAAACCCC		
		GGAC GGTTGTACC CTTTGGGG		
		C A		
GAM2477	LOC256360 5'	TGGGGTCTCCCTATGTTGCCCA 98329	AC	A A
	GG	CCTG CAACATGG GA ACCCCA		
		GGAC GTTGTATC CT TGGGGT		
		CC C C		
GAM2477	LOC257463 3'	TGGAGTCTTGCTATGTTGCCCA 71627	AC	AG A C
	GG	CCTG CAACATGG A AC CCA		
		GGAC GTTGTATC T TG GGT		
		CC GT C A		
GAM2477	LOC257465 3'	TGGTGTTTCACCATGTTGGCCA 82504	A	A C
	GG	CCTG CCAACATGG GAAAC CCA		
		GGAC GGTTGTACC CTTTG GGT		
		C A T		
GAM2477	LOC257486 3'	GGGGTTTCACCATGTTGGCCAG 69777	A	A
	G	CCTG CCAACATGG GAAACCCC		
		GGAC GGTTGTACC CTTTGGGG		
		C A		
GAM2477	LOC51008 5'	TGGGGTTTCTCCATGTTGGTCA 32537		
	GG	CCTGACCAACATGGAGAAACCCA		
		GGA CTGGTTGTACCTCTTTGGGGT		
GAM2477	LOC51159 5'	GGGATTTACCATGTTGGCCAG 33032	A	A C
	G	CCTG CCAACATGG GAAA CCC		

		GGAC GGTTGTACC CTTT GGG		
		C A A		
GAM2477	LOC51193 5'	GGGGTTTCCCATGTTGGTCAG 33368	A	
	G	CCTGACCAACATGG GAAACCCC		
		GGA		
		CTTGTACC CTTTGGGG		
		C		
GAM2477	LOC51200 3'	GGGTTTCTCCATGTTGGTCAGG 33439		
		CCTGACCAACATGGAGAAACCC		
		GGA		
		CTTGTACCTCTTTGGG		
GAM2477	LOC51219 5'	GGGGTTTCTCCATGTCGGTCAG 33548	A	
	G	CCTGACC ACATGGAGAAACCCC		
		GGA		
		CTTGTACCTCTTTGGGG		
		C		
GAM2477	LOC51652 3'	GGTTCCTCCATGTCATTTCA 32703	CCA_	A
		TGA ACATGGAG AACC		
		ACT TGTACCTC TTGG		
		TTAC C		
GAM2477	LOC57107 3'	TGGGGTTTCACTATGTTGGTCA 40197	A	
	GG	CCTGACCAACATGG GAAACCCCA		
		GGA		
		CTTGTATC CTTTGGGGT		
		A		
GAM2477	LOC57146 3'	TGGGGTTTCACCATGTTGGTCA 40300	A	
	GG	CCTGACCAACATGG GAAACCCCA		
		GGA		
		CTTGTACC CTTTGGGGT		
		A		
GAM2477	LOC81034 3'	TGGGGTTTCACCATGTTAGCCA 48599	ACC	A
	GG	CCTG AACATGG GAAACCCCA		
		GGAC TTGTACC CTTTGGGGT		
		CGA A		
GAM2477	LOC89231 3'	TGGGGTCTCACTATGTTGCCCA 94303	AC	A A
	GG	CCTG CAACATGG GA ACCCCA		
		GGAC GTTGTATC CT TGGGGT		
		CC A C		
GAM2477	LOC89932 3'	GGGGTTTCTCCATGTTGGTCAG 61469		
		CTGACCAACATGGAGAAACCCC		
		GACTGGTTGTACCTCTTTGGGG		
GAM2477	LOC89932 3'	TGGGGTTTCACCATGTTGGCCA 61478	A	A
	GG	CCTG CCAACATGG GAAACCCCA		

		GGAC GGTGTACC CTTTGGGGT		
		C A		
GAM2477	LOC90288 3'	GGGGTTTCACAGTGTAGCCAG 62793	ACC	GGA
	G	CCTG AACAT GAAACCCC		
		GGAC TTGTG CTTTGGGG		
		CGA ACA		
GAM2477	LOC90288 3'	TGGGGTTTCACCATATTGGTCA 62804	C	A
	GG	CCTGACCAA ATGG GAAACCCCA		
		GGA CTGGTT TACC CTTTGGGGT		
		A A		
GAM2477	LOC90459 3'	GGGGTTTCACCATGTTGGTCAG 63558		A
	G	CCTGACCAACATGG GAAACCCC		
		GGA CTGGTTGTACC CTTTGGGG		
		A		
GAM2477	LOC90485 3'	GGGGTTTCACCATGTTGGCTAG 63702	A	A
	G	CCTG CCAACATGG GAAACCCC		
		GGAT GGTGTACC CTTTGGGG		
		C A		
GAM2477	LOC90485 3'	GGGTTTCACCATGTTGGCCAGG 63704	A	A
		CCTG CCAACATGG GAAACCC		
		GGAC GGTGTACC CTTTGGG		
		C A		
GAM2477	LOC90580 3'	GGAGGTACCACATTGGTCAG 64110	CA	AGAA _
		CTGACCAA TGG ACC CC		
		GACTGGTT ACC TGG GG		
		AC A _ A		
GAM2477	LOC90591 3'	GGGGCTTCACTATGTTGGCCAG 64178	A	A A
	G	CCTG CCAACATGG GAA CCCC		
		GGAC GGTGTATC CTT GGGG		
		C A C		
GAM2477	LOC91012 5'	GGTTTTGCCATGTTGCCCAGG 65248	AC	AG
		CCTG CAACATGG AAACC		
		GGAC GTTGTACC TTTGG		
		CC GT		
GAM2477	LOC91115 3'	TGGGGTTTCACTGTGTTAGCCG 65580	ACC	A
	GG	CCTG AACATGG GAAACCCCA		
		GGGC TTGTGTC CTTTGGGGT		
		CGA A		
GAM2477	LOC91115 3'	TGGGGTTTCATCATGTTTGCCA 65581	ACC	GA
	G	CTG AACATG GAAACCCCA		

		GAC TTGTAC CTTTGGGGT		
		CGT TA		
GAM2477	LOC91250 5'	TGGGGTTTCATCATGTTGGCCA 65924	A	GA
	GG	CCTG CCAACATG GAAACCCCA		
		GGAC GGTGTAC CTTTGGGGT		
		C TA		
GAM2477	LOC91373 3'	TGGGGTTTGACCGTGTTAGCCA 66420	ACC	AG
	GG	CCTG AACATGG AAACCCCA		
		GGAC TTGTGCC TTTGGGGT		
		CGA AG		
GAM2477	LOC91561 5'	GGGGTTTCTCCATGTTGGTCAG 67046		
	G	CCTGACCAACATGGAGAAACCCC		
		GGACTGGTTGTACCTCTTTGGGG		
GAM2477	LOC91759 5'	GGGCTCCTCACTGGTCAGG 67695	ACAT	AAAC
		CCTGACCA GGAG CCC		
		GGACTGGT CCTC GGG		
		CACT _____		
GAM2477	LOC92148 5'	GGGGTTTCACCGTGTTAGTCAG 68884	C	A
	G	CCTGAC AACATGG GAAACCCC		
		GGACTG TTGTGCC CTTTGGGG		
		A A		
GAM2477	LOC92267 3'	TGGGGTTTCACCATATTGGCCA 69181	A C	A
	GG	CCTG CCAA ATGG GAAACCCCA		
		GGAC GGT TACC CTTTGGGGT		
		C A A		
GAM2477	LOC92303 3'	GGGTTTCACCATGTTGGCCAGG 69395	A	A
		CCTG CCAACATGG GAAACCC		
		GGAC GGTGTACC CTTTGGG		
		C A		
GAM2477	LOC92661 5'	GGGGTTTCACTGTGTTAGCCAG 70633	ACC	A
	G	CCTG AACATGG GAAACCCC		
		GGAC TTGTGTC CTTTGGGG		
		CGA A		
GAM2477	LOC92689 3'	GGGTTTCACCATGTTGGCCAGG 70778	A	A
		CCTG CCAACATGG GAAACCC		
		GGAC GGTGTACC CTTTGGG		
		C A		
GAM2477	LOC92697 5'	GGGGTTTCGCTGTGTTGGCCAG 70815	A	A
	G	CCTG CCAACATGG GAAACCCC		

			GGAC GGTGTGTC CTTTGGGG		
			C G		
GAM2477	LOC92697	5'	GGGTTTCTCCATATTGGTCAGG 70816	C	
			CCTGACCAA ATGGAGAAACCC		
			GGA CTGGTT TACCTCTTTGGG		
			A		
GAM2477	LOC92841	3'	GGGGTTTCACCATGTTAGCCAG 71259	ACC	A
			G CCTG AACATGG GAAACCCC		
			GGAC TTGTACC CTTTGGGG		
			CGA A		
GAM2477	LOC92841	3'	GGGTTTCACCATGTTGGCCA 71261	A	A
			TG CCAACATGG GAAACCC		
			AC GGTGTACC CTTTGGG		
			C A		
GAM2477	LOC93349	3'	GGGGTTTCACTATGTTGGCCAG 57273	A	A
			G CCTG CCAACATGG GAAACCCC		
			GGAC GGTGTATC CTTTGGGG		
			C A		
GAM2478	MYO1D	3'	CGGCAGAACCCACCAAGTGC 72243	A	C__
			GCAC TGGTGGGT CCG		
			CGTG ACCACCCA GGC		
			A AGAC		
GAM2478	SH3BP4	3'	CGCCAATCATCCCACCAT 27999	TCCC	
			ATGGTGGG GATTGGCG		
			TACCACCC CTAACCGC		
			TA__		
GAM2478	ABHD2	3'	CAGGGGGGCACCCACCATG 23793	_	GA
			CATGGTGGGT CCC TTG		
			GTACCACCCA GGG GAC		
			C G_		
GAM2478	BCoR	3'	CAAGCTGGACCCACCATGT 35343	CGA	
			ACATGGTGGGTCC TTG		
			TGTACCACCCAGG AAC		
			TCG		
GAM2478	FLJ12488	3'	CCGATTGGCGCAAGGCCACCA 49157	C	_____ GATT
			TATGC GCA ATGGTGGGTCC CC GG		
			CGT TACCACCCGG GG CC		
			A AAC__GC TTAG		
GAM2478	FLJ20856	5'	GTTAAGCACCCACCATGTGC 47865	CCCGA	
			GCACATGGTGGGT TTGGC		

CGTGTACCACCCA AATTG
CG____

GAM2478 NXPH3 3' CCAATGGACACCCACCGTGTGC 66340 C_ G
GCACATGGTGGGT CC ATTGG
||||||| || ||||
CGTGTGCCACCCA GG TAACC
CA _

GAM2478 TSPEAR 3' GCCAATCAGAACTGTG 59375 GGG CC
CATGGT TC GATTGGC
|||| || |||||
GTGTCA AG CTAACCG
_ A_

GAM2478 LOC145453 3' CCAACCAGGATGCTTCACCATG 77656 _ CGA
CATGGTGG GTCC TTGG
||||| ||| |||
GTACCACT TAGG AACC
TCG ACC

GAM2478 LOC150935 5' CGGACACCCACCACGTGC 80825 A C_
GCAC TGGTGGGT CCG
||| ||||| |||
CGTG ACCACCCA GGC
C CA

GAM2478 LOC56270 3' CGCCACAGCACCCACCACCTGC 39504 CA CCCGAT
GCA TGGTGGGT TGGCG
|| ||||| ||||
CGT ACCACCCA ACCGC
CC CGAC_

GAM2479 ADCY8 5' GGACATGCCTTTCTCCACGTCC 8502 A A _ CA
GC GC GGAC TGGAGAA GTA TCC
|| ||| ||||| ||| |||
CG CCTG ACCTCTT CGT AGG
_ C TC AC

GAM2479 AKT2 5' GTGCCTCCTGCATGTCCTGCT 9677 G AA_
AGCAGGACATG AG GTAC
||||||| || |||
TCGTCCTGTAC TC CGTG
G CTC

GAM2479 APOBEC2 3' TACTTCTCATGCTGT 23280 GA G
GCAG CATG AGAAGTA
||| ||| |||||
TGTC GTAC TCTTCAT
_ _

GAM2479 GPD1 3' GCTTTCTCCATATCCTCT 60397 C C _
AG AGGA ATGGAGAA GT
|| ||| ||||| ||
TC TCCT TACCTCTT CG
_ A T

GAM2479 HMGN2 3' TGTCTGCCCATGTCCTGC 19810 AGA T
GCAGGACATGG AG ACA
||||||| || |||

		CGTCCTGTACC TC TGT	
		CG_ _	
GAM2479 MCM4	3'	GCTCCCTGCATGTCCTGCT 62579	G A_
		AGCAGGACATG AG AGT	
		TCGTCCTGTAC TC TCG	
		G CC	
GAM2479 MEN1	3'	GGATGTACTAAAATGTATCCT 95013	C GAGA
		AGGA ATG AGTACATCC	
		TCCT TGT TCATGTAGG	
		A AAAA	
GAM2479 MTL5	3'	GATGTGGCAACCCATGCCCCCT 18199	CA A AGAAG
		AG GG CATGG TACATC	
		TC CC GTACC GTGTAG	
		CC _ CAACG	
GAM2479 MTMR3	5'	GCCTCGCCATGTCCTGCT 41164	A A
		AGCAGGACATGG GA GT	
		TCGTCCTGTACC CT CG	
		G C	
GAM2479 PCDH9	3'	TGCTTCTCCACAGCCTGCT 83697	ACA
		AGCAGG TGGAGAAGTA	
		TCGTCC ACCTCTTCGT	
		GAC	
GAM2479 SLC39A1	3'	GCCTCTCCAGTCCTGCT 27813	A A
		AGCAGGAC TGGAGA GT	
		TCGTCCTG ACCTCT CG	
		_ C	
GAM2479 SLC6A8	3'	GGATGCACTTCCCGCACCT 20073	ACA A A
		AGG TGG GAAGT CATCC	
		TCC GCC CTTCA GTAGG	
		AC_ _ C	
GAM2479 AD-020	3'	ACTTCTCCATTCCCTGCT 39713	AC
		AGCAGG ATGGAGAAGT	
		TCGTCC TACCTCTTCA	
		CT	
GAM2479 AD-020	3'	ACTTCTCCATTCCCTGCT 60090	AC
		AGCAGG ATGGAGAAGT	
		TCGTCC TACCTCTTCA	
		CT	
GAM2479 ALDH9	3'	G TTCCTTCTCCATTCCCACT 7348	CA C T_
		AG GGA ATGGAGAAG AC	

			TC CCT TACCTCTTC TG		
			AC _ CT		
GAM2479	ARHGEF4	3'	GATGGCGCCCTGTCCTGC 53372	T	AGAA A
			GCAGGACA GG GT CATC		
			CGTCCTGT CC CG GTAG		
			_ CG _ _		
GAM2479	DDR1	3'	GGACACACTCTCATGTCC 10477	G	A ACA
			GGACATG AGA GT TCC		
			CCTGTAC TCT CA AGG		
			_ _ CAC		
GAM2479	DDR1	3'	GGACACACTCTCATGTCC 26560	G	A ACA
			GGACATG AGA GT TCC		
			CCTGTAC TCT CA AGG		
			_ _ CAC		
GAM2479	DDR1	3'	GGACACACTCTCATGTCC 26562	G	A ACA
			GGACATG AGA GT TCC		
			CCTGTAC TCT CA AGG		
			_ _ CAC		
GAM2479	FLJ20150	3'	GTCCTCCCCCATGTCCTGC 35145	AGA	T
			GCAGGACATGG AG AC		
			CGTCCTGTACC TC TG		
			CCC C		
GAM2479	FLJ23259	3'	TGATTTCCCATGTCCTACT 45638	C	A A
			AG AGGACATGG GAAGT CA		
			TC TCCTGTACC CTTTA GT		
			A _ _		
GAM2479	GAL3ST2	3'	GCTGCCTCCATGTCCTGC 53484	A_	
			GCAGGACATGGAG AGT		
			CGTCCTGTACCTC TCG		
			CG		
GAM2479	GMEB2	3'	GCTCCTCCAGGTCCTGCT 25664	A	A
			AGCAGGAC TGGAG AGT		
			TCGTCCTG ACCTC TCG		
			G C		
GAM2479	HMG17L1	3'	TGTCTGCCCCATGTCCTGCT 41049	AGA	T
			AGCAGGACATGG AG ACA		
			TCGTCCTGTACC TC TGT		
			CG _ _		
GAM2479	HNRPA3	3'	GGATATATACCCATGTCT 20453	AGAA	C
			GGACATGG GTA ATCC		

	TCTGTACC TAT TAGG	
	CA__ A	
GAM2479 KIAA0441	3' GGATGTACCACCACACCCAGCT 29636	A ACA AGAA
	AGC GG TGG GTACATCC	
	TCG CC ACC CATGTAGG	
	A CAC AC__	
GAM2479 KIAA0522	3' GTCCTCCTCCCCATGTCCT 72426	A __ T
	AGGACATGG GA AG AC	
	TCCTGTACC CT TC TG	
	C CC C	
GAM2479 KIAA1393	3' TGTCTGCCCATGTCCTGC 72576	AGA T
	GCAGGACATGG AG ACA	
	CGTCCTGTACC TC TGT	
	CG_ _	
GAM2479 KIAA1922	3' ATGTGGCATCATGTCCTGC 73987	AGAAG
	GCAGGACATGG TACAT	
	CGTCCTGTACT GTGTA	
	ACG__	
GAM2479 LOC113220	5' GGATGTACCATCTGCCCTTCT 57359	C A TG GAA
	AG AGG CA GA GTACATCC	
	TC TCC GT CT CATGTAGG	
	T C __ AC__	
GAM2479 LOC143153	3' GGCTGTTCTCCATCTCCCGCT 76980	A C AGT T
	AGC GGA ATGGAGA ACA CC	
	TCG CCT TACCTCT TGT GG	
	C C __ C	
GAM2479 LOC145540	3' TGTCTGCCCATGTCCTGC 77779	AGA T
	GCAGGACATGG AG ACA	
	CGTCCTGTACC TC TGT	
	CG_ _	
GAM2479 LOC148915	3' TGTCTGCCCATGTCCTGC 79810	AGA T
	GCAGGACATGG AG ACA	
	CGTCCTGTACC TC TGT	
	CG_ _	
GAM2479 LOC150166	5' GATATACTTCTTTCTTGCT 86038	CATG C
	AGCAGGA GAGAAGTA ATC	
	TCGTTCT TTCTTCAT TAG	
	__ A	
GAM2479 LOC150580	3' TGTCTGCCCATGTCCTGC 61068	AGA T
	GCAGGACATGG AG ACA	

	CGTCCTGTACC TC TGT		
	CG_ _		
GAM2479 LOC152212 3'	TGTCTGCCCATGTCCTGC 83712	AGA T	
	GCAGGACATGG AG ACA		
	CGTCCTGTACC TC TGT		
	CG_ _		
GAM2479 LOC152300 3'	ATGCACTTGTCTGTT 81380	TGGAGA A	
	AGCAGGACA AGT CAT		
	TTGTCCTGT TCA GTA		
	_____ C		
GAM2479 LOC153346 5'	ATGCACTAGCTGTCCTGT 87203	TG AGA A	
	GCAGGACA G AGT CAT		
	TGTCCTGT C TCA GTA		
	__GA_ C		
GAM2479 LOC153811 3'	GGACATACCATCTTGTCTGCT 81839	T GAA CA	
	AGCAGGACA GGA GTA TCC		
	TCGTCCTGT TCT CAT AGG		
	_ AC_ AC		
GAM2479 LOC154807 5'	GATGGCGGCTCCCGTCCTGCT 87464	AT AA A	
	AGCAGGAC GGAG GT CATC		
	TCGTCCTG CCTC CG GTAG		
	C_ GG _		
GAM2479 LOC196453 5'	ATGACATTTTCATGTCCCACT 92341	CA AA A	
	AG GGACATGGAG GT CAT		
	TC CCTGTACTTT CA GTA		
	AC A_ _		
GAM2479 LOC221468 3'	ACTTCTCCATAGTCCTGCT 60003	_	
	AGCAGGAC ATGGAGAAGT		
	TCGTCCTG TACCTCTTCA		
	A		
GAM2479 LOC254000 3'	TGTCTGCCCATGTCCTGC 96615	AGA T	
	GCAGGACATGG AG ACA		
	CGTCCTGTACC TC TGT		
	CG_ _		
GAM2479 LOC257153 5'	GGCTGTTTCTCACATCCTGC 97467	CA _ GT T	
	GCAGGA TG GAGAA ACA CC		
	CGTCCT AC CTCTT TGT GG		
	_ A _ C		
GAM2479 LOC88584 3'	GATTATCTGCCCATGTCCTGC 61102	AGA TAC	
	GCAGGACATGG AG ATC		

			CGTCCTGTACC TC TAG		
			CG_ TAT		
GAM2480	DGAT1	3'	CTGAGGGCCTGGCTTCTCA 65151	T	GA_
			TGAGA AGCCAGGCT AG		
			ACTCT TCGGTCCGG TC		
			_ GAG		
GAM2480	DIO3	3'	GCTTCTGTAACGTCTCTCA 9073	CCAG	TGA
			TGAGATAG GC AGAAGC		
			ACTCTGTC TG TCTTCG		
			AA_ _		
GAM2480	DLST	3'	TGCTTCTTCAATGGCACCTTCA 10417	ATA	GGC
			TGAG GCCA TGAAGAAGCA		
			ACTT CGGT ACTTCTTCGT		
			CCA A_		
GAM2480	GYPB	3'	TGCCCCTACCCCTGGCTATC 10897	CTGA	AA
			GATAGCCAGG AG GCA		
			CTATCGGTCC TC CGT		
			CCA_ CC		
GAM2480	HNRPF	3'	TCTTCAGTGTTTTCTCA 18305	T	CAG
			TGAGA AGC GCTGAAGA		
			ACTCT TTG TGACTTCT		
			T _		
GAM2480	LAMB1	5'	GCCCCTTCAGCCCCGGCTCTC 11263	TA	A_ AA
			GAGA GCC GGCTGAAG GC		
			CTCT CGG CCGACTTC CG		
			_ CC CC		
GAM2480	LIFR	3'	CTTCAGTCAGCCATCTCA 11312	A	CA
			TGAGAT GC GGCTGAAG		
			ACTCTA CG CTGACTTC		
			C A_		
GAM2480	NR0B2	3'	TGCTGATTCAGCCTGGCCATC 42020	A	GA
			GAT GCCAGGCTGAA AGCA		
			CTA CGGTCCGACTT TCGT		
			C AG		
GAM2480	OCRL	3'	TGCTTCCCTACCATGGCTATTC 6061	AG	_ C AA
	CA		TG ATAGCCA GG TG GAAGCA		
			AC TATCGGT CC AT CTTCGT		
			CT A_ CC		
GAM2480	PLCG2	3'	TGCTCCTCATTTTTGGCCTCTC 72883	TA	C_ A A
	A		TGAGA GCCAGG TGA GA GCA		

			ACTCT CGGTTT ACT CT CGT			
			C_ TT C _			
GAM2480	RAB31	3'	GCTCGGTGGCCTGGCACCTCA 23441	ATA	AA	A
			TGAG GCCAGGCTG GA GC			
			ACTC CGGTCCGGT CT CG			
			CA_ GG _			
GAM2480	UBE2A	5'	TGCTTCTCCAGCCTCTTCGGCC 13930	ATA	___	A
	TC		GAG GCC AGGCTG AGAAGCA			
			CTC CGG TCCGAC TCTTCGT			
			___ CTTC C			
GAM2480	C17orf31	3'	TGCCCCTTTAGCTGGTACCTCA 34546	ATA	G	AA
			TGAG GCCAG CTGAAG GCA			
			ACTC TGGTC GATTTC CGT			
			CA_ _ CC			
GAM2480	CNOT3	5'	TGCTTCTTCTCTTTACCAGTCC 27989	A	AGCC_	CT
	CA		TG GAT AGG GAAGAAGCA			
			AC CTG TTC CTTCTTCGT			
			C ACCAT T_			
GAM2480	DKFZP434C0826	5'	TCAGCGGCCAGCTATCTC 85155		CA	AA
			GAGATAGC GGCTG GA			
			CTCTATCG CCGGC CT			
			AC GA			
GAM2480	DKFZP434N1511	5'	CTTGGGCCTGGCTGCCTCA 93060	A		G
			TGAG TAGCCAGGCT AAG			
			ACTC GTCGGTCCGG TTC			
			C G			
GAM2480	ERp44	3'	TGCTTCTTAGCCAGCTACCTC 82606	A	CA	A
			GAG TAGC GGCTGA GAAGCA			
			CTC ATCG CCGATT CTTCGT			
			C A_ _			
GAM2480	FADS1	3'	GCCTCTTCAGCAGCATCT 26381	A	CAG	A
			AGAT GC GCTGAAGA GC			
			TCTA CG CGACTTCT CG			
			_ A_ C			
GAM2480	FLJ00024	3'	TGCTCCTTCAGCCTCCTTGCTC 64508	A	CC	A
	A		TGAG TAG AGGCTGAAG AGCA			
			ACTC GTT TCCGACTTC TCGT			
			_ CC C			
GAM2480	KIAA0337	3'	GCTTCTTCAGCTAAACTC 29478	ATAGCCA		
			GAG GGCTGAAGAAGC			

			CTC	TCGACTTCTTCG			
			AAAA	_____			
GAM2480	KIAA0365	5'	GCCCCTAGGCTTGGCCTC	79369	ATA	GA	AA
			GAG GCCAGGCT AG GC				
			CTC CGGTTCGG TC CG				
			_____ A_ CC				
GAM2480	KIAA0513	3'	GCCCTTCCTGGCTACCTC	29037	A	CTG	AA
			GAG TAGCCAGG AAG GC				
			CTC ATCGGTCC TTC CG				
			C _____ C_				
GAM2480	KIAA0976	5'	TGCTTCAGATACTGATATCTCA	30557		GC	GCTGAA
			TGAGATA CAG GAAGCA				
			ACTCTAT GTC CTCGT				
			A_ ATAGA_				
GAM2480	KIAA1719	5'	GCTGGGCCTGACTATCTCA	68732	C	GAAGA	
			TGAGATAG CAGGCT AGC				
			ACTCTATC GTCCGG TCG				
			A G_____				
GAM2480	MT01	3'	CTTCTTCAGGAAATCCTCA	56935	_	AG	AGGC
			TGAG AT CC TGAAGAAG				
			ACTC TA GG ACTTCTTC				
			C AA _____				
GAM2480	NINJ2	3'	CTCCTTCAGTCACTATCCCA	33722	A	CCA	A
			TG GATAG GGCTGAAG AG				
			AC CTATC CTGACTTC TC				
			C A_ C				
GAM2480	PIP3-E	3'	TGCCTCTTCAGCACATCTCA	67361	AGCCAG		A
			TGAGAT GCTGAAGA GCA				
			ACTCTA CGACTTCT CGT				
			CA_____ C				
GAM2480	PRKCL2	3'	CTTCTTCAAAAGTGGCTCCTCA	21816	AT	GGC_	
			TGAG AGCCA TGAAGAAG				
			ACTC TCGGT ACTTCTTC				
			C_ GAAA				
GAM2480	PRO0641	5'	CTTTGTGCCCAACTGTCTCA	27064	CCA	TGAA	
			TGAGATAG GGC GAAG				
			ACTCTGTC CCG TTTC				
			AAC TG_____				
GAM2480	SR-BP1	3'	GCCTCAGTCTGACTCCTCA	20788	AT C	AGAA	
			TGAG AG CAGGCTGA GC				

ACTC TC GTCTGACT CG
 C_ A C___
 GAM2480 TRIM40 3' GCTTCTTCAGCCCCCTCA 57733 ATAGCCA
 TGAG GGCTGAAGAAGC
 |||| |||||
 ACTC CCGACTTCTTCG
 CC___
 GAM2480 LOC121838 5' TGCTTCTTCAAGCAAACACCT 76518 ATAGCCAG _
 CA TGAG GCT GAAGAAGCA
 |||| ||| |||||
 ACTC CGA CTTCTTCGT
 CACCAA_ A
 GAM2480 LOC125704 3' CTTGTACCTGGTTATCCCA 74879 A CTG
 TG GATAGCCAGG AAG
 || ||||| ||
 AC CTATTGGTCC TTC
 C ATG
 GAM2480 LOC145474 3' TGCTTCTTCAGTCCACACTCA 77730 ATAGCCA
 TGAG GGCTGAAGAAGCA
 |||| |||||
 ACTC CTGACTTCTTCGT
 ACAC___
 GAM2480 LOC154881 3' TCCTTGCGTGCTATCTCA 82078 CA TG A
 TGAGATAGC GGC A GA
 ||||| ||| ||
 ACTCTATCG TCG T CT
 _ GT C
 GAM2480 LOC164714 3' TTTCCAGAGCCTGGCCATC 88591 A GAA
 GAT GCCAGGCT GAAG
 ||| ||||| |||
 CTA CGGTCCGA CTTT
 C GAC
 GAM2480 LOC222493 5' TGCCCCCTCTCACTTTGGCCAA 96012 A A_ C _ AA_
 TCCCA TG GAT GCCAGG TGA AG GCA
 || ||| ||||| ||| |||
 AC CTA CGGTTT ACT TC CGT
 C AC C C CCC
 GAM2480 LOC255196 3' CTCCTGTAGTCCTGGCTACTCA 98956 A _ A A
 TGAG TAGCCAGG CTG AG AG
 |||| ||||| ||| |||
 ACTC ATCGGTCC GAT TC TC
 _ T G C
 GAM2481 FLJ22160 3' GGCACCAGCCCTGGTAACTGC 45033 _ _
 GCAGTTAC GGC GTGCC
 ||||| ||| |||||
 CGTCAATG CCG CACGG
 GTC AC
 GAM2481 KIAA0514 5' GTATTGGCCTGTCCAACCTGTG 28753 AC T
 CGCAGTT GGCG GCCAATAC
 ||||| ||| |||||

		GTGTCAA CTGT CGGTTATG	
		C_ C	
GAM2481	KIAA0893	3' GGTATTAGAAGTGTAAGTGTG 31063	G GTGCC
		CGCAGTTACG C AATACC	
		GTGTCAATGT G TTATGG	
		AAGA	
GAM2481	LOC154007	3' TATTGGCAAGTCAACTGC 81930	AC G
		GCAGTT GGC TGCCAATA	
		CGTCAA CTG ACGGTTAT	
		_ A	
GAM2481	LOC255232	3' GCATCTAGCACGTAAGTGTG 98433	- _
		GCAGTTACG GC GTGC	
		CGTCAATGC CG TACG	
		A ATC	
GAM2481	LOC92573	5' GTATTGGCTCGCAACCCGT 70378	CA ACG T
		ACG GTT GCG GCCAATAC	
		TGC CAA CGC CGGTTATG	
		C_ _ T	
GAM2482	CDH12	3' CTTATCATTTAAAGTGGTGTA 15777	CCCAA GA
		TACACCACT GAA ATAAG	
		ATGTGGTGA TTT TATTC	
		AA_ AC	
GAM2482	GOCAP1	3' ATTGTTCTTGGGAGCAGTGTA 43007	CA G
		TACAC CTCCCAAGAA AAT	
		ATGTG GAGGGTTCTT TTA	
		AC G	
GAM2482	DKFZp434N2435	5' CTTATTACTGTGGGGTGGT 98090	T AGAAG
		ACCAC CCCA AATAAG	
		TGGTG GGGT TTATTC	
		_ GTCA_	
GAM2482	DKFZP564I122	3' CTTATTCTTCTCCCTCATGTGT 63877	CACTCCCA
	A	TACAC AGAAGAATAAG	
		ATGTG TCTTCTTATTC	
		TACTCCC_	
GAM2482	FLJ21791	3' CTTATTTGCAGAAAGTGGTGTA 62126	CCCAAGAA
		TACACCACT GAATAAG	
		ATGTGGTGA TTTATTC	
		AGACG_	
GAM2482	HMP19	3' CTTATTCTTTGTTAGGAAAATG 88860	CCAC CAA_
	TA	TACA TCC GAAGAATAAG	

		ATGT AGG TTTCTTATTC	
		AAA_ ATTG	
GAM2482 KIAA1719	3'	TCTGTCTTGGGAGTGGTGTA 68742	_
		TACACCACTCCCAAGA AGA	
		ATGTGGTGAGGGTTCT TCT	
		G	
GAM2482 KIAA1853	3'	TTTTTCTTGGAAGCAGTG 69929	CA C
		CAC CT CCAAGAAGAA	
		GTG GA GGTTCCTTTT	
		AC A	
GAM2482 KIAA1877	3'	CTTATTCTTCTGCCATGAGT 66748	CCA__
		ACTC AGAAGAATAAG	
		TGAG TCTTCTTATTC	
		TACCG	
GAM2482 KIAA1906	3'	CTTATTCTTCTTGACTTTTGG 73571	CTCC_
		CCA CAAGAAGAATAAG	
		GGT GTTCTTCTTATTC	
		TTTCA	
GAM2482 OSBPL11	3'	CTTAATTTCCCAAGAGTGGTG 43206	CCAA AA
		CACCACTC GAAG TAAG	
		GTGGTGAG CTTT ATTC	
		AACC A_	
GAM2482 YME1L1	3'	TCATTCTTGATGTGGTGTA 58438	TCC _
		TACACCAC CAAGAA GA	
		ATGTGGTG GTTCTT CT	
		TA_ A	
GAM2482 ZNF262	3'	CTTATTTTGTGGGAGT 18723	A
		ACTCCCAAG AGAATAAG	
		TGAGGGTTT TTTTATTC	
		G	
GAM2482 LOC91960	3'	TGTGGCTTGGAACGTGGTGTA 68294	TC_ AAGA
		TACACCAC CCAAG ATA	
		ATGTGGTG GGTTC TGT	
		CAA GG__	
GAM2483 EPHA2	3'	CAGCCTTCGGACAGACAT 16674	CC GCGG
		ATGTC TTC GAAGGCTG	
		TACAG AGG CTTCCGAC	
		AC ____	
GAM2483 EPHB6	3'	ACACTGGTCCGAGAAGGGACAT 16713	G AA C
	G	CATGTCCCTTC CGGG GG TGT	

			GTACAGGGAAG GCCT TC ACA		
			A GG _		
GAM2483	PRPF31	3'	CTTCCCACTGAAGGGACA 32212	C_	
			TGTCCCTTCG GGGAAG		
			ACAGGGAAGT CCCTTC		
			CA		
GAM2483	RHO	3'	CAGCCTGAGAAGGGACAT 6767	GCGGGA	
			ATGTCCCTTC AGGCTG		
			TACAGGGAAG TCCGAC		
			AG____		
GAM2483	CHFR	3'	ACAGCCCCCTGAGGGAAGGGAC 37188	G__ AA	
	G		TGTCCCTTC CGGG GGCTGT		
			GCAGGGAAG GTCC CCGACA		
			GGA C_		
GAM2483	MGC11352	3'	CAACCTTCCTGGAACGTG 65425	CCCT G C	
			CATGT TC CGGGAAGG TG		
			GTGCA AG GTCCTTCC AC		
			____ _ A		
GAM2483	MGC2803	3'	ACAGCCTTCCTGAGAGGAC 44085	C C	
			GTCC TTCG GGGAAGGCTGT		
			CAGG GAGT CCCTCCGACA		
			A _		
GAM2483	PRC1	3'	ACAGCCTTCCTCCTGAAGAGA 15625	C C_	
			TC CTTCG G GGAAGGCTGT		
			AG GAAGT C CCTCCGACA		
			A C T		
GAM2483	LOC148089	3'	ACAGCCTTCCCGCAGG 79322	TC	
			CCT GCGGGAAGGCTGT		
			GGA CGCCCTTCCGACA		

GAM2484	AKAP1	3'	ACTATGGGTTCTCTTCGCAAA 14472	A CTT C	
			TTTGT GA GGAACCCA AGT		
			AAACG CT TCTTGGGT TCA		
			_ TC_ A		
GAM2484	AKAP1	3'	ACTATGGGTTCTCTTCGCAAA 58373	A CTT C	
			TTTGT GA GGAACCCA AGT		
			AAACG CT TCTTGGGT TCA		
			_ TC_ A		
GAM2484	EGF	3'	ACTATAGGTTTTGGTTCCACAA 10488	A C TG CAC	
			TTGT GA T GAACC AGT		

			AACA CT G TTTGG TCA	
			C T GT ATA	
GAM2484	EZH1	3'	GACTGTGGGTTCCAAATTAC 10551	AC
			GTAG TTGGAACCCACAGTC	
			CATT AACCTTGGGTGTCAG	
			A_	
GAM2484	STAC	3'	GACTGTGGAGTAATAGCCACAA 13427	AGA TGGA _
	A		TTTGT CT AC CCACAGTC	
			AAACA GA TG GGTGTCAG	
			CC_ TAA_ A	
GAM2484	CCR1	3'	GACTGTGGGCTCCATTC 8927	CT A
			GA TGGA CCCACAGTC	
			CT ACCT GGGTGTCTAG	
			T_ C	
GAM2484	FLJ10483	3'	GACTGTGGAAGAGATTACAAA 36652	A GGAAC
			TTTGTAG CTT CCACAGTC	
			AAACATT GAG GGTGTCAG	
			A AA_	
GAM2484	KIAA1871	3'	ACTGTAAGAGTCTACAAA 61890	GGAACCC
			TTTGTAGACTT ACAGT	
			AAACATCTGAG TGTCA	
			AA_	
GAM2484	LOC150821	3'	GGGTTCCACATCCACAAA 60944	A CT
			TTTGT GA TGGAACCC	
			AAACA CT ACCTTGGG	
			C AC	
GAM2484	LOC151057	3'	ACTGTGGGTACACCTATAAA 86379	ACT GA
			TTTGTAG TG ACCCACAGT	
			AAATATC AC TGGGTGTCA	
			C_ A_	
GAM2484	LOC157507	5'	ACTGTAAAAGTCTGCAAA 82377	GGAACCC
			TTTGTAGACTT ACAGT	
			AAACGTCTGAA TGTCA	
			AA_	
GAM2484	LOC203339	5'	GGATTCCCAGTCTACAAA 92214	T C
			TTTGTAGACT GGAA CC	
			AAACATCTGA CCTT GG	
			C A	
GAM2484	LOC51030	3'	ACTGTAAATTAACCAATCTAC 32695	C AACCC_
	AAA		TTTGTAGA TTGG ACAGT	

		AAACATCT AACC	TGTCA	
		— AAATTAAA		
GAM2484	LOC90906	3' GACTGTGGATCCCAAACCTTTGC	64951	C_ AAC
	A	TGTAGA TTGG CCACAGTC		
		ACGTTT AACC GGTGTCAG		
		CA CTA		
GAM2485	CD8A	3' ATCTCCTGTTAATATGGTGTA	10095	— A
		TACACCAT TGGCA GGAGAT		
		ATGTGGTA ATTGT CCTCTA		
		TA —		
GAM2485	MLLT2	3' CTTTCTGCCAATGAACAGTG	21029	ACAC AG
		CACT CATTGGCA GAG		
		GTGA GTAACCGT TTC		
		CAA_ CT		
GAM2485	NCOA6	3' ATCTCCTAATGATGTATTG	26826	C C GGCA
		CA TACA CATT AGGAGAT		
		GT ATGT GTAA TCCTCTA		
		T A ____		
GAM2485	PKIA	3' ATCTCCTTGCAATCATGTG	23342	CC G
		TACA ATTG CAAGGAGAT		
		GTGT TAAC GTTCCTCTA		
		AC —		
GAM2485	RAD21	3' GATCTCCTTTTCCAGTGCTG	21836	C C_
		CA CATTGG AAGGAGATC		
		GT GTGACC TTCCTCTAG		
		C TT		
GAM2485	SDHC	3' GATCTCCTTGGAGCAGTAG	69912	ACCA GG
		CTAC TT CAAGGAGATC		
		GATG AG GTTCCTCTAG		
		ACG_ —		
GAM2485	TRIM37	3' ATCTCCTTTTTTGGAGTATGT	31622	_ A TTGGC
		AC TAC CCA AAGGAGAT		
		TG ATG GGT TTCCTCTA		
		T A TT__		
GAM2485	FLJ21140	3' GATCTCCTTTAGAGGGCACAGT	45837	ACA A GGC
	G	CACT CC TT AAGGAGATC		
		GTGA GG AG TTCCTCTAG		
		CAC G AT_		
GAM2485	KIAA0159	3' ATCTCCTTGTTTTCTAATG	30138	_____
		CATTGG CAAGGAGAT		

		GTAATC GTTCCTCTA	
		TTTT	
GAM2485	MDS031	3' GATCTCCTCTCACAGTGGT 38066	GCA_
		ACCATTG AGGAGATC	
		TGGTGAC TCCTCTAG	
		ACTC	
GAM2485	PER3	3' ATCTCCTTTCAAAGTAGTG 34173	ACCA C
		CACTAC TTGG AAGGAGAT	
		GTGATG AACT TTCCTCTA	
		A__ _	
GAM2485	LOC145453	3' CTTGCCAATGGTGGAGTG 77661	A
		CACT CACCATTGGCAAG	
		GTGA GTGGTAACCGTTC	
		G	
GAM2485	LOC148824	3' TTTTGCCAATAATGTGTA 85382	C__
		TACAC ATTGGCAAGG	
		ATGTG TAACCGTTTT	
		TAA	
GAM2485	LOC220662	3' ATCTCCTTTACCAATAGGTAGT 92806	ACC C_
		ACTAC ATTGG AAGGAGAT	
		TGATG TAACC TTCCTCTA	
		GA_ AT	
GAM2486	ADAM28	3' AGGTTGCGAACTGGTG 27327	ACTT TT
		TACCAGTTC GC GACCT	
		GTGGTCAAG CG TTGGA	

GAM2486	AF1Q	5' AGGGGGAGAGTGAAGTGA 23331	TG GA
		CAGTTCCT CTT CCT	
		GTCAAGTGA GAG GGA	
		__ GG	
GAM2486	DGKE	3' CAGATAAGTGAATTGGTA 14680	C
		TACCAGTTCCTTG TTG	
		ATGGTTAAGTGAAT GAC	
		A	
GAM2486	DSC2	3' GTAGGTTGTTGCAGTGAAC 18247	T T_
		GTTCACT GC TGACCTAC	
		CAAGTGA CG GTTGGATG	
		_ TT	
GAM2486	GRB10	5' CAGGCCCACTGACTGGTA 19194	T T_
		TACCAGT CACT GCTTG	

		ATGGTCA GTGA CGGAC	
		— CC	
GAM2486	KRT16	5' TCCAGCAGTGAAGTGGTA 96892	T T
		TACCAGTTCACT GCT GA	
		ATGGTCAAGTGA CGA CT	
		— C	
GAM2486	BTN3A3	3' GTAGACATGACAAAGTGAAC 23767	CT_ AC
		GTTCACTTG TG CTAC	
		CAAGTGAAC AC GATG	
		AGT A_	
GAM2486	CAS1	3' GTAGAATTTTAAAGTAAACTGGT 43495	C CTTGAC
	G	TACCAGTT ACTTG CTAC	
		GTGGTCAA TGAAT GATG	
		A TTAA_	
GAM2486	KIAA0323	3' AGGTCCATAAAGTGAAGTGA 63946	GCTT
		CAGTTCACCT GACCT	
		GTCAAGTGAA CTGGA	
		ATAC	
GAM2486	LGALS12	5' AGGTCGCAGGTGAGACT 53547	_ TT
		AGT TCACTTGC GACCT	
		TCA AGTGGACG CTGGA	
		G _	
GAM2486	LOC139065	3' CAAACTCAAGAAAAGTGGTA 76324	CA C_
		TACCAGTT CTTG TTG	
		ATGGTCAA GAAC AAC	
		AA TCA	
GAM2486	LOC148760	3' GTCAATTCATTTAGACTGGTA 85365	CACT C_
		TACCAGTT TG TTGAC	
		ATGGTCAG AC AACTG	
		ATTT TT	
GAM2486	LOC157381	3' CAGGCAAGTAAATCAGTA 87732	CA C
		TAC GTT ACTTGCTTG	
		ATG TAA TGAACGGAC	
		AC A	
GAM2486	LOC204084	5' GTGGGAAGCAAACGGGC 91001	AC GA
		GTTC TTGCTT CCTAC	
		CGGG AACGAA GGGTG	
		CA _	
GAM2486	LOC220662	3' AGGTTGCAGTGAAGTGA 92804	T TT
		CAGTTCACCT GC GACCT	

GTCAAGTGA CG TTGGA

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      - -
GAM2486 LOC220776 3' GTAGGTCACAGGCCAAATGG 68933 GTTCA CT
      CCA CTTG TGACCTAC
      ||| ||| |||||
      GGT GGAC ACTGGATG
      AAACC _
GAM2486 LOC255475 5' GTCAACGGCTTTGAACTGG 99462 CTT _
      CCAGTTCA GCT TGAC
      ||||| ||| |||
      GGTCAAGT CGG ACTG
      TT_ CA
GAM2486 LOC51659 3' GCAGGTGTTTCAGTGACTGGTA 96214 _
      TACCAGTT CACTTGC
      ||||| |||||
      ATGGTCAG GTGGACG
      TGA CTT
GAM2486 LOC51659 3' GCAGGTGTTTCAGTGACTGGTA 32736 _
      TACCAGTT CACTTGC
      ||||| |||||
      ATGGTCAG GTGGACG
      TGA CTT
GAM2486 LOC92521 3' AGGCTCAATCCAAGTGGAC 70200 C_ _
      GTTCACTTG TTGA CCT
      ||||| ||| |||
      CAGGTGAAC AACT GGA
      CT C
GAM2487 FLJ10971 5' CCAATTAGGGGAAGGCAGATCA 37481 A_ GAA
      CCAA TTGGTGATCT TCC AATTGG
      ||||| ||| |||||
      AACCACTAGA AGG TTAACC
      CGGA GGA
GAM2487 KIAA1423 3' TCCAACCCTTCACGTCACCAA 62397 CTATCC AA_
      TTGGTGAT GAA TTGGA
      ||||| ||| |||||
      AACCACTG CTT AACCT
      CA_ CCC
GAM2487 KIAA1871 3' CCAACTTTTTAATCACCAA 61899 CTATCC A
      TTGGTGAT GAAA TTGG
      ||||| ||| |||||
      AACCACTA TTTT AACC
      AT_ C
GAM2487 MAP2K6 3' CCAATCCTGGGTGATCACCA 50079 T AAA
      TGGTGATC ATCCG ATTGG
      ||||| ||||| |||||
      ACCACTAG TGGGT TAACC
      _ CC_
GAM2487 MAP2K6 3' CCAATCCTGGGTGATCACCA 12331 T AAA
      TGGTGATC ATCCG ATTGG
      ||||| ||||| |||||
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		ACCACTAG TGGGT TAACC	
		_ CC_	
GAM2487	PDCD10	5' CCAATTCTTTTATCACCAA 24273	CTATCC A
		TTGGTGAT GA AATTGG	
		AACCACTA TT TTAACC	
		TT____ C	
GAM2487	SHARP	3' CCAAGGACACATCACCAA 31101	CTA GAAAA
		TTGGTGAT TCC TTGG	
		AACCACTA AGG AACC	
		CAC _____	
GAM2487	LOC151414	3' CCAACCTCTAAGTAGATCAC 81035	CC_ AAA
		GTGATCTAT GA TTGG	
		CACTAGATG CT AACC	
		AAT CC_	
GAM2488	ADORA1	3' TGGGCCACCAGCTCCACTGG 7275	GAA AAGA
		CCAG GAG GTGGCCCA	
		GGTC CTC CACCGGGT	
		AC_ GAC_	
GAM2488	ADRA2B	3' TGGGACCCCTGCTTCCTGGTT 7299	AGAAG T _ _
		AACCAGGAAG AG GG CC CA	
		TTGGTCCTTC TC CC GG GT	
		G____ C A A	
GAM2488	ATP2C1	5' GGGGGCTTCTCTTCCTTGT 27664	C AGTGG
		AC AGGAAGAGAAG CCC	
		TG TCCTTCTCTTC GGG	
		T GG____	
GAM2488	ATP8B2	5' CTCTCCCTGTCCTGGTT 65833	_ A
		AACCAGGA AG GAAGAG	
		TTGGTCCT TC CTTCTC	
		G C	
GAM2488	BACE	3' GGGCTCTGTCTTCCTGGT 58090	GA GTG
		ACCAGGAAGA AGA GCCC	
		TGGTCCTTCT TCT CGGG	
		G_ ____	
GAM2488	CAPN1	5' GGGAGGAGCGCTCTTCCTGGTT 19011	AAGAGTGG
		AACCAGGAAGAG CCC	
		TTGGTCCTTCTC GGG	
		GCGAGGA_	
GAM2488	CD83	3' TGGGCCCTTCCTTCTTGGTT 16172	A AGT
		AACCAGGAAG GAAG GGCCCA	

			TTGGTTCTTC CTTC CCGGGT		
			C ____		
GAM2488	CHRNE	3'	GGAAACCCTCTTCTTCCCTGGT 5378	AA	T C__
			ACCAGG GAGAAGAG GG CC		
			TGGTCC TTCTTCTC CC GG		
			C_ _ AAA		
GAM2488	CYLN2	3'	GGGCATCCCTTCCTGGT 14093	A	AGAGTG _
			ACCAGGAAG GA GC CC		
			TGGTCCTTC CT CG GG		
			C A_____ A		
GAM2488	CYP46	3'	TGGGCCACCCTTCACGCTGG 22865	GAAGA	A
			CCAG GAAG GTGGCCCA		
			GGTC CTTC CACCGGGT		
			GCA_ C		
GAM2488	DACH	3'	GGGATTCTTTTCCTAGTT 55824	C	GAGTGG
			AAC AGGAAGAGAA CCC		
			TTG TCCTTTTCTT GGG		
			A A_____		
GAM2488	DRPLA	3'	TGGACCAGGTCTCTTTCCTTG 10428	C	A G_ C
	T		AC AGGAAGAGA GA TGG CCA		
			TG TCCTTCTCT CT ACC GGT		
			T _ GG A		
GAM2488	DVL3	3'	CACCCTTCTCCCCTTCCTGGT 16638	_____	A
			ACCAGGAA GAGAAG GTG		
			TGGTCCTT CTCTTC CAC		
			CCC C		
GAM2488	EGFR	3'	GCCACTCTGTCCCTTCCTGG 19087	A	_
			CCAGGAAG GA AGAGTGGC		
			GGTCCTTC CT TCTCACCG		
			C G		
GAM2488	EGLN2	3'	GCCACTCTTTGACCGGTT 54914	A	AAGA
			AACC GG GAAGAGTGGC		
			TTGG CC TTTCTCACCG		
			_ AG_		
GAM2488	EHD3	3'	CGCTCTTCCCCTCTCCTCGG 28203	_ _	A_
			CC AGGA AG GAAGAGTG		
			GG TCCT TC CTTCTCGC		
			C C CC		
GAM2488	EPB42	5'	GGCCTGCCTCTCTCCGAGT 5503	CA	A A _
			AC GGAAGAGA G GT GGCC		

			TG CCTTCTCT C CG CCGG		
			AG _ _ T		
GAM2488	EXT1	3'	GCTGCTCTCTTCCCAGT 5522	CA	A TG
			AC GGAAGAGA GAG GC		
			TG CCTTCTCT CTC CG		
			AC _ GT		
GAM2488	GFRA2	3'	ACCTGTCTCCTCCCAGGTT 9462	A_ A _ A	
			AACC GGA GAGA AG GT		
			TTGG CCT CTCT TC CA		
			AC C G _		
GAM2488	GNPI	3'	TGGATGCTGCCTCCTCCTGG 19619	A	AAGA TG _
			CCAGGA GAG G GC CCA		
			GGTCCT CTC C CG GGT		
			C _ _ _ GT TA		
GAM2488	GRIK5	3'	ACTGCTTCTCTTCTCGGT 10876	AG	_
			ACC GAAGAGAAG AGT		
			TGG CTTCTCTTC TCA		
			CT G		
GAM2488	GYG2	3'	CCGATTCACTTCCTGGTT 15361	A	GAGT
			AACCAGGAAG GAA GG		
			TTGGTCCTTC CTT CC		
			A AG _		
GAM2488	HOXC4	5'	GCCCCTCCTCTCTCCCAGG 28247	A A	A T
			CC GG AGAGA GAG GGC		
			GG CC TCTCT CTC CCG		
			A C C C		
GAM2488	IMPDH1	3'	GGCCGCTCCCCTGTCCCTGG 7953	AAG	AA
			CCAGG AG GAGTGGCC		
			GGTCC TC CTCGCCGG		
			CTG CC		
GAM2488	JAM2	5'	GGGCGCTGCTCTCCTCCTG 41385	A	AG G
			CAGGA GAGA AGTG CCC		
			GTCCT CTCT TCGC GGG		
			C CG _		
GAM2488	LENG4	5'	TGGGCCACCCTCCCTTGCTG 44421	G	A A A
			CAG AAG GA G GTGGCCCA		
			GTC TTC CT C CACCGGGT		
			G C _ C		
GAM2488	LGR6	5'	GGGCCACTGGCTTCCTGG 85356	AGAAG	
			CCAGGAAG AGTGGCCC		

GGTCCTTC TCACCGGG
GG__

GAM2488 MECP2 3' GTCCTCCTCCTTCCTAGTT 18411 C A A T
AAC AGGAAG GA GAG GGC
||| ||||| || ||| |||
TTG TCCTTC CT CTC CTG
A _ C _

GAM2488 MTF1 3' GTCCTTGCCTTCCTGGTT 21051 AGAA T
AACCAGGAAG GAG GGC
||||||| ||| |||
TTGGTCCTTC TTC CTG
CG__ _

GAM2488 PCDH11X 3' GGGCACCTCTTCTTGGTT 28014 AAGA G
AACCAGGAAGAG GTG CCC
||||||| ||| |||
TTGGTTCTTCTC CAC GGG
C__ _

GAM2488 PCDH11Y 3' GGGCACCTCTTCTTGGTT 53166 AAGA G
AACCAGGAAGAG GTG CCC
||||||| ||| |||
TTGGTTCTTCTC CAC GGG
C__ _

GAM2488 PEA15 3' TGAGCCAGGGATCCTTTCCTGG 15014 A AGAG C
T ACCAGGAAG GA TGGC CA
||||||| || ||| |||
TGGTCCTTT CT ACCG GT
C AGGG A

GAM2488 PLCB2 3' GGCTCACCCCTCTTCCTAGG 17113 _ AAGA _
CC AGGAAGAG GTG GCC
|| ||||| ||| |||
GG TCCTTCTC CAC CGG
A CC__ T

GAM2488 PPP2R2B 3' CCCTCCCCTCCTCCTGGTT 17121 A AA T
AACCAGGA GAG GAG GG
||||||| ||| ||| |||
TTGGTCCT CTC CTC CC
C CC _

GAM2488 PTK2B 3' TGGGCCAAATCCGCTCTCTTCC 15909 A__ G_
TG CAGGAAGAGA GA TGGCCCA
||||||| || |||||
GTCCTTCTCT CT ACCGGGT
CGC AA

GAM2488 PTK7 3' GGCCTTTCCTCCTCTTCCT 12550 AA_ T
AGGAAGAG GAG GGCC
||||||| ||| |||
TCCTTCTC CTT CCGG
CTC T

GAM2488 PYGO2 3' TATTCCTGCTTCCTGG 64688 __ AA
CCAGGAAG AG GAGTG
||||||| || |||||

			GGTCCTTC TC CTTAT		
			CG CC		
GAM2488	SARDH	5'	TGGGCCACACTCCTTCCT 24019	A A A	
			AGGAAG GA G GTGGCCCA		
			TCCTTC CT C CACCGGGT		
			_ _ A		
GAM2488	SLC2A4	3'	ATGGGCCACTCTCCCCTCCCTC 8307	A _____	_____
			TTCCT AGGAAGAG AGAGTGGCCCA T		
			TCCTTCTC TCTCACCGGGT A		
			CCTCCCC		
GAM2488	TULP2	5'	TGAGCCGTCTTTCTTCTCCTCC 13905	A ____ C	
			GGA GAGAAGAG TGGC CA		
			CCT CTCTTCTT GCCG GT		
			C TCT A		
GAM2488	WNT1	3'	TGGCCATGCCTCCCTGG 19479	AA AAGA C	
			CCAGG GAG GTGGC CA		
			GGTCC CTC TACCG GT		
			_ CG_ A		
GAM2488	WNT1	3'	TGGTCCCTCTTCTCTCCTCAGT 19480	C_ A T C	
			T AAC AGGA GAGAAGAG GG CCA		
			TTG TCCT CTCTTCTC CC GGT		
			AC _ _ T		
GAM2488	WNT3A	3'	TGGGCCCGCCCCCTTCCTGG 53613	AGAAGAG	
			CCAGGAAG TGGCCCA		
			GGTCCTTC GCCGGGT		
			CCCCG_		
GAM2488	ZNF179	3'	TGACCACTCTTTGCTGG 24090	GAAGA CC	
			CCAG GAAGAGTGG CA		
			GGTC TTTCTCACC GT		
			G_ AA		
GAM2488	AF9Q34	3'	TGAGCCCTGCTCTTCTCTCCC 51723	A ____ C	
			GG AGAGAAGAGT GGC CA		
			CC TCTCTTCTCG CCG GT		
			C TC A		
GAM2488	AQP10	3'	GGCAATCCTCTTCCTGGT 55396	AA GTG	
			ACCAGGAAGAG GA GCC		
			TGGTCCTTCTC CT CGG		
			_ AA_		
GAM2488	ARHF	3'	GGAACCTCTCTCCTTTCTGG 39270	_ A GG	
			CCAGGAA GAGA GAGT CC		

GGTCCTT CTCT CTCA GG
TC _ A_
GAM2488 C11orf21 3' TATTCTTCTTTCCCCAGT 27109 CA A
AC GG AGAGAAGAGTG
|| || |||||
TG CC TTTCTTCTTAT
AC C
GAM2488 C16orf5 3' TGGGCCTCTGCTCTCTTGCCTG 26357 _ AG T
G CCAGG AAGAGA AG GGCCCA
||||| || |||||
GGTCC TTCTCT TC CCGGGT
G CG T
GAM2488 C20orf102 3' GGGCACACCTGCCCCCTGGTT 55510 AAGAGA A _
AACCAGG AG GTG GCCC
||||| || ||| ||||
TTGGTCC TC CAC CGGG
CCCG_ _ A
GAM2488 C20orf39 5' GCCCTCCTTCTCTTCCCTG 46576 _ _ T
CAGG AAGAGAAG AG GGC
||| ||||| || |||
GTCC TTCTCTTC TC CCG
C C _
GAM2488 C20orf4 5' TGGGCCGCCCTCTTCTCGG 31950 AG AAGA
CC GAAGAG GTGGCCCA
|| ||||| |||||
GG CTTCTC CGCCGGGT
CT CC_
GAM2488 C20orf98 3' GCCCCTCACCTTCCTGGTT 72007 AGAA T
AACCAGGAAG GAG GGC
||||||| ||| |||
TTGGTCCTTC CTC CCG
CA_ C
GAM2488 C9orf16 3' TGGGCCACCCTTCCTGCCTGG 44359 A A A
CCAGG AG GAAG GTGGCCCA
||||| || ||| |||||
GGTCC TC CTTC CACCGGGT
G _ C
GAM2488 C9orf7 3' GGGCCGCTCCTGCCTGGT 34585 A AGAA
ACCAGG AG GAGTGGCCC
||||| || |||||
TGGTCC TC CTCGCCGGG
G _
GAM2488 CGI-57 3' GGTTTCCCTCTCTTCTGGTT 74309 G AGAGT
AACCAG AAGAGA GGCC
||||| ||||| |||
TTGGTC TTCTCT TTGG
_ CCCT_
GAM2488 CLECSF9 3' GTCTGTCTTCTCTTCTTGGTT 27623 GT
AACCAGGAAGAGAAGA GGC
||||||| ||||| |||

		TTGGTTCTTCTCTTCT CTG	
		GT	
GAM2488	CTRP5	3' TGGGGTGCTCTCTTCCTGGT 32232	AGA G
		ACCAGGAAGAGA GTG CCCA	
		TGGTCCTTCTCT CGT GGGT	
		___ G	
GAM2488	CXYorf1	3' TGGGCTATGGCTCCTTCCTGGT 82924	A AGA
	T	AACCAGGAAG GA GTGGCCCA	
		TTGGTCCTTC CT TATCGGGT	
		_ CGG	
GAM2488	DEFCAP	5' TGGGCTCCTCCCTCCCCTGG 53389	AA AA TG
		CCAGG GAG GAG GCCCA	
		GGTCC CTC CTC CGGGT	
		C_ C_ CT	
GAM2488	DKFZp547l094	5' CAGTTCCTCTCTCCTGGTT 50554	A A _
		AACCAGGA GAGA GAG TG	
		TTGGTCCT CTCT CTT AC	
		_ C G	
GAM2488	DQX1	5' TGGGCTTCCCTTCTCTTCC 56911	AGT
		GGAAGAGAAG GGCCCA	
		CCTTCTCTTC TCGGGT	
		CCT	
GAM2488	DRIM	5' TGAGCCGCTTTCCCCTCCT 27958	AGA A C
		AGGA GA GAGTGGC CA	
		TCCT CT TTCGCCG GT	
		CCC _ A	
GAM2488	ERAL1	3' GGGAGATTTCTCTTCCTG 63312	AGTGG
		CAGGAAGAGAAG CCC	
		GTCCTTCTCTTT GGG	
		AGA__	
GAM2488	FLJ10565	3' TGGGCCACCCCTTAAGCTTCCT 36808	AG_ A_
	GGT	ACCAGGAAG AAG GTGGCCCA	
		TGGTCCTTC TTC CACCGGGT	
		GAA CC	
GAM2488	FLJ10748	3' CCACTTTCTTCTCCCTTGG 37097	AA _
		CCAGG GAGAAGA GTGG	
		GGTTC CTCTTCT CACC	
		C_ TT	
GAM2488	FLJ12242	3' TGGATGTGCTCCTTCCTGG 45506	AGAA GC_
		CCAGGAAG GAGTG CCA	

			GGTCCTTC CTCGT GGT		
			_____ GTA		
GAM2488	FLJ12425	3'	GCCTCTTTTCTCTCCCTGG 87094	A	T
			CCAGG AGAGAAGAG GGC		
			GGTCC TCTCTTTTC CCG		
			C T		
GAM2488	FLJ13265	3'	GGGACTTACCTTCCTGGT 46412	AGAA	GG
			ACCAGGAAG GAGT CCC		
			TGGTCCTTC TTCA GGG		
			CA__ _		
GAM2488	FLJ13769	3'	GCCACTCTCAGCTTCCTG 47253	AGA	
			CAGGAAG AGAGTGGC		
			GTCCTTC TCTACCG		
			GAC		
GAM2488	FLJ13848	3'	GGCCTTTCCTCTTTCCTGGT 45827	A A	T
			ACCAGGA GAGA GAG GGCC		
			TGGTCCT TTCT CTT CCGG		
			_ C T		
GAM2488	FLJ14166	3'	TGGGTGCTTTTCTTTCCCTGG 44993	A	G
			CCAGG AGAGAAGAGTG CCCA		
			GGTCC TTTCTTTTCGT GGGT		
			C _		
GAM2488	FLJ20079	3'	TGGGAATTTCTCTTCCT 34981	A	GTGG
			AGGAAGAG AGA CCCA		
			TCCTTCTC TTT GGGT		
			C AA__		
GAM2488	FLJ20277	3'	TGGACCAGGCCTCCTCTCAGCC 35315	AA A	__ C
			GG GAGA GAG TGG CCA		
			CC CTCT CTC ACC GGT		
			GA C CGG A		
GAM2488	FLJ21736	3'	GGGTCCTCCCTCCCTTCCTGG 46786	A A_	T
			CCAGGAAG GA GAG GGCCC		
			GGTCCTTC CT CTC CTGGG		
			C CC _		
GAM2488	FLJ22639	5'	GGCCCTTCCTCCCTAGTT 45997	C A A	AGT
			AAC AGG AG GAAG GGCC		
			TTG TCC TC CTTC CCGG		
			A C _ _		
GAM2488	FLJ23042	3'	GGGCCGCTCCTCGCTAACT 47948	GA A A	
			AG AG GA GAGTGGCCC		

		TC TC CT CTCGCCGGG	
		AA G C	
GAM2488	FLJ23506	3' CCTCTCTTCTCTCCCCAGT 46165	CA A T
		AC GG AGAGAAGAG GG	
		TG CC TCTCTTCTC CC	
		AC C T	
GAM2488	FLJ32934	3' CACCTCCCTCTCTTCCTG 58880	A_ _
		CAGGAAGAGA GAG TG	
		GTCCTTCTCT CTC AC	
		CC C	
GAM2488	FTSJ3	3' TGGGCCACTTAAGCCCTCCCC 34938	AA AA__
		GG GAG GAGTGGCCCA	
		CC CTC TTCACCGGGT	
		C_ CCGAA	
GAM2488	FYCO1	3' GCTGCACTCTCTTTCTGG 44773	A A TG
		CCAGGAAGAGA G G GC	
		GGTCTTTCTCT C C CG	
		_ A GT	
GAM2488	GABARAPL3	3' GCTGCTTCCCTTCTTGTT 51783	A AG TG
		AACCAGGAAG GA AG GC	
		TTGGTTCTTC CT TC CG	
		C _ GT	
GAM2488	GAL3ST2	3' TGGGCCACCCTCTCCTTCC 53486	_ A A
		GGAAG AGA G GTGGCCCA	
		CCTTC TCT C CACCGGGT	
		C _ C	
GAM2488	GR6	3' TGAGCCTTACTTCTCTTCCTGG 24753	AGT C
		CCAGGAAGAGAAG GGC CA	
		GGTCCTTCTCTTC CCG GT	
		ATT A	
GAM2488	JAM1	3' GGTCCCTGCCCTTCCTGGTT 34236	AGAAG T
		AACCAGGAAG AG GGCC	
		TTGGTCCTTC TC CTGG	
		CCCG_ _	
GAM2488	JAM1	3' GGTCCCTGCCCTTCCTGGTT 58522	AGAAG T
		AACCAGGAAG AG GGCC	
		TTGGTCCTTC TC CTGG	
		CCCG_ _	
GAM2488	KIAA0427	3' GCCTTCTTCCTCCCTCCACGGT 29385	___ A A T
	T	AACC AGG AG GAAGAG GGC	

TTGG TCC TC CTTCTT CCG
 CACC C _ _
 GAM2488 KIAA0441 3' GGGCCACCTGTTTCTAACT 29640 GA _ A
 AG AGAGA AG GTGGCCC
 || ||||| || |||||
 TC TCTTT TC CACCGGG
 AA G _
 GAM2488 KIAA0450 5' TGGGCCACTGACCACCTCCCCG 28375 A A AGAAG_
 G CC GG AG AGTGGCCCA
 || ||| |||||
 GG CC TC TCACCGGGT
 C C CACCAG
 GAM2488 KIAA0534 3' GGCCACTCTTTTTCTACC 71932 A _
 GG AGAGAA GAGTGGCC
 || ||||| |||||
 CC TCTTTT CTCACCGG
 A T
 GAM2488 KIAA0769 5' TGGGCCGTCCCCTCCTCTCCGG 29760 A A AA ____
 CC GGA GAG GAG TGGCCCA
 || ||| ||| |||||
 GG CCT CTC CTC GCCGGGT
 _ _ _ CCCT
 GAM2488 KIAA0781 3' TGGATGTTGCTTCCTCCTGGTT 68062 A GAAG TG _
 AACCAGGA GA AG GC CCA
 ||||| || || |||
 TTGGTCCT CT TC TG GGT
 C ____ GT TA
 GAM2488 KIAA0795 3' GTCCCTCTCCTCTTTCTGG 47231 A T
 CCAGGAAGAG AGAG GGC
 ||||| ||| |||
 GGTCTTTCTC TCTC CTG
 C C
 GAM2488 KIAA0930 3' GGAACCTCTTCCCCTGGTT 71071 AAGA GG
 AACCAGG GAAGAGT CC
 ||||| ||||| ||
 TTGGTCC CTTCTCA GG
 C_ A_
 GAM2488 KIAA1172 5' GGGCGCAGCCTCTTCCTG 71397 AAGA G
 CAGGAAGAG GTG CCC
 ||||| ||| |||
 GTCCTTCTC CGC GGG
 CGA_ _
 GAM2488 KIAA1277 3' TGGACCTGACTCTTCTTGA CT 65088 GAA _ C
 AG GAGAAGAGT GG CCA
 || ||||| || |||
 TC TTCTTCTCA CC GGT
 AG_ GT A
 GAM2488 KIAA1437 5' TGGGCCACTCTCCCAGCTCCTG 61222 AGAGA_
 G CCAGGA AGAGTGGCCCA
 ||||| |||||

		GGTCCT TCTCACCGGGT		
		CGACCC		
GAM2488 KIAA1494	3'	ATTCCCTCTCTTTCTAGTT 68980	C	A_
		AAC AGGAAGAGA GAGT		
		TTG TCTTTCTCT CTTA		
		A CC		
GAM2488 KIAA1554	3'	TGGACTAATTTCTCTTCCT 96864	AG	C
		AGGAAGAGAAG TGG CCA		
		TCCTTCTCTTT ATC GGT		
		A_ A		
GAM2488 KIAA1766	3'	GTCTTTCTCTTCCAGTT 71876	CA	AGT
		AAC GGAAGAGAAG GGC		
		TTG CCTTCTCTTT CTG		
		AC _		
GAM2488 KIAA1813	5'	GGACACCTCTTCCTGGTT 70826	AAGA	GC
		AACCAGGAAGAG GTG CC		
		TTGGTCCTTCTC CAC GG		
		_ A_		
GAM2488 KIAA1924	3'	GGGCCACCTGGGCTTCCTGG 74054	AGA	A
		CCAGGAAG AG GTGGCCC		
		GGTCCTTC TC CACCGGG		
		GGG _		
GAM2488 MacGAP	3'	GGAAATGTCTTCTCTTCC 54299	_	GG
		GGAAGAGAAGA GT CC		
		CCTTCTCTTCT TA GG		
		G AA		
GAM2488 MAD3	3'	TGGGCCTCTTCCCTTCCTGG 49341	A	GT
		CCAGGAAG GAAGA GGCCCA		
		GGTCCTTC CTTCT CCGGGT		
		C _		
GAM2488 MGC17330	3'	TGGGCCCAGGGACTCTTCCTG 54632	AAGAGT	
		CAGGAAGAG GGCCCA		
		GTCCTTCTC CCGGGT		
		AGGGAC		
GAM2488 MGC23280	3'	TGGACATCTCTTTTCCTGGTT 59055	A G	GC
		AACCAGGAAGAGA GA TG CCA		
		TTGGTCCTTTTCT CT AC GGT		
		_ _ A_		
GAM2488 MGC4832	3'	TGAGTTTTGTTTCTCTTCC 59660	AGT	C
		GGAAGAGAAG GGC CA		

		CCTTCTCTTT TTG GT	
		GTT A	
GAM2488 MIG	3'	GGTGCTGGCTCTTTCCTGG 11587	GAGA _ _
		CCAGGAA AGAGT GGC CC	
		GGTCCTT TCTCG TCG GG	
		_____ G T	
GAM2488 NCKX3	5'	TGAGCCAGCTCTGCTTCCTGG 40728	AGA _ C
		CCAGGAAG AGAG TGGC CA	
		GGTCCTTC TCTC ACCG GT	
		G_ G A	
GAM2488 OSBPL7	5'	CATCTCCTTCCTTCCTGGTT 35304	A _ _
		AACCAGGAAG GAAG AG TG	
		TTGGTCCTTC CTTC TC AC	
		_ C T	
GAM2488 P2RX1	3'	TGGCCCTGTTTCTTCCTGG 67752	AG T C
		CCAGGAAGAGA AG GGC CA	
		GGTCCTTCTTT TC CCG GT	
		G_ _ A	
GAM2488 P4HA2	3'	GTCCTTCCCCTTCCTGGT 16100	A_ AGT
		ACCAGGAAG GAAG GGC	
		TGGTCCTTC CTTC CTG	
		CC _____	
GAM2488 PDZ-	3'	GGGCCACTCTTCTGAAGGCC 65629	AAG_
		GG AGAAGAGTGGCCC	
		CC TCTTCTCACCGGG	
		GGAAG	
GAM2488 PGLYRP	3'	TGGGCCACTGTCCCCTCCCTG 54672	A A_ AG
		CAGG AG GA AGTGGCCCA	
		GTCC TC CT TCACCGGGT	
		C CC G_	
GAM2488 PPAP2A	5'	GGCTGCTCTCCTCCTCCGG 68442	A A A TG
		CC GGA GAG AGAG GCC	
		GG CCT CTC TCTC CGG	
		_ C C GT	
GAM2488 PRRDH	3'	TGGACCAAGGGGTCATTCCTGG 32328	GA AGAG_ C
T		ACCAGGAA GA TGG CCA	
		TGGTCCTT CT ACC GGT	
		A_ GGGGA A	
GAM2488 SCGF	3'	GGAATCGCCCTTCCTTCCTGG 12946	A A C_
		CCAGGAAG GAAG GTGG CC	

GGTCCTTC CTTC CGCT GG
C C AA

GAM2488 SEMA6A 5' CATTTACCCTCTTCCTTGTT 40816 C AA_
AAC AGGAAGAG GAGTG
||| ||||| ||||
TTG TCCTTCTC TTTAC
T CCA

GAM2488 SPEC1 3' GCCCTTCTCCTCCTTCCTGG 40006 _ A T
CCAGGAAG AG AGAG GGC
||||||| || ||||| |||
GGTCCTTC TC TCTT CCG
C C C

GAM2488 STX12 5' GCCCTTGCTCTTCCCAGTT 66951 CA AA T
AAC GGAAGAG GAG GGC
||| ||||| ||| |||
TTG CTTCTC TTC CCG
AC G_ _

GAM2488 THTPA 3' TGGGCCGCCCTCTCCCCTGG 44513 AA AGA
CCAGG GAGA GTGGCCCA
||||| ||| |||||
GGTCC CTCT CGCCGGGT
C_ CCC

GAM2488 TPARL 3' GGGTTTTTCTTCTCTTCC 38072 T_
GGAAGAGAAGAG GGCCC
||||||| |||||
CCTTCTCTTCTT TTGGG
TT

GAM2488 TRAF6 5' GGGGAGCCCTGCCCTCCTGGTT 17288 AGAGA A GG
AACCAGGA AG GT CCC
||||||| || || |||
TTGGTCCT TC CG GGG
CCCG_ C AG

GAM2488 TRIAD3 3' TGAGCAGCTTTTCCCCCTGG 96140 AAGA G C
CCAGG GAAGAGT GC CA
||||| ||||| || |||
GGTCC CTTTTCG CG GT
CCC_ A A

GAM2488 ZDHC9 5' GGCCGGCTCCCCCTTCCTGGT 62355 AGAA _
ACCAGGAAG GAGT GGCC
||||||| ||| |||||
TGGTCCTTC CTCG CCGG
CCC_ G

GAM2488 ZNF17 3' ACCTCCTCCACCTCCTGGTT 83266 A__ A A
AACCAGGA GAG AG GT
||||||| || || |||
TTGGTCCT CTC TC CA
CCAC C _

GAM2488 ZNF282 3' GGTCTCTCTTCCTTTCCTGGT 90695 A T
ACCAGGAAG GAAGAG GGCC
||||||| ||||| |||||

	TGGTCCTTT CTTCTC CTGG	
	C T	
GAM2488 LOC115110 3'	GCCTCCTCCTCTTCCTGG 72179	AA T_
	CCAGGAAGAG GAG GGC	
	GGTCCTTCTC CTC CCG	
	_ CT	
GAM2488 LOC115708 3'	GCTCCTCCCTGTCCTGGTT 73918	AG AA TG
	AACCAGGA AG GAG GC	
	TTGGTCCT TC CTC CG	
	G_ C_ CT	
GAM2488 LOC123096 3'	TGGGCCACCCCTCTGGTCTGTG 74656	_ A_ AAGA
TT	AAC CAGG AGAG GTGGCCCA	
	TTG GTCT TCTC CACCGGGT	
	T GG CC_	
GAM2488 LOC124538 3'	GCCACCCAGCTTTTCTTGG 76151	AAGA
	CCAGGAAGAG GTGGC	
	GGTTCTTTTC CACCG	
	GACC	
GAM2488 LOC125967 3'	GGAACCCTTCCCCTTCCTGG 74895	A_ A GG
	CCAGGAAG GAAG GT CC	
	GGTCCTTC CTTC CA GG	
	CC C A_	
GAM2488 LOC126133 3'	TGGGACTTTCCCCTTCTGGTT 74917	G AGA GG
	AACCAG AAG AGAGT CCCA	
	TTGGTC TTC TTTCA GGGT	
	_ CCC _	
GAM2488 LOC144583 3'	GGACGGTCCTGTTCTGGT 77419	G AA G GC
	ACCAGGAA AG GA TG CC	
	TGGTCCTT TC CT GC GG	
	G _ G A_	
GAM2488 LOC144866 5'	GGCCCCTCCTCTTCCTGG 84137	AA T
	CCAGGAAGAG GAG GGCC	
	GGTCCTTCTC CTC CCGG	
	_ C	
GAM2488 LOC145216 3'	TGGCCAGAGCCTTCCTGGTT 84229	AGAAGAG C
	AACCAGGAAG TGGC CA	
	TTGGTCCTTC ACCG GT	
	CGAG_ A	
GAM2488 LOC146823 3'	TGGGTGTCCTCTTCTCCTCC 84829	A TG_
	GGA GAGAAGAG GCCCA	

		CCT CTCTTCTC TGGGT		
		C CTG		
GAM2488	LOC146854 5'	GGTGCCCTCACTCTTCCTG 78746	AA	T _
		CAGGAAGAG GAG GGC CC		
		GTCCTTCTC CTC CCG GG		
		A_ C T		
GAM2488	LOC147138 5'	GGCCTTCGCCTTCCTGGT 78867	AGAA	T
		ACCAGGAAG GAG GGCC		
		TGGTCCTTC CTT CCGG		
		CG _ _		
GAM2488	LOC148046 3'	TGAGCCTCTGCCTTTTCCTGGT 85248	A_	GT C
	T	AACCAGGAAGAG AGA GGC CA		
		TTGGTCCTTTTC TCT CCG GT		
		CG _ A		
GAM2488	LOC148171 5'	GGGCCAGCTCTTCTTCCTGGT 79428	GA	_
	T	AACCAGGAAGA AGAGT GGCCC		
		TTGGTCCTTCT TCTCG CCGGG		
		_ AC		
GAM2488	LOC148195 5'	GTCTTCTCCTCTTCCTTGT 85289	C	A T
		AC AGGAAGAG AGAG GGC		
		TG TCCTTCTC TCTT CTG		
		T C _		
GAM2488	LOC148529 5'	GGGCCACTCCTCCCTTCCT 85323	A	A
		AGGAAG GA GAGTGGCCC		
		TCCTTC CT CTCACCGGG		
		C C		
GAM2488	LOC149124 5'	GGGCCAGCTCTTCTTCCTGGT 79921	GA	_
	T	AACCAGGAAGA AGAGT GGCCC		
		TTGGTCCTTCT TCTCG CCGGG		
		_ AC		
GAM2488	LOC150245 3'	GGCCACTCTCCAGCCTGGT 86115	AAGA	A
		ACCAGG GA GAGTGGCC		
		TGGTCC CT CTCACCGG		
		GAC_ _		
GAM2488	LOC150271 5'	TGAACCAGCCCTTCTTCTCA 86148	CA	A_ CC
	GTT	AAC GGAAGAGAAG G TGG CA		
		TTG TCTTCTCTTC C ACC GT		
		AC C G AA		
GAM2488	LOC150606 3'	TGGAGCTGTTCTCCTCTAACT 86277	GA	A TG _
		AG AGAG AGAG GC CCA		

	TC TCTC TCTT CG GGT		
	AA C GT A		
GAM2488 LOC151742 5'	CCTCTTTTTCTTCCCAGT 58345	CA	A T
	AC GGAAGAGA GAG GG		
	TG CCTTCTTT TTC CC		
	AC _ T		
GAM2488 LOC151878 5'	ACTGTGTCTCTTCTTAGTT 81195	C	AG_
	AAC AGGAAGAGA AGT		
	TTG TTCTTCTCT TCA		
	A GTG		
GAM2488 LOC152426 5'	TGGGCCACCTTGCCTTCCCTGG 86903	_	AG A
	CCAGG AAG AAG GTGGCCCA		
	GGTCC TTC TTC CACCGGGT		
	C CG _		
GAM2488 LOC153688 3'	TGGAACAATCCCCTTCCTGGT 87339		AGAA G GC
	ACCAGGAAG GA TG CCA		
	TGGTCCTTC CT AC GGT		
	CC_ A AA		
GAM2488 LOC155064 5'	TGGGCCGCGCTCCCTCCCT 82180	A A A A	
	AGG AG GA G GTGGCCCA		
	TCC TC CT C CGCCGGGT		
	C C _ G		
GAM2488 LOC169286 5'	TGGATCCTCCCCTTCCTGG 83614		AGAA T GC
	CCAGGAAG GAG G CCA		
	GGTCCTTC CTC C GGT		
	CC_ _ TA		
GAM2488 LOC196707 3'	TGGGAATTCTTCTCCTGGT 88926		GAGTGG _
	ACCAGGAAGAGAA CC CA		
	TGGTCCTTCTCTT GG GT		
	AA_ A		
GAM2488 LOC196955 5'	TGGCTGTTCTCATCCCTGGTT 77878		AA GA TG C
	AACCAGG GA AGAG GC CA		
	TTGGTCC CT TCTT CG GT		
	_ AC GT A		
GAM2488 LOC197125 3'	GGTTCTACCTCTTCCTGG 89245		AAG T
	CCAGGAAGAG AG GGCC		
	GGTCCTTCTC TC TTGG		
	CA_ _		
GAM2488 LOC197135 5'	TGGGAAGTACTTCTTCCTG 89239		AG GG
	CAGGAAGAGAAG T CCA		

	GTCCTTCTCTTC G GGGT	
	AT AA	
GAM2488 LOC200093 3'	TGGGCTATGGCTCCTTCCTGGT 63780	A AGA
T	AACCAGGAAG GA GTGGCCCA	
	TTGGTCCTTC CT TATCGGGT	
	_ CGG	
GAM2488 LOC200269 3'	GGGCCGCTCTTGCTGGTT 90075	G AGAGA
	AACCAG A AGAGTGGCCC	
	TTGGTC T TCTCGCCGGG	
	G _____	
GAM2488 LOC202126 3'	CACTCTCCTGCCCTTCCTGG 91907	___ A
	CCAGGAAG AG AGAGTG	
	GGTCCTTC TC TCTCAC	
	CCG C	
GAM2488 LOC221191 5'	GCTGCCCTCTCTTCTCTGG 95221	_ A A TG
	CCAG GAAGAGA G G GC	
	GGTC CTTCTCT C C CG	
	T _ C GT	
GAM2488 LOC221466 3'	GGACTGCCCTCCTTCCTGG 95315	A A A TG C
	CCAGGAAG GA G G G CC	
	GGTCCTTC CT C C C GG	
	_ _ C GT A	
GAM2488 LOC221692 3'	TGGGAGTTCCTCCTTCTGGTT 93860	A AA TGG
	AACCAGGA GAG GAG CCCA	
	TTGGTCTT CTC CTT GGGT	
	C C_ GA_	
GAM2488 LOC253291 3'	TGGAACACTCTCTTCCTGG 98757	AGA GC
	CCAGGAAGAGA GTG CCA	
	GGTCCTTCTCT CAC GGT	
	___ AA	
GAM2488 LOC254181 5'	TGGTACCTTTTCTCCCTGG 99443	AA TG C
	CCAGG GAGAAGAG GC CA	
	GGTCC CTCTTTTC TG GT	
	_ CA A	
GAM2488 LOC254873 3'	ATGGGCCACTCTCCCCTCCCTC 96211	A _____
TTCCT	AGGAAGAG AGAGTGGCCCA T	_____
	TCCTTCTC TCTACCGGGT A	
	CCTCCCC _____	
GAM2488 LOC255360 3'	TGGACACCTCCTCCTCCTG 98764	A A A GC
	CAGGA GAG AG GTG CCA	

	GTCCT CTC TC CAC GGT	
	C C _ A_	
GAM2488 LOC256948 3'	TGGGCTGCCCTGCTCCTGGT 96119	AGAGA A TG
	ACCAGGA AG G GCCCA	
	TGGTCCT TC C CGGGT	
	CG__ C GT	
GAM2488 LOC257451 3'	TATTCCCCTGCCTTCCTGG 97300	__ AA
	CCAGGAAG AG GAGTG	
	GGTCCTTC TC CTTAT	
	CG CC	
GAM2488 LOC51093 5'	TGGACCCAAAACCTTCCTG 32594	AAGAG C_
	CAGGAAGAG TGG CCA	
	GTCCTTCTC ACC GGT	
	AAA__ CA	
GAM2488 LOC51219 5'	GGAGTTACTTTCCTCCTG 33547	A GAA _
	CAGGA GA GAGTGGC CC	
	GTCCT CT TTCATTG GG	
	C __ A	
GAM2488 LOC51236 3'	TGGGCCACTCCTCCCTGG 33625	AA AA
	CCAGG GAG GAGTGGCCCA	
	GGTCC CTC CTCACCGGGT	
	__ __	
GAM2488 LOC51312 3'	TCCTCTTCTCTTGCCAGTT 33994	CA _ T
	AAC GG AAGAGAAGAG GG	
	TTG CC TTCTCTTCTC CT	
	AC G _	
GAM2488 LOC89941 3'	GGGCTCTACCCCTTCCTGG 57851	AGAAG__ T
T	ACCAGGAAG AG GGCCC	
	TGGTCCTTT TC TCGGG	
	CCCCCA _	
GAM2488 LOC91040 3'	TGGGCTATGGCTCCTTCCTGGT 65355	A AGA
T	AACCAGGAAG GA GTGGCCCA	
	TTGGTCCTTC CT TATCGGGT	
	_ CGG	
GAM2488 LOC92078 5'	TGGATATTCTCCTTTTCCT 68614	A GC
	AGGAAGAG AGAGTG CCA	
	TCCTTTTC TCTTAT GGT	
	C A_	
GAM2488 LOC92973 5'	TGGGATTCCTGCTTCCTGG 71595	AGAA GG
	CCAGGAAG GAGT CCA	

			GGTCCTTC	CTTA	GGGT		
			GTC_ _				
GAM2488	LOC93613	5'	GGTGT	TTTCTCCTCCGGG	73079	A A	GTG
			CC	GGA GAGAAGA GCC			
			GG	CCT CTCTTTT TGG			
			G C	G_			
GAM2489	B3GALT5	3'	AAGCCTGAGCCAAGCTC	53720	AAAA	A	
			GA	TTGG CTCAGGCTT			
			CT	AACC GAGTCCGAA			
			CG_ _				
GAM2489	B3GALT5	3'	AAGCCTGAGCCAAGCTC	53724	AAAA	A	
			GA	TTGG CTCAGGCTT			
			CT	AACC GAGTCCGAA			
			CG_ _				
GAM2489	B3GALT5	3'	AAGCCTGAGCCAAGCTC	53728	AAAA	A	
			GA	TTGG CTCAGGCTT			
			CT	AACC GAGTCCGAA			
			CG_ _				
GAM2489	B3GALT5	3'	AAGCCTGAGCCAAGCTC	53732	AAAA	A	
			GA	TTGG CTCAGGCTT			
			CT	AACC GAGTCCGAA			
			CG_ _				
GAM2489	B3GALT5	3'	AAGCCTGAGCCAAGCTC	21337	AAAA	A	
			GA	TTGG CTCAGGCTT			
			CT	AACC GAGTCCGAA			
			CG_ _				
GAM2489	CNN2	3'	TAAGCCTGACCCCTCTCCA	16464	AAAATT	AC	
			TGGA	GG TCAGGCTTA			
			ACCT	CC AGTCCGAAT			
			CTC_ _	CC			
GAM2489	FGFR2	5'	AAGCCTGAGTCCTTTCTTCC	43631	A	TT	
			GGAA	AA GGA			
			CCTT	TT CCTGAGTCCGAA			
			C T_				
GAM2489	FGFR2	5'	AAGCCTGAGTCCTTTCTTCC	43636	A	TT	
			GGAA	AA GGA			
			CCTT	TT CCTGAGTCCGAA			
			C T_				
GAM2489	FGFR2	5'	AAGCCTGAGTCCTTTCTTCC	43640	A	TT	
			GGAA	AA GGA			

			CCTT TT CCTGAGTCCGAA		
			C T_		
GAM2489	FGFR2	5'	AAGCCTGAGTCCTTTCTTCC 43645	A TT	
			GGAA AA GGACTCAGGCTT		
			CCTT TT CCTGAGTCCGAA		
			C T_		
GAM2489	FGFR2	5'	AAGCCTGAGTCCTTTCTTCC 43658	A TT	
			GGAA AA GGACTCAGGCTT		
			CCTT TT CCTGAGTCCGAA		
			C T_		
GAM2489	FGFR2	5'	AAGCCTGAGTCCTTTCTTCC 43671	A TT	
			GGAA AA GGACTCAGGCTT		
			CCTT TT CCTGAGTCCGAA		
			C T_		
GAM2489	FGFR2	5'	AAGCCTGAGTCCTTTCTTCC 43676	A TT	
			GGAA AA GGACTCAGGCTT		
			CCTT TT CCTGAGTCCGAA		
			C T_		
GAM2489	FGFR2	5'	AAGCCTGAGTCCTTTCTTCC 43761	A TT	
			GGAA AA GGACTCAGGCTT		
			CCTT TT CCTGAGTCCGAA		
			C T_		
GAM2489	FGFR2	5'	AAGCCTGAGTCCTTTCTTCC 5556	A TT	
			GGAA AA GGACTCAGGCTT		
			CCTT TT CCTGAGTCCGAA		
			C T_		
GAM2489	ITPR2	3'	AAGCCTGAACCAATCCTTCCA 11077	AA AC	
			TGGAA ATTGG TCAGGCTT		
			ACCTT TAACC AGTCCGAA		
			CC A_		
GAM2489	LYZ	3'	TTAAGCCTACAACATTTTTC 5904	T GACTC	
			GAAAAAT G AGGCTTAA		
			CTTTTTC C TCCGAATT		
			AACA		
GAM2489	SGCB	3'	TTAAGCCTGAGCCATATTCT 5878	AAAT A	
			GGAA TGG CTCAGGCTTAA		
			TCTT ACC GAGTCCGAATT		
			AT__ _		
GAM2489	WISP1	3'	AAGCCTGATCCAGCCTTTCCA 15279	AA C	
			TGGAAA TTGGA TCAGGCTT		

ACCTTT GACCT AGTCCGAA
 CC _
 GAM2489 ZNF144 3' AAGCCTCTCCACTCCTTCCA 24072 AAAT CTC
 TGGAA TGGAGGCTT
 |||| ||| |||||
 ACCTT ACCT TCCGAA
 CCTC C_
 GAM2489 DKFZP434B172 3' TTAAGTAGCTCCAATTTTTC 70578 CTCAG
 GAAAAATTGGA GCTTAA
 ||||| |||||
 CTTTTTAACCT TGAATT
 CGA_
 GAM2489 FLJ00007 3' AAGCCCCAATTTCCCCA 71772 AA ACTCA
 TGG AAATTGG GGCTT
 || ||||| |||||
 ACC TTAAACC CCGAA
 CC _
 GAM2489 KIAA0258 3' TGGGACCCACTTTTTTCCA 29473 T A_
 TGGAAAAA TGG CTCA
 ||||| ||| |||||
 ACCTTTTT ACC GGGT
 C CA
 GAM2489 KIAA1870 3' TAACCGAGTCTCAATTTTCCCA 52904 A _ A C
 TGG AAAATTG GACTC GG TTA
 || ||||| |||| || |||||
 ACC TTTTAAC CTGAG CC AAT
 C T _ _
 GAM2489 MCM10 3' AAGCCCAGCTAATTTTGTGCA 38172 G A CA
 TG AAAAATTGG CT GGCTT
 || ||||| || |||||
 AC TTTTAATC GA CCGAA
 G _ C_
 GAM2489 TSGA14 3' AAGCCATGCCCAATTTTCCA 38663 A ACT _
 TGGAAAA TTGG CA GGCTT
 ||||| |||| || |||||
 ACCTTTT AACC GT CCGAA
 _ C_ A
 GAM2489 LOC219919 5' AAGCCTGAGTCTCCAGCCCA 94914 AAAAATT
 TGG GGAAGCTCAGGCTT
 || ||||| |||||
 ACC TCTGAGTCCGAA
 CGACC_
 GAM2489 LOC51301 3' TTAAGCCTAAGTCCTCAATTC 33911 AAATT C
 GAA GGAAGCT AGGCTTAA
 || |||| |||||
 CTT CCTGA TCCGAATT
 AACT_ A
 GAM2489 LOC90786 3' TAAGCCTGAGCACTTTCC 64733 AAT GA
 GGAAA TG CTCAGGCTTA
 |||| || ||||| |||||

			CCTTT AC GAGTCCGAAT		
			C_ _		
GAM2489	LOC90826	3'	TTGATCCAATTTTACA 64790	G	C
			TG AAAAATTGGA TCAG		
			AC TTTTAACT AGTT		
			A _		
GAM2489	LOC93097	3'	AAGCCTGATTATTTTCTA 71878		TGGAC
			TGGAAAAAT TCAGGCTT		
			ATCTTTTA AGTCCGAA		
			TT_		
GAM2490	DRIL1	3'	GTGAAACCCCTGAACCAA 19080		AT AGAG
			TTGGTTCAGG GG TCAC		
			AACCAAGTCC CC AGTG		
			_ AA_		
GAM2490	MUCDHL	3'	CGGTGAGGTCCATCCTGACCAA 49204	T	GAG
			TTGGT CAGGATGGA TCACCG		
			AACCA GTCCTACCT AGTGGC		
			_ GG_		
GAM2490	FLJ11116	5'	ACATTCCCTGGACCAA 83473		ATG A
			TTGGTTCAGG GAG GT		
			AACCAGGTCC CTT CA		
			_ A		
GAM2490	FLJ20330	3'	CGGTGACCGACCCCAAACCAAG 39142		CA AT AGA
			TTGGTT GG GG GTCACCG		
			GACCAA CC CC CAGTGGC		
			A_ _ AGC		
GAM2490	KIAA1328	3'	GCTGCCCATCCCATAACCAA 62326	CA_	AG
			TTGGTT GGATGG AGT		
			AACCAA CCTACC TCG		
			TAC CG		
GAM2490	KIAA1879	5'	GTGTCCTCCATGCTGAACCAA 73945	G	AGT
			TTGGTTCAG ATGGAG CAC		
			AACCAAGTC TACCTC GTG		
			G CT_		
GAM2490	LOC51308	3'	GGGTCCCCATCCTGTACCAA 33970	T	A G
			TTGGT CAGGATGG GA TC		
			AACCA GTCCTACC CT GG		
			T C G		
GAM2491	GP9	3'	AGGCCCCCAGAACCTGGCTCCA 5724		A G AACAT
	G		CTGGAGCCA GT CT GTCT		

		GACCTCGGT CA GA CGGA	
		C A CCCC_	
GAM2491	MHC2TA	3' GACACAGGCCCGGCTCCAG 5984	AAGT AACA
		CTGGAGCC GCT TGTC	
		GACCTCGG CGG ACAG	
		CC_ AC_	
GAM2491	RAB5B	3' GCACACTAGCCCTGGCTCCA 12710	A T ACA
		TGGAGCCA G GCTA TGT	
		ACCTCGGT C CGAT ACG	
		_C CAC	
GAM2491	TGM3	3' AGACATGGACTCCGGGCTCCAG 13745	AAGTGCTAA
		CTGGAGCC CATGTCT	
		GACCTCGG GTACAGA	
		GCCTCAG_	
GAM2491	ZNF266	5' AGACATGTTTTGTGGCTC 89688	AGTGCT
		GAGCCA AACATGTCT	
		CTCGGT TTGTACAGA	
		GTT_	
GAM2491	ABCA10	3' AGACATGTTATTCATCCCCA 55361	AGCCAA C_
		TGG GTG TAACATGTCT	
		ACC TAC ATTGTACAGA	
		CC_ TT	
GAM2491	FLJ10193	3' GGCAGCCCCTGGCTCCAG 36349	AGT AACAT
		CTGGAGCCA GCT GTC	
		GACCTCGGT CGA CGG	
		CCC _	
GAM2491	FLJ14297	3' AGACATGTTATTCATCCCCA 46613	AGCCAA C_
		TGG GTG TAACATGTCT	
		ACC TAC ATTGTACAGA	
		CC_ TT	
GAM2491	FLJ20084	3' AGAGGTAAACACTTGGTCCA 34993	G CTAAC G
		TGGA CCAAGTG AT TCT	
		ACCT GGTTCAC TG AGA	
		_ AAA_ G	
GAM2491	KIAA0648	3' TGCTTAACACTTGGTTCCAG 83546	C _
		CTGGAGCCAAGTG TAA CA	
		GACCTTGGTTCAC ATT GT	
		A C	
GAM2491	KIAA1878	3' AGACATGTTGATGCTAGCCACA 93363	GA CA GC
		TG GC AGT TAACATGTCT	

		AC CG TCG GTTGTACAGA		
		AC A_ TA		
GAM2491	PRO1598	5' TATGAAGCACTCGGTTCCAG 38131	A	AA
		CTGGAGCC AGTGCT CATG		
		GACCTTGG TCACGA GTAT		
		C A_		
GAM2491	TUSP	5' ACATGCTAGAGGGTGGCTTCAG 40015	AGTG	A
		CTGGAGCCA CTA CATGT		
		GACTTCGGT GAT GTACA		
		GGA C		
GAM2491	ZNF333	5' AGACCTCAAACCCTGGCTCCAG 51583	A_	GCTAACAT
		CTGGAGCCA GT GTCT		
		GACCTCGGT CA CAGA		
		CC AACTC__		
GAM2491	LOC137362	5' AGACACATAGTCTTGGCTCCAG 75779	T	ACA
		CTGGAGCCAAG GCTA TGTCT		
		GACCTCGGTTC TGAT ACAGA		
		_ AC_		
GAM2491	LOC149722	5' GACATGTCAGCTGCTGCAG 85753	G	CAAGT A
		CTG AGC GCT ACATGTC		
		GAC TCG CGA TGTACAG		
		G T__ C		
GAM2491	LOC150837	5' AGACATGTGAGCTTGGACTCCA 80799	_	GCTA
	G	CTGGAG CCAAGT ACATGTCT		
		GACCTC GGTTCTG TGTACAGA		
		A AG__		
GAM2491	LOC150838	5' AGACATGTGAGCTTGGACTCCA 86313	_	GCTA
	G	CTGGAG CCAAGT ACATGTCT		
		GACCTC GGTTCTG TGTACAGA		
		A AG__		
GAM2491	LOC158450	3' AGACATGTTACATGGCCCA 82813	A	A CT
		TGG GCCA GTG AACATGTCT		
		ACC CGGT CAC TTGTACAGA		
		_ A _		
GAM2491	LOC158490	3' AGACATGAAAACCTCTGGCTCCA 82820	_	GCTAA
		TGGAGCCA AGT CATGTCT		
		ACCTCGGT TCA GTACAGA		
		C AAA__		
GAM2491	LOC158504	3' AGACATGTTACATGGCCCA 82827	A	A CT
		TGG GCCA GTG AACATGTCT		

		ACC CGGT CAC TTGTACAGA	
		— A —	
GAM2491	LOC203025 5'	AGACACATAGTCTTGGCTCCAG 90740	T ACA
		CTGGAGCCAAG GCTA TGTCT	
		GACCTCGGTTC TGAT ACAGA	
		— AC—	
GAM2491	LOC219917 3'	AGACATGAAATCTCTGGCTCCA 93163	— TGCTAA
		TGGAGCCA AG CATGTCT	
		ACCTCGGT TC GTACAGA	
		C TAAA—	
GAM2491	LOC221510 3'	GTTAGCATCTGGCTCCAG 92704	AG
		CTGGAGCCA TGCTAAC	
		GACCTCGGT ACGATTG	
		CT	
GAM2491	LOC91445 3'	AGACATGTGGCTTAACTCACAG 61161	— CCAAGT A
		CTG GAG GCTA CATGTCT	
		GAC CTC CGGT GTACAGA	
		A AATT— —	
GAM2492	CRAT 3'	ACTCCCAGGACCTGGAGACAGG 15674	G GA_ CAA
		CCTG CTCCAGG TGG AGT	
		GGAC GAGGTCC ACC TCA	
		A AGG C—	
GAM2492	CTNS 3'	GACCAGCTCCCCTGGAGCGAGG 18220	G AT AAA
		CCT GCTCCAGGG GGC GTC	
		GGA CGAGGTCCC TCG CAG	
		G C_ AC—	
GAM2492	DDX1 5'	GA CTCCGAACGCCGAAGACCAG 18230	— CCA GA_ CAA
G		CCTGG CT GG TGG AGTC	
		GGACC GA CC GCC TCAG	
		A AG_ GCAA —	
GAM2492	EPAC 3'	GA CTGAGTCCCTGGAGCAGG 21452	G GGCAA
		CCTG CTCCAGGGAT AGTC	
		GGAC GAGGTCCCTG TCAG	
		— AGC—	
GAM2492	IGJ 3'	GA CTTTGCCTTGGAGAGCCAG 58960	CAGGGAT
		CTGGCTC GGCAAAGTC	
		GACCGAG CCGTTTCAG	
		AGGTT—	
GAM2492	MYO1C 3'	G CCACTCCCAGAGCCAGG 61865	CA _
		CCTGGCTC GGGA TGGC	

GGACCGAG CCCT ACCG
A_ C
GAM2492 PKM2 3' GACTGGAGGCCCTGGAGCCAG 12142 ATG AA__
CTGGCTCCAGGG GC AGTC
||||||| || |||
GACCGAGGTCCC CG TCAG
__ GAGG
GAM2492 SLC9A3R1 3' GCCCATCCCTGAGCCAGG 70939 C _
CCTGGCTC AGGGATGG C
||||| ||||| |
GGACCGAG TCCCTACC G
_ C
GAM2492 TESK1 5' GACCCTGCCATGTGAGGCAGG 21887 G _ GGGA AA
CCTG CTC CA TGGCA GTC
||| ||| || ||| |||
GGAC GAG GT ACCGT CAG
G T ____ CC
GAM2492 TNFRSF14 3' GACTCTGCACCCCGACGCCAG 15112 TCCA ATG A
CTGGC GGG GCA AGTC
|||| | ||| |||
GACCG CCC CGT TCAG
CAG_ CA_ C
GAM2492 WNT3A 3' ACTCCTACCTGAAGGCAGG 53607 G C GAT CAA
CCTG CT CAGG GG AGT
|||| ||| || |||
GGAC GA GTCC CC TCA
G A AT_ ____
GAM2492 C21orf108 5' GACCCGCAGGGCCCCGGGCCAG 90114 T A ATG_ AAA
G CCTGGC CC GGG GC GTC
||||| ||| || |||
GGACCG GG CCC CG CAG
_ C GGGA CC_
GAM2492 CDC14B 3' ACTCTAGAACTGGAGCCAGG 14769 GGA CAA
CCTGGCTCCAG TGG AGT
||||||| ||| |||
GGACCGAGGTC ATC TCA
AAG ____
GAM2492 DKFZp566H0824 5' GACCTGAGATCACTGGAGCCA 34485 G GG AA
TGGCTCCAG GAT CA GTC
||||||| ||| |||
ACCGAGGTC CTA GT CAG
A GA C_
GAM2492 EZF-2 5' CTTTGCCCCCTGGGCCAGG 37677 T AT
CCTGGC CCAGGG GGCAAAG
||||| ||||| |||||
GGACCG GGTCCC CCGTTTC
_ _
GAM2492 GTPBP1 3' CCATCTTCCCTGAGCCAGG 16263 C ____
CCTGGCTC AGGGA TGG
||||| ||||| |||

GGACCGAG TCCCT ACC
_ TCT
GAM2492 KIAA0354 3' TGCAATCCCTGAAACCAGG 30195 CTC G
CCTGG CAGGGAT GCA
||||| ||||| |||
GGACC GTCCCTA CGT
AAA A
GAM2492 KIAA0427 3' GACCTACCTCCCCAGAGCAAGG 29381 G CA T CAAA
CCT GCTC GGGA GG GTC
||| ||| ||||| || |||
GGA CGAG CCCT CC CAG
A AC _ ATC_
GAM2492 KIAA0939 3' GACAGGCCTCTGGAGCCAGG 62715 GAT AAA
CCTGGCTCCAGG GGC GTC
||||||| ||| |||
GGACCGAGGTCT CCG CAG
_ GA_
GAM2492 KIAA1884 3' GACCTCAGGCTGCTGGAGTCAG 73727 GGA AAA_
CTGGCTCCAG TGGC GTC
||||||| ||| |||
GACTGAGGTC GTCG CAG
_ GACTC
GAM2492 KLF12 3' ACCCTGCCATCTCAGAGCACA 33274 _ CA AA
TG GCTC GGGATGGCA GT
|| ||| ||||| ||
AC CGAG CTCTACCGT CA
A A_ CC
GAM2492 MGC12904 3' CTAAACAAACCCTGGAGACAG 49162 G A_ GCA
G CCTG CTCCAGGG TG AAG
||||| ||||| || |||
GGAC GAGGTCCC AC TTC
A AA AAA
GAM2492 MGC15631 5' CCGATTTCCCCGGAGCCGGG 52227 A _
CCTGGCTCC GGGA TGG
||||||| ||||| |||
GGGCCGAGG CCCT GCC
C TTA
GAM2492 MGC26744 5' GACCCTCCGAGCCCCTGGAGCC 58957 T A_ CAAA
CGG CC GGCTCCAGGG TGG GTC
|| ||||| ||| |||
GG CCGAGGTCCC GCC CAG
C CGA TCC_
GAM2492 RAB10 5' CCGACTCCCCGGAACCGGG 86352 C A _
CCTGG TCC GGGA TGG
||||| ||| ||||| |||
GGGCC AGG CCCT GCC
A C CA
GAM2492 SLC31A2 3' ACTTTGAGCTGAAGCCAG 60756 C GGATGG
CTGGCT CAG CAAAGT
||||| ||| |||||

	GACCGA GTC GTTTCA	
	A GA_____	
GAM2492 LOC118851 5'	GACTTTGATTGGACCAGGAGCC 76014	A GA _
AGG	CCTGGCTCC GG TGG CAAAGTC	
	GGACCGAGG CC GTT GTTTCAG	
	A AG A	
GAM2492 LOC145757 5'	ACCTGGTCTCCCGGAGCCAGG 77911	A T AAA
	CCTGGCTCC GGGA GGC GT	
	GGACCGAGG CCCT CTG CA	
	_ _ GTC	
GAM2492 LOC146280 5'	ACTGAAGTTCCCAAGAGCCAGG 78347	CA TGGCAA
	CCTGGCTC GGGA AGT	
	GGACCGAG CCCT TCA	
	AA TGAAG_	
GAM2492 LOC147343 5'	CCTTTTGCCCTGGAGCCAGG 85125	AT____
	CCTGGCTCCAGGG GG	
	GGACCGAGGTCCC CC	
	GTTTT	
GAM2492 LOC148764 5'	GACTCTGCCAGGGCCAGAGCCA 79737	CA GA_ A
GG	CCTGGCTC GG TGGCA AGTC	
	GGACCGAG CC ACCGT TCAG	
	A_ GGG C	
GAM2492 LOC149910 3'	GACCCTGCCATCCTACCCCTAG 80356	CTCCA AA
	CTGG GGGATGGCA GTC	
	GATC TCCTACCGT CAG	
	CCCA_ CC	
GAM2492 LOC150197 5'	GACTGGCTGGACCCCTAGGAGC 80422	_ A_ AA
CAGG	CCTGGCTCC AGGG TGGC AGTC	
	GGACCGAGG TCCC GTCG TCAG	
	A CAG G_	
GAM2492 LOC151996 5'	GACCTGCCCCCATGAGCCAGG 86720	CA AT AA
	CCTGGCTC GGG GGCA GTC	
	GGACCGAG CCC CCGT CAG	
	TA C_ C_	
GAM2492 LOC158292 5'	GACCTGCCACCCACAGCCAG 88049	CCA A AA
	CTGGCT GGG TGGCA GTC	
	GACCGA CCC ACCGT CAG	
	CA_ C C_	
GAM2492 LOC158428 3'	ACTTTGCTCAGAGCTCAG 71079	_ CAGGGA _
	CTG GCTC TG GCAAAGT	

		GAC CGAG	AC CGTTTCA		
		T	_____	T	
GAM2492	LOC201915	5'	GACTTCGCCGCCGCCTGGAGCC	90555	GA_ A
		GG	CTGGCTCCAGG	TGGC AAGTC	
			GGCCGAGGTCC	GCCG TTCAG	
			GCC	C	
GAM2492	LOC220020	3'	ACCCTGCTCCATGGAGCCA	95042	G TG AA
			TGGCTCCA	GGA GCA GT	
			ACCGAGGT	CCT CGT CA	
			A	__	CC
GAM2492	LOC255452	5'	GACTCTAAGCAGACTCCAGAGC	99394	CA ATG AA__
		CAGG	CCTGGCTC	GGG GC AGTC	
			GGACCGAG	CTC CG TCAG	
			AC	AGA AATC	
GAM2492	LOC255650	3'	GTGATCCCCAGGGCCAGG	98527	CA G
			CCTGGCTC	GGGAT GC	
			GGACCGGG	CCCTA TG	
			AC	G	
GAM2492	LOC257455	5'	GACTCTGATTGGCTGAGCCAGG	79491	C GGATGG A
			CCTGGCTC	AG CA AGTC	
			GGACCGAG	TC GT TCAG	
			_	GGTTA_	C
GAM2492	LOC91409	3'	ACTTTGCCGAGAGGCAG	66569	G CAGGGA
			CTG CTC	TGGCAAAGT	
			GAC GAG	GCCGTTTCA	
			G	A_____	
GAM2492	LOC92370	3'	ACTCTGTTTCTGAAGCAGG	69664	G C GG CAA
			CCTG CT	CAG ATGG AGT	
			GGAC	GA GTC TGTC TCA	
			_	A TT	__
GAM2492	LOC96573	3'	ACTTTGGCTGTGAGCCAGG	63870	_ GGATGG
			CCTGGCTC	CAG CAAAGT	
			GGACCGAG	GTC GTTTCA	
			T	G_____	
GAM2493	EXTL2	3'	TGGCTAATGTTCCAATAATGAG	9328	CACC_ CAA
		GT	ACCTT	TGGAACAT CCA	
			TGGAG	ACCTTGTA GGT	
			TAATA	ATC	
GAM2493	GRIN2A	3'	TGGCCAATGTTCTGGAGGGTA	7726	ACC CAA
			TACCTTC	TGGAACAT CCA	

		ATGGGAG GTCTTGTA GGT	
		ACC	
GAM2493 MYB	3'	TGGTTAATGACATTGAAGGTA 60284	CC GAA C
		TACCTTCA TG CAT AACCA	
		ATGGAAGT AC GTA TTGGT	
		T_ A_ A	
GAM2493 TRIP15	3'	GGTTGATGTGTCCTGAA 16176	CCT _
		TTCA GGA ACATCAACC	
		AAGT CCT TGTAGTTGG	
		G	
GAM2493 C20orf28	3'	GGTCCTGCAGATGAAGGTA 31847	C GAA TCA
		TACCTTCA CTG CA ACC	
		ATGGAAGT GAC GT TGG	
		A _ CC_	
GAM2493 C5orf3	3'	TGGTTGATAAGCCAGAGAA 38594	AC AAC
		TTC CTGG ATCAACCA	
		AAG GACC TAGTTGGT	
		A_ GAA	
GAM2493 DOK4	3'	TGGTTGACGCCTCAGGTGAA 36665	AACA
		TTCACCTGG TCAACCA	
		AAGTGGACT AGTTGGT	
		CCGC	
GAM2493 KIAA0146	5'	TGGCTGAAACAGGTGAAGG 82324	GAACA A
		CCTTCACCTG TCA CCA	
		GGAAGTGGAC AGT GGT	
		AA_ C	
GAM2493 KIAA1068	3'	TGGCTGACACTGAGTGAAGGTG 31689	CT AACA A
		TACCTTCAC GG TCA CCA	
		GTGGAAGTG TC AGT GGT	
		AG AC_ C	
GAM2493 KIAA1305	3'	TGGGCTCCAGGTGAAGG 47624	ACA
		CCTTCACCTGGA TCA	
		GGAAGTGGACCT GGT	
		CG_	
GAM2493 KIAA1856	5'	TGGCTGAGCGGGAGGTGAAGG 94232	GGAACA A
		CCTTCACCT TCA CCA	
		GGAAGTGGA AGT GGT	
		GGGCG_ C	
GAM2493 RAB24	3'	TGGCTGCCTTCCAGGTGA 56259	CAT A
		TCACCTGGAA CA CCA	

		AGTGGACCTT GT GGT		
		CC_ C		
GAM2493	LOC132671 3'	TGATGCTTTTCAGGTGAA 59843	___	
		TTCACCTGGAA CATCA		
		AAGTGGACTTT GTAGT		
		TC		
GAM2493	LOC143381 3'	GGCAGTGCAGGTGAAGGTA 77061	GAA CAA	
		TACCTTCACCTG CAT CC		
		ATGGAAGTGGAC GTG GG		
		___ AC_		
GAM2493	LOC145547 3'	TGGGCTCCAGGTGAAGG 77785	ACA	
		CCTTCACCTGGA TCA		
		GGAAGTGGACCT GGT		
		CG_		
GAM2493	LOC146224 5'	TGAGCCATTGCAAATGAAGGTA 78206	CC G CA_	
		TACCTTCA TG AA TCA		
		ATGGAAGT AC TT AGT		
		AA G ACCG		
GAM2493	LOC151007 3'	TGGTTATGTGTTCCAAGTGAGG 80901	T C C_	
	TA	TACCT CAC TGGAACAT AACCA		
		ATGGA GTG ACCTTGTG TTGGT		
		_ A TA		
GAM2493	LOC91974 5'	TGACTTCCAGGTGAAGG 68364	CA	
		CCTTCACCTGGAA TCA		
		GGAAGTGGACCTT AGT		
		C_		
GAM2494	ADAMTS13 3'	CCCCAAACGTGCATGGA 58151	G CC A	
		TC GTGTACGT TGG GG		
		AG TACGTGCA ACC CC		
		G AA _		
GAM2494	PAX5 3'	CCTCCAGGACCCCAGCAAGTG 34127	CG GTAC	
		CACT GT GTCCTGGAGG		
		GTGA CG CAGGACCTCC		
		A_ ACCC		
GAM2494	RBP3 3'	CCTCTGGGACACACACCAAG 12795	C AC TG	
		CT GGTGT GTCC GAGG		
		GA CCACA CAGG CTCC		
		A CA GT		
GAM2494	TCF19 3'	CCTCCAGGAAATTGCCAGTG 99578	C TACG	
		CACT GGTG TCCTGGAGG		

			GTGA CCGT AGGACCTCC	
			_ TAA_	
GAM2494 TEM8	3'		CCTGGAGTTACGCACACTGAGT 50825	A ____ T
	G		CACTCGGTGT CG TCC GG	
			GTGAGTCACA GC AGG CC	
			C ATTG T	
GAM2494 UBASH3A	3'		CCTGCAGCATGTACACCGAGTG 39049	C G
			CACTCGGTGTACGT CTG AGG	
			GTGAGCCACATGTA GAC TCC	
			C G	
GAM2494 DOCK3	3'		CCTCCAGGGTAGAGATGCACCG 67092	C CG____
	AATG		CA TCGGTGTA TCCTGGAGG	
			GT AGCCACGT GGGACCTCC	
			A AGAGAT	
GAM2494 FLJ13782	3'		CCTCCAGGGTTCAGCAAGTG 46700	CG GTACG_
			CACT GT TCCTGGAGG	
			GTGA CG GGGACCTCC	
			A_ ACCCTT	
GAM2494 FLJ21034	3'		CCTCCCTGCAACACCGAGTG 46864	AC CCT
			CACTCGGTGT GT GGAGG	
			GTGAGCCACA CG CCTCC	
			A_ TC_	
GAM2494 KIAA0792	3'		CCTCCAGGGGGCACCAAG 28765	C ACG
			CT GGTGT TCCTGGAGG	
			GA CCACG GGGACCTCC	
			A G_	
GAM2494 KIAA1028	3'		CCTCCAGGACATAGCCAG 93589	C GTAC
			CT GGT GTCCTGGAGG	
			GA CCG CAGGACCTCC	
			_ ATA_	
GAM2494 MGC9753	5'		CCTCCAGGAAGGTCACAAAGTG 54187	CG T G_
			CACT GTG AC TCCTGGAGG	
			GTGA CAC TG AGGACCTCC	
			AA _ GA	
GAM2494 RARRES2	3'		CCTCCAGGACCGCTGCGGGTG 12778	GT AC
			CACTCG GT GTCCTGGAGG	
			GTGGGC CG CAGGACCTCC	
			GT C_	
GAM2494 RDH-E2	3'		CCTGGATACGCAGACCGAGTG 58070	_ AC T
			CACTCGGT GT GTCC GG	

			GTGAGCCA CG TAGG CC		
			GA CA T		
GAM2494	ZNF340	5'	CCTCCAGGACCTGCCCCGTGTG 85711	T T C	
			CAC CGG GTA GTCCTGGAGG		
			GTG GCC CGT CAGGACCTCC		
			T _ C		
GAM2494	LOC124411	3'	CCCCAGAGGCCACACCGGG 74772	AC _ A	
			CTCGGTGT GTC CTGG GG		
			GGGCCACA CGG GACC CC		
			CC A _		
GAM2494	LOC149076	3'	CCTCCAGGAACCACCAAG 79877	C TACG	
			CT GGTG TCCTGGAGG		
			GA CCAC AGGACCTCC		
			A CA__		
GAM2494	LOC165283	3'	CCTCCAGGATGCACAGAGTG 88545	G AC	
			CACTC GTGT GTCCTGGAGG		
			GTGAG CACG TAGGACCTCC		
			A _		
GAM2494	LOC197416	3'	CCCCAGAGGCCACACCGGG 91322	AC _ A	
			CTCGGTGT GTC CTGG GG		
			GGGCCACA CGG GACC CC		
			CC A _		
GAM2494	LOC200058	3'	CCTCCAGGTCCACGGAGTG 89959	G TACGT	
			CACTC GTG CCTGGAGG		
			GTGAG CAC GGACCTCC		
			G CT__		
GAM2494	LOC255652	3'	CCTCCAGGACTGCCACAGAG 98530	G _ C	
			CTC GTG TA GTCCTGGAGG		
			GAG CAC GT CAGGACCTCC		
			A C _		
GAM2494	LOC256581	5'	CCTCCAGGAGGCACGGAATG 99432	C G ACG	
			CA TC GTGT TCCTGGAGG		
			GT AG CACG AGGACCTCC		
			A G G__		
GAM2495	GPD1	3'	TCATGCCACCACATTTG 60398	C C	
			TAAATG GGTGGCAT GA		
			GTTTAC CCACCGTA CT		
			A _		
GAM2495	IL5RA	5'	TCGCATGGCCACCGCATTT 6906	AT__	
			AAATGCGGTGGC CGA		

		TTTACGCCACCG GCT		
		GTAC		
GAM2495 MYO1C	3'	TGCCGATGCCAAATATTTG 61873	CGG	A
		TAAATG TGGCATCG CA		
		GTTTAT ACCGTAGC GT		
		AA_ C		
GAM2495 C6orf37	3'	TGTCACACTGCATTTA 68097	GCATC	
		TAAATGCGGTG GACA		
		ATTTACGTCAC CTGT		
		A_____		
GAM2495 DNAJC6	3'	TTGCAGAACCACCGCATT 29498	CA GA	
		AATGCGGTGG TC CAA		
		TTACGCCACC AG GTT		
		A_ AC		
GAM2495 FLJ11210	3'	GTCGATGTGCATGCTTTTA 60319	T GTG	
		TAAA GCG GCATCGAC		
		ATTT CGT TG TAGCTG		
		T ACG		
GAM2495 FLJ12476	3'	TCGATCTTCTGCATTTA 43270	T C	
		TAAATGCGG GG ATCGA		
		ATTTACGTC TC TAGCT		
		T _		
GAM2495 KIAA1034	3'	TCGATGGCATCCGCATTTG 63134	_ G	
		TAAATGCGG TG CATCGA		
		GTTTACGCC AC GTAGCT		
		T G		
GAM2495 KIAA1987	3'	TCATGTAAGTGCATTTA 89391	G C	
		TAAATGCGGT GCAT GA		
		ATTTACGTCA TGTA CT		
		A _		
GAM2495 MGC16063	3'	TGTCCTGGCCACTGCATT 54929	ATC	
		AATGCGGTGGC GACA		
		TTACGTCACCG CTGT		
		GTC		
GAM2495 LOC147949	3'	TGTCAGATGTCCACATTGCA 79279	_ _ _	
		TGCG GTGG CATC GACA		
		ACGT CACC GTAG CTGT		
		TA T A		
GAM2495 LOC150577	3'	GTCCTCACCGCATTTG 86258	CATC	
		TAAATGCGGTGG GAC		

		GTTTACGCCACT	CTG		
		C___			
GAM2495	LOC158219	3'	TGTGTGTCACCACATTT	82694	C CG
			AAATG GGTGGCAT ACA		
			TTTAC CCACTGTG TGT		
			A _		
GAM2495	LOC202020	3'	TGTCTCACCACATTTA	90605	C CATC
			TAAATG GGTGG GACA		
			ATTTAC CCACT CTGT		
			A _		
GAM2495	LOC90826	5'	TGTCGATGCAGGTTTATTTG	64788	CGGTG
			TAAATG GCATCGACA		
			GTTTAT CGTAGCTGT		
			TTGGA		
GAM2495	LOC93587	3'	TTGTCTTTACCTGCATTTA	73042	_ CATC
			TAAATGC GGTGG GACAA		
			ATTTACG CCATT CTGTT		
			T T__		
GAM2496	ATF7	3'	TCCCAGCCCCGGAGCCTCATA	23404	_ TAGA CC
			TATGAGGC CC GCT GGGA		
			ATACTCCG GG CGA CCCT		
			A CCC_ _		
GAM2496	CREBBP	5'	CCCGCCGGTCCCGGGCCCCA	16495	A TA G C_
			TG GGCCC GA CT CGGG		
			AC CCGGG CT GG GCCC		
			C CC _ CC		
GAM2496	EGLN2	5'	TTGGGGCTCCAGAACCTC	34522	CC A
			GAGG CT GAGCTCCGG		
			CTCC GA CTCGGGGTT		
			AA C		
GAM2496	GNA11	5'	CCCAGTGA CTCTGGGCCTCA	10810	T C C_
			TGAGGCC AGAG TC GGG		
			ACTCCGGG TCTC AG CCC		
			_ _ TGA		
GAM2496	LATS2	3'	GTCCCGGAGCCGGTGCCCTCA	28135	_ TAGA
			TGAGG C CC GCTCCGGGAC		
			ACTCC G GG CGAGGCCCTG		
			C T C_		
GAM2496	NLGN3	3'	GTCTCTCTGGCTCTAGGACC	39121	C CC_
			GG CCTAGAGCT GGGAC		

CC GGATCTCGG CTCTG
 A TCT
 GAM2496 NOTCH1 5' GTCCCGGAGCCCCAAGTGCTT 92138 C AGA_
 AGGC CT GCTCCGGGAC
 ||| || |||||
 TTCG GA CGAGGCCCTG
 T ACCC
 GAM2496 PCDH1 3' CCCATTCCAGGGCCTCA 51575 A CTCC
 TGAGGCCCT GAG GGG
 ||||| ||| |||
 ACTCCGGGA CTT CCC
 C A____
 GAM2496 PML 3' TCCCAGAGGGGCCTCAT 53805 TAGAG C
 ATGAGGCCC CTC GGGA
 ||||| ||| |||
 TACTCCGGG GAG CCCT
 _____ A
 GAM2496 RBBP9 3' TCCGGAGTCTAGAGCCCCA 70699 A C G
 TG GGC CTAGA CTCCGGG
 || ||| ||||| |||||
 AC CCG GATCT GAGGCCT
 C A _
 GAM2496 UBQLN1 5' CCGAGCTCCGGGGGCCCA 26473 A TA C
 TG GGCCG GAGCTC GG
 || |||| ||||| ||
 AC CCGG CTGAG CC
 C GC _
 GAM2496 ARTN 5' CCCGGGCCTGGAGCCCCA 15612 A C A T
 TG GGC CTAG GC CCGG
 || ||| |||| |||||
 AC CCG GGTC CG GGCC
 C A _ _
 GAM2496 CNTNAP1 3' CCCAAAGGAGAAGCCTCATG 14641 CCTAGAG ____
 TATGAGGC CTCC GGG
 ||||| ||| |||
 GTACTCCG GAGG CCC
 AA_____ AAA
 GAM2496 FLJ10898 5' CCCCAAGCCAGGCACAGCCTCA 60130 _____ AGA CC
 TA TATGAGGC CCT GCT GGG
 ||||| ||| ||| |||
 ATACTCCG GGA CGA CCC
 ACAC C__ AC
 GAM2496 KIAA1977 5' CGAAGGCTCAGGGCCTCA 74765 A C_
 TGAGGCCCT GAGCT CG
 ||||| |||| ||
 ACTCCGGGA CTCGG GC
 _ AA
 GAM2496 P24B 3' TCCTGCTCTAGGGCCCCTCA 24774 ____ TCC
 TGA GGCCCTAGAGC GGGA
 ||| ||||| ||||| |||

ACT CCGGGATCTCG TCCT
 CC ____
 GAM2496 LOC146669 3' GTCTTTCTCCAGGGGCCTCA 78664 A_ CTCC
 TGAGGCCCT GAG GGGAC
 ||||| ||| ||||
 ACTCCGGGG CTC TTCTG
 AC T____
 GAM2496 LOC170127 5' CCCGGAGCCCCAGGGGCCCA 83456 A AGA_
 TG GGCCCT GCTCCGGG
 || ||||| |||||
 AC CCGGGG CGAGGCCC
 _ ACCC
 GAM2496 LOC256812 5' CCCGGAGCCCCCTGGGCCCA 99406 A TAGA_
 TG GGCCG GCTCCGGG
 || ||||| |||||
 AC CCGGG CGAGGCCC
 C TCCCC
 GAM2496 LOC90408 5' CCCCTCTCCGAGGCCTCATA 63342 CTA CTCC
 TATGAGGCC GAG GGG
 ||||| ||| |||
 ATACTCCGG CTC CCC
 AGC TC____
 GAM2497 MLC1 3' CCAGGTGAAATCCACACCA 31467 A T CTG TG
 TG TGT GGATT T CCTGG
 || ||| ||||| | ||||
 AC ACA CCTAA A GGACC
 C _ _ _ GT
 GAM2497 MLC1 3' CCAGGTGAAATCCACACCA 58289 A T CTG TG
 TG TGT GGATT T CCTGG
 || ||| ||||| | ||||
 AC ACA CCTAA A GGACC
 C _ _ _ GT
 GAM2497 SCA1 3' CCCACGTGCAAAATCAACATCA 6177 G C T C
 TGATGTTG ATT TGT GC TGGG
 ||||| ||| ||| ||| |||
 ACTACAAC TAA ACG TG ACCC
 _ A _ C
 GAM2497 SLC17A4 3' CCAAACAACAGAAAGCAT 19719 GGA CC
 ATGTT TTCTGTTG TGG
 |||| ||||| |||
 TACGA AAGACAAC ACC
 _ AA
 GAM2497 LOC220021 5' CCCAGACTCCTGCAAATCCAAC 95020 C TGC____
 GTTGGATT TGT CTGGG
 ||||| ||| ||||
 CAACCTAA ACG GACCC
 _ TCCTCA
 GAM2498 ALX3 3' ACAAACCTGAGTCCCCTCA 22423 C GG
 TGA GGGGACTCAGT TGT
 ||| ||||| ||| |||

			ACT CCCCTGAGTCA ACA		
			— A—		
GAM2498	CXorf6	3'	GCAAACACCACCAAGTTCCT 19707	CA	
			GGGGACT GTGGTGTTC		
			TCCTTGA CACCACAAACG		
			AC		
GAM2498	KPNA3	3'	GCAATGTGATCTGAGCCTCCAT 11223	C A	TGGTGT
	CA		TGA GGGG CTCAG TTGC		
			ACT CCTC GAGTC AACG		
			A C TAGTGT		
GAM2498	KIAA0227	5'	CGAGCACCGGCCCCCGCCA 61344	A A	CAGT
			TG CGGGG CT GGTGTTTG		
			AC GCCCC GG CCACGAGC		
			C C —		
GAM2498	LOC152200	3'	ACCACTGAGTTCCCATCA 86751	C	
			TGA GGGGACTCAGTGGT		
			ACT CCCTTGAGTCACCA		
			A		
GAM2499	CARD4	3'	AGAGTTGAGGATGTGGCACA 21439	A G	GCTCC
			TGT CCA CATCT CTCT		
			ACA GGT GTAGG GAGA		
			C _ AGTT_		
GAM2499	CBFA2T2	3'	AGAGGAGCTGGCATGGTGGTAC 18699	G _ _	C
	AG		CTGTACCA CAT CT GCTCC TCT		
			GACATGGT GTA GG CGAGG AGA		
			G C T _		
GAM2499	CD3Z	3'	AGAGAAAGCGCAGATGCTAGCA 7422	ACC	TCC_
	CA		TGT AGCATCTGC CTCT		
			ACA TCGTAGACG GAGA		
			CGA CGAAA		
GAM2499	CDC2L2	5'	AGAAGGAGCAGCGGGAGCAG 54316	A AGCAT	C
			CTGT CC CTGCTCC TCT		
			GACG GG GACGAGG AGA		
			A GC_ A		
GAM2499	FANCC	3'	AGAAGGGTGTGCTGGTA 71029	CT T C	
			TACCAGCAT GC CC TCT		
			ATGGTCGTG TG GG AGA		
			_ _ A		
GAM2499	FGFR3	3'	AGAGGAAAAGGCTGGTACA 5567	AT GCTC	
			TGTACCAGC CT CCTCT		

ACATGGGTCG GA GGAGA
 ___ AAA_
 GAM2499 GAS1 3' AGGGAAGGTGCTGACCAG 10759 TAC GC
 CTG CAGCATCT TCCCT
 ||| ||||| ||||
 GAC GTCGTGGA AGGGA
 CA_ _
 GAM2499 MTMR3 3' AGGGAGCAGGTCCCATACA 41160 CCAGC
 TGTA ATCTGCTCCCT
 ||| |||||
 ACAT TGGACGAGGGA
 ACCC_
 GAM2499 ORC1L 5' AGAAGGAGCCCTGCTGGTGCAG 15977 TCT C
 CTGTACCAGCA GCTCC TCT
 ||||| |||||
 GACGTGGTCGT CGAGG AGA
 CC_ A
 GAM2499 POU4F1 5' AGAGGGAGCGCCTGGCAGCAG 21756 A_ CATC
 CTGT CCAG TGCTCCCTCT
 ||| ||| |||||
 GACG GGTC GCGAGGGAGA
 AC C_
 GAM2499 PTGFRN 3' AGAGAGAACAGATATTTAAACA 67762 ACCAGC C C
 G CTGT ATCTG TC CTCT
 ||| |||| ||||
 GACA TAGAC AG GAGA
 AATTTA A A
 GAM2499 RTKN 3' AGAGAAAGGTGCTGGCATAG 53501 A GCTCC
 CTGT CCAGCATCT CTCT
 ||| ||||| |||
 GATA GGTCGTGGA GAGA
 C AA_
 GAM2499 AQP10 5' AGAGGGAGCAGTGAATAGCA 55392 ACCAG T
 TGT CA CTGCTCCCTCT
 || || |||||
 ACG GT GACGAGGGAGA
 ATAA_ _
 GAM2499 ATP9B 3' AGGGCACAGATGCTGAGACAG 78975 AC CT
 CTGT CAGCATCTG CCCT
 ||| ||||| |||
 GACA GTCGTAGAC GGA
 GA AC
 GAM2499 C20orf19 5' AGAGGGAGAAATACTGACACGG 38070 AC C CTG
 CTGT CAG AT CTCCCTCT
 ||| ||| |||||
 GGCA GTC TA GAGGGAGA
 CA A AA_
 GAM2499 C20orf3 3' GAGGGAGCATGGCCAG 68641 TA GCATC
 CTG CCA TGCTCCCTC
 ||| ||| |||||

GAC GGT ACGAGGGAG
 CC _____
 GAM2499 C20orf60 3' AGAGGGACAGGTGTGGTGGCAC 54804 A _ C
 AG CTGT CCA GCATCTG TCCCTCT
 |||| ||| |||||| ||||||
 GACA GGT TGTGGAC AGGGAGA
 C GG _
 GAM2499 CHST3 3' AGTGAAGCAGATGCCTGCA 16229 CCA C T
 TGTA GCATCTGCT CC CT
 |||| |||||| || ||
 ACGT CGTAGACGA GG GA
 C_ A T
 GAM2499 CHUK 3' AGAGGGAGGGCTGCTGCCACAG 8889 AC T G
 CTGT CAGCA CT CTCCCTCT
 |||| |||| || ||||||
 GACA GTCGT GG GAGGGAGA
 CC C _
 GAM2499 DJ159A19.3 5' AGAAGGAGCGGGGTGGCGCAG 32279 TA G A C
 CTG CCA C TCTGCTCC TCT
 ||| ||| |||||| |||
 GAC GGT G GGGCGAGG AGA
 GC _ _ A
 GAM2499 DKFZP564O0423 3' AGGGAGTGATGGGCCAGTACA 93342 CA _ T
 TGTAC GC ATC GCTCCCT
 |||| || || ||||||
 ACATG CG TAG TGAGGGA
 AC GG _
 GAM2499 DKFZP761G1913 3' AGAGAAAGACAGTGGTACAG 49691 GCAT _ CC
 CTGTACCA CTG CT CTCT
 |||||| ||| || ||||
 GACATGGT GAC GA GAGA
 _ A AA
 GAM2499 FLJ11710 3' GGGCAGACCTGATACAG 46247 C CA
 CTGTA CAG TCTGCTC
 |||| ||| ||||||
 GACAT GTC AGACGGG
 A C_
 GAM2499 FLJ14966 5' AGAGGGAGGGCCAGTGCTGGTA 52831 T _
 TACCAGCA CTG CTCCCTCT
 |||||| ||| ||||||
 ATGGTCGT GAC GAGGGAGA
 _ CGG
 GAM2499 FLJ20081 3' AGAAAAAATAGGATGCTGATAT 34986 C GCTCCC_
 A TGTA CAGCATCT TCT
 |||| |||||| |||
 ATAT GTCGTAGG AGA
 A ATAAAAA
 GAM2499 FLJ22477 3' AGAGAACGAGCCTGGATACAG 45665 _ CATCT C_
 CTGTA CCAG GCTC CTCT
 |||| |||| ||| ||||

GACAT GGTC CGAG GAGA
 A CAA
 GAM2499 FLJ23022 3' AGGAAGCCAGAGCTGGTTCAG 47489 T A _ C
 CTG ACCAGC TCTG CT CCT
 ||| ||||| ||| || |||
 GAC TGGTCG AGAC GA GGA
 T _ C A
 GAM2499 FLJ32332 3' GGCCCAGATGCTGATACA 58945 C CT
 TGTA CAGCATCTG CC
 |||| ||||| ||
 ACAT GTCGTAGAC GG
 A CC
 GAM2499 KIAA0125 3' GGAGAGATGCTGGTCA 29570 T G
 TG ACCAGCATCT CTCC
 || ||||| |||
 AC TGGTCGTAGA GAGG
 _ _
 GAM2499 KIAA0182 3' GAGGGAGTCTGCTACA 72499 C CATCT
 TGTA CAG GCTCCCTC
 |||| ||| |||||
 ACAT GTC TGAGGGAG
 C _
 GAM2499 KIAA1155 3' AGAAAGAGCAGGTGGTGCA 62906 GCA CC
 TGTACCA TCTGCTC TCT
 ||||| ||||| |||
 ACGTGGT GGACGAG AGA
 _ AA
 GAM2499 KIAA1393 3' AGAGAAAAGCTGATGCTGG 72566 T CC_
 CCAGCATC GCT CTCT
 ||||| ||| |||
 GGTCGTAG CGA GAGA
 T AAA
 GAM2499 MGC5466 5' AGAGGGAGCAGAGTGGGACCAG 73437 TA A A
 CTG CC GC TCTGCTCCCTCT
 ||| ||| |||||
 GAC GG TG AGACGAGGGAGA
 CA G _
 GAM2499 NK4 5' AGAGGGAGCAGGGGCCAGCCA 16158 TACCA AT
 G CTG GC CTGCTCCCTCT
 ||| || |||||
 GAC CG GACGAGGGAGA
 CGACC GG
 GAM2499 PDZD2 3' AGAGGGAGCAGAAAGGTCA 81716 T AGCA
 TG ACC TCTGCTCCCTCT
 || ||| |||||
 AC TGG AGACGAGGGAGA
 _ AA_
 GAM2499 PFDN1 3' AGAAAGAACAGATGTTACAG 12045 ACC C CC
 CTGT AGCATCTG TC TCT
 |||| ||||| || |||

GACA TTGTAGAC AG AGA
 C__ A AA
 GAM2499 PHF5A 3' AGGGAGCAGAGCCCAG 52250 TACCA A
 CTG GC TCTGCTCCCT
 ||| || |||||
 GAC CG AGACGAGGGA
 C_____
 GAM2499 PXR2b 3' AGAGGGAGCTTTGCTGG 33798 TCT
 CCAGCA GCTCCCTCT
 ||||| |||||
 GGTCGT CGAGGGAGA
 TT_
 GAM2499 LOC113523 3' GAAAGATCTACTGGTACAG 73421 C__ GC
 CTGTACCAG ATCT TC
 ||||| ||| ||
 GACATGGTC TAGA AG
 ATC A_
 GAM2499 LOC134111 3' AGAGGGAGCAAATGCCGTTCCGG 75636 T CA C
 CTG AC GCAT TGCTCCCTCT
 ||| || ||| |||||
 GGC TG CGTA ACGAGGGAGA
 T C_ A
 GAM2499 LOC142941 5' AGCTGGACGGATGCTGGCACAG 83763 A C CT
 CTGT CCAGCATCTG TCC CT
 ||| ||||| ||| ||
 GACA GGTCGTAGGC AGG GA
 C _ TC
 GAM2499 LOC143958 5' GAGGGAGGACCTGACA 77128 AC CA TG
 TGT CAG TC CTCCCTC
 ||| ||| || |||||
 ACA GTC AG GAGGGAG
 _ C_ _
 GAM2499 LOC146445 3' AGGGAGCAGGTGACAG 84679 ACCAG
 CTGT CATCTGCTCCCT
 ||| |||||
 GACA GTGGACGAGGGA

 GAM2499 LOC149935 3' AGAAAGAGCTGATGGTGCAG 60932 GCA T CC
 CTGTACCA TC GCTC TCT
 ||||| || ||| |||
 GACGTGGT AG CGAG AGA
 _ T AA
 GAM2499 LOC150245 5' AGAGGGAGCAGCCCCAGTCAG 86106 T CAGCAT
 CTG AC CTGCTCCCTCT
 ||| || |||||
 GAC TG GACGAGGGAGA
 _ ACCCCC
 GAM2499 LOC157273 3' AGAAGGAGCAGAAATGGATTCA 87715 TA_ GCA C
 G CTG CCA TCTGCTCC TCT
 ||| || ||||| |||

GAC GGT AGACGAGG AGA
 TTA AA_ A
 GAM2499 LOC161527 5' TAGAAGAAGCATGAGATACATC 83151 CA_____ CCC ____
 TGGTACAG CTGTACCAG TC TGCT TCT A
 ||||| || ||| |
 GACATGGTC AG ACGA AGA T
 TACATAG T AGA ____
 GAM2499 LOC200107 5' GAGGGAGCAGATTTACGG 89986 CCAGC
 CTGTA ATCTGCTCCCTC
 |||| |||||
 GGCAT TAGACGAGGGAG
 T____
 GAM2499 LOC203286 5' AGAAGGAGCAGATCTGGGGTCA 92140 TA_ C C
 G CTG CCAG ATCTGCTCC TCT
 || ||| ||||| ||
 GAC GGTC TAGACGAGG AGA
 TGG _ A
 GAM2499 LOC220282 5' AGGGACGGTGGTACAG 95980 GCAT C
 CTGTACCA CTG TCCCT
 ||||| || ||||
 GACATGGT GGC AGGGA
 ____ _
 GAM2499 LOC220936 3' GAAGGAGCCTGGTGCAG 93041 CATCT C
 CTGTACCAG GCTCC TC
 ||||| |||| ||
 GACGTGGTC CGAGG AG
 ____ A
 GAM2499 LOC254947 5' TAGAAGAAGCATGAGATACATC 98365 CA_____ CCC ____
 TGGTACAG CTGTACCAG TC TGCT TCT A
 ||||| || ||| |
 GACATGGTC AG ACGA AGA T
 TACATAG T AGA ____
 GAM2499 LOC256158 5' AGAAGGAAGATGCTGGCCAG 99475 TA GC C
 CTG CCAGCATCT TCC TCT
 || ||||| || |||
 GAC GGTCGTAGA AGG AGA
 C_ _ A
 GAM2500 ABR 3' GAGTCAGGAGCCAGGGA 8454 G CACTT T
 TC CTGGCTCC TG CTC
 || ||||| || |||
 AG GACCGAGG AC GAG
 G _ T
 GAM2500 ABR 3' GAGTCAGGAGCCAGGGA 42002 G CACTT T
 TC CTGGCTCC TG CTC
 || ||||| || |||
 AG GACCGAGG AC GAG
 G _ T
 GAM2500 ADAMTS4 5' GAGACAAAGATCCAGGA 18761 G CTCCCA
 TC CTGG CTTTGTCTC
 || ||| |||||

			AG GACC	GAAACAGAG		
			— TA	—		
GAM2500	B4GALT5	3'	GAGCCAGGAGCCAGGGA	17688	G	CACTT T
			TC CTGGCTCC	TG CTC		
			AG GACCGAGG	AC GAG		
			G	— C		
GAM2500	BCAT1	5'	GGAGGTGGGCAGGAGCCAGTGA	66787		CAC TG
			TCGCTGGCTCC	TT TCTCC		
			AGTGACCGAGG	GG GGAGG		
			AC	GT		
GAM2500	CCNF	3'	GAGCCTGGGAGCCAGC	10077		CTTT T
			GCTGGCTCCCA	G CTC		
			CGACCGAGGGT	C GAG		
			C	—		
GAM2500	CDX2	5'	GAGCCGCGAGGAGCCAGCGG	8851		CACT —
			TCGCTGGCTCC	TTGT CTC		
			GGCGACCGAGG	AGCG GAG		
			—	CC		
GAM2500	CYP26A1	5'	GAAATGGAAAGCCAGTGA	55123		C_ C
			TCGCTGGCT	CCA TTT		
			AGTGACCGA	GGT AAG		
			AA	A		
GAM2500	FCMD	3'	ACATAAGTGGGAACCAAAGA	23021	GC C	—
			TC TGG TCCCACTT	TGT		
			AG ACC AGGGTGAA	ACA		
			AA	A T		
GAM2500	FOXD2	5'	AGAACCCTGGGAGCCAGGA	16783	G	CTTTG
			TC CTGGCTCCCA	TCT		
			AG GACCGAGGGT	AGA		
			—	CCCA		
GAM2500	GGT1	5'	GGAGACAGAGAAACCAGC	19160		CTCCCA
			GCTGG	CTTTGTCTCC		
			CGACC	GAGACAGAGG		
			AAA	—		
GAM2500	GGT1	5'	GGAGACAGAGAAACCAGC	26438		CTCCCA
			GCTGG	CTTTGTCTCC		
			CGACC	GAGACAGAGG		
			AAA	—		
GAM2500	GRIA3	5'	GGAGGGGGGTGTAAGAGCCAGCG	7712		C_ TG
	A		TCGCTGGCTC	CACTT TCTCC		

			AGCGACCGAG GTGGG GGAGG		
			AAT _		
GAM2500	GRIA3	5'	GGAGGGGGTGTAAAGAGCCAGCG 7713	C_	TG
	A		TCGCTGGCTC CACTT TCTCC		
			AGCGACCGAG GTGGG GGAGG		
			AAT _		
GAM2500	IFNAR2	3'	GGAAACAGGGAAGAGCCATCGA 7901	C	CCA C
			TCG TGGCTC CTTTGT TCC		
			AGC ACCGAG GGGACA AGG		
			T AA_ A		
GAM2500	NIPSNAP1	3'	GGAAAGGGATGGGAGCCAGGA 14660	G	_ G
			TC CTGGCTCCCA CTTT TCT		
			AG GACCGAGGGT GGGA AGG		
			_ A A		
GAM2500	OAS1	3'	AGACAAAGCTCCTCAGTGA 34145	CTCCCA	
			TCGCTGG CTTTGTCT		
			AGTGACT GAAACAGA		
			CCTC_		
GAM2500	PAK4	3'	GGA CTCGTGGGAGCAAGCGA 20828	G	TTT
			TCGCT GCTCCAC GTCT		
			AGCGA CGAGGGTG CAGG		
			A CT_		
GAM2500	PMM2	3'	GGAGGTAGTGGAACCA 72563	C	TTG
			TGG TCCCACT TCTCC		
			ACC AGGGTGA GGAGG		
			A T_		
GAM2500	POU3F2	5'	GGAGACAGAAAGAGCGAGCGA 20026	G	CCAC
			TCGCT GCTC TTTGTCTCC		
			AGCGA CGAG AGACAGAGG		
			G AA_		
GAM2500	SDS	3'	AAGGTCGGCAGCCAGCGA 23377	_ C	
			TCGCTGGCT CC ACTTT		
			AGCGACCGA GG TGGAA		
			C C		
GAM2500	SEPN1	3'	GGA CTCGGGAGCCAGCG 66976	ACTTT	
			CGCTGGCTCCC GTCT		
			GCGACCGAGGG CAGG		
			CGT_		
GAM2500	SLC18A3	3'	GAGCACCGAGGCCAGCGA 13213	TCCCA T _	
			TCGCTGGC CTT GT CTC		

			AGCGACCG	GAG CA GAG		
			_____ C C			
GAM2500	SLC2A1	3'	GGGCCTGTGGGAGCCTGC	22516	T	TTT
			GC GGCTCCAC GTCT			
			CG CCGAGGGTG CGGG			
			T TC_			
GAM2500	SLC7A5	3'	CAAGCCGGGAGCCAACGA	14462	C	AC
			TCG TGGCTCCC TTG			
			AGC ACCGAGGG GAAC			
			A CC			
GAM2500	SLC9A3R2	3'	GAGACAGAGAGAGAGCGAGCGA	62102	G	CCA
			TCGCT GCTC CTTTGTCTC			
			AGCGA CGAG GAGACAGAG			
			G AGA			
GAM2500	SMTN	5'	GAGCTAGGGGCCAGCGA	23653		CACTTT T
			TCGCTGGCTCC G CTC			
			AGCGACCGGGG C GAG			
			AT_____			
GAM2500	SMTN	5'	GAGCTAGGGGCCAGCGA	57000		CACTTT T
			TCGCTGGCTCC G CTC			
			AGCGACCGGGG C GAG			
			AT_____			
GAM2500	SMTN	5'	GAGCTAGGGGCCAGCGA	57002		CACTTT T
			TCGCTGGCTCC G CTC			
			AGCGACCGGGG C GAG			
			AT_____			
GAM2500	STK19	3'	AGGCTTGGGAGCCAGGA	51612	G	CTTT
			TC CTGGCTCCCA GTCT			
			AG GACCGAGGGT CGGA			
			- T_____			
GAM2500	STK19	3'	AGGCTTGGGAGCCAGGA	16096	G	CTTT
			TC CTGGCTCCCA GTCT			
			AG GACCGAGGGT CGGA			
			- T_____			
GAM2500	BCDO	5'	GGACAAGTGAGAGCCAGC	34286	C	T
			GCTGGCTC CACTT GTCT			
			CGACCGAG GTGAA CAGG			
			A _			
GAM2500	C6.1A	3'	GGAGACAAAATGGGGAAAGATG	44535	_	GG T C
	A		TCG CT C CCCA TTTGTCTCC			

AGT GA G GGGT AAACAGAGG
 A AA _ A
 GAM2500 CNNM1 3' GAGACCCAACTGGGAGCCAGAG 40119 G CTTT_
 A TC CTGGCTCCCA GTCTC
 || ||||| ||||
 AG GACCGAGGGT CAGAG
 A CAACC
 GAM2500 DKFZP434E2135 3' GAAGTTACACTAGAGCCAGCGA 48686 CC____
 TCGCTGGCTC ACTTT
 ||||| ||||
 AGCGACCGAG TGAAG
 ATCACAT
 GAM2500 DKFZp434O0515 5' GAGATTGAGAGCCAGC 66511 C CTTT
 GCTGGCTC CA GTCTC
 ||||| || ||||
 CGACCGAG GT TAGAG
 A ____
 GAM2500 DKFZP564M182 3' GGAGAGCAAGGAGCCAGC 78636 CACT _
 GCTGGCTCC TTG TCTCC
 ||||| || ||||
 CGACCGAGG AAC AGAGG
 ____ G
 GAM2500 DKFZP727M111 5' GAGACAAGCTGGAGCCAG 32059 CAC
 CTGGCTCC TTTGTCTC
 ||||| |||||
 GACCGAGG GAACAGAG
 TC_
 GAM2500 FLJ20507 3' GAGAGCAGGAGCCAGCG 60846 CACTT _
 CGCTGGCTCC TG TCTC
 ||||| || ||||
 GCGACCGAGG AC AGAG
 ____ G
 GAM2500 FLJ20507 3' GAGAGCAGGAGCCAGCG 35741 CACTT _
 CGCTGGCTCC TG TCTC
 ||||| || ||||
 GCGACCGAGG AC AGAG
 ____ G
 GAM2500 FLJ21596 3' ACAAATGGAGTGTAAGCGG 46111 G__ CAC
 TCGCT GCTCC TTTGT
 |||| |||| ||||
 GGCGA TGAGG AAACA
 ATG TA_
 GAM2500 FLJ22378 3' GGACGTGGCAGATGCCAGCGA 47597 _ _ TTT
 TCGCTGGC TC CCAC GTCT
 ||||| || ||||
 AGCGACCG AG GGTG CAGG
 T AC ____
 GAM2500 GALNT12 3' GAGACTGTGGAGCCAGGA 45318 G C TTT
 TC CTGGCTCC AC GTCTC
 || ||||| || ||||

AG GACCGAGG TG CAGAG
 _ _ T_
 GAM2500 HELB 3' GGAGACAAAATGAACATCG 54449 C GCTCC C
 CG TG CA TTTGTCTCC
 || || || |||||
 GC AC GT AAACAGAGG
 T AA_ A
 GAM2500 HIC2 3' AGTCGTGTGCAGGAGCCAGC 65857 _ TT T
 GCTGGCTCC CAC TG CT
 ||||| || ||
 CGACCGAGG GTG GC GA
 AC T_ T
 GAM2500 HSPC156 5' GGAGCCGGCGCGGGAGCCGCGA 27188 T ACT T
 TCGC GGCTCCC TTG CTCC
 ||| ||||| || |||
 AGCG CCGAGGG GGC GAGG
 _ CGC C
 GAM2500 HT002 3' GGAGACAAAGCAAGACCAG 26793 C CCA
 CTGG TC CTTTGTCTCC
 ||| || |||||
 GACC AG GAAACAGAGG
 _ AAC
 GAM2500 KCNH8 3' AGAGTGTGAGGAGCCAGGGA 58903 G _
 TC CTGGCTCC CACTTT
 || ||||| |||||
 AG GACCGAGG GTGAGA
 G AGT
 GAM2500 KCNS1 3' GGAGCATCCAACAGGAGTCAGC 11194 CACTT_ T
 GCTGGCTCC TG CTCC
 ||||| || |||
 CGACTGAGG AC GAGG
 ACAACCT _
 GAM2500 KIAA0215 5' GGAGCCGGGCAGGAGCCGCGA 29084 T CA TT T
 TCGC GGCTCC CT G CTCC
 ||| ||||| || | |||
 AGCG CCGAGG GG C GAGG
 _ AC GC _
 GAM2500 KIAA1483 3' AGACAAAACAGGAGCCAG 70430 CAC
 CTGGCTCC TTTGTCT
 ||||| |||||
 GACCGAGG AAACAGA
 ACA
 GAM2500 KIAA1580 5' GGATGAGAAGAGCCAGCGA 69982 CCAC TG
 TCGCTGGCTC TT TCT
 ||||| || |||
 AGCGACCGAG GA AGG
 AA_ GT
 GAM2500 KIAA1656 3' GGAGGGCGGTGGGAGCCAGT 66376 TTG
 GCTGGCTCCCACT TCTCC
 ||||| |||||

				TGACCGAGGGTGG	GGAGG		
				CG_			
GAM2500	KIAA1814	3'	GAGGACTGGGAGCCAGGA	70879	G	CTTTG	
			TC CTGGCTCCCA	TCTC			
			AG GACCGAGGGT	GGAG			
			_ CA_				
GAM2500	KIAA1822	3'	GGAGCCGGGGTGGGAACCAGGA	68189	G	C	T
			TC CTGG TCCCACTTTG	CTCC			
			AG GACC AGGGTGGGGC	GAGG			
			_ A C				
GAM2500	LENG9	3'	AGACAAAGCAGGAGCGTGC	75021	TG	CA	
			GC GCTCC CTTTGTCT				
			CG CGAGG GAAACAGA				
			TG AC				
GAM2500	MGC4643	3'	GAGACAAAGTCTCAGC	52139		CTCCC	
			GCTGG ACTTTGTCTC				
			CGACT TGAAACAGAG				
			C_				
GAM2500	MGC861	3'	AGAGCTGGGCAGAAGCAGCGA	44131	G_ _ _		
			TCGCTG CT CCCA CTTT				
			AGCGAC GA GGGT GAGA				
			GAA C C				
GAM2500	NFAT5	3'	GAGACTCAGGTGAGCCAGC	57789	_	ACTTT	
			GCTGGCTC CC GTCTC				
			CGACCGAG GG CAGAG				
			T ACT_				
GAM2500	NUCKS	3'	GAGACTCGGAGCCAGTGA	43003		CACTTT	
			TCGCTGGCTCC GTCTC				
			AGTGACCGAGG CAGAG				
			CT_				
GAM2500	p25	3'	AGACATGCGGGAGCCAGGA	23822	G	ACTT	
			TC CTGGCTCCC TGTCT				
			AG GACCGAGGG ACAGA				
			_ CGT_				
GAM2500	PDIR	5'	GAGAAAGGAGCCAGCGG	23316		CACTTTG	
			TCGCTGGCTCC TCTC				
			GGCGACCGAGG AGAG				
			AA_				
GAM2500	PLP1	3'	GGAAACAAAGTGGGAAGGAAAG	6759	GG	C_ C	
			CT CT CCACTTTGT TCC				

			GA GG GGTGAAACA AGG		
			AA AA A		
GAM2500	RANBP1	5'	GAGGCCGCGGAGCCAGCGA 12763	CACTTT	
			TCGCTGGCTCC GTCTC		
			AGCGACCGAGG CGGAG		
			CGC__		
GAM2500	RGS7	5'	GAGGGAGAGAGCCAGCGA 12864	CCAC G	
			TCGCTGGCTC TTT TCTC		
			AGCGACCGAG AGA GGAG		
			__ G		
GAM2500	SCYA14	5'	GAGACAAAAGAGGCCAGC 16051	CCCAC	
			GCTGGCT TTTGTCTC		
			CGACCGG AAACAGAG		
			AGA__		
GAM2500	SCYA14	5'	GAGACAAAAGAGGCCAGC 53106	CCCAC	
			GCTGGCT TTTGTCTC		
			CGACCGG AAACAGAG		
			AGA__		
GAM2500	SDCCAG3	3'	AGACATTGTCATAAAAGCCAGT 22799	CCC__ TT	
			GA TCGCTGGCT AC TGTCT		
			AGTGACCGA TG ACAGA		
			AAATAC TT		
GAM2500	SLC37A1	3'	GAGAAGCAGAGAGCCAGCG 39091	CCA TTG	
			CGCTGGCTC CT TCTC		
			GCGACCGAG GA AGAG		
			A__ CGA		
GAM2500	WDR13	5'	GAGACAGAAGGAACCGGCGA 35842	C CAC	
			TCGCTGG TCC TTTGTCTC		
			AGCGGCC AGG AGACAGAG		
			A A__		
GAM2500	LOC112937	5'	GGAGAGGGGCGGAAGCCGC 93178	T C A G	
			GC GGCT CC CTTT TCTCC		
			CG CCGA GG GGGG AGAGG		
			_ A C _		
GAM2500	LOC134701	5'	GGAGAGGGGCGGAGAGGCAGCG 75696	G _ A G	
			A TCGCTG CTC CC CTTT TCTCC		
			AGCGAC GAG GG GGGG AGAGG		
			G A C _		
GAM2500	LOC143678	5'	GACGACAGGAGCCAGGA 83901	G CACTT _	
			TC CTGGCTCC TGTC TC		

		AG GACCGAGG ACAG AG	
		— C	
GAM2500	LOC145694 5'	GGAGGCGGCGGCAGCCAGCGA 84443	C A TT
		TCGCTGGCT CC CT GTCTCC	
		AGCGACCGA GG GG CGGAGG	
		C C —	
GAM2500	LOC146714 5'	GAGGCGGAAGACCAGCGA 84746	C CCAC
		TCGCTGG TC TTTGTCTC	
		AGCGACC AG AGGCGGAG	
		— A —	
GAM2500	LOC148089 3'	GGAACCGCGCATGGGAGCCAGC 79333	CTT_ TC
		GCTGGCTCCCA TG TCC	
		CGACCGAGGGT GC AGG	
		ACGC CA	
GAM2500	LOC150935 3'	GAGCCTTGGGAGCCAGGA 80828	G CTTT T
		TC CTGGCTCCCA G CTC	
		AG GACCGAGGGT C GAG	
		— TC —	
GAM2500	LOC151963 5'	AAAGCCTGGGAGCCTGCGA 81214	T —
		TCGC GGCTCCCA CTTT	
		AGCG CCGAGGGT GAAA	
		T CC	
GAM2500	LOC152283 5'	GGATGCTGAGGAAGCCAGCGA 86873	CCCA T C
		TCGCTGGCT CTT GT TCC	
		AGCGACCGA GAG CG AGG	
		AG_ T T	
GAM2500	LOC152441 5'	GAGACAAAATGGGACCAG 86917	C C
		CTGG TCCCA TTTGTCTC	
		GACC AGGGT AAACAGAG	
		— A	
GAM2500	LOC157653 5'	GAACCGGGGAGCCAGCGA 82444	ACTTT C
		TCGCTGGCTCCC GT TC	
		AGCGACCGAGGG CA AG	
		GC —	
GAM2500	LOC158943 5'	GAGGCCGCGGAGCCAGCGA 61150	CACTTT
		TCGCTGGCTCC GTCTC	
		AGCGACCGAGG CGGAG	
		CGC —	
GAM2500	LOC163101 5'	GGACAATGAGAGCCAGC 83313	C CT
		GCTGGCTC CA TTGTCT	

CGACCGAG GT AACAGG
A _
GAM2500 LOC196759 5' GAAGCTGGTGGGAGCCAGGA 88912 G TT TC
TC CTGGCTCCCACT G TC
|| ||||| | ||
AG GACCGAGGGTGG C AG
_ T_ GA
GAM2500 LOC199864 5' GAAGCTGGTGGGAGCCAGGA 91459 G TT TC
TC CTGGCTCCCACT G TC
|| ||||| | ||
AG GACCGAGGGTGG C AG
_ T_ GA
GAM2500 LOC202908 5' GAGACAAAGACCAACGA 90723 C CTCCCA
TCG TGG CTTTGTCTC
||| || |||||
AGC ACC GAAACAGAG
A A____
GAM2500 LOC206973 5' GGAGATCTGGCACGGGGGCCAG 91111 A__ TT
CGA TCGCTGGCTCCC CT GTCTCC
||||||| || |||||
AGCGACCGGGGG GG TAGAGG
CAC TC
GAM2500 LOC220522 5' GGAGACAGAGAAACCAGC 61142 CTCCCA
GCTGG CTTTGTCTCC
|||| |||||
CGACC GAGACAGAGG
AAA____
GAM2500 LOC222057 5' GAGACAAAGACCAGCGA 94353 CTCCCA
TCGCTGG CTTTGTCTC
||||| |||||
AGCGACC GAAACAGAG
A____
GAM2500 LOC222178 5' GAAGAAGAAAAGCCAGTGA 95837 CCCA G
TCGCTGGCT CTTT TC
|||||| ||| ||
AGTGACCGA GAAG AG
AAA_ A
GAM2500 LOC254205 5' AGATCAAGAGCCAGTGA 98464 CCACT _
TCGCTGGCTC TTG TCT
|||||| ||| |||
AGTGACCGAG AAC AGA
_____ T
GAM2500 LOC255452 5' GGAGCAGGGATGGAACCAGC 99396 C CA T
GCTGG TCC CTTTG CTCC
|||| ||| |||| |||
CGACC AGG GGGAC GAGG
A TA _
GAM2500 LOC255975 5' GAGACAAAGACCAACGA 97581 C CTCCCA
TCG TGG CTTTGTCTC
||| ||| |||||

		AGC ACC	GAAACAGAG		
		A A			
GAM2500	LOC256542	3'	GGAAACAAGGAGAGTCAGC	97291	CCA C
			GCTGGCTC CTTTGT TCC		
			C GACTGAG GGAACA AGG		
			A A		
GAM2500	LOC256878	5'	GAGACAAAGACCAACGA	98687	C CTCCCA
			TCG TGG CTTTGTCTC		
			AGC ACC GAAACAGAG		
			A A		
GAM2500	LOC57333	3'	GGAGGCAATAAAAGCCAGCG	74092	CCC ACT
			CGCTGGCT TTGTCTCC		
			GCGACCGA AACGGAGG		
			AAAT		
GAM2500	LOC90625	3'	GGAGGGATGGGACCCAGC	64380	C _ TTGT
			GCTGG TCCCA CT CTCC		
			CGACC AGGGT GG GAGG		
			C A		
GAM2501	C1orf1	3'	AAGTTGCCTTACAGAGCCAGGA	8675	CAGTT _
			TCCTGGCTCTG GGTA CTT		
			AGGACCGAGAC CCGT GAA		
			ATT T		
GAM2501	DGUOK	3'	AACTCTTACAGGCCAGGAA	10406	T C
			TTCCTGGC CTG AGTT		
			AAGGACCG GAC TCAA		
			_ ATTC		
GAM2501	DGUOK	3'	AACTCTTACAGGCCAGGAA	10407	T C
			TTCCTGGC CTG AGTT		
			AAGGACCG GAC TCAA		
			_ ATTC		
GAM2501	KCNA6	3'	GGGAACCACAGAGCCAGGAG	11141	CAGT A
			TTCCTGGCTCTG TGGT CTT		
			GAGGACCGAGAC ACCA GGG		
			A		
GAM2501	M6A	3'	AAGCACTTCCTTACAGAGCTAA	39555	C C_ TT A
	GAA		TTC TGGCTCTG AG GGT CTT		
			AAG ATCGAGAC TC TCA GAA		
			A AT CT C		
GAM2501	PRG2	5'	AAGTACCAGAAGGAAGCAAGAA	12258	CTG _ GCAG
			TTC GCT CT TTGGTACTT		

		AAG CGA GG GACCATGAA	
		AA_ A AA__	
GAM2501	C20orf54 3'	AAGTACCAACTACCTCACAGG 54153	GCTCTGC
		CCTG AGTTGGTACTT	
		GGAC TCAACCATGAA	
		ACTCCA_	
GAM2501	CREB-H 3'	TACACACAGAGCCAGGAG 51879	CAGT _
		TTCCTGGCTCTG TG GTA	
		GAGGACCGAGAC AC CAT	
		_____ A	
GAM2501	KIAA0633 3'	AAGGAGTCTGCATAGCCAGGAA 95700	C TTGGTA
		TTCCTGGCT TGCAG CTT	
		AAGGACCGA ACGTC GAA	
		T TGAG__	
GAM2501	LOC149684 3'	ACCCGCAGAGCCATGAA 85759	C AGTT
		TTC TGGCTCTGC GGT	
		AAG ACCGAGACG CCA	
		T C__	
GAM2501	LOC151470 3'	AAGTACTAGCTAAACCAG 81054	CTCTGC
		CTGG AGTTGGTACTT	
		GACC TCGATCATGAA	
		AAA__	
GAM2501	LOC158431 3'	TATTGACTACAGAGCAAGAA 88168	CTG C TG
		TTC GCTCTG AGT GTA	
		AAG CGAGAC TCA TAT	
		AA_ A GT	
GAM2501	LOC83690 3'	TACTCCTGCAGGCCAGGAA 49596	T TT
		TTCCTGGC CTGCAG GGTA	
		AAGGACCG GACGTC TCAT	
		_ C_	
GAM2502	AGRN 3'	CCAGGCAGCCGTGCTGCA 79584	CA _
		TGCAGCAC GCTGC TGG	
		ACGTCGTG CGACG ACC	
		C_ G	
GAM2502	ALEX1 5'	CTGCCTCAGAGCCGCGCCGCA 33974	AGCA A G GA
		TGC CC GCT CTG GCAG	
		ACG GG CGA GAC CGTC	
		CCC_ C _ TC	
GAM2502	AP1B1 3'	CCACCGACTGGCAGCTGCA 8516	A_ C C
		TGCAGC CCAG TG TGG	

ACGTCG GGTC GC ACC
 AC A C
 GAM2502 ATM 3' CTGCCGGGTAGCTGGGGCTACA 57144 C A GGA
 TG AGC CCAGCTGCT GCAG
 || ||| ||||| ||||
 AC TCG GGTCGATGG CGTC
 A G GC_
 GAM2502 BDP1 3' CTGCCGGGTAGCTGGGACTACA 37966 C CA GGA
 TG AG CCAGCTGCT GCAG
 || || ||||| ||||
 AC TC GGTCGATGG CGTC
 A AG GC_
 GAM2502 CAPON 5' CTGCTCTGGGGCCGGCGCCGC 64659 A A A G TG
 GC GC CC GCT C GAGCAG
 || || || || | |||||
 CG CG GG CGG G CTCGTC
 C C C _GT
 GAM2502 CTF1 3' CCAGCAGCTGGGACTACA 9009 C CA
 TG AG CCAGCTGCTGG
 || || ||||| ||||
 AC TC GGTCGACGACC
 A AG
 GAM2502 DDB2 3' CTGCTCCAGAGTTGGTGACACA 5456 CAG G
 TG CACCAGCT CTGGAGCAG
 || ||||| |||||
 AC GTGGTTGA GACCTCGTC
 ACA _
 GAM2502 ENDOGL1 3' CTGCCCCCTGAGCAGCTGGGAC 18823 C CA _ A
 TACA TG AG CCAGCTGCT GG GCAG
 || || ||||| || ||||
 AC TC GGTCGACGA CC CGTC
 A AG GTC C
 GAM2502 FCRH1 3' CTGCTGAGTAGCTGGGACTACA 54726 C CA GG
 TG AG CCAGCTGCT AGCAG
 || || ||||| ||||
 AC TC GGTCGATGA TCGTC
 A AG G_
 GAM2502 FTH1 5' GCTCCAGCGCCGCGCA 68713 A ACCA T
 TGC GC GC GCTGGAGC
 ||| || || |||||
 ACG CG CG CGACCTCG
 _ C _ _
 GAM2502 GAB2 3' CCACAGCTGGTGCTCA 55404 C C
 TG AGCACCAGCTG TGG
 || ||||| ||||
 AC TCGTGGTCGAC ACC
 _ _
 GAM2502 GAB2 3' CCACAGCTGGTGCTCA 25457 C C
 TG AGCACCAGCTG TGG
 || ||||| ||||

AC TCGTGGTCGAC ACC

```

GAM2502 HTR4   3' GCCCTGGCTGTGCTGCA   7885   C   GCT A
                  TGCAGCAC AGCT  GG GC
                  ||||| |||  ||
                  ACGTCGTG TCGG  CC CG
                  _ T _ _
GAM2502 KLHL3  3' TTCCAAGCAGGTGCTGCA   88855   A   GC
                  TGCAGCACC GCT  TGGAG
                  ||||| |||  ||||
                  ACGTCGTGG CGA  ACCTT
                  A _ _
GAM2502 LPIN1  3' CTGCTCCAGCAAGTAGCT   67987   ACCA _
                  AGC   GCT GCTGGAGCAG
                  |||  ||| |||||
                  TCG   TGA CGACCTCGTC
                  A _ _ A
GAM2502 MAD2L2 3' GCCTAGGGCAGTGCTGCA   22018   CA G A
                  TGCAGCAC GCT CTGG GC
                  ||||| ||| ||| ||
                  ACGTCGTG CGG GATC CG
                  A _ _ _
GAM2502 MPST   3' TGCCCACCTGGTGCTG   41210   CTGC A
                  CAGCACCAG TGG GCA
                  ||||| ||| |||
                  GTCGTGGTC ACC CGT
                  C _ _ _
GAM2502 MSF    3' GCCCCCACTGGGCTGCA   89466   A C CT A
                  TGCAGC CCAG TG GG GC
                  ||||| ||| ||| ||
                  ACGTCG GGTC AC CC CG
                  _ _ C _ _
GAM2502 OLFM1  3' GTATTTGCAGCTGGAAGTCA 27345   CA   TG A
                  TGCAG CCAGCTGC G GC
                  |||| ||||| | ||
                  ACGTC GGTCGACG T TG
                  AA   TT A
GAM2502 PTPN18 3' CTGCCGAGTAGCTGGGACTACA 27650   C CA   GGA
                  TG AG CCAGCTGCT GCAG
                  || || ||||| |||
                  AC TC GGTCGATGA CGTC
                  A AG   GC _
GAM2502 RPS18  5' CCGCCGCTTGTGCTGCA   42880   C T T
                  TGCAGCAC AGC GC GG
                  ||||| ||| || ||
                  ACGTCGTG TCG CG CC
                  T C _
GAM2502 SBF1   3' CTGGTCCAGCCAGCGGCTGCA 66069   ACCA _ G
                  TGCAGC GCTG CTGGA CAG
                  ||||| ||| ||||| |||
```

		ACGTCG CGAC GACCT GTC	
		G___ C G	
GAM2502	SCGB1A1	3' CTGCTCCAGCCTCTGCCGCT 13983	AC CT
		AGC CAG GCTGGAGCAG	
		TCG GTC CGACCTCGTC	
		CC TC	
GAM2502	SLC8A2	5' CTGCTCCAGGCTGTAGCCGCA 66934	A AC TG
		TGC GC CAGC CTGGAGCAG	
		ACG CG GTCG GACCTCGTC	
		C AT _	
GAM2502	STARD5	3' GCTCCCTCAGTCCTGTGCTGCA 48318	CA_ CT
		TGCAGCAC GCTG GGAGC	
		ACGTCGTG TGAC CCTCG	
		TCC TC	
GAM2502	TARBP2	3' CTGCAGGAGCTGGTGGTGCA 57004	G G G
		TGCA CACCAGCT CTG AG	
		ACGT GTGGTCGA GAC TC	
		G G G	
GAM2502	ARHGAP8	3' CTGCCCCAGCCCTCTGGTGT 35201	CT_ A
		GCACCAG GCTGG GCAG	
		TGTGGTC CGACC CGTC	
		TCC C	
GAM2502	BCKDK	3' CTGCTCCACACACTGCTGCA 60494	CCAGC C
		TGCAGCA TG TGGAGCAG	
		ACGTCGT AC ACCTCGTC	
		CAC_ _	
GAM2502	C11orf21	3' CTGAGATGGCAACTGGCACCGG 27103	AGCA_ C GAG
	CA	TGC CCAG TGCTG CAG	
		ACG GGTC ACGGT GTC	
		GCCAC A AGA	
GAM2502	C14orf3	5' CTGCCGGGCGGCTGGCACT 25049	CA GGA
		AG CCAGCTGCT GCAG	
		TC GGTCGGCGG CGTC	
		AC GC_	
GAM2502	CDCA4	3' CTGCTCTGTTAGACTGGTGCTG 36086	_ CT
		CAGCACCAG CTG GGAGCAG	
		GTCGTGGTC GAT TCTCGTC	
		A TG	
GAM2502	CITED2	5' CTGCCCCAGCGGCCGCTGCG 21401	ACCA A
		TGCAGC GCTGCTGG GCAG	

GCGTCG CGGCGACC CGTC
 C___ C
 GAM2502 COPS7B 3' CTGGGGCAGCTGGCACTCA 42999 C CA GG
 TG AG CCAGCTGCT AG
 || || ||||| ||
 AC TC GGTCGACGG TC
 _ AC GG
 GAM2502 CXYorf1 3' CCATCGTACAGTGGTGCTGCA 82908 G C___
 TGCAGCACCA CTG TGG
 ||||| || ||
 ACGTCGTGGT GAC ACC
 _ ATGCT
 GAM2502 CXYorf1 5' TGCTCCAGAGCGCCTGCA 82922 CACCA G
 TGCAG GCT CTGGAGCA
 |||| || |||||
 ACGTC CGA GACCTCGT
 CG___ _
 GAM2502 D2S448 3' CTGCTCCAACAGCCAAATGC 73890 GCACCA C
 GCA GCTG TGGAGCAG
 || |||| |||||
 CGT CGAC ACCTCGTC
 AAAC___ A
 GAM2502 FER1L4 3' CTGCTCTGTGCAGCTGGCCCGC 48119 AGCA _
 A TGC CCAGCTGC TGGAGCAG
 || ||||| |||||
 ACG GGTCGACG GTCTCGTC
 CCC___ T
 GAM2502 FLJ10604 3' CTCCAGCTTTCTGGTGTCA 36858 CA CT_
 TG GCACCAG GCTGGAG
 || ||||| |||||
 AC TGTGGTC CGACCTC
 AC TTT
 GAM2502 FLJ10640 5' CCGAGTAGCTGGGACTACA 39232 C CA _
 TG AG CCAGCTGCT GG
 || || ||||| ||
 AC TC GGTCGATGA CC
 A AG G
 GAM2502 FLJ11125 5' CCACGTAGCTGGGGCTACA 60322 C A _
 TG AGC CCAGCTGC TGG
 || || ||||| ||
 AC TCG GGTCGATG ACC
 A G C
 GAM2502 FLJ11280 5' CTGGAAGGCAGCTGGCACTGGC 37786 _ CA GGAG
 A TGC AG CCAGCTGCT CAG
 || || ||||| ||
 ACG TC GGTCGACGG GTC
 G AC AAG_
 GAM2502 FLJ12581 3' CCGAGCAGCTGGGACTACA 46334 C CA _
 TG AG CCAGCTGCT GG
 || || ||||| ||

		AC TC GGTCGACGA CC		
		A AG G		
GAM2502	FLJ12697	3' GCCCCAGCAGCCCCGCGCA	94158	A ACCA A
		TGC GC GCTGCTGG GC		
		ACG CG CGACGACC CG		
		_ CCCC C		
GAM2502	FLJ13710	3' CTGCCCCATCCCTGGTGCT	46098	CTGC A
		AGCACCAG TGG GCAG		
		TCGTGGTC ACC CGTC		
		CCT_ C		
GAM2502	FLJ14681	5' CTGCCTGGGGCGGTGCTGCA	52595	A G TG A
		TGCAGCACC GCT C G GCAG		
		ACGTCGTGG CGG G C CGTC		
		_ _GT_		
GAM2502	FLJ14871	3' TCAGCAATGGTGCTGCA	52731	GC
		TGCAGCACCA TGCTGG		
		ACGTCGTGGT ACGACT		
		A_		
GAM2502	FLJ20150	3' CTGCTCCAGCTGTTACATGCA	35140	GCACC T
		TGCA AGC GCTGGAGCAG		
		ACGT TTG CGACCTCGTC		
		ACAC_ T		
GAM2502	FLJ30678	5' CTGCCCCAGCAGCGGCCTG	58981	CA A A
		CAG CC GCTGCTGG GCAG		
		GTC GG CGACGACC CGTC		
		C_ _ C		
GAM2502	HCA112	3' CTGCTCCAGCAGCACTTGC	38082	CCA
		GCA GCTGCTGGAGCAG		
		CGT CGACGACCTCGTC		
		TCA		
GAM2502	HEMK	3' CTGTCGGGGCAGCTGGGGCCAC	32956	CA A GGA
	A	TG GC CCAGCTGCT GCAG		
		AC CG GGTCGACGG TGTC		
		AC G GGC		
GAM2502	ITGB8	5' CTGCTCCGCAGACGGGGCTGCA	11055	A AG_ T
		TGCAGC CC CTGC GGAGCAG		
		ACGTCG GG GACG CCTCGTC		
		_ GCA _		
GAM2502	KIAA0084	5' GCTCCAGCGGCTGCTGT	68709	CCA
		GCAGCA GCTGCTGGAGC		

TGTCGT CGGCGACCTCG

GAM2502 KIAA0290 3' CTGCCCCAGCTCTACACTGC 66716 CACC CT A
GCAG AG GCTGG GCAG
|||| || |||| ||||
CGTC TC CGACC CGTC
ACA_ T_ C

GAM2502 KIAA0415 3' GCCCAGGCCAGCTGGTGCT 94163 _ A
AGCACCAGCTG CTGG GC
||||||| ||| ||
TCGTGGTCGAC GACC CG
CG _

GAM2502 KIAA0453 3' CTGCCCTGTGGGCTGGTGCTTC 69605 C _TG T A
A TG AGCACCAG C C GG GCAG
|| ||||| | || ||||
AC TCGTGGTC G G CC CGTC
T G GT T _

GAM2502 KIAA0532 3' CCAAGCAGCTGGGACTACA 71319 C CA _
TG AG CCAGCTGCT GG
|| || ||||| ||
AC TC GGTCGACGA CC
A AG A

GAM2502 KIAA0720 3' CTCTAGTAGCTGGAAGTCA 62981 CA
TGCAG CCAGCTGCTGGAG
|||| ||||| ||||
ACGTC GGTCGATGATCTC
AA

GAM2502 KIAA0934 3' CTGCCCCAGTGTGACCCTGCA 64883 CACCA T A
TGCAG GC GCTGG GCAG
|||| || |||| ||||
ACGTC TG TGACC CGTC
CCAG_ _ C

GAM2502 KIAA1160 3' CTGCAGACACAGGCTGGTGCTG 40756 GC GA_
CA TGCAGCACCAGCT TG GCAG
||||||| || ||||
ACGTCGTGGTCGG AC CGTC
AC AGA

GAM2502 KIAA1169 5' CCAAGCAGCTGGAAGTCA 35878 C CA _
TG AG CCAGCTGCT GG
|| || ||||| ||
AC TC GGTCGACGA CC
A AA A

GAM2502 KIAA1464 3' CTCGGGACAGCTGTGTGCTGCA 68818 _ _ G
TGCAGCAC CAGCTG CT GAG
||||| |||| || |||
ACGTCGTG GTCGAC GG CTC
T A G

GAM2502 KIAA1465 3' CTGCCTAGTAGCTGGGACTACA 61494 C CA A
TG AG CCAGCTGCTGG GCAG
|| || ||||| ||||

AC TC GGTTCGATGATC CGTC
 A AG _
 GAM2502 KIAA1671 3' CTGCTCCAACCTGGTGCTG 66281 CTGC
 CAGCACCAG TGGAGCAG
 ||||| |||||
 GTCGTGGTC ACCTCGTC
 CA__
 GAM2502 KIAA1821 3' CTGCCTGAGTAGCTGGGACTAC 72264 C CA _ A
 A TG AG CCAGCTGCT GG GCAG
 || || ||||| || ||||
 AC TC GGTTCGATGA TC CGTC
 A AG G _
 GAM2502 MGC1842 5' CTGCTCCAGGATGGTGCTGCA 66254 GCTG
 TGCAGCACCA CTGGAGCAG
 ||||| |||||
 ACGTCGTGGT GACCTCGTC
 AG__
 GAM2502 MGC3178 3' CTGCTCTGGCCCTGGTGTGCA 48718 G CT TG
 TGCA CACCAG GC GAGCAG
 ||| |||| || |||||
 ACGT GTGGTC CG CTCGTC
 _ C_ GT
 GAM2502 MGC34923 5' CCAGCAGCTGGTGCTCA 59195 C
 TG AGCACCAGCTGCTGG
 || |||||
 AC TCGTGGTCGACGACC
 _
 GAM2502 moblak 3' CCAGCAGCTGGGACTACA 56389 C CA
 TG AG CCAGCTGCTGG
 || || |||||
 AC TC GGTTCGACGACC
 A AG
 GAM2502 NDRG4 3' CTGGGCCAGCTGGTGCTGTA 40381 CT AG
 TGCAGCACCAGCTG GG CAG
 ||||| || |||
 ATGTCGTGGTCGAC CC GTC
 _ GG
 GAM2502 NDRG4 3' CTGGGCCAGCTGGTGCTGTA 43578 CT AG
 TGCAGCACCAGCTG GG CAG
 ||||| || |||
 ATGTCGTGGTCGAC CC GTC
 _ GG
 GAM2502 NR4A3 5' CCGGTGCAGCGCGCGCCGCA 23718 A A A_ _
 TGC GC CC GCTGC TGG
 ||| || |||| |||
 ACG CG GG CGACG GCC
 C C CG TG
 GAM2502 NSAP1 5' CTGCCTCAGCCAGTAGCGCA 22086 A ACCA _ GA
 TGC GC GCTG CTG GCAG
 ||| || |||| ||||

ACG CG TGAC GAC CGTC
 _ A_ C TC
 GAM2502 PDCD5 5' CTGCTCCAGCGCTGACGC 17483 AC T
 GC CAGC GCTGGAGCAG
 || ||| |||||
 CG GTCG CGACCTCGTC
 CA _
 GAM2502 PDZD2 5' CTCCTCTACCAGTGGCTGCA 81720 ACCA C C
 TGCAGC GCTG TGGAG AG
 ||||| ||| ||||| ||
 ACGTCG TGAC ATCTC TC
 G_ C C
 GAM2502 PPP1R16B 3' TTCCAAAGCAGGTGCTGCA 62042 A GC
 TGCAGCACC GCT TGGAG
 ||||| ||| |||||
 ACGTCGTGG CGA ACCTT
 A A_
 GAM2502 PSIP2 5' CTGCGGCAGCTGGTGGCGCA 53781 AG G
 TGC CACCAGCTGCTG AG
 ||| ||||| ||| ||
 ACG GTGGTCGACGGC TC
 CG G
 GAM2502 RAB40C 3' CTGCCCACAGCACTGGTGCTCA 41279 C C GA_
 TG AGCACCAG TGCTG GCAG
 || ||||| ||||| |||||
 AC TCGTGGTC ACGAC CGTC
 _ _ ACC
 GAM2502 RAB40C 3' CTGCCCCAGCAGCCCCTCTGCA 41280 CACCA A
 TGCAG GCTGCTGG GCAG
 ||||| ||||| |||||
 ACGTC CGACGACC CGTC
 TCCC_ C
 GAM2502 SFXN5 3' CTGCCAGCCGCTGGTGC 58652 T GA
 GCACCAGC GCTG GCAG
 ||||| ||||| |||||
 CGTGGTCG CGAC CGTC
 C _
 GAM2502 SIMRP7 3' CTGCTCCAGCAGACCATCTGCA 93972 CACCAG
 TGCAG CTGCTGGAGCAG
 ||||| ||||| |||||
 ACGTC GACGACCTCGTC
 TACCA_
 GAM2502 ZNF297B 5' CTGTTGCGGCAGCTGAGGCTAC 82704 C AC G
 A TG AGC CAGCTGCTG AGCAG
 || ||| ||||| |||||
 AC TCG GTCGACGGC TTGTC
 A GA G
 GAM2502 LOC123242 5' CTGAGGCCAGCTGGTGCTG 76114 CT AG_
 CAGCACCAGCTG GG CAG
 ||||| ||| |||

		GTCGTGGTCGAC CC GTC		
		___ GGA		
GAM2502	LOC126603 5'	TGCTTCGCTGATCCTGCA 75914	CAC	TGCT
		TGCAG CAGC GGAGCA		
		ACGTC GTCG CTTCGT		
		CTA ____		
GAM2502	LOC127841 5'	CTGCTCCCCAGCAGCTGGTGC 75186		___
		GCACCAGCTGCT GGAGCAG		
		CGTGGTCGACGA CCTCGTC		
		CC		
GAM2502	LOC130074 3'	CCACAGCTGGTGCTGCA 76624	C	
		TGCAGCACCAGCTG TGG		
		ACGTCGTGGTCGAC ACC		
		—		
GAM2502	LOC132166 3'	CCAGCCGCTGGTGTGCA 75535	G	T
		TGCA CACCAGC GCTGG		
		ACGT GTGGTCG CGACC		
		— C		
GAM2502	LOC132332 5'	CTGCCCTTGACTGGTGCTCA 76666	C	CTGCT A
		TG AGCACCAG GG GCAG		
		AC TCGTGGTC CC CGTC		
		— AGTT_ _		
GAM2502	LOC142820 3'	GCTCCAGCTGCACTGCA 76916	CACCA	T
		TGCAG GC GCTGGAGC		
		ACGTC CG CGACCTCG		
		A___ T		
GAM2502	LOC143785 5'	CCAGACGCTGGTGTGCA 77102	G	TG
		TGCA CACCAGC CTGG		
		ACGT GTGGTCG GACC		
		— CA		
GAM2502	LOC146229 3'	CCAAGTAGCTGGGACTACA 78267	C CA	—
		TG AG CCAGCTGCT GG		
		AC TC GGTCGATGA CC		
		A AG A		
GAM2502	LOC146268 3'	CTCTGGCTGGTGCTGC 78338	GCT	
		GCAGCACCAGCT GGAG		
		CGTCGTGGTCGG TCTC		
		—		
GAM2502	LOC147080 5'	CCGAGCAGCTGGGACTACA 85031	C CA	—
		TG AG CCAGCTGCT GG		

AC TC GGTCGACGA CC
 A AG G
 GAM2502 LOC147160 5' CTGCTCCAGCACGTGTGC 85075 CA _
 GCAC GC TGCTGGAGCAG
 |||| || |||||
 CGTG TG ACGACCTCGTC
 _ C
 GAM2502 LOC148089 3' CCGGCAGCTAGTGGCA 79329 AG C
 TGC CAC AGCTGCTGG
 ||| ||| |||||
 ACG GTG TCGACGGCC
 _ A
 GAM2502 LOC150166 5' CTGCTCCAGCAGCCGGGCCTGC 86037 CA A
 A TGCAG CC GCTGCTGGAGCAG
 |||| || |||||
 ACGTC GG CGACGACCTCGTC
 CG C
 GAM2502 LOC151178 5' CTTGCAGCTGAAGCTGCA 80959 AC T
 TGCAGC CAGCTGC GG
 |||| ||||| ||
 ACGTCG GTCGACG TC
 AA T
 GAM2502 LOC151568 5' CTGCTCCGGCATCCAGCGCTGC 57495 ACCAGC
 GCAGC TGCTGGAGCAG
 |||| |||||
 CGTCG ACGGCCTCGTC
 CGACCT
 GAM2502 LOC153205 5' CTGCTCCTGACACGTGCTGCA 87157 CAGCTGCT
 TGCAGCAC GGAGCAG
 ||||| |||||
 ACGTCGTG CCTCGTC
 CACAGT_
 GAM2502 LOC154084 3' CTGCCCCAGTAGCATCTGCA 87377 CACCA A
 TGCAG GCTGCTGG GCAG
 |||| ||||| ||||
 ACGTC CGATGACC CGTC
 TA_ C
 GAM2502 LOC154813 5' CCACCAATGGTGCTGCA 82057 GC C
 TGCAGCACCA TG TGG
 ||||| || |||
 ACGTCGTGGT AC ACC
 A_ C
 GAM2502 LOC155006 3' CTGCTCTGCCCTGATGTGCA 82168 G C CT T
 TGCA CA CAG GC GGAGCAG
 ||| || ||| || |||||
 ACGT GT GTC CG TCTCGTC
 _ A C_ _
 GAM2502 LOC166129 5' CTGCTCCAAGCAGCAGCGGCTG 88609 ACCA _
 CA TGCAGC GCTGCT GGAGCAG
 |||| ||||| |||||

ACGTCG CGACGA CCTCGTC
 GCGA A
 GAM2502 LOC196500 5' GCTCCAGCGCCCTGCCGC 89084 A CCA T
 GC GCA GC GCTGGAGC
 || ||| || |||||
 CG CGT CG CGACCTCG
 C CC_ _
 GAM2502 LOC200093 3' CCATTGTACAGTGGTGCTGCA 63765 G C____
 TGCAGCACCA CTG TGG
 ||||| ||| |||
 ACGTCGTGGT GAC ACC
 _ ATGTT
 GAM2502 LOC200093 5' TGCTCCAGGGCGCCTGCA 63778 CACCA G
 TGCAG GCT CTGGAGCA
 |||| ||| |||||
 ACGTC CGG GACCTCGT
 CG_ _
 GAM2502 LOC253001 5' CTGAGGCCAGCTGGTGCTG 97993 CT AG_
 CAGCACCAGCTG GG CAG
 ||||| || |||
 GTCGTGGTCGAC CC GTC
 _ GGA
 GAM2502 LOC254266 5' CCACCGTGCTGGTGCTCA 99196 C _ C
 TG AGCACCAGC TG TGG
 || ||||| || |||
 AC TCGTGGTCG GC ACC
 _ T C
 GAM2502 LOC255189 5' GCTCCCCATTGTGCTGCA 98376 C C CT
 TGCAGCAC AG TG GGAGC
 ||||| || ||| |||||
 ACGTCGTG TT AC CCTCG
 _ _ CC
 GAM2502 LOC255738 5' CTGCCCACGTGGCTGGCATTGC 98629 CA TG_ A
 A TGCAG CCAGC C TGG GCAG
 |||| |||| | || ||||
 ACGTT GGTCG G ACC CGTC
 AC GT C _
 GAM2502 LOC91040 3' CCATCGTACAGTGGTGCTGCA 65339 G C____
 TGCAGCACCA CTG TGG
 ||||| ||| |||
 ACGTCGTGGT GAC ACC
 _ ATGCT
 GAM2502 LOC91040 5' TGCTCCAGAGCGCCTGCA 65353 CACCA G
 TGCAG GCT CTGGAGCA
 |||| ||| |||||
 ACGTC CGA GACCTCGT
 CG_ _
 GAM2503 MRPL11 3' ATCAGGCCTGAATAAACATCC 32649 CGG_
 GGA GTTCAGGCCTGAT
 ||| ||||| |||||

CCT TAAGTCCGGA
 ACAA
 GAM2503 MYOZ2 5' ATCAGGCCCAAGTGCCATCCAT 33938 CG TCA__
 ATGGA GGT GGCCTGAT
 ||||| ||| |||||
 TACCT CCG CCGGACTA
 A_ TGAAC
 GAM2503 LOC145226 3' TCAGGCCCAATCCATGCCA 77561 AC_ CA
 TGG GGGTT GGCCTGA
 ||| ||||| |||||
 ACC CCTAA CCGGACT
 GTA C_
 GAM2503 LOC146108 5' ATCAGACCCAAGGGCCCGTTCA 78146 A__ C
 TGGACGGGTTT GG CTGAT
 ||||| ||| |||||
 ACTTGCCCGGG CC GACTA
 AAC A
 GAM2504 ADD2 3' CTTTCTTCATGGAACCACT 34379 CA TTACGA
 AGT TTCC GAAGAAAG
 ||| ||||| |||||
 TCA AAGG CTTCTTTC
 CC TA____
 GAM2504 ADD2 3' CTTTCTTCATGGAACCACT 34380 CA TTACGA
 AGT TTCC GAAGAAAG
 ||| ||||| |||||
 TCA AAGG CTTCTTTC
 CC TA____
 GAM2504 BCAS2 3' GCTTTCAAAATAAGGATGACT 20798 T CGAGAA
 AGTCAT CCTTA GAAAGC
 ||||| ||||| |||||
 TCAGTA GGAAT CTTTCG
 _ AAAA_
 GAM2504 CERD4 3' TCTCAGTCATAAAGGAATGAC 24884 ____ _
 GTCATTCCTT AC GAGA
 ||||| ||| |||||
 CAGTAAGGAA TG CTCT
 ATAC A
 GAM2504 FOXF1 3' GCTTTCTTCTCGAGGTATAAC 9371 C T TA
 GT AT CCT CGAGAAGAAAGC
 || ||||| |||||
 CA TA GGA GCTCTTCTTTCG
 A T _
 GAM2504 HOXA3 3' TCTCTGTGCAAGGATGACT 48403 T _ _
 AGTCAT CCT TAC GAGA
 ||||| ||| ||| |||||
 TCAGTA GGA GTG CTCT
 _ AC T
 GAM2504 HSPA6 3' CTTTCTTCCCAGGATAACT 76822 CAT TACGA
 AGT TCCT GAAGAAAG
 ||| ||||| |||||

			TCA AGGA CTTCTTTC		
			AT_ CC__		
GAM2504	MKI67	3'	CTTTCTGTAAGGAGTGA	11595	AG
			AGTCATTCCCTTACG	AAG	
			TCAGTGAGGAATGT	TTC	
			CT		
GAM2504	RAD52	3'	CTTCCTTGCAGGAGTGA	57027	TA _
			AGTCATTCCCT	CGAG AAG	
			TCAGTGAGGA	GTTC TTC	
			C_ C		
GAM2504	RAD52	3'	CTTCCTTGCAGGAGTGA	57028	TA _
			AGTCATTCCCT	CGAG AAG	
			TCAGTGAGGA	GTTC TTC	
			C_ C		
GAM2504	RAD52	3'	CTTCCTTGCAGGAGTGA	57044	TA _
			AGTCATTCCCT	CGAG AAG	
			TCAGTGAGGA	GTTC TTC	
			C_ C		
GAM2504	TRIM9	3'	CTTCTCTCAGGGATGAC	31450	TAC
			GTCATTCCCT	GAGAAG	
			CAGTAGGGA	CTCTTC	
			CT_		
GAM2504	AP1GBP1	3'	GCTTTCTTGATCTAAGGAAGAA	24352	CA C G_
	CT		AGT TTCCTTA GA	AAGAAAGC	
			TCA AAGGAAT CT	TTCTTTTCG	
			AG _ AG		
GAM2504	AP1GBP1	3'	GCTTTCTTGATCTAAGGAAGAA	24353	CA C G_
	CT		AGT TTCCTTA GA	AAGAAAGC	
			TCA AAGGAAT CT	TTCTTTTCG	
			AG _ AG		
GAM2504	CDW92	3'	GCTTTCAGATAAATAAGGAATT	42330	C CGAGAA_
	ACT		AGT ATTCCTTA	GAAAGC	
			TCA TAAGGAAT	CTTTTCG	
			T AAATAGA		
GAM2504	DKFZP564I0422	3'	CTCTCTTTACTAAGGAATGCCT	49512	T CGA A
			AG CATTCCCTTA	GAAGA AG	
			TC GTAAGGAAT	TTTCT TC	
			C CA_ C		
GAM2504	FLJ10971	3'	CTTTCTTCTCAAGATTCATGAC	37484	TCCTTAC
	T		AGTCAT	GAGAAGAAAG	

TCAGTA CTCTTCTTTC
 CTTAGAA
 GAM2504 FLJ12389 3' GCTTCCCTCCAAGGAATGA 60900 AC AA A
 TCATTCCCTT GAG GAA GC
 ||||| ||| ||| ||
 AGTAAGGAA CTC CTT CG
 C_ C_ _
 GAM2504 FLJ20275 3' TTTCTTGTAAGGACTAAGT 35310 CAT
 AGT TCCTTACGAGAAG
 ||| |||||
 TCA AGGAATGTTCTTT
 ATC
 GAM2504 KIAA0111 3' CTTTCTTCTCATAAATGGC 29119 CCT C
 GTCATT TA GAGAAGAAAG
 ||||| || |||||
 CGGTAA AT CTCTTCTTTC
 _ A
 GAM2504 KIAA0370 5' CTTTCTCTCCAGCACTAGGAAT 73584 TAC_ A
 GACT AGTCATTCCCT GAGA GAAAG
 ||||| ||| |||||
 TCAGTAAGGA CTCT CTTTC
 TCACGAC _
 GAM2504 KIAA0420 3' CTTTCGTGTAAGGAAGAC 64089 A A
 GTC TTCCTTACG GAAG
 ||| ||||| |||
 CAG AAGGAATGT CTTC
 _ G
 GAM2504 KIAA1877 3' TTTCTTGAGCAAGAATGGCT 66768 CTTA_
 AGTCATTG CGAGAAG
 ||||| |||||
 TCGGTAAG GTTCTTT
 AACGA
 GAM2504 SRCRB4D 3' CCTCCTCTTGTGATGACT 55794 CCTT A AA
 AGTCATT ACGAGA GA G
 ||||| ||||| |||
 TCAGTAG TGTCTCT CT C
 _ C CC
 GAM2504 UBXD2 3' CTTTCCCCTAAATTGGAATGAT 68894 TTACG AA
 GTCATTCC AG GAAAG
 ||||| || |||||
 TAGTAAGG TC CTTTC
 TTAAA CC
 GAM2504 ZID 3' CTTTTCGTAAAGAAGACT 22783 A C
 AGTC TTC TTACGAGAAG
 ||| ||| |||||
 TCAG AAG AATGCTTTTC
 _ A
 GAM2504 LOC145678 5' CTCCTCTGTTGTGGAATGAT 84433 TT_ A
 GTCATTCC AC GAG AG
 ||||| || ||| ||

				TAGTAAGG	TG CTC TC			
				TGT T C				
GAM2504	LOC152084	5'	GCTTTCCTCAGCCTGGGATGAC	86739			TTAC_	AA
			GTCATTCC GAG GAAAGC					
			CAGTAGGG CTC CTTTCG					
			TCCGA _					
GAM2504	LOC257354	3'	CTTCGTGTAAGGAAGAC	96791	A A			
			GTC TTCCTTACG GAAG					
			CAG AAGGAATGT CTTC					
			_ G					
GAM2505	GORASP1	3'	CTCCTGTTAGCTCCCCAAACTT	49953		ACGA AG		
			AAGT GA TAACAGGAG					
			TTCA CT ATTGTCCTC					
			AACC CG					
GAM2505	KCNQ4	3'	CTCCGGACTCCTCTCGTACTTG	17477		_ AACAA		
			CAAGTACGAGA AGT GGAG					
			GTTCATGCTCT TCA CCTC					
			CC GG_					
GAM2505	FLJ23191	5'	CTCCAGGCTTCTCGTTCCTGGA	45008		AGT AACAA		
			TCCA ACGAGAAAGT GGAG					
			AGGT TGCTCTTCG CCTC					
			CCT GA_					
GAM2505	U5-116KD	3'	CTGCAACTCCTGTACTTG	16184		G A AA		
			CAAGTAC AG AGT CAG					
			GTTCATG TC TCA GTC					
			_ C AC					
GAM2505	LOC200310	3'	CTCCTGCATGGCCTCGTACTGG	66326		A AAGTAA		
	A		TCCA GTACGAG CAGGAG					
			AGGT CATGCTC GTCCTC					
			_ CGGTAC					
GAM2505	LOC253264	3'	CCTGTTACTGTGATTTGGA	96336		ACGAGA		
			TCCAAGT AGTAACAGG					
			AGGTTTA TCATTGTCC					
			GTG_					
GAM2505	LOC51193	5'	TCCTGTTACCCAGGCTGGA	33373		A ACGAGAA		
			TCCA GT GTAACAGGA					
			AGGT CG CATTGTCCT					
			_ GACC_					
GAM2506	ELF3	3'	TGACCTTGACCTTGACCAA	16685		T GAT AAA		
			TTGGT CAAGG GG GTCA					

			AACCA GTTCC TC CAGT		
			AGT		
GAM2506	JAK2	3'	TGACCTTCATTCTGAGACCAA 18318	CAA	AA
			TTGGTT GGGATGGA GTCA		
			AACCAG TCTTACTT CAGT		
			AG_ C_		
GAM2506	SLC10A2	5'	ACTCTCTGTCTTGACCAA 6590	CAA	A
			TTGGTT GGGATGGA AGT		
			AACCAG TTCTGTCT TCA		
			C		
GAM2506	FLJ10803	3'	GTGACTTTCAGTTAAAGCCAA 37205	CAAGG	G
			TTGGTT GAT GAAAGTCAC		
			AACCGA TTG CTTTCAGTG		
			AA_ A		
GAM2506	KIAA1958	5'	GTGACTTTGAACCCCAAACC 82788	CAA	ATGG
			GGTT GGG AAAGTCAC		
			CCAA CCC TTTTCAGTG		
			A_ CAAG		
GAM2506	MARCKS	3'	ACTTTCCACCCTGCCCA 11411	TTCA	A
			TGG AGGG TGGAAAGT		
			ACC TCCC ACCTTTCA		
			CG_ _		
GAM2506	TUB	5'	GTGGGACCATCCCTTAAACC 13898	C	AAAG
			GGTT AAGGGATGG TCAC		
			CCAA TTCCCTACC GGTG		
			A AG_		
GAM2506	LOC80298	3'	ACTTTTACCTTGAACCA 48062	GATG	
			TGGTTCAAGG GAAAGT		
			ACCAAGTTCC TTTTCA		
			A_		
GAM2507	ACT	5'	CCACAATCCAGGGGGGCCAT 40420	CCG	AAC
			ATGGCCCCT GGA TGTGG		
			TACCGGGGG CCT ACACC		
			A_ A_		
GAM2507	ADAM11	3'	GCCACAGCTCAACTCGGGGGC 41490	TC	AAA_
			GCCCC CGGG CTGTGGC		
			CGGGG GCTC GACACCG		
			_ AACTC		
GAM2507	ADAM11	3'	GCCACAGCTCAACTCGGGGGC 11487	TC	AAA_
			GCCCC CGGG CTGTGGC		

			CGGGG GCTC GACACCG		
			___ AACTC		
GAM2507 CDC34	3'	GCCGCACCCCGGAGGAGCCA	16390	C	AAAC
		TGGC CCTCCGGG TGTGGC			
		ACCG GGAGGCCC ACGCCG			
		A C___			
GAM2507 CRI1	3'	GCCACAGTTATCAAAGGCTA	27537	CCTCCG	A
		TGGCC GG AACTGTGGC			
		ATCGG CT TTGACACCG			
		AAA___ A			
GAM2507 FLII	3'	GCCACAGTCCCCAGTAGCC	10656	CC CC	AA
		GGC CT GGG ACTGTGGC			
		CCG GA CCC TGACACCG			
		AT __ C_			
GAM2507 FZD10	3'	GCCCACCCCCAGGAAGGCCA	24214	CC _	AAAC T
		TGGCC TCC GGG TG GGC			
		ACCGG AGG CCC AC CCG			
		A_ A CC__ _			
GAM2507 GNA11	5'	CCACAGCCCCGGGGGCCG	76585	TC	AAA
		TGGCCCC CGGG CTGTGG			
		GCCGGGG GCCC GACACC			
		___ C___			
GAM2507 IGHMBP2	3'	GCCACAGAGGAGCGGAGGGGCC	10984		GGAAA
		GGCCCCCTCCG CTGTGGC			
		CCGGGGAGGC GACACCG			
		GAGGA			
GAM2507 MAGEA3	5'	CCAGAGGCCCCCGGAGGAGC	19315	C	AAA G
		GC CCTCCGGG CT TGG			
		CG GGAGGCCC GA ACC			
		A CCG G			
GAM2507 PYGB	3'	CCAGGGGTCCCGGAGGAACC	12687	CC	AA G
		GG CCTCCGGGA CT TGG			
		CC GGAGGCCCT GG ACC			
		AA G_ G			
GAM2507 PYGB	3'	CCATGTTTCCAGGAGGGGCCAT	12689	G	T
		ATGGCCCCTCC GGAAAC GTGG			
		TACCGGGGAGG CCTTTG TACC			
		A _			
GAM2507 SLC6A6	3'	GCCACAGTCCTTCCTGGGGC	13183	TCC	___
		GCCCC GGGAA ACTGTGGC			

			CGGGG TCCTT TGACACCG		
			___ CC		
GAM2507	UBTF	3'	CCATTCCTTCCCAGAGGGGCC 27252	C	ACT
			GGCCCCTC GGGAA GTGG		
			CCGGGGAG CCCTT TACC		
			A CCT		
GAM2507	CBCIP2	3'	GCCACACGGA CT CAGAGGGGCC 52658	C	AAAC
	A		TGGCCCCTC GGG TGTGGC		
			ACCGGGGAG CTC ACACCG		
			A AGGC		
GAM2507	FEM-2	3'	GCCACAGTCCCATGAGGGGCC 28316	C C_	AA
			GGCCC TC GGA CTGTGGC		
			CCGGG AG CCCT GACACCG		
			_ TA _		
GAM2507	FLJ10199	3'	GCCACAGTTGAGAAGCGGAGGG 71755	GGA_	
	GCCA		TGGCCCCTCCG AACTGTGGC		
			ACCGGGGAGGC TTGACACCG		
			GAAGAG		
GAM2507	FLJ11715	3'	ACAGTGTCCCCAGGAGGCCAT 44972	_ CC	A
			ATGGCC CCT GGA ACTGT		
			TACCGG GGA CCCT TGACA		
			A C_ G		
GAM2507	FLJ12505	5'	CCCGGTCCCGGAGCAGCCA 45713	CC	AA T
			TGGC CTCCGGGA CTG GG		
			ACCG GAGGCCCT GGC CC		
			AC _ _		
GAM2507	KIAA0828	3'	GTTTCCCAGGAAGGCCAT 82119	CC _	
			ATGGCC TCC GGAAAC		
			TACCGG AGG CCCTTTG		
			A_ A		
GAM2507	KIAA1190	3'	CCACAGTTCTGGGAGCC 71643	CCC G	A
			GGC TCC GGAA CTGTGG		
			CCG AGG TCTT GACACC		
			_ G _		
GAM2507	KIAA1297	5'	CCATGCCCAGAAGGCCA 72634	CC C	AAAC
			TGGCC TC GGG TGTGG		
			ACCGG AG CCC GTACC		
			A_ A _		
GAM2507	PASK	5'	GCCACAGAGTTGGGGGGCCAT 31415	T	GAAA
			ATGGCCCC CCGG CTGTGGC		

			TACCGGGG GGTT GACACCG		
			GA__		
GAM2507	PCDH17	3'	GCCACAGTTCCTGCAGCCA 27836	CCCTC	A
			TGGC CGGG AACTGTGGC		
			ACCG GTCC TTGACACCG		
			AC__ C		
GAM2507	RIL	3'	CCATGCTGCCCTGAAGGGGCCA 14885	C	AACT
			TGGCCCT CGGG GTGG		
			ACCGGGGA GTCC TACC		
			A CGTCG		
GAM2507	SREC	3'	GCAGTGCTCCCGGAGGGGCC 14905	A_	
			GGCCCTCCGGGA ACTGT		
			CCGGGGAGGCCCT TGACG		
			CG		
GAM2507	TRAF2	3'	GCCGGCTCACGGAGGGGCCA 41236	G	AACTG
			TGGCCCTCCG GA TGGC		
			ACCGGGGAGGC CT GCCG		
			A CG__		
GAM2507	LOC123242	5'	CCACAGCCCACCTGGAGGCCA 76111	CC	AAA_
			TGGCC TCCGGG CTGTGG		
			ACCGG AGGTCC GACACC		
			__ ACCC		
GAM2507	LOC124460	5'	CCAAGAGCTCGAAGGGGCCAT 76559	C	AAA G
			ATGGCCCT CGGG CT TGG		
			TACCGGGGA GCTC GA ACC		
			A GA_ _		
GAM2507	LOC132166	3'	GCCAGCGCCCGAGGGGGCCA 75537	TC	AACTG
			TGGCCC CGGG TGGC		
			ACCGGGG GCCC ACCG		
			GA GCG__		
GAM2507	LOC146958	5'	GCCACAGTCTCAAGTGGACAT 84944	G C CC	AA
			ATG CC CT GGGA CTGTGGC		
			TAC GG GA CTCT GACACCG		
			A T A_ _		
GAM2507	LOC149420	3'	GCCACAGTTTCCTAAGCGC 80155	CC CC	
			GC CT GGGAACTGTGGC		
			CG GA TCCTTTGACACCG		
			C_ A_		
GAM2507	LOC152317	3'	GCCACAGTCTGGGAGAGCCA 86831	CC	G AA
			TGGC CTCC GGA CTGTGGC		

	ACCG GAGG TCT GACACCG	
	A_ G _	
GAM2507 LOC157450 3'	CCACAGCTTCCCGGGTCAT 71531	CTCC A
	ATGGCCC GGGAA CTGTGG	
	TACTGGG CCCTT GACACC	
	_____ C	
GAM2507 LOC157807 5'	GCCACAGTTTCAGCAGACCAT 82513	CCC CCGG
	ATGG CT GAAACTGTGGC	
	TACC GA CTTTGACACCG	
	A_ CGA_	
GAM2507 LOC157923 5'	GCCACAGTCCAGAGAAGGCCA 82526	C_ C GAA
	TGGCC CTC GG ACTGTGGC	
	ACCGG GAG CC TGACACCG	
	AA A _	
GAM2507 LOC158510 5'	CCAGAGGCCCCCGGAGGAGC 82833	C AAA G
	GC CCTCCGGG CT TGG	
	CG GGAGGCC GA ACC	
	A CCG G	
GAM2507 LOC196860 3'	CCACAGTTCCCGGAAAGTGCT 91214	CCC_ A
	GGC TCCGGG AACTGTGG	
	TCG AGGCCC TTGACACC	
	TGAA C	
GAM2507 LOC203235 5'	GCCAGGGCCCCCAGAGGGGCC 92099	C AAA G
	GGCCCTC GGG CT TGGC	
	CCGGGGAG CCC GG ACCG	
	A CC_ G	
GAM2507 LOC220739 3'	GCCACAGTAGGAGGGGCCA 94521	GGGAA
	TGGCCCTCC ACTGTGGC	
	ACCGGGGAGG TGACACCG	
	A_____	
GAM2507 LOC222166 5'	CCCGGCCCCCGGAGGAGCC 95733	C AAA T
	GGC CCTCCGGG CTG GG	
	CCG GGAGGCC GGC CC	
	A C_ _	
GAM2507 LOC253001 5'	CCACAGCCCACCTGGAGGCCA 97990	CC AAA_
	TGGCC TCCGGG CTGTGG	
	ACCGG AGGTCC GACACC	
	_ ACCC	
GAM2507 LOC254057 3'	GCCCCTATCCCAGAGGGGCC 98782	C AACTGT
	GGCCCTC GGGA GGC	

		CCGGGGAG CCCT CCG	
		A ATCC__	
GAM2507	LOC92558 3'	GCCACCTCCCAGAGGGGCC 70312	C AACT
		GGCCCCTC GGGA GTGGC	
		CCGGGGAG CCCT CACCG	
		A C__	
GAM2507	LOC93626 5'	CCACAGCCCCGGGGGCCG 73128	TC AAA
		TGGCCCC CGGG CTGTGG	
		GCCGGGG GCCC GACACC	
		__ C__	
GAM2508	ACT 5'	CCACAATCCAGGGGGCCAT 40420	CCG AAC
		ATGGCCCCT GGA TGTGG	
		TACCGGGGG CCT ACACC	
		A__ A__	
GAM2508	ADAM11 3'	GCCACAGCTCAACTCGGGGGC 41490	TC AAA__
		GCCCC CGGG CTGTGGC	
		CGGGG GCTC GACACCG	
		__ AACTC	
GAM2508	ADAM11 3'	GCCACAGCTCAACTCGGGGGC 11487	TC AAA__
		GCCCC CGGG CTGTGGC	
		CGGGG GCTC GACACCG	
		__ AACTC	
GAM2508	CDC34 3'	GCCGCACCCCGGAGGAGCCA 16390	C AAAC
		TGGC CCTCCGGG TGTGGC	
		ACCG GGAGGCCC ACGCCG	
		A C__	
GAM2508	CRI1 3'	GCCACAGTTATCAAAGGCTA 27537	CCTCCG A
		TGGCC GG AACTGTGGC	
		ATCGG CT TTGACACCG	
		AAA__ A	
GAM2508	FLII 3'	GCCACAGTCCCCAGTAGCC 10656	CC CC AA
		GGC CT GGG ACTGTGGC	
		CCG GA CCC TGACACCG	
		AT __ C__	
GAM2508	FZD10 3'	GCCCACCCCCAGGAAGGCCA 24214	CC _ AAAC T
		TGGCC TCC GGG TG GGC	
		ACCGG AGG CCC AC CCG	
		A_ A CC__ _	
GAM2508	GNA11 5'	CCACAGCCCCGGGGGCCG 76585	TC AAA
		TGGCCCC CGGG CTGTGG	

GCCGGGG GCCC GACACC
 — C—
 GAM2508 IGHMBP2 3' GCCACAGAGGAGCGGAGGGGCC 10984 GGAAA
 GGCCCCTCCG CTGTGGC
 ||||| |||||
 CCGGGGAGGC GACACCG
 GAGGA
 GAM2508 MAGEA3 5' CCAGAGGCCCGGAGGAGC 19315 C AAA G
 GC CCTCCGGG CT TGG
 || ||||| |||||
 CG GGAGGCCC GA ACC
 A CCG G
 GAM2508 PYGB 3' CCAGGGGTCCCGGAGGAACC 12687 CC AA G
 GG CCTCCGGGA CT TGG
 || ||||| |||||
 CC GGAGGCCCT GG ACC
 AA G_ G
 GAM2508 PYGB 3' CCATGTTTCCAGGAGGGGCCAT 12689 G T
 ATGGCCCCTCC GGAAAC GTGG
 ||||| ||||| |||||
 TACCGGGGAGG CCTTTG TACC
 A —
 GAM2508 SLC6A6 3' GCCACAGTCCTTCCTGGGGC 13183 TCC —
 GCCCC GGGAA ACTGTGGC
 |||| |||| |||||
 CGGGG TCCTT TGACACCG
 — CC
 GAM2508 UBTF 3' CCATTCTTCCCAGAGGGGCC 27252 C ACT
 GGCCCCTC GGGAA GTGG
 ||||| ||||| |||||
 CCGGGGAG CCCTT TACC
 A CCT
 GAM2508 CBCIP2 3' GCCACACGGA CTGAGGGGCC 52658 C AAAC
 A TGGCCCCTC GGG TGTGGC
 ||||| ||||| |||||
 ACCGGGGAG CTC ACACCG
 A AGGC
 GAM2508 FEM-2 3' GCCACAGTCCCATGAGGGCC 28316 C C_ AA
 GGCCC TC GGGA CTGTGGC
 |||| || |||| |||||
 CCGGG AG CCCT GACACCG
 — TA —
 GAM2508 FLJ10199 3' GCCACAGTTGAGAAGCGGAGGG 71755 GGA—
 GCCA TGGCCCCTCCG AACTGTGGC
 ||||| ||||| |||||
 ACCGGGGAGGC TTGACACCG
 GAAGAG
 GAM2508 FLJ11715 3' ACAGTGTCCCAGGAGGCCAT 44972 — CC A
 ATGGCC CCT GGGA ACTGT
 ||||| ||||| ||||| |||||

		TACCGG GGA CCCT TGACA		
		A C_ G		
GAM2508	FLJ12505	5' CCCGGTCCCGGAGCAGCCA	45713	CC AA T
		TGGC CTCCGGGA CTG GG		
		ACCG GAGGCCCT GGC CC		
		AC _ _		
GAM2508	KIAA0828	3' GTTTCCAGGAAGGCCAT	82119	CC _
		ATGGCC TCC GGGAAAC		
		TACCGG AGG CCCTTTG		
		A_ A		
GAM2508	KIAA1190	3' CCACAGTTCTGGGAGCC	71643	CCC G A
		GGC TCC GGAA CTGTGG		
		CCG AGG TCTT GACACC		
		_ G _		
GAM2508	KIAA1297	5' CCATGCCCAGAAGGCCA	72634	CC C AAAC
		TGGCC TC GGG TGTGG		
		ACCGG AG CCC GTACC		
		A_ A _		
GAM2508	PASK	5' GCCACAGAGTTGGGGGGCCAT	31415	T GAAA
		ATGGCCCC CCGG CTGTGGC		
		TACCGGGG GGTT GACACCG		
		_ GA_		
GAM2508	PCDH17	3' GCCACAGTTCCCTGCAGCCA	27836	CCCTC A
		TGGC CGGG AACTGTGGC		
		ACCG GTCC TTGACACCG		
		AC_ C		
GAM2508	RIL	3' CCATGCTGCCCTGAAGGGGCCA	14885	C AAAC
		TGGCCCCT CGGG GTGG		
		ACCGGGGA GTCC TACC		
		A CGTCG		
GAM2508	SREC	3' GCAGTGCTCCCGGAGGGGCC	14905	A_
		GGCCCCTCCGGGA ACTGT		
		CCGGGGAGGCCCT TGACG		
		CG		
GAM2508	TRAF2	3' GCCGGCTCACGGAGGGGCCA	41236	G AACTG
		TGGCCCCTCCG GA TGGC		
		ACCGGGGAGGC CT GCCG		
		A CG_		
GAM2508	LOC123242	5' CCACAGCCCACCTGGAGGCCA	76111	CC AAA_
		TGGCC TCCGGG CTGTGG		

	ACCGG AGGTCC GACACC	
	___ ACCC	
GAM2508 LOC124460 5'	CCAAGAGCTCGAAGGGGCCAT 76559	C AAA G
	ATGGCCCCT CGGG CT TGG	
	TACCGGGGA GCTC GA ACC	
	A GA_ _	
GAM2508 LOC132166 3'	GCCACGCCCCGAGGGGGCCA 75537	TC AA ACTG
	TGGCCCC CGGG TGGC	
	ACCGGGG GCCC ACCG	
	GA GCG_ _	
GAM2508 LOC146958 5'	GCCACAGTCTCAAGTGGACAT 84944	G C CC AA
	ATG CC CT GGGA CTGTGGC	
	TAC GG GA CTCT GACACCG	
	A T A_ _	
GAM2508 LOC149420 3'	GCCACAGTTTCCTAAGCGC 80155	CC CC
	GC CT GGGAAACTGTGGC	
	CG GA TCCTTTGACACCG	
	C_ A_	
GAM2508 LOC152317 3'	GCCACAGTCTGGGAGAGCCA 86831	CC G AA
	TGGC CTCC GGA CTGTGGC	
	ACCG GAGG TCT GACACCG	
	A_ G _	
GAM2508 LOC157450 3'	CCACAGCTTCCCGGGTCAT 71531	CTCC A
	ATGGCCC GGGAA CTGTGG	
	TACTGGG CCCTT GACACC	
	___ C	
GAM2508 LOC157807 5'	GCCACAGTTTCAGCAGACCAT 82513	CCC CCGG
	ATGG CT GAAACTGTGGC	
	TACC GA CTTTGACACCG	
	A_ CGA_	
GAM2508 LOC157923 5'	GCCACAGTCCAGAGAAGGCCA 82526	C_ C GAA
	TGGCC CTC GG ACTGTGGC	
	ACCGG GAG CC TGACACCG	
	AA A _	
GAM2508 LOC158510 5'	CCAGAGGCCCCCGGAGGAGC 82833	C AAA G
	GC CCTCCGGG CT TGG	
	CG GGAGGCCC GA ACC	
	A CCG G	
GAM2508 LOC196860 3'	CCACAGTTCCCGGAAAGTGCT 91214	CCC_ A
	GGC TCCGGG AACTGTGG	

		TCG AGGCCC TTGACACC		
		TGAA C		
GAM2508	LOC203235 5'	GCCAGGGCCCCCAGAGGGGCC 92099	C AAA G	
		GGCCCCTC GGG CT TGGC		
		CCGGGGAG CCC GG ACCG		
		A CC_ G		
GAM2508	LOC220739 3'	GCCACAGTAGGAGGGGCCA 94521	GGGAA	
		TGGCCCCTCC ACTGTGGC		
		ACCGGGGAGG TGACACCG		
		A ____		
GAM2508	LOC222166 5'	CCCGGCCCCGAGGAGCC 95733	C AAA T	
		GGC CCTCCGGG CTG GG		
		CCG GGAGGCCC GGC CC		
		A C_ _		
GAM2508	LOC253001 5'	CCACAGCCCACCTGGAGGCCA 97990	CC AAA_	
		TGGCC TCCGGG CTGTGG		
		ACCGG AGGTCC GACACC		
		_ ACCC		
GAM2508	LOC254057 3'	GCCCCTATCCCAGAGGGGCC 98782	C AACTGT	
		GGCCCCTC GGGA GGC		
		CCGGGGAG CCCT CCG		
		A ATCC_		
GAM2508	LOC92558 3'	GCCACCTCCCAGAGGGGCC 70312	C AACT	
		GGCCCCTC GGGA GTGGC		
		CCGGGGAG CCCT CACCG		
		A C_		
GAM2508	LOC93626 5'	CCACAGCCCCGGGGGCCG 73128	TC AAA	
		TGGCCCC CGGG CTGTGG		
		GCCGGGG GCCC GACACC		
		_ C_		
GAM2509	BAI2 3'	GCCCCTCAGCCACTGGAA 9914 A	A TTCT	
		TTC CAGTGGCT AG GC		
		AAG GTCACCGA TC CG		
		_ C CC_		
GAM2509	BTG2 3'	GCAAGGTTAGCAACTGTGAA 23147	G G C	
		TTCACAGT GCTAA TT TGC		
		AAGTGTCA CGATT GA ACG		
		A G _		
GAM2509	CABC1 3'	GTGCAAAACCCAGAAACATGAA 40043	CA GG AA C	
		TTCA GT CT GTT TGCAC		

AAGT CA GA CAA ACGTG
 A_ AA CC A
 GAM2509 CYP8B1 3' TGCAGAACTTGGCATCTG 16544 TG
 CAG GCTAAGTTCTGCA
 ||| |||||
 GTC CGGTTCAAGACGT
 TA
 GAM2509 DSCR3 3' GCAAAGTGCTAGCCACTGGAA 21316 A A TC__
 TTC CAGTGGCTA GT TGC
 ||| ||||| || |||
 AAG GTCACCGAT CG ACG
 _ _ TGAA
 GAM2509 FADD 3' GTAGCCCAGCACTGTGAA 15125 G AAGTT
 TTCACAGTG CT CTGC
 ||||| || |||
 AAGTGTAC GA GATG
 _ CCC__
 GAM2509 GBA 3' TGCAGAACTGGGCCCCTGGA 76824 AGT A
 TTCAC GGCT AGTTCTGCA
 |||| ||| |||||
 AGGTG CCGG TCAAGACGT
 C_ G
 GAM2509 GEMIN5 5' GGTGCTACTTAGCCACTGGAA 90645 A TCT _
 TTC CAGTGGCTAAGT GCA CC
 ||| ||||| ||| ||
 AAG GTCACCGATTCA CGT GG
 _ T_ T
 GAM2509 NOS1 3' GTGCATGAAACCACTGGAA 7098 A CTAAG _
 TTC CAGTGG TTC TGCAC
 ||| |||| ||| ||||
 AAG GTCACC AAG ACGTG
 _ A_ T
 GAM2509 SORBS1 3' GCACAAAAATAGCCATTGT 31806 AG_ C
 ACAGTGGCTA TT TGC
 ||||| || |||
 TGTTACCGAT AA ACG
 AAA C
 GAM2509 SORD 3' TGCAGAACTTTCTCTTTTGAA 13302 C T CT
 TTCA AG GG AAGTTCTGCA
 ||| || ||| |||||
 AAGT TT TC TTCAAGACGT
 T C T_
 GAM2509 CABIN1 3' GCCGCCTTAGCCATGTGAA 25454 G TTCT
 TTCACA TGGCTAAG GC
 |||| ||||| ||
 AAGTGT ACCGATTC CG
 _ CGCC
 GAM2509 DKFZP564D172 3' GATGTGGCCAACACTGTGAA 50197 _ AGT
 TTCACAGT GGCTA TC
 ||||| |||| ||

		AAGTGTCA CCGGT AG	
		CAA GT_	
GAM2509 EFS2	5'	GGTGC GGGGCAGCCACCGCTGA 20778	CA_ AA
	A	TTCA GTGGCT GTTCTGCACC	
		AAGT CACCGA CGGGGCGTGG	
		CGC _	
GAM2509 FLJ12586	3'	TGCTTCTAATTCAGCCACTGTG 45215	A CT_
	AA	TTCACAGTGGCT AGTT GCA	
		AAGTGT CACCGA TTAA CGT	
		C TCTT	
GAM2509 FLJ12800	3'	TGCAGAAGCAGAGCCACTGTGA 90404	AA _
	A	TTCACAGTGGCT GTT CTGCA	
		AAGTGT CACCGA CGA GACGT	
		GA A	
GAM2509 FLJ12934	3'	GCACTTACAAGCACTGTGAA 43491	G AA TC_
		TTCACAGTG CT GT TGC	
		AAGTGT CAC GA CA ACG	
		_ A_ TTC	
GAM2509 FLJ14621	3'	GCACACCACACTGGCCACTGT 52537	A TC_____
		ACAGTGGCTA GT TGC	
		TGTCACCGGT CA ACG	
		_ CACCAC	
GAM2509 KIAA0450	5'	GGCTTCCCAGCCACTGTGA 28366	_____
		TCACAGTGGCT AAGTT	
		AGTGT CACCGA TTCGG	
		CCC	
GAM2509 MGC12458	3'	GGTGCAGAACGAACCACTCGAA 51303	AC CTAA
		TTC AGTGG GTTCTGCACC	
		AAG TCACC CAAGACGTGG	
		C_ AAG_	
GAM2509 MGC14801	3'	TGCGGAGCCCAGCACTGTGAA 52085	G AA
		TTCACAGTG CT GTTCTGCA	
		AAGTGT CAC GA CGAGGCGT	
		_ CC	
GAM2509 MGC35558	3'	CAGAAACACCGACTGTGAA 59408	_ CTAAG
		TTCACAGT GG TTCTG	
		AAGTGT CA CC AAGAC	
		G ACA_	
GAM2509 RAD51	3'	TGCAGAACTTAATCTGGA 56835	A TGGC
		TC CAG TAAGTTCTGCA	

		AG GTC ATTCAAGACGT	
		— TA__	
GAM2509	LOC116166 3'	TGCAGAACTTTCTCTTTTGAA 60471	C T CT
		TTCA AG GG AAGTTCTGCA	
		AAGT TT TC TTCAAGACGT	
		T C T_	
GAM2509	LOC144970 5'	GGTGCTGCACTTGACCACTGTG 77531	C TCT _
	AA	TTCACAGTGG TAAGT GCA CC	
		AAGTGTCAACC GTTCA CGT GG	
		A CGT T	
GAM2509	LOC149319 5'	GTGGAGGCTCAGCCACTGTGAG 80076	A T G
		TTCACAGTGGCT AGT CT CAC	
		GAGTGTCAACCGA TCG GA GTG	
		C _ G	
GAM2509	LOC149320 3'	GGGCACAGAAGTCACTGTGAA 71231	AAGTTC A
		TTCACAGTGGCT TGC CC	
		AAGTGTCACTGA ACG GG	
		AGAC__	
GAM2510	ACADM 3'	GGAAAGCATTTGTGAACTTTC 5234	C CGC
	T	AGGAAGTT CGCG GCTTTCC	
		TCTTTCAA GTGT CGAAAGG	
		A TTA	
GAM2510	HNRPD 3'	GAAAACAGCGGGAAGTTC 19600	G GCGC
		GAAGTTCC CGC TTTC	
		CTTCAAGG GCG AAAG	
		_ ACA_	
GAM2510	NUDT1 5'	AAAGCGCGCGCGGGGATTCC 11712	G
		GGAA TTCCGCGCGCGCTTT	
		CCTT GGGGCGCGCGGAAA	
		A	
GAM2510	OSBP 5'	GGAAAGCACCAATGAGCTTCC 11916	CGCGCGC
		GGAAGTTC GCTTTCC	
		CCTTCGAG CGAAAGG	
		TAACCA_	
GAM2510	RGS16 5'	GGCGCACGCGGAGCCTCCT 12870	A C
		AGGA GTTCCGCG GCGCT	
		TCCT CGAGGCGC CGCGG	
		C A	
GAM2510	TBX6 3'	GGCAACACGAGCAAACTTCCT 55814	CC G C__
		AGGAAGTT GC CG GCT	

		TCCTTCAA CG GC CGG		
		AA A ACAA		
GAM2510	TIMM17A	3' AAAGCTGGTGGAACTTACT	22015	G G C
		AG AAGTTCCGC CG GCTTT		
		TC TTCAAGGTG GT CGAAA		
		A _ _		
GAM2510	TNFRSF6B	3' GGAAAGTGCTTCCCCAGAACTT	32235	CGCGC__
	CC	GGAAGTTC GCGCTTTCC		
		CCTTCAAG CGTGAAAGG		
		ACCCCTT		
GAM2510	TNFRSF6B	3' GGAAAGTGCTTCCCCAGAACTT	33597	CGCGC__
	CC	GGAAGTTC GCGCTTTCC		
		CCTTCAAG CGTGAAAGG		
		ACCCCTT		
GAM2510	TRIM8	3' GGATTTTGACACAGCAACTTCC	48856	CC GCG__ CTT
	T	AGGAAGTT GC CG TCC		
		TCCTTCAA CG GT AGG		
		_ ACACA TTT		
GAM2510	COLEC12	5' GGCGCTCGCGCGGAGCTCCC	48613	A _
		GG AGTTCCGCGC GCGCT		
		CC TCGAGGCGCG CGCGG		
		C CT		
GAM2510	COLEC12	5' GGCGCTCGCGCGGAGCTCCC	56105	A _
		GG AGTTCCGCGC GCGCT		
		CC TCGAGGCGCG CGCGG		
		C CT		
GAM2510	DKFZP566H073	5' GGAGGGCGCAGAACTCC	32032	A CGCGC
		GGA GTTC GCGCTTTCC		
		CCT CAAG CGCGGGAGG		
		_ A__		
GAM2510	FLJ14346	5' AGAGTCAGACGCGGAACTCCC	47355	A CGC_
		GG AGTTCCGCG GCTTT		
		CC TCAAGGCGC TGAGA		
		C AGAC		
GAM2510	KIAA0493	5' AAAGTGCAAACAGAACTTCC	64922	CGCGC
		GGAAGTTC GCGCTTT		
		CCTTCAAG CGTGAAA		
		ACAAA		
GAM2510	KIAA1024	3' GAAATGCAACAACTTCCT	69616	CCGCGC C
		AGGAAGTT GCG TTTC		

		TCCTTCAA	CGT AAAG		
		ACAA__ _			
GAM2510	KIAA1045	3'	GAAAGCGCAGGACTCCT	71604	A CGCGC
			AGGA GTTC	GCGCTTTC	
			TCCT CAGG	CGCGAAAG	
			_ A__		
GAM2510	LAP1B	5'	GAAAGCGCGTACTACCT	65194	A TCCGC
			AGG AGT	GCGCGCTTTC	
			TCC TCA	TGCGCGAAAG	
			A ____		
GAM2510	LCHN	3'	GGAAAGCAAAATGAATTCCT	87474	CGCGCGC
			AGGAAGTTC	GCTTTCC	
			TCCTTTAAG	CGAAAGG	
			TAAAA__		
GAM2510	PTPNS1	3'	GGAAGTGGCCAGAACTTCCT	55842	CGC G
			AGGAAGTTC	GC CGCTTTC	
			TCCTTCAAG	CG GTGAAGG	
			AC_ _		
GAM2510	SNIP1	3'	GGAAAGCAGGGGAATTTCC	45537	GCGCGC
			GGAAGTTCC	GCTTTCC	
			CCTTTAAGG	CGAAAGG	
			GGA__		
GAM2510	TDPGD	5'	AAGGTCGCGGCGGAACTTCC	60445	G _
			GGAAGTTCCGC	CGCG CTTT	
			CCTTCAAGGCG	GCGC GGAA	
			_ T		
GAM2510	LOC149134	5'	GAAAGCGCTGGTAAAGTTCCT	85520	G __ CGC
			AGGAA TT CCG	GCGCTTTC	
			TCCTT AA GGT	CGCGAAAG	
			G AT ____		
GAM2510	LOC150113	5'	GGAAAGCGCAGCTCTGAGCCCC	88567	AA C__ GC
	C		GG GTTC	GC GCGCTTTCC	
			CC CGAG	CG CGCGAAAGG	
			CC TCT A_		
GAM2510	LOC158450	5'	GGAAAACCAAAAGCAGAGCTTC	82815	C GCGCGC_
	C		GGAAGTTC GC	TTTCC	
			CCTTCGAG CG	AAAGG	
			A AAAACCA		
GAM2510	LOC158504	5'	GGAAAACCAAAAGCAGAGCTTC	82829	C GCGCGC_
	C		GGAAGTTC GC	TTTCC	

CCTTCGAG CG AAAGG
 A AAAACCA
 GAM2510 LOC219920 3' GAAAGCACTGCAAAACTTTCT 94952 CC CGC
 AGGAAGTT GCG GCTTTC
 ||||| || |||||
 TCTTTCAA CGT CGAAAG
 AA CA_
 GAM2511 DEDD 3' TACAGCTACCTTACCACTG 53380 A C A
 CA TG TAA GTAGCTGTG
 || || || |||||
 GT AC ATT CATCGACAT
 C C C
 GAM2511 ENAM 3' CCTAGCACAGTGTCTTCAACAT 49927 CTA TA
 ATG AAG GCTGTGCTAGG
 || || |||||
 TAC TTC TGACACGATCC
 AAC TG
 GAM2511 MAP3K14 3' CCAGAGCACAGCTCAGCATCA 15544 A AAAGT A_
 C ATGCT AGCTGTGCT GG
 | |||| ||||| ||
 A TACGA TCGACACGA CC
 C C___ GA
 GAM2511 MYH11 3' CCCAGCAGACTGTACTTAGCAT 43430 A GCTG_ A
 TG CAATGCTAA GTA TGCT GG
 ||||| || || ||
 GTTACGATT CAT ACGA CC
 _ GTCAG C
 GAM2511 MYH11 3' CCCAGCAGACTGTACTTAGCAT 11739 A GCTG_ A
 TG CAATGCTAA GTA TGCT GG
 ||||| || || ||
 GTTACGATT CAT ACGA CC
 _ GTCAG C
 GAM2511 USP11 5' CCCAGCACGTGCTTGGCATT 17384 AAGT _ A
 AATGCTA AGC TGTGCT GG
 ||||| || ||||| ||
 TTACGGT TCG GCACGA CC
 ___ T C
 GAM2511 FLJ20086 3' CCTAGCACAACAGAGGCA 35012 AAA AGC
 TGCT GT TGTGCTAGG
 ||| || |||||
 ACGG CA ACACGATCC
 AGA ___
 GAM2511 KIAA0397 3' CCCAGCACAGCCTGCCCAGC 62346 AAA _ A
 GCT GTAG CTGTGCT GG
 || || ||||| ||
 CGA CGTC GACACGA CC
 CC_ C C
 GAM2511 KIAA0945 3' CCCAGCACAGCTCTGAGCTTG 30901 T AA T A
 CAA GCT AG AGCTGTGCT GG
 || || || ||||| ||

GTT CGA TC TCGACACGA CC
 _ G _ _ C
 GAM2511 KIAA1184 3' CCTAGCACGGTGCCTAGCA 42925 AAGTA
 TGCTA GCTGTGCTAGG
 |||| |||||
 ACGAT TGGCACGATCC
 CCG_

GAM2511 KIAA1434 3' TACAGCTACCTCAGTACTG 70212 A AAA
 CA TGCT GTAGCTGTG
 || ||| |||||
 GT ATGA CATCGACAT
 C CTC

GAM2511 KIAA1656 3' CCCAGCATGCCCTTGGCA 66363 AGTA T A
 TGCTAA GC GTGCT GG
 |||| || |||||
 ACGGTT CG TACGA CC
 CC_ _ C

GAM2511 LIMK2 3' AGCACAGTTCAGCATTG 34118 AAAGT
 CAATGCT AGCTGTGCT
 ||||| |||||
 GTTACGA TTGACACGA
 C_

GAM2511 LIMK2 3' AGCACAGTTCAGCATTG 19920 AAAGT
 CAATGCT AGCTGTGCT
 ||||| |||||
 GTTACGA TTGACACGA
 C_

GAM2511 LOC134957 3' CTAGCACAGTCATGCACTG 58342 A TAAA AG
 CA TGC GT CTGTGCTAG
 || ||| || |||||
 GT ACG TA GACACGATC
 C _ CT

GAM2511 LOC147639 5' CCTAGCACAGGTTAATTAG 79008 AG _
 CTAA TAGC TGTGCTAGG
 ||| ||| |||||
 GATT ATTG ACACGATCC
 A_ G

GAM2511 LOC150350 3' CCAAGACTTACGTTAGCATTG 80573 A CT G A
 CAATGCTAA GTAG GT CT GG
 ||||| ||| || |||
 GTTACGATT CATT CA GA CC
 G _ _ A

GAM2511 LOC151778 3' CCTAGCACGCGCCCCAGC 71947 AAA A T
 GCT GT GC GTGCTAGG
 ||| || || |||||
 CGA CG CG CACGATCC
 CCC _ _

GAM2511 LOC152915 3' CCTAGCACGCGCCCCAGC 67583 AAA A T
 GCT GT GC GTGCTAGG
 ||| || || |||||

CGA CG CG CACGATCC
 CCC _ _
 GAM2511 LOC256598 3' CCTAGCACGCGCCCCAGC 98103 AAA A T
 GCT GT GC GTGCTAGG
 ||| ||| |||||
 CGA CG CG CACGATCC
 CCC _ _
 GAM2511 LOC90625 3' CACAGCTACCTTATCACTG 64376 A C A
 CA TG TAA GTAGCTGTG
 || ||| |||||
 GT AC ATT CATCGACAC
 C T C
 GAM2512 EMP3 5' CGAGCGAGGGACAAGACTCCGA 9243 A _ AAAGA C
 CT AGTC GAGTC TCCT GC CG
 ||||| ||| |||
 TCAG CTCAG AGGG CG GC
 C AAC AG _ A
 GAM2512 IGFBP3 3' GGCTCAGGGAGACTCTGC 7003 T AAA
 G CAGAGTCTCCT GAGCC
 | ||||| |||||
 C GTCTCAGAGGG CTCGG
 _ A _
 GAM2512 IHPK1 3' GGCTCCTCAGCTTTGTGGCTCT 97465 TC _ AAA
 GACT AGTCAGAGTC CT GAGCC
 ||||| || |||||
 TCAGTCTCGG GA CTCGG
 TGTTTC CTC
 GAM2512 LHX5 3' CGGGCTCTCCAGGAGCCTC 42561 T AA
 GAG CTCCT AGAGCCCG
 ||| ||||| |||||
 CTC GAGGA TCTCGGGC
 C CC
 GAM2512 NT5M 3' CGGGCTCCTCTGTGGGGCTCTG 39892 C AA_
 AC GTCAGAGTCTC TA GAGCCCG
 ||||| || |||||
 CAGTCTCGGGG GT CTCGGGC
 T CTC
 GAM2512 RERE 3' GTTTGTTTAGGAGGCCCTGAC 25019 A _
 GTCAG GTCTCCTAAA GAGC
 ||||| ||||| |||||
 CAGTC CGGAGGATTT TTTG
 C G
 GAM2512 SLC9A3R1 3' GGGCTGATCAAAGAACTCTGAC 70940 _ CCTAAAG
 T AGTCAGAGT CT AGCCC
 ||||| || |||||
 TCAGTCTCA GA TCGGG
 A AACTAG _
 GAM2512 AP3D1 3' GGGCAAGGAGACTCCGCT 15451 CA AAAGA
 AGT GAGTCTCCT GCCC
 ||| ||||| |||||

			TCG CTCAGAGGA	CGGG		
			C_	A_____		
GAM2512	CSNK1G1	3'	GGCCCTGGGGACTCTGACT	42130	TAA	A
			AGTCAGAGTCTCC	AG GCC		
			TCAGTCTCAGGGG	TC CGG		
			_____	C		
GAM2512	FLJ21916	3'	CGAGCCCTTCAGGGTTCTGCT	43894	T	TT A A C
			AG CAGAG C CCT AAG GC CG			
			TC GTCTT G GGA TTC CG GC			
			_____	C C A		
GAM2512	HGC6.1.1	3'	GGGAAGCCAGGAACTCTGAC	27614	C	AAAGAG
			GTCAGAGT TCCT	CCC		
			CAGTCTCA AGGA	GGG		
			A	CCGAA_		
GAM2512	HOOK2	3'	CTCAGGAGACTCTGATT	26159	AAA	
			AGTCAGAGTCTCCT	GAG		
			TTAGTCTCAGAGGA	CTC		

GAM2512	KIAA0821	3'	CTCAGGGGACTCTAAC	30605	C	AAA
			GT AGAGTCTCCT	GAG		
			CA TCTCAGGGGA	CTC		
			A	_____		
GAM2512	KIAA1240	3'	GGCTCTTTAGAACTGCCT	67290	T	AGTCTC
			AG CAG	CTAAAGAGCC		
			TC GTC	GATTTCTCGG		
			C	AA_____		
GAM2512	MGC11287	3'	CGGGCTCTTCAGGAGACTGAGA	49613	AG	A
	C		GTC AGTCTCCT AAGAGCCCG			
			CAG TCAGAGGA TTCTCGGGC			
			AG	C		
GAM2512	MGC2656	5'	GGACCTGGGAGACCCTGAC	44720	A	AA AG
			GTCAG GTCTCCT AG CC			
			CAGTC CAGAGGG TC GG			
			C	_____	CA	
GAM2512	MGC35558	3'	GCTCTTTAGGGAGCATCT	59415	_	CT
			AGA GT CCTAAAGAGC			
			TCT CG GGATTTCTCG			
			A	AG		
GAM2512	MGC5149	5'	GGCTCTTTACGGTCCCCTGGC	72759	AGTCT	_
			GTCAG	CC TAAAGAGCC		

CCGTC GG ATTTCTCGG
 CCCT_ C
 GAM2512 NFAT5 3' GCCCTCCAGGTGATTCTGAT 57791 T AA A
 GTCAGAGTC CCT AG GC
 ||||| || ||
 TAGTCTTAG GGA TC CG
 T CC C
 GAM2512 RBM14 5' CGGGCTCTCCAGGAAGGTGGCT 21992 GAG _ AA
 AGTCA TCT CCT AGAGCCCG
 |||| ||| ||| |||||
 TCGGT GGA GGA TCTCGGGC
 _ A CC
 GAM2512 SYT12 3' GCCTGGGAGACCCCGACT 96383 AGA AA A
 AGTC GTCTCCT AG GC
 ||| ||||| ||
 TCAG CAGAGGG TC CG
 CCC _ _
 GAM2512 LOC149722 5' GGCTCTCCAGGCTTTCCAGACT 85756 A_ TCT AA
 AGTC GAG CCT AGAGCC
 ||| || ||| |||||
 TCAG CTT GGA TCTCGG
 AC TC_ CC
 GAM2512 LOC158363 3' GGCTCTAAACTCTGATT 88117 CTCCTAA
 AGTCAGAGT AGAGCC
 ||||| |||||
 TTAGTCTCA TCTCGG
 AA____
 GAM2512 LOC254381 5' GGCTCCCCGGCCCTCTGGCT 99330 TCT TAAA
 AGTCAGAG CC GAGCC
 ||||| || |||||
 TCGGTCTC GG CTCGG
 CC_ CCC_
 GAM2512 LOC257476 3' GGCTCCTCAGCTTTGTGGCTCT 61924 TC____ AAA
 GACT AGTCAGAGTC CT GAGCC
 ||||| || |||||
 TCAGTCTCGG GA CTCGG
 TGTTTC CTC
 GAM2513 EHF 3' TCCAAAACCCAAGGTTGGCT 25127 AT _ C
 AGT GCCT GGGT TTGGA
 || ||| ||| |||||
 TCG TGGA CCA AACCT
 GT A A
 GAM2513 EPHA2 3' CCATCGGCCAAGAATACTTGAA 16675 GC G T_
 G CTTCAAGTAT CT GGTC TGG
 ||||| || ||| |||
 GAAGTTCATA GA CCGG ACC
 A_ A CT
 GAM2513 ITGA5 3' CCCAGAGACATACTTGAAG 61933 C_
 CTTCAAGTATG CTGGG
 ||||| |||||

			GAAGTTCATAC GACCC			
			AGA			
GAM2513	TREM2	3'	TCCAAGACTGTCATATTT 39098	CCTG		
			AAGTATG GGTCTTGGA			
			TTTATAC TCAGAACCT			
			TG__			
GAM2513	UQCRB	3'	CCAACATAGGCATACTTAAG 21939	C	GGTC	
			CTT AAGTATGCCTG TTGG			
			GAA TTCATACGGAT AACC			
			AC__			
GAM2513	ATP10D	3'	CAGAGACCACTTGAAG 73526	ATGCCTG		
			CTTCAAGT GGTCT TG			
			GAAGTTCA CCAGA AC			
			G			
GAM2513	B3GNT7	3'	CCCTTCCAGGCAACCTGAA 71678	A A	TCTT	
			TTCA GT TGCCTGGG GG			
			AAGT CA ACGGACCT CC			
			C _ TC__			
GAM2513	DKFZp547I224	3'	TCCAAAATTGACCACATACTTG 39963	CCTG		
			GA TTCAAGTATG GGTC TTGGA			
			AGGTTCATAC CCAG AACCT			
			A__ TTAA			
GAM2513	FLJ22341	3'	CCAAGCTCAGGCACACCCAAG 45114	CAA A	T	
			CTT GT TGCCTGGG CTTGG			
			GAA CA ACGGACTC GAACC			
			CC_ C _			
GAM2513	KIAA0779	3'	CCGAACAGCATACTTGAAG 86908	C	GGTC	
			CTTCAAGTATGC TG TTGG			
			GAAGTTCATACG AC AGCC			
			_ A__			
GAM2513	LOC144233	3'	CCAAGGCACATAATTGAA 77246	G	CCTGG	
			TTCAA TATG GTCTTG			
			AAGTT ATAC CGGAACC			
			A A__			
GAM2513	LOC147341	3'	ACCCAGGCATAACTGAAG 85116	AG		
			CTTCA TATGCCTGGGT			
			GAAGT ATACGGACCCA			
			CA			
GAM2513	LOC221088	5'	TCCAAGGTGCTGGCCACTCGAA 94888	A AT	TGGG	
			G CTTTCA AGT GCC TCTTGGA			

			GAAG TCA CGG GGAACCT		
			C C_ TCGT		
GAM2514 CDC6	3'	TGACCTTTTTT	ACTTGAAGCCA 8831	_	GGAT A
A			TTGGTT CAAG GGAAA GTCA		
			AACCGA GTTC TTTT CAGT		
			A AT_ C		
GAM2514 ELF3	3'	GACCTTGACCTTGACCAA	16682	T	GAT AAAA
			TTGGT CAAGG GG GTC		
			AACCA GTTCC TC CAG		
			_ AGT _		
GAM2514 SLC10A2	5'	ACTCTCTGTCTTGACCAA	6591	CAA	AA
			TTGGTT GGGATGGA AGT		
			AACCAG TTCTGTCT TCA		
			_ C_		
GAM2514 FLJ10829	3'	ACTTTTCCACCAAAGCTA	37252	CAAG	A
			TGGTT GG TGGAAAAGT		
			ATCGA CC ACCTTTTCA		
			AA_ _		
GAM2514 HEAB	3'	TGACTCTTCTAATCTTGAACCA	23363	GA	A
A			TTGGTTCAAGG TGGAA AGTCA		
			AACCAAGTTCT ATCTT TCAGT		
			A_ C		
GAM2514 HEMK	5'	TGACCTCTCCATCTCCACC	32966	TCAA	AAA
			GGT GGGATGGA GTCA		
			CCA CTCTACCT CAGT		
			C_ CTC		
GAM2514 KIAA0298	3'	TCCAAGTTCATGAGCCAA	77080	A	A_
			TTGGTTCA GGG TGGA		
			AACCGAGT CTT ACCT		
			A GA		
GAM2514 KIAA1228	3'	ACTTTTCTACCTTGAGCCAA	65664	GA	
			TTGGTTCAAGG TGGAAAAGT		
			AACCGAGTTCC ATCTTTTCA		
			_		
GAM2514 KIAA1486	3'	TGACTTTTCTCTTATACCAA	67982	TC	TG
			TTGGT AAGGGA GAAAAGTCA		
			AACCA TTCTCT CTTTTCAGT		
			TA _		
GAM2514 MGC21854	3'	ACTTTTCAATTTGATCCAA	54601	T	GGATG
			TTGG TCAAG GAAAAGT		

		AACC AGTTT CTTTCA		
		T AA__		
GAM2514	LOC148697 3'	ACTTTTCCTGCTCAAACC 79671	CAA	AT
		GGTT GGG GGAAAAGT		
		CCAA CTC CCTTTTCA		
		A__ GT		
GAM2514	LOC80298 3'	ACTTTTACCTTGAACCA 48063	GATGG	
		TGGTTCAAGG AAAAGT		
		ACCAAGTTCC TTTTCA		
		A__		
GAM2515	GPD1 3'	TCATGCCACCACATTTG 60398	C	C
		TAAATG GGTGGCAT GA		
		GTTTAC CCACCGTA CT		
		A _		
GAM2515	IL5RA 5'	TCGCATGGCCACCGCATTT 6906	AT__	
		AAATGCGGTGGC CGA		
		TTTACGCCACCG GCT		
		GTAC		
GAM2515	MYO1C 3'	TGCCGATGCCAAATATTTG 61873	CGG	A
		TAAATG TGGCATCG CA		
		GTTTAT ACCGTAGC GT		
		AA_ C		
GAM2515	C6orf37 3'	TGTCACACTGCATTTA 68097	GCATC	
		TAAATGCGGTG GACA		
		ATTTACGTAC CTGT		
		A__		
GAM2515	DNAJC6 3'	TTGCAGAACCACCGCATT 29498	CA	GA
		AATGCGGTGG TC CAA		
		TTACGCCACC AG GTT		
		A_ AC		
GAM2515	FLJ11210 3'	GTCGATGTGCATGCTTTTA 60319	T	GTG
		TAAA GCG GCATCGAC		
		ATTT CGT TGTAGCTG		
		T ACG		
GAM2515	FLJ12476 3'	TCGATCTTCTGCATTTA 43270	T	C
		TAAATGCGG GG ATCGA		
		ATTTACGTC TC TAGCT		
		T _		
GAM2515	KIAA1034 3'	TCGATGGCATCCGCATTTG 63134	_	G
		TAAATGCGG TG CATCGA		

	GTTTACGCC AC GTAGCT		
	T G		
GAM2515 KIAA1987	3' TCATGTAAGTGCATTTA 89391	G	C
	TAAATGCGGT GCAT GA		
	ATTTACGTCA TGTA CT		
	A _		
GAM2515 MGC16063	3' TGTCCTGGCCACTGCATT 54929		ATC
	AATGCGGTGGC GACA		
	TTACGTCACCG CTGT		
	GTC		
GAM2515 LOC147949	3' TGTCAGATGTCCACATTGCA 79279	_	- -
	TGCG GTGG CATC GACA		
	ACGT CACC GTAG CTGT		
	TA T A		
GAM2515 LOC150577	3' GTCCTCACCGCATTTG 86258		CATC
	TAAATGCGGTGG GAC		
	GTTTACGCCACT CTG		
	C_		
GAM2515 LOC158219	3' TGTGTGTCACCACATTT 82694	C	CG
	AAATG GGTGGCAT ACA		
	TTTAC CCACTGTG TGT		
	A _		
GAM2515 LOC202020	3' TGTCTCACACATTTA 90605	C	CATC
	TAAATG GGTGG GACA		
	ATTTAC CCACT CTGT		
	A _		
GAM2515 LOC90826	5' TGTCGATGCAGTTTATTTG 64788		CGGTG
	TAAATG GCATCGACA		
	GTTTAT CGTAGCTGT		
	TTGGA		
GAM2515 LOC93587	3' TTGTCTTTACCTGCATTTA 73042	_	CATC
	TAAATGC GGTGG GACAA		
	ATTTACG CCATT CTGTT		
	T T_		
GAM2516 BRF1	5' GGTGCCTGTCCCATCCCGCGG 9505	A	A T_
	TC CGGGATGG ACG CACC		
	GG GCCCTACC TGT GTGG		
	C C CC		
GAM2516 COL7A1	3' GTGACTTGGTCCCGTGG 5412	G	AC
	TCACGGGAT GA GTCAC		

		GGTGCCCTG TT CAGTG		
		G _		
GAM2516	MEOX1	3' GTGACAGTGTCTGTGA 16953		GGA _
		TCACGGGAT AC GTCAC		
		AGTGTCTCTG TG CAGTG		
		_ A		
GAM2516	MEOX1	3' GTGACAGTGTCTGTGA 26581		GGA _
		TCACGGGAT AC GTCAC		
		AGTGTCTCTG TG CAGTG		
		_ A		
GAM2516	NCOA6IP	5' GGTGACACCGCCCGTGG 46158		A AAC
		TCACGGG TGG GTCACC		
		GGTGCCC GCC CAGTGG		
		_ A		
GAM2516	USP14	3' GTGCTGCTGTCCATCCCATGG 18937	C	AC _
		TCA GGGATGGA GT CAC		
		GGT CCCTACCT CG GTG		
		A GT TC		
GAM2516	C20orf3	3' GTAACGTCTTGTCTGTGA 68643	AT	A C
		TCACGGG GGA CGT AC		
		AGTGTCT TCT GCA TG		
		GT _ A		
GAM2516	DKFZp434H2215	5' GGTGACGGGTGTCATCCCG 34527		AA _
		CGGGATGG CGTCACC		
		GCCCTACT GCAGTGG		
		GTGG		
GAM2516	DKFZP434K1172	5' GGCCATCTCCATCCTGTGA 49265		AC _
		TCACGGGATGGA GTC		
		AGTGTCTCTACCT CGG		
		CTAC		
GAM2516	FLJ10932	3' GTGCCTTTCCATCCGTGA 37431	G	CGT
		TCACGG ATGGAA CAC		
		AGTGCC TACCTT GTG		
		_ TCC		
GAM2516	HHLA2	3' TGACATTCCACCATTTGTGA 23954	_ A	C
		TCACG GG TGGAA GTCA		
		AGTGT CC ACCTT CAGT		
		TA _ A		
GAM2516	HHLA3	3' TGACATTCCACCATTTGTGA 23951	_ A	C
		TCACG GG TGGAA GTCA		

		AGTGT CC ACCTT CAGT	
		TA _ A	
GAM2516 KIAA0125	3'	GACACCACTGTCCATCCTGTGA 29565	AC_____
		TCACGGGATGGA GTC	
		AGTGTCTACCT CAG	
		GTCACCA	
GAM2516 KIAA1219	3'	GTGTGGCATTCCGTGA 62028	GAA T
		TCACGGGATG CG CAC	
		AGTGCCTTAC GT GTG	
		G__ _	
GAM2516 KIAA1244	3'	GGTGTTTGTTCATCCC 72449	_ T_
		GGGATGGAA CG CACC	
		CCCTACCTT GT GTGG	
		T TT	
GAM2516 KIAA1348	3'	GATGAATTCATCTCATGA 69124	C _
		TCA GGGATGGAA CGTC	
		AGT CTCTACTTT GTAG	
		A AA	
GAM2516 KIAA1349	3'	GGTGATCATTATCCTGTGA 71294	AAC
		TCACGGGATGG GTCACC	
		AGTGTCTATT TAGTGG	
		AC_	
GAM2516 KLK15	3'	GGTGACGTCCCTTGTGA 57516	AT A
		TCACGGG GGA CGTCACC	
		AGTGTTT CCT GCAGTGG	
		_ _	
GAM2516 KLK15	3'	GGTGACGTCCCTTGTGA 43714	AT A
		TCACGGG GGA CGTCACC	
		AGTGTTT CCT GCAGTGG	
		_ _	
GAM2516 MKRN4	3'	GATCGAGACCATCCTGTGA 48464	AA_ _
		TCACGGGATGG CG TC	
		AGTGTCTACC GC AG	
		AGA T	
GAM2516 PIP3-E	3'	GGTGACACTTTCCGTGA 67356	T AAC
		TCACGGGA GG GTCACC	
		AGTGCCTT TC CAGTGG	
		_ A_	
GAM2516 TRAF3	5'	GGTGTTTCTCCATCCCGT 60456	_ T
		ACGGGATGGA ACG CACC	

			TGCCCTACCT	TGT GTGG		
			CTT _			
GAM2516	LOC146485	5'	GGTGTGCAGCATCCCTTGA	60493	C	GAA T
			TCA GGGATG	CG CACC		
			AGT CCCTAC	GT GTGG		
			T GAC _			
GAM2516	LOC149837	3'	GGTATGGGCATCCCGTGG	85904		GAA C
			TCACGGGATG	CGT ACC		
			GGTGCCCTAC	GTA TGG		
			GG_ _			
GAM2516	LOC161742	3'	GATGATCTTCATCCCTGA	83168	C	A__
			TCA GGGATGGA	CGTC		
			AGT CCCTACTT	GTAG		
			_ CTA			
GAM2516	LOC163255	5'	GGTGACGTTTCAGGGATGTGG	83344		GGATG
			TCACG	GAACGTCACC		
			GGTGT	CTTGCACTGG		
			AGGGA			
GAM2516	LOC221362	3'	GGTGTAACCATCCCGTGA	95402		AACGT
			TCACGGGATGG	CACC		
			AGTGCCCTACC	GTGG		
			AAT__			
GAM2517	DTNA	3'	ATATCCCACTCACTAGCA	9139		TGATC TA
			TGCTAGTGA	TGG ATAT		
			ACGATCACT	ACC TATA		
			C__ C_			
GAM2517	TCTE1L	3'	ATATTACCACTAACACTA	71526	A	ATC
			TAGTG TG	TGGTAATAT		
			ATCAC AT	ACCATTATA		
			A C_			
GAM2517	VAPA	3'	TATATTACCAGATCATCACTAG	14546		
	CA		TGCTAGTGATGATCTGGTAATATA			
			ACGATCACTACTAGACCATTATAT			
GAM2517	FLJ13576	3'	ATACTACCAATTATCACTA	42806	C	A
			TAGTGATGAT	TGGTA TAT		
			ATCACTATTA	ACCAT ATA		
			_ C			
GAM2517	HEMK	3'	ATATTACCTTCACATAGCA	32950	_	TGATCT
			TGCTA GTGA	GGTAATAT		

		ACGAT CACT CCATTATA	
		A T_____	
GAM2517	MGC12217 3'	TACCAGATTAGCCACCATTAGC 52289	A_____
	A	TGCTAGTG TGATCTGGTA	
		ACGATTAC ATTAGACCAT	
		CACCG	
GAM2517	LOC146220 3'	ACCAGACCATCACTGGCA 84600	A
		TGCTAGTGATG TCTGGT	
		ACGGTCACTAC AGACCA	
		C	
GAM2517	LOC146515 3'	TATCAGACACCACTAGTA 78520	A A
		TGCTAGTG TG TCTGGTA	
		ATGATCAC AC AGACTAT	
		C _	
GAM2517	LOC149711 5'	TATAATGATCATCACCAGCA 85855	A TG_
		TGCT GTGATGATC GTA	
		ACGA CACTACTAG TAT	
		C TAA	
GAM2518	CALM3 3'	GCTTTGAGAATCTCTTCTCA 19005	C CCC CT_
		TGAGAAGA ATTC TC GC	
		ACTCTTCT TAAG AG CG	
		C _ TTT	
GAM2518	FGD1 5'	CGGGAGGAAGAACGCTTCCCA 16751	A ACA C_
		TG GAAG TTC CCTCCTG	
		AC CTTC AAG GGAGGGC	
		C GC_ AA	
GAM2518	GOT2 3'	CAGCATTGGAATGTTTCTCA 94495	A CCCTC
		TGAGA GACATTC CTG	
		ACTCT TTGTAAG GAC	
		_ TTTAC	
GAM2518	HAS3 3'	GCAGGAGGCAAGCGTGTCTCA 57602	G A CC
		TGAGAA AC TT CCTCCTGC	
		ACTCTT TG GA GGAGGACG	
		G C AC	
GAM2518	HDAC6 5'	GGCAGGGGCCAAGCCTCCTCA 21279	A ACA CC T
		TGAG AG TT CC CCTGCC	
		ACTC TC AA GG GGACGG	
		C CG_ CC _	
GAM2518	PBX2 3'	TGGCAGGAAGAATGGGGCCTC 11983	AAGA CCC
		GAG CATTG TCCTGCCA	

		CTC GTAAG AGGACGGT		
		CGGG A__		
GAM2518	PTGIS	3' TGGCAGGAGGCAGGATATC 8234	C C_	
		GA ATTC CCTCCTGCCA		
		CT TAGG GGAGGACGGT		
		A AC		
GAM2518	UBE3A	3' TGGCAGGAAAAATGCAGCTTTC 6628	AGA_ CCCC	
	A	TGAGA CATT TCCTGCCA		
		ACTTT GTAA AGGACGGT		
		CGAC AA__		
GAM2518	ZNF175	3' AGAAGAGAACATCTTCTCA 24083	CA CC C	
		TGAGAAGA TTC CT CT		
		ACTCTTCT AAG GA GA		
		AC A_ A		
GAM2518	AD-020	3' TGGCAGAAGGGAATGTCACTC 60094	AA CTC	
		GAG GACATTCCC CTGCCA		
		CTC CTGTAAGGG GACGGT		
		A_ AA_		
GAM2518	C21orf18	3' CAGGAGGAGGGAATGTCCTCT 34302	A _	
		AGA GACATTCCC CTCCTG		
		TCT CTGTAAGGG GAGGAC		
		C AG		
GAM2518	C8orf6	3' GAGGGAGAATTTCTTCTCA 90780	C _	
		TGAGAAGA ATTC CCCTC		
		ACTCTTCT TAAG GGGAG		
		T A		
GAM2518	CARD14	3' CAGGAGGGACATCTTCCCA 54486	A CATT C	
		TG GAAGA CCCTCCTG		
		AC CTTCT GGGAGGAC		
		C ACA__		
GAM2518	DKFZP434K1772	3' CAGCAGGGATGTCCTCCA 68332	A A TC C	
		TG GA GACAT CCCT CTG		
		AC CT CTGTA GGGG GAC		
		_ C _ C		
GAM2518	DKFZP566F2124	3' GGCAAGATTGTCTTTTCA 32217	T CCCTCC	
		TGAGAAGACA TC TGCC		
		ACTTTTCTGT AG ACGG		
		T A_____		
GAM2518	FLJ12783	3' TGGCAGAAGAGAGGGT TTTCTC 49491	ATT C _	
	A	TGAGAAGAC CC CTC CTGCCA		

ACTCTTTTG GG GAG GACGGT
 ____ A AA
 GAM2518 FLJ14297 3' TGGCAGGAAAGATATTCCTCT 46615 A CAT CCC
 AGA GA TC TCCTGCCA
 ||| || || |||||
 TCT CT AG AGGACGGT
 C TAT AA_
 GAM2518 FLJ21615 3' GCTCTAAGAACTGTCTTCTCA 50810 _ CCCTCCT
 TGAGAAGACA TTC GC
 ||||| || ||
 ACTCTTCTGT AAG CG
 C AATCT_
 GAM2518 FLJ22833 5' GGCAGAAGTGTCCCCTCA 43405 AA CCCCTC
 TGAG GACATT CTGCC
 ||| |||| ||||
 ACTC CTGTGA GACGG
 CC A____
 GAM2518 IPT 3' TGGCAGGAAAGGGCCATCTC 34934 AGACATT C_
 GAGA CCC TCCTGCCA
 ||| ||| |||||
 CTCT GGG AGGACGGT
 ACC____ AA
 GAM2518 KIAA0057 3' GGGAGGACATGTCTTCCCA 25420 A TCC
 TG GAAGACAT CCTCCT
 || ||||| |||||
 AC CTTCTGTA GGAGGG
 C CA_
 GAM2518 KIAA0802 3' CAGGAGAGATCTAGTTTTCTCA 63247 AT__ CC
 TGAGAAGAC TC CTCCTG
 ||||| || |||||
 ACTCTTTTG AG GAGGAC
 ATCT A_
 GAM2518 LMOD1 5' GCAGGAGGTTTTCTCCTCA 25101 A CATTCC
 TGAG AGA CCTCCTGC
 ||| || |||||
 ACTC TCT GGAGGACG
 C TTT_
 GAM2518 MGC12972 3' TGACAGAAGGGGAATGGGCTC 52055 AAGA C C
 GAG CATTCCCCT CTG CA
 || ||||| ||| ||
 CTC GTAAGGGGA GAC GT
 GG__ A A
 GAM2518 MGC5528 3' GGCTTCGAAATGTCTTTCA 44274 A CCCC CT_
 TGAGA GACATT TC GCC
 |||| |||| || |||
 ACTTT CTGTAA AG CGG
 _ ____ CTT
 GAM2518 MO25 3' GGCAGAACAATGTCTTCT 33291 CCCCTC
 AGAAGACATT CTGCC
 ||||| ||||

			TCTTCTGTAA	GACGG		
			CAA__			
GAM2518	NCOA2	3'	TGGCAGGAGGAGCTGCCTCTTC	22573	CATTCC_	
	TC		GAGAAGA	CCTCCTGCCA		
			CTCTTCT	GGAGGACGGT		
			CCGTCGA			
GAM2518	PARVA	3'	TGGCAGGAGTCATGTCCCTCA	37185	AA	TCCC
			TGAG	GACAT	CTCCTGCCA	
			ACTC	CTGTA	GAGGACGGT	
			C_	CT__		
GAM2518	PGS1	3'	TGGCAGGAAGGGTGGGGTCCTC	44595	AA	A _ _
	A		TGAG	GAC	TTC	CCCT
			ACTC	CTG	GGG	GGGA
			_ _	T	A	
GAM2518	SFXN2	3'	GCAAAGGCCAATGTCTTCT	74377	CC	CC
			AGAAGACATT	CCT	TGC	
			TCTTCTGTAA	GGA	ACG	
			CC	A_		
GAM2518	SH3KBP1	5'	GGCAGGAGAGGTTTGTTCCT	66947	AA	TT C
			AG	GACA	CC	CTCCTGCC
			TC	TTGT	GG	GAGGACGG
			CC	TT	A	
GAM2518	SOX30	3'	TGGAACCTTGGAGAATGTCTTC	23802	C	TCCTG_
			GAAGACATTC	CC	CCA	
			CTTCTGTAAG	GG	GGT	
			A	TTCCAA		
GAM2518	SRPUL	3'	AGGAGGAAATGTTTTCCCA	27844	A	CC
			TG	GAAGACATT	CCTCCT	
			AC	CTTTTGTA	GGAGGA	
			C	A_		
GAM2518	LOC158267	3'	CAGAAGAAAATGTCTTCCCA	82720	A	CCC C
			TG	GAAGACATT	CT	CTG
			AC	CTTCTGTAA	GA	GAC
			C	AA_	A	
GAM2518	LOC165552	3'	TGGCAGGAGGAGGGTACCACTC	83380	AAGACAT	_
	A		TGAG	TCC	CCTCCTGCCA	
			ACTC	GGG	GGAGGACGGT	
			ACCAT_	A		
GAM2518	LOC201564	3'	TGGGAGTGGGGAATGCCTTCT	81278	A	TC G
			AGAAG	CATTCCCC	CT	CCA

TCTTC GTAAGGGG GA GGT
 C T_ G
 GAM2518 LOC256307 5' GGCAGGAGGAGACACTCA 98841 AAGACAT C
 TGAG TC CCTCCTGCC
 |||| || |||||
 ACTC AG GGAGGACGG
 AC_____ A
 GAM2519 DEDD 3' TACAGCTACCTTACCACTG 53380 A C A
 CA TG TAA GTAGCTGTG
 || || || |||||
 GT AC ATT CATCGACAT
 C C C
 GAM2519 ENAM 3' CCTAGCACAGTGTCTTCAACAT 49927 CTA TA
 ATG AAG GCTGTGCTAGG
 ||| ||| |||||
 TAC TTC TGACACGATCC
 AAC TG
 GAM2519 MAP3K14 3' CCAGAGCACAGCTCAGCATCA 15544 A AAAGT A_
 C ATGCT AGCTGTGCT GG
 | |||| ||||| ||
 A TACGA TCGACACGA CC
 C C_____ GA
 GAM2519 MYH11 3' CCCAGCAGACTGTACTTAGCAT 43430 A GCTG_ A
 TG CAATGCTAA GTA TGCT GG
 ||||| ||| ||| ||
 GTTACGATT CAT ACGA CC
 _ GTCAG C
 GAM2519 MYH11 3' CCCAGCAGACTGTACTTAGCAT 11739 A GCTG_ A
 TG CAATGCTAA GTA TGCT GG
 ||||| ||| ||| ||
 GTTACGATT CAT ACGA CC
 _ GTCAG C
 GAM2519 USP11 5' CCCAGCACGTGCTTGGCATT 17384 AAGT _ A
 AATGCTA AGC TGTGCT GG
 ||||| ||| ||||| ||
 TTACGGT TCG GCACGA CC
 _____ T C
 GAM2519 FLJ20086 3' CCTAGCACAACAGAGGCA 35012 AAA AGC
 TGCT GT TGTGCTAGG
 |||| || |||||
 ACGG CA ACACGATCC
 AGA _____
 GAM2519 KIAA0397 3' CCCAGCACAGCCTGCCCAGC 62346 AAA _ A
 GCT GTAG CTGTGCT GG
 ||| ||| ||||| ||
 CGA CGTC GACACGA CC
 CC_ C C
 GAM2519 KIAA0945 3' CCCAGCACAGCTCTGAGCTTG 30901 T AA T A
 CAA GCT AG AGCTGTGCT GG
 ||| ||| || ||||| ||

GTT CGA TC TCGACACGA CC
 _ G _ _ C
 GAM2519 KIAA1184 3' CCTAGCACGGTGCCTAGCA 42925 AAGTA
 TGCTA GCTGTGCTAGG
 |||| |||||
 ACGAT TGGCACGATCC
 CCG_

GAM2519 KIAA1434 3' TACAGCTACCTCAGTACTG 70212 A AAA
 CA TGCT GTAGCTGTG
 || ||| |||||
 GT ATGA CATCGACAT
 C CTC

GAM2519 KIAA1656 3' CCCAGCATGCCCTTGGCA 66363 AGTA T A
 TGCTAA GC GTGCT GG
 |||| || |||||
 ACGGTT CG TACGA CC
 CC_ _ C

GAM2519 LIMK2 3' AGCACAGTTCAGCATTG 34118 AAAGT
 CAATGCT AGCTGTGCT
 ||||| |||||
 GTTACGA TTGACACGA
 C_

GAM2519 LIMK2 3' AGCACAGTTCAGCATTG 19920 AAAGT
 CAATGCT AGCTGTGCT
 ||||| |||||
 GTTACGA TTGACACGA
 C_

GAM2519 LOC134957 3' CTAGCACAGTCATGCACTG 58342 A TAAA AG
 CA TGC GT CTGTGCTAG
 || ||| || |||||
 GT ACG TA GACACGATC
 C _ CT

GAM2519 LOC147639 5' CCTAGCACAGGTTAATTAG 79008 AG _
 CTAA TAGC TGTGCTAGG
 ||| ||| |||||
 GATT ATTG ACACGATCC
 A_ G

GAM2519 LOC150350 3' CCAAGACTTACGTTAGCATTG 80573 A CT G A
 CAATGCTAA GTAG GT CT GG
 ||||| ||| || |||
 GTTACGATT CATT CA GA CC
 G _ _ A

GAM2519 LOC151778 3' CCTAGCACGCGCCCCAGC 71947 AAA A T
 GCT GT GC GTGCTAGG
 ||| || || |||||
 CGA CG CG CACGATCC
 CCC _ _

GAM2519 LOC152915 3' CCTAGCACGCGCCCCAGC 67583 AAA A T
 GCT GT GC GTGCTAGG
 ||| || || |||||

CGA CG CG CACGATCC
 CCC _ _
 GAM2519 LOC256598 3' CCTAGCACGCGCCCCAGC 98103 AAA A T
 GCT GT GC GTGCTAGG
 ||| ||| |||||
 CGA CG CG CACGATCC
 CCC _ _
 GAM2519 LOC90625 3' CACAGCTACCTTATCACTG 64376 A C A
 CA TG TAA GTAGCTGTG
 || ||| |||||
 GT AC ATT CATCGACAC
 C T C
 GAM2520 EMP1 3' GTAAACCATGTATTCCCT 9240 CAGC
 AGGGAATACA GTTTAC
 ||||| |||||
 TCCCTTATGT CAAATG
 AC_
 GAM2520 IL2RB 3' TGTTGCACATGCTATTCCCT 7946 _ _
 AGGGAATA CA CAGCG
 ||||| || |||||
 TCCCTTAT GT GTTGT
 C ACAC
 GAM2520 PSCD4 3' TGA CTGCTGTGTACCCT 26327 AA TT TA
 AGGG TACACAGCG CA
 ||| ||||| ||
 TCCC ATGTGTCGC GT
 _ TCA_
 GAM2520 TEGT 3' AAAAGTAATGTGTTCCCT 65224 CA G
 AGGGAATACA GC TTT
 ||||| || |||
 TCCCTTGTGT TG AAA
 AA A
 GAM2520 CAT56 3' CTTTGTGAAACTGTGCATCCCC 48280 A A CG
 T AGGG AT CACAG TTTACAAAG
 ||| || ||| |||||
 TCCC TA GTGTC AAGTGTTTC
 C C A_
 GAM2520 DKFZp761G2113 3' CTTTGTAAACGCTGTGTATTCC 70466
 CT AGGGAATACACAGCGTTTACAAAG
 ||||| ||||| |||||
 TCCCTTATGTGTCGCAAATGTTTC
 _ G
 GAM2520 FLJ10008 3' ACGGTGAATGTGTTCCCT 36176
 AGGGAATACA CA CGT
 ||||| || |||
 TCCCTTGTGT GT GCA
 AA G
 GAM2520 FLJ20499 3' TTTGTAGCAGTGTCTCCCT 35715 AT A GTT
 AGGGA ACAC GC TACAAA
 |||| ||| || |||||

TCCCT TGTG CG ATGTTT
 C_ A _
 GAM2520 FLJ22127 3' CTTCGTGCACATGTGTTCCC 43199 CAGC T A
 GGGAATACA GT TAC AAG
 ||||| || ||| ||
 CCCTTGTGT CA GTG TTC
 A_ C C
 GAM2520 FLJ25461 3' TTGTAAGTGTATTCTC 59300 CAGC T
 GGGAATACA GTT ACAA
 ||||| || |||
 CTCTTATGT CAA TGTT
 _ _
 GAM2520 KIAA0635 3' CTTTGTAAATTTTATGTATCCC 28415 A CAGCGT
 GGGA TACA TTACAAAG
 ||| ||| |||||
 CCCT ATGT AATGTTTC
 _ ATTT_ _
 GAM2520 P24B 3' CTTGGTGAGCTGTGTATTTCCCT 24772 GT A
 AGGGAATACACAGC TTAC AAG
 ||||| ||| |||
 TCCTTTATGTGTCG AGTG TTC
 _ G
 GAM2520 LOC148545 3' CTTTGTAAAAAGATCATTCCC 79642 ACACAGCG
 T AGGGAAT TTTACAAAG
 ||||| |||||
 TCCCTTA AAATGTTTC
 CTAGAAA_
 GAM2520 LOC148930 3' AGCTGCTGCCTATTCCCT 79838 CA _
 AGGGAATA CAGC GTT
 ||||| ||| |||
 TCCCTTAT GTCG CGA
 CC T
 GAM2520 LOC200515 5' AGGCATCTGTGTATGCCC 91655 A C_
 GGG ATACACAG GTTT
 || ||||| |||
 CCC TATGTGTC CGGA
 G TA
 GAM2520 LOC222166 3' CTTTGTAAACTGCCTTTCCCT 95738 TACACA _
 AGGGAA GC GTTTACAAAG
 |||| || |||||
 TCCCTT CG CAAATGTTTC
 TC_ T
 GAM2520 LOC253039 3' TAAGCTGCTGTGTATTCCC 97866 _
 GGGAATACACAGC GTTTA
 ||||| |||||
 CCCTTATGTGTCG CGAAT
 T
 GAM2520 LOC256957 5' TAAAAGCCTTGTATTCCC 96828 CA G
 GGGAATACA GC TTTA
 ||||| || |||

CCCTTATGT CG AAAT
 TC A
 GAM2520 LOC51281 3' TTTGTAGCAGTGTCTCCCT 33775 AT A GTT
 AGGGA ACAC GC TACAAA
 |||| ||| || |||||
 TCCCT TGTG CG ATGTTT
 C_ A ____
 GAM2520 LOC54499 3' AGGCACTGTGTATGCCCT 71158 A C
 AGGG ATACACAG GTTT
 ||| ||||| |||
 TCCC TATGTGTC CGGA
 G A
 GAM2521 BPHL 3' AACAGCCTCTAGCTTCAGG 16330 TT__
 CCTGAAGCTG CTGTT
 ||||| |||
 GGA CTTCGAT GACAA
 CTCC
 GAM2521 CNTNAP2 3' AGGTAACAGAACAAAAGGG 27089 GAAGC
 CCT TGTTCCTGTTACCT
 || |||||
 GGG ACAAGACAATGGA
 AAA__
 GAM2521 HNRPA2B1 3' GAGGTAACAGAACAGCTTCAGG 49187
 TT AACCTGAAGCTGTTCTGTTACCTC
 |||||
 TTGGACTTCGACAAGACAATGGAG

 GAM2521 HNRPA2B1 3' GAGGTAACAGAACAGCTTCAGG 10947
 TT AACCTGAAGCTGTTCTGTTACCTC
 |||||
 TTGGACTTCGACAAGACAATGGAG

 GAM2521 MYCL1 3' AGGCAGTAGAACTCCAGG 19363 AAGCT A
 CCTG GTTCTGTT CCT
 ||| ||||| |||
 GGAC CAAGATGA GGA
 CT__ C
 GAM2521 RPE65 3' AGAAAATCAGCTTCAGGT 6168 ____
 ACCTGAAGCTG TTCT
 ||||| |||
 TGGACTTCGAC AAGA
 TAA
 GAM2521 SNRPN 5' AACACTTAACAGCTTCAGG 43317 C__
 CCTGAAGCTGTT TGTT
 ||||| |||
 GGA CTTCGACAA ACAA
 TTC
 GAM2521 TPO 3' GCAGAACAGCTTCATGTT 6810 C
 AAC TGAAGCTGTTCTGT
 || |||||

TTG ACTTCGACAAGACG
 T
 GAM2521 COPS7B 3' AACTTGAACAGTTTCAGGTT 42996 T_
 AACCTGAAGCTGTTT GTT
 ||||| |||||
 TTGGACTTTGACAAG CAA
 TT
 GAM2521 DKFZp434K1210 3' GACAACCCCCAGCTTCAGGT 34689 TTC__
 ACCTGAAGCTG TGTT
 ||||| |||||
 TGGACTTCGAC ACAG
 CCCC
 GAM2521 DKFZp547N157 3' GAGACTGTAACAGGCCCAGGT 69525 AA TGTT ____
 ACCTG GC CTGTTAC CTC
 |||| || ||||| |||||
 TGGAC CG GACAATG GAG
 C_ ____ TCA
 GAM2521 FEM-2 3' GAGGCAGTCCCAGCCTCAG 28314 A TT_ TTA
 CTGA GCTG CTG CCTC
 |||| |||| ||||| |||||
 GACT CGAC GAC GGAG
 C CCT ____
 GAM2521 FLJ20013 3' AGCTGGGAACAGCTTCAGAGT 34793 _ ____
 AC CTGAAGCTGTTCT GTT
 || ||||| ||||| |||||
 TG GACTTCGACAAGG CGA
 A GT
 GAM2521 FLJ21551 3' AGGTGACACAGTCTTCAAGTT 46028 C _ TCT
 AAC TGAAG CTGT GTTACCT
 ||||| ||||| ||||| |||||
 TTG ACTTC GACA CAGTGGA
 A T ____
 GAM2521 FLJ21736 3' AGACAACAGAATCCATCAGG 46775 AGCT AC
 CCTGA GTTCTGTT CT
 ||||| ||||| ||||| |||||
 GGA CT TAAGACAA GA
 ACC_ CA
 GAM2521 FLJ21791 3' GAGGCAACAGTCCACTTCAGG 62127 C TT A
 CCTGAAG TG CTGTT CCTC
 ||||| ||||| ||||| |||||
 GGA CT AC GACAA GGAG
 _ CT C
 GAM2521 FLJ23594 3' AGGTAACAGATAACCAGGT 45854 AAGCTGT
 ACCTG TCTGTTACCT
 ||||| ||||| ||||| |||||
 TGGAC AGACAATGGA
 CAAT____
 GAM2521 GOLPH2 3' GTAGCAACAGCTTTAAGT 33772 C TC
 AC TGAAGCTGT TGTTAC
 || ||||| ||||| |||||

			TG ATTTCGACA ACGATG		
			A _		
GAM2521	HSPC065	3'	AGGCGAACAGCTCCAGGT 27139	A	TGTTA
			ACCTG AGCTGTTC CCT		
			TGGAC TCGACAAG GGA		
			C C_		
GAM2521	IMPACT	3'	AGGTAACAGTTGCCCAGG 38001	AA	TGTT
			CCTG GC CTGTTACCT		
			GGAC CG GACAATGGA		
			C_ TT_		
GAM2521	KIAA1164	3'	GAGGTAACCTCAAACCTCAGG 70043	AGCT	CT_
			CCTGA GTT GTTACCTC		
			GGACT CAA CAATGGAG		
			C_ ACT		
GAM2521	KIAA1317	3'	AGGTAACCTGAAGCTCCAGAGTT 87209	_ A	GT T
			AAC CTG AGCT TC GTTACCT		
			TTG GAC TCGA AG CAATGGA		
			A C _ T		
GAM2521	KIAA1579	3'	GTACTAGAACAGCCCAAGTT 37153	C AA	T
			AAC TG GCTGTTCTG TAC		
			TTG AC CGACAAGAT ATG		
			A C_ C		
GAM2521	MCF2L	3'	AGGCACTTTACAGCTTCATGTT 61523	C	TCT TA
			AAC TGAAGCTGT GT CCT		
			TTG ACTTCGACA CA GGA		
			T TTT C_		
GAM2521	MGC16175	5'	AGGTTGAGGACAGCCTCGGGT 52272	A	GTT
			ACCTGA GCTGTTCT ACCT		
			TGGGCT CGACAGGA TGGA		
			C GT_		
GAM2521	MGC2541	3'	AGGTAACATCAATACCTAGG 55619	GA C	C_
			CCT AG TGTT TGTTACCT		
			GGA TC ATAA ACAATGGA		
			_ C CT		
GAM2521	MGC5139	5'	GTAACAGAACCATTTCAGG 74575	GCT	
			CCTGAA GTTCTGTTAC		
			GGACTT CAAGACAATG		
			AC_		
GAM2521	PMI	3'	GAGACAACAGAGTATTCAG 15267	GCTG	AC
			CTGAA TTCTGTT CTC		

				GACTT	GAGACAA	GAG			
				AT__	CA				
GAM2521	RDC1	3'	AGCAAAGTAGCTTCGGGT	72831				C	
			ACCTGAAGCTGTT TGTT						
			TGGGCTTCGATGA ACGA						
			A						
GAM2521	SKB1	3'	GAGCCTTGGAAGCAGCTTCAGG	21471				_	TTAC
	TT		AACCTGAAGCTGTT CTG CTC						
			TTGGACTTCGACGA GGT GAG						
			A TCC_						
GAM2521	LOC118491	5'	GAGGCCTCCAAACAGCTTCAGG	74356					CTGTTA
			CCTGAAGCTGTT CCTC						
			GGA						
			CTTCGACAA GGAG						
			ACCTCC						
GAM2521	LOC148864	5'	GCAGATCAGCTTCAGGTT	79803				T	
			AACCTGAAGCTG TCTGT						
			TTGGACTTCGAC AGACG						
			T						
GAM2521	LOC149600	5'	GAGACACAATCACAGCTTCA	85686				TC_	TAC
			TGAAGCTGT TGT CTC						
			ACTTCGACA ACA GAG						
			CTA CA_						
GAM2521	LOC150397	3'	AGGTAACAGAACGAGGCT	80651				_	
			AGCT GTTCTGTTACCT						
			TCGG CAAGACAATGGA						
			AG						
GAM2521	LOC152404	5'	AATAGGAACAGCTCCGGT	81455				T A	_
			ACC GA GCTGTTC TGTT						
			TGG CT CGACAAG ATAA						
			C _ G						
GAM2521	LOC153910	3'	AGGTACATCCCAGCTTCAGG	81902				TTC	T
			CCTGAAGCTG TGT ACCT						
			GGA						
			CTTCGAC ACA TGGA						
			CCT _						
GAM2521	LOC157506	3'	AGCAGTGTGACATCTTCAGGTT	82362				C	__
			AACCTGAAG TGTT CTGTT						
			TTGGACTTC ACAG GACGA						
			T TGT						
GAM2521	LOC161734	3'	AATAGGAACAGCTCCGGT	88457				T A	_
			ACC GA GCTGTTC TGTT						

		TGG CT CGACAAG ATAA		
		C _ G		
GAM2521	LOC170425 5'	AATAGGAACAGCTCCGGT	76881	T A _
		ACC GA GCTGTTC TGTT		
		TGG CT CGACAAG ATAA		
		C _ G		
GAM2521	LOC196477 5'	TGACGACAGCTTCAGGT	89065	CT
		ACCTGAAGCTGTT GTTA		
		TGGACTTCGACAG CAGT		
		—		
GAM2521	LOC200448 5'	AGGTAACAGCTTCAGCTTCAG	90246	TT_
		CTGAAGCTG CTGTTACCT		
		GACTTCGAC GACAATGGA		
		TTC		
GAM2521	LOC220840 3'	GAAGTAACAGGGAAGCTACAGG	92482	A G C
	TT	AACCTG AGCT TTCTGTTAC TC		
		TTGGAC TCGA GGGACAATG AG		
		A A A		
GAM2521	LOC222233 5'	GACCCCAACATGCTTCAGG	95905	_ CT_
		CCTGAAGC TGTT GTT		
		GGA CTTCG ACAA CAG		
		T CCC		
GAM2521	LOC92379 3'	AGGCCTTCAGGAACAGCTCAGG	69675	A GTTA_
		CCTGA GCTGTTCT CCT		
		GGA CT CGACAAGG GGA		
		— ACTTCC		
GAM2522	PIP5K1A 3'	TATCCCACCCTGCCTTGATA	14520	A CA C
		TATCAAGG AGGG GG GTG		
		ATAGTTCC TCCC CC TAT		
		G A_ C		
GAM2522	SOX11 3'	ACCCACCCCCCTTG GTA	13308	AA CA C
		TATCAAGG GGG GG GT		
		ATGGTTCC CCC CC CA		
		CC A_ _		
GAM2522	CHL1 3'	TGTTACCTTTCCTCAATA	22768	CA CA
		TAT AGGAAGGG GGCG		
		ATA TCCTTTCC TTGT		
		AC A_		
GAM2522	EPB41L1 3'	CATTCTGCCCTTCCCTGA	71104	A C
		TCA GGAAGGGCAGG GTG		

AGT CCTTCCCGTCT TAC
 C _
 GAM2522 FLJ00060 3' CATACCCCTGCCCTCCTCTGA 61741 _ A CGTG
 TCA AGGA GGGCAGG ATG
 ||| ||| ||||| |||
 AGT TCCT CCCGTCC TAC
 C _ CCCA
 GAM2522 FLJ10898 5' CACCACAGCCCTTTCTCAATA 60126 CA AGGC
 TAT AGGAAGGGC GTG
 ||| ||||| |||
 ATA TCTTTCCCG CAC
 AC ACAC
 GAM2522 FLJ22557 3' ATCATCCCATCCTTAATA 45581 C A CAGGC
 TAT AAGGA GGG GTGAT
 ||| ||||| ||| |||||
 ATA TTCCT CCC TACTA
 A A _____
 GAM2522 KIAA0574 3' CATCCCCTGCCCTCCCCTGA 69808 A A CGT
 TCA GG AGGGCAGG GATG
 ||| || ||||| |||||
 AGT CC TCCCGTCC CTAC
 C C C_
 GAM2522 KIAA0632 3' CACCTCAGAAACCCTTCCTTGA 32071 CA__ C
 TCAAGGAAGGG GG GTG
 ||||| ||| |||
 AGTTCCTTCCC CT CAC
 AAAGA C
 GAM2522 KIAA1354 5' CAGTGA CTGCCTTCCCTTGATA 61572 A G _
 TATCAAGG AGGGCAG CG TG
 ||||| ||||| ||| |||
 ATAGTTCC TTCCGTC GT AC
 C A G
 GAM2522 MGC20460 5' CACCGCCTCCTACCCTTCTT 54901 C__ _
 AGGAAGGG AGGCG TG
 ||||| ||||| |||
 TTCTTCCC TCCGC AC
 ATCC C
 GAM2522 LOC158476 3' CACGCCCCGCCCCCCCCATTGA 88186 _ AA_ A
 TCAA GG GGGC GGC GTG
 ||| || ||| |||||
 AGTT CC CCG CCGCAC
 A CCC C
 GAM2522 LOC90459 3' CACACCCGCCTAATTTTGT 63550 A_ A C
 CAAGGA GGGC GG GTG
 ||||| ||| ||| |||
 GTTTTT TCCG CC CAC
 AA C A
 GAM2523 A1BG 3' GAGATGGGGTTTCACCTTGTT 56292 C
 AACA GGTGAAACTCCGTCTC
 ||| ||||| ||||| |||||

			TTGT CCACTTTGGGGTAGAG			
			T			
GAM2523	ACT	3'	AGCATGGGTTTCAACACGT 40419	_	_	T _
			ACG GT GAAAC CCGT CT			
			TGC CA CTTTG GGTA GA			
			A A _ C			
GAM2523	ADAMTS4	3'	GAGACAGGGTTTCACCATGTT 18762	C		C
			AACA GGTGAAACTC GTCTC			
			TTGT CCACTTTGGG CAGAG			
			A A			
GAM2523	ADAMTS4	3'	GAGACGGGGTTTCACCATGTT 18763	C		
			AACA GGTGAAACTCCGTCTC			
			TTGT CCACTTTGGGGCAGAG			
			A			
GAM2523	ADCY6	5'	GAGACGGAGTCTCACTCTGT 40954	C		A
			ACA GGTGA ACTCCGTCTC			
			TGT TCACT TGAGGCAGAG			
			C C			
GAM2523	ALOX15	3'	GAGACGGGGCCTCACTATGTT 8547	CG		AA
			AACA GTGA CTCCGTCTC			
			TTGT CACT GGGGCAGAG			
			AT CC			
GAM2523	APAF1	3'	GAGACGGGGTTTCACCATGTT 25973	C		
			AACA GGTGAAACTCCGTCTC			
			TTGT CCACTTTGGGGCAGAG			
			A			
GAM2523	APOL1	3'	GAGATGGGGTTTCACCATGTT 14740	C		
			AACA GGTGAAACTCCGTCTC			
			TTGT CCACTTTGGGGTAGAG			
			A			
GAM2523	APPL	3'	GAGACGGGGTTTCACCGTGTT 24948			
			AACACGGTGAAACTCCGTCTC			
			TTGTGCCACTTTGGGGCAGAG			
GAM2523	ARCN1	3'	GAGACGGGGTTTCACCGTGTT 9754			
			AACACGGTGAAACTCCGTCTC			
			TTGTGCCACTTTGGGGCAGAG			
GAM2523	ATP7A	3'	GAGACGGGGTTTCGCCATGTT 5322	C		
			AACA GGTGAAACTCCGTCTC			

			TTGT CCGCTTTGGGGCAGAG		
			A		
GAM2523	AXL	3'	GAGACAGGGTTTCACCATGTT 41886	C	C
			AACA GGTGAAACTC GTCTC		
			TTGT CCACTTTGGG CAGAG		
			A A		
GAM2523	BRIP1	3'	GAGATGGGGTTTCACCATGTT 50209	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2523	C7	3'	GAGATGGGGTTTCACCATGTT 6986	C	T
			AACA GGTGAAAC CCGTCTC		
			TTGT CCACTTTG GGTAGAG		
			A _		
GAM2523	CAMLG	3'	GAGACAGAGTTTCGCTCTTGT 9999	C _	C
			ACA G GTGAAACTC GTCTC		
			TGT C CGCTTTGAG CAGAG		
			T T A		
GAM2523	CASP10	3'	GAGATGGGGTTTCACTATGTT 53258	CG	
			AACA GTGAAACTCCGTCTC		
			TTGT CACTTTGGGGTAGAG		
			AT		
GAM2523	CASP10	3'	GAGATGGGGTTTCACTATGTT 53259	CG	
			AACA GTGAAACTCCGTCTC		
			TTGT CACTTTGGGGTAGAG		
			AT		
GAM2523	CASP2	3'	GAGACAGGGTTTCACCATGTT 53332	C	C
			AACA GGTGAAACTC GTCTC		
			TTGT CCACTTTGGG CAGAG		
			A A		
GAM2523	CASP2	3'	GAGACAGGGTTTCACCATGTT 53333	C	C
			AACA GGTGAAACTC GTCTC		
			TTGT CCACTTTGGG CAGAG		
			A A		
GAM2523	CASP2	3'	GAGACAGGGTTTCACCATGTT 8709	C	C
			AACA GGTGAAACTC GTCTC		
			TTGT CCACTTTGGG CAGAG		
			A A		
GAM2523	CASP8	3'	GAGACAGGGTTTCACTGTGTT 54076		C
			AACACGGTGAAACTC GTCTC		

			TTGTGTCACTTTGGG CAGAG		
			A		
GAM2523	CASP8	3'	GAGACAGGGTTTCACTGTGTT 54077	C	
			AACACGGTGAAACTC GTCTC		
			TTGTGTCACTTTGGG CAGAG		
			A		
GAM2523	CCNF	3'	GAGACGGGATTTACCATGTT 10075	C	CT
			AACA GGTGAAA CCGTCTC		
			TTGT CCACTTT GGCAGAG		
			A AG		
GAM2523	CDC6	3'	GAGACAGGGTTTTACCATGTT 8821	C	C
			AACA GGTGAAACTC GTCTC		
			TTGT CCATTTTGGG CAGAG		
			A A		
GAM2523	CLECSF11	5'	GAGATGGGGTTTCACTATGTT 56149	CG	
			AACA GTGAAACTCCGTCTC		
			TTGT CACTTTGGGGTAGAG		
			AT		
GAM2523	CLECSF12	3'	GAGACAGAGTTTCGCTCTTGT 77212	C _	C
			ACA G GTGAAACTC GTCTC		
			TGT C CGCTTTGAG CAGAG		
			T T A		
GAM2523	CLNS1A	3'	GAGAGCTCCTTTGCGCCATGTT 8921	C	CTCCG
			AACA GGTGAAA TCTC		
			TTGT CCGCTTT AGAG		
			A CCTCG		
GAM2523	CNGA1	5'	GAGATGGGATTTACCATGTT 60240	C	CT
			AACA GGTGAAA CCGTCTC		
			TTGT CCACTTT GGTAGAG		
			A AG		
GAM2523	CNN2	3'	GAGATGGGGTTTCCCATGTT 16461	C T	
			AACA GG GAAACTCCGTCTC		
			TTGT CC CTTTGGGGTAGAG		
			A C		
GAM2523	COX15	3'	GAGACAGAGTTTCACTCTTGT 55286	C _	C
			ACA G GTGAAACTC GTCTC		
			TGT C CACTTTGAG CAGAG		
			T T A		
GAM2523	CR1	3'	GAGACGGGGTTTACCATGTT 6944	C	
			AACA GGTGAAACTCCGTCTC		

			TTGT CCACTTTGGGGCAGAG		
			A		
GAM2523	CTF1	3'	GAGACGAGGTTTCGCCATGTT 9016	C	TC
			AACA GGTGAAAC CGTCTC		
			TTGT CCGCTTTG GCAGAG		
			A GA		
GAM2523	CXCL16	3'	GAGACGGAGTCTCGCTCTGT 42168	C	A
			ACA GGTGA ACTCCGTCTC		
			TGT TCGCT TGAGGCAGAG		
			C C		
GAM2523	CXCL16	3'	GAGACGGGGTTTCACCATGTT 42169	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGCAGAG		
			A		
GAM2523	CYP1A2	3'	GAGACGGGTTTCACCATGTT 69659	C	T
			AACA GGTGAAAC CCGTCTC		
			TTGT CCACTTTG GGCAGAG		
			A _		
GAM2523	CYP1A2	3'	GAGACGAGGTTTCACTGTGTT 7515		TC
			AACACGGTGAAAC CGTCTC		
			TTGTGTCACTTTG GCAGAG		
			GA		
GAM2523	CYP1A2	3'	GAGATGGGGTTTCACCATGTT 7517	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2523	CYP51	3'	GAGACGGGGGTTTCACTATGTT 7616	CG	_
			AACA GTGAAACTCC GTCTC		
			TTGT CACTTTGGGG CAGAG		
			AT G		
GAM2523	DFFB	3'	ACGGGGTTTCACCATGTT 88749	C	
			AACA GGTGAAACTCCGT		
			TTGT CCACTTTGGGGCA		
			A		
GAM2523	DFFB	3'	GAGACGGGGTTTCACCATGTT 88771	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGCAGAG		
			A		
GAM2523	DHFR	3'	GAGATGGGGTTTCACCATGTT 7648	C	
			AACA GGTGAAACTCCGTCTC		

			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2523	DSC3	3'	GAGACGGAGTCTCGCTCTG 10439	C	A
			CA GGTGA ACTCCGTCTC		
			GT TCGCT TGAGGCAGAG		
			C C		
GAM2523	DSC3	3'	GAGACGGGGTTTCACTGTGTT 10440		
			AACACGGTGAAACTCCGTCTC		
			TTGTGTCACTTTGGGGCAGAG		
GAM2523	DSC3	3'	GAGACGGGGTTTCACTGTGTT 10441		
			AACACGGTGAAACTCCGTCTC		
			TTGTGTCACTTTGGGGCAGAG		
GAM2523	DSC3	3'	GAGACGGAGTCTCGCTCTG 44621	C	A
			CA GGTGA ACTCCGTCTC		
			GT TCGCT TGAGGCAGAG		
			C C		
GAM2523	DSCR3	3'	GAGACGGAGTCTCAGTCTGT 21314	—	A
			ACGG TGA ACTCCGTCTC		
			TGTC ACT TGAGGCAGAG		
			TG C		
GAM2523	EHD2	3'	GAGACGGGGTTTCACCATGTT 28222	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGCAGAG		
			A		
GAM2523	EIF2S3	3'	GAGACGGGGTTTCAGCATGTT 9208	CGG	
			AACA TGAAACTCCGTCTC		
			TTGT ACTTTGGGGCAGAG		
			ACG		
GAM2523	ENDOGL1	3'	GAGATGTGGTCTCGCCGTGT 18824	A	TC
			ACACGGTGA AC CGTCTC		
			TGTGCCGCT TG GTAGAG		
			C GT		
GAM2523	EPB72	3'	GAGACGGGGTTTCACCATGTT 15876	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGCAGAG		
			A		
GAM2523	F2RL2	3'	GAGACGGGGTTTCACCATGTT 15897	C	
			AACA GGTGAAACTCCGTCTC		

			TTGT CCACTTTGGGGCAGAG		
			A		
GAM2523	F2RL3	3'	AGACGGAGTTTCACCATGTT 15487	C	
			AACA GGTGAAACTCCGTCT		
			TTGT CCACTTTGAGGCAGA		
			A		
GAM2523	F3	3'	GAGACGGAGTCTTGCTCTGTT 67678	C	TG A
			AACA GG A ACTCCGTCTC		
			TTGT TC T TGAGGCAGAG		
			C GT C		
GAM2523	FANCF	3'	GAGACGGGGTTTCACCATG 42980	C	
			CA GGTGAAACTCCGTCTC		
			GT CCACTTTGGGGCAGAG		
			A		
GAM2523	FCAR	3'	GACAGGGTTTCACCATGTT 56573	C	C
			AACA GGTGAAACTC GTC		
			TTGT CCACTTTGGG CAG		
			A A		
GAM2523	FCAR	3'	GAGATGGGGTTTCACTGTGTT 56574		
			AACACGGTGAAACTCCGTCTC		
			TTGTGTCACTTTGGGGTAGAG		
GAM2523	FCRH1	3'	GAGACAAGATTTACCGT 54727		_ CC
			ACGGTGAAA CT GTCTC		
			TGCCACTTT GA CAGAG		
			A A_		
GAM2523	FEZ1	3'	GAGATGGGAGTTTCACCATGTT 18785	C	_
			AACA GGTGAAACTCC GTCTC		
			TTGT CCACTTTGAGG TAGAG		
			A G		
GAM2523	FGF5	3'	GAGACGGGGTTTCACCATGTT 53659	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGCAGAG		
			A		
GAM2523	FGF5	3'	GAGACGGGGTTTCACCATGTT 53660	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGCAGAG		
			A		
GAM2523	FSHPRH1	5'	GAGACATTGGTCTCACTGTGTT 23067	A	CC_
			AACACGGTGA ACT GTCTC		

			TTGTGTCACT TGG CAGAG		
			C TTA		
GAM2523	FUT1	3'	GAGACAGGGTTTCACCATGTT 5592	C	C
			AACA GGTGAAACTC GTCTC		
			TTGT CCACTTTGGG CAGAG		
			A A		
GAM2523	FUT1	3'	GAGACGGAGTCTTGCTCTGT 5593	C	TG A
			ACA GG A ACTCCGTCTC		
			TGT TC T TGAGGCAGAG		
			C GT C		
GAM2523	FUT1	3'	GAGACGGGGTTTCATCGTGTT 5594		
			AACACGGTGAAACTCCGTCTC		
			TTGTGCTACTTTGGGGCAGAG		
GAM2523	G6PC	3'	GAGATGGGATTTTCATCATGTT 5661	C	CT
			AACA GGTGAAA CCGTCTC		
			TTGT CTACTTT GGTAGAG		
			A AG		
GAM2523	GHR	3'	GAGACGGGGTTTCACCATGTT 5700	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGCAGAG		
			A		
GAM2523	GM2A	3'	GAGATGGGGTTTCACCATGTT 68382	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2523	GNE	3'	GACAGGGTTTCACCATGTT 19670	C	C
			AACA GGTGAAACTC GTC		
			TTGT CCACTTTGGG CAG		
			A A		
GAM2523	GPR4	3'	GAGACAGGGTCTCACTGTGTT 60578		A C
			AACACGGTGA ACTC GTCTC		
			TTGTGTCACT TGGG CAGAG		
			C A		
GAM2523	GRM7	5'	GAGATTGGGTTTCACCATGTT 7787	C	C
			AACA GGTGAAACTC GTCTC		
			TTGT CCACTTTGGG TAGAG		
			A T		
GAM2523	HCS	3'	GAGATGGTGTTTCACCATGTT 38981	C	T
			AACA GGTGAAAC CCGTCTC		

			TTGT CCACTTTG GGTAGAG		
			A T		
GAM2523	HTR1D	3'	AGACGGGGTTTCATCATGTT 7834	C	
			AACA GGTGAAACTCCGTCT		
			TTGT CTACTTTGGGGCAGA		
			A		
GAM2523	HTR1E	5'	GAGACGGGATTTCACCATGTT 7861	C	CT
			AACA GGTGAAA CCGTCTC		
			TTGT CCACTTT GGCAGAG		
			A AG		
GAM2523	HUNK	3'	ATGGGGTTTCGCCATGTT 28176	C	
			AACA GGTGAAACTCCGT		
			TTGT CCGCTTTGGGGTA		
			A		
GAM2523	HUS1	3'	GAGACAGGGTCTCACTGTGTT 92739	A	C
			AACACGGTGA ACTC GTCTC		
			TTGTGTCACT TGGG CAGAG		
			C A		
GAM2523	HYAL4	5'	GAGATGGGGTTTCACCGTGTT 25369		
			AACACGGTGAAACTCCGTCTC		
			TTGTGCCACTTTGGGGTAGAG		
GAM2523	IGF1	3'	GAGACGGGGTTTTACCATGTT 7074	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCATTTTGGGGCAGAG		
			A		
GAM2523	IL11	3'	GAGACAGGGTTTCACCATGTT 7185	C	C
			AACA GGTGAAACTC GTCTC		
			TTGT CCACTTTGGG CAGAG		
			A A		
GAM2523	IMPA2	5'	GAGATGGGGCTTCGCCATG 96946	C	A
			CA GGTGAA CTCCGTCTC		
			GT CCGCTT GGGGTAGAG		
			A C		
GAM2523	INMT	3'	GAGACGGAGTCTGGCTCTGT 23215	C	GAA
			ACA GGT ACTCCGTCTC		
			TGT TCG TGAGGCAGAG		
			C GTC		
GAM2523	INMT	3'	GAGACGGAGTTTCGCTCTGT 23216	C	
			ACA GGTGAAACTCCGTCTC		

			TGT TCGCTTTGAGGCAGAG		
			C		
GAM2523	ITGAM	3'	GAGACGGAGTCTCGCTCTGT 72311	C	A
			ACA GGTGA ACTCCGTCTC		
			TGT TCGCT TGAGGCAGAG		
			C C		
GAM2523	JRK	3'	GAGACAGGGTCTCACTGTGTT 87827	A	C
			AACACGGTGA ACTC GTCTC		
			TTGTGTCACT TGGG CAGAG		
			C A		
GAM2523	LLGL1	3'	AGACGGAGTCTTGCTCTGT 67410	C	TG A
			ACA GG A ACTCCGTCT		
			TGT TC T TGAGGCAGA		
			C GT C		
GAM2523	LLGL1	3'	GAGATGGGGTTTCACCATGTT 67419	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2523	LNK	3'	GAGACAGGGTTTCACCATGTT 19645	C	C
			AACA GGTGAAACTC GTCTC		
			TTGT CCACTTTGGG CAGAG		
			A A		
GAM2523	LTB4R	5'	GAGACGGGGTTTCACCATGTT 7464	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGCAGAG		
			A		
GAM2523	LYZ	3'	GAGACAGGGTTTCACCGTGTT 5895		C
			AACACGGTGAAACTC GTCTC		
			TTGTGCCACTTTGGG CAGAG		
			A		
GAM2523	MAGEA10	3'	AGACAGATTCTTCACTGTGTT 41082	AC_	C
			AACACGGTGAA TC GTCT		
			TTGTGTCACTT AG CAGA		
			CTT A		
GAM2523	MAK	3'	GAGACAGGGTTTCACCATGTT 20947	C	C
			AACA GGTGAAACTC GTCTC		
			TTGT CCACTTTGGG CAGAG		
			A A		
GAM2523	MDM2	3'	GAGACAGGGTTTCACCGTGTT 11493		C
			AACACGGTGAAACTC GTCTC		

			TTGTGCCACTTTGGG CAGAG		
			A		
GAM2523	MEF2A	5'	GAGATGGAGTTTCACCATGTT 20000	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGAGGTAGAG		
			A		
GAM2523	MEFV	3'	GAGACGGGGTTTCACCATGTT 5938	C	—
			AACA GGTGAAACTCC GTCTC		
			TTGT CCACTTTGGGG CAGAG		
			A G		
GAM2523	MHC2TA	3'	GAGACGGAGTCCCACCTTG 5986	C	AA
			CA GGTG ACTCCGTCTC		
			GT CCAC TGAGGCAGAG		
			T CC		
GAM2523	MLANA	3'	GAGACGGGGTTTCTCCATGTT 19763	C	T
			AACA GG GAAACTCCGTCTC		
			TTGT CC CTTTGGGGCAGAG		
			A T		
GAM2523	MRPL49	3'	GAGACGGAGTCTCACTCTGTT 70168	C	A
			AACA GGTGA ACTCCGTCTC		
			TTGT TCACT TGAGGCAGAG		
			C C		
GAM2523	MRPL49	3'	GAGATGGGGTTTCACCATGTT 70169	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2523	MTR	3'	GAGACAGGATTTCACTGTGTT 6018	C	—
			AACACGGTGAAA TCC GTCTC		
			TTGTGTCACTTT AGG CAGAG		
			— A		
GAM2523	NCOA6	5'	GATGGGGTTTCATCATGTT 26837	C	
			AACA GGTGAAACTCCGTC		
			TTGT CTACTTTGGGGTAG		
			A		
GAM2523	NDRG3	3'	GAGATGGAGTTTCACCATGTT 42766	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGAGGTAGAG		
			A		
GAM2523	NONO	3'	GAGACGGAGTCTTACTCTGT 82890	C	A
			ACA GGTGA ACTCCGTCTC		

			TGT TCATT TGAGGCAGAG		
			C C		
GAM2523	NQO1	3'	GAGACGGCGTTTCACCATGTT 8049	C	T
			AACA GGTGAAAC CCGTCTC		
			TTGT CCACTTTG GGCAGAG		
			A C		
GAM2523	PCDHA9	3'	GAGATGGGGTTTCACCGTGTT 49845		
			AACACGGTGAAACTCCGTCTC		
			TTGTGCCACTTTGGGGTAGAG		
GAM2523	PCDHA9	3'	GAGATGGGGTTTCATCATGTT 49846	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CTACTTTGGGGTAGAG		
			A		
GAM2523	PCDHB9	3'	GAGACGGAGTCTCGCTCTGT 39445	C	A
			ACA GGTGA ACTCCGTCTC		
			TGT TCGCT TGAGGCAGAG		
			C C		
GAM2523	PER2	3'	GAGACAGGGTTTCACCATGTT 43352	C	C
			AACA GGTGAAACTC GTCTC		
			TTGT CCACTTTGGG CAGAG		
			A A		
GAM2523	PIGR	3'	GAGACAAAGTCTCACTGTGT 72998	A	CC
			ACACGGTGA ACT GTCTC		
			TGTGTCACT TGA CAGAG		
			C AA		
GAM2523	PIGR	3'	GAGACAGGGTTTCACCGTGTT 72999		C
			AACACGGTGAAACTC GTCTC		
			TTGTGCCACTTTGGG CAGAG		
			A		
GAM2523	PIGR	3'	GAGACAGGGTTTCGCCATGTT 73000	C	C
			AACA GGTGAAACTC GTCTC		
			TTGT CCGCTTTGGG CAGAG		
			A A		
GAM2523	PIGR	3'	GAGACGGAGTCTCTCACTGT 73001	A	__
			ACGGTGA ACTCCGTCTC		
			TGTCACT TGAGGCAGAG		
			CTC		
GAM2523	PIK3C2B	3'	GAGACGGAGTCTCGCCCTGT 12100	C	A
			ACA GGTGA ACTCCGTCTC		

			TGT CCGCT TGAGGCAGAG		
			C C		
GAM2523	PIK3C2B	3'	GAGACGGGGTTTCACCATGTT 12101	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGCAGAG		
			A		
GAM2523	PIK3CD	3'	GAGACGGGGTTTCACCATGTT 18492	C	—
			AACA GGTGAAACTCC GTCTC		
			TTGT CCACTTTGGGG CAGAG		
			A G		
GAM2523	POU2AF1	3'	GAGACGGGGTTTCACCATGTT 21743	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGCAGAG		
			A		
GAM2523	PRKR	3'	AGACAGGGTTTCACCATGTT 12339	C	C
			AACA GGTGAAACTC GTCT		
			TTGT CCACTTTGGG CAGA		
			A A		
GAM2523	PRKWNK3	3'	GATGGGGTTTCACTATGTT 62233	CG	
			AACA GTGAAACTCCGTC		
			TTGT CACTTTGGGGTAG		
			AT		
GAM2523	PTGES	3'	GAGACGGGTTTCACCATGTT 18061	C	A T
			AACA GGTGAA C CCGTCTC		
			TTGT CCACTT G GGCAGAG		
			A —		
GAM2523	PTGIS	3'	GAGACGGGGTTTCCCATGTT 8209	C T	
			AACA GG GAAACTCCGTCTC		
			TTGT CC CTTTGGGGCAGAG		
			A C		
GAM2523	PTGIS	3'	GAGATGGGATTTCACCGT 8210	CT	
			ACGGTGAAA CCGTCTC		
			TGCCACTTT GGTAGAG		
			AG		
GAM2523	RAB36	3'	GAGATGGGGTTTCTCCATGTT 18171	C T	
			AACA GG GAAACTCCGTCTC		
			TTGT CC CTTTGGGGTAGAG		
			A T		
GAM2523	RABL2A	3'	GAGACGGAGTCTCGCTCTGT 23995	C	A
			ACA GGTGA ACTCCGTCTC		

			TGT TCGCT TGAGGCAGAG		
			C C		
GAM2523	RABL2A	3'	GAGACGGGGTTTCACCATGTT 23996	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGCAGAG		
			A		
GAM2523	RABL2B	3'	GAGACGGGGTTTCACCATGTT 23978	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGCAGAG		
			A		
GAM2523	RABL2B	3'	GAGACGGAGTCTCGCTCTGT 23977	C	A
			ACA GGTGA ACTCCGTCTC		
			TGT TCGCT TGAGGCAGAG		
			C C		
GAM2523	RBBP9	3'	GAGACAGGGTTTCACCATGTT 70691	C	C
			AACA GGTGAAACTC GTCTC		
			TTGT CCACTTTGGG CAGAG		
			A A		
GAM2523	RHD	3'	AGATGGGGTTTCACCATGTT 32807	C	
			AACA GGTGAAACTCCGTCT		
			TTGT CCACTTTGGGGTAGA		
			A		
GAM2523	RHD	3'	AGATGGGGTTTCACCATGTT 32809	C	
			AACA GGTGAAACTCCGTCT		
			TTGT CCACTTTGGGGTAGA		
			A		
GAM2523	RHD	3'	GACAGGGTTTCACCATGTT 32828	C	C
			AACA GGTGAAACTC GTC		
			TTGT CCACTTTGGG CAG		
			A A		
GAM2523	RHD	3'	GACAGGGTTTCACCATGTT 32829	C	C
			AACA GGTGAAACTC GTC		
			TTGT CCACTTTGGG CAG		
			A A		
GAM2523	RPH3AL	3'	GAGATGGGGTTTCTCCATGTT 23734	C	T
			AACA GG GAAACTCCGTCTC		
			TTGT CC CTTTGGGGTAGAG		
			A T		
GAM2523	RPP30	3'	GAGACGGGGTTTCACCGTGTT 22199		
			AACACGGTGAAACTCCGTCTC		

TTGTGCCACTTTGGGGCAGAG

GAM2523	S100B	3'	GAGCTTTCCAGCCGTGTT	21850	—	—
			AACACGGT GAAA CTC			
			TTGTGCCG CTTT GAG			
			AC C			
GAM2523	SAS	3'	GAGACAGGGTTTCACCATGTT	21101	C	C
			AACA GGTGAAACTC GTCTC			
			TTGT CCACTTTGGG CAGAG			
			A A			
GAM2523	SCML2	3'	GAGATGGGGTTTCTCCATGTT	21426	C	T
			AACA GG GAAACTCCGTCTC			
			TTGT CC CTTTGGGGTAGAG			
			A T			
GAM2523	SEPN1	3'	GAGACGGAGTCTTGCTCTGT	66972	C	TG A
			ACA GG A ACTCCGTCTC			
			TGT TC T TGAGGCAGAG			
			C GT C			
GAM2523	SERPINB9	3'	GAGACGGGGTTTCACCGTGTT	16021		
			AACACGGTGAAACTCCGTCTC			
			TTGTGCCACTTTGGGGCAGAG			
GAM2523	SH3BP2	3'	GAACCGGGGTTTCACCATGTT	13070	C	TC
			AACA GGTGAAACTCCG TC			
			TTGT CCACTTTGGGGC AG			
			A CA			
GAM2523	SH3GL3	5'	GAGATGGGTTTCACCATGTT	13108	C	T
			AACA GGTGAAAC CCGTCTC			
			TTGT CCACTTTG GGTAGAG			
			A —			
GAM2523	SHOX	3'	GAGACGGCGTTTCACCGTGTT	6575		T
			AACACGGTGAAAC CCGTCTC			
			TTGTGCCACTTTG GGCAGAG			
			C			
GAM2523	SHOX	3'	GAGATGGGGTTTGACCATGTT	6576	C	G
			AACA GGT AAACCTCCGTCTC			
			TTGT CCA TTTGGGGTAGAG			
			A G			
GAM2523	SIL	5'	GAGACGGGGTTTCACCATGTT	13155	C	
			AACA GGTGAAACTCCGTCTC			

			TTGT CCACTTTGGGGCAGAG		
			A		
GAM2523	SLA2	3'	GAGACGGAGTCTTGCCCTGTT 50890	C	TG A
			AACA GG A ACTCCGTCTC		
			TTGT CC T TGAGGCAGAG		
			C GT C		
GAM2523	SLC15A1	3'	GAGATGGGGTTTCACCATGTT 18642	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2523	SMAC	5'	GAGATGGGGTTTCACCATGTT 58001	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2523	SNAP23	3'	GAGACAGGGTTTCACCATGT 15139	C	C
			ACA GGTGAAACTC GTCTC		
			TGT CCACTTTGGG CAGAG		
			A A		
GAM2523	SNX15	3'	GACGGGGTTACACCATGTT 74120	C	A
			AACA GGTG AACTCCGTC		
			TTGT CCAC TTGGGGCAG		
			A A		
GAM2523	SPN	3'	GAGACAGAGTTTCGCTTTGT 13375	C	C
			ACA GGTGAAACTC GTCTC		
			TGT TCGCTTTGAG CAGAG		
			T A		
GAM2523	SPN	3'	GAGATGGGGTTTCACCATGTT 13376	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2523	TAPBP	3'	GAGACGGGGTTTCACCATGTT 13562	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGCAGAG		
			A		
GAM2523	TAPBP	3'	GAGACGGGGTTTCACCGTGTT 13563		
			AACACGGTGAAACTCCGTCTC		
			TTGTGCCACTTTGGGGCAGAG		
GAM2523	TAPBP	3'	GAGACGGGGTTTCACCGTGTT 13564		
			AACACGGTGAAACTCCGTCTC		

TTGTGCCACTTTGGGGCAGAG

GAM2523 TAT 3' GAGACAGGGTTTCACCATGTT 6255 C C
AACAGGTGAAACTC GTCTC
||||| |||||
TTGT CCACTTTGGG CAGAG
A A

GAM2523 TBXA2R 3' GAGACGGGGTTTCACCGTGTT 8358
AACACGGTGAAACTCCGTCTC
||||| |||||
TTGTGCCACTTTGGGGCAGAG

GAM2523 TDGF1 3' GAGACGGAGTCTCACTCTGT 13657 C A
ACA GGTGA ACTCCGTCTC
||| ||||| |||||
TGT TCACT TGAGGCAGAG
C C

GAM2523 TEM7 3' GAGACAGGGTCTCACTGTGT 40261 A C
ACACGGTGA ACTC GTCTC
||||| |||||
TGTGTCACT TGGG CAGAG
C A

GAM2523 TERF1 3' GAGGCGGGGTTTCACCATG 34394 C
CA GGTGAAACTCCGTCTC
|| ||||| |||||
GT CCACTTTGGGGCGGAG
A

GAM2523 TERF2 3' GAGACGGGGTTTCACCGTGTT 20152
AACACGGTGAAACTCCGTCTC
||||| |||||
TTGTGCCACTTTGGGGCAGAG

GAM2523 TIM3 3' GAGACAGGGTTTCACCATGTT 52356 C C
AACAGGTGAAACTC GTCTC
||||| |||||
TTGT CCACTTTGGG CAGAG
A A

GAM2523 TMPRSS3 3' GAGACAGGGTTTCACCATGTT 44025 C C
AACAGGTGAAACTC GTCTC
||||| |||||
TTGT CCACTTTGGG CAGAG
A A

GAM2523 TNFRSF10B 3' GAGACGGGGTTTCACCATGTT 15227 C
AACAGGTGAAACTCCGTCTC
||||| |||||
TTGT CCACTTTGGGGCAGAG
A

GAM2523 TP53 3' GAGATGGGGTCTCACAGTGTT 6801 G A
AACAC GTGA ACTCCGTCTC
||||| |||||

			TTGTG CACT TGGGGTAGAG		
			A C		
GAM2523	TPMT	3'	GAGACGGGGTTTCACCATGTT 6310	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGCAGAG		
			A		
GAM2523	TRAF5	3'	GAGACAGAGTTTCATTGT 17274	C	
			ACGGTGAAACTC GTCTC		
			TGTTACTTTGAG CAGAG		
			A		
GAM2523	TRAF5	3'	GAGACGGAGTTTTGCCATGTT 17275	C TG	
			AACA GG AAACCTCCGTCTC		
			TTGT CC TTTGAGGCAGAG		
			A GT		
GAM2523	TRIM9	5'	GAGACGGAGTCTCGCTCTGT 31452	C A	
			ACA GGTGA ACTCCGTCTC		
			TGT TCGCT TGAGGCAGAG		
			C C		
GAM2523	TRIM9	5'	GAGACGGAGTTTCGCTCTTGT 31453	C _	
			ACA G GTGAAACTCCGTCTC		
			TGT C CGCTTTGAGGCAGAG		
			T T		
GAM2523	TRPM6	3'	GAGATGGGGTTTCACCATGTT 35033	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2523	TRPV1	3'	GAGACAGAGTTTCACTCTTGT 55673	C _ C	
			ACA G GTGAAACTC GTCTC		
			TGT C CACTTTGAG CAGAG		
			T T A		
GAM2523	TRPV1	3'	GAGACAGAGTTTCACTCTTGT 55674	C _ C	
			ACA G GTGAAACTC GTCTC		
			TGT C CACTTTGAG CAGAG		
			T T A		
GAM2523	TRPV1	3'	GAGACGGGGTTTCACCATGTT 55675	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGCAGAG		
			A		
GAM2523	TRPV1	3'	GAGACGGGGTTTCACCATGTT 55676	C	
			AACA GGTGAAACTCCGTCTC		

			TTGT CCACTTTGGGGCAGAG		
			A		
GAM2523	UGDH	3'	GAGACAGGGTTTCACCATGT 13997	C	C
			ACA GGTGAAACTC GTCTC		
			TGT CCACTTTGGG CAGAG		
			A A		
GAM2523	VENTX2	3'	ATGGGGTTTCACCATGTT 27853	C	
			AACA GGTGAAACTCCGT		
			TTGT CCACTTTGGGGTA		
			A		
GAM2523	VHL	3'	GAGACAGTGTTCGCCATGTT 6857	C	TCC
			AACA GGTGAAAC GTCTC		
			TTGT CCGCTTTG CAGAG		
			A TGA		
GAM2523	VHL	3'	GAGACGGGGTTTCACCATGTT 6858	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGCAGAG		
			A		
GAM2523	VIPR2	3'	GAGACAGGGTTTCACCATGTT 14063	C	C
			AACA GGTGAAACTC GTCTC		
			TTGT CCACTTTGGG CAGAG		
			A A		
GAM2523	VIPR2	3'	GAGACGGAGTCTTGCTCTGT 14064	C	TG A
			ACA GG A ACTCCGTCTC		
			TGT TC T TGAGGCAGAG		
			C GT C		
GAM2523	WBSCR5	5'	GAGATGGAATTTACCGTGTT 42111		C
			AACACGGTGAAA TCCGTCTC		
			TTGTGCCACTTT AGGTAGAG		
			A		
GAM2523	XRCC2	3'	GAGACGGGGTTTCACCATGTT 19501	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGCAGAG		
			A		
GAM2523	YES1	3'	GAGACGCAGTTTCACCGTGTT 19536		C
			AACACGGTGAAACT CGTCTC		
			TTGTGCCACTTTGA GCAGAG		
			C		
GAM2523	YES1	3'	GAGACGGAGTCTCGCTCTG 19537	C	A
			CA GGTGA ACTCCGTCTC		

			GT TCGCT TGAGGCAGAG		
			C C		
GAM2523	ZNF157	3'	AGACGGGTTTCACCATGTT 14323	C	T
			AACA GGTGAAAC CCGTCT		
			TTGT CCACTTTG GGCAGA		
			A _		
GAM2523	ZNF264	3'	GAGACGGGGTTTCACCATGTT 14215	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGCAGAG		
			A		
GAM2523	AAK1	3'	GAGACAGAGTTTCACTCTTGT 30523	C _	C
			ACA G GTGAAACTC GTCTC		
			TGT C CACTTTGAG CAGAG		
			T T A		
GAM2523	AAK1	3'	GAGATGGGGTTTCTCCATGTT 30524	C T	
			AACA GG GAAACTCCGTCTC		
			TTGT CC CTTTGGGGTAGAG		
			A T		
GAM2523	ANAPC11	5'	GAGACGGAGTTTCGTCATGTT 33633	C GT	
			AACA G GAAACTCCGTCTC		
			TTGT C CTTTGAGGCAGAG		
			A TG		
GAM2523	ANKT	3'	GAGACAGGGTCTCACTGTGTT 33457	A	C
			AACACGGTGA ACTC GTCTC		
			TTGTGTCACT TGGG CAGAG		
			C A		
GAM2523	AP3S2	3'	GAGACAGGGTTTCACCATGTT 20652	C	C
			AACA GGTGAAACTC GTCTC		
			TTGT CCACTTTGGG CAGAG		
			A A		
GAM2523	APOL2	3'	GAGACGGGGTTTCACTGTGTT 48789		
			AACACGGTGAAACTCCGTCTC		
			TTGTGTCACTTTGGGGCAGAG		
GAM2523	ARHF	3'	GAGACAGGGTTTCACCATGTT 39269	C	C
			AACA GGTGAAACTC GTCTC		
			TTGT CCACTTTGGG CAGAG		
			A A		
GAM2523	ARHGAP5	5'	GAGATGGGGTTTCTCCATGTT 77602	C T	
			AACA GG GAAACTCCGTCTC		

			TTGT CC CTTTGGGGTAGAG		
			A T		
GAM2523	ASB16	3'	GAGACGGGGTCTCGCCATGTT 55983	C	A
			AACA GGTGA ACTCCGTCTC		
			TTGT CCGCT TGGGGCAGAG		
			A C		
GAM2523	ATP1B4	3'	GAGACAGGGTTTCACCATGTT 24844	C	C
			AACA GGTGAAACTC GTCTC		
			TTGT CCACTTTGGG CAGAG		
			A A		
GAM2523	BA108L7.2	3'	GAGATGGGGGTTTCACCATGTT 49075	C	—
			AACA GGTGAAACTCC GTCTC		
			TTGT CCACTTTGGGG TAGAG		
			A G		
GAM2523	BAGE	3'	GAGATGGAGTTTCACTGTGT 8639		
			ACACGGTGAAACTCCGTCTC		
			TGTGTCACCTTTGAGGTAGAG		
GAM2523	BNIP-S	3'	GAGACGGAGTCTCGCTCTGT 57101	C	A
			ACA GGTGA ACTCCGTCTC		
			TGT TCGCT TGAGGCAGAG		
			C C		
GAM2523	BNIP-S	3'	GAGACGGGGTTTCACCATGTT 57102	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGCAGAG		
			A		
GAM2523	BRAG	3'	GAGATGGGGTCTCGCCGTGTT 30101		A
			AACACGGTGA ACTCCGTCTC		
			TTGTGCCGCT TGGGGTAGAG		
			C		
GAM2523	C11orf17	3'	GAGACGGGGTTTAACCATGTT 40581	C	G
			AACA GGT AAACCTCCGTCTC		
			TTGT CCA TTTGGGGCAGAG		
			A A		
GAM2523	C13orf1	3'	GAGATGGGGTTTCACCATGTT 40362	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2523	C1orf24	3'	GAGATGGGGTTTCACCATGTT 54790	C	CT
			AACA GGTGAAA CCGTCTC		

			TTGT CCACTTT GGTAGAG		
			A TG		
GAM2523	C20orf142	3'	GAGATGGGGTTTCTCCATGTT 75283	C T	
			AACA GG GAAACTCCGTCTC		
			TTGT CC CTTTGGGGTAGAG		
			A T		
GAM2523	C9orf9	3'	GAGACAGCGTTTCACCATGTT 39020	C	TCC
			AACA GGTGAAAC GTCTC		
			TTGT CCACTTTG CAGAG		
			A CGA		
GAM2523	C9orf9	3'	GAGACGGAGTCTCGCTCTGT 39021	C	A
			ACA GGTGA ACTCCGTCTC		
			TGT TCGCT TGAGGCAGAG		
			C C		
GAM2523	CARD6	3'	GAGACAGAGTTTCACTCTTGT 51842	C _	C
			ACA G GTGAAACTC GTCTC		
			TGT C CACTTTGAG CAGAG		
			T T A		
GAM2523	CCRN4L	3'	GAGACGGGGTTTCACCGTGTT 25068		
			AACACGGTGAAACTCCGTCTC		
			TTGTGCCACTTTGGGGCAGAG		
GAM2523	CDC14B	3'	GAGACAGGGTTTCACCATGTT 53989	C	C
			AACA GGTGAAACTC GTCTC		
			TTGT CCACTTTGGG CAGAG		
			A A		
GAM2523	CDC14B	3'	GAGACGGAAGATGCCGTGTT 53990		GAAAC
			AACACGGT TCCGTCTC		
			TTGTGCCG AGGCAGAG		
			TAGA_		
GAM2523	CENPH	3'	GAGACGGGGTTTCACCGTGTT 43566		
			AACACGGTGAAACTCCGTCTC		
			TTGTGCCACTTTGGGGCAGAG		
GAM2523	CGI-96	3'	GGGTGGATTTTCATCGTGT 32295	C	GT
			ACACGGTGAAA TCC CT		
			TGTGCTACTTT AGG GG		
			_ TG		
GAM2523	CHRA1	3'	GAGACGGGGTTTCACCATGTT 34335	C	A
			AACA GGTGAA CTCCGTCTC		

			TTGT CCACTT GGGGCAGAG		
			A _		
GAM2523	CHSY1	3'	GAGACGGAGTCTCACTCTGTT 30568	C	A
			AACA GGTGA ACTCCGTCTC		
			TTGT TCACT TGAGGCAGAG		
			C C		
GAM2523	CHSY1	3'	GAGACGGGGTTTCACCATG 30569	C	
			CA GGTGAAACTCCGTCTC		
			GT CCACTTTGGGGCAGAG		
			A		
GAM2523	CIP29	3'	GAGACGGGGTTTCACCATGTT 51377	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGCAGAG		
			A		
GAM2523	COLEC12	3'	GAGGGGTTTCACAGTGTT 56104	G	G
			AACAC GTGAAACTCC TC		
			TTGTG CACTTTGGGG AG		
			A _		
GAM2523	CPSF2	3'	GAGACAGGGTTTCACCATGTT 62270	C	C
			AACA GGTGAAACTC GTCTC		
			TTGT CCACTTTGGG CAGAG		
			A A		
GAM2523	CPSF2	3'	GAGACGGGGTTTCTCCATGTT 62271	C	T
			AACA GG GAAACTCCGTCTC		
			TTGT CC CTTTGGGGCAGAG		
			A T		
GAM2523	DBR1	3'	GACAGGGTTTCACCGTGTT 33065		C
			AACACGGTGAAACTC GTC		
			TTGTGCCACTTTGGG CAG		
			A		
GAM2523	DCOHM	3'	GAGATGGGGTTTCGCCATGTT 50526		C
			AACA GGTGAAACTCCGTCTC		
			TTGT CCGCTTTGGGGTAGAG		
			A		
GAM2523	DGKD	3'	GAGACGGAGCTGCTGCTGT 60108	_	AAA
			ACA CCGTG CTCCGTCTC		
			TGT GTCGT GAGGCAGAG		
			C C_		
GAM2523	DKFZp434A2417	3'	GAGACGGGGTTTCTCCATGTT 66679	C	T
			AACA GG GAAACTCCGTCTC		

		TTGT CC CTTTGGGGCAGAG		
		A T		
GAM2523	DKFZP434C212 3'	ACGGGGTTTCACCATGTT	69477	C
		AACA GGTGAAACTCCGT		
		TTGT CCACTTTGGGGCA		
		A		
GAM2523	DKFZP434D146 3'	GAGACAGGGTTTCATCATGTT	32135	C C
		AACA GGTGAAACTC GTCTC		
		TTGT CTACTTTGGG CAGAG		
		A A		
GAM2523	DKFZP434F0318 3'	GAGACAGGGTTTCGCCATGTT	48758	C C
		AACA GGTGAAACTC GTCTC		
		TTGT CCGCTTTGGG CAGAG		
		A A		
GAM2523	DKFZp434F1719 3'	GAGATGGGATTTTCGCCATGTT	51015	C CT
		AACA GGTGAAA CCGTCTC		
		TTGT CCGCTTT GGTAGAG		
		A AG		
GAM2523	DKFZP564G092 5'	GAGACGGAGTTTCGCTCTTGT	32160	C _
		ACA G GTGAAACTCCGTCTC		
		TGT C CGCTTTGAGGCAGAG		
		T T		
GAM2523	DKFZP564O0423 3'	GAGATGGGGTCTCACTATGTT	93350	CG A
		AACA GTGA ACTCCGTCTC		
		TTGT CACT TGGGGTAGAG		
		AT C		
GAM2523	DKFZP586A0522 3'	GAGACAGGGTCTCACTGTGTT	26727	A C
		AACACGGTGA ACTC GTCTC		
		TTGTGTCACT TGGG CAGAG		
		C A		
GAM2523	DKFZp761F2014 3'	AGCACCTGGTTTCACCATG	39936	C CC _
		CA GGTGAAACT GT CT		
		GT CCACTTTGG CA GA		
		A TC C		
GAM2523	DKFZp761J139 5'	GAGATGGGGTTTGACCATGTT	51106	C G
		AACA GGT AAACCTCCGTCTC		
		TTGT CCA TTTGGGGTAGAG		
		A G		
GAM2523	DKFZp761N1114 3'	GAGACGGGATTTACCGTGTT	79786	CT
		AACACGGTGAAA CCGTCTC		

			TTGTGCCACTTT GGCAGAG		
			AG		
GAM2523	DKFZp761O0113	5'	GAGACGGGGTTTCTCCATGTT	37893	C T
			AACA GG GAAACTCCGTCTC		
			TTGT CC CTTTGGGGCAGAG		
			A T		
GAM2523	DKFZp762P2111	3'	GAGACAGGGTTTCATCATGTT	87635	C C
			AACA GGTGAAACTC GTCTC		
			TTGT CTACTTTGGG CAGAG		
			A A		
GAM2523	DSCR6	3'	GAGACTCGGTTTCACCATGTT	39068	C CC
			AACA GGTGAAACT GTCTC		
			TTGT CCACTTTGG CAGAG		
			A CT		
GAM2523	EREG	3'	GAGGCGGGGTTTCACCATGTT	9307	C
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGCGGAG		
			A		
GAM2523	ET	3'	GAGACGGAAGGATCGCTTC	44469	C AA _
			A GGTGA CT CCGTCTC		
			C TCGCT GA GGCAGAG		
			T AG A		
GAM2523	EVI5	3'	GAGACAGGTGTCTCACTGTGTT	20209	A T _
			AACACGGTGA AC CC GTCTC		
			TTGTGTCACT TG GG CAGAG		
			C T A		
GAM2523	EVI5	3'	GAGATGGGGTTTCACCATGTT	20211	C
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2523	FBP17	3'	GAGACAGGGTTTCACCGTGTT	73150	C
			AACACGGTGAAACTC GTCTC		
			TTGTGCCACTTTGGG CAGAG		
			A		
GAM2523	FER1L4	3'	GAGACAGGGTTTCACCATGTT	48122	C C
			AACA GGTGAAACTC GTCTC		
			TTGT CCACTTTGGG CAGAG		
			A A		
GAM2523	FKBP9	3'	GAGACGGGGTTTCACCGTGTT	95716	
			AACACGGTGAAACTCCGTCTC		

TTGTGCCACTTTGGGGCAGAG

GAM2523	FLJ00060	5'	GAGATGGAATTTACCATGTT	61748	C	C
			AACA GGTGAAA TCCGTCTC			
			TTGT CCACTTT AGGTAGAG			
			A A			
GAM2523	FLJ10298	3'	GAGACGGGGTTTCACCATGTT	36458	C	
			AACA GGTGAAACTCCGTCTC			
			TTGT CCACTTTGGGGCAGAG			
			A			
GAM2523	FLJ10346	5'	GAGGCAGGGTTTCACCATGTT	36524	C	C
			AACA GGTGAAACTC GTCTC			
			TTGT CCACTTTGGG CGGAG			
			A A			
GAM2523	FLJ10535	3'	GAGATGGGGTTTCACCATGTT	36748	C	
			AACA GGTGAAACTCCGTCTC			
			TTGT CCACTTTGGGGTAGAG			
			A			
GAM2523	FLJ10560	3'	GAGACGGGGTTTCACCGTGTT	36795		
			AACACGGTGAAACTCCGTCTC			
			TTGTGCCACTTTGGGGCAGAG			
GAM2523	FLJ10713	3'	GAGATGGGGTTTCACCATGTT	37003	C	
			AACA GGTGAAACTCCGTCTC			
			TTGT CCACTTTGGGGTAGAG			
			A			
GAM2523	FLJ10901	3'	GAGATGGGGTTTCATCATGTT	37363	C	
			AACA GGTGAAACTCCGTCTC			
			TTGT CTACTTTGGGGTAGAG			
			A			
GAM2523	FLJ10956	3'	GAGACGGGGTTTCACCATGTT	37467	C	
			AACA GGTGAAACTCCGTCTC			
			TTGT CCACTTTGGGGCAGAG			
			A			
GAM2523	FLJ11193	3'	GAGATGGGGTCTCACCATGTT	37750	C	A
			AACA GGTGA ACTCCGTCTC			
			TTGT CCACT TGGGGTAGAG			
			A C			
GAM2523	FLJ12363	3'	GATGGGGTTTCACCATGTT	50636	C	
			AACA GGTGAAACTCCGTCTC			

			TTGT CCACTTTGGGGTAG		
			A		
GAM2523	FLJ12409	3'	GAGACGGAGTTTGCTCTTGTT 47771	C _	G
			AACA G GT AACTCCGTCTC		
			TTGT C CG TTTGAGGCAGAG		
			T T _		
GAM2523	FLJ12581	3'	GAGACAGGGTTTCACTGTGTT 46335		C
			AACACGGTGAAACTC GTCTC		
			TTGTGTCACTTTGGG CAGAG		
			A		
GAM2523	FLJ12581	3'	GAGACGGAGTCTTGCTCTGT 46336	C TG	A
			ACA GG A ACTCCGTCTC		
			TGT TC T TGAGGCAGAG		
			C GT C		
GAM2523	FLJ12649	3'	GAGACGGAGTCTTGCCCTGT 45090	C TG	A
			ACA GG A ACTCCGTCTC		
			TGT CC T TGAGGCAGAG		
			C GT C		
GAM2523	FLJ12649	3'	GAGATAGGGTTTTACCATGTT 45091	C	CG
			AACA GGTGAAACTC TCTC		
			TTGT CCATTTTGGG AGAG		
			A AT		
GAM2523	FLJ12687	3'	GAGACAGGGTTTCACCATGTT 46751	C	C
			AACA GGTGAAACTC GTCTC		
			TTGT CCACTTTGGG CAGAG		
			A A		
GAM2523	FLJ12876	3'	GAGACGGAGTCTCGCTCTGT 43091	C	A
			ACA GGTGA ACTCCGTCTC		
			TGT TCGCT TGAGGCAGAG		
			C C		
GAM2523	FLJ12903	3'	GAGACGGAGTTTCGCTGTTGT 43071		_
			ACA CGGTGAAACTCCGTCTC		
			TGT GTCGCTTTGAGGCAGAG		
			T		
GAM2523	FLJ12960	3'	GAGACGGAGCCTTGCTCTGT 45296	C TG	AA
			ACA GG A CTCCGTCTC		
			TGT TC T GAGGCAGAG		
			C GT CC		
GAM2523	FLJ12960	3'	GAGATGGGGTTTCACCGT 45298		
			ACGGTGAAACTCCGTCTC		

TGCCACTTTGGGGTAGAG

GAM2523	FLJ12973	3'	GAGATGGGGTTTCATCATGTT	46642	C	
			AACA GGTGAAACTCCGTCTC			
			TTGT CTACTTTGGGGTAGAG			
			A			
GAM2523	FLJ13072	5'	GAGACAGGGTTTCACCATGTT	91391	C	C
			AACA GGTGAAACTC GTCTC			
			TTGT CCACTTTGGG CAGAG			
			A A			
GAM2523	FLJ13114	3'	GAGACGGAGTCTCACTCTGT	44902	C	A
			ACA GGTGA ACTCCGTCTC			
			TGT TCACT TGAGGCAGAG			
			C C			
GAM2523	FLJ13114	3'	GAGATGGAGTTTCACCATGTT	44903	C	
			AACA GGTGAAACTCCGTCTC			
			TTGT CCACTTTGAGGTAGAG			
			A			
GAM2523	FLJ13188	3'	GAGACAGAGTTTTGCTGTGTT	42190	TG	C
			AACACGG AAACTC GTCTC			
			TTGTGTC TTTGAG CAGAG			
			GT A			
GAM2523	FLJ13197	3'	AGACGGAGTCTCACTCTGTT	45173	C	A
			AACA GGTGA ACTCCGTCT			
			TTGT TCACT TGAGGCAGA			
			C C			
GAM2523	FLJ13197	3'	GAGACAAGAGTTTCACCATGTT	45180	C	C_
			AACA GGTGAAACTC GTCTC			
			TTGT CCACTTTGAG CAGAG			
			A AA			
GAM2523	FLJ13305	5'	GAGATGGGGTTTCACCATGTT	91711	C	
			AACA GGTGAAACTCCGTCTC			
			TTGT CCACTTTGGGGTAGAG			
			A			
GAM2523	FLJ13456	3'	GAGACAGAGTTTCACTCTGT	66547	C	C
			ACA GGTGAAACTC GTCTC			
			TGT TCACTTTGAG CAGAG			
			C A			
GAM2523	FLJ13769	5'	GAGATGGGGTTTCACTATGTT	47250	CG	
			AACA GTGAAACTCCGTCTC			

			TTGT CACTTTGGGGTAGAG		
			AT		
GAM2523	FLJ14442	3'	GAGATGGGGTTTTACCATGTT 52384	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCATTTTGGGGTAGAG		
			A		
GAM2523	FLJ14950	3'	GAGACAGGGTTTCACCATGTT 52789	C	C
			AACA GGTGAAACTC GTCTC		
			TTGT CCACTTTGGG CAGAG		
			A A		
GAM2523	FLJ14957	3'	GAGACGGGGTTTCACCATGTT 52820	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGCAGAG		
			A		
GAM2523	FLJ20034	3'	GAGATGGGGTCTCTCCATGTT 34847	C T A	
			AACA GG GA ACTCCGTCTC		
			TTGT CC CT TGGGGTAGAG		
			A T C		
GAM2523	FLJ20045	3'	GAGACGGAGTCTCGCTTTGTT 34885	C	A
			AACA GGTGA ACTCCGTCTC		
			TTGT TCGCT TGAGGCAGAG		
			T C		
GAM2523	FLJ20136	3'	GAGATGAGTTTCACCATGTT 35098	C	C
			AACA GGTGAAACTC GTCTC		
			TTGT CCACTTTGAG TAGAG		
			A -		
GAM2523	FLJ20344	3'	GAGACAGGGTTTCACCATGTT 35482	C	C
			AACA GGTGAAACTC GTCTC		
			TTGT CCACTTTGGG CAGAG		
			A A		
GAM2523	FLJ20507	3'	GAGACAGGGTTTCACCATGTT 35740	C	C
			AACA GGTGAAACTC GTCTC		
			TTGT CCACTTTGGG CAGAG		
			A A		
GAM2523	FLJ20511	3'	GAGGCGCAGTTTCACCGTGTT 35774		C
			AACACGGTGAAACT CGTCTC		
			TTGTGCCACTTTGA GCGGAG		
			C		
GAM2523	FLJ20897	5'	GAGACGGGGTTTCAACGTGTT 51475	G	
			AACACG TGAAACTCCGTCTC		

			TTGTGC ACTTTGGGGCAGAG		
			A		
GAM2523	FLJ21302	3'	GAGACAGGGTTTCACCATGTT 43509	C	C
			AACA GGTGAAACTC GTCTC		
			TTGT CCACTTTGGG CAGAG		
			A A		
GAM2523	FLJ21324	5'	GAGATGGGGTTTCACCATGTT 92855	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2523	FLJ21603	3'	GAGATGGGGTTTCACCCTGTT 45772	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGTAGAG		
			C		
GAM2523	FLJ22167	5'	GAGATGGGGTCTCACTGTGTT 44872		A
			AACACGGTGA ACTCCGTCTC		
			TTGTGTCACT TGGGGTAGAG		
			C		
GAM2523	FLJ22329	3'	GAGACGGGGTTTCACCATGTT 45401	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGCAGAG		
			A		
GAM2523	FLJ22529	3'	GAGACAGGGTTTTCATCATGTT 45944	C	C
			AACA GGTGAAACTC GTCTC		
			TTGT CTACTTTGGG CAGAG		
			A A		
GAM2523	FLJ22684	3'	GAGACAGGGTTTCACCATGTT 47469	C	C
			AACA GGTGAAACTC GTCTC		
			TTGT CCACTTTGGG CAGAG		
			A A		
GAM2523	FLJ22794	3'	GAGACAGGGTTTCACCATGTT 93247	C	C
			AACA GGTGAAACTC GTCTC		
			TTGT CCACTTTGGG CAGAG		
			A A		
GAM2523	FLJ22969	3'	GAGACAGGGTTTCACCATGTT 69205	C	C
			AACA GGTGAAACTC GTCTC		
			TTGT CCACTTTGGG CAGAG		
			A A		
GAM2523	FLJ23024	3'	GAGACGGGGTTTCACCATGTT 46842	C	
			AACA GGTGAAACTCCGTCTC		

			TTGT CCACTTTGGGGCAGAG		
			A		
GAM2523	FLJ23263	5'	GAGACGGAGTCTCACTCTGT 47802	C	A
			ACA GGTGA ACTCCGTCTC		
			TGT TCACT TGAGGCAGAG		
			C C		
GAM2523	FLJ23392	3'	GAGACAGGGTTTCACCATGTT 45892	C	C
			AACA GGTGAAACTC GTCTC		
			TTGT CCACTTTGGG CAGAG		
			A A		
GAM2523	FLJ23392	3'	GAGACAGGGTTTCACCGTGTT 45893		C
			AACACGGTGAAACTC GTCTC		
			TTGTGCCACTTTGGG CAGAG		
			A		
GAM2523	FLJ23392	3'	GAGACGGGGTTTCACCGTGTT 45894		
			AACACGGTGAAACTCCGTCTC		
			TTGTGCCACTTTGGGGCAGAG		
GAM2523	FLJ23519	3'	GAGATGGGGTTTCACCGTGTT 50951		
			AACACGGTGAAACTCCGTCTC		
			TTGTGCCACTTTGGGGTAGAG		
GAM2523	FLJ23556	3'	GAGACGGAGTCTTGCTCTGT 46441	C	TG A
			ACA GG A ACTCCGTCTC		
			TGT TC T TGAGGCAGAG		
			C GT C		
GAM2523	FLJ23556	3'	GAGACGGGGTTTCACCGTGTT 46442		
			AACACGGTGAAACTCCGTCTC		
			TTGTGCCACTTTGGGGCAGAG		
GAM2523	FLJ25416	5'	GAGATGGGGTTTCACCATGTT 59455	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2523	FLJ31101	3'	GAGACGGAGTCTTGCTCTG 36163	C	TG A
			CA GG A ACTCCGTCTC		
			GT TC T TGAGGCAGAG		
			C GT C		
GAM2523	FLJ31153	3'	GAGATGGGGTTTCACCATG 58748	C	
			CA GGTGAAACTCCGTCTC		

			GT CCACTTTGGGGTAGAG		
			A		
GAM2523	FLJ32865	3'	GAGACAGAGTTTCGCTCTTGT 58811	C _	C
			ACA G GTGAAACTC GTCTC		
			TGT C CGCTTTGAG CAGAG		
			T T A		
GAM2523	FLJ32865	3'	GAGACGGGGTTTCTCCGTGTT 58812		T
			AACACGG GAAACTCCGTCTC		
			TTGTGCC CTTTGGGGCAGAG		
			T		
GAM2523	FLJ32894	3'	GAGATGGGATTTCACTGTGTT 58998		CT
			AACACGGTGAAA CCGTCTC		
			TTGTGTCACTTT GGTAGAG		
			AG		
GAM2523	GMFB	3'	GAGGTTTTGTTTCACCTGTT 15941	C	TCCG
			AACA GGTGAAAC TCTC		
			TTGT CCACTTTG GGAG		
			_ TTTT		
GAM2523	GMPPB	5'	GAGACAGGGTTTCACCAGGTT 26221	AC	C
			AAC GGTGAAACTC GTCTC		
			TTG CCACTTTGGG CAGAG		
			GA A		
GAM2523	GNG4	3'	AGACGGGGTTTCACCATGTT 16837		C
			AACA GGTGAAACTCCGTCT		
			TTGT CCACTTTGGGGCAGA		
			A		
GAM2523	GOLGA3	3'	ATGGGGTTTCACCATGTT 20880		C
			AACA GGTGAAACTCCGT		
			TTGT CCACTTTGGGGTA		
			A		
GAM2523	GREB1	3'	GAGACGGGGTTTCACCATGTT 28568		C
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGCAGAG		
			A		
GAM2523	GRWD	3'	GAGACGGAGTCTTGGTCTGT 49782	_ G _	
			ACGG T AA ACTCCGTCTC		
			TGTC G TT TGAGGCAGAG		
			T G C		
GAM2523	GRWD	3'	GAGACGGGGTTTCACCATGTT 49783		C
			AACA GGTGAAACTCCGTCTC		

			TTGT CCACTTTGGGGCAGAG		
			A		
GAM2523	GTF2E1	3'	GAGGCAGGGTTTCACCATGTT 19799	C	C
			AACA GGTGAAACTC GTCTC		
			TTGT CCACTTTGGG CGGAG		
			A A		
GAM2523	GTPBG3	3'	GAGACAAGGTTTCACCATGTT 51897	C	CC
			AACA GGTGAAACT GTCTC		
			TTGT CCACTTTGG CAGAG		
			A AA		
GAM2523	HARS2	3'	GAGACGGGGTTTTACCATGTT 55865	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCATTTTGGGGCAGAG		
			A		
GAM2523	HRH4	3'	GAGATGAAGTCTCACTGTGTT 41540	A	C
			AACACGGTGA ACT CGTCTC		
			TTGTGTCACT TGA GTAGAG		
			C A		
GAM2523	HSMPP8	3'	GAGACGGAGTTTCGCTCTTGT 95134	C	_
			ACA G GTGAAACTCCGTCTC		
			TGT C CGCTTTGAGGCAGAG		
			T T		
GAM2523	HSNOV1	3'	GAGATGGGGTTTCGCCATGTT 34436	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCGCTTTGGGGTAGAG		
			A		
GAM2523	HSPC065	3'	GAGATGGGGTTTCACCATGTT 27152	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2523	HSPC065	3'	GAGATGGGGTTTCACGATGTT 27153	CG	
			AACA GTGAAACTCCGTCTC		
			TTGT CACTTTGGGGTAGAG		
			AG		
GAM2523	HSPC232	3'	GAGATGGGGTTCACCATGTT 33657	C	A
			AACA GGTGAA CTCCGTCTC		
			TTGT CCACTT GGGGTAGAG		
			A _		
GAM2523	HT002	3'	ACAGGGTTTCACCGTGTT 26783	C	
			AACACGGTGAAACTC GT		

			TTGTGCCACTTTGGG CA		
			A		
GAM2523	ICK	3'	GAGACGGGGTTTCACTGTGTT 33688		
			AACACGGTGAAACTCCGTCTC		
			TTGTGTCACTTTGGGGCAGAG		
GAM2523	JAM1	3'	AGACGGAGTCTCGCTCTGT 34213	C	A
			ACA GGTGA ACTCCGTCT		
			TGT TCGCT TGAGGCAGA		
			C C		
GAM2523	JAM1	3'	AGACGGAGTCTCGCTCTGT 34214	C	A
			ACA GGTGA ACTCCGTCT		
			TGT TCGCT TGAGGCAGA		
			C C		
GAM2523	JAM1	3'	GAGACAGGGTTTCACCATGTT 34228	C	C
			AACA GGTGAAACTC GTCTC		
			TTGT CCACTTTGGG CAGAG		
			A A		
GAM2523	JAM1	3'	GAGACAGGGTTTCACCATGTT 34229	C	C
			AACA GGTGAAACTC GTCTC		
			TTGT CCACTTTGGG CAGAG		
			A A		
GAM2523	JM11	3'	GAGACGGAGTCTTGCTCTGT 54360	C	TG A
			ACA GG A ACTCCGTCTC		
			TGT TC T TGAGGCAGAG		
			C GT C		
GAM2523	KIAA0063	3'	GAGATGGGGTTTCTCCATGTT 30258	C	T
			AACA GG GAAACTCCGTCTC		
			TTGT CC CTTTGGGGTAGAG		
			A T		
GAM2523	KIAA0161	3'	GAGACGGAGTTTCGCTTTTGT 29201	C_	
			ACA GGTGAAACTCCGTCTC		
			TGT TCGCTTTGAGGCAGAG		
			TT		
GAM2523	KIAA0161	3'	GAGACGGGGTTTCACCATGTT 29202	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGCAGAG		
			A		
GAM2523	KIAA0186	3'	GAGACAGAGTTTTACCATGTT 41108	C	C
			AACA GGTGAAACTC GTCTC		

			TTGT CCATTTTGAG CAGAG		
			A A		
GAM2523	KIAA0186	3'	GAGATGGGGTTTCACCATGTT 41109	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2523	KIAA0205	3'	GAGATGGGGTTTCACCATGTT 30214	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2523	KIAA0210	5'	GAGACGGAGGAGTTTCACCATG 29160	C	—
	TT		AACA GGTGAAACTCC GTCTC		
			TTGT CCACTTTGAGG CAGAG		
			A AGG		
GAM2523	KIAA0391	3'	GAGACGGGTTTTCACCATGTT 28611	C	CT
			AACA GGTGAAA CCGTCTC		
			TTGT CCACTTT GGCAGAG		
			A TG		
GAM2523	KIAA0426	3'	GAGACGGGGTTTTCACCATGTT 28927	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGCAGAG		
			A		
GAM2523	KIAA0441	3'	GAGACGGGGTCTCACTGT 29635	A	
			ACGGTGA ACTCCGTCTC		
			TGTCACT TGGGGCAGAG		
			C		
GAM2523	KIAA0446	5'	GAGACGGAGTCTCCCTATGTT 69451	CG T A	
			AACA G GA ACTCCGTCTC		
			TTGT C CT TGAGGCAGAG		
			AT C C		
GAM2523	KIAA0459	3'	GAGACGGGGTTTTCACCATGTT 61653	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGCAGAG		
			A		
GAM2523	KIAA0469	3'	GAGACGGGATTTCACTGTGTT 29982		CT
			AACACGGTGAAA CCGTCTC		
			TTGTGTCACTTT GGCAGAG		
			AG		
GAM2523	KIAA0472	5'	GAGACGGAGTCTCACTCTGT 72353	C	A
			ACA GGTGA ACTCCGTCTC		

			TGT TCACT TGAGGCAGAG		
			C C		
GAM2523	KIAA0495	3'	GAGATGGGATTTACCATGTT 63268	C	CT
			AACA GGTGAAA CCGTCTC		
			TTGT CCACTTT GG TAGAG		
			A AG		
GAM2523	KIAA0513	5'	GAGACAGGGTTTCGCCATGTT 29031	C	C
			AACA GGTGAAACTC GTCTC		
			TTGT CCGCTTTGGG CAGAG		
			A A		
GAM2523	KIAA0513	3'	GAGATGGGGTTTCACCATG 29032	C	
			CA GGTGAAACTCCGTCTC		
			GT CCACTTTGGGGTAGAG		
			A		
GAM2523	KIAA0527	3'	GAGATGGAGTTTCACCATGTT 97498	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGAGGTAGAG		
			A		
GAM2523	KIAA0555	3'	GAGACAGGGTTTCACTATG 60742	CG	C
			CA GTGAAACTC GTCTC		
			GT CACTTTGGG CAGAG		
			AT A		
GAM2523	KIAA0557	3'	GAGATGGGGTTTCTCCATGTT 78564	C	T
			AACA GG GAAACTCCGTCTC		
			TTGT CC CTTTGGGGTAGAG		
			A T		
GAM2523	KIAA0561	3'	GACGGGGTTTCACCATGTT 66478	C	
			AACA GGTGAAACTCCGTC		
			TTGT CCACTTTGGGGCAG		
			A		
GAM2523	KIAA0562	3'	GAGACGGAGTCTTGCTCTGTT 28822	C	TG A
			AACA GG A ACTCCGTCTC		
			TTGT TC T TGAGGCAGAG		
			C GT C		
GAM2523	KIAA0563	5'	GAGGCGGAGTTTCGCCATGTT 29884	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCGCTTTGAGGCGGAG		
			A		
GAM2523	KIAA0599	3'	GAGACGGGGTTTCGCCGTGTT 77693		
			AACACGGTGAAACTCCGTCTC		

TTGTGCCGCTTTGGGGCAGAG

GAM2523	KIAA0682	3'	GACGGGGTTTCACCATGT	33008	C	
			ACA GGTGAAACTCCGTC			
			TGT CCACTTTGGGGCAG			
			A			
GAM2523	KIAA0682	3'	GAGACTGGGTTTCACCATGT	30024	C	C
			ACA GGTGAAACTC GTCTC			
			TGT CCACTTTGGG CAGAG			
			A T			
GAM2523	KIAA0737	3'	GAGACAGGGTTTCACCATGTT	29809	C	C
			AACA GGTGAAACTC GTCTC			
			TTGT CCACTTTGGG CAGAG			
			A A			
GAM2523	KIAA0737	3'	GAGATGGGGTCTCACTATGTT	29810	CG	A
			AACA GTGA ACTCCGTCTC			
			TTGT CACT TGGGGTAGAG			
			AT C			
GAM2523	KIAA0798	3'	GAGACGGGGTTTCACTGTGTT	28447		
			AACACGGTGAAACTCCGTCTC			
			TTGTGTCACTTTGGGGCAGAG			
GAM2523	KIAA0828	3'	GAGACAGGGTTTCACTATGTT	82115	CG	C
			AACA GTGAAACTC GTCTC			
			TTGT CACTTTGGG CAGAG			
			AT A			
GAM2523	KIAA0831	3'	GAGACGGGGGTTTTCACCATGT	30637	C	—
			ACA GGTGAAA CTCCGTCTC			
			TGT CCACTTT GGGGCAGAG			
			A TG			
GAM2523	KIAA0841	3'	GACGGGGTTTCATCATGTT	71896	C	
			AACA GGTGAAACTCCGTC			
			TTGT CTACTTTGGGGCAG			
			A			
GAM2523	KIAA0861	3'	GAGACGGAGTCTCGCTCTGT	90348	C	A
			ACA GGTGA ACTCCGTCTC			
			TGT TCGCT TGAGGCAGAG			
			C C			
GAM2523	KIAA0861	3'	GAGACGGGGTTTCCCCGTGTT	90349		T
			AACACGG GAAACTCCGTCTC			

			TTGTGCC CTTTGGGGCAGAG		
			C		
GAM2523	KIAA0889	3'	GAGACGGGGTTTCACCGTGTT 31777		
			AACACGGTGAAACTCCGTCTC		
			TTGTGCCACTTTGGGGCAGAG		
GAM2523	KIAA0931	3'	GAGACGGGGTTTCACCATGTT 68012	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGCAGAG		
			A		
GAM2523	KIAA0961	3'	GAGATGGGGTTTCACCATGTT 30400	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2523	KIAA1040	3'	GAGACGGAGTCTCGCTCTGT 72687	C	A
			ACA GGTGA ACTCCGTCTC		
			TGT TCGCT TGAGGCAGAG		
			C C		
GAM2523	KIAA1041	3'	GAGATGGGGTTTCACCATGTT 30823	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2523	KIAA1054	3'	GAGGTGGGGTTTCACCGTGTT 68965		GT
			AACACGGTGAAACTCC CTC		
			TTGTGCCACTTTGGGG GAG		
			TG		
GAM2523	KIAA1115	5'	GAGACAGGGTTTCGCCATGTT 30691	C	C
			AACA GGTGAAACTC GTCTC		
			TTGT CCGCTTTGGG CAGAG		
			A A		
GAM2523	KIAA1161	5'	GAGATGGGGTTTACCATGTT 82646	C	A
			AACA GGTGAA CTCCGTCTC		
			TTGT CCATTT GGGGTAGAG		
			A _		
GAM2523	KIAA1170	3'	ACAGGGTTTCACCATGTT 70403	C	C
			AACA GGTGAAACTC GT		
			TTGT CCACTTTGGG CA		
			A A		
GAM2523	KIAA1170	3'	GAGACAGAGTTTCGCTCTTGT 70416	C _	C
			ACA G GTGAAACTC GTCTC		

			TGT C CGCTTTGAG CAGAG		
			TT A		
GAM2523	KIAA1198	3'	GAGACAGTGTTCACCATGTT 64036	C	TCC
			AACA GGTGAAAC GTCTC		
			TTGT CCACTTTG CAGAG		
			A TGA		
GAM2523	KIAA1198	3'	GAGACGGGGTTTCACCATGTT 64037	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGCAGAG		
			A		
GAM2523	KIAA1198	3'	GAGACGGGGTTTCACCATGTT 64038	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGCAGAG		
			A		
GAM2523	KIAA1198	3'	GAGACGGGGTTTCACCGTGTT 64039		
			AACACGGTGAAACTCCGTCTC		
			TTGTGCCACTTTGGGGCAGAG		
GAM2523	KIAA1198	3'	GAGATGGGGTTTCACCATGTT 64040	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2523	KIAA1198	3'	GAGATGGGGTTTCTCCATGTT 64041	C T	
			AACA GG GAAACTCCGTCTC		
			TTGT CC CTTTGGGGTAGAG		
			A T		
GAM2523	KIAA1200	3'	GAGACGGGGTTTCACCATGTT 63038	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGCAGAG		
			A		
GAM2523	KIAA1210	3'	GAGACGGGGTTTCACCATGTT 98070	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGCAGAG		
			A		
GAM2523	KIAA1254	3'	GAGATGGGGTTTCACCATGTT 70561	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2523	KIAA1443	3'	GAGACGGGGTTTCATCATGTT 64571	C T	
			AACA GGTGAAAC CCGTCTC		

		TTGT CTA	TTTG	GGCAGAG		
		A	—			
GAM2523	KIAA1456	3'	GAGACGGGGTTTCACCGTGTT	67555		
			AACACGGTGAAACTCCGTCTC			
			TTGTGCCACTTTGGGGCAGAG			
GAM2523	KIAA1465	3'	GAGACGGGGTTTCACCATGTT	61496	C	
			AACA GGTGAAACTCCGTCTC			
			TTGT CCACTTTGGGGCAGAG			
			A			
GAM2523	KIAA1467	3'	GAGACGGGGTTTCACCATGTT	72068	C	
			AACA GGTGAAACTCCGTCTC			
			TTGT CCACTTTGGGGCAGAG			
			A			
GAM2523	KIAA1493	3'	GAGATGGGGTTTCACCTTGTT	64841	C	
			AACA GGTGAAACTCCGTCTC			
			TTGT CCACTTTGGGGTAGAG			
			T			
GAM2523	KIAA1497	5'	GAGACAGGGTTTCACCATGTT	68123	C	C
			AACA GGTGAAACTC GTCTC			
			TTGT CCACTTTGGG CAGAG			
			A A			
GAM2523	KIAA1508	3'	ACAAGGTTTCACCATGTT	62532	C	CC
			AACA GGTGAAACT GT			
			TTGT CCACTTTGG CA			
			A AA			
GAM2523	KIAA1530	3'	GAGACGGGATTTCACTGTGTT	68561		CT
			AACACGGTGAAA CCGTCTC			
			TTGTGTCACTTT GGCAGAG			
			AG			
GAM2523	KIAA1600	5'	GAGCCGGGCTGCCACCGTGT	71942	AAAC	T
			ACACGGTG TCCG CTC			
			TGTGCCAC GGGC GAG			
			CGTC C			
GAM2523	KIAA1615	3'	GAGACGGGATATCTCCGTGTT	69277	T AAC	
			AACACGG GA TCCGTCTC			
			TTGTGCC CT GGGCAGAG			
			T ATA			
GAM2523	KIAA1617	3'	GAGACAGGGTTTCACCATGTT	93078	C	C
			AACA GGTGAAACTC GTCTC			

			TTGT CCACTTTGGG CAGAG		
			A A		
GAM2523	KIAA1655	3'	GAGACAGGTTTCACCATGTT 67187	C	CC
			AACA GGTGAAACT GTCTC		
			TTGT CCACTTTGG CAGAG		
			A A_		
GAM2523	KIAA1668	3'	GAGACGGGGTTTCACCGTGTT 67069		
			AACACGGTGAAACTCCGTCTC		
			TTGTGCCACTTTGGGGCAGAG		
GAM2523	KIAA1712	3'	GAGACAGGGTTTCACCATGTT 68158	C	C
			AACA GGTGAAACTC GTCTC		
			TTGT CCACTTTGGG CAGAG		
			A A		
GAM2523	KIAA1727	3'	GAGATGGGATCTCACTATGTT 64761	CG	AAC
			AACA GTGA TCCGTCTC		
			TTGT CACT GGGTAGAG		
			AT CTA		
GAM2523	KIAA1737	3'	ATGGGGTTTTACCGTGTT 67931		
			AACACGGTGAAACTCCGT		
			TTGTGCCATTTTGGGGTA		
GAM2523	KIAA1784	3'	ACGGGGTTTCACCATGTT 65738	C	
			AACA GGTGAAACTCCGT		
			TTGT CCACTTTGGGGCA		
			A		
GAM2523	KIAA1821	3'	GAGACAGGGTCTCACTGTGTT 72265	A	C
			AACACGGTGA ACTC GTCTC		
			TTGTGTCACT TGGG CAGAG		
			C A		
GAM2523	KIAA1877	3'	GAGACAGGGTTTCACCGTGTT 66749		C
			AACACGGTGAAACTC GTCTC		
			TTGTGCCACTTTGGG CAGAG		
			A		
GAM2523	KIAA1922	5'	GAGACAAAGTTTCGCTCTTGT 73994	C_	CC
			ACA G GTGAAACT GTCTC		
			TGT C CGCTTTGA CAGAG		
			T T AA		
GAM2523	KIAA1971	3'	GAGACGAGGTTTCACCGTGTT 74681		TC
			AACACGGTGAAAC CGTCTC		

			TTGTGCCACTTTG GCAGAG		
			GA		
GAM2523	KIAA1975	5'	GAGATGGGGTTTCACCATGTT 74422	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2523	KIAA1987	3'	GAGACGGAGCCAGGCTGTGT 89384	GAAA	
			ACACGGT CTCCGTCTC		
			TGTGTCG GAGGCAGAG		
			GACC		
GAM2523	KLK7	3'	GAGACAGGGTTTCACCATGTT 18544	C	C
			AACA GGTGAAACTC GTCTC		
			TTGT CCACTTTGGG CAGAG		
			A A		
GAM2523	LAMP3	3'	GACGGGGTTTCACCATGTT 60204	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGCAG		
			A		
GAM2523	LAMP3	3'	GAGACGGAGTTTCACTCTTGT 60205	C _	
			ACA G GTGAAACTCCGTCTC		
			TGT C CACTTTGAGGCAGAG		
			T T		
GAM2523	LIECG3	3'	GAGGGGGGTCTCACTGTGTT 88799	A	G
			AACACGGTGA ACTCC TCTC		
			TTGTGTCACT TGGGG GGAG		
			C _		
GAM2523	LNIR	3'	GAGATGGAGTCTCACTATGTT 48872	CG	A
			AACA GTGA ACTCCGTCTC		
			TTGT CACT TGAGGTAGAG		
			AT C		
GAM2523	LY75	3'	GAGATGGGGTTTCACCATGTT 11394	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2523	MAP-1	3'	GAGACGGGGTTTCACCATGTT 42441	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGCAGAG		
			A		
GAM2523	MCLC	3'	GAGATGGGGTTTCACCATGTT 31382	C	
			AACA GGTGAAACTCCGTCTC		

			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2523	MEF-2	3'	GAGACTGGGTTTCACCATGTT 65022	C	C
			AACA GGTGAAACTC GTCTC		
			TTGT CCACTTTGGG CAGAG		
			A T		
GAM2523	MGC10200	3'	GAGATGGGTTTCACCATGTT 59644	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2523	MGC13007	5'	GAATTGGTTCCACTGTGTT 51279	A	CCG
			AACACGGTG AACT TC		
			TTGTGTCAC TTGG AG		
			C TTA		
GAM2523	MGC15563	3'	GAGATGGGATCTCACCATGTT 52861	C	AAC
			AACA GGTGA TCCGTCTC		
			TTGT CCACT GGGTAGAG		
			A CTA		
GAM2523	MGC21675	3'	GAGACAGAGTTTCGCTCTTGT 54592	C _	C
			ACA G GTGAAACTC GTCTC		
			TGT C CGCTTTGAG CAGAG		
			TT A		
GAM2523	MGC21675	3'	GAGATGGGTTTCACCATGTT 54593	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2523	MGC2474	3'	GAGATGGGTTTCACCATGTT 43959	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2523	MGC4766	5'	GAGACGGGGTTTCACCGTGTT 49558		
			AACACGGTGAAACTCCGTCTC		
			TTGTGCCACTTTGGGGCAGAG		
GAM2523	moblak	3'	GAGACAGGGTTTCACCGTGTT 56400		C
			AACACGGTGAAACTC GTCTC		
			TTGTGCCACTTTGGG CAGAG		
			A		
GAM2523	MOCS3	3'	GAGGGGGTTTCACCATGTT 27932	C	G
			AACA GGTGAAACTCC TC		

			TTGT CCACTTTGGGG AG		
			A G		
GAM2523	MRPL20	3'	GAGACGGAGTCTCGCGCTGT 36203	AA__	
			ACGGTG ACTCCGTCTC		
			TGTCGC TGAGGCAGAG		
			GCTC		
GAM2523	MRPS27	3'	GAGATGGGGTTTCACCATGTT 31330	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2523	MtFMT	3'	GAGATGGGGTTTCACCATGTT 58336	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2523	MYO5C	3'	GAGACAGGTTTCACCATGTT 38719	C	CC
			AACA GGTGAAACT GTCTC		
			TTGT CCACTTTGG CAGAG		
			A A_		
GAM2523	NDP52	3'	GAGACAGGGTTTCACTATGTT 20671	CG	C
			AACA GTGAAACTC GTCTC		
			TTGT CACTTTGGG CAGAG		
			AT A		
GAM2523	NDUFC2	3'	GAGACGGGGTTTCACCATGTT 17031	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGCAGAG		
			A		
GAM2523	NINJ2	3'	GAGACGGGGTTTCTCCATGTT 33725	C T	
			AACA GG GAAACTCCGTCTC		
			TTGT CC CTTTGGGGCAGAG		
			A T		
GAM2523	Nup43	3'	GAGACGACAGGGTTTCACCATG 45347	C	__
	TT		AACA GGTGAAACTC CGTCTC		
			TTGT CCACTTTGGG GCAGAG		
			A ACA		
GAM2523	Nup43	3'	GAGATGGGGTTTCACTGTGTT 45348		
			AACACGGTGAAACTCCGTCTC		
			TTGTGTCACTTTGGGGTAGAG		
GAM2523	NXN	3'	GAGATGGGGTTTCACCATGTT 42675	C	
			AACA GGTGAAACTCCGTCTC		

			TTGT CCACTTTGGGGTAGAG			
			A			
GAM2523	OCT11	3'	GAGATGGGGTTTCACCATGTT 27590	C		
			AACA GGTGAAACTCCGTCTC			
			TTGT CCACTTTGGGGTAGAG			
			A			
GAM2523	OR51E2	3'	GAGACAGAGTTTCACCATGTT 48509	C		C
			AACA GGTGAAACTC GTCTC			
			TTGT CCACTTTGAG CAGAG			
			A A			
GAM2523	OSBPL2	3'	GAGACGGAGTTTCACTCTTGT 58486	C		_
			ACA G GTGAAACTCCGTCTC			
			TGT C CACTTTGAGGCAGAG			
			T T			
GAM2523	PASK	5'	GAGACAGAGTTTCGCTCTTGT 31411	C		C
			ACA G GTGAAACTC GTCTC			
			TGT C CGCTTTGAG CAGAG			
			T T A			
GAM2523	PASK	5'	GAGACGGGGTTTCTCCATGTT 31412	C		T
			AACA GG GAAACTCCGTCTC			
			TTGT CC CTTTGGGGCAGAG			
			A T			
GAM2523	PELI1	5'	GAGACGGAGTCTCACTCTGT 40640	C		A
			ACA GGTGA ACTCCGTCTC			
			TGT TCACT TGAGGCAGAG			
			C C			
GAM2523	PELI1	5'	GAGACGGGGTTTCACCATGTT 40641	C		
			AACA GGTGAAACTCCGTCTC			
			TTGT CCACTTTGGGGCAGAG			
			A			
GAM2523	PELI1	5'	GAGATGGGGTTTCACCATGTT 40642	C		
			AACA GGTGAAACTCCGTCTC			
			TTGT CCACTTTGGGGTAGAG			
			A			
GAM2523	PIP3-E	3'	GAGACCGGGGTTTACCATGTT 67352	C		A _
			AACA GGTGAA CTCCG TCTC			
			TTGT CCATTT GGGGC AGAG			
			A _ C			
GAM2523	PIP5K1C	3'	GAGACGGAAGCACGTGTGT 71302	_		AAAC
			ACACG GTG TCCGTCTC			

			TGTGT CAC AGGCAGAG		
			G GA__		
GAM2523	PRO0365	5'	GAGACGGGGTTTCACTATGTT 26982	CG	
			AACA GTGAAACTCCGTCTC		
			TTGT CACTTTGGGGCAGAG		
			AT		
GAM2523	PRO1992	3'	GAGACAGAGTTTCGCTCTTGT 26905	C _	C
			ACA G GTGAAACTC GTCTC		
			TGT C CGCTTTGAG CAGAG		
			T T A		
GAM2523	PRO2955	3'	GAGACAGGGTTTACCATGTT 38239	C	C
			AACA GGTGAAACTC GTCTC		
			TTGT CCATTTTGGG CAGAG		
			A A		
GAM2523	PSPH	3'	GAGACGGGGTTTGACCGTGTT 17134	G	
			AACACGGT AAACTCCGTCTC		
			TTGTGCCA TTTGGGGCAGAG		
			G		
GAM2523	PSTPIP2	3'	GAGACAGGGTTTACCATGTT 44655	C	C
			AACA GGTGAAACTC GTCTC		
			TTGT CCATTTTGGG CAGAG		
			A A		
GAM2523	RAB21	3'	GAGACGGAGTCTCGCTCTGT 31088	C	A
			ACA GGTGA ACTCCGTCTC		
			TGT TCGCT TGAGGCAGAG		
			C C		
GAM2523	RAB21	3'	GAGACGGGGTTTCACCAGGTT 31089	AC	
			AAC GGTGAAACTCCGTCTC		
			TTG CCACTTTGGGGCAGAG		
			GA		
GAM2523	RAB33B	3'	GATGGGGTTTCACCATGTT 49328	C	
			AACA GGTGAAACTCCGTC		
			TTGT CCACTTTGGGGTAG		
			A		
GAM2523	RAP140	3'	GAGACAGGGTTTCACTGTGTT 31515		C
			AACACGGTGAAACTC GTCTC		
			TTGTGTCACTTTGGG CAGAG		
			A		
GAM2523	RES4-25	3'	GAGACGGGGTTTCTCCATGTT 65267	C T	
			AACA GG GAAACTCCGTCTC		

			TTGT CC CTTTGGGGCAGAG		
			A T		
GAM2523	RNF8	3'	GAGACAGGGTTTCACCATGTT 15568	C	C
			AACA GGTGAAACTC GTCTC		
			TTGT CCACTTTGGG CAGAG		
			A A		
GAM2523	RNO2	5'	GAGATGGGGTGTTCACCATGTT 53937	C	A
			AACA GGTGA ACTCCGTCTC		
			TTGT CCACT TGGGGTAGAG		
			A G		
GAM2523	SCAMP-4	3'	GAGACAGAGTTTCACTCTGT 55348	C	C
			ACA GGTGAAACTC GTCTC		
			TGT TCACTTTGAG CAGAG		
			C A		
GAM2523	SCAMP-4	3'	GATGGGGTTTCACCATGTT 55350	C	
			AACA GGTGAAACTCCGTC		
			TTGT CCACTTTGGGGTAG		
			A		
GAM2523	SCYA16	3'	GAGACGGGATTCTACCATGTT 17172	C	A CT
			AACA GGTG AA CCGTCTC		
			TTGT CCAT TT GGCAGAG		
			A C AG		
GAM2523	SCYA28	3'	GACGGGGTTTCACCGTGTT 39543		
			AACACGGTGAAACTCCGTC		
			TTGTGCCACTTTGGGGCAG		
GAM2523	SERF1B	3'	GAGATGGGGTTTCACCATGTT 43697	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2523	SFXN2	3'	GAGACGGGGTTTCACCATG 74376	C	
			CA GGTGAAACTCCGTCTC		
			GT CCACTTTGGGGCAGAG		
			A		
GAM2523	SIRPB1	3'	GAGATGGGGTTTCTCCATGTT 21367	C	T
			AACA GG GAAACTCCGTCTC		
			TTGT CC CTTTGGGGTAGAG		
			A T		
GAM2523	SLC12A8	3'	GAGACAGGGTTTCACCATGTT 45237	C	C
			AACA GGTGAAACTC GTCTC		

			TTGT CCACTTTGGG CAGAG		
			A A		
GAM2523	SLC16A4	3'	GAGGCGGGGTTTCACCATGTT 17451	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGCGGAG		
			A		
GAM2523	SLC19A3	3'	GAGATGGGGTTTCACAATGTT 48243	CG	
			AACA GTGAAACTCCGTCTC		
			TTGT CACTTTGGGGTAGAG		
			AA		
GAM2523	SLC2A10	3'	GAGATGGGGTTTCACTGTGTT 48552		
			AACACGGTGAAACTCCGTCTC		
			TTGTGTCACTTTGGGGTAGAG		
GAM2523	SREC	3'	GAGACAGGGTTTCACCATGTT 14903	C	C
			AACA GGTGAAACTC GTCTC		
			TTGT CCACTTTGGG CAGAG		
			A A		
GAM2523	SS-56	3'	GAGACGGAGTTTCACCATGTT 60351	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGAGGCAGAG		
			A		
GAM2523	SULT1C2	3'	GAGACGAGGTTTCACCGTGTT 22713		TC
			AACACGGTGAAAC CGTCTC		
			TTGTGCCACTTTG GCAGAG		
			GA		
GAM2523	SULT1C2	3'	GAGACGGAGTCTCGCTCTGT 22714	C	A
			ACA GGTGA ACTCCGTCTC		
			TGT TCGCT TGAGGCAGAG		
			C C		
GAM2523	SUN1	3'	GAGACAGGGTTTCACTGTGTT 47914		C
			AACACGGTGAAACTC GTCTC		
			TTGTGTCACTTTGGG CAGAG		
			A		
GAM2523	SYT13	3'	GAGATGGGGTTTCACCATGTT 95101	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2523	TADA3L	3'	GAGACGGGGTTTCACCGTGTT 22040		
			AACACGGTGAAACTCCGTCTC		

TTGTGCCACTTTGGGGCAGAG

GAM2523	TBCC	3'	GAGACGGGGTTTCGCCATGTT	13604	C
			AACA GGTGAAACTCCGTCTC		
			TTGT CCGCTTTGGGGCAGAG		
			A		
GAM2523	TCL6	3'	GAGACAGGGTTTCACCGTGTT	40477	C
			AACACGGTGAAACTC GTCTC		
			TTGTGCCACTTTGGG CAGAG		
			A		
GAM2523	TCL6	5'	GAGACGAGGTTTCACCATGTT	40478	C TC
			AACA GGTGAAAC CGTCTC		
			TTGT CCACTTTG GCAGAG		
			A GA		
GAM2523	THEA	3'	GAGACACTTTTCACTGTGTT	66889	CTCC
			AACACGGTGAAA GTCTC		
			TTGTGTCACTTT CAGAG		
			CA__		
GAM2523	THEA	3'	GAGATGGGGTTTCACTGTGTT	66890	
			AACACGGTGAAACTCCGTCTC		
			TTGTGTCACTTTGGGGTAGAG		
GAM2523	TRIM16	3'	GAGACGGAGTCTCGCACTGTT	22371	CG A
			AACA GTGA ACTCCGTCTC		
			TTGT CGCT TGAGGCAGAG		
			CA C		
GAM2523	TRIM16	3'	GAGATGGGGTTTCACCATGTT	22372	C
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2523	TRIM5	3'	GAGACGGGGTTTCCCCATGTT	53470	C T
			AACA GG GAAACTCCGTCTC		
			TTGT CC CTTTGGGGCAGAG		
			A C		
GAM2523	TRIM5	3'	GAGACGGGGTTTCCCCATGTT	53471	C T
			AACA GG GAAACTCCGTCTC		
			TTGT CC CTTTGGGGCAGAG		
			A C		
GAM2523	TRIM6	3'	GAGATAGGGTTTCACCGTGTT	55181	CG
			AACACGGTGAAACTC TCTC		

			TTGTGCCACTTTGGG AGAG		
			AT		
GAM2523	TU12B1-TY 3'	GAGACGGGGTTTCACCATGTT 33849		C	
		AACA GGTGAAACTCCGTCTC			
		TTGT CCACTTTGGGGCAGAG			
		A			
GAM2523	TU12B1-TY 3'	GAGATGGGGTTTCACCATGTT 33850		C	
		AACA GGTGAAACTCCGTCTC			
		TTGT CCACTTTGGGGTAGAG			
		A			
GAM2523	TUCAN 3'	GAGACAGAGTTTTGCTATGTT 30977	CG TG	C	
		AACA G A AACTC GTCTC			
		TTGT C TTTGAG CAGAG			
		AT GT A			
GAM2523	TUSP 3'	GAGACGGAGTCCCACTCTTGT 40027	C _	AA	
		ACA G GTG ACTCCGTCTC			
		TGT C CAC TGAGGCAGAG			
		T T CC			
GAM2523	UBF-fl 3'	GATGGGGTTTTACCATGTT 52625		C	
		AACA GGTGAAACTCCGTC			
		TTGT CCATTTTGGGGTAG			
		A			
GAM2523	VDU1 3'	GAGATGGGGTTTCACCATGTT 31125		C	
		AACA GGTGAAACTCCGTCTC			
		TTGT CCACTTTGGGGTAGAG			
		A			
GAM2523	VPS33A 3'	GAGACGGAGTCTTGCTCTGT 43613	C TG	A	
		ACA GG A ACTCCGTCTC			
		TGT TC T TGAGGCAGAG			
		C GT C			
GAM2523	WBSCR23 3'	GAGACGGGGTTTCACCATGTT 47435		C	
		AACA GGTGAAACTCCGTCTC			
		TTGT CCACTTTGGGGCAGAG			
		A			
GAM2523	ZNF221 3'	ACGGGGTTTCACCGTGTT 26262			
		AACACGGTGAAACTCCGT			
		TTGTGCCACTTTGGGGCA			
GAM2523	ZNF338 3'	GAGACGGAGTCTCGCTCTGTT 42256	C	A	
		AACA GGTGA ACTCCGTCTC			

		TTGT TCGCT TGAGGCAGAG		
		C C		
GAM2523	LOC112687 3'	GAGACGGAGTCTCGCCCTGT 73234	C	A
		ACA GGTGA ACTCCGTCTC		
		TGT CCGCT TGAGGCAGAG		
		C C		
GAM2523	LOC112817 3'	GAGACAGAGTTTCACTCTGT 57326	C	C
		ACA GGTGAAACTC GTCTC		
		TGT TCACTTTGAG CAGAG		
		C A		
GAM2523	LOC112817 3'	GAGATGGGGTTTCACCGTGTT 57327		
		AACACGGTGAAACTCCGTCTC		
		TTGTGCCACTTTGGGGTAGAG		
GAM2523	LOC113523 5'	GAGACAGGGTTTCACCATGTT 73423	C	C
		AACA GGTGAAACTC GTCTC		
		TTGT CCACTTTGGG CAGAG		
		A A		
GAM2523	LOC113675 5'	GAGACGGAGTCTCGATCTGT 57379	C	_ A
		ACA GGT GA ACTCCGTCTC		
		TGT CTA CT TGAGGCAGAG		
		_ G C		
GAM2523	LOC115219 5'	GAGACGGGGTTTCATCATGTT 73695	C	
		AACA GGTGAAACTCCGTCTC		
		TTGT CTACTTTGGGGCAGAG		
		A		
GAM2523	LOC115648 3'	GAGACGGGGTTTCACCATGTT 60022	C	
		AACA GGTGAAACTCCGTCTC		
		TTGT CCACTTTGGGGCAGAG		
		A		
GAM2523	LOC120114 3'	GAGATGGGGTTTCACCATGTT 76045	C	
		AACA GGTGAAACTCCGTCTC		
		TTGT CCACTTTGGGGTAGAG		
		A		
GAM2523	LOC120224 5'	GAGACAGGGTTTCACCATGTT 57888	C	C
		AACA GGTGAAACTC GTCTC		
		TTGT CCACTTTGGG CAGAG		
		A A		
GAM2523	LOC120939 3'	GAGGGGGTTTCACCATGTT 76763	C	G
		AACA GGTGAAACTCC TC		

		TTGT CCACTTTGGGG AG		
		A G		
GAM2523	LOC121504 3'	GATACGGGGTTTCACCATGTT 74547	C	C
		AACA GGTGAAACTCCGT TC		
		TTGT CCACTTTGGGGCA AG		
		A T		
GAM2523	LOC124871 3'	GAGACGGGTCTCACTATGTT 74817	CG	A T
		AACA GTGA AC CCGTCTC		
		TTGT CACT TG GGCAGAG		
		AT C _		
GAM2523	LOC126364 3'	GAGATGGGGTTTCGCCATGTT 76192	C	
		AACA GGTGAAACTCCGTCTC		
		TTGT CCGCTTTGGGGTAGAG		
		A		
GAM2523	LOC126661 3'	GAGATGGGGTTTCACCATGTT 75057	C	
		AACA GGTGAAACTCCGTCTC		
		TTGT CCACTTTGGGGTAGAG		
		A		
GAM2523	LOC126669 3'	GAGACGAAGTCTCGCTGTGTT 75935	A	C
		AACACGGTGA ACT CGTCTC		
		TTGTGTCGCT TGA GCAGAG		
		C A		
GAM2523	LOC126917 3'	AGGCAGAGCCTCACTGTGTT 75082	AA	C
		AACACGGTGA CTC GTCT		
		TTGTGTCACT GAG CGGA		
		CC A		
GAM2523	LOC128077 3'	GAGACAGGGTTTCACCATGTT 75215	C	C
		AACA GGTGAAACTC GTCTC		
		TTGT CCACTTTGGG CAGAG		
		A A		
GAM2523	LOC128077 3'	GAGACGGAGTCTTGCTCTGT 75216	C	TG A
		ACA GG A ACTCCGTCTC		
		TGT TC T TGAGGCAGAG		
		C GT C		
GAM2523	LOC128077 3'	GAGACGGGGTTTCACCATGTT 75217	C	
		AACA GGTGAAACTCCGTCTC		
		TTGT CCACTTTGGGGCAGAG		
		A		
GAM2523	LOC128989 3'	GAGACGGAGTCTTGCTCTGT 75316	C	TG A
		ACA GG A ACTCCGTCTC		

		TGT TC T TGAGGCAGAG	
		C GT C	
GAM2523	LOC128989 3'	GAGACGGGGTTTCACCATGTT 75317	C
		AACA GGTGAAACTCCGTCTC	
		TTGT CCACTTTGGGGCAGAG	
		A	
GAM2523	LOC130813 3'	GAGATGGGGTTTCTCCATGTT 76275	C T
		AACA GG GAAACTCCGTCTC	
		TTGT CC CTTTGGGGTAGAG	
		A T	
GAM2523	LOC132241 5'	GAGAGTGGGGTTTCACTATGTT 75562	CG T _
		AACA GTGAAAC CCG TCTC	
		TTGT CACTTTG GGT AGAG	
		AT _ G	
GAM2523	LOC132625 3'	GAGATGGGGTTTCACCATGTT 76440	C
		AACA GGTGAAACTCCGTCTC	
		TTGT CCACTTTGGGGTAGAG	
		A	
GAM2523	LOC135154 3'	AGACAAGGTTTCACCATGTT 75718	C CC
		AACA GGTGAAACT GTCT	
		TTGT CCACTTTGG CAGA	
		A AA	
GAM2523	LOC142820 5'	GAGACGGAGTTTTGCCATGTT 76913	C TG
		AACA GG AAACCTCCGTCTC	
		TTGT CC TTTGAGGCAGAG	
		A GT	
GAM2523	LOC143187 3'	GAGATGGAGTTTCACCATGTT 59758	C
		AACA GGTGAAACTCCGTCTC	
		TTGT CCACTTTGAGGTAGAG	
		A	
GAM2523	LOC143916 3'	GAGATGGGGTTTCACCTTGTT 77141	C
		AACA GGTGAAACTCCGTCTC	
		TTGT CCACTTTGGGGTAGAG	
		T	
GAM2523	LOC144317 5'	GAGACTGGGGTTTCTCCATGTT 77295	C T _
		AACA GG GAAACTCC GTCTC	
		TTGT CC CTTTGGGG CAGAG	
		A T T	
GAM2523	LOC144871 3'	ATGGGGTTTCACTGTGTT 84118	
		AACACGGTGAAACTCCGT	

TTGTGTCACTTTGGGGTA

GAM2523	LOC145268	5'	GAGACAGAGTTTCACCATGTT	77579	C	C
			AACA GGTGAAACTC GTCTC			
			TTGT CCACTTTGAG CAGAG			
			A A			
GAM2523	LOC145453	5'	GAGACAGGGTCTCACTGTGT	77663	A	C
			ACACGGTGA ACTC GTCTC			
			TGTGTCACT TGGG CAGAG			
			C A			
GAM2523	LOC146050	3'	GAGATGGGGTTTCACCATGTT	78117	C	
			AACA GGTGAAACTCCGTCTC			
			TTGT CCACTTTGGGGTAGAG			
			A			
GAM2523	LOC146050	3'	GAGATGGGGTTTCTCCATGTT	78118	C	T
			AACA GG GAAACTCCGTCTC			
			TTGT CC CTTTGGGGTAGAG			
			A T			
GAM2523	LOC146229	3'	GACGGGGTTTCACCATGTT	78279	C	
			AACA GGTGAAACTCCGTC			
			TTGT CCACTTTGGGGCAG			
			A			
GAM2523	LOC146229	3'	GAGACGGAGTCTCGCTCTGT	78281	C	A
			ACA GGTGA ACTCCGTCTC			
			TGT TCGCT TGAGGCAGAG			
			C C			
GAM2523	LOC146229	3'	GAGACGGGGTTTCACCATGTT	78282	C	
			AACA GGTGAAACTCCGTCTC			
			TTGT CCACTTTGGGGCAGAG			
			A			
GAM2523	LOC146229	3'	GAGACGGGGTTTTACCGTGTT	78283		
			AACACGGTGAAACTCCGTCTC			
			TTGTGCCATTTTGGGGCAGAG			
GAM2523	LOC146346	5'	GAGACGGGGTTTCACCGTGTT	78397		
			AACACGGTGAAACTCCGTCTC			
			TTGTGCCACTTTGGGGCAGAG			
GAM2523	LOC146429	5'	AGACAGGGTTTCACCATG	84658	C	C
			CA GGTGAAACTC GTCT			

			GT CCACTTTGGG CAGA		
			A A		
GAM2523	LOC146603	5'	GAGACGGGGTTTCACCGTGTT 78595		
			AACACGGTGAAACTCCGTCTC		
			TTGTGCCACTTTGGGGCAGAG		
GAM2523	LOC146784	5'	GAGATGGGGTTTCACCATGTT 78713	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2523	LOC146839	3'	GAGACGGGGTTTCACCGTGTT 84842		
			AACACGGTGAAACTCCGTCTC		
			TTGTGCCACTTTGGGGCAGAG		
GAM2523	LOC146894	3'	GAGATGGGGTTTCACCATGTT 59862	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2523	LOC146901	3'	GAGACGGGGTTTCACCATGTT 84901	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGCAGAG		
			A		
GAM2523	LOC146909	3'	GAGATGGGGTTTCACCGTGTT 78772		
			AACACGGTGAAACTCCGTCTC		
			TTGTGCCACTTTGGGGTAGAG		
GAM2523	LOC146952	5'	GAGACGGAGTCTGGCTCTGTT 84928	C	GAA
			AACA GGT ACTCCGTCTC		
			TTGT TCG TGAGGCAGAG		
			C GTC		
GAM2523	LOC147054	3'	GATGGGGTTTCTCCATGTT 85007	C	T
			AACA GG GAAACTCCGTC		
			TTGT CC CTTTGGGGTAG		
			A T		
GAM2523	LOC147071	5'	GAGACGGAGTTTCACCATGTT 73365	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGAGGCAGAG		
			A		
GAM2523	LOC147080	5'	GAGACAAGGTTTCACCATGTT 85037	C	CC
			AACA GGTGAAACT GTCTC		

	TTGT CCACTTTGG CAGAG	
	A AA	
GAM2523 LOC147080 5'	GAGACGGAGTCTGGCTCTGT 85038	C GAA
	ACA GGT ACTCCGTCTC	
	TGT TCG TGAGGCAGAG	
	C GTC	
GAM2523 LOC147166 3'	GAGACGGAGTCTCGCACTGTT 78888	CG A
	AACA GTGA ACTCCGTCTC	
	TTGT CGCT TGAGGCAGAG	
	CA C	
GAM2523 LOC147166 3'	GAGATGGGGTTTCACCATGTT 78889	C
	AACA GGTGAAACTCCGTCTC	
	TTGT CCACTTTGGGGTAGAG	
	A	
GAM2523 LOC147219 5'	ATGCTGTTTACCGTGTT 85110	A TC
	AACACGGTGAA C CGT	
	TTGTGCCATTT G GTA	
	_ TC	
GAM2523 LOC147276 3'	GAGACGGGGCTTCTCCATGTT 78962	C T A
	AACA GG GAA CTCCGTCTC	
	TTGT CC CTT GGGGCAGAG	
	A T C	
GAM2523 LOC147429 3'	GAGATGGGGTTTCACCATGTT 78996	C
	AACA GGTGAAACTCCGTCTC	
	TTGT CCACTTTGGGGTAGAG	
	A	
GAM2523 LOC147694 3'	GAGACGGGGTTTCACCGTGTT 79097	
	AACACGGTGAAACTCCGTCTC	
	TTGTGCCACTTTGGGGCAGAG	
GAM2523 LOC147817 3'	GAGACGGAGTCTTCCTCTGT 79177	T_ _
	ACGG GAA ACTCCGTCTC	
	TGTC CTT TGAGGCAGAG	
	TC C	
GAM2523 LOC147841 3'	GAGACAGAGTTTCACTCTTGT 79228	C_ C
	ACA G GTGAAACTC GTCTC	
	TGT C CACTTTGAG CAGAG	
	T T A	
GAM2523 LOC147841 3'	GAGATGGAGTTTCACCATG 79229	C
	CA GGTGAAACTCCGTCTC	

		GT CCACTTTGAGGTAGAG		
		A		
GAM2523	LOC148137 3'	GAGACGGTGTTTCACTGTGTT	59099	T
		AACACGGTGAAAC CCGTCTC		
		TTGTGTCACTTTG GGCAGAG		
		T		
GAM2523	LOC148189 5'	GAGACGGGGTTTCACCATGTT	79448	C
		AACA GGTGAAACTCCGTCTC		
		TTGT CCACTTTGGGGCAGAG		
		A		
GAM2523	LOC148195 5'	GACGGGGTCTCAACACGT	85283	_ _ A
		ACG GT GA ACTCCGTC		
		TGC CA CT TGGGGCAG		
		A A C		
GAM2523	LOC148887 5'	GAGACAGGGTTTCACCATGTT	85401	C C
		AACA GGTGAAACTC GTCTC		
		TTGT CCACTTTGGG CAGAG		
		A A		
GAM2523	LOC149171 5'	GAGATGGGGTTTCTCCATGTT	79968	C T
		AACA GG GAAACTCCGTCTC		
		TTGT CC CTTTGGGGTAGAG		
		A T		
GAM2523	LOC149478 3'	GAGACGGGGTTTCACCATGTT	80170	C _
		AACA GGTGAAACTCC GTCTC		
		TTGT CCACTTTGGGG CAGAG		
		A G		
GAM2523	LOC149692 3'	GAGACAGGGTTTCACCATGTT	85735	C C
		AACA GGTGAAACTC GTCTC		
		TTGT CCACTTTGGG CAGAG		
		A A		
GAM2523	LOC149711 3'	GAGATGGGGTTTTACCATGTT	85852	C
		AACA GGTGAAACTCCGTCTC		
		TTGT CCATTTTGGGGTAGAG		
		A		
GAM2523	LOC149821 5'	GACGGAGTTTCACCGTGTT	85932	
		AACACGGTGAAACTCCGTC		
		TTGTGCCACTTTGAGGCAG		
GAM2523	LOC150054 5'	GATGGGGTTTCCCATGTT	85974	C T
		AACA GG GAAACTCCGTC		

		TTGT CC CTTTGGGGTAG			
		A _			
GAM2523	LOC150166 5'	ATGGGGTTTCACCATGTT	86032	C	
		AACA GGTGAAACTCCGT			
		TTGT CCACTTTGGGGTA			
		A			
GAM2523	LOC150282 5'	GAGATGGCGTTTCACCATGTT	80544	C	T
		AACA GGTGAAAC CCGTCTC			
		TTGT CCACTTTG GGTAGAG			
		A C			
GAM2523	LOC150397 3'	GAGACGCAGTTTCACCGTGTT	80663		C
		AACACGGTGAAACT CGTCTC			
		TTGTGCCACTTTGA GCAGAG			
		C			
GAM2523	LOC150848 5'	AGACAGAGTTTTATAAATGT	86316	CG_	C
		ACA GTGAAACTC GTCT			
		TGT TATTTTGAG CAGA			
		AAA A			
GAM2523	LOC150960 3'	GAGATGGGGTCTCACCCTGTT	80875	C	A
		AACA GGTGA ACTCCGTCTC			
		TTGT CCACT TGGGGTAGAG			
		C C			
GAM2523	LOC151050 5'	GAGACAGAGTTTCACCATGTT	80917	C	C
		AACA GGTGAAACTC GTCTC			
		TTGT CCACTTTGAG CAGAG			
		A A			
GAM2523	LOC151057 3'	GAGACGGGGTTTCACCATGTT	86388	C	
		AACA GGTGAAACTCCGTCTC			
		TTGT CCACTTTGGGGCAGAG			
		A			
GAM2523	LOC151201 3'	GAGACGGGGTTTCACCATGTT	86477	C	
		AACA GGTGAAACTCCGTCTC			
		TTGT CCACTTTGGGGCAGAG			
		A			
GAM2523	LOC151475 5'	GAGACGAGGTTTCACCATGTT	86593	C	TC
		AACA GGTGAAAC CGTCTC			
		TTGT CCACTTTG GCAGAG			
		A GA			
GAM2523	LOC151701 3'	GAGACGGGGTTTCACCATGTT	86672	C	
		AACA GGTGAAACTCCGTCTC			

		TTGT CCACTTTGGGGCAGAG			
		A			
GAM2523	LOC151826 3'	GAGACAGGGTTTCACCGTGTT 81182		C	
		AACACGGTGAAACTC GTCTC			
		TTGTGCCACTTTGGG CAGAG			
		A			
GAM2523	LOC151979 5'	GAGACGGGGTTTCACCATGTT 81249		C	
		AACA GGTGAAACTCCGTCTC			
		TTGT CCACTTTGGGGCAGAG			
		A			
GAM2523	LOC152137 3'	GAGCGGGTTTCACCATGTT 81317	C	T	T
		AACA GGTGAAAC CCG CTC			
		TTGT CCACTTTG GGC GAG			
		A _ _			
GAM2523	LOC152343 3'	GACTGGGTTTCACCATGTT 81427	C	C	
		AACA GGTGAAACTC GTC			
		TTGT CCACTTTGGG CAG			
		A T			
GAM2523	LOC152445 3'	GAGACAGGGTTTCACCATGTT 86948	C	C	
		AACA GGTGAAACTC GTCTC			
		TTGT CCACTTTGGG CAGAG			
		A A			
GAM2523	LOC152445 3'	GAGACGGAGTCTCGATCTGTT 86949	C	_	A
		AACA GGT GA ACTCCGTCTC			
		TTGT CTA CT TGAGGCAGAG			
		_ G C			
GAM2523	LOC152719 5'	GACGGGTTTCACCATGTT 87026	C	T	
		AACA GGTGAAAC CCGTC			
		TTGT CCACTTTG GGCAG			
		A _			
GAM2523	LOC152719 5'	GAGACGGAGTCTCGCTCTGT 87028	C	A	
		ACA GGTGA ACTCCGTCTC			
		TGT TCGCT TGAGGCAGAG			
		C C			
GAM2523	LOC152719 5'	GAGACGGGGTTTCACCATGTT 87029	C		
		AACA GGTGAAACTCCGTCTC			
		TTGT CCACTTTGGGGCAGAG			
		A			
GAM2523	LOC152794 5'	GAGATGGGGTTTCATCATGTT 81559	C		
		AACA GGTGAAACTCCGTCTC			

		TTGT CTACTTTGGGGTAGAG		
		A		
GAM2523	LOC153077 3'	GAGATGGGGCTTCACCATGTT 87126	C	A
		AACA GGTGAA CTCCGTCTC		
		TTGT CCACTT GGGGTAGAG		
		A C		
GAM2523	LOC153606 5'	GAGATAGGGTTTCACCATGTT 87257	C	CG
		AACA GGTGAACTC TCTC		
		TTGT CCACTTTGGG AGAG		
		A AT		
GAM2523	LOC153688 3'	GAGACAGGATTTTCATCGTGTT 87315	C	_
		AACACGGTGAAA TCC GTCTC		
		TTGTGCTACTTT AGG CAGAG		
		_ A		
GAM2523	LOC153688 3'	GAGACAGGGTTTCACCATGTT 87316	C	C
		AACA GGTGAACTC GTCTC		
		TTGT CCACTTTGGG CAGAG		
		A A		
GAM2523	LOC153688 3'	GAGACGGAGTCTCACTCTGT 87317	C	A
		ACA GGTGA ACTCCGTCTC		
		TGT TCACT TGAGGCAGAG		
		C C		
GAM2523	LOC153883 5'	ATGGGGTTTTACCATGTT 81887	C	
		AACA GGTGAACTCCGT		
		TTGT CCATTTTGGGGTA		
		A		
GAM2523	LOC154282 5'	GAGATGGTGTTTCACCATGTT 87404	C	T
		AACA GGTGAAAC CCGTCTC		
		TTGT CCACTTTG GGTAGAG		
		A T		
GAM2523	LOC154726 5'	GAGACAGAGTTTCGCTCTTGT 82009	C _	C
		ACA G GTGAACTC GTCTC		
		TGT C CGCTTTGAG CAGAG		
		T T A		
GAM2523	LOC154877 5'	GAGACAGGGTTTCACCCTGTT 87550	C	C
		AACA GGTGAACTC GTCTC		
		TTGT CCACTTTGGG CAGAG		
		C A		
GAM2523	LOC154877 3'	GAGTCGGGGTTTCACCATGTT 87553	C	T
		AACA GGTGAACTCCG CTC		

		TTGT CCACTTTGGGGC GAG		
		A T		
GAM2523	LOC155372 3'	GAGACGGAATTTACCATG	82258	C C
		CA GGTGAAA TCCGTCTC		
		GT CCACTTT AGGCAGAG		
		A A		
GAM2523	LOC157247 5'	GAGACAGAGTTTCATTCTTGT	82297	C_ C
		ACA GGTGAAACTC GTCTC		
		TGT TTACTTTGAG CAGAG		
		TC A		
GAM2523	LOC157506 3'	GAGACGGGGTTTCACCATGTT	82367	C
		AACA GGTGAAACTCCGTCTC		
		TTGT CCACTTTGGGGCAGAG		
		A		
GAM2523	LOC157798 5'	GAGACGGAGTCTTGCTGTGT	87858	TG A
		ACACGG A ACTCCGTCTC		
		TGTGTC T TGAGGCAGAG		
		GT C		
GAM2523	LOC157798 5'	GAGACGGGGTTTCACCTTGTT	87859	C
		AACA GGTGAAACTCCGTCTC		
		TTGT CCACTTTGGGGCAGAG		
		T		
GAM2523	LOC157858 5'	GAGACGGAATCTCACTCTGT	87890	C AAC
		ACA GGTGA TCCGTCTC		
		TGT TCACT AGGCAGAG		
		C CTA		
GAM2523	LOC158014 5'	GAGACGGAGTTTCACCATGTT	82559	C
		AACA GGTGAAACTCCGTCTC		
		TTGT CCACTTTGAGGCAGAG		
		A		
GAM2523	LOC158310 5'	GAGACAGGGTTTCACAATGTT	88082	CG C
		AACA GTGAAACTC GTCTC		
		TTGT CACTTTGGG CAGAG		
		AA A		
GAM2523	LOC158402 5'	GAGGGGGGTTTCACCGTGTT	88148	G
		AACACGGTGAAACTCC TCTC		
		TTGTGCCACTTTGGGG GGAG		
		-		
GAM2523	LOC158476 3'	GAGACAGGGTTTCACCATGTT	88194	C C
		AACA GGTGAAACTC GTCTC		

			TTGT CCACTTTGGG CAGAG		
			A A		
GAM2523	LOC158549 5'		GAGATAGGGGTTTCACCGTGTT 88224		—
			AACACGGTGAAACTCC GTCTC		
			TTGTGCCACTTTGGGG TAGAG		
			A		
GAM2523	LOC158668 3'		GAGGTGGGGTTTCACCATG 69901	C	GT
			CA GGTGAAACTCC CTC		
			GT CCACTTTGGGG GAG		
			A TG		
GAM2523	LOC158865 5'		GAGATGGGGACTTCACCGTGTT 88309		A_
			AACACGGTGAA CTCCGTCTC		
			TTGTGCCACTT GGGGTAGAG		
			CA		
GAM2523	LOC160646 3'		GAGACGGAGTCTCGGTCTGT 83112	—	A
			ACGG TGA ACTCCGTCTC		
			TGTC GCT TGAGGCAGAG		
			TG C		
GAM2523	LOC160646 3'		GAGATGGGGCTTCACCATGTT 83113	C	A
			AACA GGTGAA CTCCGTCTC		
			TTGT CCACTT GGGGTAGAG		
			A C		
GAM2523	LOC161829 3'		GAGATGGGGTTTCACCATGTT 83190		C
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2523	LOC162427 3'		ATGGGGTTTCACCATGTT 83220		C
			AACA GGTGAAACTCCGT		
			TTGT CCACTTTGGGGTA		
			A		
GAM2523	LOC162962 3'		GAGACGGAGTCTCTCTCTGT 83257	C T	A
			ACA GG GA ACTCCGTCTC		
			TGT TC CT TGAGGCAGAG		
			C T C		
GAM2523	LOC169611 3'		GAGACAGAGTTTCGCTTTTGTT 83649	C_	C
			AACA GGTGAAACTC GTCTC		
			TTGT TCGCTTTGAG CAGAG		
			TT A		
GAM2523	LOC170082 5'		GAGATGGGGTTTCACCATGTT 83443		C
			AACA GGTGAAACTCCGTCTC		

			TTGT CCACTTTGGGGTAGAG		
			A		
GAM2523	LOC196047 5'	GAGCCAGGGTTTCACCATGT	91154	C	CGT
		ACA GGTGAAACTC	CTC		
		TGT CCACTTTGGG	GAG		
		A	ACC		
GAM2523	LOC196411 3'	GAGATGGGGTTTCACTATGTT	89047	CG	
		AACA GTGAAACTCCGTCTC			
		TTGT CACTTTGGGGTAGAG			
		AT			
GAM2523	LOC196529 3'	GAGACAGGGTCTCACTGTGTT	89133	A	C
		AACACGGTGA ACTC	GTCTC		
		TTGTGTCACT TGGG	CAGAG		
		C	A		
GAM2523	LOC196529 3'	GAGACAGGGTTTCACTACGTT	89134	AC	C
		AAC GGTGAAACTC	GTCTC		
		TTG TCACTTTGGG	CAGAG		
		CA	A		
GAM2523	LOC197358 3'	GAGACGGGGTTTCATCATGTT	89432	C	
		AACA GGTGAAACTCCGTCTC			
		TTGT CTACTTTGGGGCAGAG			
		A			
GAM2523	LOC197358 3'	GAGATGGGGTTTCACCATGTT	89433	C	
		AACA GGTGAAACTCCGTCTC			
		TTGT CCACTTTGGGGTAGAG			
		A			
GAM2523	LOC199699 3'	AGACAGGGTTTCACCGTGTT	89664		C
		AACACGGTGAAACTC	GTCT		
		TTGTGCCACTTTGGG	CAGA		
		A			
GAM2523	LOC199725 5'	GAGACGGAGTCACTCTGT	91419	C	AA
		ACA GGTGA	CTCCGTCTC		
		TGT TCACT	GAGGCAGAG		
		C	—		
GAM2523	LOC199725 5'	GAGACGGGATTTACCATGTT	91420	C	CT
		AACA GGTGAAA	CCGTCTC		
		TTGT CCACTTT	GGCAGAG		
		A	AG		
GAM2523	LOC199786 3'	GAGACGGTGGTTTCACCATGTT	89753	C	—
		AACA GGTGAAACT	CCGTCTC		

		TTGT CCACTTTGG GGCAGAG		
		A T		
GAM2523	LOC199786 3'	GAGATGGGGTTTCACCATGTT 89754	C	
		AACA GGTGAAACTCCGTCTC		
		TTGT CCACTTTGGGGTAGAG		
		A		
GAM2523	LOC199906 3'	AGACAGGGTTTCATCATGTT 89842	C	C
		AACA GGTGAAACTC GTCT		
		TTGT CTACTTTGGG CAGA		
		A A		
GAM2523	LOC199907 3'	AGACAAAGTTGACCGCTGTT 89826	_	GA CC
		AACA CGGT AACT GTCT		
		TTGT GCCA TTGA CAGA		
		C G_ AA		
GAM2523	LOC200014 3'	GAGACGGTGTTCACCATGTT 89935	C	T
		AACA GGTGAAAC CCGTCTC		
		TTGT CCACTTTG GGCAGAG		
		A T		
GAM2523	LOC200107 5'	GATCCGGTTTCATCGTGTT 89987		CC
		AACACGGTGAAACT GTC		
		TTGTGCTACTTTGG TAG		
		CC		
GAM2523	LOC200169 5'	GAGACGGAGTTTCACCATGTT 91556	C	
		AACA GGTGAAACTCCGTCTC		
		TTGT CCACTTTGAGGCAGAG		
		A		
GAM2523	LOC200301 5'	GAGACGGGGTTTCACCGTGTT 90140		
		AACACGGTGAAACTCCGTCTC		
		TTGTGCCACTTTGGGGCAGAG		
GAM2523	LOC200310 3'	GAGACGGGGTTTCACCATGTT 66327	C	
		AACA GGTGAAACTCCGTCTC		
		TTGT CCACTTTGGGGCAGAG		
		A		
GAM2523	LOC200316 3'	GACTGGGTTTCACCATGTT 90181	C	C
		AACA GGTGAAACTC GTC		
		TTGT CCACTTTGGG CAG		
		A T		
GAM2523	LOC200316 3'	GAGACGGAGTTTCACTCTGT 90182	C	
		ACA GGTGAAACTCCGTCTC		

		TGT TCACTTTGAGGCAGAG		
		C		
GAM2523	LOC200316 5'	GAGACGGGGTTTCTCCATGTT 90183	C	T
		AACA GG GAAACTCCGTCTC		
		TTGT CC CTTTGGGGCAGAG		
		A T		
GAM2523	LOC200845 5'	GAGATGGGGTTTCACTATGTT 90317	CG	
		AACA GTGAAACTCCGTCTC		
		TTGT CACTTTGGGGTAGAG		
		AT		
GAM2523	LOC200860 3'	GAGACGGGGTTTCTCCATGTT 91749	C	T
		AACA GG GAAACTCCGTCTC		
		TTGT CC CTTTGGGGCAGAG		
		A T		
GAM2523	LOC201164 3'	GAGACAGGGTTTCACCATGTT 89494	C	C
		AACA GGTGAAACTC GTCTC		
		TTGT CCACTTTGGG CAGAG		
		A A		
GAM2523	LOC201173 5'	GAGACGGAGTTTCACCATGTT 88685	C	
		AACA GGTGAAACTCCGTCTC		
		TTGT CCACTTTGAGGCAGAG		
		A		
GAM2523	LOC201220 5'	GAGATGGAGTTTCACCATGTT 88720	C	
		AACA GGTGAAACTCCGTCTC		
		TTGT CCACTTTGAGGTAGAG		
		A		
GAM2523	LOC201294 3'	GAGACGGAGTCTCGCTCTGT 89583	C	A
		ACA GGTGA ACTCCGTCTC		
		TGT TCGCT TGAGGCAGAG		
		C C		
GAM2523	LOC201294 3'	GAGACGGGGTTTCACCATGTT 89584	C	
		AACA GGTGAAACTCCGTCTC		
		TTGT CCACTTTGGGGCAGAG		
		A		
GAM2523	LOC201411 3'	GAGACAGGGTTTCACCATGTT 63642	C	C
		AACA GGTGAAACTC GTCTC		
		TTGT CCACTTTGGG CAGAG		
		A A		
GAM2523	LOC201627 3'	GAGATGGGGTTTCTCCATGTT 90455	C	T
		AACA GG GAAACTCCGTCTC		

		TTGT CC CTTTGGGGTAGAG		
		A T		
GAM2523	LOC202460 5'	GAGATGGGGTTTCACCATGT	90671	C
		ACA GGTGAAACTCCGTCTC		
		TGT CCACTTTGGGGTAGAG		
		A		
GAM2523	LOC202908 5'	GAGATGGGGTCTCACCCCTGT	90725	C A
		ACA GGTGA ACTCCGTCTC		
		TGT CCACT TGGGGTAGAG		
		C C		
GAM2523	LOC203197 3'	GAGATGGGGTTTCGCCATGTT	90812	C
		AACA GGTGAAACTCCGTCTC		
		TTGT CCGCTTTGGGGTAGAG		
		A		
GAM2523	LOC203339 3'	GAGATGGGGTTTCACCATGTT	92211	C
		AACA GGTGAAACTCCGTCTC		
		TTGT CCACTTTGGGGTAGAG		
		A		
GAM2523	LOC203350 3'	GAGACGGGGTTTCACCGTGTT	92240	
		AACACGGTGAAACTCCGTCTC		
		TTGTGCCACTTTGGGGCAGAG		
GAM2523	LOC203369 3'	GAGACGGAGTCTTGCCGCGT	90887	A TG A
		AC CGG A ACTCCGTCTC		
		TG GCC T TGAGGCAGAG		
		C GT C		
GAM2523	LOC203369 3'	GATGGGGTTTCACTGTGTT	90889	
		AACACGGTGAAACTCCGTC		
		TTGTGTCACTTTGGGGTAG		
GAM2523	LOC204804 3'	GAGACAGGGTCTCACTGTGT	91043	A C
		ACACGGTGA ACTC GTCTC		
		TGTGTCACT TGGG CAGAG		
		C A		
GAM2523	LOC205251 5'	GACAGGGTTTCACCATGTT	92357	C C
		AACA GGTGAAACTC GTC		
		TTGT CCACTTTGGG CAG		
		A A		
GAM2523	LOC219445 5'	GACGGGGTTTCACCGTGTT	93204	
		AACACGGTGAAACTCCGTC		

TTGTGCCACTTTGGGGCAG

GAM2523	LOC219731	5'	GAGACAGAGTTTCGTCATGTT	94706	C	GT	C
			AACA G GAAACTC GTCTC				
			TTGT C CTTTGAG CAGAG				
			A TG A				
GAM2523	LOC219735	3'	GAGACGGGGTTTCACCGTGTT	94728			
			AACACGGTGAAACTCCGTCTC				
			TTGTGCCACTTTGGGGCAGAG				
GAM2523	LOC219894	3'	GAGATGGGGTTTCACCGTGTT	94905			
			AACACGGTGAAACTCCGTCTC				
			TTGTGCCACTTTGGGGTAGAG				
GAM2523	LOC220064	3'	AGACGGAGTCTCACTCTGT	95059	C	A	
			ACA GGTGA ACTCCGTCT				
			TGT TCACT TGAGGCAGA				
			C C				
GAM2523	LOC220074	3'	GAGACAAGGTTTCGCCATGTT	59978	C	CC	
			AACA GGTGAAACT GTCTC				
			TTGT CCGCTTTGG CAGAG				
			A AA				
GAM2523	LOC220074	3'	GAGACGGAGTCTCACTCTGT	59979	C	A	
			ACA GGTGA ACTCCGTCTC				
			TGT TCACT TGAGGCAGAG				
			C C				
GAM2523	LOC220074	3'	GAGACGGAGTCTCGCTCTGT	59980	C	A	
			ACA GGTGA ACTCCGTCTC				
			TGT TCGCT TGAGGCAGAG				
			C C				
GAM2523	LOC220074	3'	GAGACGGGGTTTCACCATGTT	59981	C		
			AACA GGTGAAACTCCGTCTC				
			TTGT CCACTTTGGGGCAGAG				
			A				
GAM2523	LOC220074	3'	GAGATGGGGTTTCGCCATGTT	59982	C		
			AACA GGTGAAACTCCGTCTC				
			TTGT CCGCTTTGGGGTAGAG				
			A				
GAM2523	LOC221035	3'	GAGACGGAGTCTTGCTCTGT	94780	C	TG	A
			ACA GG A ACTCCGTCTC				

			TGT TC T TGAGGCAGAG		
			C GT C		
GAM2523	LOC221060 3'	GACGGTGTTCACCATGTT	94832	C	T
		AACA GGTGAAAC CCGTC			
		TTGT CCACTTTG GGCAG			
		A T			
GAM2523	LOC221271 3'	GAGGGGGTTTCATCATGTT	93518	C	G
		AACA GGTGAAACTCC TC			
		TTGT CTACTTTGGGG AG			
		A G			
GAM2523	LOC221296 3'	GAGACGGGGTTTCACCATG	93609	C	
		CA GGTGAAACTCCGTCTC			
		GT CCACTTTGGGGCAGAG			
		A			
GAM2523	LOC221663 5'	GAGACAAGGTTTCACTATGTT	95461	CG	CC
		AACA GTGAAACT GTCTC			
		TTGT CACTTTGG CAGAG			
		AT AA			
GAM2523	LOC222068 3'	GAGATGGGGTTTTACCATGTT	94276	C	
		AACA GGTGAAACTCCGTCTC			
		TTGT CCATTTTGGGGTAGAG			
		A			
GAM2523	LOC222070 5'	GAGACGGTGTTCACCATGTT	95816	C	T
		AACA GGTGAAAC CCGTCTC			
		TTGT CCACTTTG GGCAGAG			
		A T			
GAM2523	LOC222224 5'	GAGACAGGGTTTCACCATGTT	95872	C	C
		AACA GGTGAAACTC GTCTC			
		TTGT CCACTTTGGG CAGAG			
		A A			
GAM2523	LOC245771 5'	GAGATGGGGTTTCATCATGTT	94477	C	
		AACA GGTGAAACTCCGTCTC			
		TTGT CTACTTTGGGGTAGAG			
		A			
GAM2523	LOC253612 5'	GAGACAGAGTTTTGCCATGTT	98549	C TG	C
		AACA GG AA ACTC GTCTC			
		TTGT CC TTTGAG CAGAG			
		A GT A			
GAM2523	LOC253664 3'	GAGATGGGGTTTCCCATGTT	96466	C T	
		AACA GG GAAACTCCGTCTC			

	TTGT CC CTTTGGGGTAGAG		
	A C		
GAM2523 LOC253666 3'	GAGACGGGGTTTCACCATGTT 96761	C	
	AACA GGTGAAACTCCGTCTC		
	TTGT CCACTTTGGGGCAGAG		
	A		
GAM2523 LOC253805 3'	GAGATAGGGTTTCACAATGTT 98176	CG	CG
	AACA GTGAAACTC TCTC		
	TTGT CACTTTGGG AGAG		
	AA AT		
GAM2523 LOC254018 5'	GAGATGGGGTTTCGCCATGTT 98740	C	
	AACA GGTGAAACTCCGTCTC		
	TTGT CCGCTTTGGGGTAGAG		
	A		
GAM2523 LOC254268 3'	GAGATGGGGTTTCACCATGTT 97143	C	
	AACA GGTGAAACTCCGTCTC		
	TTGT CCACTTTGGGGTAGAG		
	A		
GAM2523 LOC254295 5'	GAGACGGGGTTTCACCGTGTT 97891		
	AACACGGTGAAACTCCGTCTC		
	TTGTGCCACTTTGGGGCAGAG		
GAM2523 LOC254351 5'	GACGGGGTTTCTCCGTGTT 96688	T	
	AACACGG GAAACTCCGTC		
	TTGTGCC CTTTGGGGCAG		
	T		
GAM2523 LOC254351 3'	GAGACGGAGTTTCACCCTTGT 96689	C_	
	ACA GGTGAAACTCCGTCTC		
	TGT CCACTTTGAGGCAGAG		
	TC		
GAM2523 LOC254655 3'	GAGACGGGGTTTCACCATGTT 97220	C	
	AACA GGTGAAACTCCGTCTC		
	TTGT CCACTTTGGGGCAGAG		
	A		
GAM2523 LOC255037 3'	GAGACGAAGTCTCGCTGTGT 98439	A C	
	ACACGGTGA ACT CGTCTC		
	TGTGTCGCT TGA GCAGAG		
	C A		
GAM2523 LOC255338 5'	GAGACAGGGCATCACTGTGTT 97632	AA C	
	AACACGGTGA CTC GTCTC		

			TTGTGTCACT GGG CAGAG		
			AC A		
GAM2523	LOC255465 3'	GAGACGGGTTTCACCATGTT	99114	C	T
		AACA GGTGAAAC CCGTCTC			
		TTGT CCACTTTG GGCAGAG			
		A			
GAM2523	LOC255497 3'	GAGACGGGTTTCACCATGTT	98985	C	
		AACA GGTGAAACTCCGTCTC			
		TTGT CCACTTTGGGGCAGAG			
		A			
GAM2523	LOC256221 3'	GAGACGGAGTCTCGCTCTGT	96909	C	A
		ACA GGTGA ACTCCGTCTC			
		TGT TCGCT TGAGGCAGAG			
		C C			
GAM2523	LOC256221 3'	GAGACGGGTTTCACCGTGTT	96910		
		AACACGGTGAAACTCCGTCTC			
		TTGTGCCACTTTGGGGCAGAG			
GAM2523	LOC256306 3'	GAGACGGGTTTCACCATGTT	98515	C	
		AACA GGTGAAACTCCGTCTC			
		TTGT CCACTTTGGGGCAGAG			
		A			
GAM2523	LOC257042 3'	AGACGGAGTGTGGCTCATGT	98679	C	_ GAA
		ACA G GT ACTCCGTCT			
		TGT C CG TGAGGCAGA			
		A T GTG			
GAM2523	LOC257465 3'	GAGATGGTGTTCACCATGTT	82496	C	T
		AACA GGTGAAAC CCGTCTC			
		TTGT CCACTTTG GGTAGAG			
		A T			
GAM2523	LOC257486 3'	GAGACGGGTTTCACCATGTT	69771	C	
		AACA GGTGAAACTCCGTCTC			
		TTGT CCACTTTGGGGCAGAG			
		A			
GAM2523	LOC51008 5'	GAGATGGGGTTTCTCCATGTT	32533	C	T
		AACA GG GAAACTCCGTCTC			
		TTGT CC CTTTGGGGTAGAG			
		A T			
GAM2523	LOC51159 5'	GAGACGGGATTTACCATGTT	33030	C	CT
		AACA GGTGAAA CCGTCTC			

		TTGT CCACTTT GGCAGAG		
		A AG		
GAM2523	LOC51193	5' GAGACGGGGTTTCCCATGTT 33367	C T	
		AACA GG GAAACTCCGTCTC		
		TTGT CC CTTTGGGGCAGAG		
		A C		
GAM2523	LOC51219	5' GAGACGGGGTTTCTCCATGT 33545	C T	
		ACA GG GAAACTCCGTCTC		
		TGT CC CTTTGGGGCAGAG		
		A T		
GAM2523	LOC51696	3' GAGACAGCGTTTCACCATGTT 33083	C	TCC
		AACA GGTGAAAC GTCTC		
		TTGT CCACTTTG CAGAG		
		A CGA		
GAM2523	LOC56181	5' GAGACAGGGCTTCACTGTGTT 97273	A C	
		AACACGGTGAA CTC GTCTC		
		TTGTGTCACTT GGG CAGAG		
		C A		
GAM2523	LOC56181	5' GAGACGGAGTCTCGCTCTGT 97274	C	A
		ACA GGTGA ACTCCGTCTC		
		TGT TCGCT TGAGGCAGAG		
		C C		
GAM2523	LOC57107	3' GAGATGGGGTTTCACTATGTT 40188	CG	
		AACA GTGAAACTCCGTCTC		
		TTGT CACTTTGGGGTAGAG		
		AT		
GAM2523	LOC57146	3' GATGGGGTTTTCACCATGTT 40296	C	
		AACA GGTGAAACTCCGTC		
		TTGT CCACTTTGGGGTAG		
		A		
GAM2523	LOC81034	3' ATGGGGTTTTCACCATGTT 48581	C	
		AACA GGTGAAACTCCGT		
		TTGT CCACTTTGGGGTA		
		A		
GAM2523	LOC89231	3' GAGATGGGGTCTCACTATGTT 94299	CG	A
		AACA GTGA ACTCCGTCTC		
		TTGT CACT TGGGGTAGAG		
		AT C		
GAM2523	LOC89919	3' GAGACGGGGTTTTCACCATGTT 61374	C	
		AACA GGTGAAACTCCGTCTC		

		TTGT CCACTTTGGGGCAGAG		
		A		
GAM2523	LOC89932	3' GAGACAGAGTTTCACTCTTGT	61461	C _ C
		ACA G GTGAAACTC GTCTC		
		TGT C CACTTTGAG CAGAG		
		T T A		
GAM2523	LOC89932	3' GAGACGGGGTTTCTCCATGTT	61462	C T
		AACA GG GAAACTCCGTCTC		
		TTGT CC CTTTGGGGCAGAG		
		A T		
GAM2523	LOC89932	3' GAGATGGGGTTTCACCATGTT	61463	C
		AACA GGTGAAACTCCGTCTC		
		TTGT CCACTTTGGGGTAGAG		
		A		
GAM2523	LOC90190	3' GAGACGGAATCTCCGTTGTT	62425	_ T AAC
		AACA CGG GA TCCGTCTC		
		TTGT GCC CT AGGCAGAG		
		T T A _		
GAM2523	LOC90288	3' GAGACGGGGTTTCACAGTGTT	62789	G
		AACAC GTGAAACTCCGTCTC		
		TTGTG CACTTTGGGGCAGAG		
		A		
GAM2523	LOC90288	3' GAGAGGGAGTCTCACCGTGT	62790	A G
		ACACGGTGA ACTCC TCTC		
		TGTGCCACT TGAGG AGAG		
		C G		
GAM2523	LOC90333	3' GAGACTGGGTTTCACCGTGTT	62959	C
		AACACGGTGAAACTC GTCTC		
		TTGTGCCACTTTGGG CAGAG		
		T		
GAM2523	LOC90371	5' GAGACGGAGTCTCGTTCTGT	63162	_ A
		ACGG TGA ACTCCGTCTC		
		TGTC GCT TGAGGCAGAG		
		TT C		
GAM2523	LOC90459	3' GAGGCGGGTTTCACCATGTT	63556	C
		AACA GGTGAAACTCCGTCTC		
		TTGT CCACTTTGGGGCGGAG		
		A		
GAM2523	LOC90485	3' GAGACGGAGTCTTGCTCTGT	63699	C TG A
		ACA GG A ACTCCGTCTC		

			TGT TC T TGAGGCAGAG		
			C GT C		
GAM2523	LOC90485	3'	GAGGCAGGGTTTCACCATGTT 63700	C	C
			AACA GGTGAAACTC GTCTC		
			TTGT CCACTTTGGG CGGAG		
			A A		
GAM2523	LOC90485	3'	GAGGCGGGGTTTCACCATGTT 63701	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGCGGAG		
			A		
GAM2523	LOC90591	3'	GAGACGGAGTCTTGCTCTGT 64169	C TG A	
			ACA GG A ACTCCGTCTC		
			TGT TC T TGAGGCAGAG		
			C GT C		
GAM2523	LOC90591	3'	GAGACGGAGTTTCATCGTGTT 64170		
			AACACGGTGAAACTCCGTCTC		
			TTGTGCTACTTTGAGGCAGAG		
GAM2523	LOC90591	3'	GAGACGGGGCTTCACTATGTT 64171	CG A	
			AACA GTGAA CTCCGTCTC		
			TTGT CACTT GGGGCAGAG		
			AT C		
GAM2523	LOC91115	3'	GAGATGGGGTTTCACTGTGTT 65566		
			AACACGGTGAAACTCCGTCTC		
			TTGTGTCACTTTGGGGTAGAG		
GAM2523	LOC91115	3'	GAGATGGGGTTTCATCATGTT 65567	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CTACTTTGGGGTAGAG		
			A		
GAM2523	LOC91250	5'	GAGATGGGGTTTCATCATGTT 65916	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CTACTTTGGGGTAGAG		
			A		
GAM2523	LOC91291	5'	GAGACAAGGTTTCACCCTGTT 66089	C CC	
			AACA GGTGAAACT GTCTC		
			TTGT CCACTTTGG CAGAG		
			C AA		
GAM2523	LOC91373	3'	GAGATGGGGTTTGACCGTGTT 66414	G	
			AACACGGT AAACCTCCGTCTC		

			TTGTGCCA TTTGGGGTAGAG		
			G		
GAM2523	LOC91561	5'	GACGGGGTTTCTCCATGTT 67044	C	T
			AACA GG GAAACTCCGTC		
			TTGT CC CTTTGGGGCAG		
			A T		
GAM2523	LOC91893	3'	GAGACGAGGTTTCACCGTGTT 68072		TC
			AACACGGTGAAAC CGTCTC		
			TTGTGCCACTTTG GCAGAG		
			GA		
GAM2523	LOC91893	3'	GAGACGGAGTCTTGCTCTG 68073	C	TG A
			CA GG A ACTCCGTCTC		
			GT TC T TGAGGCAGAG		
			C GT C		
GAM2523	LOC92148	5'	GAGACGGGGTTTCACCGTGTT 68879		
			AACACGGTGAAACTCCGTCTC		
			TTGTGCCACTTTGGGGCAGAG		
GAM2523	LOC92303	3'	GAGATGGGTTTCACCATGTT 69392	C	T
			AACA GGTGAAAC CCGTCTC		
			TTGT CCACTTTG GG TAGAG		
			A _		
GAM2523	LOC92689	3'	GAGACAGGGTTTCACCATGTT 70775	C	C
			AACA GGTGAAACTC GTCTC		
			TTGT CCACTTTGGG CAGAG		
			A A		
GAM2523	LOC92841	3'	GAGACAGGGTTTCACCATGTT 71253	C	C
			AACA GGTGAAACTC GTCTC		
			TTGT CCACTTTGGG CAGAG		
			A A		
GAM2523	LOC92841	3'	GAGACGGGGTTTCACCATGTT 71254	C	
			AACA GGTGAAACTCCGTCTC		
			TTGT CCACTTTGGGGCAGAG		
			A		
GAM2523	LOC93190	3'	GAGACGGAGTGTCGCTTC 72099	C	A
			A GGTGA ACTCCGTCTC		
			C TCGCT TGAGGCAGAG		
			T G		
GAM2523	LOC93206	3'	GAGACGGAGTTTCCCTCTGTT 72190	C_	T
			AACA GG GAAACTCCGTCTC		

			TTGT CC CTTTGAGGCAGAG			
			CT _			
GAM2523	LOC93349	3'	GAGACGGGGTTTCACTATGTT	57268	CG	
			AACA GTGAAACTCCGTCTC			
			TTGT CACTTTGGGGCAGAG			
			AT			
GAM2523	LOC93408	5'	ACAGAGTTTCACCATGTT	57282	C	C
			AACA GGTGAAACTC GT			
			TTGT CCACTTTGAG CA			
			A A			
GAM2524	A1BG	3'	CCCAGGCTGGAGTGCAGTG	56285		
			CACTGCACTCCAGCCTGGG			
			GTGACGTGAGGTCGGACCC			
GAM2524	A1BG	3'	GTTGCCCAGGCTGGAGTGCAAT	56297	C	AG
	GG		CCA TGCCTCCAGCCTGGG	AC		
			GGT ACGTGAGGTCGGACCC	TG		
			A GT			
GAM2524	AASS	3'	CCCAGGCTGGAGTGCAGTG	20459		
			CACTGCACTCCAGCCTGGG			
			GTGACGTGAGGTCGGACCC			
GAM2524	ABCB6	5'	TCCCGGGCCCAGAGCCAGCGG	20301	A CA CA_	
			CC CTG CTC GCCTGGGA			
			GG GAC GAG CGGGCCCT			
			C C_ ACC			
GAM2524	ACADSB	3'	GTCACCCAGGCTAGAGTGCAGT	9648	C	A
	GG		CCACTGCACTC AGCCTGGG	GAC		
			GGTGACGTGAG TCGGACCC	CTG		
			A A			
GAM2524	ADAMTS4	3'	GTCGCCCAGGCTGGAGTGCAAT	18771	C	A
	GG		CCA TGCCTCCAGCCTGGG	GAC		
			GGT ACGTGAGGTCGGACCC	CTG		
			A G			
GAM2524	ADCY2	3'	TCAGGCCGGGTGCAGTGG	65653	T A	
			CCACTGCAC CC GCCTGG			
			GGTGACGTG GG CGGACT			
			_ C			
GAM2524	ADCY6	5'	GTCACCCAGGCTGGAGTGCAAT	40962	C	A
	GG		CCA TGCCTCCAGCCTGGG	GAC		

			GGT ACGTGAGGTCGGACCC CTG		
			A A		
GAM2524	AHR	3'	CCCAAAGTGGAGTGCAGTGG 9674	CC	
			CCACTGCACTCCAG TGGG		
			GGTGACGTGAGGTC ACCC		
			AA		
GAM2524	AIM1	3'	TCTCAGGCTGGAGTGCAGTGG 93471		
			CCACTGCACTCCAGCCTGGGA		
			GGTGACGTGAGGTCGGACTCT		
GAM2524	ALDH1B1	3'	GTCGCCCAGGCTGGAGTGCAGT 7326	A	
			GG CCACTGCACTCCAGCCTGGG GAC		
			GGTGACGTGAGGTCGGACCC CTG		
			G		
GAM2524	ALOX15	3'	CCCAGGCTGGAGTGCAGTGG 8543		
			CCACTGCACTCCAGCCTGGG		
			GGTGACGTGAGGTCGGACCC		
GAM2524	APAF1	3'	CCAGGCTGGAGTGCAGTGG 25965		
			CCACTGCACTCCAGCCTGG		
			GGTGACGTGAGGTCGGACC		
GAM2524	APAF1	3'	TCACCCAGGCTGGAGTGCAGTG 25983	A	
			G CCACTGCACTCCAGCCTGGG GA		
			GGTGACGTGAGGTCGGACCC CT		
			A		
GAM2524	APM1	3'	CCAGGCTAGAGTGCAGTGG 17769	C	
			CCACTGCACTC AGCCTGG		
			GGTGACGTGAG TCGGACC		
			A		
GAM2524	APM1	3'	CCCTGGCTGGAGTTCAGTGG 17776	C	T
			CCACTG ACTCCAGCC GGG		
			GGTGAC TGAGGTCGG CCC		
			T T		
GAM2524	APM1	3'	GTCACCCAGGCTGGAGTACAGT 17789	C	A
			G CACTG ACTCCAGCCTGGG GAC		
			GTGAC TGAGGTCGGACCC CTG		
			A A		
GAM2524	APOL1	3'	GTCGCCAAGTTGGAGTGCAATG 14743	C	C GA
			G CCA TGCCTCCAGC TGG GAC		

			GGT ACGTGAGGTTG ACC CTG	
			A A G_	
GAM2524	APPL	3'	GTTGCCCAGGCTGGAGTGCAGT 24954	AG
	GG		CCACTGCACTCCAGCCTGGG AC	
			GGTGACGTGAGGTCGGACCC TG	
			GT	
GAM2524	AQP6	3'	GTTACCCAGGCTGGAGTGCAGT 55011	A
	GG		CCACTGCACTCCAGCCTGGG GAC	
			GGTGACGTGAGGTCGGACCC TTG	
			A	
GAM2524	AQP6	3'	GTTACCCAGGCTGGAGTGCAGT 55012	A
	GG		CCACTGCACTCCAGCCTGGG GAC	
			GGTGACGTGAGGTCGGACCC TTG	
			A	
GAM2524	ARCN1	3'	CCCAGGCTGGAATGCAATGG 9748 C C	
			CCA TGCA TCCAGCCTGGG	
			GGT ACGT AGGTCGGACCC	
			A A	
GAM2524	ATF5	3'	CTCTCGGCCGGGTGCAGTGG 24819 T A T	
			CCACTGCAC CC GCC GGGAG	
			GGTGACGTG GG CGG CTCTC	
			_ C _	
GAM2524	ATM	3'	GTCATTGCGGCTGGGCGCAGCG 5301 A A T A	
	G		CC CTGC C CCAGCCTGGG GAC	
			GG GACG G GGTCGGGCTT CTG	
			C C_ A	
GAM2524	ATP1B2	3'	GTTGCCCAGGCTGGAGTGCAT 9840 C	AG
	GG		CCA TGCACTCCAGCCTGGG AC	
			GGT ACGTGAGGTCGGACCC TG	
			A GT	
GAM2524	ATP6V1A1	3'	GTTGCCCAGGCTGGAGTGCAT 9874 C	AG
	GG		CCA TGCACTCCAGCCTGGG AC	
			GGT ACGTGAGGTCGGACCC TG	
			A GT	
GAM2524	ATP7A	3'	CCCAGGCTGGAGTGCAGTGG 5318	
			CCACTGCACTCCAGCCTGGG	
			GGTGACGTGAGGTCGGACCC	
GAM2524	AXL	3'	GTCACCCAGGCTGGAGTGCAGT 41892	A
	GG		CCACTGCACTCCAGCCTGGG GAC	

			GGTGACGTGAGGTCGGACCC CTG		
			A		
GAM2524	BAZ2A	5'	CCCAGGCTTGAGTGCAATG 26506	C	C
			CA TGCCTC AGCCTGGG		
			GT ACGTGAG TCGGACCC		
			A T		
GAM2524	BCL10	3'	TCGCCCAGGCTGGAGTGCAGTG 15374		A
	G		CCACTGCACTCCAGCCTGGG GA		
			GGTGACGTGAGGTCGGACCC CT		
			G		
GAM2524	BCL2	3'	TCTTCCTGAAATGCAGTGG 7243	CTC	GCCT
			CCACTGCA CA GGGAGA		
			GGTGACGT GT CCTTCT		
			AAA _		
GAM2524	BDKRB1	5'	GTCGGCCCAGACTGAAGTGCAG 7386	C	C A_
	TGG		CCACTGCACT CAG CTGGG GAC		
			GGTGACGTGA GTC GACCC CTG		
			A A GG		
GAM2524	BDP1	3'	CCCAGGCAAGAGTGCAGTGG 37964	CA	
			CCACTGCACTC GCCTGGG		
			GGTGACGTGAG CGGACCC		
			AA		
GAM2524	BRIP1	3'	GTTGCCCAGGCTGGAATGCAGT 50212	C	AG
	GG		CCACTGCA TCCAGCCTGGG AC		
			GGTGACGT AGGTCGGACCC TG		
			A GT		
GAM2524	C7	3'	GTTGCCCAGGCTGGAGCGCAGT 6988	A	AG
	GG		CCACTGC CTCCAGCCTGGG AC		
			GGTGACG GAGGTCGGACCC TG		
			C GT		
GAM2524	CAMLG	3'	GTTGCCCAGGCTAGAGTGCAAT 10006	C	C AG
	GG		CCA TGCCTC AGCCTGGG AC		
			GGT ACGTGAG TCGGACCC TG		
			A A GT		
GAM2524	CASP10	3'	CCCAGACTGGAGTGCAGGG 53203	A	C
			CC CTGCACTCCAG CTGGG		
			GG GACGTGAGGTC GACCC		
			_ A		
GAM2524	CASP10	3'	CCCAGACTGGAGTGCAGGG 53254	A	C
			CC CTGCACTCCAG CTGGG		

		GG GACGTGAGGTC GACCC			
		— A			
GAM2524	CASP2	3'	GTCGCCCAGGCTGGAGGGCAGT 53346	A	A
	GG		CCACTGC CTCCAGCCTGGG GAC		
			GGTGACG GAGGTCGGACCC CTG		
			G G		
GAM2524	CASP2	3'	GTCGCCCAGGCTGGAGGGCAGT 53347	A	A
	GG		CCACTGC CTCCAGCCTGGG GAC		
			GGTGACG GAGGTCGGACCC CTG		
			G G		
GAM2524	CASP2	3'	GTCGCCCAGGCTGGAGGGCAGT 53348	A	A
	GG		CCACTGC CTCCAGCCTGGG GAC		
			GGTGACG GAGGTCGGACCC CTG		
			G G		
GAM2524	CASP8	3'	GTCGCCCAGGCTGGAGTGCAGT 8762		A
	GG		CCACTGCACTCCAGCCTGGG GAC		
			GGTGACGTGAGGTCGGACCC CTG		
			G		
GAM2524	CASP8	3'	GTCGCCCAGGCTGGAGTGCAGT 8763		A
	GG		CCACTGCACTCCAGCCTGGG GAC		
			GGTGACGTGAGGTCGGACCC CTG		
			G		
GAM2524	CBFA2T2	3'	GTCTCCCAGGCTGGAGTGCA 18715		
			TGCACTCCAGCCTGGGAGAC		
			ACGTGAGGTCGGACCCTCTG		
GAM2524	CCNF	3'	GTCTCCCCGGCTGGAGTGCAGT 10086		T
	GG		CCACTGCACTCCAGCC GGGAGAC		
			GGTGACGTGAGGTCGG CCCTCTG		
			C		
GAM2524	CDC6	3'	GTTGCCCAGGCTGGAGTGCAAT 8827	C	AG
	GG		CCA TGCACTCCAGCCTGGG AC		
			GGT ACGTGAGGTCGGACCC TG		
			A GT		
GAM2524	CDH1	3'	TCGGCCAGGCTGGAGTGCAGTG 16409		GA
	G		CCACTGCACTCCAGCCTGG GA		
			GGTGACGTGAGGTCGGACC CT		
			GG		
GAM2524	CDH17	3'	GTCGCCCAGGCTGGAGTACAGT 15788	C	A
	GG		CCACTG ACTCCAGCCTGGG GAC		

			GGTGAC TGAGGTCGGACCC CTG		
			A G		
GAM2524	CELSR3	3'	GTCTCCCAGGCCGAAGGTCAG 9190	C	CCA_
			CTG ACT GCCTGGGAGAC		
			GAC TGG CGGACCCTCTG		
			_ AAGC		
GAM2524	CIAS1	5'	CCTAGGCTGGAGTGCAGTGG 18094		
			CCACTGCACTCCAGCCTGGG		
			GGTGACGTGAGGTCGGATCC		
GAM2524	CLECSF12	3'	GTTACCCAGGCTGGAGTGCAGT 77218		A
			GG CCACTGCACTCCAGCCTGGG GAC		
			GGTGACGTGAGGTCGGACCC TTG		
			A		
GAM2524	CLECSF12	3'	GTTGCCCAGGCTGGAGTGCAAC 77220	AC	AG
			GG CC TGCCTCCAGCCTGGG AC		
			GG ACGTGAGGTCGGACCC TG		
			CA GT		
GAM2524	CMAR	5'	CCCAGGCTGGAGTGCAGTG 19030		
			CACTGCACTCCAGCCTGGG		
			GTGACGTGAGGTCGGACCC		
GAM2524	CNGA1	5'	CCCAGGCTGGAGTGCAGTGG 60237		
			CCACTGCACTCCAGCCTGGG		
			GGTGACGTGAGGTCGGACCC		
GAM2524	CNN2	3'	GTTGCCCAGGCTGGAGTGCAGT 16463		AG
			GG CCACTGCACTCCAGCCTGGG AC		
			GGTGACGTGAGGTCGGACCC TG		
			GT		
GAM2524	CNP	3'	TTTCCCAAGCTGGAGTGCAGTG 53629		C
			G CCACTGCACTCCAGC TGGGAGA		
			GGTGACGTGAGGTCG ACCCTTT		
			A		
GAM2524	CORO2B	5'	GTTGCCCAAGCTGGAGTGCAGT 65175		C AG
			GG CCACTGCACTCCAGC TGGG AC		
			GGTGACGTGAGGTCG ACCC TG		
			A GT		
GAM2524	COX15	3'	GTTGCCCAGGCTGGAGTACAAT 55289	C C	AG
			GG CCA TG ACTCCAGCCTGGG AC		

			GGT AC TGAGGTCGGACCC TG		
			A A GT		
GAM2524	CPS1	3'	CCAGGCTGGAGTGCAGTGG 10287		
			CCACTGCACTCCAGCCTGG		
			GGTGACGTGAGGTCGGACC		
GAM2524	CR1	3'	GTCTCCCAGGCTGGAGTGCAGT 6950		
	GG		CCACTGCACTCCAGCCTGGGAGAC		
			GGTGACGTGAGGTCGGACCCTCTG		
GAM2524	CRTAP	3'	CCCAGGCTGGAGTGCAATGG 22076 C		
			CCA TGCACTCCAGCCTGGG		
			GGT ACGTGAGGTCGGACCC		
			A		
GAM2524	CSNK2A2	5'	GTCACCCAGGCTGGAGTGCAGT 10321		A
	GG		CCACTGCACTCCAGCCTGGG GAC		
			GGTGACGTGAGGTCGGACCC CTG		
			A		
GAM2524	CST	5'	TCCAGAGCTGGAGTGCAGCGG 17965 A		—
			CC CTGCACTCCAGC CTGGG		
			GG GACGTGAGGTCG GACCT		
			C A		
GAM2524	CTF1	3'	GTCGCCCAGGCTGGGGTGCAGT 9020		A
	GG		CCACTGCACTCCAGCCTGGG GAC		
			GGTGACGTGGGGTCGGACCC CTG		
			G		
GAM2524	CTSB	5'	CTGGGCTGGTGTGCAGTGG 65362 T TG		
			CCACTGCAC CCAGCC G		
			GGTGACGTG GGTCGG C		
			T GT		
GAM2524	CXCL16	3'	GTCATCCAGGCTGGAGTGCAGT 42177		GA
	GG		CCACTGCACTCCAGCCTGG GAC		
			GGTGACGTGAGGTCGGACC CTG		
			TA		
GAM2524	CYP1A2	3'	CCAGGCTGGAGTGCAGTGG 7506		
			CCACTGCACTCCAGCCTGG		
			GGTGACGTGAGGTCGGACC		
GAM2524	CYP1A2	3'	GTCTCCTAAGCTGGAGTGCAGT 7526		C
	GG		CCACTGCACTCCAGC TGGGAGAC		

			GGTGACGTGAGGTCG ATCCTCTG	
			A	
GAM2524	CYP1A2	3'	GTCACCCAGGTTGGAGTGCAGT 69661	A
	GG		CCACTGCACTCCAGCCTGGG GAC	
			GGTGACGTGAGGTTGGACCC CTG	
			A	
GAM2524	CYP2B6	3'	GTCTCCCAGGCTGGAGTGCTAT 7566 CT	
	GG		CCA GCACTCCAGCCTGGGAGAC	
			GGT CGTGAGGTCGGACCCTCTG	
			AT	
GAM2524	CYP2B6	3'	GTTGCCCAGGCTGGAGTGCAGT 7568	AG
	GG		CCACTGCACTCCAGCCTGGG AC	
			GGTGACGTGAGGTCGGACCC TG	
			GT	
GAM2524	CYP4F3	3'	CCCAGGCTGGAGTGCGGTGG 8003	
			CCACTGCACTCCAGCCTGGG	
			GGTGGCGTGAGGTCGGACCC	
GAM2524	CYP51	3'	GTTGCCCAGGCTGGAGTGCAGT 7621	AG
	GG		CCACTGCACTCCAGCCTGGG AC	
			GGTGACGTGAGGTCGGACCC TG	
			GT	
GAM2524	CYP8B1	3'	CCCAGGCTGCAGTGCAGTGG 16536	C
			CCACTGCACT CAGCCTGGG	
			GGTGACGTGA GTCGGACCC	
			C	
GAM2524	DFFB	3'	CTCAGGCTGGAGTGCAGTG 88768	
			CACTGCACTCCAGCCTGGG	
			GTGACGTGAGGTCGGACTC	
GAM2524	DFFB	3'	GTTGCCCAGGCTGGAGTGTAGT 88783	AG
	GG		CCACTGCACTCCAGCCTGGG AC	
			GGTGATGTGAGGTCGGACCC TG	
			GT	
GAM2524	DHFR	3'	GTTGCCCAGGCTAGCATGCAAT 7656	C CTCC AG
	GG		CCA TGCA AGCCTGGG AC	
			GGT ACGT TCGGACCC TG	
			A ACGA GT	
GAM2524	DISC1	3'	GTCACCCAAGTTGGAGTGCAGT 38514	C A
	GG		CCACTGCACTCCAGC TGGG GAC	

			GGTGACGTGAGGTTG ACCC CTG		
			A A		
GAM2524	DNAH11	3'	CCTCTGCTGGAGTGCAGTG 15022	CT	
			CACTGCACTCCAGC GGG		
			GTGACGTGAGGTCG TCC		
			TC		
GAM2524	DSC3	3'	CAGGCTGGAGTGCAGTGG 10435		
			CCACTGCACTCCAGCCTG		
			GGTGACGTGAGGTCGGAC		
GAM2524	DSC3	3'	CAGGCTGGAGTGCAGTGG 44615		
			CCACTGCACTCCAGCCTG		
			GGTGACGTGAGGTCGGAC		
GAM2524	DYRK1A	5'	TCCCGGCTGAAGTGCAGTGG 9165	C T	
			CCACTGCACT CAGCC GGGA		
			GGTGACGTGA GTCGG CCCT		
			A _		
GAM2524	EBI3	3'	TTGGGCTGGGCGCAGTGG 20442	A T TG	
			CCACTGC C CCAGCC G		
			GGTGACG G GGTCGG T		
			C _ GT		
GAM2524	EDG8	3'	GTCACCCAGGCTGGAGTGCAAT 79150	C A	
	GG		CCA TGCCTCCAGCCTGGG GAC		
			GGT ACGTGAGGTCGGACCC CTG		
			A A		
GAM2524	EHD2	3'	GTCGCCCAGGCTGGAGTGCAGT 28228	A	
	GG		CCACTGCACTCCAGCCTGGG GAC		
			GGTGACGTGAGGTCGGACCC CTG		
			G		
GAM2524	EIF2S3	3'	GTCACCCAGGCTGGAGTGCAGT 9213	A	
	GG		CCACTGCACTCCAGCCTGGG GAC		
			GGTGACGTGAGGTCGGACCC CTG		
			A		
GAM2524	ENDOGL1	3'	TCCAGGCTGGAGTGCGGTGG 18826		
			CCACTGCACTCCAGCCTGGG		
			GGTGGCGTGAGGTCGGACCT		
GAM2524	EPB72	3'	GTTGCCCAGGCTGGAGTGCA 15880	AG	
			TGCACTCCAGCCTGGG AC		

			ACGTGAGGTCGGACCC TG		
			GT		
GAM2524	F2RL2	3'	TCACCCAGACTGGCGTGCAGTG 15902	T	C A
	G		CCACTGCAC CCAG CTGGG GA		
			GGTGACGTG GGTC GACCC CT		
			C A A		
GAM2524	F2RL3	3'	GTTGCCCAGGCTGGAGTGCAGT 15526		AG
	GG		CCACTGCACTCCAGCCTGGG AC		
			GGTGACGTGAGGTCGGACCC TG		
			GT		
GAM2524	F3	3'	GTTGCCCAGGCTGGAGTGCAGT 67680		AG
			ACTGCACTCCAGCCTGGG AC		
			TGACGTGAGGTCGGACCC TG		
			GT		
GAM2524	FABP2	3'	CTCAGGCTGGAATGTAGTGG 5533	C	
			CCACTGCA TCCAGCCTGGG		
			GGTGATGT AGGTCGGACTC		
			A		
GAM2524	FANCC	3'	CCTGGCTGGGTGCAGTGG 71037	T	T
			CCACTGCAC CCAGCC GGG		
			GGTGACGTG GGTCGG TCC		
			— —		
GAM2524	FANCE	3'	GTCATCCAGGCTGGAGTGCAGT 41901		GA
	G		CACTGCACTCCAGCCTGG GAC		
			GTGACGTGAGGTCGGACC CTG		
			TA		
GAM2524	FANCF	3'	CCCAGTCTGGAGTGCAGTGG 42978		C
			CCACTGCACTCCAG CTGGG		
			GGTGACGTGAGGTC GACCC		
			T		
GAM2524	FCAR	3'	CCAAGGCTGGAGTGCAGTGG 10585		G
			CCACTGCACTCCAGCCT GG		
			GGTGACGTGAGGTCGGA CC		
			A		
GAM2524	FCAR	3'	GTCACCCAGGCTGGAGTGCAGT 10592		A
	GG		CCACTGCACTCCAGCCTGGG GAC		
			GGTGACGTGAGGTCGGACCC CTG		
			A		
GAM2524	FCAR	3'	CCAAGGCTGGAGTGCAGTGG 56565		G
			CCACTGCACTCCAGCCT GG		

		GGTGACGTGAGGTCGGA CC			
		A			
GAM2524	FCAR	3'	GTCACCCAGGCTGAAGTGCAGT 56580	C	A
	GG		CCACTGCACT CAGCCTGGG GAC		
		GGTGACGTGA GTCGGACCC CTG			
		A A			
GAM2524	FCGR2A	3'	GTTACCCAGGCTGGAGTGCAGT 80031		A
	GG		CCACTGCACTCCAGCCTGGG GAC		
		GGTGACGTGAGGTCGGACCC TTG			
		A			
GAM2524	FCRH1	3'	CTCAATCTGGAATGCAGTGG 54724	C	CC
			CCACTGCA TCCAG TGGG		
		GGTGACGT AGGTC ACTC			
		A TA			
GAM2524	FEZ1	3'	TCGCCCAGGCTGGAGTGCAATG 18790	C	A
	G		CCA TGCCTCCAGCCTGGG GA		
		GGT ACGTGAGGTCGGACCC CT			
		A G			
GAM2524	FGF2	3'	TCTAGGCCGGGTGCAGTGG 10623	T	A
			CCACTGCAC CC GCCTGGG		
		GGTGACGTG GG CGGATCT			
		_ C			
GAM2524	FGF5	3'	GTCACCAGGCTGGAGTGCAGTG 16764		GA
	G		CCACTGCACTCCAGCCTGG GAC		
		GGTGACGTGAGGTCGGACC CTG			
		A_			
GAM2524	FGF5	3'	GTCACCAGGCTGGAGTGCAGTG 53668		GA
	G		CCACTGCACTCCAGCCTGG GAC		
		GGTGACGTGAGGTCGGACC CTG			
		A_			
GAM2524	FHL2	5'	GTCGCCCAGGCTGGAGTGCAGT 9370		A
	GG		CCACTGCACTCCAGCCTGGG GAC		
		GGTGACGTGAGGTCGGACCC CTG			
		G			
GAM2524	FSHPRH1	5'	GTCACCCAGGCTGGAGTGCAGT 23069		A
	GG		CCACTGCACTCCAGCCTGGG GAC		
		GGTGACGTGAGGTCGGACCC CTG			
		A			
GAM2524	FUT1	3'	GTAGCCCAGGCCAGAGTGCAGT 5609	CA	AG
	GG		CCACTGCACTC GCCTGGG AC		

			GGTGACGTGAG CGGACCC TG		
			AC GA		
GAM2524	FUT1	3'	GTTGCCCAGGCTGGAGTGCAGT 5611		AG
	GG		CCACTGCACTCCAGCCTGGG AC		
			GGTGACGTGAGGTCGGACCC TG		
			GT		
GAM2524	G1P3	3'	TCCAGGCTAGAGTGCAGTGG 43455	C	
			CCACTGCACTC AGCCTGGG		
			GGTGACGTGAG TCGGACCT		
			A		
GAM2524	G6PC	3'	TCACCCAGGCTGGAGTGGAGTG 5665	G	A
	G		CCACT CACTCCAGCCTGGG GA		
			GGTGA GTGAGGTCGGACCC CT		
			G A		
GAM2524	GHR	3'	CCAGGCTAGAGTGCAGTGG 5695	C	
			CCACTGCACTC AGCCTGG		
			GGTGGCGTGAG TCGGACC		
			A		
GAM2524	GM2A	3'	GTCACCAGGCTGGAGTGCAGTG 68388		GA
	G		CCACTGCACTCCAGCCTGG GAC		
			GGTGACGTGAGGTCGGACC CTG		
			A_		
GAM2524	GNAI1	5'	CCGGCGGGAGTGCAGCGG 10820	A	A T
			CC CTGCACTCC GCC GG		
			GG GACGTGAGG CGG CC		
			C G _		
GAM2524	GNE	3'	CCCAGGCTGGAGTGCAGTGG 19665		
			CCACTGCACTCCAGCCTGGG		
			GGTGACGTGAGGTCGGACCC		
GAM2524	GNE	3'	CTTCCAGGCCGGGCACAGTGG 19668	CA T A	
			CCACTG C CC GCCTGGGAG		
			GGTGAC G GG CGGACCTTC		
			AC _ C		
GAM2524	GPR4	3'	GTTGCCCAGGCTGGAGTGCAGT 60581		AG
			ACTGCACTCCAGCCTGGG AC		
			TGACGTGAGGTCGGACCC TG		
			GT		
GAM2524	GPR56	5'	CAGGCTGGAGTGCAGTGG 20269		
			CCACTGCACTCCAGCCTG		

GGTGACGTGAGGTCGGAC

GAM2524	GPR81	3'	TCCCAGGCTGGAGTGCAGTGG	51757	
			CCACTGCACTCCAGCCTGGGA		
			GGTGACGTGAGGTCGGACCCT		
GAM2524	GRAF	3'	CCATGGCCGGGTGCAGTGG	31227	T A _
			CCACTGCAC CC GCC TGG		
			GGTGACGTG GG CGG ACC		
			_ C T		
GAM2524	GRAF	3'	GTGGCCCAGGCTGGAGTGCAGT	31244	AG
	GG		CCACTGCACTCCAGCCTGGG	AC	
			GGTGACGTGAGGTCGGACCC	TG	
			GG		
GAM2524	GRINL1A	3'	GTCGCCCAGGCTGGAGTGCAGT	70067	A
	GG		CCACTGCACTCCAGCCTGGG	GAC	
			GGTGACGTGAGGTCGGACCC	CTG	
			G		
GAM2524	GRM6	3'	TTTCTTAGGCTGGAGTGCAGTG	7778	
	G		CCACTGCACTCCAGCCTGGGAGA		
			GGTGACGTGAGGTCGGATTCTTT		
GAM2524	HCS	3'	CCAAGGCTGGAGTGCAGTGG	38971	G
			CCACTGCACTCCAGCCT	GG	
			GGTGACGTGAGGTCGGA	CC	
			A		
GAM2524	HCS	3'	CCCAGGCTGAGTACAGTGG	38974	C C
			CCACTG ACTC AGCCTGGG		
			GGTGAC TGAG TCGGACCC		
			A _		
GAM2524	HCS	3'	GTTGCCCAGGCTGGAGTGCAAT	38991	C AG
	GG		CCA TGCCTCCAGCCTGGG	AC	
			GGT ACGTGAGGTCGGACCC	TG	
			A GT		
GAM2524	HK1	3'	GTCCCCACGTGTGAAGTGTAG	5748	C _ C A
	TGG		CCACTGCACT CA GC TGGG	GAC	
			GGTGATGTGA GT TG ACCC	CTG	
			A G C C		
GAM2524	HLCS	5'	GTCGTCCAGGCTGGAGTGCAGT	6417	GA
	GG		CCACTGCACTCCAGCCTGG	GAC	

		GGTGACGTGAGGTCGGACC CTG	
		TG	
GAM2524 HMG20A	3'	CCCAGGCTGGAGTGCGGTGG 37063	
		CCACTGCACTCCAGCCTGGG	
		GGTGGCGTGAGGTCGGACCC	
GAM2524 HTR1D	3'	CCAGGCTGGAGTGTAGTGG 7842	
		CCACTGCACTCCAGCCTGG	
		GGTGATGTGAGGTCGGACC	
GAM2524 HTR1E	5'	GTCGCCCAGGCTGGAGTGCAG 7865	A
		CTGCACTCCAGCCTGGG GAC	
		GACGTGAGGTCGGACCC CTG	
		G	
GAM2524 HUNK	3'	GTCACCCAGGCTGGAGTGCAGT 28190	A
GG		CCACTGCACTCCAGCCTGGG GAC	
		GGTGACGTGAGGTCGGACCC CTG	
		A	
GAM2524 HUS1	3'	CCCAGACTGGAGTGCAGTG 92738	C
		CACTGCACTCCAG CTGGG	
		GTGACGTGAGGTC GACCC	
		A	
GAM2524 HYAL4	5'	GTTGCCCAGGCTGGAGTGTAGT 25371	AG
GG		CCACTGCACTCCAGCCTGGG AC	
		GGTGATGTGAGGTCGGACCC TG	
		GT	
GAM2524 ICAM1	3'	GTCACCCAGGCTGGAGTGCAGT 72041	A
GG		CCACTGCACTCCAGCCTGGG GAC	
		GGTGACGTGAGGTCGGACCC CTG	
		A	
GAM2524 IFIT4	3'	GTTTTTTGGCCGGGCGCAGTGG 71496	A T A T
		CCACTGC C CC GCC GGGAGAC	
		GGTGACG G GG CGG TTTTTG	
		C _ C _	
GAM2524 IGF1	3'	GTCCCCCAGGCTGGAGTGCAGT 7080	A
GG		CCACTGCACTCCAGCCTGGG GAC	
		GGTGACGTGAGGTCGGACCC CTG	
		C	
GAM2524 IGJ	5'	CCATGGCGCCGGAGCGCACGG 58959	AC A A__ _
		CC TGC CTCC GCC TGG	

			GG ACG GAGG CGG ACC		
			C_ C CCG T		
GAM2524	IHPK2	3'	CCTGGAGCTGATGTGCAGTGG 62516	TC	_TG
			CCACTGCAC CAGC C GG		
			GGTGACGTG GTCG G CC		
			TA A GT		
GAM2524	IL11	3'	CCTAGGCTGGAGTGCAGTG 7180		
			CACTGCACTCCAGCCTGGG		
			GTGACGTGAGGTCGGATCC		
GAM2524	INMT	3'	GTCACCCAGGCTAGAGTGCAAT 23223	C	C A
	GG		CCA TGCCTC AGCCTGGG GAC		
			GGT ACGTGAG TCGGACCC CTG		
			A A A		
GAM2524	INMT	3'	GTCGCCCAGGCTGGAGTGCAGT 23225		A
	GG		CCACTGCACTCCAGCCTGGG GAC		
			GGTGACGTGAGGTCGGACCC CTG		
			G		
GAM2524	ITGAM	3'	GTCACCCAGGCTGGAGTGCAAT 72315	C	A
	GG		CCA TGCCTCAGCCTGGG GAC		
			GGT ACGTGAGGTCGGACCC CTG		
			A A		
GAM2524	JAK3	3'	GTTACCCAGGGTGGAGTGCAGT 5832	G	A
	GG		CCACTGCACTCCA CCTGGG GAC		
			GGTGACGTGAGGT GGACCC TTG		
			G A		
GAM2524	JRK	3'	CCAGGCTGGAGTGAAGTGG 87821	G	
			CCACT CACTCCAGCCTGG		
			GGTGA GTGAGGTCGGACC		
			A		
GAM2524	JRK	3'	TCTTCAAGCTGGGTGCAGTGG 87838	T	CTG
			CCACTGCAC CCAGC GGAGA		
			GGTGACGTG GGTCG CTTCT		
			_ AA_		
GAM2524	KLRD1	3'	CTGCCCAGGCTGGAGCATAGTG 24708	CA	_
	G		CCACTG CTCCAGCCTGGG AG		
			GGTGAT GAGGTCGGACCC TC		
			AC G		
GAM2524	KMO	3'	CCAGGCTGGAGTGCAGTGG 14840		
			CCACTGCACTCCAGCCTGG		

GGTGACGTGAGGTCGGACC

GAM2524 LARS2 3' CTCCCAGGCCTGCTGTGG 31694 T CTCCA
 CCAC GCA GCCTGGGAG
 |||| ||| |||||
 GGTG CGT CGGACCCTC
 T C____

GAM2524 LILRA3 3' GTCACCAGGCTGGAATGCAGTG 97021 C GA
 G CCACTGCA TCCAGCCTGG GAC
 ||||| ||||| |||
 GGTGACGT AGGTCGGACC CTG
 A A_

GAM2524 LLGL1 3' GTCGCCCAGGCTGGAGTGCAGT 67421 A
 GG CCACTGCACTCCAGCCTGGG GAC
 ||||| ||||| |||
 GGTGACGTGAGGTCGGACCC CTG
 G

GAM2524 LNK 3' CCGGGCTGGAGTGCAGTGG 19641
 CCACTGCACTCCAGCCTGG
 ||||| |||||
 GGTGACGTGAGGTCGGGCC

GAM2524 LTB4R 5' GTCATTCAGGCTGGAGTGCAGT 7472 A
 GG CCACTGCACTCCAGCCTGGG GAC
 ||||| ||||| |||
 GGTGACGTGAGGTCGGACTT CTG
 A

GAM2524 LYZ 3' GTCGCCCAGGCTGGAGTGCAGT 5902 A
 GG CCACTGCACTCCAGCCTGGG GAC
 ||||| ||||| |||
 GGTGACGTGAGGTCGGACCC CTG
 G

GAM2524 LZTS1 3' GTCCCCCAGGCTGGAGTGCAGT 41039 A
 GG CCACTGCACTCCAGCCTGGG GAC
 ||||| ||||| |||
 GGTGACGTGAGGTCGGACCC CTG
 C

GAM2524 MADD 5' TCTCCCAGCGGGCGCCGCGG 56218 ACT_ A C
 CTGC CC GC TGGGAGA
 ||| || |||||
 GGCG GG CG ACCCTCT
 CCGC G _

GAM2524 MAK 3' TCCAGGCTGGAGTGCAGTGG 20954
 CCACTGCACTCCAGCCTGGG
 ||||| |||||
 GGTGACGTGAGGTCGGACCT

GAM2524 MDM2 3' GTTACCCAGGCTGGAGTGCAGT 23501 A
 GG CCACTGCACTCCAGCCTGGG GAC
 ||||| ||||| |||

			GGTGACGTGAGGTCGGACCC TTG		
			A		
GAM2524	MDM4	3'	GTCTCCCAGGCTGAAGTGCAGT 11512	C	
	G		CACTGCACT CAGCCTGGGAGAC		
			GTGACGTGA GTCGGACCCTCTG		
			A		
GAM2524	MEF2A	5'	CCCAGGCTGAAGTGCAGTGG 19997	C	
			CCACTGCACT CAGCCTGGG		
			GGTGACGTGA GTCGGACCC		
			A		
GAM2524	MEFV	3'	GTCACCCAGGCTGGAGTGCAGT 5946		A
	GG		CCACTGCACTCCAGCCTGGG GAC		
			GGTGACGTGAGGTCGGACCC CTG		
			A		
GAM2524	MEFV	3'	GTGGCCCAGGCTGGAGTGCAGT 5948		AG
	GG		CCACTGCACTCCAGCCTGGG AC		
			GGTGACGTGAGGTCGGACCC TG		
			GG		
GAM2524	MHC2TA	3'	CCCACGCTGGAGTGCAGTG 5973	C	
			CACTGCACTCCAGC TGGG		
			GTGACGTGAGGTCG ACCC		
			C		
GAM2524	MHC2TA	3'	GTTGCCCAGGCTGGCGTGCAGT 5994	T	AG
	GG		CCACTGCAC CCAGCCTGGG AC		
			GGTGACGTG GGTCGGACCC TG		
			C GT		
GAM2524	MLANA	3'	GTTGCCCAGGCTGGAGTGCAAT 19769	C	AG
	GG		CCA TGCACCTCCAGCCTGGG AC		
			GGT ACGTGAGGTCGGACCC TG		
			A GT		
GAM2524	MME	3'	GTCTCCCAGTTATGAATCAGTG 8033		CAC CAGC
	G		CCACTG TC CTGGGAGAC		
			GGTGAC AG GACCCTCTG		
			TA_ TATT		
GAM2524	MPL	3'	CCAGACTGGAGTGCAGTGG 19345	C	
			CCACTGCACTCCAG CTGG		
			GGTGACGTGAGGTC GACC		
			A		
GAM2524	MPL	3'	CCCAGGCTGCAGTGCAATGG 19350	C	C
			CCA TGCACCTCCAGCTGGG		

		GGT ACGTGA GTCGGACCC		
		A C		
GAM2524	MRPL49	3' GTTGCCCAGGGTGGAGTGCAGT 70171	G	AG
	GG	CCACTGCACTCCA CCTGGG AC		
		GGTGACGTGAGGT GGACCC TG		
		G GT		
GAM2524	MTR	3' CCCAGGCTGGAGTGCAGGG 6015 A		
		CC CTGCACTCCAGCCTGGG		
		GG GACGTGAGGTCGGACCC		
		—		
GAM2524	MYLK2	3' CTCCTAGCTGGAGTGCCATGG 53585	CT	C
		CCA GCACTCCAGC TGGGAG		
		GGT CGTGAGGTCTG ATCCTC		
		AC —		
GAM2524	MYO10	3' TTTGAGCTGGAGTGCTGCGG 25617	ACT	CT
		CC GCACTCCAGC GGG		
		GG CGTGAGGTCTG TTT		
		CGT AG		
GAM2524	NCOA6	5' CCGAGGCTGGAGTGCAGTGG 26833	G	
		CCACTGCACTCCAGCCT GG		
		GGTGACGTGAGGTCTGGA CC		
		G		
GAM2524	NCOA6	5' GTCGCCCAGGCTGGAGTGCAGT 26845	A	
		ACTGCACTCCAGCCTGGG GAC		
		TGACGTGAGGTCTGGACCC CTG		
		G		
GAM2524	NCOA6IP	3' CCCAGGCTGGAGTGCAGTG 46152		
		CACTGCACTCCAGCCTGGG		
		GTGACGTGAGGTCTGGACCC		
GAM2524	NDRG3	3' GTTACCCAGGCTGGAGTGCAAT 42769	C	A
	GG	CCA TGCCTCCAGCCTGGG GAC		
		GGT ACGTGAGGTCTGGACCC TTG		
		A A		
GAM2524	NEU3	5' GTCACCCAGGCTGGAGTGCAGT 22833	A	
	GG	CCACTGCACTCCAGCCTGGG GAC		
		GGTGACGTGAGGTCTGGACCC CTG		
		A		
GAM2524	NONO	3' GTCGCCCAGGCTGGAGTGTAGT 82892	A	
	GG	CCACTGCACTCCAGCCTGGG GAC		

			GGTGATGTGAGGTCGGACCC CTG		
			G		
GAM2524	NPR2L	3'	GTTACCCAGGCTGGAATACAGT 22598	CAC	A
	GG		CCACTG TCCAGCCTGGG GAC		
			GGTGAC AGGTCGGACCC TTG		
			ATA A		
GAM2524	NQO1	3'	GTTACCCAGGCTGGAGTGCAGT 8054		A
	GG		CCACTGCACTCCAGCCTGGG GAC		
			GGTGACGTGAGGTCGGACCC TTG		
			A		
GAM2524	NT5C2	5'	CTGCCCAGGCTGGAGTACAGTG 25263	C	—
			CACTG ACTCCAGCCTGGG AG		
			GTGAC TGAGGTCGGACCC TC		
			A G		
GAM2524	ORC1L	3'	GTCGCCCAGGCTGGAGTGCAGT 15987		A
	GG		CCACTGCACTCCAGCCTGGG GAC		
			GGTGACGTGAGGTCGGACCC CTG		
			G		
GAM2524	P2RY6	3'	CAGGGGGCGAAGTGCAGTGG 15994	—	AG
			CCACTGCACT CC CCGT		
			GGTGACGTGA GG GGAC		
			AGC G_		
GAM2524	PAICS	3'	GTCGCCCAGGCTGGAGTGCAGT 22267		A
	GG		CCACTGCACTCCAGCCTGGG GAC		
			GGTGACGTGAGGTCGGACCC CTG		
			G		
GAM2524	PCDH1	5'	TCTCCCAGGCTGGCAGCATTGG 51579	C	ACT
			CCA TGC CCAGCCTGGGAGA		
			GGT ACG GGTCCGACCCTCT		
			T AC_		
GAM2524	PCDHA9	3'	CCCAGGCTGGAGTACAGTGG 49836	C	
			CCACTG ACTCCAGCCTGGG		
			GGTGAC TGAGGTCGGACCC		
			A		
GAM2524	PCDHA9	3'	GTTGCCCAGGCTGGAGTGCAGT 49851		AG
	GG		CCACTGCACTCCAGCCTGGG AC		
			GGTGACGTGAGGTCGGACCC TG		
			GT		
GAM2524	PCDHB11	3'	CCCTGGCTGGAGTGCAATGG 38919	C	T
			CCA TGCACCTCCAGCC GGG		

		GGT ACGTGAGGTCGG CCC		
		A	T	
GAM2524	PCDHB16	3'	GTCACCCAGGCTGGAGTGCAGT 40909	A
	GG		CCACTGCACTCCAGCCTGGG GAC	
			GGTGACGTGAGGTCGGACCC CTG	
			A	
GAM2524	PCDHB9	3'	GTCGCCCAGGCTGGAGTGCAGT 39450	A
	GG		CCACTGCACTCCAGCCTGGG GAC	
			GGTGACGTGAGGTCGGACCC CTG	
			G	
GAM2524	PDCL	3'	GTCACCCAGGCTGGAGTACA 19400 C	A
			TG ACTCCAGCCTGGG GAC	
			AC TGAGGTCGGACCC CTG	
			A A	
GAM2524	PDE6B	3'	CCCAGGCTGGAGTGCCGTGG 6073 T	
			CCAC GCACTCCAGCCTGGG	
			GGTG CGTGAGGTCGGACCC	
			C	
GAM2524	PDZK1	5'	GTTGCCCAGGCTGGAGTGCAGT 12035	AG
	GG		CCACTGCACTCCAGCCTGGG AC	
			GGTGACGTGAGGTCGGACCC TG	
			GT	
GAM2524	PER2	3'	CCCAGGCTGGAGTGCAGTGG 43348	
			CCACTGCACTCCAGCCTGGG	
			GGTGACGTGAGGTCGGACCC	
GAM2524	PIGR	3'	GTCGCCCAGGCTGGAGTGCAGT 73009	A
	GG		CCACTGCACTCCAGCCTGGG GAC	
			GGTGACGTGAGGTCGGACCC CTG	
			G	
GAM2524	PIK3C2B	3'	GTCGCCAGGCTGGAGTGTAGTG 12110	GA
	G		CCACTGCACTCCAGCCTGG GAC	
			GGTGATGTGAGGTCGGACC CTG	
			G_	
GAM2524	PIK3CD	3'	GTTGCCCAGGCTGGAGTGCAGT 18499	AG
	GG		CCACTGCACTCCAGCCTGGG AC	
			GGTGACGTGAGGTCGGACCC TG	
			GT	
GAM2524	PKNOX1	3'	GTTGCCCAGGCTGGAGGGCAAT 17102 C A	AG
	GG		CCA TGC CTCCAGCCTGGG AC	

			GGT ACG GAGGTCGGACCC TG		
			A G GT		
GAM2524	PMCHL1	3'	GTTGCCCAGGCTGGAGTGCAAT 49921 C	AG	
	GG		CCA TGC ACTCCAGCCTGGG AC		
			GGT ACGTGAGGTCGGACCC TG		
			A GT		
GAM2524	PON1	3'	GTTGCCCAGGCTGGAGTGCAAGT 6540	AG	
	GG		CCACTGCACTCCAGCCTGGG AC		
			GGTGACGTGAGGTCGGACCC TG		
			GT		
GAM2524	POU2AF1	3'	CCCAGGCTGGAGTACAATGG 21735 C C		
			CCA TG ACTCCAGCCTGGG		
			GGT AC TGAGGTCGGACCC		
			A A		
GAM2524	PPEF2	3'	GTTGCCCAGGCTGGAGTGCATT 21779 C	AG	
	GG		CCA TGC ACTCCAGCCTGGG AC		
			GGT ACGTGAGGTCGGACCC TG		
			T GT		
GAM2524	PPID	3'	CCCAGGCTGGAGTGCGGTGG 88824		
			CCACTGCACTCCAGCCTGGG		
			GGTGGCGTGAGGTCGGACCC		
GAM2524	PPP1R12B	3'	CCCAGGCTGGAGTGCAAGTGG 50349		
			CCACTGCACTCCAGCCTGGG		
			GGTGACGTGAGGTCGGACCC		
GAM2524	PPP1R12B	3'	TCCCAATTCCACCAGGTGCAGT 50367	CCAGCC__	
	GG		CCACTGCACT TGGGA		
			GGTGACGTGG ACCCT		
			ACCACCTTA		
GAM2524	PRKR	3'	GTTGCCCAGGCTGGAGTGCAAT 12352 C	AG	
	G		CA TGC ACTCCAGCCTGGG AC		
			GT ACGTGAGGTCGGACCC TG		
			A GT		
GAM2524	PRKWNK3	3'	GTCACCCAGGTTGGAGTGCAAGT 62238	A	
	GG		CCACTGCACTCCAGCCTGGG GAC		
			GGTGACGTGAGGTTGGACCC CTG		
			A		
GAM2524	PRKY	3'	TCTAGGCTAGGTGCAGTGG 12386 CC		
			CCACTGCACT AGCCTGGG		

			GGTGACGTGG TCGGATCT		
			A_		
GAM2524	PSEN1	5'	TCTGAACTGGAGTGGAGT 24623	G	CC
			ACT CACTCCAG TGGG		
			TGA GTGAGGTC GTCT		
			G AA		
GAM2524	PSMB2	3'	CCCAGGCTGGAGTGCTGTGG 12463	T	
			CCAC GCACTCCAGCCTGGG		
			GGTG CGTGAGGTCGGACCC		
			T		
GAM2524	PSMD9	3'	CCCAGGCTGGAGTGCAGTG 12523		
			CACTGCACTCCAGCCTGGG		
			GTGACGTGAGGTCGGACCC		
GAM2524	PTGES	3'	GTTGCCCAAGCTGGAGTGAAGT 18072	G	C AG
	GG		CCACT CACTCCAGC TGGG AC		
			GGTGA GTGAGGTCG ACCC TG		
			A A GT		
GAM2524	PTGIS	3'	CCCAGGCTGGAGTGCAATGG 8203	C	
			CCA TGCCTCCAGCCTGGG		
			GGT ACGTGAGGTCGGACCC		
			A		
GAM2524	PTGIS	3'	CTGCCCAGGCTAGAGTGCAGTG 8207	C	_
	G		CCACTGCACTC AGCCTGGG AG		
			GGTGACGTGAG TCGGACCC TC		
			A G		
GAM2524	RAB36	3'	GTCACCCAGGCTGGAGTGCAAT 18178	C	A
	GG		CCA TGCCTCCAGCCTGGG GAC		
			GGT ACGTGAGGTCGGACCC CTG		
			A A		
GAM2524	RAB36	3'	GTTGCCCAGGCTGGAGTGCAAT 18180	C	AG
	GG		CCA TGCCTCCAGCCTGGG AC		
			GGT ACGTGAGGTCGGACCC TG		
			A GT		
GAM2524	RABL2A	3'	GTCGCCAGGCTGGAGTGCAGTG 23997		GA
	G		CCACTGCACTCCAGCCTGG GAC		
			GGTGACGTGAGGTCGGACC CTG		
			G_		
GAM2524	RABL2B	3'	GTCGCCAGGCTGGAGTGCAGTG 23985		GA
	G		CCACTGCACTCCAGCCTGG GAC		

			GGTGACGTGAGGTCGGACC CTG			
			G_			
GAM2524	RAI3	3'	GTCACCCAGGCTTGAGTGCAGT 15622	C	A	
	GG		CCACTGCACTC AGCCTGGG GAC			
			GGTGACGTGAG TCGGACCC CTG			
			T A			
GAM2524	RARG	5'	CTCCCAGGCTGGGGCAGTGG 8262	A T		
			CCACTGC C CCAGCCTGGGAG			
			GGTGACG G GGTCGGACCCTC			
			--			
GAM2524	RBBP9	3'	GTCTCCCAGGCTGGAGGTCAGT 70696	CA		
	GG		CCACTG CTCCAGCCTGGGAGAC			
			GGTGAC GAGGTCGGACCCTCTG			
			TG			
GAM2524	RHD	3'	CCAGGCTGGAGTGCAGTG 32819			
			CACTGCACTCCAGCCTGG			
			GTGACGTGAGGTCGGACC			
GAM2524	RHD	3'	CCAGGCTGGAGTGCAGTG 32820			
			CACTGCACTCCAGCCTGG			
			GTGACGTGAGGTCGGACC			
GAM2524	RHD	3'	GTCACCCAGGCTAGAGTGCAAT 32836	C	C	A
	GG		CCA TGCCTC AGCCTGGG GAC			
			GGT ACGTGAG TCGGACCC CTG			
			A A A			
GAM2524	RHD	3'	GTCACCCAGGCTAGAGTGCAAT 32837	C	C	A
	GG		CCA TGCCTC AGCCTGGG GAC			
			GGT ACGTGAG TCGGACCC CTG			
			A A A			
GAM2524	RP2	3'	GTTGCCCAAGCTGGAGTGCAAT 23606	C	C	AG
	GG		CCA TGCCTCCAGC TGGG AC			
			GGT ACGTGAGGTCG ACCC TG			
			A A GT			
GAM2524	RPH3AL	3'	GTTGCCCAAGGCTGGGGTGCAAGT 23741			AG
	GG		CCACTGCACTCCAGCCTGGG AC			
			GGTGACGTGGGGTCGGACCC TG			
			GT			
GAM2524	RPP30	3'	CTCAGGCTGGAGTACAGTGG 22197	C		
			CCACTG ACTCCAGCCTGGG			

			GGTGAC TGAGGTCGGA	CTC	
			A		
GAM2524	RPP30	3'	GTCCCCAGGCTGGAGTGCAGT	22207	A
	GG		CCACTGCACTCCAGCCTGGG	GAC	
			GGTGACGTGAGGTCGGACCC	CTG	
			C		
GAM2524	SAS	3'	GTTGCCCAGGCTGGAGTGCAAT	21107	C AG
	GG		CCA TGC	ACTCCAGCCTGGG AC	
			GGT ACGTGAGGTCGGACCC	TG	
			A	GT	
GAM2524	SCD	3'	CTCCCAGGCAAGCAGCTGG	18592	_ ACTCCA
			CCA CTGC	GCCTGGGAG	
			GGT GACG	CGGACCCTC	
			C	AA	
GAM2524	SEDL	3'	CAGGCTGGAGTGCAGTGG	28080	
			CCACTGCACTCCAGCCTG		
			GGTGACGTGAGGTCGGAC		
GAM2524	SEDL	3'	CAGGCTGTAGTGCAGTGG	28081	C
			CCACTGCACT CAGCCTG		
			GGTGACGTGA	GTCGGAC	
			T		
GAM2524	SEDL	3'	CCAGGCTGGAGTGCAGTGG	28086	
			CCACTGCACTCCAGCCTGG		
			GGTGACGTGAGGTCGGACC		
GAM2524	SEDL	3'	TCCAGGCTGGAGTGCAATGG	28111	C
			CCA TGC	ACTCCAGCCTGGG	
			GGT ACGTGAGGTCGGACCT		
			A		
GAM2524	SEPN1	3'	CCCAGGCTGGAGTGCTATGG	66967	CT
			CCA GCACTCCAGCCTGGG		
			GGT CGTGAGGTCGGACCC		
			AT		
GAM2524	SERPINB9	3'	GTCACCCAGGCTGGAGTGTAGT	16029	A
	GG		CCACTGCACTCCAGCCTGGG	GAC	
			GGTGATGTGAGGTCGGACCC	CTG	
			A		
GAM2524	SERPINB9	3'	GTCGCCCAGGCTGGAGTGCAGT	16031	A
	GG		CCACTGCACTCCAGCCTGGG	GAC	

			GGTGACGTGAGGTCGGACCC CTG			
			G			
GAM2524	SH3BP2	3'	CCCAGGCTGGAGTGCAATG 13056	C		
			CA TGC ACTCCAGCCTGGG			
			GT ACGTGAGGTCGGACCC			
			A			
GAM2524	SH3BP2	3'	CCGAGGCTGGAGCACAGGG 13059	A	CA	G
			CC CTG CTCCAGCCT GG			
			GG GAC GAGGTCGGA CC			
			— AC G			
GAM2524	SHOX	3'	GTCACCCAGGCTGGAGCACACT 6581	C	CA	A
	GG		CCA TG CTCCAGCCTGGG GAC			
			GGT AC GAGGTCGGACCC CTG			
			C AC A			
GAM2524	SIL	3'	GTAGCCAGGCTGGAGTGCAAT 13161	C		AG
	GG		CCA TGC ACTCCAGCCTGGG AC			
			GGT ACGTGAGGTCGGACCC TG			
			A GA			
GAM2524	SLA2	3'	CCCATGCTGGAGTGCAATGG 50885	C		C
			CCA TGC ACTCCAGC TGGG			
			GGT ACGTGAGGTCG ACCC			
			A T			
GAM2524	SLC14A2	5'	GTCACCCAGGCTGGAGTACACT 24124	C	C	A
	GG		CCA TG ACTCCAGCCTGGG GAC			
			GGT AC TGAGGTCGGACCC CTG			
			C A A			
GAM2524	SLC15A1	3'	TCCAGGCTGGAGTGCAATGG 18648	C		
			CCA TGC ACTCCAGCCTGGG			
			GGT ACGTGAGGTCGGACCT			
			A			
GAM2524	SLC19A2	3'	CCCAGGCTGCAGTGCAGTGG 69550			C
			CCACTGCACT CAGCCTGGG			
			GGTGACGTGA GTCGGACCC			
			C			
GAM2524	SLC24A1	3'	GTTGCCAGGCTGGTGTGCAAT 17567	C	T	AG
	GG		CCA TGCAC CCAGCCTGGG AC			
			GGT ACGTG GGTTCGGACCC TG			
			A T GT			
GAM2524	SLC39A1	5'	CCCAGGCTGGAGTGCGGTGG 27808			
			CCACTGCACTCCAGCCTGGG			

GGTGGCGTGAGGTCGGACCC

GAM2524 SLC7A6 3' CTTGGTAAAGTGCAGTGG 15640 CCA T
CCACTGCACT GCC GG
||||||| |||
GGTGACGTGA TGG TC
AA_ T

GAM2524 SMAC 5' GTCGCCCAGGCTGGAGTGCAGT 58005 A
GG CCACTGCACTCCAGCCTGGG GAC
||||||| |||
GGTGACGTGAGGTCGGACCC CTG
G

GAM2524 SMAC 5' GTTGCCCAGGCTGAAGTGCAGT 58006 C AG
GG CCACTGCACT CAGCCTGGG AC
||||||| ||||| ||
GGTGACGTGA GTCGGACCC TG
A GT

GAM2524 SMP1 3' TCTCCCAAGGGGTGAGTGG 27475 G AGCC
CCACT CACTCC TGGGAGA
||||| |||||
GGTGA GTGGGG ACCCTCT
_ A_

GAM2524 SNX15 3' GTCGCCCAGACTGGAGTGCAGT 74130 C A
GG CCACTGCACTCCAG CTGGG GAC
||||||| ||||| |||
GGTGACGTGAGGTC GACCC CTG
A G

GAM2524 SPN 3' CCCAGGCTGGAGTGCAATG 13373 C
CA TGCACTCCAGCCTGGG
|| |||||
GT ACGTGAGGTCGGACCC
A

GAM2524 SS18 3' GTCGCCCAGGCTGGAGTGCAGT 20105 A
GG CCACTGCACTCCAGCCTGGG GAC
||||||| ||||| |||
GGTGACGTGAGGTCGGACCC CTG
G

GAM2524 STAU 5' GTCGCCCAGGCTGGAGTGCAGT 17202 A
GG CCACTGCACTCCAGCCTGGG GAC
||||||| ||||| |||
GGTGACGTGAGGTCGGACCC CTG
G

GAM2524 TAF11 3' CCTAGGCTGGAGTGCAGCGG 20117 A
CC CTGCACTCCAGCCTGGG
|| |||||
GG GACGTGAGGTCGGATCC
C

GAM2524 TAL1 3' CTCAGGCTGGAGTACAGTGG 13527 C
CCACTG ACTCCAGCCTGGG
||||| |||||

			GGTGAC TGAGGTCGGA	CTC	
			A		
GAM2524	TAPBP	3'	CCCAGGCTGCAGTGCAGTGG	13556	C
			CCACTGCACT CAGCCTGGG		
			GGTGACGTGA GTCGGACCC		
			C		
GAM2524	TAPBP	3'	GTCGCCCAGGCTGGAGTGCAGT	13583	A
	GG		CCACTGCACTCCAGCCTGGG	GAC	
			GGTGACGTGAGGTCGGACCC	CTG	
			G		
GAM2524	TAPBP	3'	GTTGCCCAGGCTGGAGTGCAGT	13585	AG
	GG		CCACTGCACTCCAGCCTGGG	AC	
			GGTGACGTGAGGTCGGACCC	TG	
			GT		
GAM2524	TAT	3'	CCCATGCTGGAGTGCAGTGG	6253	C
			CCACTGCACTCCAGC	TGGG	
			GGTGACGTGAGGTCG	ACCC	
			T		
GAM2524	TBXA2R	3'	GTCCCCCAGGCTGGAGTGCAGT	8364	A
	GG		CCACTGCACTCCAGCCTGGG	GAC	
			GGTGACGTGAGGTCGGACCC	CTG	
			C		
GAM2524	TCF2	3'	CCCGAGCTGGAGTGCAGTGG	6611	C
			CCACTGCACTCCAGC	TGGG	
			GGTGACGTGAGGTCG	GCCC	
			A		
GAM2524	TDGF1	3'	CCCAGGCTGGACTGCAATG	13654	C C
			CA TGCA TCCAGCCTGGG		
			GT ACGT AGGTCGGACCC		
			A C		
GAM2524	TEM7	3'	TCCTTGCCAGGTGCAGTGG	40271	CCA T
			CCACTGCACT GCC GGGA		
			GGTGACGTGG CGG TCCT		
			AC_ T		
GAM2524	TERF1	3'	GTTGCCCAGGCTGGAGTGCAGT	34399	AG
	GG		CCACTGCACTCCAGCCTGGG	AC	
			GGTGACGTGAGGTCGGACCC	TG	
			GT		
GAM2524	TERF2	3'	GTCACCCAGGCTGGAGTGCAGT	20162	A
	GG		CCACTGCACTCCAGCCTGGG	GAC	

			GGTGACGTGAGGTCGGACCC CTG		
			A		
GAM2524	TIM3	3'	GTTGCCCAGGCTGGAGTGCAAT 52361	C	AG
	GG		CCA TGCCTCCAGCCTGGG AC		
			GGT ACGTGAGGTCGGACCC TG		
			A GT		
GAM2524	TJP1	5'	TCCAGGCAGGAGTGCAAGTGG 13767	A	
			CCACTGCACTCC GCCTGGG		
			GGTGACGTGAGG CGGACCT		
			A		
GAM2524	TLR5	5'	CCCAGGCTGGACTGCAGTG 13784	C	
			CACTGCA TCCAGCCTGGG		
			GTGACGT AGGTCGGACCC		
			C		
GAM2524	TMC1	5'	GTTGCCCAGGCTGGAGTGCAAGT 57711		AG
	GG		CCACTGCACTCCAGCCTGGG AC		
			GGTGACGTGAGGTCGGACCC TG		
			GT		
GAM2524	TMC2	3'	GTCTCCTCTCTTGAATGCATG 55804	C C	CCT
			CA TGCA TCCAG GGGAGAC		
			GT ACGT AGGTT TCCTCTG		
			_ A CTC		
GAM2524	TMPRSS3	3'	GTTGCCCAGGCTGGAGTGCAAGT 44032		AG
	GG		CCACTGCACTCCAGCCTGGG AC		
			GGTGACGTGAGGTCGGACCC TG		
			GT		
GAM2524	TNFAIP2	3'	GTTGCCCAGGCTGGAGTGCAAGT 21928		AG
	GG		CCACTGCACTCCAGCCTGGG AC		
			GGTGACGTGAGGTCGGACCC TG		
			GT		
GAM2524	TNFRSF10B	3'	CCCAGGCTGGAGTGCAACGG 15221	AC	
			CC TGCCTCCAGCCTGGG		
			GG ACGTGAGGTCGGACCC		
			CA		
GAM2524	TNFRSF10B	3'	GTCTCCAGGCTGGAGTGCAAT 15231	C	
	GG		CCA TGCCTCCAGCCTGGGAGAC		
			GGT ACGTGAGGTCGGACCCTCTG		
			A		
GAM2524	TNFRSF11A	3'	CCCAGGCTAGAGTGCAAGTGG 15192	C	
			CCACTGCACTC AGCCTGGG		

			GGTGACGTGAG TCGGACCC		
			A		
GAM2524	TNFRSF1B	3'	CTCAGGCCAGGTGCAGTGG 8392	CCA	
			CCACTGCACT GCCTGGG		
			GGTGACGTGG CGGACTC		
			AC_		
GAM2524	TNFRSF9	3'	GTCACCCAGGCTGGAGTGCAGT 9585	A	
		GG	CCACTGCACTCCAGCCTGGG GAC		
			GGTGACGTGAGGTCGGACCC CTG		
			A		
GAM2524	TP53	3'	GTTGCCCAGGCTGGAGTGGAGT 6805	G	AG
		GG	CCACT CACTCCAGCCTGGG AC		
			GGTGA GTGAGGTCGGACCC TG		
			G GT		
GAM2524	TPMT	3'	CCCAACCTGGAGTGCAGTGG 6308	CC	
			CCACTGCACTCCAG TGGG		
			GGTGACGTGAGGTC ACCC		
			CA		
GAM2524	TRAF5	3'	GTCACCCAGGCTGGAGTACAGT 17281	C	A
		GG	CCACTG ACTCCAGCCTGGG GAC		
			GGTGAC TGAGGTCGGACCC CTG		
			A A		
GAM2524	TRPM6	3'	CCCAGGCTGGAGTGCAATG 35030	C	
			CA TGCACTCCAGCCTGGG		
			GT ACGTGAGGTCGGACCC		
			A		
GAM2524	TRPV1	3'	CCCAGGCTGGAATGCAGTGG 55665	C	
			CCACTGCA TCCAGCCTGGG		
			GGTGACGT AGGTCGGACCC		
			A		
GAM2524	TRPV1	3'	GTTGCCCAGGCTGGAGTGCAGT 55685		AG
		GG	CCACTGCACTCCAGCCTGGG AC		
			GGTGACGTGAGGTCGGACCC TG		
			GT		
GAM2524	TRPV1	3'	GTTGCCCAGGCTGGAGTGCAGT 55686		AG
		GG	CCACTGCACTCCAGCCTGGG AC		
			GGTGACGTGAGGTCGGACCC TG		
			GT		
GAM2524	TUFT1	3'	GTCACCCAGGCTGGAGTGCAGT 39676		A
			ACTGCACTCCAGCCTGGG GAC		

			TGACGTGAGGTCGGACCC CTG		
			A		
GAM2524	UGDH	3'	GTTGCCCAGGCTGGAGTGCAGT 14003	AG	
	GG		CCACTGCACTCCAGCCTGGG AC		
			GGTGACGTGAGGTCGGACCC TG		
			GT		
GAM2524	UMPS	3'	CCCAGGATGGAGTGCAGTGG 6329	G	
			CCACTGCACTCCA CCTGGG		
			GGTGACGTGAGGT GGACCC		
			A		
GAM2524	VENTX2	3'	GTCACCCAGGCTGGAGTGCAT 27864	C	A
	G		CA TGCCTCCAGCCTGGG GAC		
			GT ACGTGAGGTCGGACCC CTG		
			A A		
GAM2524	VHL	3'	CCCAGGCTGGAGTGCAGAGG 6845	A	
			CC CTGCACTCCAGCCTGGG		
			GG GACGTGAGGTCGGACCC		
			A		
GAM2524	VIPR2	3'	GTCGCCCAGGCTGGAGTGCAGT 14074	A	
	GG		CCACTGCACTCCAGCCTGGG GAC		
			GGTGACGTGAGGTCGGACCC CTG		
			G		
GAM2524	WBSCR1	3'	CTCTCTGGCTGGGTGCAGTG 42481	T	T
			CACTGCAC CCAGCC GGGAG		
			GTGACGTG GGTCGG CTCTC		
			- T		
GAM2524	XRCC2	3'	GTCTCCAGGCTGCTGGAGTGC 19508		
	AGTGG		CCACTGCACTCCA GCCTGGGAGAC		
			GGTGACGTGAGGT CGGACCCTCTG		
			CGT		
GAM2524	XRCC2	3'	GTCTCCAGGCTGGAGTGCAGT 19510		
	GG		CCACTGCACTCCAGCCTGGGAGAC		
			GGTGACGTGAGGTCGGACCCTCTG		
GAM2524	YES1	3'	CCCAGGCTGGAGTGCAGTGG 19532		
			CCACTGCACTCCAGCCTGGG		
			GGTGACGTGAGGTCGGACCC		
GAM2524	ZNF133	5'	GTTGCCCAGGCTGGAGTGCAT 14299	C	AG
	GG		CCA TGCCTCCAGCCTGGG AC		

			GGT ACGTGAGGTCGGACCC TG		
			A GT		
GAM2524	ZNF157	3'	GTCACCCAGGCTGGAGTGCAAT 14337 C	A	
	GG		CCA TGCCTCCAGCCTGGG GAC		
			GGT ACGTGAGGTCGGACCC CTG		
			A A		
GAM2524	ZNF253	3'	CCGAGGCTGGAGTGCAATG 41077 C	G	
			CA TGCCTCCAGCCT GG		
			GT ACGTGAGGTCGGA CC		
			A G		
GAM2524	ZNF264	3'	CCCACGCTGGAGTGCTGTG 14206 T	C	
			CAC GCACTCCAGC TGGG		
			GTG CGTGAGGTCG ACCC		
			T C		
GAM2524	ZNF264	3'	GTCACCCAGGCTGGAGTGCAGT 14226	A	
	GG		CCACTGCACTCCAGCCTGGG GAC		
			GGTGACGTGAGGTCGGACCC CTG		
			A		
GAM2524	ZNF7	5'	GTCTCTCGGCCAGAACACGTGG 14174 _ CAC CA T		
			CCAC TG TC GCC GGGAGAC		
			GGTG AC AG CGG CTCTCTG		
			C A__ AC _		
GAM2524	20D7-FC4	5'	GTCACCCAGGCTGGAGTGCAGT 61567	A	
	GG		CCACTGCACTCCAGCCTGGG GAC		
			GGTGACGTGAGGTCGGACCC CTG		
			A		
GAM2524	AAK1	3'	CCTGGGCTGGAGTGCAGTGG 30520	TG	
			CCACTGCACTCCAGCC GG		
			GGTGACGTGAGGTCGG CC		
			GT		
GAM2524	AGMAT	3'	GTCACCCAGGCTGGAGTGCAGT 45743	A	
	GG		CCACTGCACTCCAGCCTGGG GAC		
			GGTGACGTGAGGTCGGACCC CTG		
			A		
GAM2524	AGMAT	3'	TCTTGGCTGGAGTGAGTGG 45744 G	T	
			CCACT CACTCCAGCC GGGA		
			GGTGA GTGAGGTCGG TTCT		
			- -		
GAM2524	ANKRD6	3'	GTCACCCAGACTGGAGTGCAGT 30774	C A	
	GG		CCACTGCACTCCAG CTGGG GAC		

			GGTGACGTGAGGTC GACCC CTG		
			A A		
GAM2524	AP1S3	3'	GTCACCCAGGCTGGAGTGCAGT 75429	A	
			ACTGCACTCCAGCCTGGG GAC		
			TGACGTGAGGTCGGACCC CTG		
			A		
GAM2524	AP3S2	3'	CCCAGGCTGGAGTGCTGTGG 20648	T	
			CCAC GCACTCCAGCCTGGG		
			GGTG CGTGAGGTCGGACCC		
			T		
GAM2524	APOL2	3'	CCCAGGATGGAGTGCAGTGG 48786	G	
			CCACTGCACTCCA CCTGGG		
			GGTGACGTGAGGT GGACCC		
			A		
GAM2524	APXL2	5'	GTCGCCAGGCTGGAGTGCAGTG 75684	GA	
	G		CCACTGCACTCCAGCCTGG GAC		
			GGTGACGTGAGGTCGGACC CTG		
			G_		
GAM2524	ARHF	3'	CTCAGGCTAGAGTGCAGTGG 39266	C	
			CCACTGCACTC AGCCTGGG		
			GGTGACGTGAG TCGGACTC		
			A		
GAM2524	ARHGAP11A	3'	GTCGTCCAGGCTGGAGTGCAGT 29458	GA	
	GG		CCACTGCACTCCAGCCTGG GAC		
			GGTGACGTGAGGTCGGACC CTG		
			TG		
GAM2524	ARHGAP5	5'	GTTGCCCAGGCTGGAGTGCAAT 77605	C	AG
	GG		CCA TGCCTCCAGCCTGGG AC		
			GGT ACGTGAGGTCGGACCC TG		
			A GT		
GAM2524	ASB16	5'	GTCGCCCAGGCTGGAGTGCAGT 55986	A	
	GG		CCACTGCACTCCAGCCTGGG GAC		
			GGTGACGTGAGGTCGGACCC CTG		
			G		
GAM2524	ASB16	3'	GTGGCCCAGGCTGAAGTGCAGT 55987	C	AG
	GG		CCACTGCACT CAGCCTGGG AC		
			GGTGACGTGA GTCGGACCC TG		
			A GG		
GAM2524	ASB16	3'	GTTGCCCAGGCTGGAGTGCAGT 55989	AG	
	GG		CCACTGCACTCCAGCCTGGG AC		

		GGTGACGTGAGGTCGGACCC TG		
		GT		
GAM2524	ASE-1	3' GTCACCCAGGCTGGAGTGCAGT 24991		A
	GG	CCACTGCACTCCAGCCTGGG GAC		
		GGTGACGTGAGGTCGGACCC CTG		
		A		
GAM2524	ASE-1	3' GTCGCCCAGGTTGGAGTGCAGT 24993		A
	GG	CCACTGCACTCCAGCCTGGG GAC		
		GGTGACGTGAGGTTGGACCC CTG		
		G		
GAM2524	ATP1B4	3' GTCACCCAGGCTGGAGTGCAGT 24851		A
	GG	CCACTGCACTCCAGCCTGGG GAC		
		GGTGACGTGAGGTCGGACCC CTG		
		A		
GAM2524	BA108L7.2	3' CCCAGGCTGGAGTGCATGG 49070	C	
		CCA TGCACCTCCAGCCTGGG		
		GGT GCGTGAGGTCGGACCC		
		A		
GAM2524	BAG5	3' CCCAGGCTGCAGTGCAGTGG 18035		C
		CCACTGCACT CAGCCTGGG		
		GGTGACGTGA GTCGGACCC		
		C		
GAM2524	BIA2	3' CTTAAGGCTGGGTGCAGTGG 71794	T	GG
		CCACTGCAC CCAGCCT GAG		
		GGTGACGTG GGTCGGA TTC		
		— A_		
GAM2524	BMF	3' CTCCCAGGAAGAGTGCTGTGG 54281	T	CAG
		CCAC GCACTC CCTGGGAG		
		GGTG CGTGAG GGACCCTC		
		T AA_		
GAM2524	BNIP-S	3' GTCGCCAGGCTGGAGTGCAGTG 57108		GA
	G	CCACTGCACTCCAGCCTGG GAC		
		GGTGACGTGAGGTCGGACC CTG		
		G_		
GAM2524	BTN3A1	3' CTAGGCTGGAGTGCAGTGG 23889		
		CCACTGCACTCCAGCCTGG		
		GGTGACGTGAGGTCGGATC		
GAM2524	BY55	5' GTCAACCAGGCCAGAGTGCAGT 60063	CA	GA
	G	CACTGCACTC GCCTGG GAC		

		GTGACGTGAG CGGACC CTG		
		AC AA		
GAM2524	C(27)-3BETA-HSD 3'	GTCACCCAGACTGGAGTGCAGT 48054	C	A
	GG	CCACTGCACTCCAG CTGGG GAC		
		GGTGACGTGAGGTC GACCC CTG		
		A A		
GAM2524	C11orf17 3'	GTTGCCCAGGCTGGAGTGCAGT 40588	AG	
	GG	CCACTGCACTCCAGCCTGGG AC		
		GGTGACGTGAGGTCGGACCC TG		
		GT		
GAM2524	C13orf1 3'	GTCACCCAGGCTAGAGTGCAGT 40369	C	A
	GG	CCACTGCACTC AGCCTGGG GAC		
		GGTGACGTGAG TCGGACCC CTG		
		A A		
GAM2524	C14orf4 5'	GTCTCGGCGTGGAACGCACGG 67920	AC	AC _ TGG
		CC TGC TCCA GCC GAGAC		
		GG ACG AGGT CGG CTCTG		
		C_ CA G _		
GAM2524	C16orf7 3'	CCCAGAAGAAGCTGGAGTGCA 18143	_____	
		TGCACTCCAGC CTGGG		
		ACGTGAGGTCG GACCC		
		AAGAA		
GAM2524	C1orf24 3'	CCAAGGCTGGAGTGCAGTGG 54785	G	
		CCACTGCACTCCAGCCT GG		
		GGTGACGTGAGGTCGGA CC		
		A		
GAM2524	C1QTNF6 3'	GTTGCCCAGGCTAGAGTGCAGT 49995	C	AG
	GG	CCACTGCACTC AGCCTGGG AC		
		GGTGACGTGAG TCGGACCC TG		
		A GT		
GAM2524	C20orf172 3'	TTTTGAGGCTGGGCGCAATGG 46770	C	A T G
		CCA TGC C CCAGCCT GGAG		
		GGT ACG G GGTCGGA TTTT		
		A C_ G		
GAM2524	C20orf183 3'	TCCCAACTGGGTGCAGTGG 48539	T	CC
		CCACTGCAC CCAG TGGGA		
		GGTGACGTG GGTC ACCCT		
		_ A_		
GAM2524	C21orf25 3'	CCTGACGCTGGAGTGCGGTG 64290	CT_	
		CACTGCACTCCAGC GGG		

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GTGGCGTGAGGTCG TCC
      CAG
GAM2524 C21orf25 3' GTTGCCCAGGCTGGAGTGCAAT 64300 C AG
      GG      CCA TGC ACTCCAGCCTGGG AC
      ||| ||||| ||
      GGT ACGTGAGGTCGGACCC TG
      A      GT
GAM2524 C21orf67 5' GTCGCCCAGGCTGGAGCGCAAT 55233 C A A
      GG      CCA TGC CTCCAGCCTGGG GAC
      ||| ||| ||||| |||
      GGT ACG GAGGTCGGACCC CTG
      A C      G
GAM2524 C22orf19 3' TCCAGGCTGGAGTGCAAGTGG 14828
      CCACTGCACTCCAGCCTGGG
      ||||| |||||
      GGTGACGTGAGGTCGGACCT

GAM2524 C22orf19 3' TGGGCTGGGCACAGTGG 14837 CA T
      CCACTG C CCAGCCTG
      ||||| | |||||
      GGTGAC G GGTCGGGT
      AC _
GAM2524 C3F 3' CCCACGCTGGAATGCAGTGG 20475 C C
      CCACTGCA TCCAGC TGGG
      ||||| ||||| |||
      GGTGACGT AGGTCG ACCC
      A C
GAM2524 C6orf31 3' TCTCCAGGCTCTTTCTGCAG 48385 CTCC_
      CTGCA AGCCTGGGAGA
      |||| | |||||
      GACGT TCGGACCCTCT
      CTTTC
GAM2524 C6orf33 3' GTCGCCCAGGCTGGAGTGCAAGT 56719 A
      G      CACTGCACTCCAGCCTGGG GAC
      ||||| ||||| |||
      GTGACGTGAGGTCGGACCC CTG
      G
GAM2524 C6orf5 3' CCAGGCTGCAGTACAGTG 31979 C C
      CACTG ACT CAGCCTGG
      |||| ||| |||||
      GTGAC TGA GTCGGACC
      A C
GAM2524 C6orf5 3' TCCAGGCTGGAGTGCAAGT 32005
      CACTGCACTCCAGCCTGGG
      ||||| |||||
      GTGACGTGAGGTCGGACCT

GAM2524 C6orf5 3' TTTTtaggCTGGGCGCAGTGG 32010 A T
      CCACTGC C CCAGCCTGGGAG
      ||||| | |||||

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			GGTGACG G GGTCGGATTTTT		
			C _		
GAM2524	C9orf9	3'	CCCAGGCTGGAGTGC GG TGG 39014		
			CCACTGCACTCCAGCCTGGG		
			GGTGGCGTGAGGTCGGACCC		
GAM2524	C9orf9	3'	GTCTCCCAGGCTGGAGTGCAGT 39032		
	GG		CCACTGCACTCCAGCCTGGGAGAC		
			GGTGACGTGAGGTCGGACCCTCTG		
GAM2524	CACNG4	3'	TCCCAGGCAGAGTAAGCAG 27710	__	CA
			CTGC ACTC GCCTGGGA		
			GACG TGAG CGGACCCT		
			AA A_		
GAM2524	CAPN6	3'	TCAAGAGCTGGAGTTCAATG 27401	C C	_ GG
			CA TG ACTCCAGC CT GA		
			GT AC TGAGGTCG GA CT		
			A T A A_		
GAM2524	CARD6	3'	GTTGCCCAGGCTGGAGTGC AAT 51849	C	AG
	GG		CCA TGC ACTCCAGCCTGGG AC		
			GGT ACGTGAGGTCGGACCC TG		
			A GT		
GAM2524	CDC14B	3'	TCCAGGCTGGAGTGCAGTGG 14778		
			CCACTGCACTCCAGCCTGGG		
			GGTGACGTGAGGTCGGACCT		
GAM2524	CEACAM8	3'	GTCGCCCAGGCTGGAGTGCAGT 10187		A
	GG		CCACTGCACTCCAGCCTGGG GAC		
			GGTGACGTGAGGTCGGACCC CTG		
			G		
GAM2524	CHSY1	3'	GTTACCCAGGCTGGAATGCAGT 30572	C	A
	GG		CCACTGCA TCCAGCCTGGG GAC		
			GGTGACGT AGGTCGGACCC TTG		
			A A		
GAM2524	CIP29	3'	CCCAGCTGGAGTGCAGTGG 51373		C
			CCACTGCACTCCAGC TGGG		
			GGTGACGTGAGGTCG ACCC		
GAM2524	COLEC12	3'	GTTGCCCAGGCTGGAGTGCAGT 56107		AG
	GG		CCACTGCACTCCAGCCTGGG AC		

		GGTGACGTGAGGTCGGACCC TG			
		GT			
GAM2524	CPSF2	3' GTCACCCAGGCTGGAGTGCAGT 62280		A	
	GG	CCACTGCACTCCAGCCTGGG GAC			
		GGTGACGTGAGGTCGGACCC CTG			
		A			
GAM2524	CPSF2	3' GTTGCCCAGACTGGAGTGCAAT 62282	C	C	AG
	GG	CCA TGCCTCCAG CTGGG AC			
		GGT ACGTGAGGTC GACCC TG			
		A A GT			
GAM2524	CSAD	3' CTTTGAGGCCGGGTGCAGTGG 32579	T	A	G
		CCACTGCAC CC GCCT GGAG			
		GGTGACGTG GG CGGA TTTC			
		_ C G			
GAM2524	ctm-1	3' TCTCCCAGGGCCAGAGACAGCA 75765	A__	CA	_
	G	CTGC CTC GCC TGGGAGA			
		GACG GAG CGG ACCCTCT			
		ACA AC G			
GAM2524	CXYorf1	5' TCTCCCAGCAGGTAGAGCAG 82921	A _	A	C
		CTGC CT CC GC TGGGAGA			
		GACG GA GG CG ACCCTCT			
		A T A _			
GAM2524	CYLC2	3' CCCTGGCTGGAGTTCAGTG 9032	C	T	
		CACTG ACTCCAGCC GGG			
		GTGAC TGAGGTCGG CCC			
		T T			
GAM2524	DBR1	3' CCTAGACTGGAGTGCAATGG 33062	C	C	
		CCA TGCCTCCAG CTGGG			
		GGT ACGTGAGGTC GATCC			
		A A			
GAM2524	DCOYM	3' CAGACTGGAGTGCAATGG 50514		C	
		CCACTGCACTCCAG CTG			
		GGTGACGTGAGGTC GAC			
		A			
GAM2524	DCOYM	3' GTCGCCCAGGCTGGAGTGCAAT 50535	C		A
	GG	CCA TGCCTCCAGCCTGGG GAC			
		GGT ACGTGAGGTCGGACCC CTG			
		A G			
GAM2524	DDX31	3' TCCCTGGATGGAGTGCAAT 43248	C	G	T
		C ACTGCACTCCA CC GGGA			

		A TGACGTGAGGT GG CCCT		
		C A T		
GAM2524	DKFZp434A2417 3'	GTTGCCCAGGCTGGAGGGCAAT 66685	C A	AG
	GG	CCA TGC CTCCAGCCTGGG AC		
		GGT ACG GAGGTCGGACCC TG		
		A G GT		
GAM2524	DKFZP434B044 3'	GTTGCCCAAGGTAGAGTGCAGT 49721	CA _	AG
	GG	CCACTGCACTC GCCT GGG AC		
		GGTGACGTGAG TGA CCC TG		
		A_ A GT		
GAM2524	DKFZP434B1727 3'	GTTACCCAGGCTGGAGTACAGT 50480	C	A
	GG	CCACTG ACTCCAGCCTGGG GAC		
		GGTGAC TGAGGTCGGACCC TTG		
		A A		
GAM2524	DKFZp434C0923 3'	GTCACCCAGGCTGGAGTACAGT 34652	C	A
	GG	CCACTG ACTCCAGCCTGGG GAC		
		GGTGAC TGAGGTCGGACCC CTG		
		A A		
GAM2524	DKFZP434C212 3'	GTTGCCCAGGCTGGAGTGCAAT 69499	C	AG
	GG	CCA TGC ACTCCAGCCTGGG AC		
		GGT ACGTGAGGTCGGACCC TG		
		A GT		
GAM2524	DKFZP434D146 3'	GTCGCCCAGGCTAGAGTATAGT 32140	C C	A
	GG	CCACTG ACTC AGCCTGGG GAC		
		GGTGAT TGAG TCGGACCC CTG		
		A A G		
GAM2524	DKFZp434E2220 5'	GTTGCCCAGGCTGGAGTGCAGT 34718		AG
	GG	CCACTGCACTCCAGCCTGGG AC		
		GGTGACGTGAGGTCGGACCC TG		
		GT		
GAM2524	DKFZP434F0318 3'	CCTAGGCTGGAGTTGCAGTGG 48749	_	
		CCACTGCA CTCCAGCCTGGG		
		GGTGACGT GAGGTCGGATCC		
		T		
GAM2524	DKFZp434F1719 3'	GTTTCCCAGGCTGGAGTGCAAT 51017	C	
	GG	CCA TGC ACTCCAGCCTGGGAGAC		
		GGT ACGTGAGGTCGGACCCTTTG		
		A		
GAM2524	DKFZP434J037 3'	CCCAGGCTAGAGTGCAATGG 48943	C C	
		CCA TGC ACTC AGCCTGGG		

		GGT ACGTGAG TCGGACCC			
		A A			
GAM2524	DKFZP564D166 3'	CCTAGGCCAGAGTGCAGTGG 48017	CA		
		CCACTGCACTC GCCTGGG			
		GGTGACGTGAG CGGATCC			
		AC			
GAM2524	DKFZP564G092 5'	CCCAGGCTGTAGTGCAGTGG 32156	C		
		CCACTGCACT CAGCCTGGG			
		GGTGACGTGA GTCGGACCC			
		T			
GAM2524	DKFZP564I122 3'	CCTAGGCTGGAGTGCAGTGG 63874			
		CCACTGCACTCCAGCCTGGG			
		GGTGACGTGAGGTCGGATCC			
GAM2524	DKFZP564K0322 3'	GTTGCCCAGGCTGGAGTGCAGT 50190	AG		
	GG	CCACTGCACTCCAGCCTGGG AC			
		GGTGACGTGAGGTCGGACCC TG			
		GT			
GAM2524	DKFZP564O0523 3'	GTTGCCCAGGCTGGAATGCAGT 50424	C	AG	
	GG	CCACTGCA TCCAGCCTGGG AC			
		GGTGACGT AGGTCGGACCC TG			
		A GT			
GAM2524	DKFZP566I1024 3'	GTTGCCCAGGCTAGAGTGCAGT 70652	C	C	AG
	GG	CCA TGCCTC AGCCTGGG AC			
		GGT ACGTGAG TCGGACCC TG			
		C A GT			
GAM2524	DKFZP761E2110 3'	CCTAGGCTGGAATGCAGTGG 48962	C		
		CCACTGCA TCCAGCCTGGG			
		GGTGACGT AGGTCGGATCC			
		A			
GAM2524	DKFZp761H2121 5'	CTCTTTTGGAGTGCAG 57179	CCT		
		CTGCACTCCAG GGGAG			
		GACGTGAGGTT TTCTC			
GAM2524	DKFZp761J139 5'	GTCACCCAGGCTGGAGTGCAGT 51112	A		
	GG	CCACTGCACTCCAGCCTGGG GAC			
		GGTGACGTGAGGTCGGACCC CTG			
		A			
GAM2524	DKFZp761N1114 3'	CCAGGCTGGAATGCAGTGG 79777	C		
		CCACTGCA TCCAGCCTGG			

GGTGACGT AGGTCGGACC
A
GAM2524 DKFZp761O0113 5' GTTGCCAGGCTTGAGTGCAGT 37899 C AG
G CACTGCACTC AGCCTGGG AC
||||||| ||||| ||
GTGACGTGAG TCGGACCC TG
T GT
GAM2524 DKFZp762K222 5' GTCTCCCGGGGACTGCAGCGG 71674 A C AGC
CC CTGCA TCC CTGGGAGAC
|| ||||| || |||||
GG GACGT AGG GGCCCTCTG
C C ____
GAM2524 DKFZp762P2111 3' GTTGCCAGGCTGGAGTGCAAT 87640 C AG
GG CCA TGCACCTCCAGCCTGGG AC
|| ||||| ||||| ||
GGT ACGTGAGGTCTGGACCC TG
A GT
GAM2524 DLL1 5' CCCAGGCTCGCGCGTGG 20050 _ ACTCC
CCAC TGC AGCCTGGG
||||| |||||
GGTG GCG TCGGACCC
C C ____
GAM2524 DMRTB1 3' TCCAGGTGGCTGGAGCCAGCAG 66840 A__ TG__
CTGC CTCCAGCC GGA
||||| ||||| ||
GACG GAGGTCGG CCT
ACC TGGA
GAM2524 DRIM 3' CCCAAGGCGGAGTGCAGTG 27950 A _
CACTGCACTCC GCCT GGG
||||||| |||||
GTGACGTGAGG CGGA CCC
_ A
GAM2524 DSCR6 3' GTCTCCAGGCTGGAGTGCAGT 39073
G CACTGCACTCCAGCCTGGGAGAC
||||||| |||||
GTGACGTGAGGTCTGGACCCTCTG
GAM2524 EPS8R1 3' CCCGAGAGGGTGCAGTGG 35302 CAGCC
CCACTGCACTC TGGG
||||||| |||||
GGTGACGTGGG GCCC
AGA__
GAM2524 EPS8R1 3' CCCGAGAGGGTGCAGTGG 56529 CAGCC
CCACTGCACTC TGGG
||||||| |||||
GGTGACGTGGG GCCC
AGA__
GAM2524 EREG 3' GTTGCCAGGTTGGAGTGCAGT 9315 AG
GG CCACTGCACTCCAGCCTGGG AC
||||||| |||||

			GGTGACGTGAGGTTGGACCC	TG	
			GT		
GAM2524	EVI5	3'	CCCAGGCTGGAGTGCTGTGG	20204	T
			CCAC GCACTCCAGCCTGGG		
			GGTG CGTGAGGTCGGACCC		
			T		
GAM2524	EVI5	3'	CTCAGGCTGGAGTGCAGTGG	20205	
			CCACTGCACTCCAGCCTGGG		
			GGTGACGTGAGGTCGGACTC		
GAM2524	FBP17	3'	TTCAGACTGGAGTGCAGTGG	73164	C
			CCACTGCACTCCAG CTGGG		
			GGTGACGTGAGGTC GACTT		
			A		
GAM2524	FBXO26	3'	CTTGCAGCCAGGTGCAGTGG	46627	CCA C G
			CCACTGCACT GC TG GAG		
			GGTGACGTGG CG AC TTC		
			AC_ _ G		
GAM2524	FER1L4	3'	GTCTCCCAGGTTGGAGTGCAGT	48132	
	GG		CCACTGCACTCCAGCCTGGGAGAC		
			GGTGACGTGAGGTTGGACCCTCTG		
GAM2524	FER1L4	3'	GTCTCCCAGGTTGGAGTGCAGT	48133	
	GG		CCACTGCACTCCAGCCTGGGAGAC		
			GGTGACGTGAGGTTGGACCCTCTG		
GAM2524	FKBP9	3'	GTCGCCAGGCTGGAGTGCAGTG	95722	GA
	G		CCACTGCACTCCAGCCTGG GAC		
			GGTGACGTGAGGTCGGACC CTG		
			G_		
GAM2524	FLJ00024	5'	GTCACCCAGGCTGGAGTGCAAT	64502	C A
	GG		CCA TGCCTCCAGCCTGGG GAC		
			GGT ACGTGAGGTCGGACCC CTG		
			A A		
GAM2524	FLJ00060	5'	GTCACCCAGGCTGGAGTGCAGT	61753	A
	GG		CCACTGCACTCCAGCCTGGG GAC		
			GGTGACGTGAGGTCGGACCC CTG		
			A		
GAM2524	FLJ10101	3'	GTGGCCCAGGCTGGAGTGCAGT	45604	AG
	GG		CCACTGCACTCCAGCCTGGG AC		

GGTGACGTGAGGTCGGACCC TG
GG
GAM2524 FLJ10232 3' CCCAGGCTGGAGTGCGATGG 36376 C
CCA TGC ACTCCAGCCTGGG
||| |||||
GGT GCGTGAGGTCGGACCC
A
GAM2524 FLJ10297 3' GTTGCCCAGGCTAGAGTGCAGT 36445 C AG
GG CCACTGCACTC AGCCTGGG AC
||||||| ||||| ||
GGTGACGTGAG TCGGACCC TG
A GT
GAM2524 FLJ10298 3' GTTGCCCAGGCTGGAGTGCAGT 36462 AG
ACTGCACTCCAGCCTGGG AC
||||||| ||||| ||
TGACGTGAGGTCGGACCC TG
GT
GAM2524 FLJ10346 5' GTCTCCCAGGCTGAAGTGCAGT 36529 C
GG CCACTGCACT CAGCCTGGGAGAC
||||||| |||||
GGTGACGTGA GTCGGACCCTCTG
A
GAM2524 FLJ10535 3' GTCACCCAGGCTGGAGTGCAGT 36755 A
GG CCACTGCACTCCAGCCTGGG GAC
||||||| ||||| |||
GGTGACGTGAGGTCGGACCC CTG
A
GAM2524 FLJ10560 3' GTCGCCCAGGCTGGCGTGCAGT 36801 T A
GG CCACTGCAC CCAGCCTGGG GAC
||||||| ||||| |||
GGTGACGTG GGTTCGGACCC CTG
C G
GAM2524 FLJ10583 3' TCTCCCAGGCTCACTGCAG 36831 CTCC
CTGCA AGCCTGGGAGA
||||| |||||
GACGT TCGGACCCTCT
CAC_
GAM2524 FLJ10607 3' CCCAGGCTAGAGCGCAGGG 77627 A A C
CC CTGC CTC AGCCTGGG
|| ||| ||| |||||
GG GACG GAG TCGGACCC
_ C A
GAM2524 FLJ10607 3' CCCAGGCTGGAGTCCAGTGG 77628 C
CCACTG ACTCCAGCCTGGG
||||| |||||
GGTGAC TGAGGTCGGACCC
C
GAM2524 FLJ10640 5' CCTAGGCTGAGTGCAGTGG 39234 C
CCACTGCACTC AGCCTGGG
||||||| |||||

GGTGACGTGAG TCGGATCC

GAM2524 FLJ10713 3' GTTGCCCAGGCTGGAGTGCAGT 37006 AG
GG CCACTGCACTCCAGCCTGGG AC
||||| ||
GGTGACGTGAGGTCGGACCC TG
GT

GAM2524 FLJ10846 3' GTCACCCAGGCTGGAGTGCAGT 37291 A
GG CCACTGCACTCCAGCCTGGG GAC
||||| |||
GGTGACGTGAGGTCGGACCC CTG
A

GAM2524 FLJ10847 3' CAGGCTGGAGTGCGGTGG 37298
CCACTGCACTCCAGCCTG
|||||
GGTGGCGTGAGGTCGGAC

GAM2524 FLJ10900 3' CCGGGGCTGGAGCGGAGTG 66206 GCA G
CACT CTCCAGCCT GG
||| ||||| ||
GTGA GAGGTCGGG CC
GGC G

GAM2524 FLJ10901 3' CCCAGGCTGGAATGCTGT 37358 T C
AC GCA TCCAGCCTGGG
|| ||| |||||
TG CGT AGGTCGGACCC
T A

GAM2524 FLJ10922 3' GTTGCCCAGGCTGGAATGCAAT 37408 C C AG
GG CCA TGCA TCCAGCCTGGG AC
||| ||| ||||| ||
GGT ACGT AGGTCGGACCC TG
A A GT

GAM2524 FLJ10956 3' CCCACATTGGAGTGCAGTGG 37463 CC
CCACTGCACTCCAG TGGG
||||| |||
GGTGACGTGAGGTT ACCC
AC

GAM2524 FLJ10989 3' CTTTTAGGCTGGGTGCAGTGG 37501 T
CCACTGCAC CCAGCCTGGGAG
||||| |||||
GGTGACGTG GGTCGGATTTTC

GAM2524 FLJ11004 5' CCCAGACTGGAGTGCTGTGG 37531 T C
CCAC GCACTCCAG CTGGG
||| ||||| |||
GGTG CGTGAGGTC GACCC
T A

GAM2524 FLJ11029 3' CCCAGCTGGGTGCAGTGG 61633 T C
CCACTGCAC CCAGC TGGG
||||| ||| |||

GGTGACGTG GGTCG ACCC

GAM2524 FLJ11467 3' GTCACCCAGGCTGGAGTACAGT 46977 C A
GG CCACTG ACTCCAGCCTGGG GAC
||||| ||||||||| |||
GGTGAC TGAGGTCGGACCC CTG
A A

GAM2524 FLJ11710 3' GTCTCCCAGGCTGGAGTGCAGT 46250
GG CCACTGCACTCCAGCCTGGGAGAC
|||||||||||||||
GGTGACGTGAGGTCGGACCCTCTG

GAM2524 FLJ11710 5' TTTGAGGCTGGATGCAGTGG 46256 C G
CCACTGCA TCCAGCCT GGA
||||| ||||||| |||
GGTGACGT AGGTCGGA TTT

GAM2524 FLJ11715 3' GTTGCCCAGGCTGGAGGGCAGT 44982 A AG
G CACTGC CTCCAGCCTGGG AC
||||| ||||||||| ||
GTGACG GAGGTCGGACCC TG
G GT

GAM2524 FLJ11800 3' GTCACCCAGGCCGGAGTGCAGT 47041 A A
GG CCACTGCACTCC GCCTGGG GAC
||||||||| ||||| |||
GGTGACGTGAGG CGGACCC CTG
C A

GAM2524 FLJ12363 3' GTCCCCCAGGCTGGAGTGCCGT 50640 T A
GG CCAC GCACTCCAGCCTGGG GAC
||| ||||||||||| |||
GGTG CGTGAGGTCGGACCC CTG
C C

GAM2524 FLJ12572 5' GTCACCCAGGCTGGAGTATAGT 43546 C A
GG CCACTG ACTCCAGCCTGGG GAC
||||| ||||||||||| |||
GGTGAT TGAGGTCGGACCC CTG
A A

GAM2524 FLJ12581 3' GTCGCCCAGGCTGGAGTGCAGT 46342 A
GG CCACTGCACTCCAGCCTGGG GAC
||||||||||||||| |||
GGTGACGTGAGGTCGGACCC CTG
G

GAM2524 FLJ12649 3' CCCAGGCTGCAGTGCAGTGG 45088 C
CCACTGCACT CAGCCTGGG
||||||| |||||||
GGTGACGTGA GTCGGACCC
C

GAM2524 FLJ12666 3' TTTGGGCTGGGCGCAGTGG 45075 A T TG
CCACTGC C CCAGCC GG
||||||| ||||| ||

			GGTGACG G GGTCGG TT		
			C _ GT		
GAM2524	FLJ12668	3'	GTTGCCCAGGCTGGAGTACAGT 47161	C	AG
	GG		CCACTG ACTCCAGCCTGGG AC		
			GGTGAC TGAGGTCGGACCC TG		
			A GT		
GAM2524	FLJ12747	3'	GTCACCCAGGCTGGAGTGCAAT 50671	C	A
	GG		CCA TGC ACTCCAGCCTGGG GAC		
			GGT ACGTGAGGTCGGACCC CTG		
			A A		
GAM2524	FLJ12787	3'	TCGCCCAGGCTGGAGTACAGTG 50696	C	A
			CACTG ACTCCAGCCTGGG GA		
			GTGAC TGAGGTCGGACCC CT		
			A G		
GAM2524	FLJ12876	3'	GTCACCCAGGCTGGAGTGCAGT 43099		A
	GG		CCACTGCACTCCAGCCTGGG GAC		
			GGTGACGTGAGGTCGGACCC CTG		
			A		
GAM2524	FLJ12888	3'	GTTGCCCAGGCTAGAGTGCAGT 46892	C	AG
	GG		CCACTGCACTC AGCCTGGG AC		
			GGTGACGTGAG TCGGACCC TG		
			A GT		
GAM2524	FLJ12903	3'	GTTGCCCAGGCTGGAGTGCAAT 43077	C	AG
	GG		CCA TGC ACTCCAGCCTGGG AC		
			GGT ACGTGAGGTCGGACCC TG		
			A GT		
GAM2524	FLJ12960	3'	GTCGCCCAGGCTGGAGTGCAGT 45305		A
	GG		CCACTGCACTCCAGCCTGGG GAC		
			GGTGACGTGAGGTCGGACCC CTG		
			G		
GAM2524	FLJ12973	3'	GTTGCCCAGGCTGGAGTGCA 46643		AG
			TGCACTCCAGCCTGGG AC		
			ACGTGAGGTCGGACCC TG		
			GT		
GAM2524	FLJ12975	3'	CCCAGGCTGGAGTGCAGTG 70190		
			CACTGCACTCCAGCCTGGG		
			GTGACGTGAGGTCGGACCC		
GAM2524	FLJ13072	5'	GTCGGCCAGGCTGGAGTGCAGT 91396		GA
	GG		CCACTGCACTCCAGCCTGG GAC		

GGTGACGTGAGGTCGGACC CTG
GG

GAM2524 FLJ13114 3' GTCGCCCAGGCTGGAATGCAGT 44908 C A
GG CCACTGCA TCCAGCCTGGG GAC
||||| ||||||| ||
GGTGACGT AGGTCGGACCC CTG
A G

GAM2524 FLJ13188 3' GTCACCCAGGCTAGAGTGCAGT 42194 C A
ACTGCACTC AGCCTGGG GAC
||||| ||||||| ||
TGACGTGAG TCGGACCC CTG
A A

GAM2524 FLJ13193 3' CCCAGGCTGGAGTACAGTGG 50718 C
CCACTG ACTCCAGCCTGGG
||||| |||||||
GGTGAC TGAGGTCGGACCC
A

GAM2524 FLJ13197 3' GTTGCCCAGGCTGGAGTGCAGT 45183 AG
GG CCACTGCACTCCAGCCTGGG AC
||||| ||
GGTGACGTGAGGTCGGACCC TG
GT

GAM2524 FLJ13352 3' CAGGCTGGGTGCAATGG 45049 C T
CCA TGCAC CCAGCCTG
||| ||| |||||||
GGT ACGTG GGTCGGAC
A _

GAM2524 FLJ13441 3' TCTCCCAGGCAGGCCATGG 43919 CT A CCA
CCA GC CT GCCTGGGAGA
||| ||| |||||||
GGT CG GA CGGACCCTCT
AC _ _

GAM2524 FLJ13448 3' TTTGGGCTGGGCACAGTGG 47888 CA T TG
CCACTG C CCAGCC GG
||||| | ||||| ||
GGTGAC G GGTCGG TT
AC _ GT

GAM2524 FLJ13456 3' GTCGCCCCAAGCTGGAGTGCAGT 66560 C A
GG CCACTGCACTCCAGC TGGG GAC
||||| ||| |||
GGTGACGTGAGGTCG ACCC CTG
A G

GAM2524 FLJ13590 5' TCAGGCTTGAGTGCAGTGG 46209 C
CCACTGCACTC AGCCTGG
||||| |||||||
GGTGACGTGAG TCGGACT
T

GAM2524 FLJ13909 5' GTCCCCCAGGCTGGTGGC 47782 ACT A
GC CCAGCCTGGG GAC
|| ||||||| |||

				CG	GGTCGGACCC CTG			
				GT_	C			
GAM2524	FLJ13952	3'	GTTGCCCAAGGCTGGAATGCAGT	46019		C		AG
	GG		CCACTGCA TCCAGCCTGGG AC					
			GGTGACGT AGGTCGGACCC TG					
			A GT					
GAM2524	FLJ13984	5'	CCTAGGCTGGAGTGCAGTGG	45804				
			CCACTGCACTCCAGCCTGGG					
			GGTGACGTGAGGTCTGGATCC					
GAM2524	FLJ14326	3'	CTCAGGCTGGGTGCAGTGG	50769		T		
			CCACTGCAC CCAGCCTGGG					
			GGTGACGTG GGTCTGGACTC					
			-					
GAM2524	FLJ14351	3'	GTCGCCCAGGCTGGAGTGCAGT	45650				A
	GG		CCACTGCACTCCAGCCTGGG GAC					
			GGTGACGTGAGGTCTGGACCC CTG					
			G					
GAM2524	FLJ14442	3'	GTTACCCAGGCTAGAGTGTAGT	52390		C		A
	GG		CCACTGCACTC AGCCTGGG GAC					
			GGTGATGTGAG TCGGACCC TTG					
			A A					
GAM2524	FLJ14803	3'	CAGACTGGAGTGCAGTGG	52691		C		
			CCACTGCACTCCAG CTG					
			GGTGACGTGAGGTC GAC					
			A					
GAM2524	FLJ14950	3'	CCCAGGCTGAACTGCAGTGG	52787		CTC		
			CCACTGCA CAGCCTGGG					
			GGTGACGT GTCGGACCC					
			CAA					
GAM2524	FLJ14957	3'	CCGAGGCTGGAGTGCAATGG	52814		C		G
			CCA TGCACTCCAGCCT GG					
			GGT ACGTGAGGTCTGGA CC					
			A G					
GAM2524	FLJ20034	3'	GTTGCCCAAGGCTGGAGTACAAT	34854		C C		AG
	GG		CCA TG ACTCCAGCCTGGG AC					
			GGT AC TGAGGTCTGGACCC TG					
			A A GT					
GAM2524	FLJ20045	3'	GTTTCCCAGGCTGGAGTGCAGT	34891				
	GG		CCACTGCACTCCAGCCTGGGAGAC					

GGTGACGTGAGGTCGGACCCTTTG

GAM2524 FLJ20079 3' GTTGCCCAGGCTGGAGTGCAAT 34975 C AG
GG CCA TGC ACTCCAGCCTGGG AC

||| ||||| ||
GGT ACGTGAGGTCGGACCC TG
A GT

GAM2524 FLJ20136 3' GTCGCCCAGGCTGGAATGCAGT 35100 C A
GG CCACTGCA TCCAGCCTGGG GAC

||||| ||||| |||
GGTGACGT AGGTCGGACCC CTG
A G

GAM2524 FLJ20147 3' GTTGCCCAGGCTAGAGTGCAG 35136 C AG
CTGCACTC AGCCTGGG AC

||||| ||||| ||
GACGTGAG TCGGACCC TG
A GT

GAM2524 FLJ20257 3' CTCCCAGGCTGGATGGCATGG 39486 C AC
CCA TGC TCCAGCCTGGGAG

||| ||| ||||| |||
GGT ACG AGGTCGGACCCTC
_ GT

GAM2524 FLJ20342 3' GTCCCCCAGGCTGGAGTGGTGC 35467 ____ A
AGTGG CCACTGCAC TCCAGCCTGGG GAC

||||| ||||| |||
GGTGACGTG AGGTCGGACCC CTG
GTG C

GAM2524 FLJ20344 3' GTCATCCAACTGGAGTGCAGT 35487 CC GA
GG CCACTGCACTCCAG TGG GAC

||||| ||| |||
GGTGACGTGAGGTC ACC CTG
AA TA

GAM2524 FLJ20452 3' CTAAAGGCCAGGTGCAGTGG 35646 CCA GGG
CCACTGCACT GCCT AG

||||| ||| ||
GGTGACGTGG CGGA TC
AC_ AA_

GAM2524 FLJ20511 3' GTCACCCAGGCTGGAGTGCAGT 35780 A
GG CCACTGCACTCCAGCCTGGG GAC

||||| ||||| |||
GGTGACGTGAGGTCGGACCC CTG
A

GAM2524 FLJ20555 3' CCCACAAGCCTGAGTGCAGTGG 35828 CA C_
CCACTGCACTC GC TGGG

||||| || |||
GGTGACGTGAG CG ACCC
TC AAC

GAM2524 FLJ20671 3' GTTGCCCAGGCTGGAGTGCAGT 35944 AG
GG CCACTGCACTCCAGCCTGGG AC

||||| ||||| ||

		GGTGACGTGAGGTCGGACCC	TG		
		GT			
GAM2524	FLJ20700	3'	CCCAGGCTGGAGTGCAGTGG	36004	
			CCACTGCACTCCAGCCTGGG		
			GGTGACGTGAGGTCGGACCC		
GAM2524	FLJ20813	3'	CCCAGGCTGGAGTGCAGTGG	36129	
			CCACTGCACTCCAGCCTGGG		
			GGTGACGTGAGGTCGGACCC		
GAM2524	FLJ21162	3'	TCTTGGGCTGGGTGCAGTGG	46377	T TG
			CCACTGCAC CCAGCC	GGA	
			GGTGACGTG GGTCGG	TCT	
			—	GT	
GAM2524	FLJ21302	3'	GTCTCCCAGGCTGGACTGCAG	43513	C
			CTGCA TCCAGCCTGGGAGAC		
			GACGT AGGTCGGACCCTCTG		
			C		
GAM2524	FLJ21324	5'	CCCAGGCTGGCGTGCAGTGG	92851	T
			CCACTGCAC CCAGCCTGGG		
			GGTGACGTG GGTCGGACCC		
			C		
GAM2524	FLJ21459	3'	GTCACCCAGGCTGGGGTGCAGT	44811	A
		GG	CCACTGCACTCCAGCCTGGG	GAC	
			GGTGACGTGGGGTCGGACCC	CTG	
			A		
GAM2524	FLJ21603	3'	GTCACCCAGGCTGGAGTACAGT	45776	C A
		GG	CCACTG ACTCCAGCCTGGG	GAC	
			GGTGAC TGAGGTCGGACCC	CTG	
			A	A	
GAM2524	FLJ21777	3'	GTCACCCAGGCTGGAGTGCAAT	50848	C A
		GG	CCA TGCCTCCAGCCTGGG	GAC	
			GGT ACGTGAGGTCGGACCC	CTG	
			A	A	
GAM2524	FLJ22167	5'	CTCAGGCTGCAGTGCAGTGG	44867	C
			CCACTGCACT CAGCCTGGG		
			GGTGACGTGA GTCGGACTC		
			C		
GAM2524	FLJ22316	5'	GTCTCCCAGGCTGGAGTGCAGT	47617	
		GG	CCACTGCACTCCAGCCTGGGAGAC		

GGTGACGTGAGGTCGGACCCTCTG

GAM2524 FLJ22329 3' GTCACCCAGGCTGGAGTGCAGT 45407 A
GG CCACTGCACTCCAGCCTGGG GAC
|||||
GGTGACGTGAGGTCGGACCC CTG
A
GAM2524 FLJ22531 5' GTTACCCAGGCCGGAGTGCAGT 45374 A A
GG CCACTGCACTCC GCCTGGG GAC
|||||
GGTGACGTGAGG CGGACCC TTG
C A
GAM2524 FLJ22644 3' CTCAGCCTGGAGTGCAGTG 47699 C
CACTGCACTCCAG CTGGG
|||||
GTGACGTGAGGTC GACTC
C
GAM2524 FLJ22794 3' CCTGGGCTGGAGTACAGTGG 93243 C TG
CCACTG ACTCCAGCC GG
|||||
GGTGAC TGAGGTCGG CC
A GT
GAM2524 FLJ22800 3' GTCTCAAAAAGGCTGGAGTAC 45993 C GG____
AGT ACTG ACTCCAGCCT GAGAC
|||||
TGAC TGAGGTCGGA CTCTG
A AAAAA
GAM2524 FLJ22814 3' GTCCCCCAGGCTCCTGCACGG 46730 AC CTCC A
CC TGCA AGCCTGGG GAC
|| |||
GG ACGT TCGGACCC CTG
C_ CC_ C
GAM2524 FLJ22965 3' CCCAGGATGGAGTGCAGTGG 42295 G
CCACTGCACTCCA CCTGGG
|||||
GGTGACGTGAGGT GGACCC
A
GAM2524 FLJ22969 3' CCTAGGCTGGAGTGCAGTGG 69199
CCACTGCACTCCAGCCTGGG
|||||
GGTGACGTGAGGTCGGATCC
GAM2524 FLJ23024 3' GTCTCCCAGGCTAGAGTGCAAT 46846 C C
GG CCA TGCATC AGCCTGGGAGAC
|||
GGT ACGTGAG TCGGACCCTCTG
A A
GAM2524 FLJ23040 3' TCACCCAAGCCAGAGTGCAGTG 47991 CA C A
G CCACTGCACTC GC TGGG GA
|||||

		GGTGACGTGAG CG ACCC CT		
		AC A A		
GAM2524	FLJ23040	3' TTTTGAGGCTGGGTGCAGTGG 47996	T	G
		CCACTGCAC CCAGCCT GGAG		
		GGTGACGTG GGTGCGGA TTTT		
		— G		
GAM2524	FLJ23053	3' CCCAGGCTGGAGTGCAGTGG 43554		
		CCACTGCACTCCAGCCTGGG		
		GGTGACGTGAGGTCGGACCC		
GAM2524	FLJ23186	3' CTTAGCTGGAGTGCAGTGG 61041	C	
		CCACTGCACTCCAGC TGGG		
		GGTGGCGTGAGGTCG ATTC		
GAM2524	FLJ23263	5' GTCGCCCAGGCTGGAGTGCAGT 47804		A
		GG CCACTGCACTCCAGCCTGGG GAC		
		GGTGACGTGAGGTCGGACCC CTG		
		G		
GAM2524	FLJ23356	3' CTGAGGCTGGAGTGCAGTG 50922	G	
		CACTGCACTCCAGCCT GG		
		GTGACGTGAGGTCGGA TC		
		G		
GAM2524	FLJ23392	3' CTGAGGCTGGAGTGCAGTGG 45891	G	
		CCACTGCACTCCAGCCT GG		
		GGTGACGTGAGGTCGGA TC		
		G		
GAM2524	FLJ23392	3' GTCACCCAGACTGGAGTGCAGT 45905	C	A
		GG CCACTGCACTCCAG CTGGG GAC		
		GGTGACGTGAGGTC GACCC CTG		
		A A		
GAM2524	FLJ23392	3' GTCCCCCAGGCTGGAGTGCAGT 45908		A
		GG CCACTGCACTCCAGCCTGGG GAC		
		GGTGACGTGAGGTCGGACCC CTG		
		C		
GAM2524	FLJ23416	3' GTTGCCCAGGCTGGAGTGCAGT 50936		AG
		GG CCACTGCACTCCAGCCTGGG AC		
		GGTGACGTGAGGTCGGACCC TG		
		GT		
GAM2524	FLJ23519	3' GTCACCCAGGCTGGAGTGCAGT 50957		A
		GG CCACTGCACTCCAGCCTGGG GAC		


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GGTGACGTGAGGTCGGACCC CTG
      A
GAM2524 FLJ23556 3' GTCGCCCAGGCTGGAGTGCAGT 46453      A
      GG      CCACTGCACTCCAGCCTGGG GAC
      |||||
GGTGACGTGAGGTCGGACCC CTG
      G
GAM2524 FLJ23563 3' GTTGCCCAGGCTAGAGTGCAAT 68218      C      C      AG
      GG      CCA TGCCTC AGCCTGGG AC
      ||| ||||| ||||| ||
GGT ACGTGAG TCGGACCC TG
      A      A      GT
GAM2524 FLJ25416 5' CCCAGGCTGAAGTGCCATGG 59452      CT      C
      CCA GCACT CAGCCTGGG
      ||| ||||| |||||
GGT CGTGA GTCGGACCC
      AC      A
GAM2524 FLJ25416 5' CCCAGGCTGGAGTGCCATGG 59453      CT
      CCA GCACTCCAGCCTGGG
      ||| ||||| |||||
GGT CGTGAGGTCGGACCC
      AC
GAM2524 FLJ30532 3' GTTGCCCAGGCTGGAGTACAGT 59226      C      AG
      GG      CCACTG ACTCCAGCCTGGG AC
      ||||| ||||| ||||| ||
GGTGAC TGAGGTCGGACCC TG
      A      GT
GAM2524 FLJ31101 3' GTCGCCCAGGCTGGAATGCAGT 36170      C      A
      GG      CCACTGCA TCCAGCCTGGG GAC
      ||||| ||||| ||||| |||
GGTGACGT AGGTCGGACCC CTG
      A      G
GAM2524 FLJ31153 3' GTCACCCAGACTGGAGTGCAGT 58752      C      A
      GG      CCACTGCACTCCAG CTGGG GAC
      ||||| ||||| ||||| |||
GGTGACGTGAGGTC GACCC CTG
      A      A
GAM2524 FLJ32499 3' CCCAGTCTGGAGTGCAAGTGG 58777      C
      CCACTGCACTCCAG CTGGG
      ||||| ||||| |||||
GGTGACGTGAGGTC GACCC
      T
GAM2524 FLJ32762 3' GTCTCCCAAACCTTCAGAGAGT 59486      GCA C__ CC_
      GG      CCACT CTC AG TGGGAGAC
      |||| ||| || |||||
GGTGA GAG TC ACCCTCTG
      __ ACT CAA
GAM2524 FLJ32783 3' TCTCCCAGTTGCATAGTACAGT 59308      C C__ C
      G      CACTG ACT CAGC TGGGAGA
      |||| ||| |||| |||||

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			GTGAC TGA GTTG ACCCTCT		
			A TAC _		
GAM2524	FLJ32865	3'	GTCACCCAGGCTGGAGTACAAT 58819	C C	A
	G		CA TG ACTCCAGCCTGGG GAC		
			GT AC TGAGGTCGGACCC CTG		
			A A A		
GAM2524	GAL3ST-4	3'	GTCCCCCAGGCTGGAGTGCAGT 45281		A
	GG		CCACTGCACTCCAGCCTGGG GAC		
			GGTGACGTGAGGTCGGACCC CTG		
			C		
GAM2524	GALNT6	3'	TTCAGGCTGGGCACAGTGG 24255	CA T	
			CCACTG C CCAGCCTGGG		
			GGTGAC G GGTCGGACTT		
			AC _		
GAM2524	GGA2	3'	CTCAGGCTGGAGTGCGGTGG 57663		
			CCACTGCACTCCAGCCTGGG		
			GGTGGCGTGAGGTCGGACTC		
GAM2524	GGA2	3'	CTCAGGCTGGAGTGCGGTGG 57664		
			CCACTGCACTCCAGCCTGGG		
			GGTGGCGTGAGGTCGGACTC		
GAM2524	GMPPB	5'	CCCAGGCTGGAGTGCGATGG 97442	C	
			CCA TGCACTCCAGCCTGGG		
			GGT GCGTGAGGTCGGACCC		
			A		
GAM2524	GNG4	3'	GTCACCCAGGCTGGAGTGCAAT 16853	C	A
	GG		CCA TGCACTCCAGCCTGGG GAC		
			GGT ACGTGAGGTCGGACCC CTG		
			A A		
GAM2524	GOLGA3	3'	GTTGCCCAGGCTGGAGTGCAGT 20895		AG
	GG		CCACTGCACTCCAGCCTGGG AC		
			GGTGACGTGAGGTCGGACCC TG		
			GT		
GAM2524	GP5	3'	GTGGCCCAGGCTGGCGTGCAGT 16882	T	AG
	GG		CCACTGCAC CCAGCCTGGG AC		
			GGTGACGTG GGTCGGACCC TG		
			C GG		
GAM2524	GR6	5'	GTCACCCAGGCTGGAATGCAGT 24748	C	A
	GG		CCACTGCA TCCAGCCTGGG GAC		

			GGTGACGT AGGTCGGACCC CTG		
			A A		
GAM2524	GREB1	3'	GTCACCCAGGCTGGAGTGCAGT 72840	A	
	GG		CCACTGCACTCCAGCCTGGG GAC		
			GGTGACGTGAGGTCGGACCC CTG		
			A		
GAM2524	GREB1	3'	CTGCCCAGGCTGGAGTGCAATG 28567	C	—
	G		CCA TGCACCTCCAGCCTGGG AG		
			GGT ACGTGAGGTCGGACCC TC		
			A G		
GAM2524	GRWD	3'	GTCGCCCAGGCTGGAGTGCAGT 49787	A	
			ACTGCACTCCAGCCTGGG GAC		
			TGACGTGAGGTCGGACCC CTG		
			G		
GAM2524	GTF2E1	3'	CCCAGGCTGGAGTGCAATGG 19795	C	
			CCA TGCACCTCCAGCCTGGG		
			GGT ACGTGAGGTCGGACCC		
			A		
GAM2524	GTPBG3	3'	CCCAGGCTGGAGTGCAGTGG 51893		
			CCACTGCACTCCAGCCTGGG		
			GGTGACGTGAGGTCGGACCC		
GAM2524	GTPBG3	3'	CCCAGGCTGGAGTTCAGTGG 51894	C	
			CCACTG ACTCCAGCCTGGG		
			GGTGAC TGAGGTCGGACCC		
			T		
GAM2524	H-plk	5'	CCAGGATGGAGTGCAGTGG 32377	G	
			CCACTGCACTCCA CCTGG		
			GGTGACGTGAGGT GGACC		
			A		
GAM2524	H105E3	5'	TCCGGGCCTGGAGTTCAGTGG 32491	C	—
			CCACTG ACTCCAG CCTGGG		
			GGTGAC TGAGGTC GGGCCT		
			T C		
GAM2524	H2AV	3'	CCCAGACTGGAGTGCATGG 25758	C	C
			CCA TGCACCTCCAG CTGGG		
			GGT GCGTGAGGTC GACCC		
			A A		
GAM2524	HCA4	3'	GTCGCCCAGGCTGGAGTGCATT 57744	C	A
	GG		CCA TGCACCTCCAGCCTGGG GAC		

			GGT ACGTGAGGTCGGACCC CTG		
			T G		
GAM2524	HRH4	3'	CCCACGCAGGAGTGCAGTGG 41532	A	C
			CCACTGCACTCC GC TGGG		
			GGTGACGTGAGG CG ACCC		
			A C		
GAM2524	HRH4	3'	GTCACCCAGGCTGGAGTGCAGT 41546	A	
			ACTGCACTCCAGCCTGGG GAC		
			TGACGTGAGGTCGGACCC CTG		
			A		
GAM2524	HRH4	3'	GTCTCCCAGGCTGGAGCGTAGT 41547	A	
			ACTGC CTCCAGCCTGGGAGAC		
			TGATG GAGGTCGGACCCTCTG		
			C		
GAM2524	HRK	5'	CCCGGCGGCTGGAGCGCGGCGG 15071	A	A
			CC CTGC CTCCAGCC TGGG		
			GG GGCG GAGGTCGG GCCC		
			C C CG		
GAM2524	HSA6591	5'	GTCTCCCGCGCGAAAGTGAG 73249	G	CCA T
			CT CACT GCC GGGAGAC		
			GA GTGA CGG CCCTCTG		
			_ AAG _		
GAM2524	HSC3	3'	CTTAGCTGGGTGCAGTGG 59732	T	C
			CCACTGCAC CCAGC TGGG		
			GGTGACGTG GGTCG ATTC		
			- -		
GAM2524	HSMPP8	3'	GTTGCCCAGGCTGGAGTGCAAT 95140	C	AG
	GG		CCA TGCCTCCAGCCTGGG AC		
			GGT ACGTGAGGTCGGACCC TG		
			A GT		
GAM2524	HSNOV1	3'	CAGAGTCTAGAGTGCAGTGG 34431	C	_ _
			CCACTGCACTC AG C CTG		
			GGTGACGTGAG TC G GAC		
			A T A		
GAM2524	HSPC065	3'	GTCCCCAAGGCTGGAGTGCAGT 27160	_	A
	GG		CCACTGCACTCCAGCCT GGG GAC		
			GGTGACGTGAGGTCGGA CCC CTG		
			A _		
GAM2524	HSPC065	3'	GTCCCCCATGCTGGAGTGCAGT 27161	C	A
	GG		CCACTGCACTCCAGC TGGG GAC		

			GGTGACGTGAGGTCG ACCC CTG		
			T C		
GAM2524	ICK	3'	GTCACCCAGGCTGGAGTGCAGT 33691		A
	GG		CCACTGCACTCCAGCCTGGG GAC		
			GGTGACGTGAGGTCGGACCC CTG		
			A		
GAM2524	IMPACT	3'	CCTAGGCTGGAGTGCAGTGG 38004		
			CCACTGCACTCCAGCCTGGG		
			GGTGACGTGAGGTCGGATCC		
GAM2524	INPP5E	3'	CCCAGCGCTGGAGTGCAG 73504		—
			CTGCACTCCAGC CTGGG		
			GACGTGAGGTCG GACCC		
			C		
GAM2524	JAM1	3'	GTCACCCAGGCTGGAGTGCAGT 34243		A
	GG		CCACTGCACTCCAGCCTGGG GAC		
			GGTGACGTGAGGTCGGACCC CTG		
			A		
GAM2524	JAM1	3'	GTCACCCAGGCTGGAGTGCAGT 34244		A
	GG		CCACTGCACTCCAGCCTGGG GAC		
			GGTGACGTGAGGTCGGACCC CTG		
			A		
GAM2524	JM11	3'	GTCACCAGGCTGGAGTGCAGCG 54371	A	GA
	G		CC CTGCACTCCAGCCTGG GAC		
			GG GACGTGAGGTCGGACC CTG		
			C A_		
GAM2524	KIAA0022	3'	CCCAGGCTACAGTGCAGTGG 30278		CC
			CCACTGCACT AGCCTGGG		
			GGTGACGTGA TCGGACCC		
			CA		
GAM2524	KIAA0063	3'	GTTGCCCAGGCTGGAGTGCAAT 30261	C	AG
	GG		CCA TGCCTCCAGCCTGGG AC		
			GGT ACGTGAGGTCGGACCC TG		
			A GT		
GAM2524	KIAA0087	3'	GTCACCCAGGCTGGAGTGCAGT 29347		A
	GG		CCACTGCACTCCAGCCTGGG GAC		
			GGTGACGTGAGGTCGGACCC CTG		
			A		
GAM2524	KIAA0090	3'	GTCACCCAGGCTGGAGAGCAGT 89818	A	A
	GG		CCACTGC CTCCAGCCTGGG GAC		

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GGTGACG GAGGTCGGACCC CTG
      A      A
GAM2524 KIAA0161 3' GTCCCCCAAGCTGGAGTACAAT 29206 C C C A
      G      CA TG ACTCCAGC TGGG GAC
              || || || || || || || || || ||
              GT AC TGAGGTCG ACCC CTG
              A A A C
GAM2524 KIAA0186 3' GTCACCCAGGCTGGGGTGCAGT 41113 A
      GG      CCACTGCACTCCAGCCTGGG GAC
              || || || || || || || || || ||
              GGTGACGTGGGGTCGGACCC CTG
              A
GAM2524 KIAA0205 3' CCCAGGCTGTAGTGCAGTGG 30206 C
              CCACTGCACT CAGCCTGGG
              || || || || || || || || || ||
              GGTGACGTGA GTCGGACCC
              T
GAM2524 KIAA0210 5' GTCGCCCAGGCTGGAGTGCAGT 29172 A
      GG      CCACTGCACTCCAGCCTGGG GAC
              || || || || || || || || || ||
              GGTGACGTGAGGTCGGACCC CTG
              G
GAM2524 KIAA0210 5' TCCAGGCTGGAGTATAATGG 29177 C C
              CCA TG ACTCCAGCCTGGG
              || || || || || || || || || ||
              GGT AT TGAGGTCGGACCT
              A A
GAM2524 KIAA0391 3' TCTAGGCTGGAGTGCAATGG 28622 C
              CCA TGCACTCCAGCCTGGG
              || || || || || || || || || ||
              GGT ACGTGAGGTCGGATCT
              A
GAM2524 KIAA0410 3' GTCTCCCAGGCCTTCCCAGTCA 29428 C CACTCCA
              C ACTG GCCTGGGAGAC
              | || || || || || || || || ||
              A TGAC CGGACCCTCTG
              C CCTTC__
GAM2524 KIAA0418 5' CTCAGGCTGGATTGCAGTGG 28294 C
              CCACTGCA TCCAGCCTGGG
              || || || || || || || || || ||
              GGTGACGT AGGTCGGACTC
              T
GAM2524 KIAA0426 3' GTCGCCCAGGCTGGAGTGCAAT 28932 C A
      GG      CCA TGCACTCCAGCCTGGG GAC
              || || || || || || || || || ||
              GGT ACGTGAGGTCGGACCC CTG
              A G
GAM2524 KIAA0435 3' TCAAGCACCAGAGTTGCAGTGG 29664 _ CA_ C
              CCACTGCA CTC GC TGG
              || || || || || || || || || ||

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			GGTGACGT GAG CG ACT		
			T ACCA A		
GAM2524	KIAA0441	3'	TCACCCAGGCCAGAGTGTAGTG 29644	CA	A
		G	CCACTGCACTC GCCTGGG GA		
			GGTGATGTGAG CGGACCC CT		
			AC A		
GAM2524	KIAA0446	5'	GTCCCCCAGGCTGAGGCTGGGG 69455	ACT A C	A
			CC GC CTC AGCCTGGG GAC		
			GG CG GAG TCGGACCC CTG		
			GGT _ _ C		
GAM2524	KIAA0446	5'	GTCTCCTAGGCTGGAGTGCAGT 69457		
		GG	CCACTGCACTCCAGCCTGGGAGAC		
			GGTGACGTGAGGTCGGATCCTCTG		
GAM2524	KIAA0447	3'	GTCACCCAGGCTGGAGTACAGT 72128	C	A
		GG	CCACTG ACTCCAGCCTGGG GAC		
			GGTGAC TGAGGTCGGACCC CTG		
			A A		
GAM2524	KIAA0469	3'	GTCACCCAGGCTGGAGTGCAGT 29993		A
		GG	CCACTGCACTCCAGCCTGGG GAC		
			GGTGACGTGAGGTCGGACCC CTG		
			A		
GAM2524	KIAA0469	3'	GTCACCCAGGCTGGAGTGCAGT 29994		A
		GG	CCACTGCACTCCAGCCTGGG GAC		
			GGTGACGTGAGGTCGGACCC CTG		
			A		
GAM2524	KIAA0475	3'	GTTGCCCAGGCTGGAGTGCAGT 30128		AG
		GG	CCACTGCACTCCAGCCTGGG AC		
			GGTGACGTGAGGTCGGACCC TG		
			GT		
GAM2524	KIAA0493	5'	CCCAAGCTGGAGTGCAGTG 64931		C
			CACTGCACTCCAGC TGGG		
			GTGACGTGAGGTCG ACCC		
			A		
GAM2524	KIAA0495	3'	GTCACCCAGGCTGGAGTGCAAT 63273	C	A
		GG	CCA TGCCTCCAGCCTGGG GAC		
			GGT ACGTGAGGTCGGACCC CTG		
			A A		
GAM2524	KIAA0513	3'	CCCAAGTGCGGTGCAGTG 29024	T G C	
			CACTGCAC CCA C TGGG		

			GTGACGTG GGT G ACCC		
			C _ A		
GAM2524	KIAA0513	3'	GTTGCCCAGGCTGGAGTGCAGT 29048		AG
	G		CACTGCACTCCAGCCTGGG AC		
			GTGACGTGAGGTCGGACCC TG		
			GT		
GAM2524	KIAA0513	5'	TTTCCCAGGCTGGAGTGCAGAG 29060 A		
	G		CC CTGCACTCCAGCCTGGGAGA		
			GG GACGTGAGGTCGGACCCTTT		
			A		
GAM2524	KIAA0527	3'	CCCAGGCTGGAGTGCAGTG 97493		
			CACTGCACTCCAGCCTGGG		
			GTGACGTGAGGTCGGACCC		
GAM2524	KIAA0532	3'	GTCACCCAGGCTAGAGTACAGT 71325	C C A	
	GG		CCACTG ACTC AGCCTGGG GAC		
			GGTGAC TGAG TCGGACCC CTG		
			A A A		
GAM2524	KIAA0544	3'	CTGCCCAGGCTGGAGTGCAGTG 71464		—
	G		CCACTGCACTCCAGCCTGGG AG		
			GGTGACGTGAGGTCGGACCC TC		
			G		
GAM2524	KIAA0555	3'	CCCATGCTGGAGTGCATTGG 60738	C C	
			CCA TGCACTCCAGC TGGG		
			GGT ACGTGAGGTCG ACCC		
			T T		
GAM2524	KIAA0561	3'	CCCGGGCTGGAGTGCAGCGG 66469 A		
			CC CTGCACTCCAGCCTGGG		
			GG GACGTGAGGTCGGGCCC		
			C		
GAM2524	KIAA0562	3'	CCTAGGCTGGAGTGCAGTGG 28819		
			CCACTGCACTCCAGCCTGGG		
			GGTGACGTGAGGTCGGATCC		
GAM2524	KIAA0563	5'	CCCAGGCTGAAGTGCAGTG 29875	C	
			CACTGCACT CAGCCTGGG		
			GTGACGTGA GTCGGACCC		
			A		
GAM2524	KIAA0594	3'	GTTGCCCAGGCTGGAGTGCAGT 65517		AG
	GG		CCACTGCACTCCAGCCTGGG AC		

			GGTGACGTGAGGTCGGACCC TG		
			GT		
GAM2524	KIAA0599	3'	GTCACCCAGGCTGGAGTGCAAT 77698	C	A
		GG	CCA TGCCTCCAGCCTGGG GAC		
			GGT ACGTGAGGTCGGACCC CTG		
			A A		
GAM2524	KIAA0599	3'	GTCGCCCAGGCTGGAGCGCAGT 77700	A	A
		GG	CCACTGC CTCCAGCCTGGG GAC		
			GGTGACG GAGGTCGGACCC CTG		
			C G		
GAM2524	KIAA0682	3'	CCGAGAGGGCTGGAGTGCAAGT 30018		_____
		G	CCACTGCACTCCAGCCT GG		
			GGTGACGTGAGGTCGGG CC		
			AGAG		
GAM2524	KIAA0737	3'	GTCACCCAGGCTGGAGTGCAAGT 29817		A
		GG	CCACTGCACTCCAGCCTGGG GAC		
			GGTGACGTGAGGTCGGACCC CTG		
			A		
GAM2524	KIAA0841	3'	GTTGCCCAAGTTGGAGTGCAAGT 71903	C	AG
		GG	CCACTGCACTCCAGC TGGG AC		
			GGTGACGTGAGGTTG ACCC TG		
			A GT		
GAM2524	KIAA0841	3'	GTTTCCCAGGCTGAAGTGCAAGT 71905	C	
		GG	CCACTGCACT CAGCCTGGGAGAC		
			GGTGACGTGA GTCGGACCCTTTG		
			A		
GAM2524	KIAA0861	3'	GTCGCCCAGGCTGGAGTGCAAGT 90359		A
		GG	CCACTGCACTCCAGCCTGGG GAC		
			GGTGACGTGAGGTCGGACCC CTG		
			G		
GAM2524	KIAA0889	3'	GTCCCCCAGGCTTGAGTGCAAT 31783	C	C A
		G	CA TGCCTC AGCCTGGG GAC		
			GT ACGTGAG TCGGACCC CTG		
			A T C		
GAM2524	KIAA0924	3'	CCCAGGCTAGAGTGCAAGTGG 30358	C	
			CCACTGCACTC AGCCTGGG		
			GGTGACGTGAG TCGGACCC		
			A		
GAM2524	KIAA0924	3'	CCTGGGCTGGAGTGCAAGTGG 30361		TG
			CCACTGCACTCCAGCC GG		

			GGTGACGTGAGGTCGG	CC		
			GT			
GAM2524	KIAA0924	3'	GTTGCCCAGGCTAGAGTGCAGT	30373	C	AG
		GG	CCACTGCACTC AGCCTGGG	AC		
			GGTGACGTGAG TCGGACCC	TG		
			A	GT		
GAM2524	KIAA0930	3'	TTGGGGCTGGGCGCAGTGG	71078	A T	G
			CCACTGC C CCAGCCT	GG		
			GGTGACG G GGTCGGG	TT		
			C _	G		
GAM2524	KIAA0931	3'	CTCAGGCTGGAGTGCAATGG	68009	C	
			CCA TGCCTCCAGCCTGGG			
			GGT ACGTGAGGTCGGA	CTC		
			A			
GAM2524	KIAA0961	3'	CCCAGGCTGGCGTGCAGTGG	30397	T	
			CCACTGCAC CCAGCCTGGG			
			GGTGACGTG GGTCGGACCC			
			C			
GAM2524	KIAA1001	3'	TTTAGGCTGGGCGCAGTGG	31018	A T	
			CCACTGC C CCAGCCTGGG			
			GGTGACG G GGTCGGATT	T		
			C _			
GAM2524	KIAA1017	3'	TGGGACTGGGTGCAGTGG	24272	T _	
			CCACTGCAC CCAG CCTG			
			GGTGACGTG GGTC GGGT			
			_ A			
GAM2524	KIAA1026	3'	CCCAGGATGGAGTGCAGTG	71734	G	
			CACTGCACTCCA CCTGGG			
			GTGACGTGAGGT GGACCC			
			A			
GAM2524	KIAA1028	3'	GTCACCCAAGCTGGAGTGCAGT	93591	C A	
		GG	CCACTGCACTCCAGC TGGG	GAC		
			GGTGACGTGAGGTCG ACCC	CTG		
			A A			
GAM2524	KIAA1029	5'	CTCCCAGGCCATGCACCGG	24427	AC	CTCCA
			CC TGCA GCCTGGGAG			
			GG ACGT CGGACCCTC			
			CC AC__			
GAM2524	KIAA1040	3'	GTCACCCAGGCTGGAATGCAGT	72691	C	A
		GG	CCACTGCA TCCAGCCTGGG	GAC		

			GGTGACGT AGGTCGGACCC CTG		
			A A		
GAM2524	KIAA1041	3'	GTTGCCCAGGCTGGAGTGCAGT 30829		AG
		GG	CCACTGCACTCCAGCCTGGG AC		
			GGTGACGTGAGGTCGGACCC TG		
			GT		
GAM2524	KIAA1045	3'	CCCTGAGGCTGGGCACAGTGG 71602	CA T	—
			CCACTG C CCAGCCT GGG		
			GGTGAC G GGTCGGA CCC		
			AC_ GT		
GAM2524	KIAA1052	5'	CTCAGGCTGCAGTGCAGTGG 30941		C
			CCACTGCACT CAGCCTGGG		
			GGTGACGTGA GTCGGA CTC		
			C		
GAM2524	KIAA1054	3'	GTTGCCCAGGCTGGAGTGCAGT 68969		AG
		GG	CCACTGCACTCCAGCCTGGG AC		
			GGTGACGTGAGGTCGGACCC TG		
			GT		
GAM2524	KIAA1110	3'	CTCCTGGGAGAGGCAGTG 62500	A CAG TG	
			CACTGC CTC CC GGAG		
			GTGACG GAG GG CCTC		
			_ A_ GT		
GAM2524	KIAA1128	3'	CCCAGGCTGGATTACAGTGG 68999		CAC
			CCACTG TCCAGCCTGGG		
			GGTGAC AGGTCGGACCC		
			ATT		
GAM2524	KIAA1143	3'	GTCACCCAGGCTGGAGTGCAGT 69248		A
		GG	CCACTGCACTCCAGCCTGGG GAC		
			GGTGACGTGAGGTCGGACCC CTG		
			A		
GAM2524	KIAA1155	3'	GTCACCCAGGCTGGAGTGCAGT 62916		A
		GG	CCACTGCACTCCAGCCTGGG GAC		
			GGTGACGTGAGGTCGGACCC CTG		
			A		
GAM2524	KIAA1161	5'	GTCACCCAGGTTGGAGTGCAGT 82650		A
		GG	CCACTGCACTCCAGCCTGGG GAC		
			GGTGACGTGAGGTTGGACCC CTG		
			A		
GAM2524	KIAA1169	5'	CCTGGGCTGGAGTCCAGTGG 35881	C TG	
			CCACTG ACTCCAGCC GG		

		GGTGAC TGAGGTCGG CC		
		C GT		
GAM2524	KIAA1170	3' GTTGCCCAAGCTGGAGTGCAT 70422	C	C AG
	GG	CCA TGCCTCCAGC TGGG AC		
		GGT ACGTGAGGTCG ACCC TG		
		A A GT		
GAM2524	KIAA1185	3' GTCGCCAGGCTGGAGTGCAGTG 63294		GA
	G	CCACTGCACTCCAGCCTGG GAC		
		GGTGACGTGAGGTCGGACC CTG		
		G_		
GAM2524	KIAA1193	3' GTCGCCAGGCTGGAGTGCAGTG 68277		GA
	G	CCACTGCACTCCAGCCTGG GAC		
		GGTGACGTGAGGTCGGACC CTG		
		G_		
GAM2524	KIAA1198	3' CCAAGCTGGACTGCAGTGG 64011	C	C
		CCACTGCA TCCAGC TGG		
		GGTGACGT AGGTCG ACC		
		C A		
GAM2524	KIAA1198	3' CCAGGCTGGAGTGCAGTGG 64016		
		CCACTGCACTCCAGCCTGG		
		GGTGACGTGAGGTCGGACC		
GAM2524	KIAA1198	3' CCCAGGCTGGAGTGCAGTGG 64020		
		CCACTGCACTCCAGCCTGGG		
		GGTGACGTGAGGTCGGACCC		
GAM2524	KIAA1198	3' CCCAGGCTGGAGTGCAGTGG 64021		
		CCACTGCACTCCAGCCTGGG		
		GGTGACGTGAGGTCGGACCC		
GAM2524	KIAA1198	3' GTTGCCCAGGCTGGAGTGCAGT 64057		AG
	GG	CCACTGCACTCCAGCCTGGG AC		
		GGTGACGTGAGGTCGGACCC TG		
		GT		
GAM2524	KIAA1210	3' GTTACCCAGATTGGAGTGCAGT 98081	GC	A
	GG	CCACTGCACTCCA CTGGG GAC		
		GGTGACGTGAGGT GACCC TTG		
		TA A		
GAM2524	KIAA1254	3' GTCAGCCAGGCTGGAGTGCAGT 70564		GA
	G	CACTGCACTCCAGCCTGG GAC		

			GTGACGTGAGGTCGGACC CTG		
			GA		
GAM2524	KIAA1257	3'	GTCGCCCAGGCTGGAGTGCAGT 63411	A	
	GG		CCACTGCACTCCAGCCTGGG GAC		
			GGTGACGTGAGGTCGGACCC CTG		
			G		
GAM2524	KIAA1257	3'	GTTGCCCAGGCTGGAGTACAAT 63414 C C	AG	
	GG		CCA TG ACTCCAGCCTGGG AC		
			GGT AC TGAGGTCGGACCC TG		
			A A GT		
GAM2524	KIAA1280	5'	CCAAGCTGGAGTACACGG 70276 AC C C		
			CC TG ACTCCAGC TGG		
			GG AC TGAGGTCG ACC		
			C_ A A		
GAM2524	KIAA1280	5'	GTTGCCCAGGCTGGAGTGCAGT 70287	AG	
	G		CACTGCACTCCAGCCTGGG AC		
			GTGACGTGAGGTCGGACCC TG		
			GT		
GAM2524	KIAA1287	3'	GTTGCCCAGGCTGGAGTGCAGT 78941	AG	
	GG		CCACTGCACTCCAGCCTGGG AC		
			GGTGACGTGAGGTCGGACCC TG		
			GT		
GAM2524	KIAA1320	5'	CCCAGGCTGGAGTATAGTG 69836 C		
			CACTG ACTCCAGCCTGGG		
			GTGAT TGAGGTCGGACCC		
			A		
GAM2524	KIAA1320	5'	GTCACCCAGGCTGGAGTGCAGT 69847	A	
	GG		CCACTGCACTCCAGCCTGGG GAC		
			GGTGACGTGAGGTCGGACCC CTG		
			A		
GAM2524	KIAA1373	3'	GTCGCCCAGGCTGGAGTGCAGT 71511	A	
	GG		CCACTGCACTCCAGCCTGGG GAC		
			GGTGACGTGAGGTCGGACCC CTG		
			G		
GAM2524	KIAA1404	3'	TTTTTAGGCTGGGCGCAGTGG 62697 A T		
			CCACTGC C CCAGCCTGGGAG		
			GGTGACG G GGTCGGATTTTT		
			C_		
GAM2524	KIAA1443	3'	CCCAGGCTGTAGTGCAATGG 64568 C C		
			CCA TGCACT CAGCCTGGG		

		GGT ACGTGA GTCGGACCC	
		A T	
GAM2524	KIAA1456	3' GTCGCCCAGGCTGGAGTGCAGT 67567	C A
	GG	CCA TGCCTCCAGCCTGGG GAC	
		GGT ACGTGAGGTCGGACCC CTG	
		C G	
GAM2524	KIAA1465	3' GTCGCCCAGGCTGGAGTGCAGTG 61508	GA
	G	CCACTGCACTCCAGCCTGG GAC	
		GGTGACGTGAGGTCGGACC CTG	
		G_	
GAM2524	KIAA1467	3' GTCGCCCAGGCTGGAGTGCAGT 72076	A
	GG	CCACTGCACTCCAGCCTGGG GAC	
		GGTGACGTGAGGTCGGACCC CTG	
		G	
GAM2524	KIAA1473	3' CCCAGGCTGGAGTACAGTGG 71208	C
		CCACTG ACTCCAGCCTGGG	
		GGTGAC TGAGGTCGGACCC	
		A	
GAM2524	KIAA1497	5' GTTGCCCAGGCTGGAGTGCAGT 68130	AG
	GG	CCACTGCACTCCAGCCTGGG AC	
		GGTGACGTGAGGTCGGACCC TG	
		GT	
GAM2524	KIAA1508	3' GTCACCCAGGCTGGAGTGCA 62560	A
		TGCACTCCAGCCTGGG GAC	
		ACGTGAGGTCGGACCC CTG	
		A	
GAM2524	KIAA1530	3' CCCAGGCTGAGTGCAGTGG 68553	C
		CCACTGCACTC AGCCTGGG	
		GGTGACGTGAG TCGGACCC	
		-	
GAM2524	KIAA1530	3' GTCGCCCAGGCTGGAGTGCAATG 68569	C GA
	G	CCA TGCCTCCAGCCTGG GAC	
		GGT ACGTGAGGTCGGACC CTG	
		A G_	
GAM2524	KIAA1559	3' GTCCCCCAGGCTGGAGTGCAGT 73460	A
	GG	CCACTGCACTCCAGCCTGGG GAC	
		GGTGACGTGAGGTCGGACCC CTG	
		C	
GAM2524	KIAA1571	3' GTCTTGCCCAGGCTGGAGTGCA 61622	—
	GTGG	CCACTGCACTCCAGCCTGGG AGAC	

		GGTGACGTGAGGTCGGACCC TCTG		
		GT		
GAM2524	KIAA1615	3' CCTAGGCTGGAGTGCAGTGG 69273		
		CCACTGCACTCCAGCCTGGG		
		GGTGACGTGAGGTCGGATCC		
GAM2524	KIAA1615	3' GTCACCAGGCCGGAGTGCAGTG 69282	A	GA
	G	CCACTGCACTCC GCCTGG GAC		
		GGTGACGTGAGG CGGACC CTG		
		C A_		
GAM2524	KIAA1649	3' CCAAGGCTGGAGTGCAGTGG 51223	G	
		CCACTGCACTCCAGCCT GG		
		GGTGACGTGAGGTCGGA CC		
		A		
GAM2524	KIAA1655	3' GTTGCCCAGGCTGGAGTGCAGT 67201	AG	
	GG	CCACTGCACTCCAGCCTGGG AC		
		GGTGACGTGAGGTCGGACCC TG		
		GT		
GAM2524	KIAA1668	3' GTCGCCCAGGCTGGAGTGCAGT 67079	A	
	GG	CCACTGCACTCCAGCCTGGG GAC		
		GGTGACGTGAGGTCGGACCC CTG		
		G		
GAM2524	KIAA1671	3' CCAGGCTGGAATGCAGTGG 66272	C	
		CCACTGCA TCCAGCCTGG		
		GGTGACGT AGGTCGGACC		
		A		
GAM2524	KIAA1671	3' CTCAAGCTGGAGTGGAGTGG 66275	G	C
		CCACT CACTCCAGC TGGG		
		GGTGA GTGAGGTCG ACTC		
		G A		
GAM2524	KIAA1712	3' CCCAGGCTGGAGTGCAGTGG 68152	C	
		CCA TGCACTCCAGCCTGGG		
		GGT ACGTGAGGTCGGACCC		
		C		
GAM2524	KIAA1712	3' GTTGCCCAGGCTGGAGTGCA 68164	AG	
		TGCACTCCAGCCTGGG AC		
		ACGTGAGGTCGGACCC TG		
		GT		
GAM2524	KIAA1727	3' GTCTCCCAGACTGGACTGCAGT 64763	C	C
	GG	CCACTGCA TCCAG CTGGGAGAC		

		GGTGACGT AGGTC GACCCTCTG		
		C A		
GAM2524 KIAA1751	3'	CCTAGGCTGGAGTGCAGTGG 72153		
		CCACTGCACTCCAGCCTGGG		
		GGTGACGTGAGGTCGGATCC		
GAM2524 KIAA1755	3'	TCCAGGCTGGAGTGCAGTGG 62023		
		CCACTGCACTCCAGCCTGGG		
		GGTGACGTGAGGTCGGACCT		
GAM2524 KIAA1784	3'	CCTAGGCTGGAGTGCAGTGG 65746		
		CCACTGCACTCCAGCCTGGG		
		GGTGACGTGAGGTCGGATCC		
GAM2524 KIAA1821	3'	GTTGCCCAGGCTGGAGTGTAGT 72274	AG	
	GG	CCACTGCACTCCAGCCTGGG AC		
		GGTGATGTGAGGTCGGACCC TG		
		GT		
GAM2524 KIAA1829	3'	GTTGCCCAGGCTGGAGTGCAGT 62654	AG	
	GG	CCACTGCACTCCAGCCTGGG AC		
		GGTGACGTGAGGTCGGACCC TG		
		GT		
GAM2524 KIAA1829	3'	TCCAGGCTGGAATGCGGTG 62657	C	
		CACTGCA TCCAGCCTGGG		
		GTGGCGT AGGTCGGACCT		
		A		
GAM2524 KIAA1877	3'	GTCGCCCAGGCTAGAGTGCAGT 66759	C	A
	GG	CCACTGCACTC AGCCTGGG GAC		
		GGTGACGTGAG TCGGACCC CTG		
		A G		
GAM2524 KIAA1908	5'	CTCCCAGGCTGGGCTTTGTAG 73787	C__	
		CTGCA TCCAGCCTGGGAG		
		GATGT GGGTCGGACCCTC		
		TTC		
GAM2524 KIAA1922	5'	GTTGCCCAGGCTGGAGTGCAAT 74004	C	AG
	GG	CCA TGCCTCCAGCCTGGG AC		
		GGT ACGTGAGGTCGGACCC TG		
		A GT		
GAM2524 KIAA1924	3'	CCCAGGATGGAGTGCAGTGG 74043	G	
		CCACTGCACTCCA CCTGGG		

			GGTGACGTGAGGT GGACCC			
			A			
GAM2524	KIAA1924	3'	CCTAGGCTGGAATGCAGTGG 74044	C		
			CCACTGCA TCCAGCCTGGG			
			GGTGACGT AGGTCGGATCC			
			A			
GAM2524	KIAA1971	3'	CCAGGCTGGGGTGCAGTGG 74673			
			CCACTGCACTCCAGCCTGG			
			GGTGACGTGGGGTCGGACC			
GAM2524	KIAA1971	3'	GTCATCCAGGCTAGAGTGCAGT 74691	C		GA
		GG	CCACTGCACTC AGCCTGG GAC			
			GGTGACGTGAG TCGGACC CTG			
			A TA			
GAM2524	KIAA1971	3'	GTCGCCCAGGCTGGGGTGCAGT 74693			A
		GG	CCACTGCACTCCAGCCTGGG GAC			
			GGTGACGTGGGGTCGGACCC CTG			
			G			
GAM2524	KIAA1975	5'	GTCTCCCGGCCTGGAGTGCAGT 74427	C		
		GG	CCACTGCACTCCAG CTGGGAGAC			
			GGTGACGTGAGGTC GGCCCTCTG			
			C			
GAM2524	KIAA1987	5'	GTTGCCCAGGTTAGAGTGCAGT 89389	C		AG
		GG	CCACTGCACTC AGCCTGGG AC			
			GGTGACGTGAG TTGGACCC TG			
			A GT			
GAM2524	LAMP3	3'	GTCACCCAGGCTGGAGTACAGT 60210	C		A
		GG	CCACTG ACTCCAGCCTGGG GAC			
			GGTGAC TGAGGTCTGGACCC CTG			
			A A			
GAM2524	LENG1	5'	CCTGGGCCAGAGTGCAGCGG 85194	A	CA	TG
			CC CTGCACTC GCC GG			
			GG GACGTGAG CGG CC			
			C AC GT			
GAM2524	LIECG3	3'	GTTGCCCAGGTTGGAGTGCAGT 88803			AG
		GG	CCACTGCACTCCAGCCTGGG AC			
			GGTGACGTGAGGTTGGACCC TG			
			GT			
GAM2524	LY75	3'	GTTGCCCAGGCTGGAGTACAAT 11398	C C		AG
		GG	CCA TG ACTCCAGCCTGGG AC			

			GGT AC TGAGGTCGGACCC TG		
			A A GT		
GAM2524	LZIC	3'	TCCCCACTCATTGGAGTGAACA 51399	CC	A
	G		CTG CACTCCAG TGGG GA		
			GAC GTGAGGTT ACCC CT		
			AA ACTC _		
GAM2524	MAIL	3'	CCCAGGCTGGAGTACAGTGG 49471	C	
			CCACTG ACTCCAGCCTGGG		
			GGTGAC TGAGGTCGGACCC		
			A		
GAM2524	MAP-1	3'	GTCACCCAGGCTGGAGTGCAGT 42448		A
	GG		CCACTGCACTCCAGCCTGGG GAC		
			GGTGACGTGAGGTCGGACCC CTG		
			A		
GAM2524	MCM10	3'	CCCTGGCTGGAGTGCAGT 38174	T	
			ACTGCACTCCAGCC GGG		
			TGACGTGAGGTCGG CCC		
			T		
GAM2524	MEF-2	3'	CCCAGGCTGCTGGAGTGCCGTG 65019	T	
	G		CCAC GCACTCCA GCCTGGG		
			GGTG CGTGAGGT CGGACCC		
			C CGT		
GAM2524	MESDC2	3'	TTGGGCTGGGTACAGTGG 72928	C T	TG
			CCACTG AC CCAGCC G		
			GGTGAC TG GGTCGG T		
			A _ GT		
GAM2524	MGC10200	3'	CAGGCTAGAGTGCAGTGG 59638	C	
			CCACTGCACTC AGCCTG		
			GGTGACGTGAG TCGGAC		
			A		
GAM2524	MGC10818	3'	GTCGCCCAGGCTGGAGTACAAT 48304	C C	A
	GG		CCA TG ACTCCAGCCTGGG GAC		
			GGT AC TGAGGTCGGACCC CTG		
			A A G		
GAM2524	MGC11386	3'	CCTAGGCTGAAGCACAGTGG 53061	CA C	
			CCACTG CT CAGCCTGGG		
			GGTGAC GA GTCGGATCC		
			AC A		
GAM2524	MGC12466	3'	CTAGGCTGAAGTGTAGTGG 79796	C	
			CCACTGCACT CAGCCTGG		

		GGTGATGTGA GTCGGATC		
		A		
GAM2524	MGC13017	3' TTTTGGGCTGGGCACAGTGG 55584	CA T	TG
		CCACTG C CCAGCC GGAG		
		GGTGAC G GGTCGG TTTT		
		AC_ GT		
GAM2524	MGC13138	3' GTCACCCAGGCTGGAGTGCAGT 54160		A
	GG	CCACTGCACTCCAGCCTGGG GAC		
		GGTGACGTGAGGTCGGACCC CTG		
		A		
GAM2524	MGC13138	3' GTTGCCCAGGCTGGAGTGCA 54162		AG
		TGCACTCCAGCCTGGG AC		
		ACGTGAGGTCGGACCC TG		
		GT		
GAM2524	MGC13204	3' GTTGCCCAGGCTGGAGTGCAGT 49632		AG
	GG	CCACTGCACTCCAGCCTGGG AC		
		GGTGACGTGAGGTCGGACCC TG		
		GT		
GAM2524	MGC14289	3' GTTGCCCAGGCTGGAGTGCAGT 55593		AG
	G	CACTGCACTCCAGCCTGGG AC		
		GTGACGTGAGGTCGGACCC TG		
		GT		
GAM2524	MGC14836	3' GTTGCCCAGGCTGGAGTGCAGT 54176		AG
	GG	CCACTGCACTCCAGCCTGGG AC		
		GGTGACGTGAGGTCGGACCC TG		
		GT		
GAM2524	MGC15606	5' GTTGCCCAGGCTGGAGTACATT 59525	C C	AG
	GG	CCA TG ACTCCAGCCTGGG AC		
		GGT AC TGAGGTCGGACCC TG		
		T A GT		
GAM2524	MGC1842	3' GTTGCCCAGACTGGAGTGCAGT 66262	C	AG
	GG	CCACTGCACTCCAG CTGGG AC		
		GGTGACGTGAGGTC GACCC TG		
		A GT		
GAM2524	MGC20235	3' GTCTTACAGCTGGGTGCAGTGG 59559	T	C GG
		CCACTGCAC CCAGC TG AGAC		
		GGTGACGTG GGTCG AC TCTG		
		_ _ AT		
GAM2524	MGC20481	3' TCTCGGGTCCAGAGCGAGCAG 63369	A_	CA_
		CTGC CTC GCCTGGGA		

			GACG GAG TGGGCTCT		
			AGC ACC		
GAM2524	MGC21675	3'	GTTGCCCAGGCTGGAGTGCAAT 54596	C	AG
		GG	CCA TGCACCTCCAGCCTGGG AC		
			GGT ACGTGAGGTCGGACCC TG		
			A GT		
GAM2524	MGC2474	3'	CCCAGGCTGGAATGCAGTGG 43956	C	
			CCACTGCA TCCAGCCTGGG		
			GGTGACGT AGGTCGGACCC		
			A		
GAM2524	MGC2474	3'	GTTGCCCAGGCTGGAGTGCAAT 43964	C	AG
		GG	CCA TGCACCTCCAGCCTGGG AC		
			GGT ACGTGAGGTCGGACCC TG		
			A GT		
GAM2524	MGC2477	5'	CCCAGCTGGAGTGCAGTGG 44295	C	
			CCACTGCACTCCAGC TGGG		
			GGTGACGTGAGGTCG ACCC		
			—		
GAM2524	MGC2477	5'	CCCAGGGCTGGAGTGCAGTGG 44296	—	
			CCACTGCACTCCAGCC TGGG		
			GGTGACGTGAGGTCGG ACCC		
			G		
GAM2524	MGC2603	3'	GTCGCCAGGCTGGAGTGCAGTG 44082		GA
		G	CCACTGCACTCCAGCCTGG GAC		
			GGTGACGTGAGGTCGGACC CTG		
			G_		
GAM2524	MGC29891	3'	CCCAGGCTGGAGTGCGGTGG 58857		
			CCACTGCACTCCAGCCTGGG		
			GGTGGCGTGAGGTCGGACCC		
GAM2524	MGC29898	3'	GTTGCCCAGACTGGAGTGCAGT 59588	C	AG
		GG	CCACTGCACTCCAG CTGGG AC		
			GGTGACGTGAGGTC GACCC TG		
			A GT		
GAM2524	MGC3113	3'	GTTCCCCAGGCCGGAGTGCAGT 44063	A	AG
		GG	CCACTGCACTCC GCCTGGG AC		
			GGTGACGTGAGG CGGACCC TG		
			C CT		
GAM2524	MGC32043	3'	CTCCTGTATCCAGAGATGCAGT 58662	—	CAGCCT_
		GG	CCACTGCA CTC GGGAG		

			GGTGACGT GAG TCCTC		
			A ACCTATG		
GAM2524	MGC3329	3'	TCTAGGCTGGAGTGCCGTGG 44251	T	
			CCAC GCACTCCAGCCTGGG		
			GGTG CGTGAGGTCGGATCT		
			C		
GAM2524	MGC4248	3'	CCAGGCTGGGTGCAGTGG 51312	T	
			CCACTGCAC CCAGCCTGG		
			GGTGACGTG GGTCGGACC		
			—		
GAM2524	MGC4638	3'	GTCACCAGGCTGGAGTGCAGTG 49744		GA
			CACTGCACTCCAGCCTGG GAC		
			GTGACGTGAGGTCGGACC CTG		
			A_		
GAM2524	MGC5149	3'	GTCACCAGGCTAGAGTGCAGTG 72762	C	GA
	G		CCACTGCACTC AGCCTGG GAC		
			GGTGACGTGAG TCGGACC CTG		
			A A_		
GAM2524	MGC9912	3'	GTCGCCAGACTGGAGTGCAGTG 55609	C	GA
	G		CCACTGCACTCCAG CTGG GAC		
			GGTGACGTGAGGTC GACC CTG		
			A G_		
GAM2524	MKRN4	3'	GTCACCCAGGCTGGAGTGCAGT 48473		A
	GG		CCACTGCACTCCAGCCTGGG GAC		
			GGTGACGTGAGGTCGGACCC CTG		
			A		
GAM2524	MMPL1	3'	GTCCTCCAGGCTGGAGTGCAAT 15966	C	GA
	G		CA TGCACTCCAGCCTGG GAC		
			GT ACGTGAGGTCGGACC CTG		
			A TC		
GAM2524	MO25	5'	CAGGCGGAGTGCAGCGG 33285	A	A
			CC CTGCACTCC GCCTG		
			GG GACGTGAGG CGGAC		
			C		
			—		
GAM2524	moblak	3'	CCAGGCTGGAGTGCAGTGG 56391		
			CCACTGCACTCCAGCCTGG		
			GGTGACGTGAGGTCGGACC		
GAM2524	MOCS3	3'	GTTGCCCAGGCTGGAGTGTAGT 27935		AG
	GG		CCACTGCACTCCAGCCTGGG AC		

			GGTGATGTGAGGTCGGACCC	TG		
			GT			
GAM2524	MRAS	5'	CCGGGGCTGGAGCGCGCGG	25236	AC A	G
			CC TGC CTCCAGCCT	GG		
			GG GCG GAGGTCGGG	CC		
			C_ C	G		
GAM2524	MRPL20	3'	GTCACCCAGGCTGGAGTGCAAT	36208	C	A
	GG		CCA TGC ACTCCAGCCTGGG	GAC		
			GGT ACGTGAGGTCGGACCC	CTG		
			A	A		
GAM2524	MRPL35	3'	GTTGCCCAGGCTGGAGTGCAAGT	34023		AG
	GG		CCACTGCACTCCAGCCTGGG	AC		
			GGTGACGTGAGGTCGGACCC	TG		
			GT			
GAM2524	MRPL44	3'	CCCAGGCTGGACTGCAGTGG	43594	C	
			CCACTGCA TCCAGCCTGGG			
			GGTGACGT AGGTCGGACCC			
			C			
GAM2524	MRPS27	3'	GTCACCCAGGCTGGAGTGCAAGT	31333		A
	GG		CCACTGCACTCCAGCCTGGG	GAC		
			GGTGACGTGAGGTCGGACCC	CTG		
			A			
GAM2524	MT-ACT48	3'	TTTTTAGGCCAGGCACAGTGG	25611	CACT A_	
			CCACTG CC GCCTGGGAG			
			GGTGAC GG CGGATTTTT			
			AC_ AC			
GAM2524	MtFMT	3'	CCCAGGCTGGAATCCAGTGG	58333	CAC	
			CCACTG TCCAGCCTGGG			
			GGTGAC AGGTCGGACCC			
			CTA			
GAM2524	MYO5C	3'	TCGCCAGGCTGGAGTGTAGTGG	38727		_
			CCACTGCACTCCAGCCTGG	GA		
			GGTGATGTGAGGTCGGACC	CT		
			G			
GAM2524	NAPG	5'	CCCAGGCTGGAGTGCAGTGG	15145		
			CCACTGCACTCCAGCCTGGG			
			GGTGACGTGAGGTCGGACCC			
GAM2524	NDP52	3'	GTCACCCAGGCTGGCGTGCAAT	20676	C T	A
	GG		CCA TGCA C CAGCCTGGG	GAC		

			GGT ACGTG GGTCTGGACCC CTG	
			A C A	
GAM2524	NDUFB1	5'	TCCCCCAGGCTGGAGTGTAGTG 17016	A
	G		CCACTGCACTCCAGCCTGGG GA	
			GGTGATGTGAGGTCGGACCC CT	
			C	
GAM2524	NDUFC2	3'	TCAGGCTGGAGTGCAGTGG 17037	
			CCACTGCACTCCAGCCTGG	
			GGTGACGTGAGGTCGGACT	
GAM2524	NINJ2	3'	CTAGGCTGGAGTAAAATGG 33721 CTGC	
			CCA ACTCCAGCCTGG	
			GGT TGAGGTCGGATC	
			AAAA	
GAM2524	NOSIP	5'	CCTAGGCTGGAGTGCAATGG 32542 C	
			CCA TGCACTCCAGCCTGGG	
			GGT ACGTGAGGTCGGATCC	
			A	
GAM2524	Nup43	3'	GTCTTGCTCTGCTGGAGTGCGG 45353	CT _
	TGG		CCACTGCACTCCAGC GG GAGAC	
			GGTGGCGTGAGGTCG TC TTCTG	
			TC G	
GAM2524	NXN	3'	GTCGCCCAGGCTGGAGTGCAGT 42680	A
	GG		CCACTGCACTCCAGCCTGGG GAC	
			GGTGACGTGAGGTCGGACCC CTG	
			G	
GAM2524	OCT11	3'	CCCAGGCTGGAGTGCAGTGG 27585	
			CCACTGCACTCCAGCCTGGG	
			GGTGACGTGAGGTCGGACCC	
GAM2524	OR51E2	3'	GTCACCAGGCTGGAGTGCAGTG 48516	GA
	G		CCACTGCACTCCAGCCTGG GAC	
			GGTGACGTGAGGTCGGACC CTG	
			A_	
GAM2524	OSBPL2	3'	GTTGCCCAGGCTGGAGTGCAAT 58492 C	AG
	GG		CCA TGCACTCCAGCCTGGG AC	
			GGT ACGTGAGGTCGGACCC TG	
			A GT	
GAM2524	PASK	5'	CTGAGGCTGGAGTGCAGTGG 31408	G
			CCACTGCACTCCAGCCT GG	

		GGTGACGTGAGGTCGGA TC	
		G	
GAM2524	PCBP3	3' CCCATGCACCGGCATGCAGTGG 40443	CT A__ C
		CCACTGCA CC GC TGGG	
		GGTGACGT GG CG ACCC	
		AC CCA T	
GAM2524	PELI1	5' GTCACCCAGGCTGGAGTGCAGT 40648	A
	GG	CCACTGCACTCCAGCCTGGG GAC	
		GGTGACGTGAGGTCGGACCC CTG	
		A	
GAM2524	PELI1	5' GTCGCCCAGGCTGGAGTGCAGT 40650	A
	GG	CCACTGCACTCCAGCCTGGG GAC	
		GGTGACGTGAGGTCGGACCC CTG	
		G	
GAM2524	PELI1	5' GTTGCCCAGGTTGGAGTGCAGT 40652	AG
	GG	CCACTGCACTCCAGCCTGGG AC	
		GGTGACGTGAGGTTGGACCC TG	
		GT	
GAM2524	PI4KII	3' TCTCCCATCAGTGCTGTGG 37954 T CCAGCC	
		CCAC GCACT TGGGAGA	
		GGTG CGTGA ACCCTCT	
		T CT____	
GAM2524	PIP3-E	3' GTTGCCCAGGCTGGAGTGCAGT 67359	AG
	GG	CCACTGCACTCCAGCCTGGG AC	
		GGTGACGTGAGGTCGGACCC TG	
		GT	
GAM2524	POFUT1	3' GTCTCCCAGGCTGGAGTGCAGT 70981	
	GG	CCACTGCACTCCAGCCTGGGAGAC	
		GGTGACGTGAGGTCGGACCCTCTG	
GAM2524	POLE3	3' GTGGCCCAGGCTGGAGTGCAGT 34319	AG
	GG	CCACTGCACTCCAGCCTGGG AC	
		GGTGACGTGAGGTCGGACCC TG	
		GG	
GAM2524	POLE3	3' TCTCCCAGACTTGTGACTATGG 34322	CTG_ TCC C
		CCA CAC AG CTGGGAGA	
		GGT GTG TC GACCCTCT	
		ATCA T__ A	
GAM2524	PRO0365	5' GTCGCCAGGCTGAAGTGCAGTG 26993	C GA
	G	CCACTGCACT CAGCCTGG GAC	

				GGTGACGTGA GTCGGACC CTG			
				A G_			
GAM2524	PRO0456	3'	TTTAGGCTGGGTGCAGTGG	27011	T		
		CCACTGCAC CCAGCCTGGG					
		GGTGACGTG GGTCGGATTT					
GAM2524	PRO0478	3'	TCCCAGCCTGGAATGCAGTGG	27040	C C		
		CCACTGCA TCCAG CTGGGA					
		GGTGACGT AGGTC GACCCT					
		A C					
GAM2524	PRO0611	3'	TCTTCTGGCTGGGCGCAGTGG	26861	A T T		
		CCACTGC C CCAGCC GGGAGA					
		GGTGACG G GGTCGG TCTTCT					
		C _ _					
GAM2524	PRO0902	3'	GTCACCCAGGCTGGAGTGTAGT	54969		A	
	GG		CCACTGCACTCCAGCCTGGG GAC				
		GGTGATGTGAGGTCCGACCC CTG					
		A					
GAM2524	PRO1048	3'	CTGCCCAGGCTGGAGTACAGTG	38113	C	_	
	G		CCACTG ACTCCAGCCTGGG AG				
		GGTGAC TGAGGTCCGACCC TC					
		A G					
GAM2524	PRO1386	3'	TCTGGCCAGGTGCAGTGG	49219	CCA TG		
		CCACTGCACT GCC GGA					
		GGTGACGTGG CGG TCT					
		AC_ _					
GAM2524	PRO1992	5'	GTCACCCAGACTGGAGTGCAGT	26910	C A		
	GG		CCACTGCACTCCAG CTGGG GAC				
		GGTGACGTGAGGTC GACCC CTG					
		A A					
GAM2524	PRO1992	3'	GTCACCCAGGCTGGAGTGCAGT	26912		A	
	GG		CCACTGCACTCCAGCCTGGG GAC				
		GGTGACGTGAGGTCCGACCC CTG					
		A					
GAM2524	PRO2955	3'	GTCCCCCAGGCTGAAGTGCAGC	38244	A C A		
	GG		CC CTGCACT CAGCCTGGG GAC				
		GG GACGTGA GTCGGACCC CTG					
		C A C					
GAM2524	PSPH	3'	GTTGCCCAGGCTGGAGTGCAGT	17139		AG	
	GG		CCACTGCACTCCAGCCTGGG AC				

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GGTGACGTGAGGTCGGACCC TG
GT
GAM2524 PSR 3' CCAAGGCCAGGTGCAGTGG 65781 CCA G
CCACTGCACT GCCT GG
||||||| ||| ||
GGTGACGTGG CGGA CC
AC_ A
GAM2524 PSTPIP2 3' GTCCCCCAGGCTGAAGTGCAGC 44661 A C A
GG CC CTGCACT CAGCCTGGG GAC
|| ||||| ||||| |||
GG GACGTGA GTCGGACCC CTG
C A C
GAM2524 PTD011 5' CAGGCTGGAGTGCAGTGG 26759
CCACTGCACTCCAGCCTG
|||||||
GGTGACGTGAGGTCGGAC

GAM2524 RAB21 3' GTCACCCAGGCTGGAGTGCAGT 31097 C A
GG CCA TGCCTCCAGCCTGGG GAC
||| ||||| |||
GGT ACGTGAGGTCGGACCC CTG
C A
GAM2524 RAB33B 3' GTCTCCAGGCTGGAGTGCAGTG 49333 G
G CCACTGCACTCCAGCCTGG AGAC
||||||| |||
GGTGACGTGAGGTCGGACC TCTG

GAM2524 RAB39 3' GTCACCCAGGCTGGAGTGCAGT 77125 A
GG CCACTGCACTCCAGCCTGGG GAC
||||||| |||
GGTGACGTGAGGTCGGACCC CTG
A
GAM2524 RAP140 3' GTCGCCCAAGCTGGAGTACAGT 31523 C C A
GG CCACTG ACTCCAGC TGGG GAC
||||| ||||| ||| |||
GGTGAC TGAGGTCG ACCC CTG
A A G
GAM2524 RASSF2 3' GTTTCACAGGCTGGAGTGCAGT 29111
GG CCACTGCACTCCAGCCTGGGAGAC
|||||||
GGTGACGTGAGGTCGGACCCTTTG

GAM2524 RES4-25 3' GTTGCCCAGGCTGGAGTGCAAT 65273 C AG
GG CCA TGCCTCCAGCCTGGG AC
||| ||||| ||| ||
GGT ACGTGAGGTCGGACCC TG
A GT
GAM2524 RIL 3' TCCTAGGCTCTGGGTGCAGT 14889 C_
ACTGCACTC AGCCTGGGA
||||||| |||||

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		TGACGTGGG TCGGATCCT			
		TC			
GAM2524	RNF8	3'	GTTGCCCAAGCTGGAGTACAGT 15573	C	C AG
			ACTG ACTCCAGC TGGG AC		
			TGAC TGAGGTCG ACCC TG		
			A A GT		
GAM2524	RNO2	5'	CCAAGGCTGGAGTGCAGGG 53928	A	G
			CC CTGCACTCCAGCCT GG		
			GG GACGTGAGGTCGGA CC		
			— A		
GAM2524	SARM	3'	TCCAGGCTGGAGGGCAGTG 31306	A	
			CACTGC CTCCAGCCTGGG		
			GTGACG GAGGTCGGACCT		
			G		
GAM2524	SCAMP-4	3'	GTCGCCCAGGCTGGAGTGCAGT 55354		A
	GG		CCACTGCACTCCAGCCTGGG GAC		
			GGTGACGTGAGGTCGGACCC CTG		
			G		
GAM2524	SCAND2	3'	TCACCCAGGCTGGAGTGGAGTG 42145	G	A
	G		CCACT CACTCCAGCCTGGG GA		
			GGTGA GTGAGGTCGGACCC CT		
			G A		
GAM2524	SCYA13	3'	TCAAGCTGGAGTACGTG 19431	T C	C
			CAC G ACTCCAGC TGG		
			GTG C TGAGGTCG ACT		
			_ A A		
GAM2524	SCYA16	3'	GTCACCCAGGCTGGAGTGCAGT 17177		A
	GG		CCACTGCACTCCAGCCTGGG GAC		
			GGTGACGTGAGGTCGGACCC CTG		
			A		
GAM2524	SCYA22	3'	CCCACGCTGGAGTGCAATGG 92585	C	C
			CCA TGCCTCCAGC TGGG		
			GGT ACGTGAGGTCG ACCC		
			A C		
GAM2524	SCYA22	3'	GTCGCCCAGGCTGGAGTGCAGT 92606		A
	GG		CCACTGCACTCCAGCCTGGG GAC		
			GGTGACGTGAGGTCGGACCC CTG		
			G		
GAM2524	SCYA22	3'	GTCTCCCAAGCCTGGCATGTGG 92607	TG CT	_ C
			C CA CCAG C TGGGAGAC		

			G GT GGTC G ACCCTCTG		
			GT AC C A		
GAM2524	SCYA28	3'	CAGGCTGGAGGGCAGTGG 39538	A	
			CCACTGC CTCCAGCCTG		
			GGTGACG GAGGTCGGAC		
			G		
GAM2524	SERF1B	3'	CCCAGGCTGGACTGCAGTGG 43693	C	
			CCACTGCA TCCAGCCTGGG		
			GGTGACGT AGGTCGGACCC		
			C		
GAM2524	SERF1B	3'	GTCACCAGACTGGAGTGCAGTG 43702	C	GA
	G		CCACTGCACTCCAG CTGG GAC		
			GGTGACGTGAGGTC GACC CTG		
			A A_		
GAM2524	SERF2	5'	CCCATGCTGGAGTACGGTGG 20488	C	C
			CCACTG ACTCCAGC TGGG		
			GGTGGC TGAGGTCG ACCC		
			A T		
GAM2524	SFXN2	3'	GTCGCCCAGGCTGGAATGCAGT 74384	C	A
	GG		CCACTGCA TCCAGCCTGGG GAC		
			GGTGACGT AGGTCGGACCC CTG		
			A G		
GAM2524	SIRPB1	3'	TTCCCAGGCTGGAGTGCAATG 21372	C	
			CA TGCACTCCAGCCTGGGAG		
			GT ACGTGAGGTCGGACCCTT		
			A		
GAM2524	SLC11A1	3'	CCAAGGCTGGAGTGCAGTGG 60157		G
			CCACTGCACTCCAGCCT GG		
			GGTGACGTGAGGTCGGA CC		
			A		
GAM2524	SLC12A8	3'	CCCAGGCTGGAGTCCAGTGG 45235	C	
			CCACTG ACTCCAGCCTGGG		
			GGTGAC TGAGGTCGGACCC		
			C		
GAM2524	SLC16A4	3'	CCCAGGCTGGAGTGCAGTGG 17450		
			CCACTGCACTCCAGCCTGGG		
			GGTGACGTGAGGTCGGACCC		
GAM2524	SLC16A6	5'	GTCATTCAAGCAAGAGTGCAGT 17442	CA	A
			ACTGCACTC GCCTGGG GAC		

			TGACGTGAG CGGACTT CTG		
			AA A		
GAM2524	SLC19A3	3'	TCAGAGGCTGGAGTGCAATGG 48251	C	GG
			CCA TGCACTCCAGCCT GA		
			GGT ACGTGAGGTCGGA CT		
			A GA		
GAM2524	SLC19A3	3'	TCTATGGGCCAGGTGCAGTGG 48253	CCA	GG
			CCACTGCACT GCCTG AGA		
			GGTGACGTGG CGGGT TCT		
			AC_ A_		
GAM2524	SLC6A14	3'	CCTGGGCTGGAGTGCACTGG 24307		TG
			CCACTGCACTCCAGCC GG		
			GGTGACGTGAGGTCGG CC		
			GT		
GAM2524	SREC	3'	GTCCCCCAGGCTGGAGTGCACT 14910		A
	GG		CCACTGCACTCCAGCCTGGG GAC		
			GGTGACGTGAGGTCGGACCC CTG		
			C		
GAM2524	SS-56	3'	GTTGCCCAGGCTGGAGTGCACT 60359		AG
	GG		CCACTGCACTCCAGCCTGGG AC		
			GGTGACGTGAGGTCGGACCC TG		
			GT		
GAM2524	STAF65(gamma)	3'	GTCACCCAGGCTGGAGTGCAAT 30073	C	A
	GG		CCA TGCACTCCAGCCTGGG GAC		
			GGT ACGTGAGGTCGGACCC CTG		
			A A		
GAM2524	STAM2	3'	GTCACCCAGGCTGGAGTGCACT 20706		A
			ACTGCACTCCAGCCTGGG GAC		
			TGACGTGAGGTCGGACCC CTG		
			A		
GAM2524	SULT1C2	3'	GTCGCCCAGGCTGGAGTGCACT 22720		A
	GG		CCACTGCACTCCAGCCTGGG GAC		
			GGTGACGTGAGGTCGGACCC CTG		
			G		
GAM2524	SUN1	3'	GTTGCCCAGGCTGGAGTGCACT 47922		AG
	GG		CCACTGCACTCCAGCCTGGG AC		
			GGTGACGTGAGGTCGGACCC TG		
			GT		
GAM2524	SYT12	5'	TCAGGCTGGAGTGCACTGG 96388		
			CCACTGCACTCCAGCCTGG		

GGTGACGTGAGGTCGGACT

GAM2524	SYT13	3'	GTTGCCCAGGCTGGAGTGCAGT 95105	AG
	GG		CCACTGCACTCCAGCCTGGG AC	
			GGTGACGTGAGGTCGGACCC TG	
			GT	
GAM2524	T54	3'	TCCCCCAGGCTGGTACCAG 32278 CACT	A
			CTG CCAGCCTGGG GA	
			GAC GGTCCGACCC CT	
			CAT_ C	
GAM2524	TADA3L	3'	GTCACCCAGGCTGGAGTGCAGT 22044	A
	GG		CCACTGCACTCCAGCCTGGG GAC	
			GGTGACGTGAGGTCGGACCC CTG	
			A	
GAM2524	TCL6	5'	CCAGGCCAGAGTGCAGTGG 40465 CA	
			CCACTGCACTC GCCTGG	
			GGTGACGTGAG CGGACC	
			AC	
GAM2524	TCL6	5'	CTCAGGCTGGAATGCAGTGG 40470 C	
			CCACTGCA TCCAGCCTGGG	
			GGTGACGT AGGTCGGA	
			CTC	
			A	
GAM2524	TERA	3'	GTTACCCAGGCTGGAGTGCAGT 41422	A
	GG		CCACTGCACTCCAGCCTGGG GAC	
			GGTGACGTGAGGTCGGACCC TTG	
			A	
GAM2524	TGIF2	3'	CCCGGGCTGGAGTGCAGTGG 41743	
			CCACTGCACTCCAGCCTGGG	
			GGTGACGTGAGGTCGGGCCC	
GAM2524	THEA	3'	GTTGCCCAGGCTGGAGTGCAGT 66894	AG
	G		CACTGCACTCCAGCCTGGG AC	
			GTGACGTGAGGTCGGACCC TG	
			GT	
GAM2524	TOR1B	3'	GTCATCCAAGCTGGAGTGCAGT 27977	C GA
	GG		CCACTGCACTCCAGC TGG GAC	
			GGTGACGTGAGGTCG ACC CTG	
			A TA	
GAM2524	TRIM16	3'	GTTGCCCAGGCTGGAGAGCAGT 22376	A AG
	GG		CCACTGC CTCCAGCCTGGG AC	

			GGTGACG GAGGTCGGACCC TG		
			A GT		
GAM2524	TRIM35	3'	TCACCCAGGCTGGAGTACAGTG 61520	C	A
	G		CCACTG ACTCCAGCCTGGG GA		
			GGTGAC TGAGGTCGGACCC CT		
			A A		
GAM2524	TRIM5	3'	GTTCCCCAGGCTGGAGTGCAAT 53475	C	AG
	GG		CCA TGCACCTCCAGCCTGGG AC		
			GGT ACGTGAGGTCGGACCC TG		
			A CT		
GAM2524	TRIM6	3'	GTCGCCCAGGCTGGAGTGCACT 55186	C	A
	GG		CCA TGCACCTCCAGCCTGGG GAC		
			GGT ACGTGAGGTCGGACCC CTG		
			C G		
GAM2524	TU12B1-TY	3'	CCCAGGCCGGAGTGCAATGG 33837	C	A
			CCA TGCACCTCC GCCTGGG		
			GGT ACGTGAGG CGGACCC		
			A C		
GAM2524	TU12B1-TY	3'	CCCAGGCTGGAGTGCACTGG 33838		
			CCACTGCACTCCAGCCTGGG		
			GGTGACGTGAGGTCGGACCC		
GAM2524	TU12B1-TY	3'	CCCATTCTGGAGTGCACTGG 33839		CC
			CCACTGCACTCCAG TGGG		
			GGTGACGTGAGGTC ACCC		
			TT		
GAM2524	TUCAN	3'	GTTACCCAGGCTGGAGTGCACT 30985		A
	GG		CCACTGCACTCCAGCCTGGG GAC		
			GGTGACGTGAGGTCGGACCC TTG		
			A		
GAM2524	TUCAN	3'	TCTAGGCTGGAGTGCACTGG 30991		
			CCACTGCACTCCAGCCTGGG		
			GGTGACGTGAGGTCGGATCT		
GAM2524	TUSP	3'	CCCAACTAGAGTGTAGTGG 40018	C CC	
			CCACTGCACTC AG TGGG		
			GGTGATGTGAG TC ACCC		
			A A_		
GAM2524	TXNL2	3'	CCAGGCTGGGCACAATGG 22579	C CA T	
			CCA TG C CCAGCCTGG		

			GGT AC G GGTCGGACC		
			A AC _		
GAM2524	TXNL2	3'	GTCACCCAGGCTGGAGTGCAGT 22585		A
	GG		CCACTGCACTCCAGCCTGGG GAC		
			GGTGACGTGAGGTCGGACCC CTG		
			A		
GAM2524	UBF-fl	3'	GTCTCCCAGGCTAGAGTACCGT 52632	TGC	C
	GG		CCAC ACTC AGCCTGGGAGAC		
			GGTG TGAG TCGGACCCTCTG		
			CCA A		
GAM2524	VDU1	3'	CCCAGGCTGGAGTGCTGTGG 31121	T	
			CCAC GCACTCCAGCCTGGG		
			GGTG CGTGAGGTCGGACCC		
			T		
GAM2524	VPS33A	3'	GTCACCCAGACTAGAGTGCAGT 43615	C C	A
	GG		CCACTGCACTC AG CTGGG GAC		
			GGTGACGTGAG TC GACCC CTG		
			A A A		
GAM2524	WNT2B	3'	CTGAGGTGGAATGCAGTGG 44679	C G G	
			CCACTGCA TCCA CCT GG		
			GGTGACGT AGGT GGA TC		
			A _ G		
GAM2524	ZNF17	3'	GTTGCCCAGACTAGAGTGCAGT 83276	C C	AG
	GG		CCACTGCACTC AG CTGGG AC		
			GGTGACGTGAG TC GACCC TG		
			A A GT		
GAM2524	ZNF197	3'	TGGGCTGGGTGCAGTGG 23763	T	
			CCACTGCAC CCAGCCTG		
			GGTGACGTG GGTCGGGT		
			-		
GAM2524	ZNF338	3'	GTTTCCCAGGCTGGAGTGCAGT 42261		
	GG		CCACTGCACTCCAGCCTGGGAGAC		
			GGTGACGTGAGGTCGGACCCTTTG		
GAM2524	ZNF339	3'	GTCACCCAGGCTGGAGTACAGT 41396	C	A
	GG		CCACTG ACTCCAGCCTGGG GAC		
			GGTGAC TGAGGTCGGACCC CTG		
			A A		
GAM2524	ZTL1	3'	CCCAGGCTGCAGTGCAGTG 43517	C	
			CACTGCACT CAGCCTGGG		

		GTGACGTGA GTCGGACCC		
		C		
GAM2524	LOC112687 3'	CAGGCTGGGTGCAATGG 73226	C T	
		CCA TGCAC CCAGCCTG		
		GGT ACGTG GGTCGGAC		
		A _		
GAM2524	LOC112687 3'	GTCACCCAGGCTGGAGTGCAGT 73242		A
	GG	CCACTGCACTCCAGCCTGGG GAC		
		GGTGACGTGAGGTCGGACCC CTG		
		A		
GAM2524	LOC112724 5'	GTCGCCAGGCTGGAATGCAGT 57306	C	GA
		ACTGCA TCCAGCCTGG GAC		
		TGACGT AGGTCGGACC CTG		
		A G_		
GAM2524	LOC112817 3'	GTCACCCAGGCTGGAGTGCAAT 57332	C	A
	GG	CCA TGCACCTCCAGCCTGGG GAC		
		GGT ACGTGAGGTCGGACCC CTG		
		A A		
GAM2524	LOC113675 5'	GTCACCCAGGCTGGAGTGCAGT 57382		A
	GG	CCACTGCACTCCAGCCTGGG GAC		
		GGTGACGTGAGGTCGGACCC CTG		
		A		
GAM2524	LOC115196 3'	CCCAGGCTGGAGTCCAGTGG 73654	C	
		CCACTG ACTCCAGCCTGGG		
		GGTGAC TGAGGTCGGACCC		
		C		
GAM2524	LOC115219 5'	GTCCCCCAGGCTGGAGTGCGAT 73705	C	A
	GG	CCA TGCACCTCCAGCCTGGG GAC		
		GGT GCGTGAGGTCGGACCC CTG		
		A C		
GAM2524	LOC115343 5'	CTGAGAGCTGGAGTACAG 72532	C _ G	
		CTG ACTCCAGC CT GG		
		GAC TGAGGTCG GA TC		
		A A G		
GAM2524	LOC115648 3'	CCTGGCTGGAGTGCAGTGG 60020		T
		CCACTGCACTCCAGCC GGG		
		GGTGACGTGAGGTCGG TCC		
		_		
GAM2524	LOC116411 5'	TCCAGGCTGGAGTGCAGTGG 74303		
		CCACTGCACTCCAGCCTGGG		

GGTGACGTGAGGTCGGACCT

GAM2524 LOC120114 3' GTCACCCAGGCTAGAGTGCAAT 76050 C C A
GG CCA TGC ACTC AGCCTGGG GAC
||| ||||| ||||| |||
GGT ACGTGAG TCGGACCC CTG
A A A

GAM2524 LOC120224 5' GTCACCCAGGCTGGAGTGCAAT 57893 C A
GG CCA TGC ACTCCAGCCTGGG GAC
||| ||||| ||||| |||
GGT ACGTGAGGTCGGACCC CTG
A A

GAM2524 LOC120939 3' GTAGCCCAGGCTGGGATGCAAT 76769 C CT AG
GG CCA TGCA CCAGCCTGGG AC
||| ||| ||||| ||
GGT ACGT GGTCGGACCC TG
A AG GA

GAM2524 LOC121219 3' CTCCTGGAAGGCTGGAGCACA 74487 CA ____
TG CTCCAGCCT GGGAG
|| ||||| ||||
AC GAGGTCGGA TCCTC
AC AGG

GAM2524 LOC121504 3' CCGAGGCTGGAGTGCA GTG 74543 G
CCACTGCACTCCAGCCT GG
||||| ||||| ||
GGTGACGTGAGGTCGGA CC
G

GAM2524 LOC123591 5' GTCCCCCAGGCTGGGACG GGG 76132 A CAC A
CC CTG TCCAGCCTGGG GAC
|| ||| ||||| |||
GG GGC GGGTCGGACCC CTG
_ A _ C

GAM2524 LOC124602 3' GTTTTTCAGGCTGGGCACAGTG 74790 CA T GG
CACTG C CCAGCCTG AGAC
|||| | ||||| |||
GTGAC G GGTCGGAC TTTG
AC _ TT

GAM2524 LOC125268 3' TCTCCCAGGCACGCATGG 76581 C ACTCCA
CCA TGC GCCTGGGAGA
||| ||| ||||| |||
GGT ACG CGGACCCTCT
_ CA ____

GAM2524 LOC125268 3' TCTCCCAGGTGCCACTGCAG 76582 CTCCA
CTGCA GCCTGGGAGA
|||| ||||| |||
GACGT TGGACCCTCT
CACCG

GAM2524 LOC126133 3' GTCACCCAGGCTGGAGCGCAGT 74915 A A
GG CCACTGC CTCCAGCCTGGG GAC
||||| ||||| |||

		GGTGACG GAGGTCGGACCC CTG		
		C A		
GAM2524	LOC126364 3'	CCCAGGCTGGAGTGCAATG 76186 C		
		CA TGCCTCCAGCCTGGG		
		GT ACGTGAGGTCGGACCC		
		A		
GAM2524	LOC126661 3'	GTTGCCCAGGCTGGAGTGCAGT 75063	AG	
	GG	CCACTGCACTCCAGCCTGGG AC		
		GGTGACGTGAGGTCGGACCC TG		
		GT		
GAM2524	LOC126669 3'	GTTGCCCAGGCTGGAGTGCAT 75948 C	AG	
	GG	CCA TGCCTCCAGCCTGGG AC		
		GGT ACGTGAGGTCGGACCC TG		
		A GT		
GAM2524	LOC128077 3'	CCCAGGCTGGAGTGCAGTGG 75209		
		CCACTGCACTCCAGCCTGGG		
		GGTGACGTGAGGTCGGACCC		
GAM2524	LOC128077 3'	GTCGCCCAGGCTAGAGTGCAGT 75229	C	A
	GG	CCACTGCACTC AGCCTGGG GAC		
		GGTGACGTGAG TCGGACCC CTG		
		A G		
GAM2524	LOC128387 3'	GTTGCCCAGGCTGGAGTGCAT 75259 C	AG	
	GG	CCA TGCCTCCAGCCTGGG AC		
		GGT ACGTGAGGTCGGACCC TG		
		A GT		
GAM2524	LOC128989 3'	GTCACCCAGGCTGGAGTGCAGT 75324	A	
	GG	CCACTGCACTCCAGCCTGGG GAC		
		GGTGACGTGAGGTCGGACCC CTG		
		A		
GAM2524	LOC130813 3'	CCTAGGCTAGAGGGCAGTG 76270	A	C
		CACTGC CTC AGCCTGGG		
		GTGACG GAG TCGGATCC		
		G A		
GAM2524	LOC131308 3'	CTCAGGCTGGAGTGCAGTGG 75494		
		CCACTGCACTCCAGCCTGGG		
		GGTGACGTGAGGTCGGACTC		
GAM2524	LOC131965 3'	CAGGCTGGAGTGCAGTGG 75519		
		CCACTGCACTCCAGCCTG		

GGTGACGTGAGGTCGGAC

GAM2524 LOC132241 5' TTCCCAGGCTGGAGTGCAGTGG 75568
CCACTGCACTCCAGCCTGGGAG
|||||||
GGTGACGTGAGGTCGGACCCTT

GAM2524 LOC133686 3' CCCAGGCTGGACTGCAGTGG 75615 C
CCACTGCA TCCAGCCTGGG
||||| |||||
GGTGACGT AGGTCGGACCC
C

GAM2524 LOC135154 3' CCCAGGCTGGAGTGGAGTGG 75728 G
CCACT CACTCCAGCCTGGG
|||| |||||
GGTGA GTGAGGTCGGACCC
G

GAM2524 LOC135293 3' GTTGCCAGGCTGAAGTGTAGT 76690 C AG
GG CCACTGCACT CAGCCTGGG AC
||||| ||||| ||
GGTGATGTGA GTCGGACCC TG
A GT

GAM2524 LOC135293 3' TCTCCAGGCTGGAGTGCAGTG 76692
G CCACTGCACTCCAGCCTGGGAGA
|||||||
GGTGACGTGAGGTCGGACCCTCT

GAM2524 LOC135398 3' CCCAGCCTGGAATGTAGTGG 76468 C C
CCACTGCA TCCAG CTGGG
||||| |||||
GGTGATGT AGGTC GACCC
A C

GAM2524 LOC135763 3' GTCACCCAGGCTGGAGTGCAGT 57562 A
GG CCACTGCACTCCAGCCTGGG GAC
||||||| |||||
GGTGACGTGAGGTCGGACCC CTG
A

GAM2524 LOC138050 5' CCCAGGCTGGAGTGCAGTGG 75813
CCACTGCACTCCAGCCTGGG
|||||||
GGTGGCGTGAGGTCGGACCC

GAM2524 LOC138199 3' GTCTCCAGGCCGGAGTGCAGT 75827 A
GG CCACTGCACTCC GCCTGGGAGAC
||||||| |||||
GGTGACGTGAGG CGGACCCTCTG
C

GAM2524 LOC138428 3' CTTGAGGCCGGGTGCAGTGG 75857 T A GG
CCACTGCAC CC GCCT GAG
||||||| || |||||

		GGTGACGTG GG CGGA TTC		
		_ C GG		
GAM2524	LOC139422 5'	GTTGCCCAGACTGGAGTGCAGT 76355	C	AG
	GG	CCACTGCACTCCAG CTGGG AC		
		GGTGACGTGAGGTC GACCC TG		
		A GT		
GAM2524	LOC142913 5'	CCCAGGCTGGAGTAGAGTG 76932	GC	
		CACT ACTCCAGCCTGGG		
		GTGA TGAGGTCGGACCC		
		GA		
GAM2524	LOC143153 3'	GTCACCCAGGCTGGAGTGCAG 76982	A	
		CTGCACTCCAGCCTGGG GAC		
		GACGTGAGGTCGGACCC CTG		
		A		
GAM2524	LOC143154 3'	GTCACCCAGGCTGGAGTGCAG 76993	A	
		CTGCACTCCAGCCTGGG GAC		
		GACGTGAGGTCGGACCC CTG		
		A		
GAM2524	LOC143187 3'	CCTGGCTGGAGTGGAGTGG 59757	G	T
		CCACT CACTCCAGCC GGG		
		GGTGA GTGAGGTCGG TCC		
		G _		
GAM2524	LOC143241 5'	GTTGCCCAGGCTGGAGTGCAAT 57975	C	AG
	GG	CCA TGCACTCCAGCCTGGG AC		
		GGT ACGTGAGGTCGGACCC TG		
		A GT		
GAM2524	LOC144248 5'	CCCAGGCTGGAGTGCAATGG 77251	C	
		CCA TGCACTCCAGCCTGGG		
		GGT ACGTGAGGTCGGACCC		
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GAM2524	LOC144519 5'	CCTGGGCTGGAGTGCAGTGG 77370	TG	
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GAM2524 LOC144776 5' GTTGCCCAAGCTGGAGTGCAAT 77495 C AG
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GAM2524 LOC146839 3'	GTTGCCCAGGCTGGAGTGCAGT 84849	AG	
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GAM2524 LOC146894 3'	CTGCCCAGGCTGGAGTGCAGTG 59858	—	
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GAM2524 LOC146895 5'	GTCACCCAGGCTGGAGTGCAGT 84872	A	
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GAM2524 LOC146909 3'	GTCGCCCAGGCTGGAGTGCAGT 78780	A	
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GAM2524	LOC147817 3'	GTCGCCCAGGCTGGAGTGCAAT 79190	C	A	
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GAM2524	LOC147895 5'	CCTACGCTGGAGTGCAGTGG 85199		C	
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		C			
GAM2524	LOC147990 3'	CCCAGGCTGGAGTGCGGTGG 85218			
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GAM2524	LOC148137	3'	CCCAGGCTGTAGTACAATGG	59091	C C C	
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GAM2524	LOC148147	3'	GTCACCAGGCTGGAGTGCAGTG	79405		GA
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GAM2524	LOC148198	3'	CCCAGGCTGGAGTACAGTGG	71224	C	
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GAM2524	LOC148443	3'	GTCACCCAGGCTGGGATGCAGT	79606	CT	A
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GAM2524	LOC148709	5'	CTCAGGCTGGAGTGCGGTGG	79690		
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			ACTGCACTCCAGCCT	GGA		
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			GGTGACG	GAGGTCGGACCC	CTG	
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GAM2524	LOC149506	3'	CCCAGGCTGTAGTGCAGTGG	85628	C	
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GAM2524	LOC150587	3'	CCCAAGCTGGAATGCGGTGG	86241	C	C		
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GAM2524	LOC150696	3'	GTCACCCAGGCTGGAGTGTAGT	59166				A
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GAM2524 LOC152220 3'	CTCAGGCTGGAGTGCAGTG 86763		
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GAM2524 LOC152282 5'	GTTGCCCAGGCTGGAGTATAGT 81407	C	AG
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GAM2524 LOC154007 3'	TCTACTGGCTGGAGTGCAGTGG 81933	TG_
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GAM2524 LOC154282 5'	GTCGCCAGGTTGGAGTGCAGTG 87412	GA
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GAM2524 LOC154726 5'	GTTGCCCAGGCTGGAGTGCAGT 82013	AG
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GAM2524 LOC154822 3'	CCAGGCTGGAGTGCAATG 87484 C	
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		TG ACTC AGCCTGGG GAC	
		AC TGAG TCGGACCC CTG	
		— — C	
GAM2524	LOC158310 5'	GTCGCCCAGGCTGGAGTGCAGT 88088	A
	GG	CCACTGCACTCCAGCCTGGG GAC	
		GGTGACGTGAGGTCGGACCC CTG	
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GAM2524	LOC158402 5'	GTTGCCCAGGCTGGAGTGCAGT 88152	AG
	GG	CCACTGCACTCCAGCCTGGG AC	
		GGTGACGTGAGGTCGGACCC TG	
		GT	
GAM2524	LOC158476 3'	CCCAGCTTGAGTGCAGTGG 88189	C C
		CCACTGCACTC AGC TGGG	
		GGTGACGTGAG TCG ACCC	
		T —	
GAM2524	LOC158476 3'	GTCGCCCAGGCTGGAGTGCAGT 88203	A
	GG	CCACTGCACTCCAGCCTGGG GAC	

GGTGACGTGAGGTCGGACCC CTG
G
GAM2524 LOC158549 5' GTCTCCCAGGCTGGAGTGCAGT 88228
GG CCACTGCACTCCAGCCTGGGAGAC
|||||
GGTGACGTGAGGTCGGACCCTCTG

GAM2524 LOC158668 3' GTTGCCCAGGCTGGAGTGCAAT 69905 C AG
GG CCA TGCCTCCAGCCTGGG AC
||| ||||| ||
GGT ACGTGAGGTCGGACCC TG
A GT

GAM2524 LOC159184 5' TCTTCTTCTGGAGCAAGT 60683 GCA CCT
ACT CTCCAG GGGAGA
||| ||||| |||||
TGA GAGGTC TCTTCT
AC_ T_

GAM2524 LOC160646 3' GTCACCCAGGCTGGAGTGCAGT 83120 A
GG CCACTGCACTCCAGCCTGGG GAC
|||||
GGTGACGTGAGGTCGGACCC CTG
A

GAM2524 LOC161829 3' GTCACCCAGGCTGGAGTGTAGT 83193 A
GG CCACTGCACTCCAGCCTGGG GAC
|||||
GGTGATGTGAGGTCGGACCC CTG
A

GAM2524 LOC162427 3' GTTGCCCAGGCTGGAGTGCAGT 83229 AG
GG CCACTGCACTCCAGCCTGGG AC
||||| ||
GGTGACGTGAGGTCGGACCC TG
GT

GAM2524 LOC162962 3' CCAGGCTGGAATGCAGTG 83254 C
CACTGCA TCCAGCCTGG
|||||
GTGACGT AGGTCGGACC
A

GAM2524 LOC165552 3' CCCTCGCGGAGTGCGTGG 83378 T A CT
CCAC GCACTCC GC GGG
||| ||||| || |||
GGTG CGTGAGG CG CCC
_ _ CT

GAM2524 LOC169611 3' CCCGGGCTGGAATGCAATGG 83642 C C
CCA TGCA TCCAGCCTGGG
||| ||| |||||
GGT ACGT AGGTCGGGCCC
A A

GAM2524 LOC170409 5' CTCATAAGGGCTGGAGTGCTGT 83743 T GG_
GG CCAC GCACTCCAGCCT GAG
||||| |||

		GGTG CGTGAGGTCGGG	CTC		
		T	AATA		
GAM2524	LOC196047 5'	GTCTCCCAGGCTGGAGTGCA	91162		
		TGCACTCCAGCCTGGGAGAC			
		ACGTGAGGTCGGACCCTCTG			
GAM2524	LOC196074 5'	CTGAGGCTGGAAACAGCGG	88969	A CAC	G
		CC CTG TCCAGCCT GG			
		GG GAC AGGTCGGA TC			
		C AA_ G			
GAM2524	LOC196264 3'	GTCGCCAGGCTGGAGTGCA	88992		GA
	G	CCACTGCACTCCAGCCTGG	GAC		
		GGTGACGTGAGGTCGGACC	CTG		
		G_			
GAM2524	LOC196411 3'	CCTGGGCTGGAATGCAGTGG	89045	C	TG
		CCACTGCA TCCAGCC GG			
		GGTGACGT AGGTCGG CC			
		A GT			
GAM2524	LOC196529 3'	CCCAGGCTGGAGTGCAATG	89129	C	
		CA TGCACTCCAGCCTGGG			
		GT ACGTGAGGTCGGACCC			
		A			
GAM2524	LOC196529 3'	GTTGCCCAGGCTGGAGTGCAAT	89138	C	AG
	G	CA TGCACTCCAGCCTGGG	AC		
		GT ACGTGAGGTCGGACCC	TG		
		A GT			
GAM2524	LOC196812 3'	CCTCTGCGGAGTGTAGTG	91123	A CT	
		CACTGCACTCC GC GGG			
		GTGATGTGAGG CG TCC			
		_ TC			
GAM2524	LOC196957 3'	GTCACCAGGCTGGAGTACAGTG	89193	C	GA
		CACTG ACTCCAGCCTGG	GAC		
		GTGAC TGAGGTCGGACC	CTG		
		A A_			
GAM2524	LOC196961 3'	GTCACCAGGCTGGAGTACAGTG	89206	C	GA
		CACTG ACTCCAGCCTGG	GAC		
		GTGAC TGAGGTCGGACC	CTG		
		A A_			
GAM2524	LOC197138 3'	GTCACCAGGCTGGAGTACAGTG	89255	C	GA
		CACTG ACTCCAGCCTGG	GAC		

		GTGAC TGAGGTCGGACC CTG	
		A A_	
GAM2524	LOC197358 3'	GTCACCCAGGCTGGAGTGCAGT 89441	A
	GG	CCACTGCACTCCAGCCTGGG GAC	
		GGTGACGTGAGGTCGGACCC CTG	
		A	
GAM2524	LOC197358 3'	GTCGCCCAGGCTGGAGTGCAGT 89443	A
	GG	CCACTGCACTCCAGCCTGGG GAC	
		GGTGACGTGAGGTCGGACCC CTG	
		G	
GAM2524	LOC199699 3'	GTCACCCAGGCTGGAGTGCAAT 89681 C	A
	GG	CCA TGCCTCCAGCCTGGG GAC	
		GGT ACGTGAGGTCGGACCC CTG	
		A A	
GAM2524	LOC199699 3'	GTCGCCCAGGCTGGAGTGCAGT 89683	A
	GG	CCACTGCACTCCAGCCTGGG GAC	
		GGTGACGTGAGGTCGGACCC CTG	
		G	
GAM2524	LOC199725 5'	CCTAGGCTGGATTGCAATGG 91414 C C	
		CCA TGCA TCCAGCCTGGG	
		GGT ACGT AGGTCGGATCC	
		A T	
GAM2524	LOC199786 3'	CCCGGGCTGGAGTGCAGTGG 89746	
		CCACTGCACTCCAGCCTGGG	
		GGTGACGTGAGGTCGGGCCC	
GAM2524	LOC199899 5'	TCTCAGGCTGGAGTACAGTGG 91472 C	
		CCACTG ACTCCAGCCTGGGA	
		GGTGAC TGAGGTCGGACTCT	
		A	
GAM2524	LOC199906 3'	TCCAGGCTGGAGTGCAGTGG 89860	
		CCACTGCACTCCAGCCTGGG	
		GGTGACGTGAGGTCGGACCT	
GAM2524	LOC200014 3'	CCAGGCTGGAGTGCAGTGG 89926	
		CCACTGCACTCCAGCCTGG	
		GGTGACGTGAGGTCGGACC	
GAM2524	LOC200093 5'	TCTCCAGCAGGCTAGAGCAG 63777 A _ A C	
		CTGC CT CC GC TGGGAGA	

		GACG GA GG CG ACCCTCT		
		A T A _		
GAM2524	LOC200107 3'	CCAGGCTGGAGTGCAGTG 89982		
		CACTGCACTCCAGCCTGG		
		GTGACGTGAGGTCGGACC		
GAM2524	LOC200169 5'	GTCGTCCAGGCTGGAGTGCAGT 91560		GA
		ACTGCACTCCAGCCTGG GAC		
		TGACGTGAGGTCGGACC CTG		
		TG		
GAM2524	LOC200301 5'	TCGCCCAGGCTGGAGTACAGTG 90156	C	A
	G	CCACTG ACTCCAGCCTGGG GA		
		GGTGAC TGAGGTCGGACCC CT		
		A G		
GAM2524	LOC200310 3'	CCTAGGCTGGAGTGCAGTG 66323		
		CACTGCACTCCAGCCTGGG		
		GTGACGTGAGGTCGGATCC		
GAM2524	LOC200314 3'	CCAGGCTGGGGTGCAGTGG 91594		
		CCACTGCACTCCAGCCTGG		
		GGTGACGTGGGGTCGGACC		
GAM2524	LOC200860 3'	GTCACCCAGGCTGGAGTGCAGT 91756		A
	GG	CCACTGCACTCCAGCCTGGG GAC		
		GGTGACGTGAGGTCGGACCC CTG		
		A		
GAM2524	LOC200860 3'	TCCAGGCTGGAGTGCAATGG 91759	C	
		CCA TGCACTCCAGCCTGGG		
		GGT ACGTGAGGTCGGACCT		
		A		
GAM2524	LOC201164 3'	GTGGCCCAGGCTGGAGTGCAGT 89501		AG
	GG	CCACTGCACTCCAGCCTGGG AC		
		GGTGACGTGAGGTCGGACCC TG		
		GG		
GAM2524	LOC201173 5'	CCCAGGCTGAAGTGCAATG 88677	C	C
		CA TGCACT CAGCCTGGG		
		GT ACGTGA GTCGGACCC		
		A A		
GAM2524	LOC201220 5'	CCCAGGCTGAAGTGCAATG 88712	C	C
		CA TGCACT CAGCCTGGG		

		GT ACGTGA GTCGGACCC		
		A A		
GAM2524	LOC201294 3'	CCAGGCCAGAGTGCAGTGG 89578	CA	
		CCACTGCACTC GCCTGG		
		GGTGACGTGAG CGGACC		
		AC		
GAM2524	LOC201294 3'	GTCGCCCAGGCTGGAGTGCAGT 89595	A	
	GG	CCACTGCACTCCAGCCTGGG GAC		
		GGTGACGTGAGGTCGGACCC CTG		
		G		
GAM2524	LOC201411 3'	CCCAACCTGGAGTGCAATGG 63639	C CC	
		CCA TGCCTCCAG TGGG		
		GGT ACGTGAGGTC ACCC		
		A CA		
GAM2524	LOC201626 3'	GTTGCCCAGGCTGGAGTGCAAT 90438	C AG	
	GG	CCA TGCCTCCAGCCTGGG AC		
		GGT ACGTGAGGTCGGACCC TG		
		A GT		
GAM2524	LOC201627 3'	GTTGCCCAGGCTGGAGTGCAAT 90459	C AG	
	GG	CCA TGCCTCCAGCCTGGG AC		
		GGT ACGTGAGGTCGGACCC TG		
		A GT		
GAM2524	LOC201696 3'	GTTGCCCAGGCTGGAGTGCAAT 63827	C AG	
	GG	CCA TGCCTCCAGCCTGGG AC		
		GGT ACGTGAGGTCGGACCC TG		
		A GT		
GAM2524	LOC201702 5'	GTCACCCAGGCTGGAGTGCAAT 90473	C A	
	GG	CCA TGCCTCCAGCCTGGG GAC		
		GGT ACGTGAGGTCGGACCC CTG		
		A A		
GAM2524	LOC201868 5'	TTGGGGCCAGGTGCAGTGG 90535	CCA G	
		CCACTGCACT GCCT GG		
		GGTGACGTGG CGGG TT		
		AC_ G		
GAM2524	LOC202460 5'	GTCACCAGGCTGGAGTGCAGTG 90676	GA	
	G	CCACTGCACTCCAGCCTGG GAC		
		GGTGACGTGAGGTCGGACC CTG		
		A_		
GAM2524	LOC202908 5'	CAGGCTGGAGTACAGTGG 90714	C	
		CCACTG ACTCCAGCCTG		

		GGTGAC TGAGGTCGGAC		
		A		
GAM2524	LOC202908 5'	GTCACCCAGGCTGGAGTACAGT 90731	C	A
	GG	CCACTG ACTCCAGCCTGGG GAC		
		GGTGAC TGAGGTCGGACCC CTG		
		A A		
GAM2524	LOC202908 5'	TCCAAGGCTGGAGTGTAGT 90733	G	
		ACTGCACTCCAGCCT GGA		
		TGATGTGAGGTCGGA CCT		
		A		
GAM2524	LOC202934 3'	GTCACCAGGCTGGAGTGCAGTG 92048		GA
	G	CCACTGCACTCCAGCCTGG GAC		
		GGTGACGTGAGGTCGGACC CTG		
		A_		
GAM2524	LOC202934 3'	GTCACCCAGGCTGGAGTACAGT 92050	C	A
	GG	CCACTG ACTCCAGCCTGGG GAC		
		GGTGAC TGAGGTCGGACCC CTG		
		A A		
GAM2524	LOC203197 3'	GTCACCCAGGCTGGAGTGCAGT 90816		A
	GG	CCACTGCACTCCAGCCTGGG GAC		
		GGTGACGTGAGGTCGGACCC CTG		
		A		
GAM2524	LOC203297 5'	GTCACCCAGGCTGGAGTGCAAT 75874	C	A
	GG	CCA TGCCTCCAGCCTGGG GAC		
		GGT ACGTGAGGTCGGACCC CTG		
		A A		
GAM2524	LOC203350 3'	GTTGCCCAGGCTGGAGTGCAGT 92247		AG
	GG	CCACTGCACTCCAGCCTGGG AC		
		GGTGACGTGAGGTCGGACCC TG		
		GT		
GAM2524	LOC203369 3'	GTCTCCCAGGCTGGAGTGCAGT 90892		
	GG	CCACTGCACTCCAGCCTGGGAGAC		
		GGTGACGTGAGGTCGGACCCTCTG		
GAM2524	LOC203378 3'	GTCGCCCAGGCTGGAGAGCAGT 92297	A	A
	GG	CCACTGC CTCCAGCCTGGG GAC		
		GGTGACG GAGGTCGGACCC CTG		
		A G		
GAM2524	LOC203397 3'	GTTTTTCAGGCTGGGCACAGTG 90903	CA T	GG
		CACTG C CCAGCCTG AGAC		

		GTGAC G GGTCCGAC TTTG		
		AC _ TT		
GAM2524	LOC204804 3'	GTCACCCAGGCTAGAGTGCAGT 91048	C	A
	GG	CCACTGCACTC AGCCTGGG GAC		
		GGTGACGTGAG TCGGACCC CTG		
		A A		
GAM2524	LOC204804 3'	GTCTCCCAGGCTGGAGTACAGT 91050	C	
	GG	CCACTG ACTCCAGCCTGGGAGAC		
		GGTGAC TGAGGTCGGACCCTCTG		
		A		
GAM2524	LOC219294 3'	GTCACCCAGGCTGGAGTGCAG 94598	A	
		CTGCACTCCAGCCTGGG GAC		
		GACGTGAGGTCGGACCC CTG		
		A		
GAM2524	LOC219295 3'	GTCACCCAGGCTGGAGTGCAG 94589	A	
		CTGCACTCCAGCCTGGG GAC		
		GACGTGAGGTCGGACCC CTG		
		A		
GAM2524	LOC219529 5'	CCCAGCCTGGAGTGCAGTGG 94565	C	
		CCACTGCACTCCAG CTGGG		
		GGTGACGTGAGGTC GACCC		
		C		
GAM2524	LOC219673 5'	CCCAGTCTGGAGTGCAGTGG 94621	C	
		CCACTGCACTCCAG CTGGG		
		GGTGACGTGAGGTC GACCC		
		T		
GAM2524	LOC219673 5'	GTTGCCCAGGCTGGAGGGCAGT 94631	A	AG
	GG	CCACTGC CTCCAGCCTGGG AC		
		GGTGACG GAGGTCGGACCC TG		
		G GT		
GAM2524	LOC219731 5'	GTCATCCAGGCTGGAGTGCAGT 94713	GA	
	GG	CCACTGCACTCCAGCCTGG GAC		
		GGTGACGTGAGGTCGGACC CTG		
		TA		
GAM2524	LOC219735 3'	GTTGCCCAGGCTGGAGTGCAGT 94734	AG	
		ACTGCACTCCAGCCTGGG AC		
		TGACGTGAGGTCGGACCC TG		
		GT		
GAM2524	LOC219894 3'	CCCAGGCTGGAGTGCAGTGG 94902		
		CCACTGCACTCCAGCCTGGG		

GGTGACGTGAGGTCGGACCC

GAM2524 LOC220074 3' CAGGCTGGAGTGCAGTGG 59966
CCACTGCACTCCAGCCTG
|||||||
GGTGACGTGAGGTCGGAC

GAM2524 LOC220074 3' CCCAGCTGGAGTGCAGTGG 59970 C
CCACTGCACTCCAGC TGGG
||||||| |||
GGTGACGTGAGGTCG ACCC

GAM2524 LOC220074 3' GTCACCCAGGCTGGAGTGCAGT 59993 A
GG CCACTGCACTCCAGCCTGGG GAC
||||||| |||
GGTGACGTGAGGTCGGACCC CTG
A

GAM2524 LOC220575 3' GTCACCCAGGCCGGAGTGCAGT 76816 A A
GG CCACTGCACTCC GCCTGGG GAC
||||||| ||| |||
GGTGACGTGAGG CGGACCC CTG
C A

GAM2524 LOC220662 3' CCCAGGCTGGAGTGCAGTGG 92814
CCACTGCACTCCAGCCTGGG
|||||||
GGTGGCGTGAGGTCGGACCC

GAM2524 LOC220662 3' CTTGGCTGGATGCAGTGG 92817 C T
CCACTGCA TCCAGCC GG
||||| ||||| ||
GGTGACGT AGGTCGG TC
T

GAM2524 LOC220739 3' TCAGGGGCCAGAGTGCAGGG 94530 A CA GG
CC CTGCACTC GCCT GA
|| ||||| ||| ||
GG GACGTGAG CGGG CT
AC GA

GAM2524 LOC221035 3' GTCACCAGGCTGGAGTGCAGTG 94782 GA
G CCACTGCACTCCAGCCTGG GAC
||||||| |||
GGTGACGTGAGGTCGGACC CTG
A_

GAM2524 LOC221060 3' GTTGCCCAGGCTGGAGTGCAAT 94836 C AG
GG CCA TGCCTCCAGCCTGGG AC
||| ||||| ||| ||
GGT ACGTGAGGTCGGACCC TG
A GT

GAM2524 LOC221271 3' CTCAGGCTGGAGTGCAATG 93514 C
CA TGCCTCCAGCCTGGG
|| |||||

		GT ACGTGAGGTCGGA		
		A		
GAM2524	LOC221296 3'	GTCGCCCAGGTTGGAGTGCAGT 93616		A
	GG	CCACTGCACTCCAGCCTGGG GAC		
		GGTGACGTGAGGTTGGACCC CTG		
		G		
GAM2524	LOC221641 3'	TTCTAGGCCAGGCACAATGG 95351 C__ A CCA		
		CCA TGC CT GCCTGGGA		
		GGT ACG GA CGGATCTT		
		AAC _ C__		
GAM2524	LOC221663 5'	CCAAGGCTGGAGTGCAGTGG 95459		G
		CCACTGCACTCCAGCCT GG		
		GGTGACGTGAGGTCGGA CC		
		A		
GAM2524	LOC221773 3'	GTCTCCCAGGCTGGAGTGCAGT 92696		
	G	CACTGCACTCCAGCCTGGGAGAC		
		GTGACGTGAGGTCGGACCCTCTG		
GAM2524	LOC221814 5'	GTCGCCAAGCCAGAGTGCAGTG 95559		CA C GA
	G	CCACTGCACTC GC TGG GAC		
		GGTGACGTGAG CG ACC CTG		
		AC A G_		
GAM2524	LOC221960 3'	CCCAGGCTGGAATGCAATGG 92724 C C		
		CCA TGCA TCCAGCCTGGG		
		GGT ACGT AGGTCGGACCC		
		A A		
GAM2524	LOC221964 3'	GTCTCCCAGGCTGGACTGCAGT 95611		C
	GG	CCACTGCA TCCAGCCTGGGAGAC		
		GGTGACGT AGGTCGGACCCTCTG		
		C		
GAM2524	LOC222057 5'	TCCAAGGCTGGAGTGTAGT 94361		G
		ACTGCACTCCAGCCT GGA		
		TGATGTGAGGTCGGA CCT		
		A		
GAM2524	LOC222060 5'	CTCCCAGGTGAGGGCAGTGG 95753		A CA
		CCACTGC CTC GCCTGGGAG		
		GGTGACG GAG TGGACCCTC		
		G _		
GAM2524	LOC222068 3'	GTCGCCCAGGCTGGAGTGCAAT 94279	C	A
	GG	CCA TGCACTCCAGCCTGGG GAC		

		GGT ACGTGAGGTCGGACCC CTG		
		A G		
GAM2524	LOC222070 5'	GTCTCCCAGGCTGGAGTGCAGT 95822		
	GG	CCACTGCACTCCAGCCTGGGAGAC		
		GGTGACGTGAGGTCGGACCCTCTG		
GAM2524	LOC222112 5'	CTCCCAGGATGCTAGTGG 94378	_	CTCCAG
		CCACT GCA CCTGGGAG		
		GGTGA CGT GGACCCTC		
		T A		
GAM2524	LOC222160 3'	TAGGCTGGGCGCAGTGG 95790	A	T
		CCACTGC C CCAGCCTG		
		GGTGACG G GGTCCGAT		
		C		
GAM2524	LOC222189 5'	CTGAGAGCTGGAGTACAG 95834	C	_ G
		CTG ACTCCAGC CT GG		
		GAC TGAGGTCG GA TC		
		A A G		
GAM2524	LOC245771 5'	GTCGCCCAGGCTGGAATGCAGT 94486	C	A
		ACTGCA TCCAGCCTGGG GAC		
		TGACGT AGGTCGGACCC CTG		
		A G		
GAM2524	LOC253142 3'	TCTCCCAAATGCTGAGCAG 99226	ACTC	C
		CTGC CAGC TGGGAGA		
		GACG GTCG ACCCTCT		
		A TAA		
GAM2524	LOC253532 3'	TTCAGGCTGGGTGCAGTGG 97743	T	
		CCACTGCAC CCAGCCTGGG		
		GGTGACGTG GGTCCGACTT		
GAM2524	LOC253612 5'	GTCTCCCAGGCTGGAGTGCGGT 98556		
	GG	CCACTGCACTCCAGCCTGGGAGAC		
		GGTGGCGTGAGGTCGGACCCTCTG		
GAM2524	LOC253664 3'	GTTGCCCAGGCTGGAGTGCAGT 96474		AG
	GG	CCACTGCACTCCAGCCTGGG AC		
		GGTGACGTGAGGTCGGACCC TG		
		GT		
GAM2524	LOC253779 3'	GTCACCCAGGTTGGAGTGCAGT 98926		A
	GG	CCACTGCACTCCAGCCTGGG GAC		

		GGTGACGTGAGGTTGGACCC CTG	
		A	
GAM2524	LOC253805 3'	GTTGCCCAGGCTGGAGTGCAGT 98183	AG
	G	CACTGCACTCCAGCCTGGG AC	
		GTGACGTGAGGTCGGACCC TG	
		GT	
GAM2524	LOC253868 5'	CCCAGGACTCTGAGTGCAG 97320	C_ _
		CTGCACTC AG CCTGGG	
		GACGTGAG TC GGACCC	
		TC A	
GAM2524	LOC254013 3'	CTCCCAGGCTGGAATGCAGTGG 96533	C
		CCACTGCA TCCAGCCTGGGAG	
		GGTGACGT AGGTTCGGACCCTC	
		A	
GAM2524	LOC254013 3'	GTCGTCCAGGCTGGAGTGCAGT 96535	GA
	G	CACTGCACTCCAGCCTGG GAC	
		GTGACGTGAGGTCGGACC CTG	
		TG	
GAM2524	LOC254082 5'	GTCGCCCAAGCTAGAGTGCAGT 98997	C C A
	GG	CCACTGCACTC AGC TGGG GAC	
		GGTGACGTGAG TCG ACCC CTG	
		A A G	
GAM2524	LOC254351 3'	TCCAGGCTGGAGTGCAATGG 96695	C
		CCA TGCACTCCAGCCTGGG	
		GGT ACGTGAGGTCGGACCT	
		A	
GAM2524	LOC254381 5'	CCGGGGCTGGAGCGCAGCGG 99326	A A G
		CC CTGC CTCCAGCCT GG	
		GG GACG GAGGTCGGG CC	
		C C G	
GAM2524	LOC254423 5'	TTTCCTGGGAGCACAAATGG 99304	C CA AGCC
		CCA TG CTCC TGGGAGA	
		GGT AC GAGG GTCCTTT	
		A AC _	
GAM2524	LOC254655 3'	GTCTCCCAGGCTGGAGTGCAGT 97225	
	GG	CCACTGCACTCCAGCCTGGGAGAC	
		GGTGACGTGAGGTCGGACCCTCTG	
GAM2524	LOC254672 3'	GTTGCCCAGGCTGGAGTGCAAT 96299	C AG
	GG	CCA TGCACTCCAGCCTGGG AC	

		GGT ACGTGAGGTCGGACCC TG		
		A GT		
GAM2524	LOC254875 3'	TTCAGGCTGGGTGCAGTGG 97787	T	
		CCACTGCAC CCAGCCTGGG		
		GGTGACGTG GGTTCGGA		
GAM2524	LOC255027 5'	CCGGCTGCTGCAGTGCAGT 96775	C	—
		ACTGCACT CAGC CTGG		
		TGACGTGA GTCG GGCC		
		C TC		
GAM2524	LOC255031 3'	CCCAGGCTAGAGTGCAGTGG 99033	C	
		CCACTGCACTC AGCCTGGG		
		GGTGACGTGAG TCGGACCC		
		A		
GAM2524	LOC255177 3'	GTTGCCCAGGCTGGAGTGCAAT 98400	C	AG
	GG	CCA TGCACCTCCAGCCTGGG AC		
		GGT ACGTGAGGTCGGACCC TG		
		A GT		
GAM2524	LOC255196 5'	CTCAGGCTGGAGTGCAGTG 98955		
		CACTGCACTCCAGCCTGGG		
		GTGACGTGAGGTCGGA		
GAM2524	LOC255326 3'	TCTGGCCGGGTGCAGTGG 98126	T A	TGGG
		CCACTGCAC CC GCC AGA		
		GGTGACGTG GG CGG TCT		
		— C —		
GAM2524	LOC255458 5'	CCAGGCTGGAGTATAGTGG 98932	C	
		CCACTG ACTCCAGCCTGG		
		GGTGAT TGAGGTCGGACC		
		A		
GAM2524	LOC255465 3'	GTCACCAGGCTGGAGTGCAGTG 99123		GA
	G	CCACTGCACTCCAGCCTGG GAC		
		GGTGACGTGAGGTCGGACC CTG		
		A_		
GAM2524	LOC255465 3'	GTCACCCAGGCTGGAGTACAGT 99125	C	A
	GG	CCACTG ACTCCAGCCTGGG GAC		
		GGTGAC TGAGGTCGGACCC CTG		
		A A		
GAM2524	LOC255620 5'	GTCTCCTACCTGCGGATGCAG 98875	C A C	—
		CTGCA TCC GC TGGGAGAC		

	GACGT AGG CG ATCCTCTG		
	— _ TCC		
GAM2524 LOC255919 3'	CCAGGCTGGAGGGCAGTGG 96744	A	
	CCACTGC CTCCAGCCTGG		
	GGTGACG GAGGTCGGACC		
	G		
GAM2524 LOC255975 5'	TCCAAGGCTGGAGTGTAGT 97590	G	
	ACTGCACTCCAGCCT GGA		
	TGATGTGAGGTCGGA CCT		
	A		
GAM2524 LOC256055 5'	TCTCCGTCAAGTGCAGT 97623	CCA CTG	
	ACTGCACT GC GGAGA		
	TGACGTGA TG CCTCT		
	AC_ _		
GAM2524 LOC256158 5'	CCTGTGGCGCTGGAGTGCCTGG 99491	T	_ _
	CCAC GCACTCCAGC CT GGG		
	GGTG CGTGAGGTCG GG TCC		
	_ C TG		
GAM2524 LOC256221 3'	CTCAGGCTGGAGTGCAGTGG 96908		
	CCACTGCACTCCAGCCTGGG		
	GGTGACGTGAGGTCGGA CTC		
GAM2524 LOC256267 5'	CCCAGGTTCTAGAGTGCAGTGG 98609	C_	
	CCACTGCACTC AGCCTGGG		
	GGTGACGTGAG TTGGACCC		
	ATC		
GAM2524 LOC256306 3'	CCCAGGCTGGAGTGCAGAGG 98510	A	
	CC CTGCACTCCAGCCTGGG		
	GG GACGTGAGGTCGGACCC		
	A		
GAM2524 LOC256476 5'	GTCACCCAGGCTGGAGTGCATG 98625	C	A
	CA TGCCTCCAGCCTGGG GAC		
	GT ACGTGAGGTCGGACCC CTG		
	_ A		
GAM2524 LOC256878 5'	TCCAAGGCTGGAGTGTAGT 98691	G	
	ACTGCACTCCAGCCT GGA		
	TGATGTGAGGTCGGA CCT		
	A		
GAM2524 LOC256923 5'	CCTGGGCTGGAGTGCAGTG 96846	TG	
	CACTGCACTCCAGCC GG		

		GTGACGTGAGGTCGG	CC		
		GT			
GAM2524	LOC256940 5'	CCAGTGCTGAAGTGCAGT	98245	C	_
		ACTGCACT CAGC CTGG			
		TGACGTGA GTCG GACC			
		A T			
GAM2524	LOC257054 5'	CCCAGGCTGGAGTGCAGTG	97371		
		CACTGCACTCCAGCCTGGG			
		GTGACGTGAGGTCGGACCC			
GAM2524	LOC257463 3'	TCCCCAGGCTGGAGTGCAATGG	71625	C	A
		CCA TGCACTCCAGCCTGGG GA			
		GGT ACGTGAGGTCGGACCC CT			
		A _			
GAM2524	LOC257465 3'	GTCTTCCAGGCTGGAGTGCAGT	82499		
	GG	CCACTGCACTCCAGCCTGGGAGAC			
		GGTGACGTGAGGTCGGACCTTCTG			
GAM2524	LOC257486 3'	GTTACCCAGATTGGAGTGCAGT	69781	GC	A
	GG	CCACTGCACTCCA CTGGG GAC			
		GGTGACGTGAGGT GACCC TTG			
		TA A			
GAM2524	LOC51031 5'	TCAGGCTGGAGTGCAGTGG	32711		
		CCACTGCACTCCAGCCTGG			
		GGTGACGTGAGGTCGGACT			
GAM2524	LOC51122 3'	CTAAGCTGGGTGCAGTGG	66197	T	C
		CCACTGCAC CCAGC TGG			
		GGTGACGTG GGTCG ATC			
		_ A			
GAM2524	LOC51193 5'	GTTACCCAGGCTGGAGGACAGT	33369	CA	A
	G	CACTG CTCCAGCCTGGG GAC			
		GTGAC GAGGTCGGACCC TTG			
		AG A			
GAM2524	LOC51193 3'	TCCAGGATGGAGTGCAGTGG	33370	G	
		CCACTGCACTCCA CCTGGG			
		GGTGACGTGAGGT GGACCT			
		A			
GAM2524	LOC51219 5'	GTCGCCCAGGCTGGAGTGCAT	33550	C	A
	GG	CCA TGCACTCCAGCCTGGG GAC			

			GGT ACGTGAGGTCGGACCC CTG		
			A G		
GAM2524	LOC51336	3'	GTTACCCAGGCTGGAGTGCAAT 34076	C	A
		GG	CCA TGC ACTCCAGCCTGGG GAC		
			GGT ACGTGAGGTCGGACCC TTG		
			A A		
GAM2524	LOC51622	3'	CCCAGGCTGGAATGCAATGG 32206	C C	
			CCA TGCA TCCAGCCTGGG		
			GGT ACGT AGGTCGGACCC		
			A A		
GAM2524	LOC51696	3'	GTCACCCAGGCTGGAGTGCAAGT 33087		A
			ACTGCACTCCAGCCTGGG GAC		
			TGACGTGAGGTCGGACCC CTG		
			A		
GAM2524	LOC55954	5'	GTCACCCAGGCTGGAGTGTAGT 39399		A
		GG	CCACTGCACTCCAGCCTGGG GAC		
			GGTGATGTGAGGTCGGACCC CTG		
			A		
GAM2524	LOC56181	5'	GTCACCCAGGTTGGAGTGCAAGT 97283		A
		GG	CCACTGCACTCCAGCCTGGG GAC		
			GGTGACGTGAGGTTGGACCC CTG		
			A		
GAM2524	LOC57107	3'	GTTGCCCAGGCTGGAGTGCAAT 40193	C	AG
		GG	CCA TGC ACTCCAGCCTGGG AC		
			GGT ACGTGAGGTCGGACCC TG		
			A GT		
GAM2524	LOC57118	3'	CGGGCTGGGTGCAGTGG 40219	T TG	
			CCACTGCAC CCAGCC G		
			GGTGACGTG GGTCGG C		
			GT		
GAM2524	LOC57146	3'	GTTGCCCAGGCTGGAGTGCAAC 40298	AC	AG
		GG	CC TGC ACTCCAGCCTGGG AC		
			GG ACGTGAGGTCGGACCC TG		
			CA GT		
GAM2524	LOC63929	3'	TCAGGGCTGGGCACAGCGG 42284	A CA T	GG
			CC CTG C CCAGCCT GA		
			GG GAC G GGTCGGG CT		
			C AC_ A_		
GAM2524	LOC81034	3'	GTCGCCCAGGCTGGAGTGCAAGT 48594		A
		GG	CCACTGCACTCCAGCCTGGG GAC		

			GGTGACGTGAGGTCGGACCC CTG		
			G		
GAM2524	LOC89231	3'	GTTGCCCAGGCTGGAGTGCAAT 94301	C	AG
	GG		CCA TGC ACTCCAGCCTGGG AC		
			GGT ACGTGAGGTCGGACCC TG		
			A GT		
GAM2524	LOC89932	3'	CCCAGGCTGGAGTACAATGG 61453	C C	
			CCA TG ACTCCAGCCTGGG		
			GGT AC TGAGGTCGGACCC		
			A A		
GAM2524	LOC89932	3'	GTTGCCCAGGCTGGAGGGCAAT 61473	C A	AG
	GG		CCA TGC CTCCAGCCTGGG AC		
			GGT ACG GAGGTCGGACCC TG		
			A G GT		
GAM2524	LOC90141	3'	CCTAAGCTGGAGTACAGTG 62302	C C	
			CACTG ACTCCAGC TGGG		
			GTGAC TGAGGTCG ATCC		
			A A		
GAM2524	LOC90155	3'	TCCCAGGCTAGAGTGCAGTGG 62369	C	
			CCACTGCACTC AGCCTGGGA		
			GGTGACGTGAG TCGGACCCT		
			A		
GAM2524	LOC90288	3'	CCTAGGCTGGAGTGAAGTGG 62782	G	
			CCACT CACTCCAGCCTGGG		
			GGTGA GTGAGGTCGGATCC		
			A		
GAM2524	LOC90288	3'	GTCACCCAGGCTGGAGTGCAGT 62797		A
	GG		CCACTGCACTCCAGCCTGGG GAC		
			GGTGACGTGAGGTCGGACCC CTG		
			A		
GAM2524	LOC90333	3'	GTCGCCCAGGTTGGAGTGCAGT 62962		A
	GG		CCACTGCACTCCAGCCTGGG GAC		
			GGTGACGTGAGGTTGGACCC CTG		
			G		
GAM2524	LOC90371	5'	GTCACCCAGGCTGGAGTGCAGT 63165		A
	GG		CCACTGCACTCCAGCCTGGG GAC		
			GGTGACGTGAGGTCGGACCC CTG		
			A		
GAM2524	LOC90408	5'	GTTACCCAGGCTGGAGTGCAGT 63346		A
	GG		CCACTGCACTCCAGCCTGGG GAC		

GGTGACGTGAGGTCTGGACCC TTG
A
GAM2524 LOC90459 3' CCAGGATGGAGTGCAGTGG 63552 G
CCACTGCACTCCA CCTGG
||||||| ||||
GGTGACGTGAGGT GGACC
A
GAM2524 LOC90485 3' GTCACCCAGGCTAGAGTGCAGT 63707 C A
GG CCACTGCACTC AGCCTGGG GAC
||||||| ||||| |||
GGTGACGTGAG TCGGACCC CTG
A A
GAM2524 LOC90485 3' GTCGCCCAGGCTGGAGTGCAGT 63708 A
G CACTGCACTCCAGCCTGGG GAC
||||||| ||||| |||
GTGACGTGAGGTCTGGACCC CTG
G
GAM2524 LOC90557 5' CTGAGCCGGGGTGCAGTGG 57855 A CT
CCACTGCACTCC GC GG
||||||| || ||
GGTGACGTGGGG CG TC
C AG
GAM2524 LOC90591 3' GTCACCCAGGCTGGAGTGCAGT 64184 A
GG CCACTGCACTCCAGCCTGGG GAC
||||||| ||||| |||
GGTGACGTGAGGTCTGGACCC CTG
A
GAM2524 LOC90591 3' GTTGCCCAGGCTGGAGTGCAGT 64187 AG
GG CCACTGCACTCCAGCCTGGG AC
||||||| ||||| |||
GGTGACGTGAGGTCTGGACCC TG
GT
GAM2524 LOC90639 3' CAGGCTGGGCGCAGCGG 64406 A A T
CC CTGC C CCAGCCTG
|| ||| | |||||
GG GACG G GGTCGGAC
C C _
GAM2524 LOC90999 3' GTTGCCCAGGCTGGAGTACAGT 65185 C AG
GG CCACTG ACTCCAGCCTGGG AC
||||| ||||| ||||| |||
GGTGAC TGAGGTCTGGACCC TG
A GT
GAM2524 LOC91040 5' TCTCCCAGCAGGTAGAGCAG 65351 A _ A C
CTGC CT CC GC TGGGAGA
||| || || || |||||
GACG GA GG CG ACCCTCT
A T A _
GAM2524 LOC91115 3' CCCAGGCTGGAGTGCTGTGG 65556 T
CCAC GCACTCCAGCCTGGG
||||| ||||| ||||| |||||

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GGTG CGTGAGGTCGGACCC
T
GAM2524 LOC91115 3' GTCACCCAGGCTGGAGTGCAAT 65575 C A
GG CCA TGC ACTCCAGCCTGGG GAC
||| |||
GGT ACGTGAGGTCGGACCC CTG
A A
GAM2524 LOC91115 3' GTTGCCCAGGCTGGAGTGCAAT 65577 C AG
GG CCA TGC ACTCCAGCCTGGG AC
||| |||
GGT ACGTGAGGTCGGACCC TG
A GT
GAM2524 LOC91291 5' GTCGCCCAGACTAGAATGCAGT 66093 C C C A
GG CCA CTG CA TC AG CTGGG GAC
||| ||| ||| |||
GGTGACGT AG TC GACCC CTG
A A A G
GAM2524 LOC91373 3' GTTGCCCAGGCTGGAGTGAAGT 66419 G AG
GG CCA CT CACTCCAGCCTGGG AC
||| ||| ||| |||
GGTGA GTGAGGTCGGACCC TG
A GT
GAM2524 LOC91380 3' TCCAGGCTGGAGTTCAGTGG 66455 C
CCACTG ACTCCAGCCTGGG
||| ||| ||| |||
GGTGAC TGAGGTCGGACCT
T
GAM2524 LOC91445 3' CCCCTCAGTGCAGTGG 61166 CC CCT
CCACTGCACT AG GGG
||| ||| |||
GGTGACGTGA TC CCC
C_ C_
GAM2524 LOC91661 3' CTCAGACCTAGAGTGCAGGG 57211 A C C_
CC CTGCACTC AG CTGGG
|| ||| ||| |||
GG GACGTGAG TC GACTC
_ A CA
GAM2524 LOC91661 3' GTCGGCCAGGCTGGAATGCAAT 57219 C C GA
GG CCA TGCA TCCAGCCTGG GAC
||| ||| ||| ||| |||
GGT ACGT AGGTCGGACC CTG
A A GG
GAM2524 LOC91893 3' CCCAGGCGGGAGTGCAGTGG 68070 A
CCACTGCACTCC GCCTGGG
||| ||| ||| |||
GGTGACGTGAGG CGGACCC
G
GAM2524 LOC92148 5' CCCAGGCTAGAGTGCAGTGG 68873 C
CCACTGCACTC AGCCTGGG
||| ||| ||| ||| |||

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			GGTGACGTGAG TCGGACCC		
			A		
GAM2524	LOC92267	3'	GTCCCCCAGGCTGGAGTGCCGT 69175	T	A
		GG	CCAC GCACTCCAGCCTGGG GAC		
			GGTG CGTGAGGTCGGACCC CTG		
			C C		
GAM2524	LOC92283	3'	CCCAGGCTGGAGTCCAGTGG 69301	C	
			CCACTG ACTCCAGCCTGGG		
			GGTGAC TGAGGTCGGACCC		
			C		
GAM2524	LOC92299	3'	TTAGGCTGGGCGCAGTGG 69376	A T	
			CCACTGC C CCAGCCTGG		
			GGTGACG G GGTCCGATT		
			C _		
GAM2524	LOC92303	3'	CCCGGGCTGGAGTGCAATGG 69389	C	
			CCA TGC ACTCCAGCCTGGG		
			GGT ACGTGAGGTCGGGCC		
			A		
GAM2524	LOC92466	5'	CCCAGGTTCTAGAGTGCAGTGG 69965	C__	
			CCACTGCACTC AGCCTGGG		
			GGTGACGTGAG TTGGACCC		
			ATC		
GAM2524	LOC92609	3'	GTTGCCCAGGCTGGAGTGCATT 73210	C	AG
		G	CA TGC ACTCCAGCCTGGG AC		
			GT ACGTGAGGTCGGACCC TG		
			T GT		
GAM2524	LOC92661	5'	CCCAGGCTGGAGTGCAGTGG 70625		
			CCACTGCACTCCAGCCTGGG		
			GGTGACGTGAGGTCGGACCC		
GAM2524	LOC92697	5'	CCCAGGCTGGAGTGCAGTGG 70808		
			CCACTGCACTCCAGCCTGGG		
			GGTGACGTGAGGTCGGACCC		
GAM2524	LOC92841	3'	GTTGCCCAGGCTGGAGTGCAAT 71263	C	AG
		GG	CCA TGC ACTCCAGCCTGGG AC		
			GGT ACGTGAGGTCGGACCC TG		
			A GT		
GAM2524	LOC93129	3'	CCAGGCTGGAGTGTAGTG 71954		
			CACTGCACTCCAGCCTGG		

GTGATGTGAGGTCGGACC

GAM2524 LOC93132 5' GTCACCAGGCTGGAGGGCAGTG 71998 A GA
G CCACTGC CTCCAGCCTGG GAC
||||| ||||||| |||
GGTGACG GAGGTCGGACC CTG
G A_

GAM2524 LOC93408 5' GTCGCCCAGGCTGGAGCGCAAT 57289 C A A
GG CCA TGC CTCCAGCCTGGG GAC
||| ||| ||||||| |||
GGT ACG GAGGTCGGACCC CTG
A C G

GAM2524 LOC93613 5' TCCTGGCTTCTGGGCACAATGG 73083 C CA C__ T
CCA TG CTC AGCC GGGA
||| || ||| ||| |||
GGT AC GGG TCGG TCCT
A AC TCT _

GAM2525 PIP5K1A 3' TATCCCACCCTGCCTTGATA 14520 A CA C
TATCAAGG AGGG GG GTG
||||| ||| ||| |||
ATAGTTCC TCCC CC TAT
G A_ C

GAM2525 SOX11 3' ACCCACCCCCCCTTG GTA 13308 AA CA C
TATCAAGG GGG GG GT
||||| ||| ||| |||
ATGGTTCC CCC CC CA
CC A_ _

GAM2525 CHL1 3' TGTTACCTTTCCTCAATA 22768 CA CA
TAT AGGAAGGG GGCG
||| |||||| |||
ATA TCCTTTCC TTGT
AC A_

GAM2525 EPB41L1 3' CATTCTGCCCTTCCCTGA 71104 A C
TCA GGAAGGGCAGG GTG
||| ||||||| |||
AGT CCTTCCCGTCT TAC
C _

GAM2525 FLJ00060 3' CATACCCCCTGCCCTCCTCTGA 61741 _ A CGTG
TCA AGGA GGGCAGG ATG
||| ||| |||||| |||
AGT TCCT CCGTCC TAC
C _ CCCA

GAM2525 FLJ10898 5' CACCACAGCCCTTTCTCAATA 60126 CA AGGC
TAT AGGAAGGGC GTG
||| |||||| |||
ATA TCTTTCCCG CAC
AC ACAC

GAM2525 FLJ22557 3' ATCATCCCATCCTTAATA 45581 C A CAGGC
TAT AAGGA GGG GTGAT
||| |||| ||| ||||

		ATA TTCCT CCC TACTA		
		A A _____		
GAM2525	KIAA0574	3' CATCCCCTGCCCTCCCCTGA	69808	A A CGT
		TCA GG AGGGCAGG GATG		
		AGT CC TCCCGTCC CTAC		
		C C C__		
GAM2525	KIAA0632	3' CACCTCAGAAACCCTTCCTTGA	32071	CA__ C
		TCAAGGAAGGG GG GTG		
		AGTTCCTTCCC CT CAC		
		AAAGA C		
GAM2525	KIAA1354	5' CAGTGA CTGCCTTCCCTTGATA	61572	A G _
		TATCAAGG AGGGCAG CG TG		
		ATAGTTCC TTCCGTC GT AC		
		C A G		
GAM2525	MGC20460	5' CACCGCCTCCTACCCTTCTT	54901	C__ _
		AGGAAGGG AGGCG TG		
		TTCTTCCC TCCGC AC		
		ATCC C		
GAM2525	LOC158476	3' CACGCCCGCCCCCCCCATTGA	88186	_ AA_ A
		TCAA GG GGGC GGC GTG		
		AGTT CC CCG CCGCAC		
		A CCC C		
GAM2525	LOC90459	3' CACACCCGCCTAATTTTGT	63550	A_ A C
		CAAGGA GGGC GG GTG		
		GTTTTT TCCG CC CAC		
		AA C A		
GAM2526	SCAMP1	3' GCTAAATAAATATTCTCC	54500	T C
		GGA AATATT ATTTAGC		
		CCT TTATAA TAAATCG		
		C A		
GAM2526	SCAMP1	3' GCTAAATAAATATTCTCC	54501	T C
		GGA AATATT ATTTAGC		
		CCT TTATAA TAAATCG		
		C A		
GAM2526	NX-17	3' TGAATATCAGCCCCTAATA	40706	ATA_
		TATTAGGG ATATTCA		
		ATAATCCC TATAAGT		
		CGAC		
GAM2526	LOC161589	3' GCTAAATGAATATTATCCCTAA	83159	
	TA	TATTAGGGATAATATTCATTTAGC		

ATAATCCCTATTATAAGTAAATCG

GAM2527	BAZ2A	5'	ATGACCTGTTCTCAGCTTACTC	26505	C	GT ACA
	A		TGAG AGGCTGAGA G TCAT			
			ACTC TTCGACTCT T AGTA			
			A TG CC_			
GAM2527	CLTB	3'	TCCTCTCAGTCTACTCA	10218	C	T
			TGAG AGGCTGAGAG GA			
			ACTC TCTGACTCTC CT			
			A _			
GAM2527	CPNE6	3'	CACTCCCTCAGCCTCTCA	21229	C	_
			TGAG AGGCTGA GAGTG			
			ACTC TCCGACT CTCAC			
			_ CC			
GAM2527	ECM2	5'	ATGACACCAAGCAAAGCCTACT	9148	C	GAGAG ACA
	TA		TGAG AGGCT TG TCAT			
			ATTC TCCGA AC AGTA			
			A AACGA CAC			
GAM2527	GRIN2B	3'	ATGATGCCATGGGCCCTCTCA	7729	CA	GAGA A
			TGAG GGCT GTG CATCAT			
			ACTC CCGG TAC GTAGTA			
			TC G__ C			
GAM2527	PCDHB11	3'	ATGCACTCCCCTCAGCCT	38917	_	A
			AGGCTGA GAGTG CAT			
			TCCGACT CTCAC GTA			
			CCC _			
GAM2527	PSMD5	3'	GCATCATATAATCTCAGCTACT	18560	CA	A_____ ACAT
	CA		TGAG GGCTGAG GTG C			
			ACTC TCGACTC TAC G			
			A_ TAATA__ TACA			
GAM2527	VPS41	3'	ATGTACCCCTCAGCCTTCTCA	27687	C	AGTG
			TGAG AGGCTGAG ACAT			
			ACTC TCCGACTC TGTA			
			T CCCA			
GAM2527	CGI-01	3'	TGGA CTCCAGCCTGCCA	32509	A	A GA
			TG GCAGGCTG GAGT CA			
			AC CGTCCGAC CTCA GT			
			_ C G_			
GAM2527	FLJ14431	3'	ATGACACCAACATCTGCTCA	52366	C	AGA A
			TGAGCAGG TG GTG CAT			

		ACTCGTCT AC CAC GTA	
		_ AAC A	
GAM2527	FLJ20006 3'	ATGATGTCACCTATTCCCTCC 34778	CT _
		GG GA GAGTGACATCAT	
		CC CT TTCACTGTAGTA	
		TC TA	
GAM2527	KIAA1546 3'	ATGATGGTGCTACTCAGCCTGC 68495	_ GA
	T	AGCAGGCTGAG AGT CATCAT	
		TCGTCCGACTC TCG GTAGTA	
		A TG	
GAM2527	MGC10812 3'	TCACTCTCTGCCTGCCCA 49480	A T
		TG GCAGGC GAGAGTGA	
		AC CGTCCG CTCTCACT	
		C T	
GAM2527	MGC1842 3'	ATGACACCGACAGCTGCCCA 66248	A G AGA A
		TG GCAG CTG GTG CAT	
		AC CGTC GAC CAC GTA	
		C _ AGC A	
GAM2527	LOC163231 3'	TGTTCACTCTCAACCACTCA 83337	CA C _
		TGAG GG TGAGAGTGA CA	
		ACTC CC ACTCTCACT GT	
		A_ A T	
GAM2527	LOC163231 5'	TGTTCACTCTCAACCACTCA 83338	CA C _
		TGAG GG TGAGAGTGA CA	
		ACTC CC ACTCTCACT GT	
		A_ A T	
GAM2527	LOC163231 5'	TGTTCACTCTCACCACTCA 83339	CA C _
		TGAG GG TGAGAGTGA CA	
		ACTC CC ACTCTCACT GT	
		AC _ T	
GAM2527	LOC245757 3'	ATGGAGCACTCAGCCTGCCA 92455	A A GA
		TG GCAGGCTGAG GT CAT	
		AC CGTCCGACTC CG GTA	
		_ A AG	
GAM2528	AQP6 5'	CATTCCACCCCATACACATGC 9725	CTTTATA A
	A	TGCATGTGT GT GAATG	
		ACGTACACA CA CTTAC	
		TACCCC_ C	
GAM2528	AQP6 5'	CATTCCACCCCATACACATGC 54991	CTTTATA A
	A	TGCATGTGT GT GAATG	

			ACGTACACA	CA CTTAC		
			TACCCC_	C		
GAM2528	CARPX	3'	TACATACAAACACATGCA	39815	CTT	A
			TGCATGTGT	TAT GTA		
			ACGTACACA	ATA CAT		
			AAC	_		
GAM2528	CYP1B1	3'	ACATATAGACACATACA	5442	C	T A
			TG ATGTGTCT	TAT GT		
			AC TACACAGA	ATA CA		
			A	T _		
GAM2528	FACL3	3'	CATTCTCACTAAGACACATG	16739	TTA	_
			CATGTGTCT	TAGT AGAATG		
			GTACACAGA	ATCA TCTTAC		
			_	C		
GAM2528	XRCC2	3'	TTGTTATAAAGACACATGCA	19514		
			TGCATGTGTCTTTATAGTAG			
			ACGTACACAGAAATATTGTT			
GAM2528	ABCA9	3'	GCATTCTACTATAAAGACACAT	55365		
	GCA		TGCATGTGTCTTTATAGTAGAATG			
			ACGTACACAGAAATATCATCTTAC		G	
GAM2528	FPGT	3'	CATTCCATAGGAAGACACA	15179	A	GTA
			TGTGTCTTT	TA GAATG		
			ACACAGAAG	AT CTTAC		
			G	AC_		
GAM2528	KIAA1229	3'	CATGCTGCTATAGAGACACATG	62753		A
	CA		TGCATGTGTCTTTATAGTAG	ATG		
			ACGTACACAGAGATATCGTC	TAC		
			G			
GAM2528	KIAA1344	3'	ACTAGCTAGCACACATGCA	72864	_	TTA
			TGCATGTGT	CT TAGT		
			ACGTACACA	GA ATCA		
			C	TCG		
GAM2528	MGC11349	5'	CTCTAAGAAACACGTGCA	47789	C	A T
			TGCATGTGT	TTT TAG AG		
			ACGTGCACA	AAG ATC TC		
			_	A _		
GAM2528	MGC32104	3'	CATTCCACCATAAAGACA	59065	A	A
			TGTCTTTAT	GT GAATG		

ACAGAAATA CA CTTAC
 C C
 GAM2528 PRO0618 3' ATTATAAGACACACACA 27047 CA T
 TG TGTGTCTT ATAGT
 || ||||| ||||
 AC ACACAGAA TATTA
 AC _
 GAM2528 LOC123264 3' CATCCTAAGCCAGACACATG 74659 TTATAG A
 CATGTGTCT TAG ATG
 ||||| ||||
 GTACACAGA ATC TAC
 CCGA_ C
 GAM2528 LOC142941 3' CTACCAAAGACACATGCA 83765 ATA
 TGCATGTGTCTTT GTAG
 ||||| ||||
 ACGTACACAGAAA CATC
 AC_
 GAM2528 LOC144766 3' CATGCTGCTATAAAGACACATA 77480 C A
 CA TG ATGTGTCTTTATAGTAG ATG
 || ||||| ||||
 AC TACACAGAAATATCGTC TAC
 A G
 GAM2528 LOC145384 3' CATGCTGCTATAAAGACACATG 77713 A
 CA TGCATGTGTCTTTATAGTAG ATG
 ||||| ||||
 ACGTACACAGAAATATCGTC TAC
 G
 GAM2528 LOC145858 3' TCTACACCCAAGACACGCA 78005 AT TATA
 TGC GTGTCTT GTAGA
 || ||||| ||||
 ACG CACAGAA CATCT
 _ CCCA
 GAM2528 LOC148529 5' ACTCAAAAACACATGCA 85319 C AT
 TGCATGTGT TTT AGT
 ||||| ||||
 ACGTACACA AAA TCA
 A C_
 GAM2528 LOC149401 3' GCATTCTACTATAAAGACACAT 80113 _
 GCA TGCATGTGTCTTTATAGTAGAATG C
 ||||| ||||
 ACGTACACAGAAATATCATCTTAC G
 _
 GAM2528 LOC151040 3' CATGCTGCTATAAAGACACATG 80905 A
 CA TGCATGTGTCTTTATAGTAG ATG
 ||||| ||||
 ACGTACACAGAAATATCGTC TAC
 G
 GAM2528 LOC157958 3' CATCCTACTGAAGACACATG 82530 AT A
 CATGTGTCTTT AGTAG ATG
 ||||| ||||
 ||||| ||||

GTACACAGAAG TCATC TAC
 — C
 GAM2528 LOC222252 3' CATGCTGCTATGAAGACACACG 95965 A A
 CA TGC TGTGTCTTTATAGTAG ATG
 ||| |||||
 ACG ACACAGAAGTATCGTC TAC
 C G
 GAM2529 AVPR1A 3' CGGCACTATTTCTGAACAAAGA 7379 CTA GT
 TCTTTG TT GAATAGTGCCG
 ||||| || |||||
 AGAAAC AG TTTATCACGGC
 A__ TC
 GAM2529 FLJ11218 3' CGGCTTTATTCACAACAGC 37757 A T
 GCT TTGTGAATAG GCCG
 ||| |||||
 CGA AACACTTATT CGGC
 C T
 GAM2529 KIAA1229 3' GGCCTATTTCACAATAGCAAAG 62756
 A TCTTTGCTATTGTGAATAGTGCC
 |||||
 AGAAACGATAAACTTATCACGG
 T
 GAM2529 MGC32104 3' GCACTATTCTCAATAGCAAAGA 59067 T
 TCTTTGCTATTG GAATAGTGC
 |||||
 AGAAACGATAAC CTTATCACG
 T
 GAM2529 PCSK7 5' CACTACTCACAGTGAAAG 17519 GC A
 CTTT TATTGTGA TAGTG
 ||| |||||
 GAAA GTGACACT ATCAC
 — C
 GAM2529 PRO2289 5' GCAGTATTCACAATAACCAAGA 38413 TGC G
 TCTT TATTGTGAATA TGC
 ||| |||||
 AGAA ATAACACTTAT ACG
 CCA G
 GAM2529 SCAMP-4 3' GCACCATTTCACAACGGTTGGG 55351 TT TA A
 CT GC TTGTGAAT GTGC
 || || |||||
 GG TG AACACTTA CACG
 GT GC C
 GAM2529 LOC142941 3' CTATTCACAATAGCAAAGA 83766
 TCTTTGCTATTGTGAATAG
 |||||
 AGAAACGATAAACTTATC
 A
 GAM2529 LOC144766 3' GGCCTATTTCACAACAGCAAAG 77482 A
 A TCTTTGCT TTGTGAATAGTGCC
 |||||

			AGAAACGA AACACTTATCACGG		
			C		
GAM2529	LOC145384	3'	GGCACTATTCACAATAGCAAAG 77716		
	A		TCTTTGCTATTGTGAATAGTGCC		
			AGAAACGATAAACTTATCACGG		
GAM2529	LOC147599	3'	GCACTATTTGCAATAGCCAAGA 85163	T	TG
			TCTT GCTATTG AATAGTGC		
			AGAA CGATAAC TTATCACG		
			C GT		
GAM2529	LOC149401	3'	GCACTATTCACAATAACAAAGA 80112	C	
			TCTTTG TATTGTGAATAGTGC		
			AGAAAC ATAACACTTATCACG		
			A		
GAM2529	LOC151040	3'	GGCACTATTCACAATAGCAAAG 80907		
	A		TCTTTGCTATTGTGAATAGTGCC		
			AGAAACGATAAACTTATCACGG		
GAM2529	LOC158046	3'	GCACTG TTCACAACAGCCAAGA 59904	T	A
			TCTT GCT TTGTGAATAGTGC		
			AGAA CGA AACACTTGTACAG		
			C C		
GAM2529	LOC222252	3'	GGCACTATTCACAATAGCAAAG 95967		
	A		TCTTTGCTATTGTGAATAGTGCC		
			AGAAACGATAAACTTATCACGG		
GAM2529	LOC257085	3'	GCACTATTCACAATAGCCAAGA 99214	T	
			TCTT GCTATTGTGAATAGTGC		
			AGAA CGATAAACTTATCACG		
			C		
GAM2529	LOC90509	3'	GCACTATTCACAATAGCCAAGA 63794	T	
			TCTT GCTATTGTGAATAGTGC		
			AGAA CGATAAACTTATCACG		
			C		
GAM2530	ADCY6	3'	GCTCCCCAGTCCCTTGTGAAGC 31589	CC TG	_ C A
	C		GGC T CGAGG AC GG GAGC		
			CCG A GTTCC TG CC CTCG		
			A_GT C A C		
GAM2530	ADCY6	3'	GCTCCCCAGTCCCTTGTGAAGC 40958	CC TG	_ C A
	C		GGC T CGAGG AC GG GAGC		

			CCG A GTTCC TG CC CTCG		
			A_ GT C A C		
GAM2530	DRIL1	5'	CCCCTCCCCG CAGGGGCC 19077	A	CC
			GGCCCTTGCG GGA GG		
			CCGGGGACGC CCT CC		
			C CC		
GAM2530	GSTM3	3'	CTCCCCAACTGAGTTCAAGGGC 68637	__	GA ACC A
	T		GGCCCTTG C GG GG GAG		
			TCGGGAAC G TC CC CTC		
			TT AG AAC _		
GAM2530	LETM1	3'	CCGTCACCCTGGCAAGGGCC 25552	G	AC__
			GGCCCTTGC AGG CGG		
			CCGGGAACG TCC GCC		
			G CACT		
GAM2530	MSX1	5'	CCGGGCCCTCGCAGAGGCC 11710	C	A_
			GGCC TTGCGAGG CCGG		
			CCGG GACGCTCC GGCC		
			A CG		
GAM2530	MYO1C	3'	CTCCTACCCTCAAGGGCC 61863	GC	ACC
			GGCCCTT GAGG GGAG		
			CCGGGAA CTCC CCTC		
			_ CAT		
GAM2530	N33	5'	CCGGGTCCCTCGCAAAGCC 23153	CC	A__
			GGC TTGCGAGG CCGG		
			CCG AACGCTCC GGCC		
			A_ CTG		
GAM2530	NTSR1	3'	GCCCTCCCAGTGCCCAAGGGCC 11856	CGA _ C_	A
			GGCCCTTG GG AC GGAG GC		
			CCGGGAAC CC TG CCTC CG		
			_ G AC C		
GAM2530	SLC9A5	3'	CTGGTCCTCACAGGGGCC 17181	C	
			GGCCCTTG GAGGACCGG		
			CCGGGGAC CTCCTGGTC		
			A		
GAM2530	SLC9A5	3'	CTGGTCCTCACAGGGGCC 60477	C	
			GGCCCTTG GAGGACCGG		
			CCGGGGAC CTCCTGGTC		
			A		
GAM2530	ZNF179	3'	CTGGGCCTCCGCAAGGGCC 24088	_	A
			GGCCCTTGCG AGG CCGG		

		CCGGGAACGC TCC GGTC		
		C G		
GAM2530	C8orf13	3' CTGTCCCGCAAGGGCC 82477	A	C
		GGCCCTTGCG GGAC GG		
		CCGGGAACGC CCTG TC		
		- -		
GAM2530	DKFZp547D155	3' CTGGGCCCCCGCCAGGGCC 70946	T	A A_
		GGCCCT GCG GG CCGG		
		CCGGGA CGC CC GGTC		
		C C CG		
GAM2530	DMWD	3' CTCCCCGGCCAGGGGCC 61550	GCGA	A A
		GGCCCTT GG CCGG GAG		
		CCGGGGA CC GGCC CTC		
		- - C		
GAM2530	FLJ10482	3' GCTCTTTCTGCTACAAGGGCC 36649	CGA_	CCG
		GGCCCTTG GGA GAGAGC		
		CCGGGAAC TCT TTCTCG		
		ATCG -		
GAM2530	FLJ21916	3' CCGGAAACTCACAGGGGCC 43893	C	GA_
		GGCCCTTG GAG CCGG		
		CCGGGGAC CTC GGCC		
		A AAA		
GAM2530	FLJ23231	3' CTGCCCTCCAAGGGGCC 47606	C	AC
		GGCCCTTG GAGG CGG		
		CCGGGAAC CTCC GTC		
		- C_		
GAM2530	GMPPB	5' CCTCCTCGGCAAGGGCC 97443	-	CC
		GGCCCTTGC GAGGA GG		
		CCGGGAACG CTCCT CC		
		G -		
GAM2530	KIAA0599	3' CTCTTTTCCCCAAGGGGCC 77691	CGA	CC
		GGCCCTTG GGA GGAGAG		
		CCGGGAAC CCT TTTCTC		
		C_ -		
GAM2530	KIAA1297	3' CCAGGGCCCCTCGCAGGGCC 72633	T	A_ -
		GGCCCT GCGAGG CC GG		
		CCGGGA CGCTCC GG CC		
		- CCG A		
GAM2530	KLK6	5' GCTCCCCAGCCCGGGGCAGGGG 12425	GA_	ACC A
	C	GCCCTTGC GG GG GAGC		

			CGGGGACG CC CC CTCG		
			GGG CGA C		
GAM2530	LAP3	5'	CCGCCCGCAAGGGCT 32480	A AC	
			GGCCCTTGCG GG CGG		
			TCGGGAACGC CC GCC		
			— —		
GAM2530	MGC11257	3'	CCAGAGCCTCGCAAGGGCC 51353	ACC_	
			GGCCCTTGCGAGG GG		
			CCGGGAACGCTCC CC		
			GAGA		
GAM2530	PTK6	3'	CTCCTGCGCTGACAAGGGCC 21075	CGA AC A	
			GGCCCTTG GG CGG GAG		
			CCGGGAAC TC GTC CTC		
			AG_ GC _		
GAM2530	SARM	3'	GCTCTTTCCCCGCAAGGGCC 31296	A CCG	
			GGCCCTTGCG GGA GAGAGC		
			CCGGGAACGC CCT TTCTCG		
			C _		
GAM2530	SDC3	3'	CCTCCTTCACAGGGCC 28470	_ C CC	
			GGCCCT TG GAGGA GG		
			CCGGGA AC TTCCT CC		
			C _ _		
GAM2530	SLC1A7	3'	CTCTCCAACCCTCCTGAGCAGC 22881	C_ C ACC	
	C		GGC CTTG GAGG GGAGAG		
			CCG GAGT CTCC CCTCTC		
			AC C CAA		
GAM2530	SMOC1	5'	GCTCCCCGCCGCCGCGAGGGCC 42412	A_ AC A	
			GGCCCTTGCG GG CGG GAGC		
			CCGGGAGCGC CC GCC CTCG		
			CG _ C		
GAM2530	SMOC1	3'	GCTCTCCGGACCCCAAAGGGC 42413	GCGA A	
	C		GGCCCTT GG CCGGAGAGC		
			CCGGGAA CC GGCCTCTCG		
			ACCC A		
GAM2530	TTY9	5'	CTCTGGTCCCTCCAAAAGCC 50022	CC C _	
			GGC TTG GAGG ACCGGAG		
			CCG AAC CTCC TGGTCTC		
			AA _ C		
GAM2530	LOC121036	3'	CTGAGCCCTGCAAGGGCC 74482	A AC	
			GGCCCTTGCG GG CGG		

CCGGGAACGT CC GTC
 C GA
 GAM2530 LOC137991 5' GCTTAGGGGTTCTCGCAAGAA 75807 CC _ GGA
 CC GG CTTGCGAGGA CC GAGC
 || ||||| || ||||
 CC GAACGCTCCT GG TTCG
 AA T GGA
 GAM2530 LOC138623 3' CTGGCCCCGCAAGGGCC 76486 A A
 GGCCCTTGCG GG CCGG
 ||||| || ||||
 CCGGGAACGC CC GGTC
 C _
 GAM2530 LOC150370 3' CTCCAGGCCAGCAAGGGCC 86124 GA A _
 GGCCCTTGC GG CC GGAG
 ||||| || || ||||
 CCGGGAACG CC GG CCTC
 A_ _ A
 GAM2530 LOC151610 3' GCTCCTCTACTGCACAAGGGCC 81095 CGA ACC _
 GGCCCTTG GG GGAG AGC
 ||||| || |||| ||||
 CCGGGAAC TC TCTC TCG
 ACG A_ _ C
 GAM2530 LOC152274 5' TCAGTCCTCACAGGGCC 81345 T C C
 GGCCCT G GAGGAC GG
 ||||| | ||||| ||
 CCGGGA C CTCCTG CT
 _A A
 GAM2530 LOC165288 5' GCCCTCCGGCGGACCCTCAAGG 83375 GC A_ _ A
 GCC GGCCCTT GAGG CCGGAG GC
 ||||| ||| ||||| ||
 CCGGGAA CTCC GGCCTC CG
 _ CAGGC C
 GAM2530 LOC223009 5' CTCATGCCTCACAAGGGCC 96033 C ACCG
 GGCCCTTG GAGG GAG
 ||||| ||| |||
 CCGGGAAC CTCC CTC
 A GTA_
 GAM2530 LOC253027 5' GCCCAGCTGCCCCACAGGGGCC 98769 CGA AC AGA_
 GGCCCTTG GG CGG GC
 ||||| || ||| ||
 CCGGGGAC CC GTC CG
 A_ CC GACC
 GAM2530 LOC254100 5' CTCTCCTCCGGTCGCAAGACC 98154 CC _ CC
 GG CTTGCGA GGA GGAGAG
 || ||||| || |||||
 CC GAACGCT CCT CCTCTC
 A_ GG _
 GAM2530 LOC255975 5' CTCATGCTTCACAAGGGCC 97578 C ACCG
 GGCCCTTG GAGG GAG
 ||||| ||| |||

			CCGGGAAC CTTC CTC			
			A GTA_			
GAM2530	LOC57115	3'	CCAACATCCTCCAAGGGCC 40208	C	CC__	
			GGCCCTTG GAGGA GG			
			CCGGGAAC CTCCT CC			
			_ ACAA			
GAM2531	DLEC1	3'	CATCTGGCCCTCCCTTG 24716	A	A C	
			CAAGG AGGGC GG GTG			
			GTTCC TCCCG TC TAC			
			C G _			
GAM2531	DLEC1	3'	CATCTGGCCCTCCCTTG 24728	A	A C	
			CAAGG AGGGC GG GTG			
			GTTCC TCCCG TC TAC			
			C G _			
GAM2531	PIP5K1A	3'	TATCCCACCCTGCCTTGATA 14520	A	CA C	
			TATCAAGG AGGG GG GTG			
			ATAGTTCC TCCC CC TAT			
			G A_ C			
GAM2531	SOX11	3'	ACCCACCCCCCTTG GTA 13308	AA	CA C	
			TATCAAGG GGG GG GT			
			ATGGTTCC CCC CC CA			
			CC A_ _			
GAM2531	CHL1	3'	TGTTACCTTTCCTCAATA 22768	CA	CA	
			TAT AGGAAGGG GGCG			
			ATA TCCTTTCC TTGT			
			AC A_			
GAM2531	EPB41L1	3'	CATTCTGCCCTTCCCTGA 71104	A	C	
			TCA GGAAGGGCAGG GTG			
			AGT CCTTCCCGTCT TAC			
			C _			
GAM2531	FLJ00060	3'	CATACCCCCTGCCCTCCTCTGA 61741	_	A	CGTG
			TCA AGGA GGGCAGG ATG			
			AGT TCCT CCCGTCC TAC			
			C _ CCCA			
GAM2531	FLJ10898	5'	CACCACAGCCCTTTCTCAATA 60126	CA	AGGC	
			TAT AGGAAGGGC GTG			
			ATA TCTTTCCCG CAC			
			AC ACAC			
GAM2531	FLJ22557	3'	ATCATCCCATCCTTAATA 45581	C	A	CAGGC
			TAT AAGGA GGG GTGAT			

ATA TTCCT CCC TACTA
 A A ____
 GAM2531 KIAA0574 3' CATCCCCTGCCCTCCCCTGA 69808 A A CGT
 TCA GG AGGGCAGG GATG
 ||| || ||||| |||
 AGT CC TCCCGTCC CTAC
 C C C__
 GAM2531 KIAA0632 3' CACCTCAGAAACCCTTCCTTGA 32071 CA__ C
 TCAAGGAAGGG GG GTG
 ||||| || |||
 AGTTCCTTCCC CT CAC
 AAAGA C
 GAM2531 KIAA1045 3' CATCACATGTCCTTCC 71599 GGC
 GGAAGGGCA GTGATG
 ||||| |||||
 CCTTCCTGT CACTAC
 A__
 GAM2531 KIAA1354 5' CAGTGA CTGCCTTCCCTTGATA 61572 A G _
 TATCAAGG AGGGCAG CG TG
 ||||| ||||| || ||
 ATAGTTCC TTCCGTC GT AC
 C A G
 GAM2531 MGC20460 5' CACCGCCTCCTACCCTTCTT 54901 C__ _
 AGGAAGGG AGGCG TG
 ||||| |||| ||
 TTCTTCCC TCCGC AC
 ATCC C
 GAM2531 LOC158476 3' CACGCCCGCCCCCCCCATTGA 88186 _ AA_ A
 TCAA GG GGGC GGC GTG
 ||| || ||| |||||
 AGTT CC CCG CCGCAC
 A CCC C
 GAM2531 LOC90459 3' CACACCCGCTAATTTTTG 63550 A_ A C
 CAAGGA GGGC GG GTG
 ||||| ||| || |||
 GTTTTT TCCG CC CAC
 AA C A
 GAM2532 GNAS 3' CAACGACTGCCGTGACATCATT 33914
 CA TGAATGATGTCACGGCAGTCGTTG
 |||||
 ACTTACTACAGTGCCGTCAGCAAC
 GAM2532 HIC2 3' CAACGACTGATCTCTCCATTCA 65860 ATGTCACGG
 TGAATG CAGTCGTTG
 ||||| |||||
 ACTTAC GTCAGCAAC
 CTCTCTA__
 GAM2532 MGC13114 3' CTGCCGTGGCACCCTCA 51392 A A
 TGA TG TGTCACGGCAG
 ||| || |||||

ACT AC ACGGTGCCGTC
 C C
 GAM2532 MGC19556 5' CTGCCGTGACACCCTTCA 54339 TGA
 TGAA TGTCACGGCAG
 ||| |||||
 ACTT ACAGTGCCGTC
 CCC
 GAM2532 NY-BR-1 5' CAACGACTCCTACATCGTCCA 54849 A CAC C
 TG ATGATGT GG AGTCGTTG
 || ||||| || |||||
 AC TGCTACA CC TCAGCAAC
 C T__ _
 GAM2533 ADARB1 5' CCAGGTTGGCGGCCGGGGC 8485 A_ _ G
 GCCCCGGTC CG C TGG
 ||||| || |||
 CGGGGCCGG GT G ACC
 CG T G
 GAM2533 ADARB1 5' CCAGGTTGGCGGCCGGGGC 32337 A_ _ G
 GCCCCGGTC CG C TGG
 ||||| || |||
 CGGGGCCGG GT G ACC
 CG T G
 GAM2533 MYLK2 3' CCACACAGTGGCCGGGGC 53582 GC_
 GCCCCGGTCAC GTGG
 ||||| |||
 CGGGGCCGGTG CACC
 ACA
 GAM2533 PDGFB 5' CCAGCGACGGAGCCGGGGC 12022 CA _ _
 GCCCCGGT CG CG TGG
 ||||| || |||
 CGGGGCCG GC GC ACC
 AG A G
 GAM2533 DKFZP434N1511 5' CCACGCGGGGCAGGCCGGGGC 93054 A____
 GCCCCGGTC CGCGTGG
 ||||| |||||
 CGGGGCCGG GCGCACC
 ACGGG
 GAM2533 FLJ10769 3' CCACGCGTGTGCTGAAGGC 37142 C_ _
 GCC CGGT CACGCGTGG
 || ||| |||||
 CGG GTCG GTGCGCACC
 AA T
 GAM2533 KIAA1404 3' CCACTGAATGACTGGGGC 62684 CG_
 GCCCCGGTCA C GTGG
 ||||| |||||
 CGGGGTCAGT G CACC
 AA T
 GAM2533 LAIR2 5' GCCACGCGTCCGGGGACCGGGG 41478 _____
 C GCCCCGGTC ACGCGTGG C
 ||||| ||||| |

		CGGGGCCAG	TGCGCACC	G		
		GGGCC	_____			
GAM2533	LAIR2	5'	GCCACGCGTCCGGGGACCGGGG	11255	_____	_____
	C		GCCCCGGTC	ACGCGTGG	C	
			CGGGGCCAG	TGCGCACC	G	
			GGGCC	_____		
GAM2533	MGC12904	5'	CCACCGTGGGACCTGAGGC	49161	C _	A _
			GCC C	GGTC CGCG TGG		
			CGG G	CCAG GTGC ACC		
			A T	G C		
GAM2533	MGC15827	3'	CCACATCGGGATCGGGGC	52871	A C _	
			GCCCCGGTC	CG GTGG		
			CGGGGCTAG	GC CACC		
			G TA			
GAM2533	SLC17A3	5'	CCACGCGTCCGGTCGGGGC	22788	GT _	
			GCCCCG C	ACGCGTGG		
			CGGGGC	G TGCGCACC		
			TG CC			
GAM2533	LOC143437	5'	CCACACCAGTGGCCGGGGT	83855	GC _	
			GCCCCGGTCAC	GTGG		
			TGGGGCCGGTG	CACC		
			ACCA			
GAM2533	LOC146745	5'	CCACGTCGCGGCTGGGGC	78690	A _	
			GCCCCGGTC	CG CGTGG		
			CGGGGTCGG	GC GCACC		
			C T			
GAM2533	LOC147080	3'	CCACACTCTGAGACCGGGGC	85028	A C _	
			GCCCCGGTC	CG GTGG		
			CGGGGCCAG	GT CACC		
			A CTCA			
GAM2533	LOC149319	5'	CCATGTGTACACCAGGGC	80069	C C _	
			GCCC GGT	ACGCGTGG		
			CGGG CCA	TGTGTACC		
			A CA			
GAM2533	LOC201175	5'	CCACGCGCGCCTGCCGGGGC	89511	CA _	
			GCCCCGGT	CGCGTGG		
			CGGGGCCG	GCGCACC		
			TCCGC			
GAM2533	LOC201243	5'	CCACGTCGCGGCTGGGGC	89539	A _	
			GCCCCGGTC	CG CGTGG		

			CGGGGTCGG GC GCACC		
			C T		
GAM2533	LOC253531	5'	CCACACCAGTGGCCGGGGT	98221	GC__
			GCCCCGGTCAC GTGG		
			TGGGGCCGGTG CACC		
			ACCA		
GAM2533	LOC92973	5'	CCAGGTTTGAATCGGGGC	71588	_ C G
			GCCCCGGT CA GC TGG		
			CGGGGCTA GT TG ACC		
			A T G		
GAM2534	ABCC3	3'	AATTCTGCAAGGGTTCTTGG	39608	AGAA
			CCAAGGG TTGCAGAATT		
			GGTTCTT AACGTCTTAA		
			GGG_		
GAM2534	AKAP2	3'	GCGAACTCTGCCTTGGAG	24228	G A_
			CTCCAAGG AGA TTGC		
			GAGGTTCC TCT AGCG		
			G CA		
GAM2534	CDH1	3'	CTGCAATCACTTTTTTGGG	16403	AGA
			TCCAAGGG ATTGCAG		
			AGGTTTTT TAACGTC		
			CAC		
GAM2534	SEL1L	3'	TCTGATTTTCCCTAGAGG	18607	CA TG
			CCTC AGGGAGAAT CAGA		
			GGAG TCCCTTTTA GTCT		
			A_ _		
GAM2534	TMEPAI	3'	TTTGTCTCTCTTGAAG	39831	C TT
			CT CAAGGGAGAA GCAGA		
			GA GTTCTCTCTT TGTTT		
			A _		
GAM2534	C20orf152	5'	TTTGTAGTCCTCCCCTTG	55939	_ A
			CAAGGG AG ATTGCAGA		
			GTTCCC TC TGATGTTT		
			C C		
GAM2534	EDG2	3'	GCCGTCCTCTCTTGGAGG	55132	A T
			CCTCCAAGGGAG AT GC		
			GGAGGTTCTCTC TG CG		
			C C		
GAM2534	EDG2	3'	GCCGTCCTCTCTTGGAGG	9173	A T
			CCTCCAAGGGAG AT GC		

GGAGGTTCTCTC TG CG
C C
GAM2534 FLJ10961 3' CTGCCAATTTTCCCCAAAGG 64223 CCAA _
CCT GGGAGAATTG CAG
||| ||||| |||
GGA CCCTTTTAAC GTC
AAC_ C
GAM2534 NLI-IF 3' TTTGCCTCTGCCTTGGAGG 41347 G ATT
CCTCCAAGG AGA GCAGA
||||| ||| ||||
GGAGGTTCC TCT CGTTT
G C_
GAM2534 UBE1C 3' TTTGTAACCTTCCCTTGAAG 15605 C AA
CT CAAGGGAG TTGCAGA
|| ||||| |||||
GA GTTCCCTT AATGTTT
A CC
GAM2534 LOC145678 3' TTCTCAGCCTCCCTTGGAG 84437 AA C
CTCCAAGGGAG TTG AGAA
||||||| ||| ||||
GAGGTTCCCTC GAC TCTT
C_ _
GAM2534 LOC147381 3' AATTCTGCTTATTCTCTC 85139 T_
GGGAGAAT GCAGAATT
||||| |||||
CTCTCTTA CGTCTTAA
TT
GAM2534 LOC162333 5' GCCAGTTTCTCCCTGGAGG 88495 A _
CCTCCA GGGAGAATTG C
||||| ||||| |||
GGAGGT CCCTCTTGAC G
C C
GAM2534 LOC196214 5' TGCAATCCTCCCTCAGGA 91185 A_ A
TCC AGGGAG ATTGCA
||| ||||| |||||
AGG TCCCTC TAACGT
AC C
GAM2534 LOC196478 3' AATTCTGCAATGTTTCCTT 89067 A
AAGGGAG ATTGCAGAATT
||||| ||||| |||||
TTCCTTT TAACGTCTTAA
G
GAM2534 LOC220776 3' TCTGTTTTCTCCCTTGAAG 68937 C TT
CT CAAGGGAGAA GCAGA
|| ||||| |||||
GA GTTCCCTCTT TGTCT
A T_
GAM2535 COL19A1 3' CAGACCAAAGAGTTCACA 10261 T C C
TGT GAGC TTTTGG CTG
||| ||| ||||| |||

		ACA CTTG AGAAACC GAC	
		— — A	
GAM2535	RRM2B	3' CAAAACTTAACATTTA 68431	CC
		TAAATGTTGAG TTTTGT	
		ATTTACAATTC AAAAAC	
		—	
GAM2535	TCF2	3' CAGGCTGGAGCCCAGCATT 22402	A CTT TG
		AATGTTG GC TT GCCTG	
		TTACGAC CG AG CGGAC	
		C — GT	
GAM2535	BY55	3' AGACAGACCTCAACATT 60061	CCTT GC
		AATGTTGAG TTTG CT	
		TTACAACTC AGAC GA	
		C — A —	
GAM2535	C8orf2	3' CAAGTCAGGCTGAACATT 24145	G T —
		AATGTT AGCCT TTTG	
		TTACAA TCGGA GAAC	
		G CT	
GAM2535	FLJ13409	3' CAGGCTTCAACTTAACATTTA 45194	CCTTTTT
		TAAATGTTGAG GGCCTG	
		ATTTACAATTC TCGGAC	
		AACT —	
GAM2535	FLJ22774	3' CTAAAAAGGCTGAACATTTA 64471	G
		TAAATGTT AGCCTTTTTGG	
		ATTTACAA TCGGAAAAATC	
		G	
GAM2535	HSOBRGRP	3' CAGACCAAGAGCCTCAACATTT 34462	C T C
		AAATGTTGAG CTTT GG CTG	
		TTTACAACTC GAGAA CC GAC	
		C — A	
GAM2535	KIAA0435	3' GCTAGAACTCAGCATT 29661	CCT
		AATGTTGAG TTTTGGC	
		TTACGACTC AAGATCG	
		—	
GAM2535	MGC10940	3' CAAAAAGTAAAAAAGCTCAAC 51183	—————
	A	TGTTGAGC CTTTTTG	
		ACAACTCG GAAAAAC	
		AAAAAAT	
GAM2535	ZIN	3' CAGGCCAGGGATTGCCCAACA 26391	A C —
		TGTTG GC TTTTGGCCTG	

		ACAAC CG AGGGACCGGAC	
		C TT	
GAM2535	LOC256158 5'	CAGGCCACTGGAGAGCCCACA 99482	T A _ T_
		TGT G GC CTTT TGGCCTG	
		ACA C CG GAGG ACCGGAC	
		_ C A TC	
GAM2536	BSN 3'	CCACAGTCAAAGAACAGCAGTG 14378	CTG CCA A
	G	CCACTGCTG CT GCTG GG	
		GGTGACGAC GA TGAC CC	
		AA_ AAG A	
GAM2536	BTAF1 3'	CTCAGCTGTACAATAACAG 72871	C C CTC
		CTG TG TG CAGCTGAG	
		GAC AT AC GTCGACTC	
		A A AT_	
GAM2536	CACNA1A 3'	CAGCAGCAGCAGCAGCAG 5353	CCA
		CTGCTGCTGCT GCTG	
		GACGACGACGA CGAC	
		CGA	
GAM2536	CACNA1A 3'	CAGCAGCAGCAGCAGCAG 5354	CCA
		CTGCTGCTGCT GCTG	
		GACGACGACGA CGAC	
		CGA	
GAM2536	CACNA1A 3'	CAGCAGCAGCAGCAGCAG 5355	CCA
		CTGCTGCTGCT GCTG	
		GACGACGACGA CGAC	
		CGA	
GAM2536	CACNA1A 3'	CAGCAGCAGCAGCAGCAG 5356	CCA
		CTGCTGCTGCT GCTG	
		GACGACGACGA CGAC	
		CGA	
GAM2536	CACNA1A 3'	CCGCAGCAGCAGCAGCAGCAG 5358	CCA A
		CTGCTGCTGCT GCTG GG	
		GACGACGACGA CGAC CC	
		CGA G	
GAM2536	CALM1 5'	CAGCAGCAGCAGCAGCAG 23536	CCA
		CTGCTGCTGCT GCTG	
		GACGACGACGA CGAC	
		CGA	
GAM2536	CALM1 5'	CCTTAGCAGCAGCAGCAGCAG 23537	CCA
		CTGCTGCTGCT GCTGAGG	

			GACGACGACGA CGATTCC		
			CGA		
GAM2536	CAPN11	3'	CAGCAGCAGCAGCAG 23911	CCA	
			CTGCTGCTGCT GCTG		
			GACGACGACGA CGAC		
			—		
GAM2536	CSRP1	3'	CCCAGAGGAGCAGCAGCA 15812	AG A	
			TGCTGCTGCTCC CTG GG		
			ACGACGACGAGG GAC CC		
			A_ _		
GAM2536	DNAJB9	5'	CCTCAGCTCTGTGGAGGAGCAG 25605	G	—
	CAGT		ACTGCTGCT CTCCA GCTGAGG		
			TGACGACGA GAGGT CGACTCC		
			G GTCT		
GAM2536	DPH2L1	5'	CTCAGCTGCAGGCAGCA 9111	GCTC	
			TGCTGCT CAGCTGAG		
			ACGACGG GTCGACTC		
			AC_		
GAM2536	DUOX2	3'	CCTCAGCTGGAGGGCTGCAG 26866	T G	
			CTGC GCT CTCCAGCTGAGG		
			GACG CGG GAGGTCGACTCC		
			T _		
GAM2536	EGFL5	5'	CCCAGCAGCAGCAACAGCAG 87911	C CCA A	
			CTGCTG TGCT GCTG GG		
			GACGAC ACGA CGAC CC		
			A CGA _		
GAM2536	EIF2C1	3'	CAGCAGCAGCAGCAGCAG 25184	CCA	
			CTGCTGCTGCT GCTG		
			GACGACGACGA CGAC		
			CGA		
GAM2536	EIF2C1	3'	TCAGCAGCAGCAGCAGCAG 25199	CCA	
			CTGCTGCTGCT GCTGA		
			GACGACGACGA CGACT		
			CGA		
GAM2536	ENG	3'	CCTCGGAGAGCAGCAGCA 5492	CAG	
			TGCTGCTGCTC CTGAGG		
			ACGACGACGAG GGCTCC		
			A_		
GAM2536	ESPN	3'	CCCAGCCCTTGGAACACTGG 49702	C C GCTCCA A	
			CCA TG TGCT GCTG GG		

		GGT AC ACGG CGAC CC	
		C A TTCC__ _	
GAM2536 FBXL7	3'	CTCCCTAGAGCAGCAGCG 25492	C CT
		TGCTGCTGCTC AG GAG	
		GCGACGACGAG TC CTC	
		A C_	
GAM2536 FGFR1	3'	CTCAGGGCTACAGCAGTAG 32372	CT_ AG
		CTGCTGCTG CC CTGAG	
		GATGACGAC GG GACTC	
		ATC _	
GAM2536 FGFR1	3'	CTCAGGGCTACAGCAGTAG 43885	CT_ AG
		CTGCTGCTG CC CTGAG	
		GATGACGAC GG GACTC	
		ATC _	
GAM2536 FGFR1	3'	CTCAGGGCTACAGCAGTAG 7021	CT_ AG
		CTGCTGCTG CC CTGAG	
		GATGACGAC GG GACTC	
		ATC _	
GAM2536 GGT1	3'	CTGTGAGCAGCAGAGCAG 19159	_ _
		CTGCT GCTGCTC CAG	
		GACGA CGACGAG GTC	
		GA T	
GAM2536 GGT1	3'	CTGTGAGCAGCAGAGCAG 26421	_ _
		CTGCT GCTGCTC CAG	
		GACGA CGACGAG GTC	
		GA T	
GAM2536 GGT1	3'	CTGTGAGCAGCAGAGCAG 26437	_ _
		CTGCT GCTGCTC CAG	
		GACGA CGACGAG GTC	
		GA T	
GAM2536 GGT2	3'	CTGTGAGCAGCAGAGCAG 74086	_ _
		CTGCT GCTGCTC CAG	
		GACGA CGACGAG GTC	
		GA T	
GAM2536 GLS	5'	CAGCAGCAGCAGCAG 30462	CCA
		CTGCTGCTGCT GCTG	
		GACGACGACGA CGAC	
		—	
GAM2536 GLS	5'	CAGCAGCAGCAGCAG 30463	CCA
		CTGCTGCTGCT GCTG	

			GACGACGACGA CGAC	
			CGA	
GAM2536	GLS	5'	CAGCAGCAGCAGCAGCAG 30464	CCA
			CTGCTGCTGCT GCTG	
			GACGACGACGA CGAC	
			CGA	
GAM2536	GLS	5'	CAGCAGCAGCAGCAGCAG 30465	CCA
			CTGCTGCTGCT GCTG	
			GACGACGACGA CGAC	
			CGA	
GAM2536	GLS	5'	CAGCAGCAGCAGCAGCAG 30466	CCA
			CTGCTGCTGCT GCTG	
			GACGACGACGA CGAC	
			CGA	
GAM2536	GLS	5'	CAGCAGCAGCAGCAGCAG 30467	CCA
			CTGCTGCTGCT GCTG	
			GACGACGACGA CGAC	
			CGA	
GAM2536	GLS	5'	CAGCAGCAGCAGCAGCAG 30468	CCA
			CTGCTGCTGCT GCTG	
			GACGACGACGA CGAC	
			CGA	
GAM2536	GLS	5'	CAGCAGCAGCAGCAGCAG 30469	CCA
			CTGCTGCTGCT GCTG	
			GACGACGACGA CGAC	
			CGA	
GAM2536	GLS	5'	CAGCAGCAGCAGCAGCAG 30470	CCA
			CTGCTGCTGCT GCTG	
			GACGACGACGA CGAC	
			CGA	
GAM2536	GLS	5'	CAGCAGCAGCAGCAGCAG 30471	CCA
			CTGCTGCTGCT GCTG	
			GACGACGACGA CGAC	
			CGA	
GAM2536	GSPT1	5'	CAGCGGCAGCAGCAGCAG 10882	_ A
			CTGCTGCTGCT CC GCTG	
			GACGACGACGA GG CGAC	
			C _	
GAM2536	HDAC2	5'	CAGCAGCAGCAGCAGCAG 92626	CCA
			CTGCTGCTGCT GCTG	

		GACGACGACGA CGAC	
		CGA	
GAM2536 HDAC2	5'	CAGCAGCAGCAGCAGCAG 92627	CCA
		CTGCTGCTGCT GCTG	
		GACGACGACGA CGAC	
		CGA	
GAM2536 HDAC2	5'	CAGCAGCAGCAGCAGCAG 92628	CCA
		CTGCTGCTGCT GCTG	
		GACGACGACGA CGAC	
		CGA	
GAM2536 HDAC2	5'	CGGCGGCAGCAGCAGCAG 92630	_ A
		CTGCTGCTGCT CC GCTG	
		GACGACGACGA GG CGGC	
		C _	
GAM2536 HS3ST3B1	5'	CCTGGGGAAGAGCAGCAGCAG 21271	CAG G
		CTGCTGCTGCTC CT AGG	
		GACGACGACGAG GG TCC	
		AAG G	
GAM2536 IRS1	5'	CAGCAGCAGCAGCAG 19869	CCA
		CTGCTGCTGCT GCTG	
		GACGACGACGA CGAC	
		—	
GAM2536 IRS1	5'	CAGCAGCAGCAGCAGCAG 19870	CCA
		CTGCTGCTGCT GCTG	
		GACGACGACGA CGAC	
		CGA	
GAM2536 IRS1	5'	CAGCAGCAGCAGCAGCAG 19871	CCA
		CTGCTGCTGCT GCTG	
		GACGACGACGA CGAC	
		CGA	
GAM2536 IRS1	5'	CAGCAGCAGCAGCAGCAG 19872	CCA
		CTGCTGCTGCT GCTG	
		GACGACGACGA CGAC	
		CGA	
GAM2536 IRS1	5'	CAGCAGCAGCAGCAGCAG 19873	CCA
		CTGCTGCTGCT GCTG	
		GACGACGACGA CGAC	
		CGA	
GAM2536 IRS1	5'	CGGCGGCAGCAGCAGCAG 19875	_ A
		CTGCTGCTGCT CC GCTG	

			GACGACGACGA GG CGGC		
			C _		
GAM2536	ISG20	5'	GCTGAGAGCAGCTGCAGT 11021	T _	
			ACTGC GCTGCTC CAGC		
			TGACG CGACGAG GTCG		
			T A		
GAM2536	KCNK3	5'	CCTCCGGGGCAGCAGCAGCGG 11172	A	AGCT
			CC CTGCTGCTGCTCC GAGG		
			GG GACGACGACGGGG CTCC		
			C C__		
GAM2536	KCNK4	3'	CTGGGCAGAGCAGCAGAGCAG 33984	_	CA G
			CTGCT GCTGCTC GCT AG		
			GACGA CGACGAG CGG TC		
			GA A_ G		
GAM2536	LNK	3'	CAGGCTCACAGCAGTGG 19635	C CTCC	GA
			CCACTGCTG TG AGCT G		
			GGTGACGAC AC TCGG C		
			_ _ _ AC		
GAM2536	MAB21L1	5'	CAGCAGCAGCAGCAGCAG 19954		CCA
			CTGCTGCTGCT GCTG		
			GACGACGACGA CGAC		
			CGA		
GAM2536	MAB21L1	5'	CAGCAGCAGCAGCAGCAG 19955		CCA
			CTGCTGCTGCT GCTG		
			GACGACGACGA CGAC		
			CGA		
GAM2536	MAB21L1	5'	CAGCAGCAGCAGCAGCAG 19956		CCA
			CTGCTGCTGCT GCTG		
			GACGACGACGA CGAC		
			CGA		
GAM2536	MAB21L1	5'	CAGCAGCAGCAGCAGCAG 19957		CCA
			CTGCTGCTGCT GCTG		
			GACGACGACGA CGAC		
			CGA		
GAM2536	MAB21L1	5'	CAGCAGCAGCAGCAGCAG 19958		CCA
			CTGCTGCTGCT GCTG		
			GACGACGACGA CGAC		
			CGA		
GAM2536	MAB21L1	5'	CAGCAGCAGCAGCAGCAG 19959		CCA
			CTGCTGCTGCT GCTG		

			GACGACGACGA CGAC		
			CGA		
GAM2536	MAB21L1	5'	CAGCAGCAGCAGCAGCAG	19960	CCA
			CTGCTGCTGCT GCTG		
			GACGACGACGA CGAC		
			CGA		
GAM2536	MAB21L1	5'	CAGCAGCAGCAGCAGCAG	19966	CCA
			CTGCTGCTGCT GCTG		
			GACGACGACGA CGAC		
			CGA		
GAM2536	MAB21L1	5'	CAGCAGCAGCAGCAGCAG	19967	CCA
			CTGCTGCTGCT GCTG		
			GACGACGACGA CGAC		
			CGA		
GAM2536	MAB21L1	5'	CAGCAGCAGCAGCAGCAG	19968	CCA
			CTGCTGCTGCT GCTG		
			GACGACGACGA CGAC		
			CGA		
GAM2536	MAB21L1	5'	CAGCAGCAGCAGCAGCAG	19961	CCA
			CTGCTGCTGCT GCTG		
			GACGACGACGA CGAC		
			CGA		
GAM2536	MAB21L1	5'	CAGCAGCAGCAGCAGCAG	19962	CCA
			CTGCTGCTGCT GCTG		
			GACGACGACGA CGAC		
			CGA		
GAM2536	MAB21L1	5'	CAGCAGCAGCAGCAGCAG	19963	CCA
			CTGCTGCTGCT GCTG		
			GACGACGACGA CGAC		
			CGA		
GAM2536	MAB21L1	5'	CAGCAGCAGCAGCAGCAG	19964	CCA
			CTGCTGCTGCT GCTG		
			GACGACGACGA CGAC		
			CGA		
GAM2536	MAB21L1	5'	CAGCAGCAGCAGCAGCAG	19965	CCA
			CTGCTGCTGCT GCTG		
			GACGACGACGA CGAC		
			CGA		
GAM2536	MAD1L1	3'	CCACAGGGCAGCAGCATG	88869	C CCAG A
			CA TGCTGCTGCT CTG GG		

			GT ACGACGACGG GAC CC	
			— A	
GAM2536	MCCC2	5'	CCCAGCCAGGGAAGCGGCAG 42405	G CA A
			CTGCTGCT CTC GCTG GG	
			GACGGCGA GGG CGAC CC	
			A AC _	
GAM2536	MLH3	3'	CCTCTGAGCAGAGAGCAGCAGC 27660	CA_ _
	AG		CTGCTGCTGCTC GCT GAGG	
			GACGACGACGAG CGA CTCC	
			AGA GT	
GAM2536	MYO1D	3'	CTCAGCCAGGAGCCAGTGG 72245	CTGCT A_
			CCACTG GCTCC GCTGAG	
			GGTGAC CGAGG CGACTC	
			— AC	
GAM2536	NFRKB	5'	CCTCAACTCCCAGCAGCAGT 21606	CTCC C
			ACTGCTGCTG AG TGAGG	
			TGACGACGAC TC ACTCC	
			CC_ A	
GAM2536	NPPB	5'	CAGCAGAAGCAGCAGCAG 11826	CCA
			CTGCTGCTGCT GCTG	
			GACGACGACGA CGAC	
			AGA	
GAM2536	NPPB	5'	CAGCAGCAGCAGCAGCAG 11827	CCA
			CTGCTGCTGCT GCTG	
			GACGACGACGA CGAC	
			CGA	
GAM2536	NPPB	5'	CAGCAGCAGCAGCAGCAG 11828	CCA
			CTGCTGCTGCT GCTG	
			GACGACGACGA CGAC	
			CGA	
GAM2536	NPPB	5'	CCAGCAGCAGCAGCAG 11829	CCA A
			CTGCTGCTGCT GCTG G	
			GACGACGACGA CGAC C	
			— G	
GAM2536	PACSIN1	3'	CCTACGGCAAAGCCAGCAACAG 93880	C _ CCA _
	T		ACTG TGCTG CT GCTG AGG	
			TGAC ACGAC GA CGGC TCC	
			A C AA_ A	
GAM2536	PDYN	3'	CAGCAGCAGCAGCAGCAG 44583	CCA
			CTGCTGCTGCT GCTG	

			GACGACGACGA CGAC	
			CGA	
GAM2536 PDYN	3'	CAGCAGCAGCAGCAGCAG	44584	CCA
		CTGCTGCTGCT GCTG		
		GACGACGACGA CGAC		
		CGA		
GAM2536 PDYN	3'	CAGCGGCAGCAGCAGCAG	44585	_ A
		CTGCTGCTGCT CC GCTG		
		GACGACGACGA GG CGAC		
		C _		
GAM2536 PIM1	5'	CAGCAGCAGCAGCAGCAG	92678	CCA
		CTGCTGCTGCT GCTG		
		GACGACGACGA CGAC		
		CGA		
GAM2536 PIM1	5'	CAGCAGCAGCAGCAGCAG	92679	CCA
		CTGCTGCTGCT GCTG		
		GACGACGACGA CGAC		
		CGA		
GAM2536 PIM1	5'	CAGCAGCAGCAGCAGCAG	92680	CCA
		CTGCTGCTGCT GCTG		
		GACGACGACGA CGAC		
		CGA		
GAM2536 PIM1	5'	CAGCAGCAGCAGCAGCAG	92681	CCA
		CTGCTGCTGCT GCTG		
		GACGACGACGA CGAC		
		CGA		
GAM2536 PIM1	5'	CCGGCAGCAGCAGCAGCAG	92682	CCA A_
		CTGCTGCTGCT GCTG GG		
		GACGACGACGA CGAC CC		
		CGA GG		
GAM2536 POU4F1	5'	CAGCAGGAGCAGCAGCAG	21761	A
		CTGCTGCTGCTCC GCTG		
		GACGACGACGAGG CGAC		
		A		
GAM2536 PSAP	3'	TCTCAGTTGAACAAAGCAGCA	69887	GCTC_
		TGCTGCT CAGCTGAGG		
		ACGACGA GTTGACTCT		
		AACA		
GAM2536 PTP4A2	3'	CCGTCAAAGGAGCAGCAGCA	14439	AGC _
		TGCTGCTGCTCC TGA GG		

ACGACGACGAGG ACT CC
 AA_ G
 GAM2536 PTPN7 5' CCTGGGAGTGGAACAGCAGCAG 55460 C C G_ G
 TTA C ACTGCTGCTG TCCA CT AGG
 | ||||| ||| || |||
 A TGACGACGAC AGGT GG TCC
 T A GA G
 GAM2536 RFPL2 5' CCTCAGCTCAGAGCACAGTG 22759 CTGC C_
 CACTG TGCTC AGCTGAGG
 |||| |||| |||||
 GTGAC ACGAG TCGACTCC
 _____ AC
 GAM2536 RFPL3 5' CCTCAGCTCAGAGCACAGTG 22757 CTGC C_
 CACTG TGCTC AGCTGAGG
 |||| |||| |||||
 GTGAC ACGAG TCGACTCC
 _____ AC
 GAM2536 SERPINB8 5' CAGCAGCAGCAGCAGCAG 12073 CCA
 CTGCTGCTGCT GCTG
 ||||| |||
 GACGACGACGA CGAC
 CGA
 GAM2536 SERPINB8 5' CGGCGGCAGCAGCAGCAG 12074 _ A
 CTGCTGCTGCT CC GCTG
 ||||| || |||
 GACGACGACGA GG CGGC
 C _
 GAM2536 SLC11A3 5' CCTCAGCGAGAGCAGCAGCAG 28166 CA
 CTGCTGCTGCTC GCTGAGG
 ||||| |||||
 GACGACGACGAG CGACTCC
 AG
 GAM2536 SOX4 3' CCCGTTGGAAGCGCAGCAGCGG 13303 A T _ T A
 CC CTGCTGC GCT CCAGC G GG
 || ||||| || |||| | ||
 GG GACGACG CGA GGTTG C CC
 C _ A _ _
 GAM2536 STC1 5' CAGCAGCAGCAGCAGCAGCGG 13455 A CCA
 CC CTGCTGCTGCT GCTG
 || ||||| |||
 GG GACGACGACGA CGAC
 C CGA
 GAM2536 STC1 5' CAGCAGCAGCAGCAGCAGCGG 13456 A CCA
 CC CTGCTGCTGCT GCTG
 || ||||| |||
 GG GACGACGACGA CGAC
 C _
 GAM2536 STC1 3' CCAGCAGCAGCAGCAGCAG 13457 CCA A
 CTGCTGCTGCT GCTG G
 ||||| ||| |

			GACGACGACGA CGAC C		
			CGA _		
GAM2536	STC1	5'	CGGCAGCAGCAGCAGCAGCGG 13458	A	CCA
			CC CTGCTGCTGCT GCTG		
			GG GACGACGACGA CGGC		
			C CGA		
GAM2536	STC1	5'	CGGCGGCAGCAGCAGCAG 13459	_ A	
			CTGCTGCTGCT CC GCTG		
			GACGACGACGA GG CGGC		
			C _		
GAM2536	STC1	5'	CTGCAGCAGCAGCAGCAGCAG 13460	CCA	_
			CTGCTGCTGCT GCTG AG		
			GACGACGACGA CGAC TC		
			CGA G		
GAM2536	TRPV4	3'	CCCAGCTGGAACCTGGCAGAGG 61329	A	GCTGC A
			CC CTGCT TCCAGCTG GG		
			GG GACGG AGGTCGAC CC		
			A TCCA_ _		
GAM2536	WEE1	5'	CCCAGCACCGGAGGAGCAGCG 14107	G	A_ A
			TGCTGCT CTCC GCTG GG		
			GCGACGA GAGG CGAC CC		
			G CCA _		
GAM2536	ACTR3	5'	CGGCGGCAGCAGCAGCAG 20365	_ A	
			CTGCTGCTGCT CC GCTG		
			GACGACGACGA GG CGGC		
			C _		
GAM2536	ADAR3	5'	CCTCAAGCTTCGCAGCAGCGGC 38633	A	TCC _
	GG		CC CTGCTGCTGC AGCT GAGG		
			GG GGCGACGACG TCGA CTCC		
			C CT_ A		
GAM2536	AEBP1	3'	CTCAAGCTACAGCAGCAG 8520	CTCC	_
			CTGCTGCTG AGCT GAG		
			GACGACGAC TCGA CTC		
			A_ A		
GAM2536	AMOT	5'	CAGCAACAGCAGCAGCAG 56535	CCA	
			CTGCTGCTGCT GCTG		
			GACGACGACGA CGAC		
			CAA		
GAM2536	AMOT	5'	CAGCAGCAGCAGCAG 56536	CCA	
			CTGCTGCTGCT GCTG		

GACGACGACGA CGAC

GAM2536 AMOT 5' CCTGAGTCAGCAGCAGCAG 56540 CCA G
CTGCTGCTGCT GCT AGG
||||||| |||
GACGACGACGA TGA TCC
C__ G

GAM2536 BICD2 3' CCTCAACTAACCCAGCAGCAGC 70909 A CTCC C
GG CC CTGCTGCTG AG TGAGG
|| ||||| || |||||
GG GACGACGAC TC ACTCC
C CCAA A

GAM2536 BIKE 3' CAGCAACAGCAACAGCAGCAG 34590 ____ CCA
CTGCTGCT GCT GCTG
||||| ||| |||
GACGACGA CGA CGAC
CAA CAA

GAM2536 BIKE 3' CAGCAACAGCAACAGCAGCAG 34591 ____ CCA
CTGCTGCT GCT GCTG
||||| ||| |||
GACGACGA CGA CGAC
CAA CAA

GAM2536 BIKE 3' CAGCAACAGCAGCAGCAG 34592 CCA
CTGCTGCTGCT GCTG
||||||| |||
GACGACGACGA CGAC
CAA

GAM2536 BIKE 3' CAGCAACAGCAGCAGCAG 34593 CCA
CTGCTGCTGCT GCTG
||||||| |||
GACGACGACGA CGAC
CAA

GAM2536 BIKE 3' CAGCAACAGCAGCAGCAG 34594 CCA
CTGCTGCTGCT GCTG
||||||| |||
GACGACGACGA CGAC
CAA

GAM2536 BIKE 3' CAGCAACAGCAGCAGCAG 34595 CCA
CTGCTGCTGCT GCTG
||||||| |||
GACGACGACGA CGAC
CAA

GAM2536 BIKE 3' CAGCAGCAGCAGCAG 34596 CCA
CTGCTGCTGCT GCTG
||||||| |||
GACGACGACGA CGAC

GAM2536 BIKE 3' CAGCAGCAGCAGCAG 34597 CCA
CTGCTGCTGCT GCTG
||||||| |||

		GACGACGACGA CGAC	
		CGA	
GAM2536 BIKE	3'	CAGCAGCAGCAGCAGCAG 34598	CCA
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		GACGACGACGA CGAC	
		CGA	
GAM2536 BIKE	3'	CAGCAGCAGCAGCAGCAG 34599	CCA
		CTGCTGCTGCT GCTG	
		GACGACGACGA CGAC	
		CGA	
GAM2536 BIKE	3'	CAGCAGCAGCAGCAGCAG 34600	CCA
		CTGCTGCTGCT GCTG	
		GACGACGACGA CGAC	
		CGA	
GAM2536 BIKE	3'	CAGCAGCAGCAGCAGCAG 34601	CCA
		CTGCTGCTGCT GCTG	
		GACGACGACGA CGAC	
		CGA	
GAM2536 BIKE	3'	CAGCAGCAGCAGCAGCAG 34602	CCA
		CTGCTGCTGCT GCTG	
		GACGACGACGA CGAC	
		CGA	
GAM2536 BIKE	3'	CCTCACCAGCAGCAGCAGCAGC 34606	CCA ____
AG		CTGCTGCTGCT GCT GAGG	
		GACGACGACGA CGA CTCC	
		CGA CCA	
GAM2536 C14orf4	5'	CAGCAACAGCAACAGCAGCAG 67898	____ CCA
		CTGCTGCT GCT GCTG	
		GACGACGA CGA CGAC	
		CAA CAA	
GAM2536 C14orf4	5'	CAGCAACAGCAGCAGCAG 67899	CCA
		CTGCTGCTGCT GCTG	
		GACGACGACGA CGAC	
		CAA	
GAM2536 C14orf4	5'	CAGCAACAGCAGCAGCAG 67900	CCA
		CTGCTGCTGCT GCTG	
		GACGACGACGA CGAC	
		CAA	
GAM2536 C14orf4	5'	CAGCAACAGCAGCAGCAG 67901	CCA
		CTGCTGCTGCT GCTG	

			GACGACGACGA CGAC		
			CAA		
GAM2536	C14orf4	5'	CAGCAACAGCAGCAGCAG	67902	CCA
			CTGCTGCTGCT GCTG		
			GACGACGACGA CGAC		
			CAA		
GAM2536	C14orf4	5'	CAGCAGCAGCAGCAG	67903	CCA
			CTGCTGCTGCT GCTG		
			GACGACGACGA CGAC		
			—		
GAM2536	C14orf4	5'	CAGCAGCAGCAGCAG	67904	CCA
			CTGCTGCTGCT GCTG		
			GACGACGACGA CGAC		
			—		
GAM2536	C14orf4	5'	CAGCAGCAGCAGCAGCAG	67905	CCA
			CTGCTGCTGCT GCTG		
			GACGACGACGA CGAC		
			CGA		
GAM2536	C14orf4	5'	CAGCAGCAGCAGCAGCAG	67906	CCA
			CTGCTGCTGCT GCTG		
			GACGACGACGA CGAC		
			CGA		
GAM2536	C14orf4	5'	CAGCAGCAGCAGCAGCAG	67907	CCA
			CTGCTGCTGCT GCTG		
			GACGACGACGA CGAC		
			CGA		
GAM2536	C14orf4	5'	CAGCAGCAGCAGCAGCAG	67908	CCA
			CTGCTGCTGCT GCTG		
			GACGACGACGA CGAC		
			CGA		
GAM2536	C14orf4	5'	CAGCAGCAGCAGCAGCAG	67909	CCA
			CTGCTGCTGCT GCTG		
			GACGACGACGA CGAC		
			CGA		
GAM2536	C14orf4	5'	CAGCAGCAGCAGCAGCAG	67910	CCA
			CTGCTGCTGCT GCTG		
			GACGACGACGA CGAC		
			CGA		
GAM2536	C14orf4	5'	CAGCAGCAGCAGCAGCAG	67911	CCA
			CTGCTGCTGCT GCTG		

		GACGACGACGA CGAC	
		CGA	
GAM2536	C14orf4	5' CAGCAGCAGCAGCAGCAG 67912	CCA
		CTGCTGCTGCT GCTG	
		GACGACGACGA CGAC	
		CGA	
GAM2536	C20orf151	3' CCTCAGCTGAACCCACAGTG 90093	C CTGCTC
		CACTG TG CAGCTGAGG	
		GTGAC AC GTCGACTCC	
		_ CCAA _	
GAM2536	C5orf4	5' CCTGCAGCAGAGCCGCAGCAG 51489	T CA _
		CTGCTGC GCTC GCTG AGG	
		GACGACG CGAG CGAC TCC	
		C A_ G	
GAM2536	CAPN6	5' CAGCAGCAGCAGCAGCAG 27391	CCA
		CTGCTGCTGCT GCTG	
		GACGACGACGA CGAC	
		CGA	
GAM2536	CAPN6	5' CAGCAGCAGCAGCAGCAG 27392	CCA
		CTGCTGCTGCT GCTG	
		GACGACGACGA CGAC	
		CGA	
GAM2536	CAPN6	5' CAGCAGCAGCAGCAGCAG 27393	CCA
		CTGCTGCTGCT GCTG	
		GACGACGACGA CGAC	
		CGA	
GAM2536	CAPN6	5' CAGCAGCAGCAGCAGCAG 27394	CCA
		CTGCTGCTGCT GCTG	
		GACGACGACGA CGAC	
		CGA	
GAM2536	CAPN6	5' CAGCAGCAGCAGCAGCAG 27395	CCA
		CTGCTGCTGCT GCTG	
		GACGACGACGA CGAC	
		CGA	
GAM2536	CAPN6	5' CAGCAGCAGCAGCAGCAG 27396	CCA
		CTGCTGCTGCT GCTG	
		GACGACGACGA CGAC	
		CGA	
GAM2536	CAPN6	5' CAGCAGCAGCAGCAGCAG 27397	CCA
		CTGCTGCTGCT GCTG	

			GACGACGACGA CGAC		
			CGA		
GAM2536	CAPN6	5'	CGGCAGCAGCAGCAGCAG	27400	CCA
			CTGCTGCTGCT GCTG		
			GACGACGACGA CGGC		
			CGA		
GAM2536	CDIPT	3'	CCCAGCCAGAGCAAGCTTGG	21973	CT GC CA A
			CCA GCT TGCTC GCTG GG		
			GGT CGA ACGAG CGAC CC		
			T_ _ AC _		
GAM2536	CIZ1	5'	CAGCAACAGCAGCAGCAG	25094	CCA
			CTGCTGCTGCT GCTG		
			GACGACGACGA CGAC		
			CAA		
GAM2536	CLIC4	5'	CCGGAGCAGAAGCAGCAGCAG	26526	CCA GA
			CTGCTGCTGCT GCT GG		
			GACGACGACGA CGA CC		
			AGA GG		
GAM2536	DCNP1	5'	CTGATGAAAAGCAGCAGTG	56459	GC _
			CACTGCTGCT TC CAG		
			GTGACGACGA AG GTC		
			AA TA		
GAM2536	DKFZP434F0318	3'	CTTTTGGAAGCAGCAACAGT	48755	C _ CT
			ACTG TGCTGCT CCAG GAG		
			TGAC ACGACGA GGTT TTC		
			A A _		
GAM2536	DKFZp434F1719	3'	CAGCCAGCAGCAGTGG	51013	CTCCA
			CCACTGCTGCTG GCTG		
			GGTGACGACGAC CGAC		

GAM2536	DKFZp434G179	3'	CCCAGATGAAGAGCAGCAACA	80890	C _ G A
			TG TGCTGCTC CA CTG GG		
			AC ACGACGAG GT GAC CC		
			A AA A _		
GAM2536	DKFZP586M0122	3'	CAGTACAGAGCACAGCAG	31858	C CA_
			CTGCTG TGCTC GCTG		
			GACGAC ACGAG TGAC		
			_ ACA		
GAM2536	DKFZp762O076	5'	CAGCAGAGGCAGCAGCAGT	73956	CCA
			ACTGCTGCTGCT GCTG		

		TGACGACGACGG CGAC		
		AGA		
GAM2536	DSCR1L1	3' CCCAGAATGCAGCAGCAGCTG	20625	_ TCCAG A
		CA CTGCTGCTGC CTG GG		
		GT GACGACGACG GAC CC		
		C TAA__ _		
GAM2536	EFA6R	3' CCTTGAGGAGCTGCAGCAGT	31634	T AGC
		ACTGCTGC GCTCC TGAGG		
		TGACGACG CGAGG GTTCC		
		T A__		
GAM2536	FLJ10748	5' CAGAGGCAGCAGCAGTGG	37095	CCAG
		CCACTGCTGCTGCT CTG		
		GGTGACGACGACGG GAC		
		A__		
GAM2536	FLJ10898	5' CTGAGAACAGCAGCAGCAG	60132	CCAG G
		CTGCTGCTGCT CT AG		
		GACGACGACGA GA TC		
		CAA_ G		
GAM2536	FLJ10925	5' CCCAGCCGGGCGCAGCAGC	37412	_ A A
		GCTGCTGC TCC GCTG GG		
		CGACGACG GGG CGAC CC		
		C C _		
GAM2536	FLJ12505	5' CCAGCAGCAGCAGCAGCAG	45712	CCA A
		CTGCTGCTGCT GCTG G		
		GACGACGACGA CGAC C		
		CGA _		
GAM2536	FLJ13111	3' CTGAGCACCCAGCAGTGG	47627	C C
		CCACTGCTG TGCTC AG		
		GGTGACGAC ACGAG TC		
		C _		
GAM2536	FLJ20174	3' CTGGTAACAGCAGCAGCAG	35192	_____
		CTGCTGCTGCT CCAG		
		GACGACGACGA GGTC		
		CAAT		
GAM2536	FLJ20320	3' CCCAGCTAGGAGCAGCAGCA	35419	_ A
		TGCTGCTGCTCC AGCTG GG		
		ACGACGACGAGG TCGAC CC		
		A _		
GAM2536	FLJ20689	3' CCTCTTCAAACACAGCAGTGG	35960	C CTCCAGCT
		CCACTGCTG TG GAGG		

GGTGACGAC AC CTCC
_ AACTTT_
GAM2536 FLJ20689 3' CCTCTTTCAAACACAGCAGTGG 36209 C CTCCAGCT
CCACTGCTG TG GAGG
||||||| || ||||
GGTGACGAC AC CTCC
_ AACTTT_
GAM2536 FLJ21615 3' CCTCAGCTGGGATGAGGAGTG 50807 G GCTG T
CACT CT C CCAGCTGAGG
|||| || | |||||
GTGA GA G GGTCTGACTCC
G GTA_
GAM2536 FLJ22582 3' CAGCGACAGCAGCAACAGCAG 47454 _ CCA
CTGCT GCTGCT GCTG
|||| ||||| ||||
GACGA CGACGA CGAC
CAA CAG
GAM2536 FLJ22688 3' CCCAGAATGTAAACAGCAGCAG 47822 _ CTCCAG_ A
ATG CA CTGCTGCTG CTG GG
|| ||||| ||||
GT GACGACGAC GAC CC
A AAATGTAA _
GAM2536 FLJ22940 5' CCGGGGCAGAACAGCAGCATGG 44997 C C CA GA
CCA TGCTGCTG TC GCT GG
|| ||||| || ||||
GGT ACGACGAC AG CGG CC
_ A A_ GG
GAM2536 GGTL4 3' CTGTGAGCAGCAGAGCAG 55945 _ _
CTGCT GCTGCTC CAG
|||| ||||| ||||
GACGA CGACGAG GTC
GA T
GAM2536 GGTLA4 3' CTGTGAGCAGCAGAGCAG 56049 _ _
CTGCT GCTGCTC CAG
|||| ||||| ||||
GACGA CGACGAG GTC
GA T
GAM2536 HUMAGCGB 5' CGGCGAAGTAGCAGCAGCAG 26131 CCA_
CTGCTGCTGCT GCTG
||||||| ||||
GACGACGACGA CGGC
TGAAG
GAM2536 KIAA0014 3' CAGTAGTAGCAGCAGCAGCGG 28538 A CCA
CC CTGCTGCTGCT GCTG
|| ||||| ||||
GG GACGACGACGA TGAC
C TGA
GAM2536 KIAA0339 3' CCTCTGACAGCAGCAGCAGCAG 71962 CCA _
CTGCTGCTGCT GCT GAGG
||||||| || ||||

		GACGACGACGA CGA CTCC	
		___ CAGT	
GAM2536 KIAA0543	3'	CCCAGCTCTGCTGCAGGCAGTG 69519	_ T TCC A
	G	CCACTGC TGC GC AGCTG GG	
		GGTGACG ACG CG TCGAC CC	
		G T TC_ _	
GAM2536 KIAA0987	5'	CCCAAGGAGGAGCAGCAGCAG 25506	AG GA
		CTGCTGCTGCTCC CT GG	
		GACGACGACGAGG GA CC	
		AG AC	
GAM2536 KIAA1093	3'	CCTTTTTTGGAACAGCAGCAG 67145	C CT
		CTGCTGCTG TCCAG GAGG	
		GACGACGAC AGGTT TTCC	
		A TT	
GAM2536 KIAA1094	3'	CAGTGCAGCAGCAGTG 30479	TCCA
		CACTGCTGCTGC GCTG	
		GTGACGACGACG TGAC	

GAM2536 KIAA1163	3'	CCCAGCTGGGGAGAGCAAAGCA 79646	_ G_ A
	G	CTGCT GCT CTCCAGCTG GG	
		GACGA CGA GGGGTCGAC CC	
		AA GA _	
GAM2536 KIAA1169	5'	CAGGGAGCAAGAGCAGCAG 35877	___ AG
		CTGCTGCT GCTCC CTG	
		GACGACGA CGAGG GAC	
		GAA _	
GAM2536 KIAA1193	5'	CTTGCAGACAACAGCAGTGG 68270	C C CA T
		CCACTGCTG TG TC GC GAG	
		GGTGACGAC AC AG CG TTC	
		A _ A_ _	
GAM2536 KIAA1257	3'	CCAACTGTCAGCAGTGTG 63396	T CTC C A
		CAC GCTGCTG CAG TG G	
		GTG TGACGAC GTC AC C	
		_ T_ A _	
GAM2536 KIAA1483	5'	CAGCAGCAGCAGCAGCAG 70431	CCA
		CTGCTGCTGCT GCTG	
		GACGACGACGA CGAC	
		CGA	
GAM2536 KIAA1483	5'	CAGCAGCAGCAGCAGCAG 70432	CCA
		CTGCTGCTGCT GCTG	

GACGACGACGA CGAC
 CGA
 GAM2536 KIAA1483 5' CGGCGGCAGCAGCAGCAG 70433 _ A
 CTGCTGCTGCT CC GCTG
 ||||| || ||||
 GACGACGACGA GG CGGC
 C _
 GAM2536 KIAA1543 5' CCTCAGAACAACAGCGGCAGTA 71542 CCAG__
 G CTGCTGCTGCT CTGAGG
 ||||| ||||
 GATGACGGCGA GACTCC
 CAACAA
 GAM2536 KIAA1546 3' CCTCAGCTCACCAGCAACA 68496 C CTCC
 TG TGCTG AGCTGAGG
 || |||| |||||
 AC ACGAC TCGACTCC
 A CAC_
 GAM2536 KIAA1819 5' CCTGCTGAACAGTAGCA 70250 CTC TG
 TGCTGCTG CAGC AGG
 ||||| ||| ||
 ACGATGAC GTCG TCC
 AA_ _
 GAM2536 KIAA1879 3' CCGAGCACGAAGAAACAGCAGC 73937 C___ CA GA
 AG CTGCTGCTG TC GCT GG
 ||||| || ||| ||
 GACGACGAC AG CGA CC
 AAAGA CA G_
 GAM2536 KIAA1889 5' CAGCGGCAGCAACAGCAGCGG 73880 A C _ A
 CC CTGCTG TGCT CC GCTG
 || ||||| |||| || ||||
 GG GACGAC ACGA GG CGAC
 C A C _
 GAM2536 KIAA1904 3' CTGGGGCAGCAGCAGTGG 73869
 CCACTGCTGCTGCTCCAG
 |||||
 GGTGACGACGACGGGGTC
 GAM2536 KIAA1932 5' CCTCAGCTTTGCAGCAGCAGCA 73822 C __
 GT ACTGCTGCTGCT CA GCTGAGG
 ||||| || |||||
 TGACGACGACGA GT CGACTCC
 C TT
 GAM2536 LAP1B 5' CCTCAAATGGCGGCAGCAGCG 65191 _ GC_
 TGCTGCTGCT CCA TGAGG
 ||||| || ||||
 GCGACGACGG GGT ACTCC
 C AAA
 GAM2536 LOXL4 3' CCTACAGAGCAGCAAGAGT 50858 GC CAGC _
 ACT TGCTGCTC TG AGG
 || ||||| || |||

			TGA ACGACGAG AC TCC		
			GA ____ A		
GAM2536	MGC15429	5'	CAGCACAGCAGCAGCAG 52210	CCA	
			CTGCTGCTGCT GCTG		
			GACGACGACGA CGAC		
			CA_		
GAM2536	MO25	5'	CCAGCAGCAGCCGCAG 33286	T CCA A	
			CTGC GCTGCT GCTG G		
			GACG CGACGA CGAC C		
			C ____ A		
GAM2536	NSAP1	5'	TCAGCCAGTAGCGCAG 22087	T CCA	
			CTGC GCTGCT GCTGA		
			GACG CGATGA CGACT		
			_ C_		
GAM2536	PLEK2	3'	CCTCAGATTACAAACAGCAGTG 33610	CTGCTCCAG	
	G		CCACTGCTG CTGAGG		
			GGTGACGAC GACTCC		
			AAACATTA_		
GAM2536	PRO2714	3'	CCTCAGCTGAAGATGGAGAAAC 38193	ACTG G _ C	
	GG		CC CT CTG CT CAGCTGAGG		
			GG GA GGT GA GTCGACTCC		
			CAAA _ A A		
GAM2536	RNPC2	5'	CAGCAGCAGCAGCAGCAG 18128	CCA	
			CTGCTGCTGCT GCTG		
			GACGACGACGA CGAC		
			CGA		
GAM2536	RNPC2	5'	CAGCAGCAGCAGCAGCAG 18129	CCA	
			CTGCTGCTGCT GCTG		
			GACGACGACGA CGAC		
			CGA		
GAM2536	RNPC2	5'	CGGCGGCAGCAGCAGCAG 18130	_ A	
			CTGCTGCTGCT CC GCTG		
			GACGACGACGA GG CGGC		
			C _		
GAM2536	RNPC2	5'	CAGCAGCAGCAGCAGCAG 18127	CCA	
			CTGCTGCTGCT GCTG		
			GACGACGACGA CGAC		
			CGA		
GAM2536	SARM	3'	CCCAGCTGGAACAGCTGAAGTC 31284	C GCT C A	
	A		C ACT GCTG TCCAGCTG GG		

		A TGA CGAC AGGTCGAC CC	
		C AGT A _	
GAM2536	SLIT1	3' CCCAGCCGCTGCAGCAGCGG 13231	TCCA A
		CTGCTGCTGC GCTG GG	
		GGCGACGACG CGAC CC	
		TCGC _	
GAM2536	TNFAIP3	3' CCTCAGCTGCCACTGCAACAGT 21908	C TGCTC
	GG	CCACTG TGC CAGCTGAGG	
		GGTGAC ACG GTCGACTCC	
		A TCACC	
GAM2536	TRIM2	5' CCGTTATGGAACGCAGCAGCAG 31598	_ GCTGA
		CTGCTGCTGC TCCA GG	
		GACGACGACG AGGT CC	
		CA ATTG_	
GAM2536	USP20	3' CCTCCCAGCAGCAGCAGTG 22899	CCAGCT
		CACTGCTGCTGCT GAGG	
		GTGACGACGACGA CTCC	
		CC_	
GAM2536	UXS1	5' CCTCAGCCTTCCGGAGCAGCAG 47591	TG A_
	TGG	C CTGCTGCTCC GCTGAGG	
		G GACGACGAGG CGACTCC	
		GT CCTTC	
GAM2536	LOC115114	3' CAGCAGCAGCAGCAGCAG 69312	CCA
		CTGCTGCTGCT GCTG	
		GACGACGACGA CGAC	
		CGA	
GAM2536	LOC115114	3' CAGCAGCAGCAGCAGCAG 69313	CCA
		CTGCTGCTGCT GCTG	
		GACGACGACGA CGAC	
		CGA	
GAM2536	LOC115114	3' CAGCAGCAGCAGCAGCAG 69314	CCA
		CTGCTGCTGCT GCTG	
		GACGACGACGA CGAC	
		CGA	
GAM2536	LOC116411	5' CCCAACTGGAGTGCAGACA 74296	_ T C A
		TG CTGC GCTCCAG TG GG	
		AC GACG TGAGGTC AC CC	
		A _ A _	
GAM2536	LOC122618	5' CCTCTTTGGAAAGCAGCAGTGG 57903	GC CT
		CCACTGCTGCT TCCAG GAGG	

GGTGACGACGA AGGTT CTCC
A_ T_
GAM2536 LOC132617 3' CCCAGCCTGCAGCAGCA 76411 TCCA A
TGCTGCTGC GCTG GG
||||||| ||| ||
ACGACGACG CGAC CC
TC__ _
GAM2536 LOC146057 5' CAGTAACAGCAGCAGCAG 78131 CCA
CTGCTGCTGCT GCTG
||||||| |||
GACGACGACGA TGAC
CAA
GAM2536 LOC146333 5' CCCAGCGGTGACAGCAGCAGGG 83199 A CT_ A A
CC CTGCTGCTG CC GCTG GG
|| ||||| || ||| ||
GG GACGACGAC GG CGAC CC
_ AGT _ _
GAM2536 LOC147057 3' CTGAGATAAAGCAGCAGCAG 84981 CCAG G
CTGCTGCTGCT CT AG
||||||| |||
GACGACGACGA GA TC
AATA G
GAM2536 LOC147514 5' CAAAGCGAGCAGCAGTAG 68176 CA GA_
CTGCTGCTGCTC GCT G
||||||| ||| |
GATGACGACGAG CGA C
_ AAA
GAM2536 LOC147958 5' CCTGCAAGTCAGCAGCAGCAG 88520 CCA _ _
CTGCTGCTGCT GCT G AGG
||||||| ||| |||
GACGACGACGA TGA C TCC
C_ A G
GAM2536 LOC148089 3' CCTCAGCCCCGGCAGCTAGTGG 79330 _ CTCCA
CCACT GCTGCTG GCTGAGG
||||| ||||| |||||
GGTGA CGACGGC CGACTCC
T CC_
GAM2536 LOC149305 5' CAGCAGCAGCAGCAG 80036 CCA
CTGCTGCTGCT GCTG
||||||| |||
GACGACGACGA CGAC
_ _
GAM2536 LOC149305 5' CCAGGCGACAGCAGCAGCAG 80037 CCA GA
CTGCTGCTGCT GCT GG
||||||| ||| ||
GACGACGACGA CGG CC
CAG A_
GAM2536 LOC149426 3' CCCAGGGGAAAGCAAGAGCAGT 85572 GC _ AG A
G CACTGCT TGC TCC CTG GG
||||| ||| ||| ||| ||

	GTGACGA ACG AGG GAC CC		
	GA AA G_ _		
GAM2536 LOC150005 3'	CAGTTGCAGCAACAGCAGCAG 85960	___	C
	CTGCTGCT GCT CAGCTG		
	GACGACGA CGA GTTGAC		
	CAA C		
GAM2536 LOC150174 3'	CCCGGCAAACAGCAGCAG 80434	CTCCA	A
	CTGCTGCTG GCTG GG		
	GACGACGAC CGGC CC		
	AAA_ _		
GAM2536 LOC150213 3'	CCCGGCAAACAGCAGCAG 75353	CTCCA	A
	CTGCTGCTG GCTG GG		
	GACGACGAC CGGC CC		
	AAA_ _		
GAM2536 LOC151121 5'	CCTCACTTCTACAGCAGCAAGG 80933	AC	CTCC C
	CC TGCTGCTG AG TGAGG		
	GG ACGACGAC TC ACTCC		
	A_ ATCT _		
GAM2536 LOC152282 3'	CAGCAGCAGCAGCAG 81396	CCA	
	CTGCTGCTGCT GCTG		
	GACGACGACGA CGAC		

GAM2536 LOC152282 3'	CAGCAGCAGCAGCAGCAG 81397	CCA	
	CTGCTGCTGCT GCTG		
	GACGACGACGA CGAC		
	CGA		
GAM2536 LOC152282 3'	CAGCAGCAGCAGCAGCAG 81398	CCA	
	CTGCTGCTGCT GCTG		
	GACGACGACGA CGAC		
	CGA		
GAM2536 LOC152282 3'	CCCAGCCCCCGTAGCAGCAG 81400	TCCA	A
	CTGCTGCTGC GCTG GG		
	GACGACGATG CGAC CC		
	CCCC _		
GAM2536 LOC152282 3'	CCCAGTAGCAGCAACAGCAG 81401	C CCA	A
	CTGCTG TGCT GCTG GG		
	GACGAC ACGA TGAC CC		
	A CGA _		
GAM2536 LOC152282 3'	CCCAGTAGCAGCAGCAGCAG 81402	CCA	A
	CTGCTGCTGCT GCTG GG		

		GACGACGACGA	TGAC CC		
		CGA	_		
GAM2536	LOC152282 3'	CCCAGTAGCAGCGGCAGCAG	81403	CCA	A
		CTGCTGCTGCT	GCTG GG		
		GACGACGGCGA	TGAC CC		
		CGA	_		
GAM2536	LOC159090 5'	CCTCAGCCGGAAGATAGCAGC	82959	C	___ A
	ATG	CA TGCTGCTG	C TCC GCTGAGG		
		GT ACGACGAT	G AGG CGACTCC		
		_	A AA C		
GAM2536	LOC162137 3'	CCTCAGCTCTCACAGCAGTG	88478	C	CTCC
		CACTGCTG TG	AGCTGAGG		
		GTGACGAC AC	TCGACTCC		
		_	TC__		
GAM2536	LOC165162 5'	CCTGGGGGAGCAGAAGCAGT	88541	G	AG G
		ACTGCT CTGCTCC	CT AGG		
		TGACGA GACGAGG	GG TCC		
		A	_ G		
GAM2536	LOC197342 3'	CTCAGCCAGAAGCAGTAG	89362	G	CCA
		CTGCTGCT CT	GCTGAG		
		GATGACGA GA	CGACTC		
		A	C__		
GAM2536	LOC200093 3'	CTGGAGAAGCAGCAGCAG	63771	___	
		CTGCTGCTGC	TCCAG		
		GACGACGACG	AGGTC		
		AAG			
GAM2536	LOC200273 5'	CAAAGCCAGCAGCAGTAG	71334	CCA	GA_
		CTGCTGCTGCT	GCT G		
		GATGACGACGA	CGA C		
		C__	AAA		
GAM2536	LOC202038 5'	CCTCCGGGAGCGGCAGCAGT	90620		AGCT
		ACTGCTGCTGCTCC	GAGG		
		TGACGACGGCGAGG	CTCC		
		GC__			
GAM2536	LOC219855 3'	CCCAATTGGAACAGCAGCATGG	93140	C	C C A
		CCA TGCTGCTG	TCCAG TG GG		
		GGT ACGACGAC	AGGTT AC CC		
		_	A A _		
GAM2536	LOC220522 3'	CTGTGAGCAGCAGAGCAG	61139	___	_
		CTGCT	GCTGCTC CAG		

		GACGA CGACGAG GTC		
		GA T		
GAM2536	LOC221935 3'	CTCACCAGCAGCAGCGTG	94202	T CCAGC
		CAC GCTGCTGCT TGAG		
		GTG CGACGACGA ACTC		
		CC__		
GAM2536	LOC221968 5'	CAGCAGCAGCAGCAGCAG	94142	CCA
		CTGCTGCTGCT GCTG		
		GACGACGACGA CGAC		
		CGA		
GAM2536	LOC221968 5'	CAGCAGCAGCAGCAGCAG	94143	CCA
		CTGCTGCTGCT GCTG		
		GACGACGACGA CGAC		
		CGA		
GAM2536	LOC221968 5'	CAGCAGCAGCAGCAGCAG	94144	CCA
		CTGCTGCTGCT GCTG		
		GACGACGACGA CGAC		
		CGA		
GAM2536	LOC221968 5'	CAGCAGCAGCAGCAGCAG	94145	CCA
		CTGCTGCTGCT GCTG		
		GACGACGACGA CGAC		
		CGA		
GAM2536	LOC221968 5'	CAGCAGCAGCAGCAGCAG	94146	CCA
		CTGCTGCTGCT GCTG		
		GACGACGACGA CGAC		
		CGA		
GAM2536	LOC221968 5'	CAGCAGCAGCAGCAGCAG	94147	CCA
		CTGCTGCTGCT GCTG		
		GACGACGACGA CGAC		
		CGA		
GAM2536	LOC221968 5'	CAGCAGCAGCAGCAGCAG	94148	CCA
		CTGCTGCTGCT GCTG		
		GACGACGACGA CGAC		
		CGA		
GAM2536	LOC221968 5'	CAGCAGCAGCAGCAGCAG	94149	CCA
		CTGCTGCTGCT GCTG		
		GACGACGACGA CGAC		
		CGA		
GAM2536	LOC221968 5'	CAGCAGCAGCAGCAGCAG	94150	CCA
		CTGCTGCTGCT GCTG		

GACGACGACGA CGAC
 CGA
 GAM2536 LOC221968 5' CAGCAGCAGCAGCAGCAG 94151 CCA
 CTGCTGCTGCT GCTG
 ||||| |||
 GACGACGACGA CGAC
 CGA
 GAM2536 LOC222662 3' CCTCAGCTAAAAATAGCGTAG 94411 T CTCC_
 CTGC GCTG AGCTGAGG
 ||| ||| |||||
 GATG CGAT TCGACTCC
 _ AAAAA
 GAM2536 LOC253649 3' CCCAGCCTGTGAGCGGCAGTGG 97875 TG _ _ A
 C CTGCTGCTC CAG CTG GG
 | ||||| ||| ||| ||
 G GACGGCGAG GTC GAC CC
 GT T C _
 GAM2536 LOC254111 5' CCCAAGTGGGCAGCAGCAGCAG 97982 _ A GA
 CTGCTGCTGCT CC GCT GG
 ||||| ||| ||| ||
 GACGACGACGA GG TGA CC
 C G AC
 GAM2536 LOC254587 5' CGAGAGGAGCAGCAGCGG 99523 AG GA
 CTGCTGCTGCTCC CT G
 ||||| ||| ||
 GGCGACGACGAGG GA C
 A_ G_
 GAM2536 LOC254842 5' AGCAGAAGCAGCAGCAGT 99448 CCA
 ACTGCTGCTGCT GCT
 ||||| |||
 TGACGACGACGA CGA
 AGA
 GAM2536 LOC256080 5' CGCTGAGGCCCGCAGCAGCAGC 99414 T_____ AGCTGA
 AGTGG CCACTGCTGCTGC CC G
 ||||| ||| ||
 GGTGACGACGACG GG C
 ACGCC_ AGTCGA
 GAM2536 LOC256158 5' CCAGGCTGGAGAACAACAGCAG 99485 C _ GA
 CTGCTG TG CTCCAGCT GG
 ||||| ||| ||||| ||
 GACGAC AC GAGGTCGG CC
 A AA A_
 GAM2536 LOC257106 5' CCCAGGCAGAAGCAGCAGGAG 97125 G CCA GA
 CTCTGCTGCT GCT GG
 || ||||| ||| ||
 GA GACGACGA CGG CC
 G AGA AC
 GAM2536 LOC257237 5' CCTCTGGGCAGAGCAGCAG 97310 CA _
 CTGCTGCTC GCT GAGG
 ||||| ||| |||||

	GACGACGAG CGG CTCC	
	A_ GT	
GAM2536 LOC257456 3'	CTGTGAGCAGCAGAGCAG 80595	— —
	CTGCT GCTGCTC CAG	
	GACGA CGACGAG GTC	
	GA T	
GAM2536 LOC51667 3'	CCCAGGACCGCAGCAGCAG 32777	TCCAG A
	CTGCTGCTGC CTG GG	
	GACGACGACG GAC CC	
	CCAG_ _	
GAM2536 LOC91170 3'	CAGCAGCAGCAGCAGCAG 65724	CCA
	CTGCTGCTGCT GCTG	
	GACGACGACGA CGAC	
	CGA	
GAM2536 LOC91170 3'	CAGCAGCAGCAGCAGCAG 65725	CCA
	CTGCTGCTGCT GCTG	
	GACGACGACGA CGAC	
	CGA	
GAM2536 LOC91170 3'	CAGCAGCAGCAGCAGCAG 65726	CCA
	CTGCTGCTGCT GCTG	
	GACGACGACGA CGAC	
	CGA	
GAM2536 LOC91170 3'	CAGCAGCAGCAGCAGCAG 65727	CCA
	CTGCTGCTGCT GCTG	
	GACGACGACGA CGAC	
	CGA	
GAM2536 LOC91170 3'	CAGCAGCAGCAGCAGCAG 65728	CCA
	CTGCTGCTGCT GCTG	
	GACGACGACGA CGAC	
	CGA	
GAM2536 LOC91170 3'	CAGCAGCAGCAGCAGCAG 65729	CCA
	CTGCTGCTGCT GCTG	
	GACGACGACGA CGAC	
	CGA	
GAM2536 LOC91170 3'	CAGCAGCAGCAGCAGCAG 65730	CCA
	CTGCTGCTGCT GCTG	
	GACGACGACGA CGAC	
	CGA	
GAM2536 LOC91170 3'	CCGTAGCAGCAGCAGCAGCAG 65732	CCA A
	CTGCTGCTGCT GCTG GG	

			GACGACGACGA CGAT CC		
			CGA G		
GAM2536	LOC91355	5'	CCTCAACCTGCTTAGCCAGCAG 66305	_ C_ C_	
			CAG CTGCTGCTG CT CAG TGAGG		
			GACGACGAC GA GTC ACTCC		
			C TTC CA		
GAM2536	LOC92080	5'	CCTCACCTGGAGCAGCACAGCA 68626	__ C	
			G CTGCT GCTGCTCCAG TGAGG		
			GACGA CGACGAGGTC ACTCC		
			CA C		
GAM2536	LOC93463	3'	CAGCAGCAGCAGCAGCAG 72833	CCA	
			CTGCTGCTGCT GCTG		
			GACGACGACGA CGAC		
			CGA		
GAM2536	LOC93463	3'	CAGCAGCAGCAGCAGCAG 72834	CCA	
			CTGCTGCTGCT GCTG		
			GACGACGACGA CGAC		
			CGA		
GAM2536	LOC93463	3'	CAGCAGCAGCAGCAGCAG 72835	CCA	
			CTGCTGCTGCT GCTG		
			GACGACGACGA CGAC		
			CGA		
GAM2536	LOC93463	3'	CAGCAGCAGCAGCAGCAG 72836	CCA	
			CTGCTGCTGCT GCTG		
			GACGACGACGA CGAC		
			CGA		
GAM2536	LOC96597	3'	CCCAGCCAGCCAGCCAGCCAGC 67450	_ _ CCA_ A	
			AG CTGCTG CTG CT GCTG GG		
			GACGAC GAC GA CGAC CC		
			C C CCGAC _		
GAM2537	PSG6	3'	GATTAAAACATGACCCAC 12446	A ATGGTG	
			GTGG TCGTGTTT AATC		
			CACC AGTACAAA TTAG		
			C A_____		
GAM2537	TGM4	3'	TCACCATAGAGACCCAT 13723	ATC G	
			GTGG GT TTTATGGTGA		
			TACC CA AGATACCACT		
			__ G		
GAM2537	ESDN	3'	TACTGTAAACATGACCCAC 56062	A	
			GTGG TCGTGTTTATGGTG		

			CACC AGTACAAATGTCAT			
			C			
GAM2538	DLEC1	3'	CATCTGGCCCTCCCTTG	24716	A	A C
			CAAGG AGGGC GG GTG			
			GTTCC TCCCG TC TAC			
			C G _			
GAM2538	DLEC1	3'	CATCTGGCCCTCCCTTG	24728	A	A C
			CAAGG AGGGC GG GTG			
			GTTCC TCCCG TC TAC			
			C G _			
GAM2538	PIP5K1A	3'	TATCCCACCCTGCCTTGATA	14520	A	CA C
			TATCAAGG AGGG GG GTG			
			ATAGTTCC TCCC CC TAT			
			G A_ C			
GAM2538	SOX11	3'	ACCCACCCCCCCTTGGTA	13308	AA	CA C
			TATCAAGG GGG GG GT			
			ATGGTTCC CCC CC CA			
			CC A_ _			
GAM2538	CHL1	3'	TGTTACCTTTCTCAATA	22768	CA	CA
			TAT AGGAAGGG GGCG			
			ATA TCCTTTCC TTGT			
			AC A_			
GAM2538	EPB41L1	3'	CATTCTGCCCTTCCCTGA	71104	A	C
			TCA GGAAGGGCAGG GTG			
			AGT CCTTCCCGTCT TAC			
			C _			
GAM2538	FLJ00060	3'	CATACCCCCTGCCCTCCTCTGA	61741	_	A CGTG
			TCA AGGA GGGCAGG ATG			
			AGT TCCT CCCGTCC TAC			
			C _ CCCA			
GAM2538	FLJ10898	5'	CACCACAGCCCTTTCTCAATA	60126	CA	AGGC
			TAT AGGAAGGGC GTG			
			ATA TCTTTCCCG CAC			
			AC ACAC			
GAM2538	FLJ22557	3'	ATCATCCCATCCTTAATA	45581	C	A CAGGC
			TAT AAGGA GGG GTGAT			
			ATA TTCCT CCC TACTA			
			A A _____			
GAM2538	KIAA0574	3'	CATCCCCTGCCCTCCCCTGA	69808	A A	CGT
			TCA GG AGGGCAGG GATG			

AGT CC TCCCGTCC CTAC
 C C C__
 GAM2538 KIAA0632 3' CACCTCAGAAACCCTTCCTTGA 32071 CA__ C
 TCAAGGAAGGG GG GTG
 ||||| ||||
 AGTTCCTTCCC CT CAC
 AAAGA C
 GAM2538 KIAA1045 3' CATCACATGTCCTTCC 71599 GGC
 GGAAGGGCA GTGATG
 ||||| ||||
 CCTTCCTGT CACTAC
 A__
 GAM2538 KIAA1354 5' CAGTGA CTGCCTTCCTTGATA 61572 A G _
 TATCAAGG AGGGCAG CG TG
 ||||| ||||| || ||
 ATAGTTCC TTCCGTC GT AC
 C A G
 GAM2538 MGC20460 5' CACCGCCTCCTACCCTTCTT 54901 C__ _
 AGGAAGGG AGGCG TG
 ||||| |||| ||
 TTCTTCCC TCCGC AC
 ATCC C
 GAM2538 LOC158476 3' CACGCCCGCCCCCCCCATTGA 88186 _ AA_ A
 TCAA GG GGGC GGC GTG
 ||| || ||| |||||
 AGTT CC CCG CCGCAC
 A CCC C
 GAM2538 LOC90459 3' CACACCCGCCTAATTTTGT 63550 A_ A C
 CAAGGA GGGC GG GTG
 ||||| ||| || |||
 GTTTTT TCCG CC CAC
 AA C A
 GAM2539 BID 5' TCCGCGCGCCTGGGAGACGCTG 8654 A TCTTC
 CGGC TCTCCCAGGC TGGA
 ||| ||||| |||
 GTCG AGAGGGTCCG GCCT
 C CGC__
 GAM2539 EPAC 5' CCAGCTCTGGGAGCACCG 21451 CAT CTCTT
 CGG CTCCCAGG CTGG
 || ||||| |||
 GCC GAGGGTCT GACC
 AC_ C____
 GAM2539 EPB42 5' CCAGTAACTGGTCCAGGAGATA 5502 C CA CTT__
 CC GG ATCTCC GGCT CTGG
 || ||||| ||| |||
 CC TAGAGG CTGG GACC
 A AC TCAAT
 GAM2539 IL4R 3' CCATGCCTGGGAAATGCC 6457 C TCTTC
 GGCAT TCCCAGGC TGG
 ||||| ||||| |||

CCGTA AGGGTCCG ACC
 A T____
 GAM2539 KCNE2 3' TCCAGACATGAAGAGATGCC 18894 C_ GGCTCT
 GGCATCTC CA TCTGGA
 ||||| || |||||
 CCGTAGAG GT AGACCT
 AA AC____
 GAM2539 MATN1 5' CCAGCCCCTGGAAGAGCC 11467 A C CTCTT
 GGC TCT CCAGG CTGG
 ||| ||| |||| ||||
 CCG AGA GGTCC GACC
 _ A CC____
 GAM2539 MEOX2 3' CAGAGTGAAGATGCCG 20994 CCCAGGC _
 CGGCATCT TC TTCTG
 ||||| || |||||
 GCCGTAGA AG GAGAC
 _____ T
 GAM2539 MLLT4 3' CCATTTGGCCCTGAGAGATGCC 72898 C CT TTC
 GGCATCTC CAGG C TGG
 ||||| ||| | |||
 CCGTAGAG GTCC G ACC
 A CG TTT
 GAM2539 PABPN1 3' CCAGGGCTCTGGAAGGACACC 17356 CA C_ _ CTT
 GG TCT CCAG GCT CTGG
 || ||| |||| ||| ||||
 CC AGG GGTC CGG GACC
 AC AA T ____
 GAM2539 PTEN 5' CCAGGGCTGGGAACGCCG 6138 ATC G TCTT
 CGGC TCCCAG C CTGG
 |||| ||||| | ||||
 GCCG AGGGTC G GACC
 CA_ G____
 GAM2539 SHOX 3' CCAGATTTCTGGGAGATCC 6565 C A CTCT
 GG ATCTCCC GG TCTGG
 || ||||| || |||||
 CC TAGAGGG CT AGACC
 _ _ TT____
 GAM2539 VCP 5' CCACCGCCTGGAAGAGCCG 75887 A C TCTTC
 CGGC TCT CCAGGC TGG
 |||| ||| ||||| |||
 GCCG AGA GGTCCG ACC
 _ A CC____
 GAM2539 C20orf18 3' CCTGGGGGCCCAGGAGACACC 49170 CA CA CT
 GG TCTCC GGCTCTT GG
 || |||| ||||| ||
 CC AGAGG CCGGGGG CC
 AC AC T_
 GAM2539 CDV-1 5' TCCAGAAGAAAGTAGATACC 26764 C CCCAGGC
 GG ATCT TCTTCTGGA
 || |||| |||||

CC TAGA AGAAGACCT
 A TGAA____
 GAM2539 dJ309H15.1 3' TCCAGAAGAGCCCCTGCC 57572 TCTCCCA
 GGCA GGCTCTTCTGGA
 ||| |||||
 CCGT CCGAGAAGACCT
 CC____
 GAM2539 EFS2 5' CCAGCCCTGGGAGCACCG 20769 CAT CTCTT
 CGG CTCCCAGG CTGG
 || ||||| |||
 GCC GAGGGTCC GACC
 AC_ C____
 GAM2539 FLJ12768 3' CCAAGACTCAGCCATAGAAGAT 47963 _CCA CT_ _
 GCCG CGGCATCT C GGCT TCT GG
 ||||| | ||| |||
 GCCGTAGA G CCGA AGA CC
 A ATA CTC A
 GAM2539 FLJ14297 5' TCCAGAAGAGTGGAAATGCC 46614 C CAG
 GGCAT TCC GCTCTTCTGGA
 |||| ||| |||||
 CCGTA AGG TGAGAAGACCT
 A ____
 GAM2539 HIC2 3' CCAGAAGGGGGGAGGGACACCG 65862 CA__ AGG
 CGG TCTCCC CTCTTCTGG
 || ||||| |||||
 GCC GGAGGG GGGAAGACC
 ACAG ____
 GAM2539 HN1L 3' TCCAGATGGCTGGGAGATGCC 58620 G CT
 GGCATCTCCCAG CT TCTGGA
 ||||| ||| |||||
 CCGTAGAGGGTC GG AGACCT
 _ T_
 GAM2539 HSA011916 3' CGGAAGCCTAGGAGAGCCG 60905 A C CT
 CGGC TCTCC AGGCT TCTG
 ||| |||| |||| |||
 GCCG AGAGG TCCGA AGGC
 _ A ____
 GAM2539 HSA011916 3' CGGAAGCCTAGGAGAGCCG 31697 A C CT
 CGGC TCTCC AGGCT TCTG
 ||| |||| |||| |||
 GCCG AGAGG TCCGA AGGC
 _ A ____
 GAM2539 KIAA0258 3' CCAGAAAGGGAAGGAGAGCCG 29465 A CAGG _
 CGGC TCTCC CTCTT CTGG
 ||| |||| |||| |||
 GCCG AGAGG GGGAA GACC
 _ AA__ A
 GAM2539 KIAA1111 3' TCCAGAAGTGGCCTAGAAATGC 97947 C CC _
 C GGCAT TC AGGCT CTTCTGGA
 |||| || |||| |||||

CCGTA AG TCCGG GAAGACCT
 A A_ T
 GAM2539 KIAA1277 3' TCCAGAAGGGACAGTGATGCC 65085 TCCCAGG
 GGCATC CTCTTCTGGA
 ||||| |||||
 CCGTAG GGGAAGACCT
 TGACA__
 GAM2539 KIAA1423 3' TAGGAGAACCTGGAAGATGACC 62396 _ C C
 GG CATCT CCAGG TCTTCTG
 || |||| |||| |||||
 CC GTAGA GGTCC AGAGGAT
 A A A
 GAM2539 KIAA1508 3' TCCAAGGCCTTCTAGGAGACAC 62563 CA C__ T TC
 TG CGG TCTCC AGGC CT TGGA
 || |||| |||| || ||||
 GTC AGAGG TCCG GA ACCT
 AC ATCT _ _
 GAM2539 KIAA1554 5' TCCATCTGCCTGGGAGATGC 96863 TCTTC
 GCATCTCCCAGGC TGGA
 ||||| ||||
 CGTAGAGGGTCCG ACCT
 TCT__
 GAM2539 KIAA1724 3' CCAGAATTGGAAGGTGCC 67611 C GCTC
 GGCATCT CCAG TTCTGG
 ||||| |||| |||||
 CCGTGGA GGTT AAGACC
 A ____
 GAM2539 KIAA1755 3' TCCAGAAAACCTCCTGGAAGACC 62022 CA C CTC_
 CG CGG TCT CCAGG TTCTGGA
 || || |||| |||||
 GCC AGA GGTCC AAGACCT
 C_ A TCAA
 GAM2539 MAPK6 5' GAGAGCCTCGGAGACGCCG 12306 A C
 CGGC TCTCC AGGCTCTT
 |||| |||| |||||
 GCCG AGAGG TCCGAGAG
 C C
 GAM2539 MAST205 5' CCAGAAGGCTCGAAGGCGCCG 31358 AT CCCA T
 CGGC CT GGC CTTCTGG
 |||| || |||||
 GCCG GA TCG GAAGACC
 CG AGC_ _
 GAM2539 MGC11287 3' CCAGAAGCAGGGATGCC 49612 CCAG CT
 GGCATCTC GCT TCTGG
 ||||| || ||||
 CCGTAGGG CGA AGACC
 A__ _
 GAM2539 MGC15476 5' CCAAGTCCCTAGGAGACGCC 59606 A C CT TC
 GGC TCTCC AGG CT TGG
 || |||| || || ||||

CCG AGAGG TCC GA ACC
 C A CT _
 GAM2539 MGC15827 3' CCAGCGCAGTCCCGGGAGATGG 52872 G A _ CTT
 CG CG CATCTCCC GG CT CTGG
 || ||||| || || ||||
 GC GTAGAGGG CC GA GACC
 G C T CGC
 GAM2539 PASK 3' CCAGAAGAACTGGAGAAATACC 31406 C C _ GC
 GG AT TC CCAG TCTTCTGG
 || || |||| |||||
 CC TA AG GGTC AGAAGACC
 A A A A_
 GAM2539 PDE4DIP 5' CCAGAAGAGCCTTGTGGAGGCC 28403 AT _ _
 G CGGC CTCC CA GGCTCTTCTGG
 ||| ||| || |||||
 GCCG GAGG GT CCGAGAAGACC
 _ T T
 GAM2539 PDZD2 5' TCCAGTGAGCCTGGAAAACCC 81735 CATCTC TT
 GG CCAGGCTC CTGGA
 || ||||| ||||
 CC GGTCCGAG GACCT
 CAAAA_ T_
 GAM2539 PIP5K1C 3' CCAGAGCTCGGGAGATGCC 71297 AG TCT
 GGCATCTCCC GCTCT GG
 ||||| |||| ||
 CCGTAGAGGG CGAGA CC
 CT _
 GAM2539 PTPRT 3' TCCAGAAGTCCAGGGACACC 56509 CATC A CT
 GG TCCC GG CTTCTGGA
 || ||| || |||||
 CC AGGG CC GAAGACCT
 AC_ A T_
 GAM2539 SDCCAG43 3' TCCAGGGGCTGAGAGACGGC 70897 A_ C GCT
 GC TCTC CAG CTTCTGGA
 || ||| || |||||
 CG AGAG GTC GGGGACCT
 GC A _
 GAM2539 SLC17A3 5' CCAGAAGACCAAGAGCC 22789 A CCCA C
 GGC TCT GG TCTTCTGG
 ||| || || |||||
 CCG AGA CC AGAAGACC
 _ A _
 GAM2539 ZDHHC4 5' TCCAGGCTCCTGGAAGAACC 36646 CA C CTCT
 GG TCT CCAGG TCTGGA
 || ||| |||| |||||
 CC AGA GGTCC GGACCT
 A_ A TC_
 GAM2539 LOC122614 3' TCCAGAAGATGTGAGAAGCC 76101 A C GGC
 GGC TCTC CA TCTTCTGGA
 ||| ||| || |||||

CCG AGAG GT AGAAGACCT
 A T ____
 GAM2539 LOC123095 3' CCAGAAGACTAAGACAGC 76521 A_ CCCA C
 GC TCT GG TCTTCTGG
 || ||| || |||||
 CG AGA TC AGAAGACC
 AC A_____
 GAM2539 LOC123435 5' CCACCTGGACCCAGGAGACCCC 74660 CA CA C TC_
 GG TCTCC GG TCT TGG
 || ||||| || ||| |||
 CC AGAGG CC AGG ACC
 CC AC _ TCC
 GAM2539 LOC129433 5' CCAAGAGCTCCTGGGAGCACC 76220 CAT CT TC
 GG CTCCCAGG CT TGG
 || ||||| || |||
 CC GAGGGTCC GA ACC
 AC_ TC GA
 GAM2539 LOC131377 3' TCCAGAAAAGAGGCTAGGAGAG 76781 A C G ____
 GCC GGC TCTCC AG CTCT TCTGGA
 ||| ||||| || ||| |||||
 CCG AGAGG TC GAGA AGACCT
 G A G AA
 GAM2539 LOC143666 5' TCCAGGTCGTCCTGAGGATGCC 83890 CC CTCT
 G CGGCATCT CAGG TCTGGA
 ||||| ||| |||||
 GCCGTAGG GTCC GGACCT
 A_ TGCT
 GAM2539 LOC144997 3' TCAAGGAAGCCTATGAGATGCC 84139 CC C G
 GGCATCTC AGGCT TTCT GA
 ||||| |||| ||| ||
 CCGTAGAG TCCGA AGGA CT
 TA _ A
 GAM2539 LOC145644 5' CCAGACCGTGAGGAGAGCC 65286 A _ CTCT
 GGC TCTCCCA GG TCTGG
 ||| ||||| || |||||
 CCG AGAGGGT CC AGACC
 _ G ____
 GAM2539 LOC146337 3' TCCAGGCCGGCTAGGGGACACC 84647 CA T A CT
 G CGG TC CCC GGCT TCTGGA
 ||| || ||| ||||| |||||
 GCC AG GGG TCGG GGACCT
 AC _ A CC
 GAM2539 LOC148147 3' TCCAGAAGCCGAATAGATACC 79406 C CCCA CT
 GG ATCT GGCT TCTGGA
 || |||| ||| |||||
 CC TAGA CCGA AGACCT
 A TAAG ____
 GAM2539 LOC155061 5' CCAGGAAGGAGCCTGGGAAAGC 82187 ATC ____
 C GGC TCCCAGGCTCT TCTGG
 ||| ||||| ||||| |||||

CCG AGGGTCCGAGG GGACC
 AA_ AA
 GAM2539 LOC196707 3' CAGAGAGCCTGGGAGAGCC 88923 A T
 GGC TCTCCAGGCTCT CTG
 ||| ||||| |||
 CCG AGAGGGTCCGAGA GAC

 GAM2539 LOC196860 3' CCAGAAGACTAAGACAGC 91215 A_ CCCA C
 GC TCT GG TCTTCTGG
 || ||| || |||||
 CG AGA TC AGAAGACC
 AC A_ _
 GAM2539 LOC197320 5' CCAGAAGGGAAAGTCGCCG 89306 AT CCCAGG
 CGGC CT CTCTTCTGG
 ||| || |||||
 GCCG GA GGAAGACC
 CT AA_
 GAM2539 LOC220954 3' CCAGAAGGAAGGAAGATTCC 94757 C C AGG T
 GG ATCT CC C CTTCTGG
 || ||| || |||||
 CC TAGA GG G GAAGACC
 T A AA_
 GAM2539 LOC256158 5' CAGAAGGAAGATGCTG 99480 C AGGCTC
 CGGCATCT CC TTCTG
 ||||| || |||
 GTCGTAGA GG AAGAC
 A _
 GAM2539 LOC92299 5' CCAGGTCCGGGAGATG 69362 A TCTT
 CATCTCCC GGC CTGG
 ||||| || |||
 GTAGAGGG CTG GACC
 C _
 GAM2539 LOC92973 5' CCAGAAGGAGGAGAACC 71587 CA CAGGC
 GG TCTCC TCTTCTGG
 || ||| |||||
 CC AGAGG GGAAGACC
 A_ A_
 GAM2540 ADCY6 3' GGGAGCAGGGGAGGGGTCAG 31590 C G ATG
 CTG CCCCTCT CTG CCC
 ||| ||||| ||| |||
 GAC GGGGAGG GAC GGG
 T G GA_
 GAM2540 ADCY6 3' GGGAGCAGGGGAGGGGTCAG 40959 C G ATG
 CTG CCCCTCT CTG CCC
 ||| ||||| ||| |||
 GAC GGGGAGG GAC GGG
 T G GA_
 GAM2540 AGRN 3' GGGGCAGGTGCAGAGGTGGCAG 79588 C TGA
 CTGCC CCTCTGC TGCCCC
 |||| ||||| |||||

			GACGG GGAGACG ACGGGG		
			T TGG		
GAM2540 AKAP2	3'	TGGGGGCATTTT	AGAGCGGCA 24231	CC	CT
		TGCC	CTCTG GATGCCCCCA		
		ACGG	GAGAT TTACGGGGGT		
		C_	TT		
GAM2540 AQP6	3'	GGGACAGAGCAGAGGAAGGCAG 55009		C_	GA _
		CTGCC	CCTCTGCT TG CCC		
		GACGG	GGAGACGA AC GGG		
		AA	G_ A		
GAM2540 AQP6	3'	TGGGGACAGGGGCAGGGGCAG 55018		CTC	GA C
		CTGCCCC	TGCT TG CCCCCA		
		GACGGGG	ACGG AC GGGGT		
		___	GG A		
GAM2540 AQP6	3'	GGGACAGAGCAGAGGAAGGCAG 9731		C_	GA _
		CTGCC	CCTCTGCT TG CCC		
		GACGG	GGAGACGA AC GGG		
		AA	G_ A		
GAM2540 ASIC4	5'	GCGGCAGCAGAGGCAGCAG 38537		CC	A
		CTGC	CCTCTGCTG TGC		
		GACG	GGAGACGAC GCG		
		AC	G		
GAM2540 ATOX1	3'	GGATGGACCAAAGGGGGGCAG 15749		C	CTGATG C_
		CTGCCCCCT	TG CC CC		
		GACGGGGGA	AC GG GG		
		A	CA___ TA		
GAM2540 ATP1A2	3'	GGGTAGCAGCAGAGGCAG 7367		CCC	A
		CTGCC	TCTGCTG TGCCC		
		GACGG	AGACGAC ATGGG		
		___	G		
GAM2540 ATRN	3'	TGAGGACACAGCCAGGACGGCA 58447		C_	CT A C C
G		CTGCC	CCT GCTG TG CC CA		
		GACGG	GGA CGAC AC GG GT		
		CA	C_ _ A A		
GAM2540 AVP	5'	GCCAGCAGAGGCAGCAG 6675		CC	AT
		CTGC	CCTCTGCTG GC		
		GACG	GGAGACGAC CG		
		AC	___		
GAM2540 B3GNT3	3'	TGGAGGTGTGGGCAGAGGAGGG 27306		_	G C
		CCC	CCTCTGCT ATGCC CCA		

			GGG GGAGACGG TGTGG GGT		
			A G A		
GAM2540	CBFA2T2	3'	GGAGTCGGGCAGAGAAGCAG 18712	CCC	G
			CTGC CTCTGCTGAT CC		
			GACG GAGACGGCTG GG		
			AA_ A		
GAM2540	CDS2	3'	GGAACAGAACTGAGCAGGGGCA 15108	__ TG__	ATG
	G		CTGCCCC CTC CTG CC		
			GACGGGG GAG GAC GG		
			AC TCAA AA_		
GAM2540	CEP2	3'	TGGGGGCAGGGGAAGAGACAG 23250	CCCC	G GA
			CTG CTCT CT TGCCCCCA		
			GAC GAGA GG ACGGGGGT		
			A__ A GG		
GAM2540	COPA	5'	GGGGGGACAGAGGGGCAG 16479	C	CTGATG
			CTGCCCC TCTG CCCCC		
			GACGGGG AGAC GGGGG		
			_ AG__		
GAM2540	DAG1	3'	TGGGGGCACCTGGGAGGTCA 16557	T _	TCTGCTGA
			C GCC CCC TGCCCCCA		
			A TGG GGG ACGGGGGT		
			C A TCC__		
GAM2540	DBCCR1	5'	GGGAGGCAGAGGGAGTAG 28243	C	GATG
			CTGC CCCTCTGCT CCC		
			GATG GGGAGACGG GGG		
			A A__		
GAM2540	DDB2	3'	TGGGTGGTAGCAGAGGGATCA 5458	CC	GAT _
			TG CCCTCTGCT GCC CCCA		
			AC GGGAGACGA TGG GGGT		
			TA _ T		
GAM2540	DTNA	3'	GCCAGCAGGGGGAGCAG 9146	C	AT
			CTGC CCCTCTGCTG GC		
			GACG GGGGGACGAC CG		
			A _		
GAM2540	DTNA	3'	GCCAGCAGGGGGAGCAG 53270	C	AT
			CTGC CCCTCTGCTG GC		
			GACG GGGGGACGAC CG		
			A _		
GAM2540	DTNA	3'	GCCAGCAGGGGGAGCAG 53272	C	AT
			CTGC CCCTCTGCTG GC		

			GACG GGGGGACGAC CG		
		A	—		
GAM2540 DTNA	3'	GCCAGCAGGGGGAGCAG	53277	C	AT
		CTGC CCCTCTGCTG GC			
		GACG GGGGGACGAC CG			
		A	—		
GAM2540 DTR	3'	GGGGTCAGTGCAGCAGAGGACA	10457	CCC	AT—
G		CTG CCTCTGCTG GCCCC			
		GAC GGAGACGAC TGGGG			
		A— GTGAC			
GAM2540 DUSP3	3'	GGGGGCTCAGAGGGGG	15837	CTGAT	
		CCCCCTCTG GCCCC			
		GGGGGAGAC CGGGGG			
		T—			
GAM2540 EGFL4	3'	GGGGATCCAGGAGGAGCAG	62470	CC	GCT G
		CTGC CCTCT GAT CCCC			
		GACG GGAGG CTA GGGG			
		A_ AC_ _			
GAM2540 EHD2	3'	TGGAAGCATTTAGAGGGG	28231	CT	CC
		CCCCTCTG GATGC CCA			
		GGGGAGAT TTACG GGT			
		_ AA			
GAM2540 EIF2B5	3'	GGGAACAGCAGAGAGCAG	62205	CCC	ATG
		CTGC CTCTGCTG CCC			
		GACG GAGACGAC GGG			
		A— AA_			
GAM2540 EPHA8	3'	TGGAGGCATCATGGCAGAG	40441	_	C
		CTCTGCT GATGCC CCA			
		GAGACGG CTACGG GGT			
		TA A			
GAM2540 EZH1	3'	TGGGAGTGTTACAGTAGGGAGC	10558	C	_ C C
AG		CTGC CCCT CTG TGATGC CCCA			
		GACG GGGA GAC ATTGTG GGGT			
		A T _ A			
GAM2540 FGFR4	5'	GGAGGAGCCAGGAAGGCAG	10637	C_	CT GATG C
		CTGCC CCT GCT CC CC			
		GACGG GGA CGA GG GG			
		AA C_ _ A			
GAM2540 FGFR4	5'	GGAGGAGCCAGGAAGGCAG	43630	C_	CT GATG C
		CTGCC CCT GCT CC CC			

			GACGG GGA CGA GG GG			
			AA C_ ____ A			
GAM2540	GCNT2	5'	GGGGAGGCAGAGGGAGG 9455	_	GATG	
			CC CCCTCTGCT CCCC			
			GG GGGAGACGG GGGG			
			A A__			
GAM2540	GDF5	3'	GGAATCACAGAGGGGTCAG 6896	C	C G	
			CTG CCCCTCTG TGAT CC			
			GAC GGGGAGAC ACTA GG			
			T _ A			
GAM2540	GRLF1	3'	TGGGGACAGAGGCAGGGGCA 79263	CTC	GA C	
			TGCCCC TGCT TG CCCCA			
			ACGGGG ACGG AC GGGGT			
			_ AG A			
GAM2540	H1F0	5'	GGCAGAGGCAGAGGCAG 19219	CCC	GA	
			CTGCC TCTGCT TGCC			
			GACGG AGACGG ACGG			
			_ AG			
GAM2540	H1F0	5'	TGGGAAAAGGGAGGCAGAGGAG 19220	C	GATG _	
			GCAG CTGCC CCTCTGCT CC CCCA			
			GACGG GGAGACGG GG GGGT			
			A AG_ AAAA			
GAM2540	HMG20A	3'	TGGGGGCAGAGAAAGAGTGCAG 37072	CCC	GCTGA	
			CTGC CTCT TGCCCCCA			
			GACG GAGA ACGGGGGT			
			T_ AAGAG			
GAM2540	HNRPD	5'	GGGAGGCGAAGGGGGCAG 49389	CTGCTGA	_	
			CTGCCCCCT TGCC CCC			
			GACGGGGGA GCGG GGG			
			A_____ A			
GAM2540	HNRPD	5'	GGGAGGCGAAGGGGGCAG 10950	CTGCTGA	_	
			CTGCCCCCT TGCC CCC			
			GACGGGGGA GCGG GGG			
			A_____ A			
GAM2540	HOXB3	5'	GGGGGGCAGAGAGGGG 10955	_	TGATG	
			CCCC CTCTGC CCCCC			
			GGGG GAGACG GGGGG			
			A _____			
GAM2540	ISG20	5'	GGCAGCAGAGAGGCAG 11022	CC	GAT	
			CTGCC CTCTGCT GCC			

			GACGG GAGACGA CGG		
			A_ _		
GAM2540	ITIH1	3'	GGGGCCAAGGCAGAGGAGG 11058	C	GAT
			CC CCTCTGCT GCCCC		
			GG GGAGACGG CGGGG		
			A AAC		
GAM2540	JRK	5'	GGATCAGCAGAGCAGGCAG 87829	CC	G
			CTGCC CTCTGCTGAT CC		
			GACGG GAGACGACTA GG		
			AC _		
GAM2540	LEP	3'	GGGGTGATTTCAGAGAGGGCAG 5866	C	CT _
			CTGCCC CTCTG GAT GCCCC		
			GACGGG GAGAC TTA TGGGG		
			A T_ G		
GAM2540	LMO2	5'	GGAGGCCGAGCAAGCGGAGGCA 19938	_ _ C	GAT C
	G		CTGCC CC CT TGCT GCC CC		
			GACGG GG GA ACGA CGG GG		
			A C _ GC_ A		
GAM2540	LUZP1	5'	GGGGCCGCAGAGGGGACA 54404	C	TGAT
			TG CCCCTCTGC GCCCC		
			AC GGGGAGACG CGGGG		
			A C__		
GAM2540	MAP3K9	3'	GGGGCGGGCAAGGGGGACAG 61365	_	C GA
			CTG CCCCT TGCT TGCCCC		
			GAC GGGGGA ACGG GCGGGG		
			A _ _		
GAM2540	MGEA5	5'	GGAGGGCAGCAGAGGCAG 25220	CCC	GAT _
			CTGCC TCTGCT GCCC CC		
			GACGG AGACGA CGGG GG		
			_ _ A		
GAM2540	MMP14	3'	GGCAGAACAGCCAGAGGGGGCA 18430	_	A__
	G		CTGCCCCCTCTG CTG TGCC		
			GACGGGGGAGAC GAC ACGG		
			C AAG		
GAM2540	MSL3L1	3'	GGAAGTCAGCAGCAGGGGAGGC 55322	_ _	GC
	AG		CTGCC CCCT CTGCTGAT CC		
			GACGG GGGG GACGACTG GG		
			A AC AA		
GAM2540	NCOA6IP	5'	GGGGGCAGGGGCAGGGGCAG 46155	CTC	GA
			CTGCCCC TGCT TGCCCCC		

			GACGGGG	ACGG	ACGGGGG		
			___	GG			
GAM2540	NCSTN	5'	GCTCAGCAGAGAGGCA	74136	CC	T	
			TGCC	CTCTGCTGA	GC		
			ACGG	GAGACGACT	CG		
			A_	_			
GAM2540	NR4A2	3'	TGGAAACTGTCAAGAGGGGGCA	21647	GC	GCCC_	
			TGCCCCCTCT	TGAT	CCA		
			ACGGGGGAGA	ACTG	GGT		
			___	TCAA			
GAM2540	P2RY6	3'	GGAAGCTTCTTAGAAGAGGCAG	15999	CCC	CT T CC	
			CTGCC	TCTG	GA GC CC		
			GACGG	AGAT	CT CG GG		
			AGA	T_ T	AA		
GAM2540	PCSK5	5'	GGGCCAGCAGAGGGGGC	21676	AT		
			GCCCCCTCTGCTG	GCCC			
			CGGGGGAGACGAC	CGGG			

GAM2540	PEX13	5'	GGGAGCCGAGAGGAGGCGG	12043	C	GCTGAT C	
			CTGCC	CCTCT	GC CCC		
			GGCGG	GGAGA	CG GGG		
			A	GC___	A		
GAM2540	PGF	3'	TGAAGGCAGTGGCAGGGGAGCA	12067	C T	GA CC	
	G		CTGC	CCC CTGCT	TGCC CA		
			GACG	GGG GACGG	ACGG GT		
			A	_ TG	AA		
GAM2540	PHLDA3	5'	GGAGGCATCTGGCAGAGGCGG	25694	_	_ C	
			CC	CCTCTGCT	GATGCC CC		
			GG	GGAGACGG	CTACGG GG		
			C	T	A		
GAM2540	PLAB	5'	TGGGGGCACCCTGAGGGGGCA	66428	TGCTGA		
			TGCCCCCTC	TGCCCCCA			
			ACGGGGGAG	ACGGGGGT			
			TCCC_				
GAM2540	PPP2R2B	5'	GGGCAGCGGAGGCAG	17122	CCC	GAT C	
			CTGCC	TCTGCT	GCC C		
			GACGG	AGGCGA	CGG G		
			___	___	A		
GAM2540	PROK1	3'	TGGGAGCAAGGGACAGGGAGCA	51571	C	CTG GA C	
	G		CTGC	CCCT	CT TGC CCCA		

			GACG GGGG GG ACG GGGT		
			A CA_ GA A		
GAM2540	PSCD3	3'	GGAAGGCGTGGCAGGGAGGCAG 16164	C T G C_	
			CTGCC CC CTGCT ATGCC CC		
			GACGG GG GACGG TGC GG GG		
			A _ _ AA		
GAM2540	PTCRA	3'	GGGGCATTTAGGGAGCAG 57154	C CTGCT	
			CTGC CCCT GATGCCCC		
			GACG GGGG TTACGGGG		
			A T_____		
GAM2540	PTGS1	3'	GCATACAACAGAGGGGGCA 55474	C _	
			TGCCCCCTCTG TG ATGC		
			ACGGGGGAGAC AC TACG		
			A A		
GAM2540	PTGS1	3'	GCATACAACAGAGGGGGCA 8242	C _	
			TGCCCCCTCTG TG ATGC		
			ACGGGGGAGAC AC TACG		
			A A		
GAM2540	RAP1GA1	3'	GGGATTGCTCAGTGAAGCAG 12774	CCCC TG T C_	
			CTGC TC CTGA GC CCC		
			GACG AG GACT CG GGG		
			A___ GT _ TTA		
GAM2540	RIMS1	5'	GCGAGCAGAGGGGGCGG 73030	GA	
			CTGCCCCCTCTGCT TGC		
			GGCGGGGGAGACGA GCG		

GAM2540	RPA2	5'	GGAGCATGGGCAGAGGAGACAG 12899	CCC G C	
			CTG CCTCTGCT ATGC CC		
			GAC GGAGACGG TACG GG		
			AGA G A		
GAM2540	RPS6KA2	3'	GGCACAGGTGGGAGGGCAG 41225	C TG A	
			CTGCCC CTC CTG TGCC		
			GACGGG GGG GAC ACGG		
			A TG _		
GAM2540	S100A10	5'	GGGGGCAGGAAGAGGGGG 60048	GCTGA	
			CCCCCTCT TGCCCCC		
			GGGGGAGA ACGGGGG		
			AGG__		
GAM2540	SIRT1	5'	GGGAGCAGAGGAGGCG 25289	C GATG	
			TGCC CCTCTGCT CCC		

GCGG GGAGACGA GGG
 A ____
 GAM2540 SLC12A4 5' GGGGACAGCGGCGGGGACAG 18629 C T ATG
 CTG CCCC CTGCTG CCCC
 ||| ||| ||||| ||||
 GAC GGGG GGCGAC GGGG
 A C A__
 GAM2540 SLC22A12 3' GGAGAGCAGAGGGGTCAG 58690 C GATG
 CTG CCCCTCTGCT CC
 ||| ||||| || ||
 GAC GGGGAGACGA GG
 T GA__
 GAM2540 SLC5A5 5' GGGGCGGACGCAGAGACAG 6597 CCCC TGA
 CTG CTCTGC TGCCCC
 ||| ||||| |||||
 GAC GAGACG GCGGGG
 A__ CAG
 GAM2540 SOX11 3' CAAAGGCAGAGGGGGCGG 13310 GA
 CTGCCCCCTCTGCT TG
 ||||| ||||| ||
 GGCGGGGGAGACGG AC
 AA
 GAM2540 SPAG8 3' GGGGGCAGAGCGGGGCAG 25841 CTCT GA
 CTGCCCC GCT TGCCCC
 ||||| ||| |||||
 GACGGGG CGA ACGGGGG
 ____ G_
 GAM2540 STK11 3' GGGCCGGGCAGGGGGACAG 6599 C T GAT
 CTG CCCC CTGCT GCCC
 ||| ||| ||||| ||||
 GAC GGGG GACGG CGGG
 A _ GC_
 GAM2540 STX1A 3' GGGAAGAGGCAGAGGGAGGCAG 17214 _ GATG
 CTGCC CCCTCTGCT CCC
 ||||| ||||| ||||| ||||
 GACGG GGGAGACGG GGG
 A AGAA
 GAM2540 TTYH1 3' GGGAGTAGCTGAGGGGGCAG 40685 T ATG
 CTGCCCCCTC GCTG CCC
 ||||| ||||| ||||| ||||
 GACGGGGGAG CGAT GGG
 T GA_
 GAM2540 UBE2G2 3' GGGAGGCAGAGGTAGCAG 65490 CC GATG
 CTGC CCTCTGCT CCC
 ||||| ||||| ||||| ||||
 GACG GGAGACGG GGG
 AT A__
 GAM2540 USP5 3' GGGCAGAGCAGAGGGGCAG 14448 C GA
 CTGCCCC TCTGCT TGCCC
 ||||| ||||| ||||| ||||

GACGGGG AGACGA ACGGG
 _ G_
 GAM2540 WHSC1 3' TGGGGACATTGGGAAGGTGGGC 56703 _ CTG TG C
 AG CTGCCC CCT C ATG CCCCCA
 ||||| ||| | ||| |||||
 GACGGG GGA G TAC GGGGT
 T AG_ GT A
 GAM2540 ZNF219 3' GCCAGCAGGGGGGCAG 33555 CT AT
 CTGCCCCCT GCTG GC
 ||||| ||| ||
 GACGGGGGA CGAC CG
 — —
 GAM2540 20D7-FC4 3' GGACCCACCAGCAGGGAGCAG 61564 CC T A CCC
 CTGC CC CTGCTG TG CC
 ||| || ||||| || ||
 GACG GG GACGAC AC GG
 A_ _ C CCA
 GAM2540 ABIN-2 3' GGAACATCTGGCAGAGGG 44461 _ CC
 CCCTCTGCT GATG CC
 ||||| ||| ||
 GGGAGACGG CTAC GG
 T AA
 GAM2540 AIP 5' GGAAGTTGCCGAAAGGGAGCAG 15615 _ C_ T T GC
 CTGC CCC TC GC GAT CC
 ||| ||| || || ||| ||
 GACG GGG AG CG TTG GG
 A AA C _ AA
 GAM2540 ASB13 3' TGGGGAGCACAGAGGAGGC 45547 C CTGA _
 GCC CCTCTG TGC CCCCCA
 || ||||| ||| |||||
 CGG GGAGAC ACG GGGGT
 A _ _ A
 GAM2540 BATF 5' GGGCAGGCAGAGGAGGCA 22147 C GA
 TGCC CCTCTGCT TGCC
 ||| ||||| |||||
 ACGG GGAGACGG ACGGG
 A _
 GAM2540 BCDO2 3' TGAGGACTCCAAAAGGGGGGCA 50036 T GC ATGC C
 TGCCCC CT TG CC CA
 ||||| || || || ||
 ACGGGGG GA AC GG GT
 _ AA CTCA A
 GAM2540 BRP44I 5' TGGGAAGCGGCAGCAGAGGCAG 32740 CCC A C_
 CTGCC TCTGCTG TGC CCCC
 |||| ||||| || |||||
 GACGG AGACGAC GCG GGGT
 _ G AA
 GAM2540 C12orf22 3' GGAGGCAGTAGGGAGCA 48708 C CT GAT C
 TGC CCCT GCT GCC CC
 || |||| || ||| ||

ACG GGGA TGA CGG GG
 A _ _ A
 GAM2540 C12orf3 3' GGGGTCTTGAAGAGGGGGCAG 40166 GC T
 CTGCCCCCTCT TGA GCCCC
 ||||| |||||
 GACGGGGGAGA GTT TGGGG
 A_ C
 GAM2540 C17orf31 5' TGAAGGTGGCAGAGGATGCAG 34545 CC GAT CC
 CTGC CCTCTGCT GCC CA
 ||| ||||| ||| ||
 GACG GGAGACGG TGG GT
 TA _ AA
 GAM2540 C20orf110 3' TGGGGGAGACAGAAGGGGCAG 80367 C _ GATG
 CTGCCCC TCTG CT CCCCCA
 ||||| ||||| |||||
 GACGGGG AGAC GA GGGGGT
 A A _
 GAM2540 C20orf39 5' TGAGGGGAGGGCAGAGGAGG 46579 C GATG _
 CC CCTCTGCT CCCC CA
 || ||||| ||||| ||
 GG GGAGACGG GGGG GT
 A GA_ A
 GAM2540 C8orf13 3' GGGGTGTCAGAGGAAGC 82481 CC GCT
 GC CCTCT GATGCCCC
 || |||| |||||
 CG GGAGA CTGTGGGG
 AA _
 GAM2540 CAMTA1 3' GGAAATTTGCAGAGGGGCAG 68506 C T GC
 CTGCCCC TCTGC GAT CC
 ||||| ||||| ||| ||
 GACGGGG AGACG TTA GG
 _ T AA
 GAM2540 CBLN1 5' GGGAACACAGCGCGGAGGGG 16369 _ A CC
 CCCCTCT GCTG TG CCC
 ||||| ||||| ||| ||
 GGGGAGGCGAC AC GGG
 CG _ AA
 GAM2540 CENTG3 3' GGAAGAGGGCAGAGGGGCCAG 50047 C GATG_
 CTG CCCCTCTGCT CC
 ||| ||||| ||||| ||
 GAC GGGGAGACGG GG
 C GAGAA
 GAM2540 cerk 3' TGGGGGCAGTCAGGAGGAAGC 43172 CC TG _
 GC CCTC CTGA TGCCCCCA
 || |||| ||||| |||||
 CG GGAG GACT ACGGGGGT
 AA _ G
 GAM2540 COASTER 3' TGGGGGCAGGGCAAGAGGAGAC 32083 CCC _ GA
 AG CTG CCTCT GCT TGCCCCCA
 ||| ||||| ||||| |||||

GAC GGAGA CGG ACGGGGGT
 AGA A G_
 GAM2540 CXYorf1 3' TGGGGGCATCGGCAAGG 82925 C
 CCT TGCTGATGCCCCCA
 ||| |||||
 GGA ACGGCTACGGGGGT

 —
 GAM2540 DIO2 3' TGGAGAAATGAAGCAGAGGAAG 26558 C_ G_ GCCC
 G CC CCTCTGCT AT CCA
 || ||||| || |||
 GG GGAGACGA TA GGT
 AA AG AAGA
 GAM2540 DIO2 3' TGGAGAAATGAAGCAGAGGAAG 7668 C_ G_ GCCC
 G CC CCTCTGCT AT CCA
 || ||||| || |||
 GG GGAGACGA TA GGT
 AA AG AAGA
 GAM2540 DKFZP564B1162 5' GGGGGTGCTATAAAAGAAGCAG 49350 CCCC GC__ AT
 CTGC TCT TG GCCCCC
 |||| || || |||||
 GACG AGA AT TGGGGG
 A__ AAAT CG
 GAM2540 DKFZP564C103 3' GGGGGCACTGAGGAAGCAG 32241 CC TGCTGA
 CTGC CCTC TGCCCC
 |||| || |||||
 GACG GGAG ACGGGG
 AA TC__
 GAM2540 DKFZP667O116 3' CAGAAGCAGAGGAGGCAG 95939 C GA
 CTGCC CCTCTGCT TG
 |||| ||||| ||
 GACGG GGAGACGA AC
 A AG
 GAM2540 DKFZP761C169 5' GGGGCACCTCTGGTGGGGCAG 68424 C TGCTGA
 CTGCCCC TC TGCCCC
 ||||| || |||||
 GACGGGG GG ACGGGG
 T TCTCC_
 GAM2540 DKFZp762K222 5' GGGGACTGCAGCGGAGGCAG 71671 CCC ATG_
 CTGCC TCTGCTG CCCC
 |||| ||||| |||
 GACGG AGGCGAC GGGG
 __ GTCA
 GAM2540 DKFZp762O076 5' GGCAGCAGAGGCAGCAG 73957 CC GAT
 CTGC CCTCTGCT GCC
 |||| ||||| |||
 GACG GGAGACGA CGG
 AC __
 GAM2540 DPCR1 3' TGGGGGCACCAATGCAGA 56000 __ A
 TCTGC TG TGCCCCCA
 |||| || |||||

AGACG AC ACGGGGGT
 TA C
 GAM2540 DRF1 3' TGGAGGAGGCAGTGGGGGCAG 47762 T GATG C
 CTGCCCCC CTGCT CC CCA
 ||||| ||| |||
 GACGGGGG GACGG GG GGT
 T A__ A
 GAM2540 FAM3D 3' GGGGCTGAGGAGGAGGAGCAG 57947 _ _ GCTGAT
 CTGC CC CCTCT GCCC
 ||| || ||| |||
 GACG GG GGAGG CGGGG
 A A AGT__
 GAM2540 FBP17 3' TGGGAGCATCTGGCAGGCAGGG 73163 ____ _ C
 GGGCAG CTGCCCCCT CTGCT GATGC CCA
 ||||| ||| ||| |||
 GACGGGGG GACGG CTACG GGT
 ACG T A
 GAM2540 FBXO9 5' GGGGGCGGTGCAGAGGGGGCA 54251 TGA
 TGCCCCCTCTGC TGCCCC
 ||||| |||
 ACGGGGAGACG GCGGGG
 TG_
 GAM2540 FLJ10415 3' CAGCAGCAGAGGCAGCAG 36586 CC A
 CTGC CCTCTGCTG TG
 ||| ||||| ||
 GACG GGAGACGAC AC
 AC G
 GAM2540 FLJ10415 3' GGGAGGAACAGCAGCAGAGGCA 36588 CC _ ATG _
 G CTGCC CT CTGCTG CC CCC
 ||| || ||| |||
 GACGG GA GACGAC GG GGG
 A_ C AA_ A
 GAM2540 FLJ10468 3' ATCAGCAGAGCAGGACAG 36631 _ CC
 CTG CC CTCTGCTGAT
 ||| || |||||
 GAC GG GAGACGACTA
 A AC
 GAM2540 FLJ11126 3' GGCAGCAGAGAGGCCAG 37652 C C GAT
 CTG CC CTCTGCT GCC
 ||| || ||| |||
 GAC GG GAGACGA CGG
 C A ____
 GAM2540 FLJ12242 3' GGGGAGAGGCAGCAGAAGGGGC 45504 C ATG__
 GCCCC TCTGCTG CCCC
 ||| ||||| |||
 CGGGG AGACGAC GGGG
 A GGAGA
 GAM2540 FLJ12547 3' TGGAAGCACAGCGTGAGGGGGC 47136 _ A CC
 A TGCCCCCTC TGCTG TGC CCA
 ||||| ||| ||| |||

ACGGGGGAG GCGAC ACG GGT
 T _ AA
 GAM2540 FLJ12577 3' GGTGAGCAGGGGAGCA 48886 C T GA
 TGC CCC CTGCT TGCC
 ||| ||| |||| ||||
 ACG GGG GACGA GTGG
 A _ _
 GAM2540 FLJ12700 5' GGGGCAGTCAGGGAGCAG 46658 C CTGCT _
 CTGC CCCT GA TGCCCC
 |||| |||| || ||||
 GACG GGGA CT ACGGGG
 A _ _ G
 GAM2540 FLJ12770 3' GGGGCAGTTGATGAGGCAG 50680 CCC T GAT
 CTGCC TC GCT GCCCC
 |||| || ||| ||||
 GACGG AG TGA CGGGG
 AGT T _
 GAM2540 FLJ12998 3' TGGAGGGACAGAGCAGAGGGGC 43152 C GA _ _
 CAG CTG CCCCTCTGCT TG CCC CCA
 ||| |||| |||| || ||| |||
 GAC GGGGAGACGA AC GGG GGT
 C G_ A A
 GAM2540 FLJ13111 3' TGAGGGACACACAGAGGTGACA 47629 CCC C A _ C
 G CTG CCTCTG TG TG CCC CA
 ||| |||| || || ||| ||
 GAC GGAGAC AC AC GGG GT
 AGT _ _ A A
 GAM2540 FLJ13114 3' GGAGCTTGGGCAGCAGGGGCAG 44905 CT GAT C
 CTGCCCC CTGCT GC CC
 |||| |||| || ||
 GACGGGG GACGG CG GG
 AC GTT A
 GAM2540 FLJ14249 3' TGGGGACATCGGTGTGAAGGG 42647 C _ C
 CCC TC TGCTGATG CCCA
 ||| || |||| ||||
 GGG AG GTGGCTAC GGGGT
 A T A
 GAM2540 FLJ14594 3' GGAGCAGGCTAGGGGGCAG 52507 CT GA C
 CTGCCCCCT GCT TGC CC
 |||| |||| || ||| ||
 GACGGGGGA CGG ACG GG
 T_ _ A
 GAM2540 FLJ14642 3' GGGAAGCAGAGGTGGCAG 52577 C GATG
 CTGCC CCTCTGCT CCC
 |||| |||| || ||
 GACGG GGAGACGA GGG
 T A_
 GAM2540 FLJ14810 3' TGGGGACAGAGAGCAGGGGGCA 52705 CT GA_ C
 G CTGCCCCCT GCT TG CCCA
 |||| |||| || || ||||

GACGGGGGA CGA AC GGGGT
 _ GAG A
 GAM2540 FLJ20296 3' GGGCACAGCAGGGGACAG 35366 CC T A
 CTG CCC CTGCTG TGCCC
 ||| ||| ||||| |||||
 GAC GGG GACGAC ACGGG
 A _ _ _
 GAM2540 FLJ20619 5' GGGTGAGGCCAGGGGAGCAG 35894 _ CT GAT
 CTGC CCCCT GCT GCCC
 |||| |||| | |||
 GACG GGGGA CGG TGGG
 A C _ AG _
 GAM2540 FLJ20700 3' GGGAGGCCAAGGGGGCAG 36013 C CTGAT _
 CTGCCCCCT TG GCC CCC
 ||||| || ||| |||
 GACGGGGGA AC CGG GGG
 _ _ _ A
 GAM2540 FLJ22160 3' GGGCATCAGGGACGCAG 45034 CCCC G
 CTGC TCT CTGATGCCC
 |||| ||| |||||
 GACG AGG GACTACGGG
 C _ _
 GAM2540 FLJ23058 5' GGCATCTCGGGGCAGGGGGCAG 45527 _ CT
 CTGCCCCCT CTG GATGCC
 ||||| || |||||
 GACGGGGGA GGC CTACGG
 CGG T _
 GAM2540 FLJ23403 3' CAACAGCAATAGGGGGCAG 42204 C _ A
 CTGCCCCCT TGCTG TG
 ||||| |||| |
 GACGGGGGA ACGAC AC
 TA A
 GAM2540 FLJ32818 5' GGGGGTGCCAGGGAAGCAG 59074 C _ CT TGAT
 CTGC CCCT GC GCCCC
 |||| ||| || |||||
 GACG GGGA CG TGGGGG
 AA C _ _
 GAM2540 FREQ 3' TGGGAGCTGGAAGAAGGGGCA 27378 C G GAT C
 TGCCCC TCT CT GC CCA
 ||||| ||| || |||||
 ACGGGG AGA GG CG GGGT
 A A T _ A
 GAM2540 GMPPB 5' GGGCATAGCAGATGGGGCAG 97455 C A
 CTGCCCC TCTGCTG TGCCC
 ||||| ||||| |||||
 GACGGGG AGACGAT ACGGG
 T _
 GAM2540 HIC2 3' GGTGATGCAGCAGCGGGGCA 65873 CT AT _
 TGCCCC CTGCTG GCC
 ||||| ||||| |||

		ACGGGG GACGAC TGG		
		AC GTAG		
GAM2540	KBRAS2	3' TGAGGGCAAAGTAGAGG	34631	GA C
		CCTCTGCT TGCCC CA		
		GGAGATGA ACGGG GT		
		A_ A		
GAM2540	KIAA0057	3' TGGGGGCCGAGCAGGGGGCA	25426	CT GAT
		TGCCCCCT GCT GCCCCA		
		ACGGGGGA CGA CGGGGGT		
		_ GC_		
GAM2540	KIAA0265	5' GGGCTGGGACAGTGGGGGCAG	70442	T _ GAT
		CTGCCCCC CTG CT GCCC		
		GACGGGGG GAC GG CGGG		
		T A GT_		
GAM2540	KIAA0280	3' GGGAATCCAGAGAGGGGCAG	93307	_ CT G
		CTGCCCC CTCTG GAT CCC		
		GACGGGG GAGAC CTA GGG		
		A _ A		
GAM2540	KIAA0321	5' GGGTCTTTGCAGCAGGGGCAG	63059	CT T T
		CTGCCCC CTGC GA GCCC		
		GACGGGG GACG TT TGGG		
		AC T C		
GAM2540	KIAA0329	3' GGTGGCAGCAGAGGCAG	29941	CCC AT
		CTGCC TCTGCTG GCC		
		GACGG AGACGAC TGG		
		_ GG		
GAM2540	KIAA0540	3' GGGAACACCCCGGGGTGGGCAG	64616	C CTGA CC
		CTGCCC CTCTG TG CCC		
		GACGGG GGGGC AC GGG		
		T CCC_ AA		
GAM2540	KIAA0557	3' GGGCAGCGTATGGGGGCAG	78572	TC TGA
		CTGCCCCC TGC TGCCC		
		GACGGGGG ATG ACGGG		
		T_ CG_		
GAM2540	KIAA0620	3' GGGGGCTGGAGGGGGGCAG	62813	T G GAT
		CTGCCCCC CT CT GCCCC		
		GACGGGGG GA GG CGGGGG		
		_ _ T_		
GAM2540	KIAA0720	3' GGCCGAGCAGAGGGGGCA	62988	GAT
		TGCCCCCTCTGCT GCC		

ACGGGGGAGACGA CGG
 GC_
 GAM2540 KIAA0769 3' GGAGCAAAGAGGGGGGCAG 29758 T G GA C
 CTGCCCCC CT CT TGC CC
 ||||| || || ||
 GACGGGGG GA GA ACG GG
 _ _ A_ A
 GAM2540 KIAA0836 3' GCATCAAAGGGGGGCAG 65167 CTGC
 CTGCCCCCT TGATGC
 ||||| ||||
 GACGGGGGA ACTACG
 A__
 GAM2540 KIAA0913 5' TGGGGGCGAGGAAGAGAAGGC 69535 CC G GA
 GCC CTCT CT TGCCCCA
 || ||| || |||||
 CGG GAGA GG GCGGGGGT
 AA A A_
 GAM2540 KIAA0945 3' TGGGGGCGGGAAGGAGGGGCA 30907 CT GCTGA
 TGCCCC CT TGCCCCA
 |||| || |||||
 ACGGGG GA GCGGGGGT
 AG AGG_
 GAM2540 KIAA0980 3' TGGGAGCTGTACGAAGGAGCA 47999 CC C _ C
 G CTGC CCT TGCTGAT GC CCA
 ||| || ||||| || |||
 GACG GGA ACGACTG CG GGGT
 A_ _ T A
 GAM2540 KIAA1130 3' GGGAGGCAGAGGTAGCAG 63099 CC GATG
 CTGC CCTCTGCT CCC
 ||| ||||| ||
 GACG GGAGACGG GGG
 AT A_
 GAM2540 KIAA1136 3' GGCATGGGTAGAAGAGGACCAG 92959 CC _ _ G
 CTG CC CT CTGCT ATGCC
 || || || |||| ||||
 GAC GG GA GATGG TACGG
 CA A A G
 GAM2540 KIAA1193 3' GGGGCACAGAGGGCAG 68275 CC CTGA C
 CTGCCC TCTG TGCCC C
 |||| ||| |||| |
 GACGGG AGAC ACGGG G
 _ _ _ A
 GAM2540 KIAA1199 3' GGCCCAGCAGAGGGAGTAG 72931 C AT
 CTGC CCCTCTGCTG GCC
 ||| ||||| |||
 GATG GGGAGACGAC CGG
 A C_
 GAM2540 KIAA1259 3' GGGCGGAGAGAGGGGGCAG 50800 G GA
 CTGCCCCCTCT CT TGCCC
 ||||| || ||||

GACGGGGGAGA GA GCGGG
 _ G_
 GAM2540 KIAA1277 3' GCTGTCCTGCAGCGGGGACAG 65079 C T T_ _
 CTG CCCC CTGC GAT GC
 ||| ||| ||| ||| ||
 GAC GGGG GACG CTG CG
 A C TC T
 GAM2540 KIAA1277 3' GGGACAGCGGGGAGGCAG 65080 C T ATG
 CTGCC CC CTGCTG CCC
 ||||| || ||||| |||
 GACGG GG GGCGAC GGG
 A _ A_
 GAM2540 KIAA1277 3' GGGGACAGTGGGGACAG 65082 C TCT ATG
 CTG CCCC GCTG CCCC
 ||| ||| ||| |||
 GAC GGGG TGAC GGGG
 A _ A_
 GAM2540 KIAA1363 5' GGACACCGTAGAGGGGGCA 69791 T A _
 TGCCCCCTCTGC G TG CC
 ||||| ||||| ||| |||
 ACGGGGAGATG C AC GG
 _ C A
 GAM2540 KIAA1399 3' GGAGCCAACAGAGGGAGCAG 70793 C C AT C
 CTGC CCCTCTG TG GC CC
 ||| ||||| || |||
 GACG GGGAGAC AC CG GG
 A A _ A
 GAM2540 KIAA1610 5' GGGAGCGGCAGAGACGGCAG 67739 CC ATG
 CTGCC CTCTGCTG CCC
 |||| ||||| |||
 GACGG GAGACGGC GGG
 CA GA_
 GAM2540 KIAA1879 5' TGGAGGACGTGCAGAGGGTGCA 73949 C TG _ C
 G CTGC CCCTCTGC ATG CC CCA
 ||| ||||| ||| |||
 GACG GGGAGACG TGC GG GGT
 T _ A A
 GAM2540 KIAA1957 3' GGTGGGCGCGGAGGGAGCAG 76217 C TGAT _
 CTGC CCCTCTGC GCCC CC
 ||| ||||| ||| |||
 GACG GGGAGGCG CGGG GG
 A _ T
 GAM2540 KIF13B 3' CAGCAGCAGAGGGGACAG 83713 C A
 CTG CCCCTCTGCTG TG
 ||| ||||| ||| |||
 GAC GGGGAGACGAC AC
 A G
 GAM2540 KIF13B 3' CAGCAGCAGAGGGGACAG 31557 C A
 CTG CCCCTCTGCTG TG
 ||| ||||| ||| |||

GAC GGGGAGACGAC AC
 A G
 GAM2540 KRTHB2 3' TGGGGACAGACGGCAGAG 53454 A_ C
 CTCTGCTG TG CCCCCA
 ||||| || ||||
 GAGACGGC AC GGGGT
 AG A
 GAM2540 LIN-28 3' TGGGGGCAACCAGGAGGGGGG 45473 G A_
 CCCCTCT CTG TGCCCCCA
 ||||| || |||||
 GGGGGGA GAC ACGGGGGT
 G CA
 GAM2540 MESDC2 3' GGCAGGCAGAGGAAACAG 72918 CCC GA
 CTG CCTCTGCT TGCC
 || ||||| ||||
 GAC GGAGACGG ACGG
 AAA _
 GAM2540 MGC10334 5' GGGTGCGGTGCAGAGCAGAGCA 48321 CCC_ TGA C
 G CTGC CTCTGC TGC CCC
 ||| |||| || |||
 GACG GAGACG GCG GGG
 AGAC TG_ T
 GAM2540 MGC10765 3' GGGAGGCAGAGGGTGCAG 44564 C GATG
 CTGC CCCTCTGCT CCC
 ||| ||||| |||
 GACG GGGAGACGG GGG
 T A__
 GAM2540 MGC13010 5' TGGAGGCACGGCAGAGGAGGCA 52062 C A C
 G CTGCC CCTCTGCTG TGCC CCA
 |||| ||||| |||| |||
 GACGG GGAGACGGC ACGG GGT
 A _ A
 GAM2540 MGC15416 5' TGGGGGCAGCCAGGGAGAGGGC 57349 C G A_
 A TGCCC CTCT CTG TGCCCCCA
 |||| ||| || |||||
 ACGGG GAGG GAC ACGGGGGT
 A _ CG
 GAM2540 MGC16025 3' TGGAAGGTTTTAGCAGAAAAAG 53029 CCC_ T C_
 G CC TCTGCTGA GCC CCA
 || ||||| || |||
 GG AGACGATT TGG GGT
 AAAA T AA
 GAM2540 MGC21688 3' GTGTTTGGAGAGGAGGCAG 58917 C GCT
 CTGCC CCTCT GATGC
 |||| |||| ||||
 GACGG GGAGA TTGTG
 A GGT
 GAM2540 MGC35558 3' TGAGGGCATCGTGGAAGGG 59422 C TG T C
 CCC TC C GATGCCC CA
 ||| || | ||||| ||

			GGG AG G CTACGGG GT		
			A GT _ A		
GAM2540	MGC5566	3'	TGGAAGCATTGCCAGAGGGG 44125	CT	CC
			CCCCTCTG GATGC CCA		
			GGGGAGAC TTACG GGT		
			CG AA		
GAM2540	NOPAR	5'	GGGGGGAGCAGAGGAGGCAG 54860	C	GATG
			CTGCC CCTCTGCT CCCCC		
			GACGG GGAGACGA GGGGG		
			A G _		
GAM2540	NOPAR	5'	TGGAGACAAGGTAGGGGGGAGC 54861	_	GA CCC
	AG		CTGC CCCCTCTGCT TG CCA		
			GACG GGGGGGATGG AC GGT		
			A A _ AGA		
GAM2540	OBTP	3'	GGAAGCCTCCAAGCAGAGGACA 34667	CCC	_ T CC
	G		CTG CCTCTGCT GA GC CC		
			GAC GGAGACGA CT CG GG		
			A _ AC C AA		
GAM2540	P114-RHO-GEF	3'	GGGGGCATGGGCAGAGAGGGC 31674	C	G
			GCCC CTCTGCT ATGCCCCC		
			CGGG GAGACGG TACGGGGG		
			A G		
GAM2540	p25	3'	TGGGGGTGACAAGAGGAGACAG 23839	CCC	GC A
			CTG CCTCT TG TGCCCCCA		
			GAC GGAGA AC GTGGGGGT		
			AGA _ A		
GAM2540	P2RXL1	3'	TGGAGGTCTGGGAGAGAGAGCA 19565	CCC	G GAT C
	G		CTGC CTCT CT GCC CCA		
			GACG GAGA GG TGG GGT		
			AGA G TC _ A		
GAM2540	P2RXL1	3'	TGGGAGAGAGAGCAGAGGGCGG 19566	_	GATGCC
	CAG		CTGCC CCCTCTGCT CCCA		
			GACGG GGGAGACGA GGGT		
			C GAGAGA		
GAM2540	PP591	5'	TGGAGGGCCTTGCAGAGGGGCA 48152	C	TGAT _
	G		CTGCCCC TCTGC GCCC CCA		
			GACGGGG AGACG CGGG GGT		
			_ TTC _ A		
GAM2540	PRO1257	5'	TGAGGGCATGAGCAGAGG 38327	G	C
			CCTCTGCT ATGCCC CA		

GGAGACGA TACGGG GT
G A
GAM2540 REPRIMO 3' TGGGGGCAGGTGGAGAGGGCGG 39532 C TG GA
CTGCCC CTC CT TGCCCCCA
||||| ||| || |||||
GGCGGG GAG GG ACGGGGGT
A GT _
GAM2540 RINZF 5' GGGGGCGAGACAGAGGGGG 43939 _ GA
CCCCCTCTG CT TGCCCCC
||||||| || |||||
GGGGGAGAC GA GCGGGGG
A _
GAM2540 RP4-622L5 3' GGATATACAGACGGGGGCAG 39428 _ CTG G
CTGCCCCC TCTG AT CC
||||||| ||| |||
GACGGGGG AGAC TA GG
C ATA _
GAM2540 SIAT8A 5' GGAGCATCGCTCGGAGGGGACA 13144 C C_ C
TG CCCCTCTG TGATGC CC
|| ||||| ||||| ||
AC GGGGAGGC GCTACG GG
A TC A
GAM2540 SKIP 3' TGGGGGCAGGCAGAAGGG 33713 C GA
CCC TCTGCT TGCCCCCA
||| ||||| |||||
GGG AGACGG ACGGGGGT
A _
GAM2540 SKIP 3' TGGGGGCAGGCAGAAGGG 56248 C GA
CCC TCTGCT TGCCCCCA
||| ||||| |||||
GGG AGACGG ACGGGGGT
A _
GAM2540 SLC16A6 3' GGGGACACAAGGAGGCAG 17441 C CTGC A C
CTGCC CCT TG TG CCCC
||||| ||| ||| |||||
GACGG GGA AC AC GGGG
A _ _ A
GAM2540 SLC2A10 5' GGAGGGCAGGGCAGGAGGGACA 48556 C CT GA _
G CTG CCC CTGCT TGCCC CC
||| ||| ||||| ||||| ||
GAC GGG GACGG ACGGG GG
A AG G_ A
GAM2540 SLC37A1 3' GGCCAGCAGAGAAGCAG 39092 CCC AT
CTGC CTCTGCTG GCC
||| ||||| |||
GACG GAGACGAC CGG
AA_ _
GAM2540 SPRY4 3' GGATAGCAGGGGAGGCAG 49021 C ATG
CTGCC CCTCTGCTG CC
||||| ||||| |||

			GACGG GGGGACGAT GG		
			A A__		
GAM2540	SPRY4	3'	GGGCATCATCAGGCAG 49027	CCCTC C	
			CTGCC TG TGATGCCC		
			GACGG AC ACTACGGG		
			_____ T		
GAM2540	SSH-3	3'	GGAGCAGGAGCAGGGGCAG 37418	CTC GA C	
			CTGCCCC TGCT TGC CC		
			GACGGGG ACGA ACG GG		
			_____ GG A		
GAM2540	SSH-3	3'	GGAGCAGGGGCAGGGGCAG 37419	CTC GA C	
			CTGCCCC TGCT TGC CC		
			GACGGGG ACGG ACG GG		
			_____ GG A		
GAM2540	SSH-3	3'	GGGGCAGGGGCAGGGGCAG 37420	CTC GA	
			CTGCCCC TGCT TGCCCC		
			GACGGGG ACGG ACGGGG		
			_____ GG		
GAM2540	STAT2	3'	GGGTACAGAGGGGACA 19454	C CTGA	
			TG CCCCTCTG TGCCC		
			AC GGGGAGAC ATGGG		
			A _____		
GAM2540	STC2	3'	GGAGAAGGGTGGAGAGGAGGCA 14934	C G GAT _____	
	G		CTGCC CCTCT CT GCCC CC		
			GACGG GGAGA GG TGGG GG		
			A _ _ _ AAGA		
GAM2540	STX1B2	5'	GGAGCAGCAGCAGAGGCAG 54619	CCC A C	
			CTGCC TCTGCTG TGC CC		
			GACGG AGACGAC ACG GG		
			_____ G A		
GAM2540	SYT13	3'	GGCTGGCAGAGTAGGCAG 95102	CC GAT	
			CTGCC CTCTGCT GCC		
			GACGG GAGACGG CGG		
			AT T__		
GAM2540	TED	3'	GGGGGCACAGAGGGG 32273	CTGA	
			CCCCTCTG TGCCCCC		
			GGGGAGAC ACGGGGG		

GAM2540	TGIF2	3'	GCCACAGCAGGGGGCAG 41751	CT AT	
			CTGCCCCCT GCTG GC		

GACGGGGGA CGAC CG
 — AC
 GAM2540 THTPA 5' TGAGGACATCAGCAGCAGTGG 44511 C _ C C
 CC CT CTGCTGATG CC CA
 || || || || || || || || || ||
 GG GA GACGACTAC GG GT
 T C A A
 GAM2540 TM4-B 5' GGACACAGAGGGGCAG 25889 C C ATG
 CTGCCCC TCTG TG CC
 || || || || || || || || || ||
 GACGGGG AGAC AC GG
 — — A—
 GAM2540 YKT6 3' GG TAGCTGCAGAGGGGGGAG 22642 G TGA
 CT CCCCCTCTGC TGCC
 || || || || || || || || || ||
 GA GGGGGAGACG ATGG
 G TCG
 GAM2540 ZIC5 5' TGAAGCGGGGCAGAGGG 53615 GA CC
 CCCTCTGCT TGCC CA
 || || || || || || || || || ||
 GGGAGACGG GCGG GT
 — AA
 GAM2540 ZNF263 3' GGAATTGGCAGAGGAAGTAG 20427 CC TG G
 CTGC CCTCTGC AT CC
 || || || || || || || || || ||
 GATG GGAGACG TA GG
 AA GT A
 GAM2540 ZNF263 3' GGGAGGTGCAGAGGCAGCAG 20428 CC TGAT _
 CTGC CCTCTGC GCC CCC
 || || || || || || || || || ||
 GACG GGAGACG TGG GGG
 AC — A
 GAM2540 LOC116173 3' GCCAGCCAGAGAGGACAG 57427 C C _ AT
 CTG CC CTCTG CTG GC
 || || || || || || || || || ||
 GAC GG GAGAC GAC CG
 A A C _
 GAM2540 LOC124470 3' TGGAAAGGCAGGCAGAGGG 76149 GA C__
 CCCTCTGCT TGCC CCA
 || || || || || || || || || ||
 GGGAGACGG ACGG GGT
 — AAA
 GAM2540 LOC124590 3' TGGAGGCACCAGAGGGGCA 76153 C CTGA C
 TGCCCC TCTG TGCC CCA
 || || || || || || || || || ||
 ACGGGG AGAC ACGG GGT
 _ C_ A
 GAM2540 LOC124997 3' GCCTTCAGCTGAGGGGGCAG 74848 T T_
 CTGCCCCCTC GCTGA GC
 || || || || || || || || || ||

		GACGGGGGAG CGACT CG			
		T TC			
GAM2540	LOC127841 5'	GCCCAGGCAGAGAGGGCAG 75188	C	GAT	
		CTGCCC CTCTGCT GC			
		GACGGG GAGACGG CG			
		A ACC			
GAM2540	LOC129181 5'	TGGGGGCTGCAGCAGGGAGGCA 76315	C T	AT	
		TGCC CC CTGCTG GCCCCCA			
		ACGG GG GACGAC CGGGGGT			
		A _ GT			
GAM2540	LOC129303 3'	GGGAACAGCAGAGGGGATAG 75375	C	ATG	
		CTG CCCCTCTGCTG CCC			
		GAT GGGGAGACGAC GGG			
		A AA_			
GAM2540	LOC130940 5'	GGGGGTGGCGGAGAGGACAG 57939	C C	GAT	
		CTG CC CTCTGCT GCCCCC			
		GAC GG GAGGCGG TGGGGG			
		A A _			
GAM2540	LOC143437 5'	TGGGGATACAGCAGGGAGCA 83861	CC T	A C	
		TGC CC CTGCTG TG CCCCCA			
		ACG GG GACGAC AT GGGGT			
		A_ _ _ A			
GAM2540	LOC145241 5'	TGAAGGTGATCAGCAGGGGCAG 63529	CTC	_ CC	
		CTGCCCC TGCTGAT GCC CA			
		GACGGGG ACGACTA TGG GT			
		_ G AA			
GAM2540	LOC146802 3'	GCAGCAGCAGAGAGCAG 78726	CCC	A	
		CTGC CTCTGCTG TGC			
		GACG GAGACGAC ACG			
		A_ G			
GAM2540	LOC147043 5'	GGCATCAGAAGGGGAGC 88504	_	CTG	
		GC CCCCT CTGATGCC			
		CG GGGGA GACTACGG			
		A A_			
GAM2540	LOC147645 5'	CACGGTTGGGGGAGGCAG 79066	_	T A	
		CTGCC CCCTC GCTG TG			
		GACGG GGGGG TGGC AC			
		A T _			
GAM2540	LOC147912 5'	TGGGGGCGAAAAGGGGGGACAG 79266	C	GCTGA	
		CTG CCCCTCT TGCCCCCA			

GAC GGGGGGA GCGGGGGT
 A AAA__
 GAM2540 LOC148413 3' GGGGCATCGGGGGGCAG 79581 CTGCT
 CTGCCCCCT GATGCCCC
 ||||| |||||
 GACGGGGGG CTACGGGG

 GAM2540 LOC149386 5' TGGGGGCGTCAGCAGAGGGGCA 85565 C
 G CTGCCCC TCTGCTGATGCCCCCA
 ||||| |||||
 GACGGGG AGACGACTGCGGGGGT

 GAM2540 LOC150481 3' TGAGGGGATGGGCAGAGGAGGC 80717 C G G _
 GCC CCTCTGCT AT CCCC CA
 || ||||| || |||||
 CGG GGAGACGG TA GGGG GT
 A G _ A
 GAM2540 LOC152220 3' TGGGACTAGCAGCAGAGGCAG 86771 CCC ATGCC
 CTGCC TCTGCTG CCA
 |||| ||||| |||||
 GACGG AGACGAC GGGT
 GATCA
 GAM2540 LOC152627 3' GGGAGGCAGAGGGTGCAG 81512 C GATG
 CTGC CCCTCTGCT CCC
 |||| ||||| |||||
 GACG GGGAGACGG GGG
 T A__
 GAM2540 LOC155066 5' GGACCCGGCCAGAGGGACAG 82210 CC _ ATG
 CTG CCCTCTG CTG CC
 || ||||| || |||||
 GAC GGGAGAC GGC GG
 A_ C CCA
 GAM2540 LOC157860 3' GGGGCATCTGGGCGCAG 87880 C TCTGCT
 CTGC CCC GATGCCCC
 |||| ||||| |||||
 GACG GGG CTACGGGG
 C T____
 GAM2540 LOC158062 3' GGGGAGAGCCACAGAGGAGCAG 87964 CC C AT ____
 CTGC CCTCTG TG GC CCCC
 |||| ||||| || |||||
 GACG GGAGAC AC CG GGGG
 A_ _ _ AGA
 GAM2540 LOC158191 3' TGAGGGGATGGGCAGAGGAGGC 82686 C G G _
 GCC CCTCTGCT AT CCCC CA
 || ||||| || |||||
 CGG GGAGACGG TA GGGG GT
 A G _ A
 GAM2540 LOC159121 3' TGGGGGCAAGGGCAAGAGG 88389 _ GA
 CCTCT GCT TGCCCCCA
 |||| ||||| |||||

		GGAGA CGG ACGGGGGT		
		A GA		
GAM2540	LOC159199 5'	GGGCAGCAGAGTGAGCAG 83066	CCC	GAT
		CTGC CTCTGCT GCCC		
		GACG GAGACGA CGGG		
		AGT ____		
GAM2540	LOC162083 3'	GGAAAGCTGAGGGGGCAG 83208	T	GATG
		CTGCCCCCTC GCT CC		
		GACGGGGGAG CGA GG		
		T AA__		
GAM2540	LOC163682 3'	GGGGGCACAGGGGGCAG 88412	CTGCT	A
		CTGCCCCCT G TGCCCCC		
		GACGGGGGA C ACGGGGG		

GAM2540	LOC164714 3'	GGCAGCAGGGGGGGCAG 88586	GAT	
		CTGCCCCCTCTGCT GCC		
		GACGGGGGGGACGA CGG		

GAM2540	LOC169693 5'	GGGAAGCAGAGGAGCAG 88630	CC	GATG
		CTGC CCTCTGCT CCC		
		GACG GGAGACGA GGG		
		A_ A__		
GAM2540	LOC196214 5'	GTACAGCAAGGGGGCAG 91183	C	A
		CTGCCCCCT TGCTG TGC		
		GACGGGGGA ACGAC ATG		

GAM2540	LOC196410 3'	TGGGGGCACCAGGGAGAATCAG 89034	CCCC	G A
		CTG CTCT CTG TGCCCCCA		
		GAC GAGG GAC ACGGGGGT		
		TAA_ _ C		
GAM2540	LOC196955 5'	TGAGGGCATTGTAAAAGG 77876	C_ T	C
		CCT TGC GATGCCC CA		
		GGA ATG TTACGGG GT		
		AA _ A		
GAM2540	LOC200093 3'	TGGGGGCATCGGCAAGG 63781	C	
		CCT TGCTGATGCCCCCA		
		GGA ACGGCTACGGGGGT		

GAM2540	LOC200563 5'	GCATCAGTCAGTGGACAG 91656	CCC T	_
		CTG CC CTG CTGATGC		

		GAC GG GAC GACTACG		
		A__ T T		
GAM2540	LOC200734 3'	TGAAGGCATCGGTTAAGGGCA	90284	CCTCT CC
		TGCCC GCTGATGCC CA		
		ACGGG TGGCTACGG GT		
		AAT__ AA		
GAM2540	LOC201685 5'	GCCAGCAGACAGGGCAG	91842	CC AT
		CTGCCC TCTGCTG GC		
		GACGGG AGACGAC CG		
		AC _		
GAM2540	LOC203238 3'	GTTTCAGCAGAAGTGGCAG	90824	CCC T
		CTGCC TCTGCTGA GC		
		GACGG AGACGACT TG		
		TGA T		
GAM2540	LOC203554 5'	GGGAGGCAGCAGAGGGG	92328	GAT _
		CCCCTCTGCT GCC CCC		
		GGGGAGACGA CGG GGG		
		_ A		
GAM2540	LOC220024 5'	GGGAGCTGAGCGCAGCAGAGAG	95032	CCC AT__ C
	CAG	CTGC CTCTGCTG GC CCC		
		GACG GAGACGAC CG GGG		
		A__ GCGAGT A		
GAM2540	LOC221184 5'	TGGGGGTGCCCCAGCAGCGGGG	93411	T A__
	GCAG	CTGCCCC CTGCTG TGCCCCA		
		GACGGGGG GACGAC GTGGGGGT		
		C CCC		
GAM2540	LOC221922 5'	GGGAGGGTCAGGAGGGCAG	94255	CCTC G G _
		CTGCCC T CTGAT CC CCC		
		GACGGG A GACTG GG GGG		
		_ G _ A		
GAM2540	LOC221922 5'	GGGGGAGCAGGAGGGCAG	94258	C T GATG
		CTGCCC C CTGCT CCCCC		
		GACGGG G GACGA GGGGG		
		A _ _		
GAM2540	LOC221922 5'	GGGGGAGCAGGAGGGCAG	94259	C T GATG
		CTGCCC C CTGCT CCCCC		
		GACGGG G GACGA GGGGG		
		A _ _		
GAM2540	LOC221964 3'	GGGGCAGGGGCAGGGGCAG	95607	CTC GA
		CTGCCCC TGCT TGCCCC		

				GACGGGG	ACGG	ACGGGG			
				___	GG				
GAM2540	LOC253367	3'	GGGGAGTTTCGAGGGGGCA	99438			TGCT	T	_
			TGCCCCCTC	GA	GC	CCCC			
			ACGGGGGAG	CT	TG	GGGG			
			___	T	A				
GAM2540	LOC253531	5'	TGGGGATACAGCAGGGAGCA	98227			CC	T	A
			TGC	CC	CTGCTG	TG	CCCCA		
			ACG	GG	GACGAC	AT	GGGGT		
			A	_	_	_	A		
GAM2540	LOC253974	3'	TGGGGGCATCAGCAGAGGGGGC	99284					
	AG		CTGCCCCCTCTGCTGATGCCCCCA						
			GACGGGGGAGACGACTACGGGGGT						
GAM2540	LOC254050	3'	GGAAGGCAGAGGTGGCAG	96562			C		GATG
			CTGCC	CCTCTGCT	CC				
			GACGG	GGAGACGG	GG				
			T	AA	___				
GAM2540	LOC254181	5'	GGGCCCCAGCAGAGCAGGCAG	99442			CC		AT
			CTGCC	CTCTGCTG	GCCC				
			GACGG	GAGACGAC	CGGG				
			AC	CC					
GAM2540	LOC254263	3'	GGCTCAGCAGGGGGGGCAG	96369			T		T
			CTGCCCCC	CTGCTGA	GCC				
			GACGGGGG	GACGACT	CGG				
GAM2540	LOC255394	5'	TGAGGGCCCCAGAGGGGG	96544			CTGAT		C
			CCCCCTCTG	GCCC	CA				
			GGGGGAGAC	CGGG	GT				
			CC	___	A				
GAM2540	LOC256073	5'	GGAAGCTCCAAGAGGGGCAG	98487			CC	GCT	T
			CTGCCC	TCT	GA	GC	CC		
			GACGGG	AGA	CT	CG	GG		
			___	AC	_	_	AA		
GAM2540	LOC256254	3'	GTTTCAGCAGAAGTGGCAG	97902			CCC		T
			CTGCC	TCTGCTGA	GC				
			GACGG	AGACGACT	TG				
			TGA	T					
GAM2540	LOC256530	3'	GGGAGTTCAGTGGGGACAG	98622			C	TCT	T
			CTG	CCCC	GCTGA	GC	CCC		

		GAC GGGG TGACT TG GGG		
		A _ _ A		
GAM2540	LOC256949 5'	GGCTGCGGAGGAGGCAG 96985	C	TGAT
		CTGCC CCTCTGC GCC		
		GACGG GGAGGCG CGG		
		A T _		
GAM2540	LOC257095 5'	GGGCAGCGGGGGCAG 98721	TCT	GAT C
		CTGCCCCC GCT GCC C		
		GACGGGGG CGA CGG G		
		_ _ A		
GAM2540	LOC257450 3'	GGGGTCAAGCAGAGGAGG 91451	C	GAT
		CC CCTCTGCT GCCCC		
		GG GGAGACGA TGGGG		
		A AC _		
GAM2540	LOC51125 5'	GGAGGGCAGAGGAGGCGG 32743	C	GCTGAT _
		CTGCC CCTCT GCCC CC		
		GGCGG GGAGA CGGG GG		
		A _ _ A		
GAM2540	LOC56832 3'	GGCTATCAGCAGAAGGATCAG 65447	CC C	_
		CTG CC TCTGCTGAT GCC		
		GAC GG AGACGACTA CGG		
		TA A T		
GAM2540	LOC56964 5'	GGACAGTCAGTGGGAGCAG 63252	C T _	ATG
		CTGC CCC CTG CTG CC		
		GACG GGG GAC GAC GG		
		A T T A _		
GAM2540	LOC90119 5'	GGGGAGGGCAGAGGGGTCAG 62211	C	GATG
		CTG CCCCTCTGCT CCCC		
		GAC GGGGAGACGG GGGG		
		T GA _		
GAM2540	LOC90462 3'	GGCCCAGCAGAGGGCAG 63572	CC	AT
		CTGCCC TCTGCTG GCC		
		GACGGG AGACGAC CGG		
		_ C _		
GAM2540	LOC90494 5'	GGAGTAGGCAGAGGGATCAG 63734	CC	GA C
		CTG CCCTCTGCT TGC CC		
		GAC GGGAGACGG ATG GG		
		TA _ A		
GAM2540	LOC91040 3'	TGGGGGCATCGGCAAGG 65356	C	
		CCT TGCTGATGCCCCCA		

GGA ACGGCTACGGGGGT

GAM2540 LOC91974 5' TGGGAGCAAACCTTCAGAGAAGG 68365 CC CTGA_ C
CAG CTGCC CTCTG TGC CCCA

||||| ||||| ||| |||||
GACGG GAGAC ACG GGGT
AA TTCAA A

GAM2540 LOC92230 5' GGGGGCAAAGGGGCAG 69087 CTCTGC GA
CTGCCCC T TGCCCCC

||||||| | |||||
GACGGGG A ACGGGGG
____ AA

GAM2540 LOC92340 3' TGGGGACCTCAGTGGGGGCAG 69570 TCT TGC
CTGCCCCC GCTGA CCCCA

||||||| ||||| |||||
GACGGGGG TGA CT GGGGT
____ CCA

GAM2540 LOC92710 3' GGGTGCAGAGAGGCAG 70866 CC TGAT
CTGCC CTCTGC GCCC

||||| ||||| |||
GACGG GAGACG TGGG
A_ ____

GAM2541 BSN 3' CCCAGCATCATGAGCAAG 14380 A CTTCA AA
CTTGCTCAT GT GC GG

||||||| || || ||
GAACGAGTA TA CG CC
C ____ AC

GAM2541 CLCA2 3' CCTTACACTTTGGCTATGAACA 22563 C TTCAGC_
A TTG TCATAGTC AAGG

||| ||||| |||||
AAC AGTATCGG TTCC
A TTTCACA

GAM2541 CRY2 3' CCTTGCTCCGTGAGCAA 72661 AGTCTTC
TTGCTCAT AGCAAGG

||||||| |||||
AACGAGTG TCGTTCC
CC ____

GAM2541 FADD 3' TCCTCACTATGACACTGAGCAA 15126 TA TTC CA
G CTTGCTCA GTC AG AGGA

||||||| ||| || |||||
GAACGAGT CAG TC TCCT
CA TA_ AC

GAM2541 HLCS 5' TCCATTGAAGACTTGAACAAG 6421 C T CAA
CTTG TCA AGTCTTCAG GGA

||| ||| ||||| |||
GAAC AGT TCAGAAGTT CCT
A _ A_

GAM2541 MEST 3' CTGAAAGACCTATGAGCAA 70459 _ _
TTGCTCATAG TCTT CAG

||||||| ||||| |||

			AACGAGTATC AGAA GTC		
			C A		
GAM2541	PCDH7	5'	CCCCGCTGCATGAGCAG 51616	A TCTT	AA
			TTGCTCAT G CAGC GG		
			GACGAGTA C GTCG CC		
			— CC		
GAM2541	PCDH7	5'	CCCCGCTGCATGAGCAG 51619	A TCTT	AA
			TTGCTCAT G CAGC GG		
			GACGAGTA C GTCG CC		
			— CC		
GAM2541	PCDH7	5'	CCCCGCTGCATGAGCAG 11987	A TCTT	AA
			TTGCTCAT G CAGC GG		
			GACGAGTA C GTCG CC		
			— CC		
GAM2541	PLP2	5'	TCCTCGAAACCACGAGCAAG 12176	ATA C	AGCA
			CTTGCTC GT TTC AGGA		
			GAACGAG CA AAG TCCT		
			CAC _ C_		
GAM2541	PLXNA2	3'	TCCCTAAAGTTACTATGAGAAG 48003	G _	C CAA
			CTT CTCATAGT CTT AG GGA		
			GAA GAGTATCA GAA TC CCT		
			_ TT A _		
GAM2541	AP1GBP1	3'	CCTCAGACCAAGTGAGCAA 24346	A_	TCAGCA
			TTGCTCAT GTCT AGG		
			AACGAGTG CAGA TCC		
			AC C_		
GAM2541	AP1GBP1	3'	CCTCAGACCAAGTGAGCAA 55438	A_	TCAGCA
			TTGCTCAT GTCT AGG		
			AACGAGTG CAGA TCC		
			AC C_		
GAM2541	AP1GBP1	3'	CCTCAGACCAAGTGAGCAA 55444	A_	TCAGCA
			TTGCTCAT GTCT AGG		
			AACGAGTG CAGA TCC		
			AC C_		
GAM2541	CAP350	3'	CCTACTGAAGACTGGGC 29703	TA	CA
			GCTCA GTCTTCAG AGG		
			CGGGT CAGAAGTC TCC		
			_ A_		
GAM2541	DDX34	3'	TCCCTGCTGGAGACCAACAAG 28679	CTCATA	A
			CTTG GTCTTCAGCA GGA		

			GAAC	CAGAGGTCGT CCT		
			AAC__	C		
GAM2541	DKFZP586G1122	3'	CCGCAAAACTGTGAGCAA	61938	CTTCA AA	
			TTGCTCATAGT	GC GG		
			AACGAGTGTCA	CG CC		
			AAA__			
GAM2541	FAM10A6	3'	CCTTGCTGAAGGAAAAGCAA	72782	CATAG	
			TTGCT	TCTTCAGCAAGG		
			AACGA	GGAAGTCGTTCC		
			AAA__			
GAM2541	FLJ10546	5'	TGCAAAGACTATGAGCA	60184	CA	
			TGCTCATAGTCTT	GCA		
			ACGAGTATCAGAA	CGT		
			A_			
GAM2541	FLJ10726	3'	CTTAAGTATGAGCAGG	37042	CTTCAGC	
			CTTGCTCATAGT	AAG		
			GGACGAGTATCA	TTC		
			A_____			
GAM2541	KIAA0475	5'	CCTTAATACATGAGCAAG	30115	A C CAGC	
			CTTGCTCAT	GT TT AAGG		
			GAACGAGTA	CA AA TTCC		
			_ T _____			
GAM2541	KIAA1655	5'	CCTCACTGTGGATGAGCAA	67179	TAG T CA	
			TTGCTCA	TCT CAG AGG		
			AACGAGT	AGG GTC TCC		
			_____ T AC			
GAM2541	MGC3077	3'	TCCTTGTTTTTAGACTAT	44128	TC_	
			ATAGTCT	AGCAAGGA		
			TATCAGA	TTGTTCCCT		
			TTT			
GAM2541	RAB40C	3'	CCTTGTTTGGGATTATGAACAA	41278	C TC	
			TTG TCATAGTCT	AGCAAGG		
			AAC AGTATTAGG	TTGTTCC		
			A GT			
GAM2541	SENP2	3'	CTGCTGAAGAGCAGG	76832	ATAGTC A	
			CTTGCTC	TTCAGCA G		
			GGACGAG	AAGTCGT C		
			_____ C			
GAM2541	ST13	3'	CCTTGCTGAAGGAAAAGCAA	15431	CATAG	
			TTGCT	TCTTCAGCAAGG		

AACGA GGAAGTCGTTCC
AAA__
GAM2541 LOC118491 5' TCCTGTTGGAGAACTATGAGCA 74358 _ A
AG CTTGCTCATAGT CTTGAGCA GGA
||||||| ||||| |||
GAACGAGTATCA GAGGTTGT CCT
A _
GAM2541 LOC125228 3' CCTTTGGAACTATGGGCAA 74863 C GC
TTGCTCATAGT TTCA AAGG
||||||| ||| |||
AACGGGTATCA AGGT TTCC
A _
GAM2541 LOC126751 3' CCCTGCTGAGATTGAGCCAG 75072 T TA T A
CT GCTCA GTCT CAGCA GG
|| ||| ||| ||| ||
GA CGAGT TAGA GTCGT CC
C _ _ C
GAM2541 LOC144840 3' CCTACTGAAGACTGGAG 77526 A CA
CTC TAGTCTTCAG AGG
||| ||||| |||
GAG GTCAGAAGTC TCC
_ A_
GAM2541 LOC149052 3' CCTTGCTGAAGGAAAAGCAA 79872 CATAG
TTGCT TCTTCAGCAAGG
||||| |||||
AACGA GGAAGTCGTTCC
AAA__
GAM2541 LOC158886 3' CCTTGCTGAAGGAAAAGCAA 83722 CATAG
TTGCT TCTTCAGCAAGG
||||| |||||
AACGA GGAAGTCGTTCC
AAA__
GAM2541 LOC200197 3' CCCTGCCGACATGAGCAA 90016 A TTCA A
TTGCTCAT GTC GCA GG
||||||| ||| ||| ||
AACGAGTA CAG CGT CC
_ C_ C
GAM2541 LOC219731 5' CCAGGTTAAAACATGAGGAAG 94699 G C C AA
CTT CTCATAGT TT AGC GG
||| ||||| || ||| ||
GAA GAGTATCA AA TTG CC
G A _ GA
GAM2541 LOC221178 3' CCCTGCTGATGATGAGCAAG 95168 AGTCT A
CTTGCTCAT TCAGCA GG
||||||| ||||| ||
GAACGAGTA AGTCGT CC
GT_ C
GAM2541 LOC222407 5' CCTACACTGAAAACAATGAGCA 95973 A C CA_
A TTGCTCAT GT TTCAG AGG
||||||| || ||||| |||

			AACGAGTA CA AAGTC TCC		
			A A ACA		
GAM2541	LOC245718	3'	CCTTGCTGAAGGAAAAGCAA 92415	CATAG	
			TTGCT TCTTCAGCAAGG		
			AACGA GGAAGTCGTTCC		
			AAA__		
GAM2541	LOC256228	5'	CCTTGCTGAAGCAGGACAGCAA 97969	CATAGT	
			G CTTGCT CTTCAGCAAGG		
			GAACGA GAAGTCGTTCC		
			CAGGAC		
GAM2542	APM1	3'	AAGCCAACTCCATCTCT 17750 C A		
			AG AGGT GAGTTGGCTT		
			TC TCTA CTCAACCGAA		
			_ C		
GAM2542	CYP4A11	3'	AACTCCTGCCTGCCCTCCA 7584 AA _		
			TGGA GCAGGTAG AGTT		
			ACCT CGTCCGTC TCAA		
			CC C		
GAM2542	EHD2	3'	AAGCCAAGGCTTCTTCCCA 28207 A C AGAG		
			TGG AAG AGGT TTGGCTT		
			ACC TTC TTCG AACCGAA		
			C _ G__		
GAM2542	GALE	3'	AAAGCAGCAGCTGCCTGCTCTC 63858 A AGTTG		
	CA		TGGA AGCAGGTAG GCTTT		
			ACCT TCGTCCGTC CGAAA		
			C GACGA		
GAM2542	LCP1	3'	AAAGCCAACATGTGGCTCCTCC 11280 A_ AGGTAGA		
			GGA AGC GTTGGCTTT		
			CCT TCG CAACCGAAA		
			CC GTGTA__		
GAM2542	NEDD4	3'	CCACTTTCTACTTTCCA 70543 C TA T		
			TGGAAAG AGG GAGT GG		
			ACCTTTC TCT TTCA CC		
			A _ _		
GAM2542	VIPR1	3'	AGCCTACCTGCTCTCCA 17309 A A		
			TGGA AGCAGGTAG GTT		
			ACCT TCGTCCATC CGA		
			C _		
GAM2542	BTBD3	3'	AAAGCCAAACTCTTCTCTCCA 31024 AA C T _		
			TGGA G AGG AGAGTT GGCTTT		

ACCT C TCT TCTCAA CCGAAA
 — — — A
 GAM2542 FLJ20694 3' AAAGCCAAACTGACCATCTGCT 35966 AG — —
 TTCCA TGGAAAGCAGGT AGTT GGCTTT
 ||||| ||| |||||
 ACCTTTCGTCTA TCAA CCGAAA
 CCAG A
 GAM2542 HSPC157 5' GTCCTACTACCTGCTTTCCA 27191 — TT
 TGGAAAGCAGGTAG AG GGC
 ||||| || |||
 ACCTTTCGTCCATC TC CTG
 A —
 GAM2542 KIAA0543 3' AACTCTACCTCTTCCCA 69516 A C
 TGG AAG AGGTAGAGTT
 ||| ||| |||||
 ACC TTC TCCATCTCAA
 C —
 GAM2542 KIAA1522 3' CCACCCTCCTGCCTTCCA 65604 A T A T
 TGGAA GCAGG AG GT GG
 |||| ||| || |||
 ACCTT CGTCC TC CA CC
 C — C —
 GAM2542 PP1628 5' AAGCCAGCCCCTCCTCCCA 48069 AA C TAGA
 TGG AG AGG GTTGGCTT
 ||| ||| |||||
 ACC TC TCC CGACCGAA
 C_ C C_—
 GAM2542 TIX1 3' AGTTGGCTTTAAACCACCTGCT 62405 A T ——— TTGG
 TCCCA TGG AAGCAGG AGAG CT
 ||| ||||| ||| ||
 ACC TTCGTCC TTTC GA
 C ACCAAA — GGTT
 GAM2542 LOC118987 3' CCAACCCAAGGATCTGCTTTC 74393 AGA —
 GAAAGCAGGT GTTGG
 ||||| |||||
 CTTTCGTCTA CAACC
 GGAACC
 GAM2542 LOC132617 3' AAAGCCAACTCTACAATGCTCA 76405 A G_—
 A AGCA GTAGAGTTGGCTTT
 | ||| |||||
 A TCGT CATCTCAACCGAAA
 C AA
 GAM2542 LOC152503 3' CCACTTTCCTGCTTTCCA 86976 T T
 TGGAAAGCAGG AGAGT GG
 ||||| ||||| ||
 ACCTTTCGTCC TTTCA CC
 — —
 GAM2543 NFKBIL2 5' CCAGTACCTGGAGCTGGCACA 26447 G CAGG_—
 TGTG CCAGCTCCAG GG
 ||| ||||| ||

ACAC GGTCTGAGGTC CC
 _ CATGA
 GAM2543 PSD 5' CCCCTGAGCGCCTGGCCACA 12433 CTCCAG
 TGTGGCCAG CAGGGGG
 ||||| |||||
 ACACCGGTC GTCCCCC
 CGCGA_
 GAM2543 FLJ10815 5' TCTGCTGAAGCCAGCACA 37237 G CA C
 TGTG C GCT CAGCAGG
 ||| | ||| |||||
 ACAC G CGA GTCGTCT
 _AC A
 GAM2543 KIAA0237 3' TCCGCTGCAGCTGGCCACA 29233 CCA G
 TGTGGCCAGCT GCAG GGG
 ||||| ||| |||
 ACACCGGTCGA CGTC CCT
 _ G
 GAM2543 KIAA1076 3' ATCCCCCTGCCGGCAGCCCCTC 66118 T CCA _ A
 A TG GG GCT CC GCAGGGGGAT
 || || ||| ||| |||||
 AC CC CGA GG CGTCCCCCTA
 T C_ C C
 GAM2543 KIAA1649 5' CCCCTGCTGAAGTGGACC 51228 _ G C
 GG CCA CT CAGCAGGGGG
 || ||| ||| |||||
 CC GGT GA GTCGTCCCCC
 A _ A
 GAM2543 MGC17303 3' CCCCTGCTTGCGGAACCA 58232 _ A TCC
 TGG CC GC AGCAGGGGG
 ||| ||| |||||
 ACC GG CG TCGTCCCCC
 AA _ T_
 GAM2543 OASIS 3' CCCCTGCTGCTGCCCA 54563 C TCC
 TGG CAGC AGCAGGGGG
 ||| ||| |||||
 ACC GTCG TCGTCCCCC
 C _
 GAM2543 SDCCAG43 5' ATCCCCCTGCTGGCCGTAGCCC 70891 T CAGCT
 CA TG GGC CCAGCAGGGGGAT
 || ||| |||||
 AC CCG GGTGTCGCCCTA
 C ATGCC
 GAM2543 SPRY2 5' CCTGCTGGAGTGACCACA 20701 CCA
 TGTGG GCTCCAGCAGG
 |||| |||||
 ACACC TGAGGTCGTCC
 AG_
 GAM2543 LOC123242 3' CCCACTGAAGCTGGCCCA 76112 T C CA
 TG GGCCAGCT CAG GGG
 || ||||| ||| |||

		AC CCGGTCGA GTC CCC		
		— A A—		
GAM2543	LOC148738 5'	CCCCCTGGCTGGAGCTGACCCA 59888	T C	—
		TG GG CAGCTCCAGC AGGGGG		
		AC CC GTCGAGGTCG TCCCCC		
		— A G		
GAM2543	LOC151979 5'	ATCGTCCTGCTGAAGCAGGCCA 81245	A C	G
	CA	TGTGGCC GCT CAGCAGGG GAT		
		ACACCGG CGA GTCGTCCT CTA		
		A A G		
GAM2543	LOC154789 5'	CCCCCATGCATGGAGCTGCCAC 82026	C	— —
	A	TGTGGC AGCTCCA GCA GGGGG		
		ACACCG TCGAGGT CGT CCCCC		
		— A A		
GAM2543	LOC201116 5'	ATCCCCCTGCACAGACTGGCCA 89475	— CCA	
	C	GTGGCCAG CT GCAGGGGGAT		
		CACCGGTC GA CGTCCCCCTA		
		A CA—		
GAM2543	LOC202347 3'	TCTTGCTGGAGCCAACCCA 91950	T CCA	
		TG GG GCTCCAGCAGGG		
		AC CC CGAGGTCGTTCT		
		— AAC		
GAM2543	LOC222031 3'	ATCCCCCACCCTGTGGCCAC 95669	GCTC CA—	
		GTGGCCA CAG GGGGGAT		
		CACCGGT GTC CCCCCTA		
		— CCAC		
GAM2543	LOC253001 3'	CCCACTGAAGCTGGCCCA 97991	T C CA	
		TG GGCCAGCT CAG GGG		
		AC CCGGTCGA GTC CCC		
		— A A—		
GAM2543	LOC254896 5'	CCCATGGCATGGAGCTGCCAC 97859	C — AG—	
	A	TGTGG CAGCTCCA GC GGG		
		ACACC GTCGAGGT CG CCC		
		C A GTA		
GAM2543	LOC92840 3'	TCACCTGCAGCTGGCCACA 57249	CCA GG	
		TGTGGCCAGCT GCAGG GA		
		ACACCGGTCGA CGTCC CT		
		— A—		
GAM2544	ADCY2 3'	TCCAGTTTCCCAAAAACCCCA 65656	C AA C	
		TGGGGTT TTG AA ATTGGA		

			ACCCCAA AAC TT TGACCT		
			A CC _		
GAM2544	CARPX	5'	CTCTTCTTCAATAACCCCA 39814	C	AACATT
			TGGGGTT TTGAA GGAG		
			ACCCCAA AACTT TCTC		
			T CT____		
GAM2544	CNTNAP2	5'	CTCCCTTCAAGAACCCTA 27090		AACATT
			TGGGGTTCTTGAA GGAG		
			ATCCCAAGAACTT CCTC		
			C____		
GAM2544	KLHL3	3'	TCCCCAACCCCCAAGAACCCCA 88852		AAAACA A
			TGGGGTTCTTG TTGG GA		
			ACCCCAAGAAC AACC CT		
			CCCC__ C		
GAM2544	MDFI	3'	CCCATGTCCTCTCAGAACCCCA 19980		T_ AA T
			TGGGGTTCT GA ACAT GG		
			ACCCCAAGA CT TGTA CC		
			CT CC C		
GAM2544	SPAP1	3'	TCTCCAATATCTTCTTTTACCT 57838		TCTT AAC
			GGGT GAA ATTGGAGA		
			TCCA CTT TAACCTCT		
			TTTT CTA		
GAM2544	TRPM2	5'	CCCATGTGTCTCTAGAACCCCA 13862		T AA_ T
			TGGGGTTCT GA ACAT GG		
			ACCCCAAGA CT TGTA CC		
			T CTG C		
GAM2544	ARHF	3'	TCTTGTCTCGAAGAACCCCA 39279		_ A TT
			TGGGGTTCTT GA AACA GGA		
			ACCCCAAGAA CT TTGT TCT		
			G C _		
GAM2544	BM046	3'	CCAAAGCCTCCAAGAACCTCA 38056		AAAACA
			TGGGGTTCTTG TTGG		
			ACTCCAAGAAC AACC		
			CTCCGA		
GAM2544	DMRTA2	3'	CCCAAACAGGAACCCCA 61289		AAAACA A
			TGGGGTTCTTG TTGG G		
			ACCCCAAGGAC AACC C		
			A____ C		
GAM2544	FOXP1	3'	TCTTAGTGCCATCAAGAACCCC 52048		AAA G
	A		TGGGGTTCTTGA CATTG AGA		

		ACCCCAAGAACT GTGAT TCT	
		ACC _	
GAM2544 KIAA1052	3'	CTCCAATACCTCAGCCTCA 30942	TCT AAC
		TGGGGT TGA ATTGGAG	
		ACTCCG ACT TAACCTC	
		_ CCA_	
GAM2544 PTPNS1	3'	CTCCAAGTCCCAGAACCCCA 55839	T AAA A
		TGGGGTTCT G AC TTGGAG	
		ACCCCAAGA C TG AACCTC	
		_ CC_	
GAM2544 LOC116068	3'	AATATTTTCAAGACCCCA 74105	T C
		TGGGGT CTTGAAAA ATT	
		ACCCCA GAACTTTT TAA	
		_ A	
GAM2544 LOC118738	5'	CCAAGCCCTCCAGAACCCCA 76001	T AAACA
		TGGGGTTCT GA TTGG	
		ACCCCAAGA CT AACC	
		C CCCG_	
GAM2544 LOC152503	5'	CTCGTGGTTTCCAGGAACCCCA 86979	A ATTG
		TGGGGTTCTTG AAAC GAG	
		ACCCCAAGGAC TTTG CTC	
		C GTG_	
GAM2544 LOC256158	5'	CCAACATTTGAGAACCCCA 99484	TG AACA
		TGGGGTTCT AA TTGG	
		ACCCCAAGA TT AACC	
		GT AC_	
GAM2545 ADRA1A	3'	GGACAAGACAGGACCAAT 53951	TA G _
		GTTG CTTG TCTTG CC	
		TAAC GGAC AGAAC GG	
		CA _ A	
GAM2545 ATP8B2	5'	AAGACCTCCAAGTACAAT 65826	_____
		GTTGTA CTT GGTCTT	
		TAACATGAA CCAGAA	
		CCT	
GAM2545 CBS	5'	GCAAGAAGTTAACCAAGTAAAA 5363	G _____
C		GTT TACTTG TCTTGC	
		CAA ATGAACC AGAACG	
		A AATTGA	
GAM2545 CRACC	3'	GGGCAAGAAGACCAAAAC 41314	GTAC _____
		GTT TTGGTCT TGCCC	

			CAA AACCAGA ACGGG		
			____ AGA		
GAM2545 DMN	5'	GGGACAAGACCAGGGCAG	63023	A	—
		TTGT CTTGGTCTTG CCC			
		GACG GGACCAGAAC GGG			
		— A			
GAM2545 EPHB2	3'	GGGGCGGGAAATACAAGG	16701	G	CTTGG
		C TTGTA TCTTGCCCC			
		G AACAT AGGGCGGGG			
		G AA____			
GAM2545 GCNT3	3'	GGGGCAAGAGCATGTACAA	17644	T G	
		TTGTAC TG TCTTGCCCC			
		AACATG AC AGAACGGGG			
		T G			
GAM2545 LAMA2	3'	CAAGTATATCAAGTAAAAC	6464	G	—
		GTT TACTTGGT CTTG			
		CAA ATGAACTA GAAC			
		A TAT			
GAM2545 MINPP1	3'	GCAAGTCGGAAAGTACAATG	18109	GGT	—
		CGTTGTACTT CTTGC			
		GTAACATGAA GAACG			
		AGGCT			
GAM2545 PDE6C	3'	GGGGCAAAATAAAGTTCAAC	21690	T G C	
		GTTG ACTT GT TTGCCCC			
		CAAC TGAA TA AACGGGG			
		T A A			
GAM2545 BHMT	3'	GGAGCAAAATAAGTACAA	9932	GTC	—
		TTGTACTTG TTGC CC			
		AACATGAAT AACG GG			
		AA_ A			
GAM2545 CCR5	3'	GGGCAAGGAGACCACCAAC	6963	TACT	—
		GTTG TGGTCT TGCCC			
		CAAC ACCAGA ACGGG			
		C____ GGA			
GAM2545 CNR2	3'	GGGACAGGGTCAGTACAA	10235	T GT	—
		TTGTACT G CTTG CCC			
		AACATGA C GGAC GGG			
		_TG A			
GAM2545 DKFZP761C169	5'	GGAGTGGACAAGTACAAC	68423	G TG	—
		GTTGTACTTG TCT CC			

CAACATGAAC AGG GG
 _ TGA
 GAM2545 ELL2 5' GGAACAAGACCAATGAGACG 24896 GTAC CC
 CGTT TTGGTCTTG CC
 ||| ||||| ||
 GCAG AACCAGAAC GG
 AGT_ AA
 GAM2545 FLJ10774 3' GAGGCCCTTAAGTACATCG 45416 T _
 CG TGTACTT GGTCTT
 || ||||| |||||
 GC ACATGAA CCGGAG
 T TTC
 GAM2545 FLJ20274 3' GGGGCAAGATGCAGTACAA 63325 TG
 TTGTACT GTCTTGCCCC
 ||||| |||||
 AACATGA TAGAACGGGG
 CG
 GAM2545 FLJ22672 3' GGACAAGGCAGGTACAA 46597 G CC
 TTGTACTTG TCTTG CC
 ||||| ||| ||
 AACATGGAC GGAAC GG
 _ AA
 GAM2545 FXC1 3' GGAGCTATCGAAGTACAACG 69595 _ CTT _
 CGTTGTACTT GGT GC CC
 ||||| ||| ||
 GCAACATGAA CTA CG GG
 G T_ A
 GAM2545 GEMIN7 3' GGAGCTGGGCCAAGTACGAC 45559 T _
 GTTGTACTTGGTCT GC CC
 ||||| ||| ||
 CAGCATGAACCGGG CG GG
 T A
 GAM2545 KIAA0781 3' GGGGCAAGAACTCAAGAAC 68060 A _
 GT CTTGG TCTTGCCCC
 || ||| |||||
 CA GAACT AGAACGGGG
 A CAA
 GAM2545 KIAA1136 3' GGGGCAAGAGCAACAACG 92960 ACT G
 CGTTGT TG TCTTGCCCC
 |||| || |||||
 GCAACA AC AGAACGGGG
 _ G
 GAM2545 KIAA1163 3' GGAATTGGTCCCAGGTACAAC 79652 T_ TG_
 GTTGTACTTGG CT CC
 ||||| || ||
 CAACATGGACC GG GG
 CT TTAA
 GAM2545 KIAA1449 3' GGAGCAAGACTTCTAACG 40840 TACTT _
 CGTTG GGTCTTGC CC
 |||| ||||| ||

		GCAAT TCAGAACG GG	
		CT___ A	
GAM2545 KIAA1493	3'	GGGACAGATGAGTACAAC 64842	G TG
		GTTGTACTTG TCT CCC	
		CAACATGAGT AGA GGG	
		_ CA	
GAM2545 KIAA1582	5'	GGGGCAACAGCACAAATACAA 65991	C _ C_
		TTGTA TTG GT TTGCCCC	
		AACAT AAC CG AACGGGG	
		A A AC	
GAM2545 KIAA1855	3'	GGGGCAAGCAGCACACCG 93957	T A TG T
		CG TGT CT G CTTGCCCC	
		GC ACA GA C GAACGGGG	
		C C _ _	
GAM2545 LOC146714	3'	GGGACACCCCAGTACAAC 84749	T TCT _
		GTTGTACT GG TG CCC	
		CAACATGA CC AC GGG	
		C C_ A	
GAM2545 LOC146733	5'	GGCAAGAGAGATCCAGCAAC 84786	ACT _____
		GTTGT TGG TCTTGCC	
		CAACG ACC AGAACGG	
		_ TAGAG	
GAM2545 LOC158236	5'	GGGCAAAACCAGTAAGAC 88010	G T C
		GTT TACT GGT TTGCCC	
		CAG ATGA CCA AACGGG	
		A _ A	
GAM2545 LOC163412	5'	GGAACAAGACCACATACAA 83016	CT CC
		TTGTA TGGTCTTG CC	
		AACAT ACCAGAAC GG	
		AC AA	
GAM2545 LOC164382	3'	GGCAACTCCCCAAGTACAATG 88559	TC_
		CGTTGTACTTGG TTGCC	
		GTAACATGAACC AACGG	
		CCTC	
GAM2545 LOC255042	5'	GGGGCAAGGGGCAAAACG 97054	GTA TGG
		CGTT CT TCTTGCCCC	
		GCAA GG GGAACGGGG	
		AAC _	
GAM2545 LOC90120	5'	GGCCCGCACCAAGTACAAC 62215	CTT_
		GTTGTACTTGGT GCC	

		CAACATGAACCA CGG	
		CGCC	
GAM2545	LOC90620	5' GGGCAAAGGTCAGAAACAAC 64328	AC GT _
		GTTGT TTG CTT GCCC	
		CAACA GAC GAA CGGG	
		AA TG A	
GAM2546	ADAT1	3' CCAACCTGGTGAAACCCTGT 24913	T
		ACGGGGTTTCACCA GTTGG	
		TGTCCCAAAGTGGT CAACC	
		C	
GAM2546	AICDA	3' CTGGCCAACATGGCAAACCCC 40693	CA
	GT	ACGGGGTTT CCATGTTGGTTAG	
		TGCCCCAAA GGTACAACCGGTC	
		AC	
GAM2546	AK1	3' CCAACATGGCAAACCCC 6635	CA
		GGGGTTT CCATGTTGG	
		CCCCAAA GGTACAACC	
		AC	
GAM2546	ALDH3B1	3' CTAACATGGCGAAACCCCGT 93156	A
		ACGGGGTTTC CCATGTTGG	
		TGCCCCAAAG GGTACAATC	
		C	
GAM2546	ALPP	3' CTAACACGGTGAAACCCC 69417	A
		GGGGTTTCACC TGTTGG	
		CCCCAAAGTGG ACAATC	
		C	
GAM2546	ANKH	3' CTGGCCAACATGGCGAAACCCT 55068	A
	GT	ACGGGGTTTC CCATGTTGGTTAG	
		TGTCCCAAAG GGTACAACCGGTC	
		C	
GAM2546	APOL1	3' CTAACACAGTGAAACCCCGT 14738	CA
		ACGGGGTTTCAC TGTTGG	
		TGCCCCAAAGTG ACAATC	
		AC	
GAM2546	ATM	3' CCAGTATGGTGAAACCCTGT 5294	
		ACGGGGTTTCACCATGTTGG	
		TGTCCCAAAGTGGTATGACC	
GAM2546	ATP1A2	3' CTGGCCAACATGGTGAAACCCT 7364	
	GT	ACGGGGTTTCACCATGTTGGTTAG	

TGTCCCAAAGTGGTACAACCGGTC

GAM2546 BCAS1 3' CCAACATCATGAAACCCCGT 14708 CC
ACGGGGTTTCA ATGTTGG
||||||| |||||
TGCCCAAAGT TACAACC
AC

GAM2546 BHMT2 3' CTGACCAACATGGTGAAACCCT 34732
GT ACGGGGTTTCACCATGTTGGTTAG
|||||||
TGTCCCAAAGTGGTACAACCAGTC

GAM2546 BRCA1 5' CCAACGTGGTGAAACTCCGT 24551
ACGGGGTTTCACCATGTTGG
|||||||
TGCCTCAAAGTGGTGCAACC

GAM2546 BRCA1 3' CTGGCCAACATGGTGAAACCCC 24556
GGGGTTTCACCATGTTGGTTAG
|||||||
CCCCAAAGTGGTACAACCGGTC

GAM2546 BRCA1 3' CTGGCCAACATGGTGAAACCCC 24557
GGGGTTTCACCATGTTGGTTAG
|||||||
CCCCAAAGTGGTACAACCGGTC

GAM2546 BRCA1 3' CTGGCCAACATGGTGAAACCCC 24558
GGGGTTTCACCATGTTGGTTAG
|||||||
CCCCAAAGTGGTACAACCGGTC

GAM2546 BRCA1 3' CTGGCCAACATGGTGAAACCCC 24559
GGGGTTTCACCATGTTGGTTAG
|||||||
CCCCAAAGTGGTACAACCGGTC

GAM2546 C5R1 3' CCAGCATGGTGAAACCCCGT 9973
ACGGGGTTTCACCATGTTGG
|||||||
TGCCCAAAGTGGTACGACC

GAM2546 CASP10 3' CCAATACGGCAAAACCTC 53247 CA A
GGGGTTT CC TGTTGG
||||| || |||||
CTCCAAA GG ATAACC
AC C

GAM2546 CASP10 3' CCAATACGGCAAAACCTC 53248 CA A
GGGGTTT CC TGTTGG
||||| || |||||

			CTCCAAA GG ATAACC		
			AC C		
GAM2546	CD68	3'	CTGGCCAACATGGTGAAACCCT 60505		
	GT		ACGGGGTTTCACCATGTTGGTTAG		
			TGTCCCAAAGTGGTACAACCGGTC		
GAM2546	CEACAM5	3'	CCAACATCGTGAAACCCC 16421	C	
			GGGGTTTCAC ATGTTGG		
			CCCCAAAGTG TACAACC		
			C		
GAM2546	CHST5	3'	CCAACATAGTGAAACCCC 25087	C	
			GGGGTTTCAC ATGTTGG		
			CCCCAAAGTG TACAACC		
			A		
GAM2546	COG7	3'	CTGACCAACATGGTGAAACCCC 68252		
			GGGGTTTCACCATGTTGGTTAG		
			CCCCAAAGTGGTACAACCAGTC		
GAM2546	COPA	3'	CCAACATGGCAACACCCCGT 16478	TTCA	
			ACGGGGT CCATGTTGG		
			TGCCCCA GGTACAACC		
			CAAC		
GAM2546	CORO2A	3'	CTGACCAACATGGTGAAACCCC 54495		
			GGGGTTTCACCATGTTGGTTAG		
			CCCCAAAGTGGTACAACCAGTC		
GAM2546	CPM	3'	CTGACCAACATGGTGAAACCCT 60407		
	GT		ACGGGGTTTCACCATGTTGGTTAG		
			TGTCCCAAAGTGGTACAACCAGTC		
GAM2546	CRACC	3'	CTGGCCAACATGGTGAAACCCC 41310		
			GGGGTTTCACCATGTTGGTTAG		
			CCCCAAAGTGGTACAACCGGTC		
GAM2546	CTMP	3'	CAACACGATGAAACTCCGT 54945	CCA	
			ACGGGGTTTCA TGTTG		
			TGCCTCAAAGT ACAAC		
			AGC		
GAM2546	CTSS	3'	CTAACATGGTGAAACCCC 15818		
			GGGGTTTCACCATGTTGG		

CCCCAAAGTGGTACAATC

GAM2546 CUBN 3' CCAGCATGGTGAAACCTC 8419
GGGGTTTTCACCATGTTGG
|||||
CTCCAAAGTGGTACGACC

GAM2546 CYB561 3' CTAACAAACACAGTGAAACCCC 10350 CA G
GT ACGGGGTTTCAC TGTT GTTAG
||||| ||| ||||
TGCCCCAAAGTG ACAA CAATC
AC A

GAM2546 CYP4F3 3' CCAATATGGTGAAACCACGT 8000 G
ACG GGTTTTCACCATGTTGG
||| |||||||
TGC CCAAAGTGGTATAACC
A

GAM2546 DBT 3' CCAACATGGTGAAACCCC 10369
GGGGTTTTCACCATGTTGG
|||||
CCCCAAAGTGGTACAACC

GAM2546 DBT 3' CTGGCCAACATGGTGAAACCCC 10372
GGGGTTTTCACCATGTTGGTTAG
|||||
CCCCAAAGTGGTACAACCGGTC

GAM2546 DDOST 3' CTAACACGGTAAAACCCTGT 19063 C A
ACGGGGTTT ACC TGTTGG
||||| ||| |||||
TGTCCCAA TGG ACAATC
A C

GAM2546 DFFA 3' CTAACATGGTGAAACCCTGT 16593
ACGGGGTTTTCACCATGTTGG
|||||
TGTCCCAAAGTGGTACAATC

GAM2546 DMC1 3' CCAACATGGAGAAACCCC 23942 A
GGGGTTTC CCATGTTGG
||||| |||||
CCCCAAAG GGTACAACC
A

GAM2546 DNASE2 3' CTGGCCAACATGGTGAAACCCC 9100
GGGGTTTTCACCATGTTGGTTAG
|||||
CCCCAAAGTGGTACAACCGGTC

GAM2546 DVL3 3' CTGGCCAACATAGCAAAACCCT 16644 CACC
GT ACGGGGTTT ATGTTGGTTAG
||||| |||||

			TGTCCCAAA TACAACCGGTC	
			ACGA	
GAM2546	EGFL4	3'	CCAATATGGTGAAACCCC 62459	
			GGGGTTTCACCATGTTGG	
			CCCCAAAGTGGTATAACC	
GAM2546	EGFL5	3'	CAACATGGCGAAATCCCGT 87907	A
			ACGGGGTTTC CCATGTTG	
			TGCCCTAAAG GGTACAAC	
			C	
GAM2546	EHHADH	3'	CAACATAGCAAAACCCCTGT 10498	CACC
			ACGGGGTTT ATGTTG	
			TGTCCCAAA TACAAC	
			ACGA	
GAM2546	FANCD2	3'	CTGGCCAACATAGTGAAACCCC 53529	C
			GGGGTTTCAC ATGTTGGTTAG	
			CCCCAAAGTG TACAACCGGTC	
			A	
GAM2546	FCMD	3'	CTGGCCAACATAGTGAAACCCC 23036	C
	GT		ACGGGGTTTCAC ATGTTGGTTAG	
			TGCCCCAAAGTG TACAACCGGTC	
			A	
GAM2546	FGF2	3'	CCAACCTGGTGAAACCCCGT 10616	T
			ACGGGGTTTCACCA GTTGG	
			TGCCCCAAAGTGGT CAACC	
			C	
GAM2546	FGFR1	3'	GGCCAACATGGTGAAACCCC 32373	
			GGGGTTTCACCATGTTGGTT	
			CCCCAAAGTGGTACAACCGG	
GAM2546	FGFR2	3'	CTGGCCAACATGGTGAAACCCT 43774	
	GT		ACGGGGTTTCACCATGTTGGTTAG	
			TGTCCCAAGTGGTACAACCGGTC	
GAM2546	FLI1	3'	CCAACGTGGTGAAACCTC 77107	
			GGGGTTTCACCATGTTGG	
			CTCCAAAGTGGTGCAACC	
GAM2546	GAS7	3'	CTAACATGGTGAAACCCCGT 20847	
			ACGGGGTTTCACCATGTTGG	

TGCCCCAAAGTGGTACAATC

GAM2546	GGCX	3'	CCAACATGGCAAAACCCC	7701	CA
			GGGGTTT CCATGTTGG		
			CCCCAAA GGTACAACC		
			AC		
GAM2546	GNE	3'	AACATGGTGAAACCCCGT	19655	
			ACGGGGTTTCACCATGTT		
			TGCCCCAAAGTGGTACAA		
GAM2546	GRAF	3'	CGACGGTGAAGCCCCGT	31234	AT
			ACGGGGTTTCACC GTTG		
			TGCCCCGAAGTGG CAGC		
GAM2546	GRM6	3'	CCAATGTGGTGAAACCCTGT	7762	
			ACGGGGTTTCACCATGTTGG		
			TGTCCCAAAGTGGTGTAACC		
GAM2546	HCS	3'	CAACATGGCGAAACCCTGT	38970	A
			ACGGGGTTTC CCATGTTG		
			TGTCCCAAAG GGTACAAC		
			C		
GAM2546	HIP1	3'	CCAACATGGTGAAACCCC	19251	
			GGGGTTTCACCATGTTGG		
			CCCCAAAGTGGTACAACC		
GAM2546	HIP1	3'	CTGGCCAACATGGTGAAACCCC	19255	
	GT		ACGGGGTTTCACCATGTTGGTTAG		
			TGCCCCAAAGTGGTACAACCGGTC		
GAM2546	HLA-E	3'	CTAACACGGTGAACCCCGT	92675	A
			ACGGGGTTTCACC TGTTGG		
			TGCCCCAAAGTGG ACAATC		
			C		
GAM2546	HSPA5	3'	CCAACATGGTGAAACTCC	19282	
			GGGGTTTCACCATGTTGG		
			CCTCAAAGTGGTACAACC		
GAM2546	HUNK	3'	CAACATGGTGAAAGCCCGT	28178	G
			ACGGG TTTCACCATGTTG		

			TGCCC AAAGTGGTACAAC		
			G		
GAM2546	IAPP	3'	CCAACGTGGTGAAACCCTGT 6440		
			ACGGGGTTTCACCATGTTGG		
			TGTCCCAAAGTGGTGCAACC		
GAM2546	IFIT4	3'	CTAACACAGTGAAATCCCGT 71493	CA	
			ACGGGGTTTCAC TGTTGG		
			TGCCCTAAAGTG ACAATC		
			AC		
GAM2546	IFNAR1	3'	CCAACGTGGTGAAACCCC 7138		
			GGGGTTTCACCATGTTGG		
			CCCCAAAGTGGTGCAACC		
GAM2546	IL10	3'	CAACATGGTGAAACCCCGT 6923		
			ACGGGGTTTCACCATGTTG		
			TGCCCCAAAGTGGTACAAC		
GAM2546	IL11	3'	GCGAGACATGGCAAACCCCTGT 7188	CA	G_
			ACGGGGTTT CCATGTT GT		
			TGTCCCAA GGTACAG CG		
			AC AG		
GAM2546	IL12B	3'	CTGGGAAACATAACAAGACCCC 10990	CACC	GG
	GT		ACGGGGTTT ATGTT TTAG		
			TGCCCCAGA TACAA GGTC		
			ACAA AG		
GAM2546	IL17R	3'	CTGGCCAACATGGTGAAACCCC 27554		
			GGGGTTTCACCATGTTGGTTAG		
			CCCCAAAGTGGTACAACCGGTC		
GAM2546	IL18	3'	CCAACATGGTGAAACCTC 9590		
			GGGGTTTCACCATGTTGG		
			CTCCAAAGTGGTACAACC		
GAM2546	IL1R1	3'	AGCCAACATGGCAAACCCC 7920	CA	
			GGGGTTT CCATGTTGGTT		
			CCCCAAA GGTACAACCGA		
			AC		
GAM2546	IRAK4	3'	CTGGCCAACATGGTGAAACCCC 61843		
	GT		ACGGGGTTTCACCATGTTGGTTAG		

TGCCCCAAAGTGGTACAACCGGTC

GAM2546 KAI1	3' CTAACATGGTCAAACCCCGT 11123	
	ACGGGGTTTCACCATGTTGG	
	TGCCCCAAAGTGGTACAATC	
GAM2546 KCNA7	3' CTAACACGGTCAAACCCCGT 49898	A
	ACGGGGTTTCACC TGTTGG	
	TGCCCCAAAGTGG ACAATC	
	C	
GAM2546 KCNJ5	3' CTAACACGGTCAAACCCCGT 7973	A
	ACGGGGTTTCACC TGTTGG	
	TGCCCCAAAGTGG ACAATC	
	C	
GAM2546 KCNK3	3' CTAGGTGACATAGTGAGACCCC 11173	C G
	GGGGTTTCAC ATGTTG TTAG	
	CCCCAGAGTG TACAGT GATC	
	A G	
GAM2546 KIF1B	3' CCAATGTGATCAAACCCCGT 31265	C
	ACGGGGTTTCA CATGTTGG	
	TGCCCCAAAGT GTGTAACC	
	A	
GAM2546 KIF3B	3' CTGGCCAACATGGTGGAACCCC 17803	
GT	ACGGGGTTTCACCATGTTGGTTAG	
	TGCCCCAAGGTGGTACAACCGGTC	
GAM2546 KNSL1	3' CCAACGTGGCAAAACCTCGT 16941	CA
	ACGGGGTTT CCATGTTGG	
	TGCTCCAAA GGTGCAACC	
	AC	
GAM2546 LAMC2	3' CTGGCCAACATGGTCAAACCCCT 19908	
GT	ACGGGGTTTCACCATGTTGGTTAG	
	TGTCCCAAAGTGGTACAACCGGTC	
GAM2546 LAMP2	3' CTGGCCAACATGGTCAAACCCC 26572	
	GGGGTTTCACCATGTTGGTTAG	
	CCCCAAAGTGGTACAACCGGTC	
GAM2546 LDLR	3' CTAACAAGGTCAAACCCCGT 6735	A
	ACGGGGTTTCACC TGTTGG	

			TGCCCCAAAGTGG ACAATC	
			A	
GAM2546	LEP	3'	CTGGCCAACATGGTGAACCCC 5859	
	GT		ACGGGGTTTCACCATGTTGGTTAG	
			TGCCCCAAAGTGGTACAACCGGTC	
GAM2546	LILRB1	3'	CCAACATGGTGAACCCCTGT 22871	
			ACGGGGTTTCACCATGTTGG	
			TGTCCCAAAGTGGTACAACC	
GAM2546	LRR2	3'	CCAGCATGGCGAAACCCC 44741	A
			GGGGTTTC CCATGTTGG	
			CCCCAAAG GGTACGACC	
			C	
GAM2546	LRR2	3'	CTAAACAACATAGTGAACCCCT 44744	C G
	GT		ACGGGGTTTCAC ATGTTG TTAG	
			TGTCCCAAAGTG TACAAC AATC	
			A A	
GAM2546	LRR2	3'	GACATCATGACGAAACCCC 44746	AC TTG
			GGGGTTTC CATG GTT	
			CCCCAAAG GTAC CAG	
			CA TA_	
GAM2546	LUZP1	3'	CAATATAGTGAACCCCGT 54397	C
			ACGGGGTTTCAC ATGTTG	
			TGCCCCAAAGTG TATAAC	
			A	
GAM2546	MAFF	3'	CAACATGGTGAACCCCGT 25573	
			ACGGGGTTTCACCATGTTG	
			TGCCCCAAAGTGGTACAAC	
GAM2546	MAML1	3'	CCAACAGTAACACCAGTGAAC 29272	CA_____
	CCC		GGGGTTTCAC TGTTGG	
			CCCCAAAGTG ACAACC	
			ACCACAATG	
GAM2546	MCM4	3'	CCAAGATGGTGAACCCCGT 62576	G
			ACGGGGTTTCACCAT TTGG	
			TGCCCCAAAGTGGTA AACC	
			G	
GAM2546	MLLT4	3'	CTAACACGGTGAACCCCGT 21038	A
			ACGGGGTTTCACC TGTTGG	

			TGCCCCAAAGTGG ACAATC	
			C	
GAM2546	MOG	3'	CTGGCCAACATGGTGAAACCCC 11672	
			GGGGTTTTCACCATGTTGGTTAG	
			CCCCAAAGTGGTACAACCGGTC	
GAM2546	MS4A1	3'	CTGGCCAACATAGTGAAACCCC 5547	C
	GT		ACGGGGTTTTCAC ATGTTGGTTAG	
			TGCCCCAAAGTG TACAACCGGTC	
			A	
GAM2546	MSH3	3'	CTGGCCAACATGGCAAAACCCC 11690	CA
			GGGGTTT CCATGTTGGTTAG	
			CCCCAAA GGTACAACCGGTC	
			AC	
GAM2546	MTMR8	3'	CTAACACGGTGAAAACCC 31911	G A
			GGG TTTCACC TGTTGG	
			CCC AAAGTGG ACAATC	
			A C	
GAM2546	MYO1B	3'	CTGGCCAACATGGCAAAACCCT 25243	CA
	GT		ACGGGGTTT CCATGTTGGTTAG	
			TGTCCCAA GGTACAACCGGTC	
			AC	
GAM2546	NFKBIL2	3'	CTAACATGGTGAAACCCCGT 26451	
			ACGGGGTTTTCACCATGTTGG	
			TGCCCCAAAGTGGTACAATC	
GAM2546	NPHS1	3'	CTGGCCAACATGGTAAACTCC 17371	C
			GGGGTTT ACCATGTTGGTTAG	
			CCTCAA TGGTACAACCGGTC	
			A	
GAM2546	NT5C2	3'	CCAACATGGAGAAACCCC 25257	A
			GGGGTTTC CCATGTTGG	
			CCCCAAG GGTACAACC	
			A	
GAM2546	NUP62	3'	CTGGCCAACATGGTGAAACCCC 33784	
	GT		ACGGGGTTTTCACCATGTTGGTTAG	
			TGCCCCAAAGTGGTACAACCGGTC	
GAM2546	OPA3	3'	CTGGCCAACATGGTGAAACTCC 47844	
	GT		ACGGGGTTTTCACCATGTTGGTTAG	

TGCCTCAAAGTGGTACAACCGGTC

GAM2546 PA2G4 3' CTAACCAACATGGCGAAACCCT 71828 A
GT ACGGGGTTTC CCATGTTGGTTAG

||||||| |||||||||

TGTCCCAAAG GGTACAACCAATC

C

GAM2546 PAICS 3' CTGGCCAACATGGTGAAACCCT 22261
GT ACGGGGTTTCACCATGTTGGTTAG

||||||| |||||||||

TGTCCCAAAGTGGTACAACCGGTC

GAM2546 PCDH11X 3' CTAACACGGTGAAACCCC 28011 A
GGGGTTTCACC TGTTGG

||||||| |||||

CCCCAAAGTGG ACAATC

C

GAM2546 PCDH11Y 3' CTAACATGGTGAAACCCC 53160
GGGGTTTCACCATGTTGG

||||||| |||||||

CCCCAAAGTGGTACAATC

GAM2546 PDE4C 3' CTGGCCAACATGGTGAAACCCC 8102
GGGGTTTCACCATGTTGGTTAG

||||||| |||||||||

CCCCAAAGTGGTACAACCGGTC

GAM2546 PIK3R2 3' CCAAAATGGCAAAACCCCG 18510 CA G
CGGGGTTT CCAT TTGG

||||||| ||||| |||||

GCCCCAAA GGTA AACC

AC A

GAM2546 PLA2G2D 3' CCAACATGGCAAAACCTCGT 25710 CA
ACGGGGTTT CCATGTTGG

||||||| |||||||

TGCTCCAAA GGTACAACC

AC

GAM2546 POLH 3' CCAATATGGTGAAACCCC 22478
GGGGTTTCACCATGTTGG

||||||| |||||||

CCCCAAAGTGGTATAACC

GAM2546 PSD 5' CCAACGTAGTGAAACCCC 12432 C
GGGGTTTCAC ATGTTGG

||||||| |||||||

CCCCAAAGTG TGCAACC

A

GAM2546 PSMB2 3' CTGACCAACATGGTGAAACCCC 12471
GT ACGGGGTTTCACCATGTTGGTTAG

||||||| |||||||||

TGCCCCAAAGTGGTACAACCGGTC

GAM2546	PSMB2	3'	CTGGCCAACATGGTGAAACCCC	12472	
			GGGGTTTCACCATGTTGGTTAG		
			CCCCAAAGTGGTACAACCGGTC		
GAM2546	PSMB9	3'	CCAACATGGAGAAACCCCGT	12498	A
			ACGGGGTTTC CCATGTTGG		
			TGCCCCAAAG GGTACAACC		
			A		
GAM2546	PSMD5	3'	CCAATATGGCAAAACCCCTGT	18555	CA
			ACGGGGTTT CCATGTTGG		
			TGTCCCAA GGTATAACC		
			AC		
GAM2546	PTAFR	3'	CCAACATTGTAAAACCCC	8164	C C
			GGGGTTT AC ATGTTGG		
			CCCCAAA TG TACAACC		
			A T		
GAM2546	PTGIS	3'	CTGGCCAACATGGCGAAACCCC	8208	A
GT			ACGGGGTTTC CCATGTTGGTTAG		
			TGCCCCAAAG GGTACAACCGGTC		
			C		
GAM2546	RAB3B	3'	CTAACAAGGTGAAACCCCGT	12703	A
			ACGGGGTTTCACC TGTTGG		
			TGCCCCAAAGTGG ACAATC		
			A		
GAM2546	RAB7L1	3'	CCAACATACTGAAACCCCGT	15402	CC
			ACGGGGTTTCA ATGTTGG		
			TGCCCCAAAGT TACAACC		
			CA		
GAM2546	RAD1	3'	CCAACGTGGAGAAACCCC	12641	A
			GGGGTTTC CCATGTTGG		
			CCCCAAAG GGTGCAACC		
			A		
GAM2546	RAD1	3'	CCAACGTGGAGAAACCCC	56750	A
			GGGGTTTC CCATGTTGG		
			CCCCAAAG GGTGCAACC		
			A		
GAM2546	RBL1	3'	CCAACATGGAGAAACCCC	12787	A
			GGGGTTTC CCATGTTGG		

			CCCCAAAG GGTACAACC		
			A		
GAM2546	RBM3	3'	CTGACCAACATGGTGAAACCCC 71010		
			GGGGTTTTCACCATGTTGGT TAG		
			CCCCAAAGTGGTACAACCAGTC		
GAM2546	ROCK2	3'	CTGCCCAACATAGTGAAACTCC 66617	C	T
	GT		ACGGGGTTTTCAC ATGTTGG TAG		
			TGCCTCAAAGTG TACAACC GTC		
			A C		
GAM2546	SCAP2	3'	GGCCAACATGGTGAAACCCTGT 15425		
			ACGGGGTTTTCACCATGTTGGTT		
			TGTCCCAAAGTGGTACAACCGG		
GAM2546	SFRS2IP	5'	CAACATGGCAAACCCTGT 17536	CA	
			ACGGGGTTT CCATGTTG		
			TGTCCCAA GGTACAAC		
			AC		
GAM2546	SIM2	3'	CCAACAAGCTGAAACCCC 18623	CCA	
			GGGGTTTCA TGTG		
			CCCCAAAGT ACAACC		
			CGA		
GAM2546	SLC17A5	3'	CCAGCATGGTGAAACCCC 25830		
			GGGGTTTTCACCATGTTGG		
			CCCCAAAGTGGTACGACC		
GAM2546	SLC26A4	3'	CTAACATGGTAAAACCCCGT 6527	C	
			ACGGGGTTT ACCATGTTGG		
			TGCCCCAAA TGGTACAATC		
			A		
GAM2546	SLC28A2	3'	CTAACACGGTGAAACCCCGT 16149	A	
			ACGGGGTTTTCACC TGTG		
			TGCCCCAAAGTG ACAATC		
			C		
GAM2546	SLC2A6	3'	CTGGCCAACATGGTGAAACCCC 34571		
	GT		ACGGGGTTTTCACCATGTTGGT TAG		
			TGCCCCAAAGTGGTACAACCGGTC		
GAM2546	SLC31A1	3'	CCAACATGGGGAAACCCCGT 10275	A	
			ACGGGGTTTTC CCATGTTGG		

			TGCCCCAAAG GGTACAACC	
			G	
GAM2546	SMG1	3'	CTAACACGGTGAAACCCCGT 31348	A
			ACGGGGTTTCACC TGTG	
			TGCCCCAAAGTGG ACAATC	
			C	
GAM2546	STAT3	3'	CTAACACGGTGAAACCCCGT 13435	A
			ACGGGGTTTCACC TGTG	
			TGCCCCAAAGTGG ACAATC	
			C	
GAM2546	SUDD	3'	CAACATGGCGAAACCCTGT 15154	A
			ACGGGGTTTC CCATGTTG	
			TGTCCCAAAG GGTACAAC	
			C	
GAM2546	SULT2A1	3'	CTAACACGGTGAAACCCC 72228	A
			GGGGTTTCACC TGTG	
			CCCCAAAGTGG ACAATC	
			C	
GAM2546	SULT2A1	3'	CTGGCCAACATGATGAAACCCT 72229	C
			GGGGTTTCA CATGTTGGTTAG	
			TCCCAAAGT GTACAACCGGTC	
			A	
GAM2546	SUV39H2	3'	CCATCATGGTGAAACCCTGT 45455	T
			ACGGGGTTTCACCATG TGG	
			TGTCCCAAAGTGGTAC ACC	
			T	
GAM2546	SWAP70	3'	CCAACCTGGTGAAACCCTGT 71866	T
			ACGGGGTTTCACCA GTTGG	
			TGTCCCAAAGTGGT CAACC	
			C	
GAM2546	TBX6	3'	GCCAACATGGTGAAACCCTGT 55813	
			ACGGGGTTTCACCATGTTGGT	
			TGTCCCAAAGTGGTACAACCG	
GAM2546	TCF7	3'	CTGGCCAACATGGTGAAACCCT 13621	
	GT		ACGGGGTTTCACCATGTTGGTTAG	
			TGTCCCAAAGTGGTACAACCGGTC	
GAM2546	TEP1	3'	CTAACATAGTGAAACCCTGT 24046	C
			ACGGGGTTTCAC ATGTTGG	

		TGTCCCAAAGTG TACAATC	
		A	
GAM2546	TNFRSF1B	3' CTGGCCAACATGGTAAAACCCC 8396	C
		GGGGTTT ACCATGTTGGTTAG	
		CCCCAAA TGGTACAACCGGTC	
		A	
GAM2546	TNFSF10	3' CCAACATAGTGAAACCCC 15090	C
		GGGGTTTCAC ATGTTGG	
		CCCCAAAGTG TACAACC	
		A	
GAM2546	TNFSF14	3' CTAACATGGCAAACCCC 15080	CA
		GGGGTTT CCATGTTGG	
		CCCCAAA GGTACAATC	
		AC	
GAM2546	TNFSF15	3' CCAACGTGGAGAAACCCC 18864	A
		GGGGTTTC CCATGTTGG	
		CCCCAAAG GGTGCAACC	
		A	
GAM2546	TRIM14	3' CCAAGATGGTGAAACCCC 29507	G
		GGGGTTTCACCAT TTGG	
		CCCCAAAGTGGTA AACC	
		G	
GAM2546	TSNAX	3' CCAACGTGGCGAAACCTCGT 21156	A
		ACGGGGTTTC CCATGTTGG	
		TGCTCCAAAG GGTGCAACC	
		C	
GAM2546	UBE2G2	3' CTAACAGTGAAACCCTGT 65486	CA
		ACGGGGTTTCAC TGTTGG	
		TGTCCCAAAGTG ACAATC	
		—	
GAM2546	UBE2G2	3' CTAATACAGTGAAACCCC 65487	CA
		GGGGTTTCAC TGTTGG	
		CCCCAAAGTG ATAATC	
		AC	
GAM2546	UPK1B	3' CTGGCCAACATGGTGAAACCCC 23700	
	GT	ACGGGGTTTCACCATGTTGGTTAG	
		TGCCCCAAAGTGGTACAACCGGTC	
GAM2546	USP14	3' CCACATGGTGAAACCCTGT 18932	T
		ACGGGGTTTCACCATGT GG	

TGTCCCAAAGTGGTACA CC

GAM2546 VHL 3' CTAACACGGGTGAAACCCCGT 6851 A_

ACGGGGTTTCACC TGTTGG

||||||| |||||

TGCCCAAAGTGG ACAATC

GC

GAM2546 VHL 3' CTAACATGGTGAACCTC 6852

GGGGTTTCACCATGTTGG

|||||||

CTCCAAAGTGGTACAATC

GAM2546 VHL 3' CTGGCCAACATGGTAAAACCCC 6855 C

GGGGTTT ACCATGTTGGTTAG

||||| |||||||||

CCCCAAA TGGTACAACCGGTC

A

GAM2546 VHL 3' CTGGCCAACATGGTGAACCCCT 6856

GGGGTTTCACCATGTTGGTTAG

|||||||

TCCCAAAGTGGTACAACCGGTC

GAM2546 VPS41 3' CCAACATGGAGAAACCCC 27690 A

GGGGTTTC CCATGTTGG

||||| |||||||

CCCCAAAG GGTACAACC

A

GAM2546 WIG1 3' CTAACACAGTGAACCC 96100 CA

GGGGTTTCAC TGTTGG

||||||| |||||

CCCCAAAGTG ACAATC

AC

GAM2546 XT3 3' CTGGCCAACATGGCGAAACCCC 39910 A

GGGGTTTC CCATGTTGGTTAG

||||||| |||||||||

CCCCAAAG GGTACAACCGGTC

C

GAM2546 ZNF264 3' CTGGCCAACATGGCAAAACCCT 14212 CA

GT ACGGGGTTT CCATGTTGGTTAG

||||||| |||||||||

TGTCCCAA GGTACAACCGGTC

AC

GAM2546 ZNF36 3' CCAACATGGTAAAATCCCGT 95578 C

ACGGGGTTT ACCATGTTGG

||||||| |||||||

TGCCCTAAA TGGTACAACC

A

GAM2546 AF020591 3' CTAATATGGTGAACCCCTGT 27909

ACGGGGTTTCACCATGTTGG

|||||||

TGTCCCAAAGTGGTATAATC

GAM2546 AGMAT 3' CCAACATGGTGAAACCTCGT 45737
ACGGGGTTTCACCATGTTGG
|||||
TGCTCCCAAAGTGGTACAACC

GAM2546 AKAP11 3' CAACATGGTGAAACCCCGT 58457
ACGGGGTTTCACCATGTTG
|||||
TGCCCAAAGTGGTACAAC

GAM2546 AKR1D1 3' CTAACAAGGTGAAACCCCGT 21132 A
ACGGGGTTTCACC TGTTGG
|||||
TGCCCAAAGTGG ACAATC
A

GAM2546 ALTE 3' AACCAACATGGTGAAACCTCGT 60991
ACGGGGTTTCACCATGTTGGTT
|||||
TGCTCCCAAAGTGGTACAACCAA

GAM2546 ALTE 3' CTGGCCAACATGGCGAAACCCC 61000 A
GT ACGGGGTTTC CCATGTTGGTTAG
|||||
TGCCCAAAG GGTACAACCGGTC
C

GAM2546 APOF 3' CAACATGGCGAAACCCCGT 9690 A
ACGGGGTTTC CCATGTTG
|||||
TGCCCAAAG GGTACAAC
C

GAM2546 APXL2 3' CTAACACGGTGAAACCCCGT 75677 A
ACGGGGTTTCACC TGTTGG
|||||
TGCCCAAAGTGG ACAATC
C

GAM2546 ARNTL2 3' CCAATATGGTGAAACCCCGT 39842
ACGGGGTTTCACCATGTTGG
|||||
TGCCCAAAGTGGTATAACC

GAM2546 ARNTL2 3' CTGGCCAACATGGTGAAACCCC 39848
GT ACGGGGTTTCACCATGTTGGTTAG
|||||
TGCCCAAAGTGGTACAACCGGTC

GAM2546 ARSDR1 3' CTGGCCAACATGGTGAAACCCC 32623
GGGGTTTCACCATGTTGGTTAG
|||||

CCCCAAAGTGGTACAACCGGTC

GAM2546 ASAH1 3' CCAACATGGTGAAACCTCGT 64314
ACGGGGTTTCACCATGTTGG
|||||||
TGCTCCAAAGTGGTACAACC

GAM2546 ASB13 3' CCAACTTGATGAAACCCC 45543 C T
GGGGTTTCA CA GTTGG
||||||| || |||||
CCCCAAAGT GT CAACC
A T

GAM2546 BANP 3' CCAATATGGCAAAACCTC 66800 CA
GGGGTTT CCATGTTGG
||||| |||||
CTCCAAA GGTATAACC
AC

GAM2546 BFAR 3' CCAACATGGTGAAACCTC 61422
GGGGTTTCACCATGTTGG
|||||||
CTCCAAAGTGGTACAACC

GAM2546 BIA2 3' CTGGCCAACATGGTGAAACCCT 71793
GT ACGGGGTTTCACCATGTTGGTTAG
|||||||
TGTCCCAAAGTGGTACAACCGGTC

GAM2546 BIRC1 3' CCAGCATGGTGAAACCCC 16989
GGGGTTTCACCATGTTGG
|||||||
CCCCAAAGTGGTACGACC

GAM2546 BIVM 3' CTAACATGGTGAAACCCCGT 35157
ACGGGGTTTCACCATGTTGG
|||||||
TGCCCCAAAGTGGTACAATC

GAM2546 BTN3A2 3' CTAACACGGTGAAACCCCGT 23876 A
ACGGGGTTTCACC TGTTGG
||||||| |||||
TGCCCCAAAGTGG ACAATC
C

GAM2546 C1orf33 3' CTAACACGGTGAAACCCCGT 32984 A
ACGGGGTTTCACC TGTTGG
||||||| |||||
TGCCCCAAAGTGG ACAATC
C

GAM2546 C1orf34 3' CTGGCCAACATGGTGAAACCCC 61307
GT ACGGGGTTTCACCATGTTGGTTAG
|||||||

TGCCCCAAAGTGGTACAACCGGTC

GAM2546 C20orf106 3' CAACATGGTGAAACCCTGT 55896
ACGGGGTTTCACCATGTTG
|||||||
TGCCCCAAAGTGGTACAAC

GAM2546 C20orf106 3' CTGGCCAACACGGTGAAACCCC 55902 A
GGGGTTTCACC TGTTGGTTAG
||||||| |||||
CCCCAAAGTGG ACAACCGGTC
C

GAM2546 C20orf108 3' CTGGCCAACATGATGAAACCCC 55879 C
GT ACGGGGTTTCA CATGTTGGTTAG
||||||| |||||
TGCCCCAAAGT GTACAACCGGTC
A

GAM2546 C20orf12 3' CCAACATGGAGAAACCCCGT 36846 A
ACGGGGTTTC CCATGTTGG
||||||| |||||
TGCCCCAAAG GGTACAACC
A

GAM2546 C20orf142 3' CTAGCCAACATGATAAAACCCC 75281 CAC
GT ACGGGGTTT CATGTTGGTTAG
||||||| |||||
TGCCCCAAA GTACAACCGATC
ATA

GAM2546 C20orf175 3' CTGGCCAACATGATGAAACCCC 55925 C
GT ACGGGGTTTCA CATGTTGGTTAG
||||||| |||||
TGCCCCAAAGT GTACAACCGGTC
A

GAM2546 C20orf183 3' CTAACATGGTGAAACCCCGT 48533
ACGGGGTTTCACCATGTTGG
|||||||
TGCCCCAAAGTGGTACAATC

GAM2546 C20orf29 3' CTGGCCAACATAGTGAAACCCC 37709 C
GGGGTTTCAC ATGTTGGTTAG
||||||| |||||
CCCCAAAGTG TACAACCGGTC
A

GAM2546 C21orf108 3' CTTCCCAACATGGTGAAACCCC 90113 TT
GGGGTTTCACCATGTTGG AG
||||||| ||
CCCCAAAGTGGTACAACC TC
CT

GAM2546 C22orf19 3' CCGACATGGTGAAACCCTGT 14823
ACGGGGTTTCACCATGTTGG
|||||||

TGTCCCAAAGTGGTACAGCC

GAM2546 C22orf19 3' CTGGCCAACATGGTGAAACCCC 14824
GT ACGGGGTTTCACCATGTTGGTTAG
|||||||
TGTCCCAAAGTGGTACAACCGGTC

GAM2546 C22orf20 3' CTGGCCAACATAGCAAAACCCT 48196 CACC
GT ACGGGGTTT ATGTTGGTTAG
||||| |||||
TGTCCCAA TACAACCGGTC
ACGA

GAM2546 C2F 3' CCAACGTGGTGAAATCCCGT 22004
ACGGGGTTTCACCATGTTGG
|||||||
TGCCCTAAAGTGGTGCAACC

GAM2546 C4S-2 3' CTGGCCAACATGGTGAAACCCT 38449
GT ACGGGGTTTCACCATGTTGGTTAG
|||||||
TGTCCCAAAGTGGTACAACCGGTC

GAM2546 C6orf31 3' CCAGCTCTGACAAAACCCCG 48382 CAC T_
CGGGGTTT CA GTTGG
||||| || ||||
GCCCCAAA GT CGACC
ACA CT

GAM2546 C6orf5 3' CTAACACGGTGAAACTCC 31987 A
GGGGTTTCACC TGTTGG
||||||| |||||
CCTCAAAGTGG ACAATC
C

GAM2546 C6orf5 3' CTGGCCAACATGGTGAAACCCC 31989
GGGGTTTCACCATGTTGGTTAG
|||||||
CCCCAAAGTGGTACAACCGGTC

GAM2546 C8orf2 3' CCAACATGCGAAACCCC 24150 AC
GGGGTTTC CATGTTGG
||||| |||||
CCCCAAAG GTACAACC
C_

GAM2546 C9orf5 3' CTAGGCAACATGGCAAAACCCC 50106 CA G
GGGGTTT CCATGTTG TTAG
||||| ||||| ||||
CCCCAAA GGTACAAC GATC
AC G

GAM2546 CALN1 3' CCAACGTGGTGAAACCCC 49660
GGGGTTTCACCATGTTGG
|||||||

CCCCAAAGTGGTGCAACC

GAM2546 CBCIP2 3' CTGGCCAACATGGTGAAACCCT 52657
GT ACGGGGTTTCACCATGTTGGTTAG
|||||||
TGTCCCAAAGTGGTACAACCGGTC

GAM2546 CCR6 3' CCAACATGGCGAAACCCC 16440 A
GGGGTTTC CCATGTTGG
||||| |||||
CCCCAAAG GGTACAACC
C

GAM2546 cerk 3' CCAACATGGTGAAACCTCGT 43162
ACGGGGTTTCACCATGTTGG
|||||||
TGCTCCAAAGTGGTACAACC

GAM2546 CG012 5' CCAACATAGTGAAACCCC 84150 C
GGGGTTTCAC ATGTTGG
||||||| |||||
CCCCAAAGTG TACAACC
A

GAM2546 CGRP-RCP 3' CCAACATGGAAAAACCCC 27886 CA
GGGGTTT CCATGTTGG
||||| |||||
CCCCAAA GGTACAACC
AA

GAM2546 CHRFAM7A 3' CCAATGTGATAAAACCCC 96715 CAC
GGGGTTT CATGTTGG
||||| |||||
CCCCAAA GTGTAACC
ATA

GAM2546 CLDN15 3' CTGGCCAACATGGTGAAACCCT 57371
GT ACGGGGTTTCACCATGTTGGTTAG
|||||||
TGTCCCAAAGTGGTACAACCGGTC

GAM2546 CNNM1 3' CCAACATGGTGAAACCCC 40116
GGGGTTTCACCATGTTGG
|||||||
CCCCAAAGTGGTACAACC

GAM2546 CRTAM 3' CTGGCCAACATAGTGAAACCCC 39471 C
GT ACGGGGTTTCAC ATGTTGGTTAG
||||||| |||||
TGCCCCAAAGTG TACAACCGGTC
A

GAM2546 D21S2056E 3' CCAACATGGAGAAACCCC 14863 A
GGGGTTTC CCATGTTGG
||||| |||||

			CCCCAAAG GGTACAACC		
			A		
GAM2546	DDX34	3'	CCAACATGGAGAAACCCCGT 28665	A	
			ACGGGGTTTC CCATGTTGG		
			TGCCCCAAAG GGTACAACC		
			A		
GAM2546	DDX34	3'	CTAACACGGTGAAACCCCGT 28670	A	
			ACGGGGTTTCACC TGTTGG		
			TGCCCCAAAGTGG ACAATC		
			C		
GAM2546	DEGS	3'	CTGGCCAACACGGTGAAACCCC 59267	A	
			GGGGTTTCACC TGTTGGTTAG		
			CCCCAAAGTGG ACAACCGGTC		
			C		
GAM2546	DIS3	3'	CTGGCCAACATGGTAAAACGCC 30915	G	C
	GT		ACGG GTTT ACCATGTTGGTTAG		
			TGCC CAAA TGGTACAACCGGTC		
			G A		
GAM2546	DJ122O8.2	3'	CCAACATGGTGAAACCTC 40393		
			GGGGTTTCACCATGTTGG		
			CTCCAAAGTGGTACAACC		
GAM2546	dJ383J4.3	3'	CCAACATGGTGAAACCCC 67492		
			GGGGTTTCACCATGTTGG		
			CCCCAAAGTGGTACAACC		
GAM2546	DKFZP434B168	3'	CTAACACAGTGAAACCCCGT 31867	CA	
			ACGGGGTTTCAC TGTTGG		
			TGCCCCAAAGTG ACAATC		
			AC		
GAM2546	DKFZP434C171	3'	CTAACACAGTGAAACCCTGT 32191	CA	
			ACGGGGTTTCAC TGTTGG		
			TGTCCCAAAGTG ACAATC		
			AC		
GAM2546	DKFZp434E0519	3'	CAACATGGTGAAACCCCGT 50985		
			ACGGGGTTTCACCATGTTG		
			TGCCCCAAAGTGGTACAAC		
GAM2546	DKFZp434E2220	5'	CCAATATGGTGAAACCCCGT 34709		
			ACGGGGTTTCACCATGTTGG		

TGCCCCAAAGTGGTATAACC

GAM2546 DKFZP434F091 3' CTGGCCAACATGGTGAAACCCT 31894
GT ACGGGGTTTCACCATGTTGGTTAG
|||||||
TGCCCCAAAGTGGTACAACCGGTC

GAM2546 DKFZp434G171 3' CTGGCCAACACGGCAAAACCCC 80241 CA A
GT ACGGGGTTT CC TGTGTTAG
||||| || |||||
TGCCCCAA GG ACAACCGGTC
AC C

GAM2546 DKFZp434G171 3' CTGGCCAACATGGTGAAACCCT 80242
GT ACGGGGTTTCACCATGTTGGTTAG
|||||||
TGCCCCAAAGTGGTACAACCGGTC

GAM2546 DKFZP434I1735 3' CTGACCAACATGGTGAAACCCC 89169
GT ACGGGGTTTCACCATGTTGGTTAG
|||||||
TGCCCCAAAGTGGTACAACCAGTC

GAM2546 DKFZP434N1511 3' CTAACGTGGTGAAACCCCGT 93058
ACGGGGTTTCACCATGTTGG
|||||||
TGCCCCAAAGTGGTGCAATC

GAM2546 DKFZp547C176 3' CTGGCCAACATGGTGAAACCCC 67801
GT ACGGGGTTTCACCATGTTGGTTAG
|||||||
TGCCCCAAAGTGGTACAACCGGTC

GAM2546 DKFZp547G183 3' CTGGCCAACATGGCGAAACCCC 38642 A
GGGGTTTC CCATGTTGGTTAG
||||| |||||
CCCCAAAG GGTACAACCGGTC
C

GAM2546 DKFZP564A022 3' CTAACATGGTGAAACCCCGT 48973
ACGGGGTTTCACCATGTTGG
|||||||
TGCCCCAAAGTGGTACAATC

GAM2546 DKFZP564B1023 3' CAACATGGTGAAATCCCGT 49360
ACGGGGTTTCACCATGTTG
|||||||
TGCCCTAAAGTGGTACAAC

GAM2546 DKFZP564B1023 3' CTAACCAACATGGAGAAACCCT 49364 A
GT ACGGGGTTTC CCATGTTGGTTAG
||||| |||||

			TGTCCCAAAG GGTACAACCAATC		
			A		
GAM2546	DKFZP564I052	3'	CTGGCCAACATGGTGAAACCCT 67284		
			GGGGTTTTCACCATGTTGGTTAG		
			TCCCAAAGTGGTACAACCGGTC		
GAM2546	DKFZp564K142	3'	CTGGCCAACATGGTGAAACCCC 50432		
		GT	ACGGGGTTTTCACCATGTTGGTTAG		
			TGCCCCAAAGTGGTACAACCGGTC		
GAM2546	DKFZP564M182	3'	CTGGCCAACATGGTGAAACCCT 78626		
		GT	ACGGGGTTTTCACCATGTTGGTTAG		
			TGTCCCAAAGTGGTACAACCGGTC		
GAM2546	DKFZP564M182	3'	CTTACATGGTGAAACCCC 78628	T	
			GGGGTTTTCACCATGT GG		
			CCCCAAAGTGGTACA TC		
			T		
GAM2546	DKFZP566J2046	3'	CTAACAGGGTGAAACCCCGT 49138	A	
			ACGGGGTTTTCACC TGTTGG		
			TGCCCCAAAGTGG ACAATC		
			G		
GAM2546	DKFZP586C1324	3'	CTGGCCAACATGGTGAAACCCC 70358		
		GT	ACGGGGTTTTCACCATGTTGGTTAG		
			TGCCCCAAAGTGGTACAACCGGTC		
GAM2546	DKFZP586D2223	3'	CCAACATGGTTAAACCCCGT 38287	C	
			ACGGGGTTT ACCATGTTGG		
			TGCCCCAAA TGGTACAACC		
			T		
GAM2546	DKFZp727G131	3'	CTGGCCAACATGGTGAAACCCC 59694		
			GGGGTTTTCACCATGTTGGTTAG		
			CCCCAAAGTGGTACAACCGGTC		
GAM2546	DKFZP761G1913	3'	CTGGGTAATATGGCAAAACCCC 49695	CA	G
			GGGGTTT CCATGTTG TTAG		
			CCCCAAA GGTATAAT GGTC		
			AC G		
GAM2546	DRF1	3'	CCAACATGGCGAAACCCC 47743	A	
			GGGGTTTTC CCATGTTGG		

CCCCAAAG GGTACAACC
 C
 GAM2546 DRF1 3' CCAACGTGGTCAAACCCCGT 47744
 ACGGGGTTTCACCATGTTGG
 |||||
 TGCCCCAAAGTGGTGCAACC

 GAM2546 ERAP140 3' CTGGCCAACATGGTCAAACCCC 75703
 GGGGTTTCACCATGTTGGTTAG
 |||||
 CCCCAAAGTGGTACAACCGGTC

 GAM2546 ERGL 3' CTGGCCAACATGGTCAAACCCCT 41817
 GT ACGGGGTTTCACCATGTTGGTTAG
 |||||
 TGTCCCAAAGTGGTACAACCGGTC

 GAM2546 FBXO27 3' CTGGCCAACATGGTCAAACCCC 75010
 GT ACGGGGTTTCACCATGTTGGTTAG
 |||||
 TGCCCCAAAGTGGTACAACCGGTC

 GAM2546 FBXO6 3' CTGGCCAACACGGTCAAACCCCT 37993 A
 GT ACGGGGTTTCACC TGTTGGTTAG
 |||||
 TGTCCCAAAGTGG ACAACCGGTC
 C
 GAM2546 FBXO9 3' CAACATGGCAAAACACCGT 25653 G CA
 ACGG GTTT CCATGTTG
 ||| ||| |||||
 TGCC CAAA GGTACAAC
 A AC
 GAM2546 FKSG17 3' CTGGCCAACATGATCAAACCCCT 50154 C
 GT ACGGGGTTTCA CATGTTGGTTAG
 |||||
 TGTCCCAAAGT GTACAACCGGTC
 A
 GAM2546 FLJ00060 3' CTAATGTGGTCAAACCCCGT 61746
 ACGGGGTTTCACCATGTTGG
 |||||
 TGCCCCAAAGTGGTGTAATC

 GAM2546 FLJ10008 3' CTAACATGGTCAAACCCC 36185
 GGGGTTTCACCATGTTGG
 |||||
 CCCCAAAGTGGTACAATC

 GAM2546 FLJ10043 3' CCAACAAGGCGAAACCCCTGT 36231 A A
 ACGGGGTTTC CC TGTTGG
 ||||| || |||||

	TGTCCCAAAG GG ACAACC	
	C A	
GAM2546 FLJ10139 3'	CAACATGGTGAGACCCCGT 36315	
	ACGGGGTTTCACCATGTTG	
	TGCCCCAGAGTGGTACAAC	
GAM2546 FLJ10460 3'	CTGGGTAACATGGTGAAATCCC 36616	G
	GGGGTTTCACCATGTTG TTAG	
	CCCTAAAGTGGTACAAT GGTC	
	G	
GAM2546 FLJ10520 3'	CTGACCAACATGGTGAAACCCC 36706	
	GGGGTTTCACCATGTTGGTTAG	
	CCCCAAAGTGGTACAACCAGTC	
GAM2546 FLJ10547 3'	CCAACATGGTGAAATGAAACCC 36775	
C	GGGGTT TCACCATGTTGG	_____
	CCCCAA AGTGGTACAACC	
	AGTAA	
GAM2546 FLJ10607 3'	CCAAAATGGTGAAACCCTGT 77625	G
	ACGGGGTTTCACCAT TTGG	
	TGTCCCAAAGTGGTA AACC	
	A	
GAM2546 FLJ10704 3'	CTGGCCAACATGGTGAAACCCT 36978	
GT	ACGGGGTTTCACCATGTTGGTTAG	
	TGTCCCAAAGTGGTACAACCGGTC	
GAM2546 FLJ10781 3'	TTGACCAACATGGTGAAACCCC 37177	
	GGGGTTTCACCATGTTGGTTAG	
	CCCCAAAGTGGTACAACCAGTT	
GAM2546 FLJ10803 3'	CAACATGGTGAAACCCTGT 37197	
	ACGGGGTTTCACCATGTTG	
	TGTCCCAAAGTGGTACAAC	
GAM2546 FLJ10803 3'	CTGACCAACATGGCAAAACCCT 37202	CA
GT	ACGGGGTTT CCATGTTGGTTAG	
	TGTCCCAA GGTACAACCAGTC	
	AC	
GAM2546 FLJ10936 3'	CCAACGTGGTGAAACACCGT 37440	G
	ACGG GTTTCACCATGTTGG	

		TGCC CAAAGTGGTGCAACC	
		A	
GAM2546	FLJ10989 3'	CAACATGGTGAAACCCCGT 37496	
		ACGGGGTTTCACCATGTTG	
		TGCCCCAAAGTGGTACAAC	
GAM2546	FLJ11042 3'	CAACATGGTGAAACCCTGT 37562	
		ACGGGGTTTCACCATGTTG	
		TGTCCCAAAGTGGTACAAC	
GAM2546	FLJ11106 3'	CTAACACCGTGAAACCCC 37623	CA
		GGGGTTTCAC TGTTGG	
		CCCCAAAGTG ACAATC	
		CC	
GAM2546	FLJ11126 3'	CTGGCCAACATGATGAAACCCC 37650	C
	GT	ACGGGGTTTCA CATGTTGGTTAG	
		TGCCCCAAAGT GTACAACCGGTC	
		A	
GAM2546	FLJ11136 3'	CCAAGATGGTGAAACCCC 37666	G
		GGGGTTTCACCAT TTGG	
		CCCCAAAGTGGTA AACC	
		G	
GAM2546	FLJ11151 3'	CTGGCCAACATGGTGAAACTCC 68475	
		GGGGTTTCACCATGTTGGTTAG	
		CCTCAAAGTGGTACAACCGGTC	
GAM2546	FLJ11301 3'	CCAACATGGAGAAACCCCGT 37804	A
		ACGGGGTTTC CCATGTTGG	
		TGCCCCAAAG GGTACAACC	
		A	
GAM2546	FLJ11370 3'	CTGGCCAACATGGTGAAACCCT 46964	
	GT	ACGGGGTTTCACCATGTTGGTTAG	
		TGTCCCAAAGTGGTACAACCGGTC	
GAM2546	FLJ11577 3'	CCAATATGGTGAAACCCC 47956	
		GGGGTTTCACCATGTTGG	
		CCCCAAAGTGGTATAACC	
GAM2546	FLJ11637 3'	CGGCTATGGTGAAACCCCGT 46981	_ TG
		ACGGGGTTTCACCAT GT G	

		TGCCCCAAAGTGGTA CG C	
		T GT	
GAM2546	FLJ11700	3' CCAACATGGTGAAACCCC 46559	
		GGGGTTTCACCATGTTGG	
		CCCCAAAGTGGTACAACC	
GAM2546	FLJ11722	3' CTGGCCAACACAGTGAAACCCC 47001	CA
		GGGGTTTCAC TGTTGGTTAG	
		CCCCAAAGTG ACAACCGGTC	
		AC	
GAM2546	FLJ11722	3' CTGGCCAACATGGTGAAACCCC 47002	
		GGGGTTTCACCATGTTGGTTAG	
		CCCCAAAGTGGTACAACCGGTC	
GAM2546	FLJ11726	3' CTGGCCAACATGGTGAAACCCC 47020	
	GT	ACGGGGTTTCACCATGTTGGTTAG	
		TGCCCCAAAGTGGTACAACCGGTC	
GAM2546	FLJ11996	3' CCAACATGGTGAAACCTCGT 47057	
		ACGGGGTTTCACCATGTTGG	
		TGCTCCAAAGTGGTACAACC	
GAM2546	FLJ12294	5' CAACATAGCAAAACCCTGT 47708	CACC
		ACGGGGTTT ATGTTG	
		TGTCCCAA TACAAC	
		ACGA	
GAM2546	FLJ12294	3' CCAACATGGTGAAACCCC 47712	
		GGGGTTTCACCATGTTGG	
		CCCCAAAGTGGTACAACC	
GAM2546	FLJ12331	3' CTGGCCAACATGGCAAAACCCT 47111	CA
		GGGGTTT CCATGTTGGTTAG	
		TCCCAA GGTACAACCGGTC	
		AC	
GAM2546	FLJ12363	3' CCAACATGGTGAAACCCC 50632	
		GGGGTTTCACCATGTTGG	
		CCCCAAAGTGGTACAACC	
GAM2546	FLJ12409	3' CAACATGGCTAAACCCCGT 47767	CA
		ACGGGGTTT CCATGTTG	

			TGCCCCAAA GGTACAAC		
			TC		
GAM2546	FLJ12448	3'	CCAACATGGCGAGACCCC	43475	A
			GGGGTTTC CCATGTTGG		
			CCCCAGAG GGTACAACC		
			C		
GAM2546	FLJ12547	3'	CCGACATGGTGAAACCCC	47130	
			GGGGTTTCACCATGTTGG		
			CCCCAAAGTGGTACAGCC		
GAM2546	FLJ12586	3'	CCAGCATGGTGAAACCCC	45209	
			GGGGTTTCACCATGTTGG		
			CCCCAAAGTGGTACGACC		
GAM2546	FLJ12606	3'	CAACATGGTGAAACCCTGT	46062	
			ACGGGGTTTCACCATGTTG		
			TGTCCCAAAGTGGTACAAC		
GAM2546	FLJ12606	3'	CTGGCCAACACGGTGAAACCCC	46068	A
		GT	ACGGGGTTTCACC TGTTGGTTAG		
			TGCCCCAAAGTGG ACAACCGGTC		
			C		
GAM2546	FLJ12618	3'	CAACATGGCAAAACCCTGT	46502	CA
			ACGGGGTTT CCATGTTG		
			TGTCCCAA GGTACAAC		
			AC		
GAM2546	FLJ12660	3'	CTGACCAACATGGTGAAACCCC	47896	
		GT	ACGGGGTTTCACCATGTTGGTTAG		
			TGCCCCAAAGTGGTACAACCAGTC		
GAM2546	FLJ12666	3'	CCAATATGGTGAAACCCC	45067	
			GGGGTTTCACCATGTTGG		
			CCCCAAAGTGGTATAACC		
GAM2546	FLJ12921	3'	CTAACACGGTGAAACCCC	46398	A
			GGGGTTTCACC TGTTGG		
			CCCCAAAGTGG ACAATC		
			C		
GAM2546	FLJ13117	3'	CTGGCCAACATGGTGAAACCCT	43809	
		GT	ACGGGGTTTCACCATGTTGGTTAG		

TGTCCCAAAGTGGTACAACCGGTC

GAM2546 FLJ13193 3' CTGGCCAACATGGTGAAACCCT 50723
GT ACGGGGTTTCACCATGTTGGTTAG
|||||||
TGTCCCAAAGTGGTACAACCGGTC

GAM2546 FLJ13305 3' CTAACACGATGAAACCCCGT 91710 CCA
ACGGGGTTTCA TGTTGG
||||||| |||||
TGCCCAAAGT ACAATC
AGC

GAM2546 FLJ13456 3' CCAAATGGTGAAACCCTGT 66536 G
ACGGGGTTTCACCAT TTGG
||||||| |||||
TGTCCCAAAGTGGTA AACC

GAM2546 FLJ13456 3' CCAACGTGGTGAAACCCCGT 66537
ACGGGGTTTCACCATGTTGG
|||||||
TGCCCAAAGTGGTGCAACC

GAM2546 FLJ13621 3' CCAACATGGTGAAACCTC 47220
GGGGTTTCACCATGTTGG
|||||||
CTCCAAAGTGGTACAACC

GAM2546 FLJ13769 3' CTGGCCAACATAGCGAAACCCC 47249 ACC
GT ACGGGGTTTC ATGTTGGTTAG
||||||| |||||
TGCCCAAAG TACAACCGGTC
CGA

GAM2546 FLJ13952 3' CCACCATGGAGAAACCCCGT 46009 A T
ACGGGGTTTC CCATG TGG
||||||| |||||
TGCCCAAAG GGTAC ACC
A C

GAM2546 FLJ13984 3' CAACATGGCAAACCCCTGT 45801 CA
ACGGGGTTT CCATGTTG
||||||| |||||
TGTCCCAA GGTACAAC
AC

GAM2546 FLJ14100 3' CTAACACGGTGAAACCCTGT 47334 A
ACGGGGTTTCACC TGTTGG
||||||| |||||
TGTCCCAAAGTGG ACAATC
C

GAM2546 FLJ14117 3' CCAACATGGCAAATCCC 43219 CA
GGGGTTT CCATGTTG
||||||| |||||

		CCCTAAA GGTACAACC		
		AC		
GAM2546	FLJ14117	3' CCAACGTGGTGAAACCCC 43220		
		GGGGTTTTCACCATGTTGG		
		CCCCAAAGTGGTGCAACC		
GAM2546	FLJ14117	3' CTGGCCAACATGGTGAAACCCC 43225		
	GT	ACGGGGTTTTCACCATGTTGGTTAG		
		TGCCCCAAAGTGGTACAACCGGTC		
GAM2546	FLJ14129	3' CCAACATGGCAAACCCC 48806	CA	
		GGGGTTT CCATGTTGG		
		CCCCAAA GGTACAACC		
		AC		
GAM2546	FLJ14225	3' CTAACACGGTGAAACCCC 46385	A	
		GGGGTTTTCACC TGTTGG		
		CCCCAAAGTGG ACAATC		
		C		
GAM2546	FLJ14251	3' CTGGCCAACATAGTGAAACCCC 46481	C	
		GGGGTTTTCAC ATGTTGGTTAG		
		CCCCAAAGTG TACAACCGGTC		
		A		
GAM2546	FLJ14251	3' CTGGCCAACATGGTGAAACCCC 46482		
		GGGGTTTTCACCATGTTGGTTAG		
		CCCCAAAGTGGTACAACCGGTC		
GAM2546	FLJ14280	3' CTAGGCAACATGGCGAAACCCT 46520	A	G
	GT	ACGGGGTTTC CCATGTTG TTAG		
		TGTCCCAAAG GGTACAAC GATC		
		C G		
GAM2546	FLJ14327	3' CTGGCCAACACGGTGAAACCCC 46678	A	
	GT	ACGGGGTTTTCACC TGTTGGTTAG		
		TGCCCCAAAGTGG ACAACCGGTC		
		C		
GAM2546	FLJ14346	3' CTAACACGGTGAAACCCCGT 47363	A	
		ACGGGGTTTTCACC TGTTGG		
		TGCCCCAAAGTGG ACAATC		
		C		
GAM2546	FLJ14397	3' CCAACATGGAGAAACCCCGT 52320	A	
		ACGGGGTTTC CCATGTTGG		

			TGCCCCAAAG GGTACAACC		
			A		
GAM2546	FLJ14397	3'	CTAACACGGTGAAACCCTGT 52325	A	
			ACGGGGTTTCACC TGTTGG		
			TGTCCCAAAGTGG ACAATC		
			C		
GAM2546	FLJ14457	3'	CTAACACAGTGAAACCCTGT 52405	CA	
			ACGGGGTTTCAC TGTTGG		
			TGTCCCAAAGTG ACAATC		
			AC		
GAM2546	FLJ14466	3'	CCAACATGGAGAAACCCC 52424	A	
			GGGGTTTC CCATGTTGG		
			CCCCAAAG GGTACAACC		
			A		
GAM2546	FLJ14490	3'	CTAACATGGTGAAACCCCGT 52441		
			ACGGGGTTTCACCATGTTGG		
			TGCCCCAAAGTGGTACAATC		
GAM2546	FLJ14641	3'	CCAACATGGTGAAACCTC 52554		
			GGGGTTTCACCATGTTGG		
			CTCCAAAGTGGTACAACC		
GAM2546	FLJ20004	3'	CCAACATGGAGAAACCCC 34753	A	
			GGGGTTTC CCATGTTGG		
			CCCCAAAG GGTACAACC		
			A		
GAM2546	FLJ20004	3'	CTGGCCAACATGGTGAAACCC 34759		
			GGGTTTCACCATGTTGGTTAG		
			CCCAAAGTGGTACAACCGGTC		
GAM2546	FLJ20006	3'	CCAACATGGCGAAACCCC 34782	A	
			GGGGTTTC CCATGTTGG		
			CCCCAAAG GGTACAACC		
			C		
GAM2546	FLJ20013	3'	CCAACACGGTGAAAACCCGT 34796	G	A
			ACGGG TTTCACC TGTTGG		
			TGCCC AAAGTGG ACAACC		
			A C		
GAM2546	FLJ20034	3'	CTAGCCAACATGGTGAAACCCC 34844		
	GT		ACGGGGTTTCACCATGTTGGTTAG		

TGCCCCAAAGTGGTACAACCGATC

GAM2546 FLJ20045 3' CCAAATGGTGAACCCC 34877 G
GGGGTTTTCACCAT TTGG
||||||||| |||
CCCCAAAGTGGTA AACC

GAM2546 FLJ20055 3' CTAACACGGTGAAACCCTGT 34908 A
ACGGGGTTTTCACC TGTTGG
||||||||| |||||
TGTCCCAAAGTGG ACAATC

C
GAM2546 FLJ20059 3' CCAACATGGAGAAACCCCGT 34925 A
ACGGGGTTTTC CATGTTGG
||||||||| |||||
TGCCCCAAAG GGTACAACC

A
GAM2546 FLJ20059 3' CTAATATGGTGAACCCCGT 34927
ACGGGGTTTTCACCATGTTGG
||||||||| |||||
TGCCCCAAAGTGGTATAATC

GAM2546 FLJ20069 3' CTGACCAACATGGTGAACCCC 34952
GGGGTTTTCACCATGTTGGTTAG
||||||||| |||||
CCCCAAAGTGGTACAACCAGTC

GAM2546 FLJ20139 3' CAACATGGTGAACCCCTGT 35112
ACGGGGTTTTCACCATGTTG
||||||||| |||||
TGTCCCAAAGTGGTACAAC

GAM2546 FLJ20211 3' CTGGCCAACATAGTGAACCCC 35260 C
G CGGGGTTTTCAC ATGTTGGTTAG
||||||||| |||||
GCCCAAAGTG TACAACCGGTC
A

GAM2546 FLJ20280 3' GCCAACACAGTGAACCCCTGT 35331 CA
ACGGGGTTTTCAC TGTTGGT
||||||||| |||||
TGTCCCAAAGTG ACAACCG
AC

GAM2546 FLJ20306 3' CCAACGTGGTGAACCCCGT 35387
ACGGGGTTTTCACCATGTTGG
||||||||| |||||
TGCCCCAAAGTGGTGCAACC

GAM2546 FLJ20340 3' CAACATGGTGAACCCCTGT 35451
ACGGGGTTTTCACCATGTTG
||||||||| |||||

TGTCCCAAAGTGGTACAAC

GAM2546 FLJ20413 3' CTAACACGGTGAAACTCCGT 35594 A
ACGGGGTTTCACC TGTTGG
||||||| |||||
TGCCTCAAAGTGG ACAATC
C

GAM2546 FLJ20464 3' CCAACACGGAGAAACCCC 35692 A A
GGGGTTTC CC TGTTGG
||||| || |||||
CCCCAAAG GG ACAACC
A C

GAM2546 FLJ20464 3' CCAACATGGAGAAACCCCGT 35693 A
ACGGGGTTTC CCATGTTGG
||||||| |||||
TGCCCAAAG GGTACAACC
A

GAM2546 FLJ20627 3' CTGGCCAACATGGTGAAACCCC 35909
GGGGTTTCACCATGTTGGTTAG
|||||||
CCCCAAAGTGGTACAACCGGTC

GAM2546 FLJ20694 3' CCAACATATAGTGAAACCCAGT 35974 G C__
AC GGGTTTCAC ATGTTGG
|| ||||| |||||
TG CCCAAAGTG TACAACC
A ATA

GAM2546 FLJ20695 3' CCAACATGGTGAAGCCCC 35983
GGGGTTTCACCATGTTGG
|||||||
CCCCGAAGTGGTACAACC

GAM2546 FLJ20700 3' CCAACAGAATGAAACCCTGT 36001 CCA
ACGGGGTTTCA TGTTGG
||||||| |||||
TGTCCCAAAGT ACAACC
AAG

GAM2546 FLJ20700 3' CTAACCTGGTGAAACCCTGT 36007 T
ACGGGGTTTCACCA GTTGG
||||||| |||||
TGTCCCAAAGTGGT CAATC
T

GAM2546 FLJ20783 3' CTAACACGGTGAAACCCC 36099 A
GGGGTTTCACC TGTTGG
||||||| |||||
CCCCAAAGTGG ACAATC
C

GAM2546 FLJ20802 3' CCAGCATGGTGAAACCCCGT 36109
ACGGGGTTTCACCATGTTGG
|||||||

TGCCCCAAAGTGGTACGACC

GAM2546	FLJ20808	3'	CTAACACGGTGAAACCCCGT	36119		A
			ACGGGGTTTCACC TGTTGG			
			TGCCCCAAAGTGG ACAATC			
			C			
GAM2546	FLJ20825	3'	CCAACATGGAGAAACCCC	36144		A
			GGGGTTTC CCATGTTGG			
			CCCCAAAG GGTACAACC			
			A			
GAM2546	FLJ20972	3'	CCAACATGGAGAAACCCC	47384		A
			GGGGTTTC CCATGTTGG			
			CCCCAAAG GGTACAACC			
			A			
GAM2546	FLJ21106	3'	CTAACACGGTGAAACCCCGT	47694		A
			ACGGGGTTTCACC TGTTGG			
			TGCCCCAAAGTGG ACAATC			
			C			
GAM2546	FLJ21144	3'	CCAATACGGTGAAAGCCCGT	43191	G	A
			ACGGG TTTCACC TGTTGG			
			TGCCC AAAGTGG ATAACC			
			G C			
GAM2546	FLJ21162	3'	CCAGCATGGTGAAACCCC	46369		
			GGGGTTTCACCATGTTGG			
			CCCCAAAGTGGTACGACC			
GAM2546	FLJ21551	3'	CCAACCTGGTGAAACCCCGT	46033		T
			ACGGGGTTTCACCA GTTGG			
			TGCCCCAAAGTGGT CAACC			
			C			
GAM2546	FLJ21657	3'	CTGGCCAACATGGTGAAACCCC	42799		
	GT		ACGGGGTTTCACCATGTTGGTTAG			
			TGCCCCAAAGTGGTACAACCGGTC			
GAM2546	FLJ21687	3'	CCAAGATGGTGAAACCCCGT	46294		G
			ACGGGGTTTCACCAT TTGG			
			TGCCCCAAAGTGGTA AACC			
			G			
GAM2546	FLJ21777	3'	CCAACATGGTGAAACCTCGT	50837		
			ACGGGGTTTCACCATGTTGG			

TGCTCCAAAGTGGTACAACC

GAM2546 FLJ22054 3' CCAACATGGTGAAACCCC 96047
GGGGTTTTCACCATGTTGG
|||||||
CCCCAAAGTGGTACAACC

GAM2546 FLJ22167 3' CCAACATAGTGAAACCCC 44863 C
GGGGTTTTCAC ATGTTGG
|||||||
CCCCAAAGTG TACAACC

A

GAM2546 FLJ22474 3' CTGGCCAACACGGTGAAACCCC 45612 A
GT ACGGGGTTTTCACC TGTTGGTTAG
|||||||
TGCCCCAAAGTGG ACAACCGGTC

C

GAM2546 FLJ22692 3' CTAACACGGTAAAACCCTGT 47481 C A
ACGGGGTTT ACC TGTTGG
|||||||
TGTCCCAA TGG ACAATC

A C

GAM2546 FLJ22814 3' CCAGCATGGCGAAACCCTGT 46721 A
ACGGGGTTTC CCATGTTGG
|||||||
TGTCCCAAAG GGTACGACC

C

GAM2546 FLJ22814 3' CTAACATGGTGAAACCCC 46724
GGGGTTTTCACCATGTTGG
|||||||
CCCCAAAGTGGTACAATC

GAM2546 FLJ22965 3' CAACATGGTGAAACCCTGT 42293
ACGGGGTTTTCACCATGTTG
|||||||
TGTCCCAAAGTGGTACAAC

GAM2546 FLJ23022 3' CTGGCCAACATGGTGAAACCCT 47494
GT ACGGGGTTTTCACCATGTTGGTTAG
|||||||
TGTCCCAAAGTGGTACAACCGGTC

GAM2546 FLJ23040 3' CTGGCCAACATGATGAAACCCT 47986 C
GT ACGGGGTTTCA CATGTTGGTTAG
|||||||
TGTCCCAAAGT GTACAACCGGTC

A

GAM2546 FLJ23042 3' CCAACATGGAGAAACCCC 47940 A
GGGGTTTC CCATGTTGG
|||||||

CCCCAAAG GGTACAACC

A

GAM2546 FLJ23042 3' CTAGGCAACACAGTGAAACCCT 47942 CA G
GT ACGGGGTTTCAC TGTTG TTAG

||||||| |||||

TGTCCCAAAGTG ACAAC GATC

AC G

GAM2546 FLJ23120 3' CTAATACAGTGAAACCCTGT 86326 CA
ACGGGGTTTCAC TGTTGG

||||||| |||||

TGTCCCAAAGTG ATAATC

AC

GAM2546 FLJ23235 3' CTGGCCAACATGGTGAAACCCT 46879
GT ACGGGGTTTCACCATGTTGGTTAG

|||||||

TGTCCCAAAGTGGTACAACCGGTC

GAM2546 FLJ23360 3' CCACATGGTGCAACCCCGT 43826 T T
ACGGGGTT CACCATGT GG

||||| ||||| ||

TGCCCAA GTGGTACA CC

C

GAM2546 FLJ23420 3' CTGGGTAACATAGCGAGACCCC 47539 ACC G
GGGGTTTC ATGTTG TTAG

||||| |||||

CCCCAGAG TACAAT GGTC

CGA G

GAM2546 FLJ23499 3' CCAATGTGGTGAAACTCC 43130
GGGGTTTCACCATGTTGG

|||||||

CCTCAAAGTGGTGTAACC

GAM2546 FLJ23878 3' GACCATGGTGAAACCCCGT 59370 TGT
ACGGGGTTTCACCA TGTT

||||||| |||||

TGCCCAAAGTGGT ACCAG

GAM2546 FLJ25012 3' CTAACATGGTGAAACCCC 58708
GGGGTTTCACCATGTTGG

|||||||

CCCCAAAGTGGTACAATC

GAM2546 FLJ30681 3' CTGACCAACATGGTGAAACCCT 93435
GT ACGGGGTTTCACCATGTTGGTTAG

|||||||

TGTCCCAAAGTGGTACAACCAGTC

GAM2546 FLJ31168 3' CTGGCCAACATGGTGAAACCCT 59181
GT ACGGGGTTTCACCATGTTGGTTAG

|||||||

TGTCCCAAAGTGGTACAACCGGTC

GAM2546 FLJ31455 3' CTAATATGGTGAAACCTCGT 59283
ACGGGGTTTCACCATGTTGG
|||||||
TGCTCCCAAAGTGGTATAATC

GAM2546 FLJ31737 3' CTGGCCAACATGGTGAAACCCC 59349
GGGGTTTCACCATGTTGGTTAG
|||||||
CCCCAAAGTGGTACAACCGGTC

GAM2546 FLJ31952 3' CCAACATGGAGAAACCCC 59044 A
GGGGTTTC CCATGTTGG
||||| |||||
CCCCAAAG GGTACAACC
A

GAM2546 FLJ32915 5' CTGGCCAACATGGTGAAACCCT 59433
GT ACGGGGTTTCACCATGTTGGTTAG
|||||||
TGTCCCAAAGTGGTACAACCGGTC

GAM2546 FUSIP1 3' CTGACCAACACGGTGAAACCCC 55038 A
GT ACGGGGTTTCACC TGTTGGTTAG
||||||| |||||
TGCCCCAAAGTGG ACAACCAGTC
C

GAM2546 GLTP 3' CTGGCCAACATGGTGAAACCCC 33584
GGGGTTTCACCATGTTGGTTAG
|||||||
CCCCAAAGTGGTACAACCGGTC

GAM2546 GNB4 3' CTACCCAACATGGTGAAACCCC 41568 T
GGGGTTTCACCATGTTGG TAG
||||||| |||
CCCCAAAGTGGTACAACC ATC
C

GAM2546 GP5 3' CCAAGATGGTGAAACCCCGT 16868 G
ACGGGGTTTCACCAT TTGG
||||||| |||
TGCCCCAAAGTGGTA AACC
G

GAM2546 GTPBP5 3' CTAACACAGTGAAACCCCGT 65974 CA
ACGGGGTTTCAC TGTTGG
||||||| |||||
TGCCCCAAAGTG ACAATC
AC

GAM2546 HES2 3' CTAACACGGTGAAACCCC 39373 A
GGGGTTTCACC TGTTGG
||||||| |||||

			CCCCAAAGTGG ACAATC	
			C	
GAM2546	HIC	3'	GGGCAACATGGTGAAACCCC 68050	G
			GGGGTTTCACCATGTTG TT	
			CCCCAAAGTGGTACAAC GG	
			G	
GAM2546	HIG2	3'	GCCAACATGGCGAAACCCC 26202	A
			GGGGTTTC CCATGTTGGT	
			CCCCAAAG GGTACAACCG	
			C	
GAM2546	HRH4	3'	CTGGCCAACATGGTGAAACCCC 41537	
			GGGGTTTCACCATGTTGGTTAG	
			CCCCAAAGTGGTACAACCGGTC	
GAM2546	HSA250303	3'	CTGGCCAACATGGTAAAACCCT 38022	C
	GT		ACGGGGTTT ACCATGTTGGTTAG	
			TGTCCCAA TGGTACAACCGGTC	
			A	
GAM2546	HSH2	3'	CTGGCCAACATGGTGAAACCCC 52739	
	GT		ACGGGGTTTCACCATGTTGGTTAG	
			TGCCCCAAAGTGGTACAACCGGTC	
GAM2546	HSPC031	3'	CTGGCCAACATGGTGAAACCCC 32748	
			GGGGTTTCACCATGTTGGTTAG	
			CCCCAAAGTGGTACAACCGGTC	
GAM2546	HSPC043	3'	CTGGCCAACATGGTGAAACCCT 68351	
	GT		ACGGGGTTTCACCATGTTGGTTAG	
			TGTCCCAAAGTGGTACAACCGGTC	
GAM2546	HYPK	3'	CCAACATGTGAAACCCCGT 33513	C
			ACGGGGTTTCAC ATGTTGG	
			TGCCCCAAAGTG TACAACC	
			-	
GAM2546	ICAM4	3'	CAACATAGTGAGACCCCGT 42588	C
			ACGGGGTTTCAC ATGTTG	
			TGCCCCAGAGTG TACAAC	
			A	
GAM2546	ICAM4	3'	CAACATAGTGAGACCCCGT 9532	C
			ACGGGGTTTCAC ATGTTG	

TGCCCCAGAGTG TACAAC

A

GAM2546 IL10RB 3' CCAATATGGTCAAACCCAGT 7126 G
AC GGGTTTCACCATGTTGG

|| |||||

TG CCCAAAGTGGTATAACC

A

GAM2546 IMAGE:4907098 3' CCAATATGGTCAAACCCCGT 57754
ACGGGGTTTCACCATGTTGG

|||||

TGCCCCAAAGTGGTATAACC

GAM2546 KALI 3' CCAACTTGGTCAAACCCCGT 54690 T
ACGGGGTTTCACCA GTTGG

|||||

TGCCCCAAAGTGGT CAACC

T

GAM2546 KBRAS2 3' CCAACATTGTCAAACCCC 34621 C
GGGGTTTCAC ATGTTGG

|||||

CCCCAAAGTG TACAACC

T

GAM2546 KCNH6 3' CTAACACGGTCAAACCCC 48573 A
GGGGTTTCACC TGTTGG

|||||

CCCCAAAGTGG ACAATC

C

GAM2546 KIAA0042 3' CTGGCCAACATGGTCAAACCCC 30235
GT ACGGGGTTTCACCATGTTGGTTAG

|||||

TGCCCCAAAGTGGTACAACCGGTC

GAM2546 KIAA0057 3' CTGGCCAACATGGTCAAACCCC 25413
GGGGTTTCACCATGTTGGTTAG

|||||

CCCCAAAGTGGTACAACCGGTC

GAM2546 KIAA0159 3' CCAACATGGAGAAACCCC 30141 A
GGGGTTTC CCATGTTGG

|||||

CCCCAAAG GGTACAACC

A

GAM2546 KIAA0184 3' CTAACATGGTCAAACCCTGT 65809
ACGGGGTTTCACCATGTTGG

|||||

TGTCCCCAAAGTGGTACAATC

GAM2546 KIAA0226 3' CCAATGTGGTCAAACCCTGT 64256
ACGGGGTTTCACCATGTTGG

|||||

TGTCCCAAAGTGGTGTAACC

GAM2546 KIAA0252 3' CTAACACGGTGAAACCCC 63453 A
GGGGTTTTCACC TGTTGG
||||||| |||||
CCCCAAAGTGG ACAATC
C

GAM2546 KIAA0266 3' CAACATGGTGAAACCCTGT 41637
ACGGGGTTTTCACCATGTTG
|||||||
TGTCCCAAAGTGGTACAAC

GAM2546 KIAA0355 3' CCAATATGGTGAAACCCC 28703
GGGGTTTTCACCATGTTGG
|||||||
CCCCAAAGTGGTATAACC

GAM2546 KIAA0419 3' CCAAACATGGCGAAACCCC 28859 A _
GGGGTTTC CCATGTT GG
||||| ||||| ||
CCCCAAAG GGTACAA CC
C A

GAM2546 KIAA0441 3' CTGACCAACATAGTGAAACCCC 29634 C
GGGGTTTTCAC ATGTTGGTTAG
||||||| |||||
CCCCAAAGTG TACAACAGTC
A

GAM2546 KIAA0446 5' CTAACATGGTGAAACCCCGT 69449
ACGGGGTTTTCACCATGTTGG
|||||||
TGCCCCAAAGTGGTACAATC

GAM2546 KIAA0447 3' CTGGCCAACATGATGAAACCCT 72120 C
GT ACGGGGTTTCA CATGTTGGTTAG
||||||| |||||
TGTCCCAAAGT GTACAACCGGTC
A

GAM2546 KIAA0472 3' CTGGCCAACATGGTGAAACCCC 72350
GT ACGGGGTTTTCACCATGTTGGTTAG
|||||||
TGCCCCAAAGTGGTACAACCGGTC

GAM2546 KIAA0472 3' TAACATGGTGAAACCCCGT 72364
ACGGGGTTTTCACCATGTTG
|||||||
TGCCCCAAAGTGGTACAAT

GAM2546 KIAA0547 3' CCAATATGGTGAAACTCCGT 29591
ACGGGGTTTTCACCATGTTGG
|||||||

TGCCTCAAAGTGGTATAACC

GAM2546 KIAA0557 3' CTGGCCAACATGGTCAAACCCC 78559
GGGGTTTCACCATGTTGGTTAG
|||||||
CCCCAAAGTGGTACAACCGGTC

GAM2546 KIAA0563 3' CTAACATGGTCAAACCCC 29879
GGGGTTTCACCATGTTGG
|||||||
CCCCAAAGTGGTACAATC

GAM2546 KIAA0565 3' CCAACATGGTCAAACCCCGT 67435
ACGGGGTTTCACCATGTTGG
|||||||
TGCCCCAAAGTGGTACAACC

GAM2546 KIAA0570 3' AGGCAACATGGTCAAACCTC 28848 G
GGGGTTTCACCATGTTG TT
|||||||
CTCCAAAGTGGTACAAC GA
G

GAM2546 KIAA0596 3' CTGGCCAACATGGTCAAACCCT 63487
GT ACGGGGTTTCACCATGTTGGTTAG
|||||||
TGTCCCAAAGTGGTACAACCGGTC

GAM2546 KIAA0794 3' CAACATGGTCAAACCCCGT 81224
ACGGGGTTTCACCATGTTG
|||||||
TGCCCCAAAGTGGTACAAC

GAM2546 KIAA0795 3' CTGGCCAACATGGTCAAACCCT 47229
GT ACGGGGTTTCACCATGTTGGTTAG
|||||||
TGTCCCAAAGTGGTACAACCGGTC

GAM2546 KIAA0831 3' CTAACATGGTCAAACCCTGT 30633
ACGGGGTTTCACCATGTTGG
|||||||
TGTCCCAAAGTGGTACAATC

GAM2546 KIAA0872 3' CCAGCATGGCGAAACCTCGT 30746 A
ACGGGGTTTC CATGTTGG
|||||||
TGCTCCAAAG GGTACGACC
C

GAM2546 KIAA0872 3' CTGACCAACATGGTCAAACACC 30753 G
GG GTTTCACCATGTTGGTTAG
|| |||||

			CC CAAAGTGGTACAACCAGTC		
			A		
GAM2546	KIAA0884	3'	CAACATGGTCAAACCCTGT 70750		
			ACGGGGTTTCACCATGTTG		
			TGTCCCAAAGTGGTACAAC		
GAM2546	KIAA0889	3'	CCAATATGGTCAAACCCTGT 31766		
			ACGGGGTTTCACCATGTTGG		
			TGTCCCAAAGTGGTATAACC		
GAM2546	KIAA0889	3'	CTGGCCAACATGGTCAAACCCC 31775		
			GGGGTTTCACCATGTTGGTTAG		
			CCCCAAAGTGGTACAACCGGTC		
GAM2546	KIAA0894	3'	CCAACATGATCAAACCCAGT 30329	G	C
			AC GGGTTTCA CATGTTGG		
			TG CCAAAGT GTACAACC		
			A A		
GAM2546	KIAA0907	3'	CCAACATAGTCAAATCCC 30870		C
			GGGGTTTTCAC ATGTTGG		
			CCCTAAAGTG TACAACC		
			A		
GAM2546	KIAA0907	3'	CTAACACGGTCAAACCCCGT 30872		A
			ACGGGGTTTTCACC TGTTGG		
			TGCCCCAAAGTGG ACAATC		
			C		
GAM2546	KIAA0930	3'	CTAACATGCTCAAACCCC 71069		C
			GGGGTTTTCATCATGTTGG		
			CCCCAAAGT GTACAATC		
			C		
GAM2546	KIAA0953	3'	CAACATGGTCAAACCCCGT 67322		
			ACGGGGTTTTCACCATGTTG		
			TGCCCCAAAGTGGTACAAC		
GAM2546	KIAA0961	3'	CCATCATGGTCAAACCTC 30396		T
			GGGGTTTTCACCATG TGG		
			CTCCAAAGTGGTAC ACC		
			T		
GAM2546	KIAA0981	3'	CTGGCCAACATGACCAAACCCC 62086		AC
			GGGGTTTC CATGTTGGTTAG		

	CCCCAAAG GTACAACCGGTC	
	CA	
GAM2546 KIAA1001	3' CTGGCCAACATGGTCAAACCCC 31006	
	GGGGTTTCACCATGTTGGT TAG	
	CCCCAAAGTGGTACAACCGGTC	
GAM2546 KIAA1032	3' CTGGCCAACATGGCGAAACCCC 66725	A
	GGGGTTTC CCATGTTGGT TAG	
	CCCCAAAG GGTACAACCGGTC	
	C	
GAM2546 KIAA1056	3' CCAATGTGGCAAACCCCTGT 30312	CA
	ACGGGGTTT CCATGTTGG	
	TGTCCCAA GGTGTAACC	
	AC	
GAM2546 KIAA1086	3' CAACATGGTCAAACCCCTGT 71281	
	ACGGGGTTTCACCATGTTG	
	TGTCCCAAAGTGGTACAAC	
GAM2546 KIAA1130	3' CCAAAATGGTCAAACCCCGT 63080	G
	ACGGGGTTTCACCAT TTGG	
	TGCCCCAAAGTGGTA AACC	
	A	
GAM2546 KIAA1160	3' CTGGCCAACATGGTCAAACCCC 40757	
	GGGGTTTCACCATGTTGGT TAG	
	CCCCAAAGTGGTACAACCGGTC	
GAM2546 KIAA1164	3' CCAGCATGGTCAAACCCCTGT 70038	
	ACGGGGTTTCACCATGTTGG	
	TGTCCCAAAGTGGTACGACC	
GAM2546 KIAA1164	3' CTGGCCAACATGGCAAACCCCT 70042	CA
GT	ACGGGGTTT CCATGTTGGT TAG	
	TGTCCCAA GGTACAACCGGTC	
	AC	
GAM2546 KIAA1191	3' CTGGCCAACATGGTCAAACCCC 40333	
GT	ACGGGGTTTCACCATGTTGGT TAG	
	TGCCCCAAAGTGGTACAACCGGTC	
GAM2546 KIAA1202	3' CTAACACGGTCAAACCCCT 72488	A
	GGGGTTTCACC TGTTGG	

			TCCCAAAGTGG ACAATC		
			C		
GAM2546	KIAA1228	3'	CCAACATGGAGAAACCCC 65672	A	
			GGGGTTTC CCATGTTGG		
			CCCCAAAG GGTACAACC		
			A		
GAM2546	KIAA1244	3'	CAACATGGTGAAACCTCGT 72441		
			ACGGGGTTTCACCATGTTG		
			TGCTCCAAAGTGGTACAAC		
GAM2546	KIAA1253	3'	CAACATGGTGAAACCCTGT 93547		
			ACGGGGTTTCACCATGTTG		
			TGTCCCAAAGTGGTACAAC		
GAM2546	KIAA1257	3'	CTAACACGGTGAAACCCCGT 63402	A	
			ACGGGGTTTCACC TGTTGG		
			TGCCCCAAAGTGG ACAATC		
			C		
GAM2546	KIAA1271	3'	CCAACAGGGTGAAACCCCGT 70131	A	
			ACGGGGTTTCACC TGTTGG		
			TGCCCCAAAGTGG ACAACC		
			G		
GAM2546	KIAA1276	3'	CCAATATGGTGAAACCCC 67029		
			GGGGTTTCACCATGTTGG		
			CCCCAAAGTGGTATAACC		
GAM2546	KIAA1277	3'	CTGGCCAACATGGCAAACCCC 65075	CA	
			GGGGTTT CCATGTTGGTTAG		
			CCCCAAA GGTACAACCGGTC		
			AC		
GAM2546	KIAA1328	3'	CTAACACGGTGAAACCCC 62322	A	
			GGGGTTTCACC TGTTGG		
			CCCCAAAGTGG ACAATC		
			C		
GAM2546	KIAA1364	3'	CTGGCCAACATAATGAAACCCT 64348	CC	
	GT		ACGGGGTTTCA ATGTTGGTTAG		
			TGTCCCAAAGT TACAACCGGTC		
			AA		
GAM2546	KIAA1404	3'	CTGACCAACATGGCGAAACCCC 62689	A	
	GT		ACGGGGTTTC CCATGTTGGTTAG		

		TGCCCCAAAG GGTACAACCAGTC	
		C	
GAM2546	KIAA1456	3' CTGACCAACATGGTCAAACCCC 67551	
	GT	ACGGGGTTTCACCATGTTGGTTAG	
		TGCCCCAAAGTGGTACAACCAGTC	
GAM2546	KIAA1486	3' CTAACACGGTGAGACCCC 67973	A
		GGGGTTTCACC TGTTGG	
		CCCCAGAGTGG ACAATC	
		C	
GAM2546	KIAA1559	3' CCAACACTGAGAAACCCC 73451	AC _
		GGGGTTTC CA TGTTGG	
		CCCCAAAG GT ACAACC	
		A_ C	
GAM2546	KIAA1559	3' CTGGTTAACATGGTCAAACCCCT 73455	TT
	GT	ACGGGGTTTCACCATGTTGG AG	
		TGTCCCAAAGTGGTACAATT TC	
		GG	
GAM2546	KIAA1586	5' CCAGTATAGTGAAACCTC 93936	C
		GGGGTTTCAC ATGTTGG	
		CTCCAAAGTG TATGACC	
		A	
GAM2546	KIAA1630	3' CTGGCCAACACGGTCAAACCCC 38653	A
	G	CGGGGTTTCACC TGTTGGTTAG	
		GCCCCAAAGTGG ACAACCGGTC	
		C	
GAM2546	KIAA1649	3' CTAACCAACGTGGTAAAACCCCT 51232	C
	GT	ACGGGGTTT ACCATGTTGGTTAG	
		TGTCCCAA TGGTGCAACCAATC	
		A	
GAM2546	KIAA1656	5' CTGGCCAACATGGTCAAACCCC 66368	
	GT	ACGGGGTTTCACCATGTTGGTTAG	
		TGCCCCAAAGTGGTACAACCGGTC	
GAM2546	KIAA1674	3' CTAACACGGTCAAACCCCGT 69337	A
		ACGGGGTTTCACC TGTTGG	
		TGCCCCAAAGTGG ACAATC	
		C	
GAM2546	KIAA1724	3' CAACATGGCGAAACCCCGT 67607	A
		ACGGGGTTTC CCATGTTG	

		TGCCCCAAAG GGTACAAC		
		C		
GAM2546	KIAA1727	3' CTAGGCAACATGGAGAAACCCC 64757	A	G
	GT	ACGGGGTTTC CCATGTTG TTAG		
		TGCCCCAAAG GGTACAAC GATC		
		A G		
GAM2546	KIAA1751	3' CTGGCCAACATGGTGAAACCCC 72156		
		GGGGTTTCACCATGTTGGTTAG		
		CCCCAAAGTGGTACAACCGGTC		
GAM2546	KIAA1811	5' CTGACCAACATGGTGAAACCCC 65418		
		GGGGTTTCACCATGTTGGTTAG		
		CCCCAAAGTGGTACAACCGGTC		
GAM2546	KIAA1829	3' CCAACATGGAGAAACCCCGT 62635	A	
		ACGGGGTTTC CCATGTTGG		
		TGCCCCAAAG GGTACAACC		
		A		
GAM2546	KIAA1841	3' CCAACGTGGTGAAACCCCT 80848		
		GGGGTTTCACCATGTTGG		
		TCCCAAAGTGGTGCAACC		
GAM2546	KIAA1871	3' CCAACATACTAAAACCCCGT 61898	CACC	
		ACGGGGTTT ATGTTGG		
		TGCCCCAAA TACAACC		
		ATCA		
GAM2546	KIAA1872	3' CCAACATGGTGAAACCTC 63604		
		GGGGTTTCACCATGTTGG		
		CTCCAAAGTGGTACAACC		
GAM2546	KIAA1872	3' CTGGCCAACATGGTGAAACCCC 63607		
		GGGGTTTCACCATGTTGGTTAG		
		CCCCAAAGTGGTACAACCGGTC		
GAM2546	KIAA1872	3' CTGGTGAACATGGCGAAACCCC 63609	A	G TT
	GT	ACGGGGTTTC CCATGTT G AG		
		TGCCCCAAAG GGTACAA T TC		
		C G GG		
GAM2546	KIAA1941	3' CTGGCCAACATGGTGAAACCCC 75337		
		GGGGTTTCACCATGTTGGTTAG		

CCCCAAAGTGGTACAACCGGTC

GAM2546 KIAA1948 3' CTAACACGGTGAAACCCC 83303 A
GGGGTTTCACC TGTTGG
||||||| |||||
CCCCAAAGTGG ACAATC

C

GAM2546 KIAA1951 3' CTAACACGGTGAAACCCCGT 74152 A
ACGGGGTTTCACC TGTTGG
||||||| |||||
TGCCCCAAAGTGG ACAATC

C

GAM2546 KIAA1958 3' CCAACATGGTGAAACCCC 82781
GGGGTTTCACCATGTTGG
||||||| |||||
CCCCAAAGTGGTACAACC

GAM2546 KIAA1969 3' CTGGCCAACATGGTGAAACCCT 79477
GT ACGGGGTTTCACCATGTTGGTTAG
||||||| |||||
TGTCCCAAAGTGGTACAACCGGTC

GAM2546 KIAA1979 3' CTGGTTAACATGGTGAAACACC 89651 G TT
GG GTTTCACCATGTTGG AG
|| ||||| ||
CC CAAAGTGGTACAATT TC
A GG

GAM2546 KLHL8 3' CTGACCAACATGGTGAAACCCT 63514
GT ACGGGGTTTCACCATGTTGGTTAG
||||||| |||||
TGTCCCAAAGTGGTACAACCAGTC

GAM2546 KR18 3' CCAGCATAGTGAAACCCC 53887 C
GGGGTTTCAC ATGTTGG
||||||| |||||
CCCCAAAGTG TACGACC

A

GAM2546 KREMEN 3' CCAACATGGCGAAAACCC 50229 G A
GGG TTTC CCATGTTGG
||| ||| |||||
CCC AAAG GGTACAACC

A C

GAM2546 LAP1B 3' CTGGCCAACATGGTGAAACCCC 65193
GT ACGGGGTTTCACCATGTTGGTTAG
||||||| |||||
TGCCCCAAAGTGGTACAACCGGTC

GAM2546 LIM 3' CTGGCCAACATGGTGAAACCCC 22324
GGGGTTTCACCATGTTGGTTAG
||||||| |||||

CCCCAAAGTGGTACAACCGGTC

GAM2546 LIM 3' CTGGCCAACATGGTCAAACCCT 22325
GT ACGGGGTTTCACCATGTTGGTTAG
|||||||
TGTCCCAAAGTGGTACAACCGGTC

GAM2546 LRG 3' CTAACATGGTCAAACCCTGT 54818
ACGGGGTTTCACCATGTTGG
|||||||
TGTCCCAAAGTGGTACAATC

GAM2546 LRRFIP1 3' CTGGCCAACATGGTCAAACCCT 17612
GT ACGGGGTTTCACCATGTTGGTTAG
|||||||
TGTCCCAAAGTGGTACAACCGGTC

GAM2546 LSR68 3' CCGACATGGCGAAACCCTGT 38555 A
ACGGGGTTTC CATGTTGG
|||||||
TGTCCCAAAG GGTACAGCC
C

GAM2546 LYSAL1 3' CTAACACGGTCAAACCCCGT 18122 A
ACGGGGTTTCACC TGTGTTGG
|||||||
TGCCCAAAGTGG ACAATC
C

GAM2546 MACF1 3' CTAACACGGTCAAACCCCGT 53428 A
ACGGGGTTTCACC TGTGTTGG
|||||||
TGCCCAAAGTGG ACAATC
C

GAM2546 MACF1 3' CTGGCCAACATGGTCAAACCCC 53429
GGGGTTTCACCATGTTGGTTAG
|||||||
CCCCAAAGTGGTACAACCGGTC

GAM2546 MAWBP 3' CCAACATGGTCAAACCTCGT 42380
ACGGGGTTTCACCATGTTGG
|||||||
TGCTCCAAAGTGGTACAACC

GAM2546 MCAM 3' CTAACACGGTCAAACCCTGT 22461 A
ACGGGGTTTCACC TGTGTTGG
|||||||
TGTCCCAAAGTGG ACAATC
C

GAM2546 MGC10765 3' CTGACCAACATGGTCAAACGCC 44560 G
GG GTTTCACCATGTTGGTTAG
|| |||||

		CC CAAAGTGGTACAACCAAGTC	
		G	
GAM2546	MGC10771	3' CTGGCCAACATGGTGAAACCCC 44713	
	GT	ACGGGGTTTCACCATGTTGGTTAG	
		TGCCCCAAAGTGGTACAACCGGTC	
GAM2546	MGC10814	3' CCAACATGGTGAAACCCCGT 52016	
		ACGGGGTTTCACCATGTTGG	
		TGCCCCAAAGTGGTACAACC	
GAM2546	MGC10814	5' CTGGCCAACATGGTGAAACCCT 52018	
	GT	ACGGGGTTTCACCATGTTGGTTAG	
		TGTCCCAAAGTGGTACAACCGGTC	
GAM2546	MGC10999	3' CTGGCCAACATGGTGAAACCCC 51194	
		GGGGTTTCACCATGTTGGTTAG	
		CCCCAAAGTGGTACAACCGGTC	
GAM2546	MGC11352	3' CTAATACGGTGAAACCCC 65432	A
		GGGGTTTCACC TGTTGG	
		CCCCAAAGTGG ATAATC	
		C	
GAM2546	MGC11386	3' CTGGCCAACATGGTGAAACCCT 53064	
	GT	ACGGGGTTTCACCATGTTGGTTAG	
		TGTCCCAAAGTGGTACAACCGGTC	
GAM2546	MGC13017	3' CTGGCCAACACGATGAAACCCC 55573	CCA
	GT	ACGGGGTTTCA TGTTGGTTAG	
		TGCCCCAAAGT ACAACCGGTC	
		AGC	
GAM2546	MGC13053	3' CCAACATGGTGAAACCCC 52103	
		GGGGTTTCACCATGTTGG	
		CCCCAAAGTGGTACAACC	
GAM2546	MGC13053	3' CTAACACTGAAACCCCGT 52106	CCA
		ACGGGGTTTCA TGTTGG	
		TGCCCCAAAGT ACAATC	
		C__	
GAM2546	MGC14126	3' CCAACATGGTGAAACCTCG 52938	
		CGGGGTTTCACCATGTTGG	

GCTCCAAAGTGGTACAACC

GAM2546 MGC14799 3' GACCAACATGGTGAAACCCC 51329
GGGGTTTTCACCATGTTGGTT
|||||||
CCCCAAAGTGGTACAACCAG

GAM2546 MGC14817 3' CTAATACAGTGAAACCCC 51336 CA
GGGGTTTTCAC TGTTGG
||||||| |||||
CCCCAAAGTG ATAATC
AC

GAM2546 MGC16142 3' CCAACGTGATGAAACTCC 52263 C
GGGGTTTCA CATGTTGG
||||||| |||||
CCTCAAAGT GTGCAACC
A

GAM2546 MGC16385 3' TCAACATGGAGAAACCCCGT 59542 A
ACGGGGTTTC CCATGTTGG
||||||| |||||
TGCCCCAAAG GGTACAACT
A

GAM2546 MGC16703 3' CTAACACGGTGAAACCCCG 73494 A
CGGGGTTTTCACC TGTTGG
||||||| |||||
GCCCCAAAGTGG ACAATC
C

GAM2546 MGC2562 3' CAACATGGCAAAACCCTGT 51424 CA
ACGGGGTTT CCATGTTG
||||||| |||||
TGTCCCAA GGTACAAC
AC

GAM2546 MGC2562 3' CAACATGGCGAAACCCTG 51425 A
CGGGGTTTC CCATGTTG
||||||| |||||
GTCCCAAAG GGTACAAC
C

GAM2546 MGC2562 3' CCAAACATGGTGAAACCCTGT 51433 _
ACGGGGTTTTCACCATGTT GG
||||||| |||||
TGTCCCAAAGTGGTACAA CC
A

GAM2546 MGC2562 3' CTGCCCAACATGGTGAAACCCC 51441 T
GT ACGGGGTTTTCACCATGTTGG TAG
||||||| |||||
TGCCCCAAAGTGGTACAACC GTC
C

GAM2546 MGC26641 3' CAACATGGTGAAACCCTGT 59320
ACGGGGTTTTCACCATGTTG
||||||| |||||

TGTCCCAAAGTGGTACAAC

GAM2546 MGC2731 3' CCAACATGGAGAAACCCCGT 44162 A
ACGGGGTTTC CCATGTTGG
||||||| |||||
TGCCCAAAG GGTACAACC

A

GAM2546 MGC29762 3' CCAATATGGTGAGACCCC 59142
GGGGTTTCACCATGTTGG
|||||||
CCCCAGAGTGGTATAACC

GAM2546 MGC29891 3' CCAACATGGTGACACCCCGT 58854 T
ACGGGGT TCACCATGTTGG
||||| |||||
TGCCCA AGTGGTACAACC

C

GAM2546 MGC29891 3' CTAACACGGTGAAACTCC 58862 A
GGGGTTTCACC TGTTGG
||||||| |||||
CCTCAAAGTGG ACAATC

C

GAM2546 MGC29937 3' CTGACCAACATGGTGAAACCCC 58729
GGGGTTTCACCATGTTGGTTAG
|||||||
CCCCAAAGTGGTACAACCAGTC

GAM2546 MGC3169 3' CCAACATGGTGAAACCCC 44184
GGGGTTTCACCATGTTGG
|||||||
CCCCAAAGTGGTACAACC

GAM2546 MGC3207 3' CTAACATGGTGAAACCCC 63236
GGGGTTTCACCATGTTGG
|||||||
CCCCAAAGTGGTACAATC

GAM2546 MGC39350 3' CTGGCCAACATGGCGAAACCCC 59316 A
GGGGTTTC CCATGTTGGTTAG
||||| |||||
CCCCAAAG GGTACAACCGTC

C

GAM2546 MGC4248 3' CAACATGGCGAAACCCCGT 51309 A
ACGGGGTTTC CCATGTTG
||||||| |||||
TGCCCAAAG GGTACAAC

C

GAM2546 MGC4562 3' CTAACACGGTGAAACCCAGT 56739 G A
AC GGGTTTCACC TGTTGG
|| ||||| |||||

			TG CCCAAAGTGG ACAATC	
			A C	
GAM2546	MGC4663	3'	CTAACACGGTGAAACCCC 44786	A
			GGGGTTTCACC TGTTGG	
			CCCAAAGTGG ACAATC	
			C	
GAM2546	MGC4771	3'	CCAACATAGTGAAACCCC 52002	C
			GGGGTTTCAC ATGTTGG	
			CCCAAAGTG TACAAC	
			A	
GAM2546	MOST2	5'	CTGGCCAACATGGTAAAACCCCT 40062	C
	GT		ACGGGGTTT ACCATGTTGGTTAG	
			TGTCCCAA TGGTACAACCGGTC	
			A	
GAM2546	MRPS10	3'	CTAACACGGTGAAACCCCGT 36817	A
			ACGGGGTTTCACC TGTTGG	
			TGCCCCAAAGTGG ACAATC	
			C	
GAM2546	MYO3B	3'	CTGACCAACATGGTGAAACCCC 58111	
	GT		ACGGGGTTTCACCATGTTGGTTAG	
			TGCCCCAAAGTGGTACAACCAGTC	
GAM2546	N4BP2	3'	CTGGCCAACATGGTGAATCCCC 36940	T
	GT		ACGGGG TTCACCATGTTGGTTAG	
			TGCCCC AAGTGGTACAACCGGTC	
			T	
GAM2546	NCBP2	3'	CAACATAGCAAGACCCCGT 24765	CACC
			ACGGGGTTT ATGTTG	
			TGCCCCAGA TACAAC	
			ACGA	
GAM2546	NMNAT	3'	CCAATATGGTGAAACCCC 43284	
			GGGGTTTCACCATGTTGG	
			CCCAAAGTGGTATAACC	
GAM2546	NMT2	3'	CTGGCCAACATAGTGAAACCCC 17856	C
			GGGGTTTCAC ATGTTGGTTAG	
			CCCAAAGTG TACAACCGGTC	
			A	
GAM2546	NPTXR	3'	CCAACGTGGTGAAACCCC 27429	
			GGGGTTTCACCATGTTGG	

CCCCAAAGTGGTGCAACC

GAM2546 ORC6L 3' CTGGCCAACATGGTGAAACCCC 27491
GGGGTTTCACCATGTTGGT TAG
|||||||
CCCCAAAGTGGTACAACCGGTC

GAM2546 PAFAH2 3' CTGGCCAACATGGTGAAACCCC 6502
GT ACGGGGTTTCACCATGTTGGT TAG
|||||||
TGCCCCAAAGTGGTACAACCGGTC

GAM2546 PB1 3' CCAACATGGTGAAACCTC 36873
GGGGTTTCACCATGTTGG
|||||||
CTCCAAAGTGGTACAACC

GAM2546 PB1 3' CCAACGTGGTGAAACCCTGT 36874
ACGGGGTTTCACCATGTTGG
|||||||
TGTCCCAAAGTGGTGCAACC

GAM2546 PDCD7 3' CTAACACGGTGAAACCCTGT 72604 A
ACGGGGTTTCACC TGTTGG
|||||||
TGTCCCAAAGTGG ACAATC
C

GAM2546 phorbolin-1 3' CTAACACGGTGAAACCCTGT 90210 A
ACGGGGTTTCACC TGTTGG
|||||||
TGTCCCAAAGTGG ACAATC
C

GAM2546 PIWIL2 3' CTGGCCAACATGGTGAAACCCC 36544
GT ACGGGGTTTCACCATGTTGGT TAG
|||||||
TGCCCCAAAGTGGTACAACCGGTC

GAM2546 PNPASE 3' CTAACACGGTGAAACCCCGT 71439 A
ACGGGGTTTCACC TGTTGG
|||||||
TGCCCCAAAGTGG ACAATC
C

GAM2546 PPP1R3B 3' CCAACATGGTGAAACCTCGT 45135
ACGGGGTTTCACCATGTTGG
|||||||
TGCTCCAAAGTGGTACAACC

GAM2546 PPP1R3B 3' CTAACACGGTGAAACCCTGT 45141 A
ACGGGGTTTCACC TGTTGG
|||||||

			TGTCCCAAAGTGG ACAATC	
			C	
GAM2546	PRIC285	3'	CTGGCCAACATGGTCAAACCCC 62114	
	GT		ACGGGGTTTCACCATGTTGGTTAG	
			TGCCCCAAAGTGGTACAACCGGTC	
GAM2546	PRO0478	3'	CTAGCATGGTCAAACCCCGT 27030	
			ACGGGGTTTCACCATGTTGG	
			TGCCCCAAAGTGGTACGATC	
GAM2546	PRO0618	3'	CTAACATGGTCAAACCCCTGT 27053	
			ACGGGGTTTCACCATGTTGG	
			TGTCCCAAAGTGGTACAATC	
GAM2546	PRO0628	3'	CTGGCCAACACGGTCAAACCCCT 27062	A
	GT		ACGGGGTTTCACC TGTTGGTTAG	
			TGTCCCAAAGTGG ACAACCGGTC	
			C	
GAM2546	PRO1048	3'	CTAACATGGTCAAACCCCGT 38111	
			ACGGGGTTTCACCATGTTGG	
			TGCCCCAAAGTGGTACAATC	
GAM2546	PRO1853	3'	CCAAAATGGAGAAACCCC 38379	A G
			GGGGTTTC CCAT TTGG	
			CCCCAAAG GGTA AACC	
			A A	
GAM2546	PRO2015	3'	CTGGCCAACATGGCGAAACCCC 38161	A
	GT		ACGGGGTTTC CCATGTTGGTTAG	
			TGCCCCAAAG GGTACAACCGGTC	
			C	
GAM2546	PRO2730	3'	CCAACATGGAGAAACCCC 48181	A
			GGGGTTTC CCATGTTGG	
			CCCCAAAG GGTACAACC	
			A	
GAM2546	PRO2893	3'	CCAACATGGAGAAACCCCGT 38431	A
			ACGGGGTTTC CCATGTTGG	
			TGCCCCAAAG GGTACAACC	
			A	
GAM2546	PRO2949	3'	CTAACACGGTCAAACCCC 38222	A
			GGGGTTTCACC TGTTGG	

			CCCCAAAGTGG ACAATC		
			C		
GAM2546	PRO2964	3'	CTAACACGGTGAAACCTCGT	38259	A
			ACGGGGTTTCACC TGTTGG		
			TGCTCCAAAGTGG ACAATC		
			C		
GAM2546	PSR	3'	CTGGCCAACACGGTGAAACCCC	65784	A
	GT		ACGGGGTTTCACC TGTTGGTTAG		
			TGCCCCAAAGTGG ACAACCGGTC		
			C		
GAM2546	PTK6	3'	CTAACACGGTGAAACCCCGT	21074	A
			ACGGGGTTTCACC TGTTGG		
			TGCCCCAAAGTGG ACAATC		
			C		
GAM2546	PXMP4	3'	CAACATGGTGAAACCCAGT	24331	G
			AC GGGTTTCACCATGTTG		
			TG CCCAAAGTGGTACAAC		
			A		
GAM2546	RAB4B	5'	CCAACATGGAGAAACCCCGT	32902	A
			ACGGGGTTTC CCATGTTGG		
			TGCCCCAAAG GGTACAACC		
			A		
GAM2546	RAD51	3'	CCAAGATGGTGAAATCCC	56830	G
			GGGGTTTCACCAT TTGG		
			CCCTAAAGTGGTA AACC		
			G		
GAM2546	RHOBTB3	3'	CCAAAACAGTGAAACCCCGT	30425	CATG
			ACGGGGTTTCAC TTGG		
			TGCCCCAAAGTG AACC		
			ACAA		
GAM2546	RNO2	3'	CCAAGATGGTGAAACCCTGT	53927	G
			ACGGGGTTTCACCAT TTGG		
			TGTCCCAAAGTGGTA AACC		
			G		
GAM2546	RNO2	5'	CCAGCACGGTGAAACCCCGT	53929	A
			ACGGGGTTTCACC TGTTGG		
			TGCCCCAAAGTGG ACGACC		
			C		
GAM2546	RNO2	5'	CTGGCCAACATGGTGAAACCCC	53935	
			GGGGTTTCACCATGTTGGTTAG		

CCCCAAAGTGGTACAACCGGTC

GAM2546	RoXaN	3'	CTAACACGGTGAAACCCC	47287	A
			GGGGTTTCACC TGTTGG		
			CCCCAAAGTGG ACAATC		
			C		
GAM2546	RoXaN	3'	CTAACATGGTGAAACCCC	47288	
			GGGGTTTCACCATGTTGG		
			CCCCAAAGTGGTACAATC		
GAM2546	RoXaN	3'	CTGGCCAACATAATGAAACCCC	47290	CC
			GGGGTTTCA ATGTTGGTTAG		
			CCCCAAAGT TACAACCGGTC		
			AA		
GAM2546	RPP14	3'	CTGGCCAACATGGTGAAACCCC	60222	
			GGGGTTTCACCATGTTGGTTAG		
			CCCCAAAGTGGTACAACCGGTC		
GAM2546	RRP4	3'	CCAACAAGGTGAAACCCC	27355	A
			GGGGTTTCACC TGTTGG		
			CCCCAAAGTGG ACAACC		
			A		
GAM2546	SAMHD1	3'	CTAGCATGGCGAAACCCAGT	61982	G A
			AC GGGTTTC CCATGTTGG		
			TG CCCAAAG GGTACGATC		
			A C		
GAM2546	SC65	3'	CTGGCCAACATGGTGAAACCCC	22293	
			GGGGTTTCACCATGTTGGTTAG		
			CCCCAAAGTGGTACAACCGGTC		
GAM2546	SCIN	3'	CCAACATGGCGAAACCTCG	53601	A
			CGGGGTTTC CCATGTTGG		
			GCTCCAAAG GGTACAACC		
			C		
GAM2546	SCN12A	3'	CCAACCATGATGAAACTCCGT	27080	C _
			ACGGGGTTTCA CATG TTGG		
			TGCCTCAAAGT GTAC AACC		
			A C		
GAM2546	SCYA5	3'	CTGGCCAACATGATGAAACCCC	12967	C
			GGGGTTTCA CATGTTGGTTAG		

			CCCCAAAGT GTACAACCGGTC		
			A		
GAM2546	SEMA3E	3'	CTAACAAGGTGAAACCCCGT 25807	A	
			ACGGGGTTTCACC TGTTGG		
			TGCCCCAAAGTG ACAATC		
			A		
GAM2546	SGKL	3'	CCAACATGGACAAACCCCGT 26056	CA	
			ACGGGGTTT CCATGTTGG		
			TGCCCCAAA GGTACAACC		
			CA		
GAM2546	SLC7A11	3'	CCAACATGGAGAAACCCC 27530	A	
			GGGGTTTC CCATGTTGG		
			CCCCAAAG GGTACAACC		
			A		
GAM2546	SMA3	3'	CCAACGTGGCAAACTCC 23259	CA	
			GGGGTTT CCATGTTGG		
			CCTCAA GGTGCAACC		
			AC		
GAM2546	SMAP-5	3'	CTGGTTAACACGGTGAAACCCC 48659	A	TT
	G		CGGGGTTTCACC TGTTGG AG		
			GCCCCAAAGTG ACAATT TC		
			C GG		
GAM2546	SNAPC1	3'	CTAACACAGTGAAACCCCGT 13275	CA	
			ACGGGGTTTCAC TGTTGG		
			TGCCCCAAAGTG ACAATC		
			AC		
GAM2546	SPRY4	3'	CCAATATGGTAAACCCC 49004	C	
			GGGGTTT ACCATGTTGG		
			CCCCAAA TGGTATAACC		
			—		
GAM2546	SPRY4	3'	CTGGCCAACATAGTGAAACCCC 49011	C	
	GT		ACGGGGTTTCAC ATGTTGGTTAG		
			TGCCCCAAAGTG TACAACCGGTC		
			A		
GAM2546	SPTLC2	3'	CCAACATGGCGAAACCTC 17983	A	
			GGGGTTTC CCATGTTGG		
			CTCCAAAG GGTACAACC		
			C		
GAM2546	SPTLC2	3'	CTGGCCAACATGGTGAAACCCC 17991		
	GT		ACGGGGTTTCACCATGTTGGTTAG		

TGCCCCAAAGTGGTACAACCGGTC

GAM2546 SS18L1 3' CCAACATGGAGAAACCCCGT 65953 A
ACGGGGTTTC CCATGTTGG
||||||| |||||
TGCCCCAAAG GGTACAACC

A

GAM2546 SSR3 3' CTGGCCAACATGGTGAAACCCC 24035
GT ACGGGGTTTCACCATGTTGGTTAG
||||||| |||||
TGCCCCAAAGTGGTACAACCGGTC

GAM2546 SUN1 3' CCAATGTAGCAAAACCCTGT 47910 CACC
ACGGGGTTT ATGTTGG
||||||| |||||
TGTCCCAA TGTAACC

ACGA

GAM2546 SYAP1 3' GCCAACATAGTGAAACCCTGT 52472 C
ACGGGGTTTCAC ATGTTGGT
||||||| |||||
TGTCCCAAAGTG TACAACCG

A

GAM2546 TA-LRRP 3' CCAACCTGGTGAAACCCC 31711 T
GGGGTTTCACCA GTTGG
||||||| |||||
CCCCAAAGTGGT CAACC

C

GAM2546 TACTILE 3' CTAACACAGTGAAACCCCGT 20586 CA
ACGGGGTTTCAC TGTTGG
||||||| |||||
TGCCCCAAAGTG ACAATC

AC

GAM2546 TDP1 5' CAACATGGTGAAACCCCGT 37601
ACGGGGTTTCACCATGTTG
||||||| |||||
TGCCCCAAAGTGGTACAAC

GAM2546 THEA 3' CCAACATGGTGAAACCCC 66881
GGGGTTTCACCATGTTGG
||||||| |||||
CCCCAAAGTGGTACAACC

GAM2546 THEA 3' CTGGCCAACATGGCGAAACCCC 66888 A
GGGGTTTC CCATGTTGGTTAG
||||||| |||||
CCCCAAAG GGTACAACCGGTC

C

GAM2546 TIP47 3' GGCCAACATGGTGAAACCCCGT 20606
ACGGGGTTTCACCATGTTGGTT
||||||| |||||

TGCCCCAAAGTGGTACAACCGG

GAM2546 TMG4 3' CTGGCCAACATGGTGAAACCCG 44213 G
GT AC GGGTTTCACCATGTTGGTTAG
|| |||||
TG CCCAAAGTGGTACAACCGGTC
G

GAM2546 TRIM38 3' CTGGCCAACATGGTGAAACCCT 22055
GT ACGGGGTTTCACCATGTTGGTTAG
|||||
TGTCCCAAAGTGGTACAACCGGTC

GAM2546 UBCE7IP5 3' CCAACATGGCAAGACCCC 30843 CA
GGGGTTT CCATGTTGG
|||||
CCCCAGA GGTACAACC
AC

GAM2546 ust3 3' CTGGCCAACATGGTGAAACCCT 94853
GT ACGGGGTTTCACCATGTTGGTTAG
|||||
TGTCCCAAAGTGGTACAACCGGTC

GAM2546 WBSCR21 3' CTGGCCAACATGGTGAAACCCT 49301
GT ACGGGGTTTCACCATGTTGGTTAG
|||||
TGTCCCAAAGTGGTACAACCGGTC

GAM2546 WBSCR23 3' CTGGCCAACATGGTGAAACCCC 47434
GGGGTTTCACCATGTTGGTTAG
|||||
CCCCAAAGTGGTACAACCGGTC

GAM2546 WSB1 3' AACATGATGAAACCCTGT 56959 C
ACGGGGTTTCA CATGTT
|||||
TGTCCCAAAGT GTACAA
A

GAM2546 WSB1 3' AACATGATGAAACCCTGT 56960 C
ACGGGGTTTCA CATGTT
|||||
TGTCCCAAAGT GTACAA
A

GAM2546 YME1L1 3' CTGGCCAACATGGTGAAACCCC 58432
GGGGTTTCACCATGTTGGTTAG
|||||
CCCCAAAGTGGTACAACCGGTC

GAM2546 ZAK 3' CTGGCCAACATGGTGAAACCCT 34104
GT ACGGGGTTTCACCATGTTGGTTAG
|||||

TGTCCCAAAGTGGTACAACCGGTC

GAM2546	ZFD25	3'	CTGGCCAACATAGCAAAACCCC 33110	CACC
			GGGGTTT ATGTTGGTTAG	
			CCCCAAA TACAACCGGTC	
			ACGA	
GAM2546	ZFP106	3'	CTGGCCAACATAGTGAAACCCC 42725	C
	GT		ACGGGGTTTCAC ATGTTGGTTAG	
			TGCCCCAAAGTG TACAACCGGTC	
			A	
GAM2546	ZFP106	3'	CTGGCCAACATGGCAAAACCCC 42726	CA
	GT		ACGGGGTTT CCATGTTGGTTAG	
			TGCCCCAAA GGTACAACCGGTC	
			AC	
GAM2546	ZIM3	3'	CCAACATGGTGAAACCCTGT 54637	
			ACGGGGTTTCACCATGTTGG	
			TGTCCCAAAGTGGTACAACC	
GAM2546	ZNF197	3'	CTGACCAACATGGTGAAACCCC 23755	
			GGGGTTTCACCATGTTGGTTAG	
			CCCCAAAGTGGTACAACCAGTC	
GAM2546	ZNF271	3'	CTGACCAACATGGTGAAACCCT 96965	
	GT		ACGGGGTTTCACCATGTTGGTTAG	
			TGTCCCAAAGTGGTACAACCAGTC	
GAM2546	ZNF297B	3'	CTGACCAACATAGTGAAACCCC 26655	C
			GGGGTTTCAC ATGTTGGTTAG	
			CCCCAAAGTG TACAACCAGTC	
			A	
GAM2546	ZNF297B	5'	CTGGCCAACATAGTGAAACCCC 26656	C
			GGGGTTTCAC ATGTTGGTTAG	
			CCCCAAAGTG TACAACCGGTC	
			A	
GAM2546	ZNF347	3'	CTGACCAACATGGCGAAACCCC 51825	A
			GGGGTTTC CCATGTTGGTTAG	
			CCCCAAAG GGTACAACCAGTC	
			C	
GAM2546	LOC112687	3'	CTGGCCAACATGGTGAAACCCC 73233	
	GT		ACGGGGTTTCACCATGTTGGTTAG	

TGCCCCAAAGTGGTACAACCGGTC

GAM2546	LOC115129	3'	CCAACAATGGCAAACCCCGT	73612	CA	_
			ACGGGGTTT CCAT GTTGG			
			TGCCCCAAA GGTA CAACC			
			AC A			
GAM2546	LOC115196	3'	CTAACACAGTGAAACCCTGT	73657	CA	
			ACGGGGTTTCAC TGTTGG			
			TGTCCCAAAGTG ACAATC			
			AC			
GAM2546	LOC115273	3'	CTGGCCAACATGGTGAAACCCT	73750		
		GT	ACGGGGTTTCACCATGTTGGTTAG			
			TGTCCCAAAGTGGTACAACCGGTC			
GAM2546	LOC116143	3'	CTAACATGGTGAAACCCCGT	74184		
			ACGGGGTTTCACCATGTTGG			
			TGCCCCAAAGTGGTACAATC			
GAM2546	LOC116228	3'	CCAACAGGGTGAAACCCTGT	74227	A	
			ACGGGGTTTCACC TGTTGG			
			TGTCCCAAAGTGG ACAACC			
			G			
GAM2546	LOC116236	3'	CTAACACAGTGAAACCTC	74243	CA	
			GGGGTTTCAC TGTTGG			
			CTCCAAAGTG ACAATC			
			AC			
GAM2546	LOC116349	3'	CTAACATGGTGAAACCCCGT	74275		
			ACGGGGTTTCACCATGTTGG			
			TGCCCCAAAGTGGTACAATC			
GAM2546	LOC118471	3'	CAACATGGTGAAACCCCGT	74352		
			ACGGGGTTTCACCATGTTG			
			TGCCCCAAAGTGGTACAAC			
GAM2546	LOC119504	5'	CCAACATGGAGAAACCCC	74443	A	
			GGGGTTTC CCATGTTGG			
			CCCCAAAG GGTACAACC			
			A			
GAM2546	LOC121457	3'	CTAACAGGGTGAAACCCTGT	74509	A	
			ACGGGGTTTCACC TGTTGG			

		TGTCCCAAAGTGG ACAATC		
		G		
GAM2546	LOC121504 3'	CCAACATAGTGAGACCCC	74542	C
		GGGGTTTCAC ATGTTGG		
		CCCCAGAGTG TACAACC		
		A		
GAM2546	LOC122704 3'	CAACATGGTGAAACCCTGT	74600	
		ACGGGGTTTCACCATGTTG		
		TGTCCCAAAGTGGTACAAC		
GAM2546	LOC122970 3'	TAACACAGCGAGACCCCGT	74644	ACCAT _
		ACGGGGTTTC GTTG GTTA		
		TGCCCCAGAG CGAC CAAT		
		_____ A		
GAM2546	LOC124602 3'	CCAACATGGCGAAATCCCGT	74785	A
		ACGGGGTTTC CCATGTTGG		
		TGCCCTAAAG GGTACAACC		
		C		
GAM2546	LOC126282 3'	CTAACACGGTGAAACCCC	74955	A
		GGGGTTTCACC TGTTGG		
		CCCCAAAGTGG ACAATC		
		C		
GAM2546	LOC126282 3'	CTGGCCAACATGGTGAAACCCC	74956	
	GT	ACGGGGTTTCACCATGTTGGTTAG		
		TGCCCAAAGTGGTACAACCGGTC		
GAM2546	LOC126669 3'	CTGGCCAACATGGTGAAACCCT	75933	
	GT	ACGGGGTTTCACCATGTTGGTTAG		
		TGTCCCAAAGTGGTACAACCGGTC		
GAM2546	LOC127294 3'	CTGGCCAACATGACGAAACCCG	75145	G AC
	GT	AC GGGTTTC CATGTTGGTTAG		
		TG CCAAAG GTACAACCGGTC		
		G CA		
GAM2546	LOC127428 3'	CTGGCCAACATGGCGAAACCCT	75157	A
	GT	ACGGGGTTTC CCATGTTGGTTAG		
		TGTCCCAAAG GGTACAACCGGTC		
		C		
GAM2546	LOC130026 3'	CTAACATGGTGAAACCCCGT	57437	
		ACGGGGTTTCACCATGTTGG		

TGCCCCAAAGTGGTACAATC

GAM2546 LOC130535 3' CCAACATGGCGAAACCCC 76647 A
GGGGTTTC CCATGTTGG
||||||| |||||||
CCCCAAAG GGTACAACC
C

GAM2546 LOC130535 3' CCAGCATGGTGAAACCCTGT 76648
ACGGGGTTTCACCATGTTGG
||||||| |||||||
TGTCCCCAAAGTGGTACGACC

GAM2546 LOC130589 3' CTAACACGGTGAAACCCCGT 57931 A
ACGGGGTTTCACC TGTGTTGG
||||||| |||||
TGCCCCAAAGTGG ACAATC
C

GAM2546 LOC131744 3' CTGACCAACATGGTGAAACCCC 76389
GGGGTTTCACCATGTTGGTTAG
||||||| |||||||
CCCCAAAGTGGTACAACCGTC

GAM2546 LOC131965 3' CCAACATGGTGAGACCCC 75520
GGGGTTTCACCATGTTGG
||||||| |||||||
CCCCAGAGTGGTACAACC

GAM2546 LOC134147 3' CCAACATGGTGAGACCCC 57956
GGGGTTTCACCATGTTGG
||||||| |||||||
CCCCAGAGTGGTACAACC

GAM2546 LOC134147 3' CTGGCCAACATGGTGAAACCCC 57959
GGGGTTTCACCATGTTGGTTAG
||||||| |||||||
CCCCAAAGTGGTACAACCGGTC

GAM2546 LOC137362 3' CTGGCCAACATGGTGAAACCCC 75783
GT ACGGGGTTTCACCATGTTGGTTAG
||||||| |||||||
TGCCCCAAAGTGGTACAACCGGTC

GAM2546 LOC138389 3' CCAAAATGATGAAACCCC 76729 C G
GGGGTTTCA CAT TTGG
||||||| ||| |||
CCCCAAAGT GTA AACC
A A

GAM2546 LOC138428 3' CTGGCCAACATGGTGAAACCCT 75856
GT ACGGGGTTTCACCATGTTGGTTAG
||||||| |||||||

TGTCCCAAAGTGGTACAACCGGTC

GAM2546 LOC139422 3' CTAACACAGTGAAACCCCGT 76347 CA
ACGGGGTTTCAC TGTTGG
||||||| |||||
TGCCCAAAGTG ACAATC
AC

GAM2546 LOC142927 3' CAACATGGCGAAACCCCGT 76943 A
ACGGGGTTTC CCATGTTG
||||||| |||||
TGCCCAAAG GGTACAAC
C

GAM2546 LOC143196 3' CTGGCCAACATGGTGAACCCC 83803
GT ACGGGGTTTCACCATGTTGGTTAG
|||||||
TGCCCAAAGTGGTACAACCGGTC

GAM2546 LOC143310 3' CTAACATGGTGAACCCCT 77045
GGGGTTTCACCATGTTGG
|||||||
TCCCAAAGTGGTACAATC

GAM2546 LOC143465 3' CTGGCCAACATGGTGAACCCCT 83873
GT ACGGGGTTTCACCATGTTGGTTAG
|||||||
TGTCCCAAAGTGGTACAACCGGTC

GAM2546 LOC143888 3' CTGGCCAACATGGTGAACCCC 77170
GT ACGGGGTTTCACCATGTTGGTTAG
|||||||
TGCCCAAAGTGGTACAACCGGTC

GAM2546 LOC144289 3' CCACCATGGTGAACCCC 83954 T
GGGGTTTCACCATG TGG
||||||| |||
CCCCAAAGTGGTAC ACC
C

GAM2546 LOC144465 3' CCAACATGGAGAAACCCC 77345 A
GGGGTTTC CCATGTTG
||||| |||||
CCCCAAAG GGTACAACC
A

GAM2546 LOC144465 3' CCAACATGGAGAAACCCCGT 77346 A
ACGGGGTTTC CCATGTTG
||||||| |||||
TGCCCAAAG GGTACAACC
A

GAM2546 LOC144481 3' CTGGCCAACATGGCAAAACCCC 84018 CA
GGGGTTT CCATGTTGGTTAG
||||| |||||||||

	CCCCAAA GGTACAACCGGTC		
	AC		
GAM2546 LOC144486 3'	CCAACATGGTGAAATCCC 84001		
	GGGGTTTTCACCATGTTGG		
	CCCTAAAGTGGTACAACC		
GAM2546 LOC144524 3'	CTGGCCAACACGGTGAAACACC 84053	G	A
GT	ACGG GTTTCACC TGTTGGTTAG		
	TGCC CAAAGTGG ACAACCGGTC		
	A C		
GAM2546 LOC144563 3'	CTGGCCAACATGGTGAAACCCC 77396		
	GGGGTTTTCACCATGTTGGTTAG		
	CCCCAAAGTGGTACAACCGGTC		
GAM2546 LOC144583 3'	CTGGCCAACATGGTGAAACCCC 77416		
	GGGGTTTTCACCATGTTGGTTAG		
	CCCCAAAGTGGTACAACCGGTC		
GAM2546 LOC144817 3'	CTAACACGGTGAAACCCTGT 77516	A	
	ACGGGGTTTTCACC TGTTGG		
	TGTCCCAAAGTGG ACAATC		
	C		
GAM2546 LOC144817 3'	GGCCAACATAGTGAAACCCTGT 77519	C	
	ACGGGGTTTTCAC ATGTTGGTT		
	TGTCCCAAAGTG TACAACCGG		
	A		
GAM2546 LOC144845 3'	CTGGCCAACATGGTAAAACCCC 57460	C	
GT	ACGGGGTTT ACCATGTTGGTTAG		
	TGCCCCAAA TGGTACAACCGGTC		
	A		
GAM2546 LOC145035 3'	CTGGGAAACATAGCGAAACCCC 84175	ACC	GG
	GGGGTTTC ATGTT TTAG		
	CCCCAAAG TACAA GGTC		
	CGA AG		
GAM2546 LOC145082 5'	CTGACCAACATGGCAAAACCCT 84188	CA	
GT	ACGGGGTTT CCATGTTGGTTAG		
	TGTCCCAA GGTACAACCAGTC		
	AC		
GAM2546 LOC145216 3'	CTGACCAACATGACAAAACCCC 84222	CAC	
GT	ACGGGGTTT CATGTTGGTTAG		

	TGCCCCAAA GTACAACCAGTC	
	ACA	
GAM2546 LOC145231 3'	CAACATGATGAAACTCCGT 84241	C
	ACGGGGTTTCA CATGTTG	
	TGCCTCAAAGT GTACAAC	
	A	
GAM2546 LOC145299 3'	CTAACAAGGTGAAACCCCGT 84276	A
	ACGGGGTTTCACC TGTTGG	
	TGCCCCAAAGTGG ACAATC	
	A	
GAM2546 LOC145333 3'	CTAAAACGGTGAAACCCCGT 84295	ATG
	ACGGGGTTTCACC TTGG	
	TGCCCCAAAGTGG AATC	
	CAA	
GAM2546 LOC145387 3'	CCAATATGGTGAAACCCTGT 84333	
	ACGGGGTTTCACCATGTTGG	
	TGTCCCAAAGTGGTATAACC	
GAM2546 LOC145438 3'	CTAAAACGGTGAAACCCCGT 84312	ATG
	ACGGGGTTTCACC TTGG	
	TGCCCCAAAGTGG AATC	
	CAA	
GAM2546 LOC145482 3'	CTGGCCAACACGGTGAAACCCC 77742	A
	GGGGTTTCACC TGTTGGTTAG	
	CCCCAAAGTGG ACAACCGGTC	
	C	
GAM2546 LOC145483 3'	AGCCAACACGGCAAAACTCC 77750	CA A
	GGGGTTT CC TGTTGGTT	
	CCTCAA GG ACAACCGA	
	AC C	
GAM2546 LOC145662 3'	CCAAGATGGTGAAACCCCGT 77834	G
	ACGGGGTTTCACCAT TTGG	
	TGCCCCAAAGTGGTA AACC	
	G	
GAM2546 LOC145663 3'	CAACATGATGAAACCCTGT 84413	C
	ACGGGGTTTCA CATGTTG	
	TGTCCCAAAGT GTACAAC	
	A	
GAM2546 LOC145663 3'	CTAACATGGTGAAACCCCGT 84423	
	ACGGGGTTTCACCATGTTGG	

TGCCCCAAAGTGGTACAATC

GAM2546 LOC145757 3' CTGGCCAACATGGTGAAACCCC 77930
GT ACGGGGTTTCACCATGTTGGTTAG
|||||||
TGCCCCAAAGTGGTACAACCGGTC

GAM2546 LOC145820 3' CTAACATGGTGAAACCCCGT 77977
ACGGGGTTTCACCATGTTGG
|||||||
TGCCCCAAAGTGGTACAATC

GAM2546 LOC146059 3' CTGGCCAACATGGCAAACCCC 78086 CA
GGGGTTT CCATGTTGGTTAG
||||| |||||
CCCCAAA GGTACAACCGGTC
AC

GAM2546 LOC146667 3' CTAACATGGTGAAACCCCGT 84709
ACGGGGTTTCACCATGTTGG
|||||||
TGCCCCAAAGTGGTACAATC

GAM2546 LOC146669 3' CTGGCCAACATGGCGAAACCCC 78660 A
GGGGTTTC CCATGTTGGTTAG
||||| |||||
CCCCAAAG GGTACAACCGGTC
C

GAM2546 LOC146713 3' CCAATGTAGTGAAACCCCGT 84725 C
ACGGGGTTTCAC ATGTTGG
||||||| |||||
TGCCCCAAAGTG TGTAACC
A

GAM2546 LOC146713 3' CTGGCCAACATGGCGAAACCCT 84729 A
GGGGTTTC CCATGTTGGTTAG
||||| |||||
TCCCAAAG GGTACAACCGGTC
C

GAM2546 LOC146723 3' CCAACATGGAGAAACCCC 78677 A
GGGGTTTC CCATGTTGG
||||| |||||
CCCCAAAG GGTACAACC
A

GAM2546 LOC146728 5' CCAACATGGTGAAACCTCGT 84763
ACGGGGTTTCACCATGTTGG
|||||||
TGCTCCAAAGTGGTACAACC

GAM2546 LOC146756 3' CTAAAACGGTGAAACCCCGT 84800 ATG
ACGGGGTTTCACC TTGG
||||||| |||

		TGCCCCAAAGTGG AATC		
		CAA		
GAM2546	LOC146780 3'	CTAACATGGTGAAACCCCG 84819		
		CGGGGTTTCACCATGTTGG		
		GCCCCAAAGTGGTACAATC		
GAM2546	LOC146895 3'	CCAACGTGATGAAACCCC 84865	C	
		GGGGTTTCA CATGTTGG		
		CCCCAAAGT GTGCAACC		
		A		
GAM2546	LOC146901 3'	CTGGCCAACATGGTGAAACCCC 84899		
	GT	ACGGGGTTTCACCATGTTGGTTAG		
		TGCCCCAAAGTGGTACAACCGGTC		
GAM2546	LOC146923 3'	CTAACACGGTGAAACCCC 78799	A	
		GGGGTTTCACC TGTTGG		
		CCCCAAAGTGG ACAATC		
		C		
GAM2546	LOC147057 3'	CTGGCCAACACGGTGAAACCCG 84982	G	A
	GT	AC GGGTTTCACC TGTTGGTTAG		
		TG CCCAAAGTGG ACAACCGGTC		
		G C		
GAM2546	LOC147071 3'	CTAACATGGTGAAACCCC 73362		
		GGGGTTTCACCATGTTGG		
		CCCCAAAGTGGTACAATC		
GAM2546	LOC147180 5'	CTGTCCAACATGGTGAAACCCC 85098		T
	GT	ACGGGGTTTCACCATGTTGG TAG		
		TGCCCCAAAGTGGTACAACC GTC		
		T		
GAM2546	LOC147649 3'	CTGGCCAACACGGTGAAACCCC 79061		A
	GT	ACGGGGTTTCACC TGTTGGTTAG		
		TGCCCCAAAGTGG ACAACCGGTC		
		C		
GAM2546	LOC147660 3'	CTAACACGGTGAAACCTCGT 79027		A
		ACGGGGTTTCACC TGTTGG		
		TGCTCCAAAGTGG ACAATC		
		C		
GAM2546	LOC147664 3'	CCAACATGGAGAAACCCCGT 79045		A
		ACGGGGTTTC CCATGTTGG		

	TGCCCCAAAG GGTACAACC	
	A	
GAM2546 LOC147700 3'	CCAACATGGAGAAACCCCGT 59880	A
	ACGGGGTTTC CCATGTTGG	
	TGCCCCAAAG GGTACAACC	
	A	
GAM2546 LOC147727 5'	CCAGCATGGTGAAACCCCGT 79133	
	ACGGGGTTTCACCATGTTGG	
	TGCCCCAAAGTGGTACGACC	
GAM2546 LOC147727 5'	CTGGCCAACATGGTGAAACACC 79135	G
GT	ACGG GTTTCACCATGTTGGTTAG	
	TGCC CAAAGTGGTACAACCGGTC	
	A	
GAM2546 LOC148147 3'	CTAACACGGTGAAACCCCGT 79397	A
	ACGGGGTTTCACC TGTTGG	
	TGCCCCAAAGTGG ACAATC	
	C	
GAM2546 LOC148254 3'	CTGGTTAACATGGTGAAACCCT 79502	TT
GT	ACGGGGTTTCACCATGTTGG AG	
	TGTCCCAAAGTGGTACAATT TC	
	GG	
GAM2546 LOC148397 3'	CCAACATGGAGAAACCCC 79563	A
	GGGGTTTC CCATGTTGG	
	CCCCAAAG GGTACAACC	
	A	
GAM2546 LOC148534 3'	CCAACATGGTGAAACCTC 79634	
	GGGGTTTCACCATGTTGG	
	CTCCAAAGTGGTACAACC	
GAM2546 LOC148734 3'	CTAACAGAGTGAAACCCC 79711	CA
	GGGGTTTCAC TGTTGG	
	CCCCAAAGTG ACAATC	
	AG	
GAM2546 LOC148749 3'	CTGAGTAACATGGTGAAACCCC 79714	G
	GGGGTTTCACCATGTTG TTAG	
	CCCCAAAGTGGTACAAT AGTC	
	G	
GAM2546 LOC148809 5'	CTGGCCAACACAGTGAAACCCC 79752	CA
	GGGGTTTCAC TGTTGGTTAG	

		CCCCAAAGTG ACAACCGGTC		
		AC		
GAM2546	LOC148809 3'	CTGGCCAACATGGTGAACCCC 79754		
		GGGGTTTCACCATGTTGGTTAG		
		CCCCAAGGTGGTACAACCGGTC		
GAM2546	LOC148918 5'	CTGGCCAACATGGTGAAACCCT 79826		
	GT	ACGGGGTTTCACCATGTTGGTTAG		
		TGTCCCAAAGTGGTACAACCGGTC		
GAM2546	LOC148936 3'	CTGGCCAACATGGTGAAACCCC 85452		
		GGGGTTTCACCATGTTGGTTAG		
		CCCCAAAGTGGTACAACCGGTC		
GAM2546	LOC148938 3'	CTGGCCAACATGGTGAAACCCC 85435		
		GGGGTTTCACCATGTTGGTTAG		
		CCCCAAAGTGGTACAACCGGTC		
GAM2546	LOC148946 3'	GGCCAACATGGTGAAACCC 85469		
		GGGTTTCACCATGTTGGTT		
		CCCAAAGTGGTACAACCGG		
GAM2546	LOC149073 3'	CTGACCAACATGGCGAAACCCC 85484	A	
	GT	ACGGGGTTTC CCATGTTGGTTAG		
		TGCCCCAAAG GGTACAACCAGTC		
		C		
GAM2546	LOC149113 3'	CCAAGATGGTGAAACCCC 79904	G	
		GGGGTTTCACCAT TTGG		
		CCCCAAAGTGGTA AACC		
		G		
GAM2546	LOC149113 5'	CTGACCAACATGGTGAAACCCC 79910		
		GGGGTTTCACCATGTTGGTTAG		
		CCCCAAAGTGGTACAACCAGTC		
GAM2546	LOC149175 3'	CTAACAGGGTGAAACCACGT 79952	G	A
		ACG GGTTTCACC TGTTGG		
		TGC CCAAAGTGG ACAATC		
		A G		
GAM2546	LOC149194 5'	TAACATGGTGAAACCCGCGT 79989	—	
		ACG GGGTTTCACCATGTTG		

		TGC CCCAAAGTGGTACAAT	
		G	
GAM2546	LOC149271 3'	CAACATGGTGAAACCCTGT 79997	
		ACGGGGTTTCACCATGTTG	
		TGTCCCAAAGTGGTACAAC	
GAM2546	LOC149319 3'	CTGGCCAACATGGTGAAACCCT 80071	
	GT	ACGGGGTTTCACCATGTTGGTTAG	
		TGTCCCAAAGTGGTACAACCGGTC	
GAM2546	LOC149460 3'	CCAATATGGTAAAACCCCGT 85608	C
		ACGGGGTTT ACCATGTTGG	
		TGCCCCAAA TGGTATAACC	
		A	
GAM2546	LOC149668 3'	CCAATATAGTGAAACCCC 85697	C
		GGGGTTTCAC ATGTTGG	
		CCCCAAAGTG TATAACC	
		A	
GAM2546	LOC149705 3'	CTGGCCAACATGGTGAAACCCC 85777	
		GGGGTTTCACCATGTTGGTTAG	
		CCCCAAAGTGGTACAACCGGTC	
GAM2546	LOC149705 3'	CTGGCCAACATGGTGAAACCCC 85778	
	GT	ACGGGGTTTCACCATGTTGGTTAG	
		TGCCCCAAAGTGGTACAACCGGTC	
GAM2546	LOC150185 3'	CTGACCAACATGGTAGAACCCC 86069	TC
	GT	ACGGGGTTT ACCATGTTGGTTAG	
		TGCCCCAA TGGTACAACCAGTC	
		GA	
GAM2546	LOC150299 3'	CCAACATGGTGAAACCTC 86164	
		GGGGTTTCACCATGTTGG	
		CTCCAAAGTGGTACAACC	
GAM2546	LOC150358 3'	CCAACATGGTGATACCCCGT 86091	T
		ACGGGGT TCACCATGTTGG	
		TGCCCCA AGTGGTACAACC	
		T	
GAM2546	LOC150358 3'	CTAACACAGTGAAACCCCGT 86097	CA
		ACGGGGTTTCAC TGTTGG	

		TGCCCCAAAGTG ACAATC	
		AC	
GAM2546	LOC150372 3'	CCAACGTGGTGAAACCCCGT 80608	
		ACGGGGTTTCACCATGTTGG	
		TGCCCCAAAGTGGTGCAACC	
GAM2546	LOC150481 3'	CTGGCCAACATGGTGAAACCCT 80699	
	GT	ACGGGGTTTCACCATGTTGGTTAG	
		TGTCCCAAAGTGGTACAACCGGTC	
GAM2546	LOC150622 3'	CCACCATGGTGAGACCCCGT 80757	T
		ACGGGGTTTCACCATG TGG	
		TGCCCCAGAGTGGTAC ACC	
		C	
GAM2546	LOC150935 3'	CTGGCCAACATGGTGAAACCCC 80826	
	GT	ACGGGGTTTCACCATGTTGGTTAG	
		TGCCCCAAAGTGGTACAACCGGTC	
GAM2546	LOC150960 3'	CAACATGGTGAAACCCCGT 80868	
		ACGGGGTTTCACCATGTTG	
		TGCCCCAAAGTGGTACAAC	
GAM2546	LOC151195 3'	AACCAACATGGTGGTTCAGT 80966	GG TT
		AC GG TCACCATGTTGGTT	
		TG CT GGTGGTACAACCAA	
		A_ T_	
GAM2546	LOC151196 3'	CTGGCCAACATGGTGAAACCCC 86451	
	GT	ACGGGGTTTCACCATGTTGGTTAG	
		TGCCCCAAAGTGGTACAACCGGTC	
GAM2546	LOC151248 3'	CTAATCCGGTGAAACCTCGT 80993	AT
		ACGGGGTTTCACC GTTGG	
		TGCTCCAAAGTGG TAATC	
		CC	
GAM2546	LOC151429 3'	CTAACACGGTGAAACCCTGT 86534	A
		ACGGGGTTTCACC TGTGG	
		TGTCCCAAAGTGG ACAATC	
		C	
GAM2546	LOC151429 3'	GCCAACATGGTGAAACCCC 86539	
		GGGGTTTCACCATGTTGGT	

CCCCAAAGTGGTACAACCG

GAM2546 LOC151446 3' CTAGGCAACATGGTGAAACCCA 86570 G G
GT AC GGGTTTCACCATGTTG TTAG

|| |||||
TG CCCAAAGTGGTACAAC GATC
A G

GAM2546 LOC151556 3' CTGGCCAACATGGCGAAACCCC 81078 A
GT ACGGGGTTTC CCATGTTGGTTAG

||||| |||||
TGCCCCAAAG GGTACAACCGGTC
C

GAM2546 LOC151602 3' CTGGCCAACATGGTGAAACCCC 81111
GT ACGGGGTTTCACCATGTTGGTTAG

||||| |||||
TGCCCCAAAGTGGTACAACCGGTC

GAM2546 LOC151614 3' CTAACACAGTGAAACCTCGT 81121 CA
ACGGGGTTTCAC TGTTGG

||||| |||||
TGCTCCAAAGTG ACAATC
AC

GAM2546 LOC151632 3' CCAAAATGGTGAAACCCC 86642 G
GGGGTTTCACCAT TTGG

||||| |||||
CCCCAAAGTGGTA AACC
A

GAM2546 LOC151720 3' CTAACATGGTGAAACCCTGT 81152
ACGGGGTTTCACCATGTTGG

||||| |||||
TGTCCCCAAAGTGGTACAATC

GAM2546 LOC151904 3' CTGGCCAACATGGTGAAACCCC 81205
GGGGTTTCACCATGTTGGTTAG

||||| |||||
CCCCAAAGTGGTACAACCGGTC

GAM2546 LOC152271 3' CCAATGTGGTGAAACCCC 81356
GGGGTTTCACCATGTTGG

||||| |||||
CCCCAAAGTGGTGTAACC

GAM2546 LOC152283 3' CAACATAGTGAAACCCCGT 86865 C
ACGGGGTTTCAC ATGTTG

||||| |||||
TGCCCCAAAGTG TACAAC
A

GAM2546 LOC152317 3' CAACATGGTGAAACTCCGT 86823
ACGGGGTTTCACCATGTTG

||||| |||||

TGCCTCAAAGTGGTACAAC

GAM2546 LOC152426 3' CTAACATGGTGAAACCCTGT 86895
ACGGGGTTTCACCATGTTGG
|||||||
TGTCCCAAAGTGGTACAATC

GAM2546 LOC152445 3' CCAACATGGAGAAACCCCGT 86941 A
ACGGGGTTTC CCATGTTGG
|||||||
TGCCCCAAAG GGTACAACC
A

GAM2546 LOC152453 3' TCAACATGGAGAAACCCCGT 81479 A
ACGGGGTTTC CCATGTTGG
|||||||
TGCCCCAAAG GGTACAAC
A

GAM2546 LOC152627 5' CTGGCCAACATGGTGAAACCCT 81509
GT ACGGGGTTTCACCATGTTGGTTAG
|||||||
TGTCCCAAAGTGGTACAACCGGTC

GAM2546 LOC152804 3' CTAGTCAACATGGTGAAACCCC 87077 GT
GT ACGGGGTTTCACCATGTTG TAG
|||||||
TGCCCCAAAGTGGTACAAC ATC
TG

GAM2546 LOC152804 3' CTGGCCAACATGGTGAAACCCC 87079
GGGGTTTCACCATGTTGGTTAG
|||||||
CCCCAAAGTGGTACAACCGGTC

GAM2546 LOC152860 3' CCAACGTGGAGAAACCCCGT 81576 A
ACGGGGTTTC CCATGTTGG
|||||||
TGCCCCAAAG GGTGCAACC
A

GAM2546 LOC152926 3' CTGGCCAACATGGTGAAACCCT 81631
GT ACGGGGTTTCACCATGTTGGTTAG
|||||||
TGTCCCAAAGTGGTACAACCGGTC

GAM2546 LOC153077 3' CTAACACAGTGAAACCCC 87123 CA
GGGGTTTCAC TGTTGG
|||||||
CCCCAAAGTG ACAATC
AC

GAM2546 LOC153146 3' CAACATGGTGAAACCTCGT 87142
ACGGGGTTTCACCATGTTG
|||||||

TGCTCCAAAGTGGTACAAC

GAM2546 LOC153260 3' CTGACCAACATGGTGAAACCCC 81672
GT ACGGGGTTTCACCATGTTGGTTAG
|||||||
TGCCCCAAAGTGGTACAACCAGTC

GAM2546 LOC153338 3' CTGGCCAACATGGTGAAACCC 87196
GGGTTTCACCATGTTGGTTAG
|||||||
CCCAAAGTGGTACAACCGGTC

GAM2546 LOC153579 3' CTAACACAGTGAAACCCCGT 81769 CA
ACGGGGTTTCAC TGTTGG
|||||||
TGCCCCAAAGTG ACAATC
AC

GAM2546 LOC153642 3' CTGGCCAACATGGTGAAACCCT 81787
GT ACGGGGTTTCACCATGTTGGTTAG
|||||||
TGTCCCCAAAGTGGTACAACCGGTC

GAM2546 LOC153682 3' CTAACACAGTGAAACCCC 87273 CA
GGGGTTTCAC TGTTGG
|||||||
CCCAAAGTG ACAATC
AC

GAM2546 LOC153727 3' CTGGCCAACATGGTGAAACCCC 87362
GT ACGGGGTTTCACCATGTTGGTTAG
|||||||
TGCCCCAAAGTGGTACAACCGGTC

GAM2546 LOC154089 3' CTAGGCAACATGGTGAAACCCT 81941 G
GT ACGGGGTTTCACCATGTTG TTAG
|||||||
TGTCCCCAAAGTGGTACAAC GATC
G

GAM2546 LOC154403 3' CCAAGATGGTGAAACCCC 81970 G
GGGGTTTCACCAT TTGG
|||||||
CCCAAAGTGGTA AACC
G

GAM2546 LOC154403 5' CTGACCAACATGGTGAAACCCC 81976
GGGGTTTCACCATGTTGGTTAG
|||||||
CCCAAAGTGGTACAACCAGTC

GAM2546 LOC154739 3' CAACATATCAAAACCCCGT 87430 CACC
ACGGGGTTT ATGTTG
|||||||

		TGCCCCAAA	TACAAC	
		ACTA		
GAM2546	LOC154739 5'	CTGACCAACATGGTGAAACCCT	87439	
		GGGGTTTTCACCATGTTGGTTAG		
		TCCCAAAGTGGTACAACCAGTC		
GAM2546	LOC154791 3'	CCAACATGGAAAAACCCCGT	82051	CA
		ACGGGGTTT CCATGTTGG		
		TGCCCCAAA GGTACAACC		
		AA		
GAM2546	LOC154992 3'	CCAAGATGGTGAAACTCC	82132	G
		GGGGTTTTCACCAT TTGG		
		CCTCAAAGTGGTA AACC		
		G		
GAM2546	LOC154992 5'	CTGACCAACATGGTGAAACCCC	82137	
	GT	ACGGGGTTTTCACCATGTTGGTTAG		
		TGCCCCAAAAGTGGTACAACCAGTC		
GAM2546	LOC155006 3'	CTGGCCAACATGGTGAAACCCT	82169	
	GT	ACGGGGTTTTCACCATGTTGGTTAG		
		TGTCCCAAAGTGGTACAACCGGTC		
GAM2546	LOC155072 3'	CTAACATGGTGAAACCCCGT	87663	
		ACGGGGTTTTCACCATGTTGG		
		TGCCCCAAAAGTGGTACAATC		
GAM2546	LOC155072 3'	CTAACATGGTGAAACCCTGT	87664	
		ACGGGGTTTTCACCATGTTGG		
		TGTCCCAAAGTGGTACAATC		
GAM2546	LOC155376 3'	CTGGCCAACATGGTGAAACCCT	82245	
	GT	ACGGGGTTTTCACCATGTTGGTTAG		
		TGTCCCAAAGTGGTACAACCGGTC		
GAM2546	LOC157464 5'	CTGGCCAACATGGCAAACCCC	87746	CA
	GT	ACGGGGTTT CCATGTTGGTTAG		
		TGCCCCAAA GGTACAACCGGTC		
		AC		
GAM2546	LOC157657 3'	CTGGCCAACATGATAAACACC	82434	G CAC
		GG GTTT CATGTTGGTTAG		

		CC CAAA GTACAACCGGTC	
		A ATA	
GAM2546	LOC157660 3'	CTGACCAACATGGTGAAACCCC 87803	
	GT	ACGGGGTTTCACCATGTTGGTTAG	
		TGCCCCAAAGTGGTACAACCAGTC	
GAM2546	LOC157983 3'	CCAACGTGGTGAAACCCCGT 82538	
		ACGGGGTTTCACCATGTTGG	
		TGCCCCAAAGTGGTGCAACC	
GAM2546	LOC158088 3'	CTAACACGGTGAAATCCCGT 87973	A
		ACGGGGTTTCACC TGTTGG	
		TGCCCTAAAGTGG ACAATC	
		C	
GAM2546	LOC158191 3'	CTGGCCAACATGGTGAAACCCT 82672	
	GT	ACGGGGTTTCACCATGTTGGTTAG	
		TGTCCCAAAGTGGTACAACCGGTC	
GAM2546	LOC158288 3'	CTAACACAGTGAAACCCCGT 88020	CA
		ACGGGGTTTCAC TGTTGG	
		TGCCCCAAAGTG ACAATC	
		AC	
GAM2546	LOC158292 5'	CTAACACGGTGAAACCCCGT 88048	A
		ACGGGGTTTCACC TGTTGG	
		TGCCCCAAAGTGG ACAATC	
		C	
GAM2546	LOC158337 3'	CGACACGGTGAAACCCTGT 88109	A TG
		ACGGGGTTTCACC TGT G	
		TGTCCCAAAGTGG ACA C	
		C GT	
GAM2546	LOC158677 5'	CTGGCCAACATGGCGAAACCCT 88248	A
	GT	ACGGGGTTTC CCATGTTGGTTAG	
		TGTCCCAAAG GGTACAACCGGTC	
		C	
GAM2546	LOC158819 3'	CCAAGATGGTGAAATCCCGT 88273	G
		ACGGGGTTTCACCAT TTGG	
		TGCCCTAAAGTGGTA AACC	
		G	
GAM2546	LOC158819 5'	CTGGCCAACATGGTGAAACCCC 88275	
	GT	ACGGGGTTTCACCATGTTGGTTAG	

TGCCCCAAAGTGGTACAACCGGTC

GAM2546 LOC158863 3' CCAGCATAGTGAAACCCTGT 88296 C
ACGGGGTTTCAC ATGTTGG
||||||| |||||
TGTCCCCAAAGTG TACGACC

A

GAM2546 LOC158987 3' CTGGCCAACATGGTGAAACCCT 88324
GT ACGGGGTTTCACCATGTTGGTTAG
||||||| |||||
TGTCCCCAAAGTGGTACAACCGGTC

GAM2546 LOC159036 3' CCAATATGGTGAAACCCC 88346
GGGGTTTCACCATGTTGG
||||||| |||||
CCCCAAAGTGGTATAACC

GAM2546 LOC159053 3' CTAACACGGTGAAACCCTGT 88370 A
ACGGGGTTTCACC TGTTGG
||||||| |||||
TGTCCCCAAAGTGG ACAATC

C

GAM2546 LOC159053 3' CTGGCCAACATGGTGAAACCCC 88371
GT ACGGGGTTTCACCATGTTGGTTAG
||||||| |||||
TGCCCCAAAGTGGTACAACCGGTC

GAM2546 LOC159110 3' CTGGCCAACATGGTGAAACCCT 82991
GT ACGGGGTTTCACCATGTTGGTTAG
||||||| |||||
TGTCCCCAAAGTGGTACAACCGGTC

GAM2546 LOC159116 3' CTGGCCAACATGGTGAAACCCT 82974
GT ACGGGGTTTCACCATGTTGGTTAG
||||||| |||||
TGTCCCCAAAGTGGTACAACCGGTC

GAM2546 LOC170395 3' CCAACATGGAGAAACCCCGT 76866 A
ACGGGGTTTC CCATGTTGG
||||||| |||||
TGCCCCAAAG GGTACAACC

A

GAM2546 LOC196047 5' CCAACATGGTGAAACCTC 91148
GGGGTTTCACCATGTTGG
||||||| |||||
CTCCAAAGTGGTACAACC

GAM2546 LOC196529 3' CTGGCCAACATGGCAAAACCCT 89131 CA
GGGGTTT CCATGTTGGTTAG
||||| |||||

		TCCCAA	GGTACAACCGGTC		
		AC			
GAM2546	LOC197196 3'	CTGGCCAACATGATGAAACCCC	91302	C	
	GT	ACGGGGTTTCA	CATGTTGGTTAG		
		TGCCCCAAAGT	GTACAACCGGTC		
		A			
GAM2546	LOC197201 3'	CCAACATGGAGAAACCCC	89270	A	
		GGGGTTTC	CCATGTTGG		
		CCCCAAAG	GGTACAACC		
		A			
GAM2546	LOC197319 3'	CCAACACAGTGAAACCTCGT	89316	CA	
		ACGGGGTTTCAC	TGTTGG		
		TGCTCCAAAGTG	ACAACC		
		AC			
GAM2546	LOC197319 3'	CTGGCCAACATGGTGAAACGCC	89321	G	
		GG GTTTCACCATGTTGGTTAG			
		CC CAAAGTGGTACAACCGGTC			
		G			
GAM2546	LOC199733 3'	AGGCAACATGGTGAAACCCC	91432	G	
		GGGGTTTCACCATGTTG	TT		
		CCCCAAAGTGGTACAAC	GA		
		G			
GAM2546	LOC199733 3'	CTAACATGGTGAAACCCC	91439		
		GGGGTTTCACCATGTTGG			
		CCCCAAAGTGGTACAATC			
GAM2546	LOC199858 3'	CTAACACGGCGAAACGCC	89797	G	A A
		GG GTTTC	CC TGTTGG		
		CC CAAAG	GG ACAATC		
		G	C C		
GAM2546	LOC200014 3'	CTGGCCAACATGGTGAAACCCC	89931		
	GT	ACGGGGTTTCACCATGTTGGTTAG			
		TGCCCCAAAGTGGTACAACCGGTC			
GAM2546	LOC200251 5'	CTGACCAACACGATGAAACCCT	90062	CCA	
	GT	ACGGGGTTTCA	TGTTGGTTAG		
		TGTCCCAAAGT	ACAACCAGTC		
		AGC			
GAM2546	LOC200251 3'	TTGACCAACATGGTGAAACCCC	90070		
		GGGGTTTCACCATGTTGGTTAG			

CCCCAAAGTGGTACAACCAAGTT

GAM2546 LOC200317 3' CCAAGGTGGTGAAACCCC 90223 G
GGGGTTTTCACCAT TTGG
||||||| |||
CCCCAAAGTGGTG AACC
G

GAM2546 LOC200803 3' CTGGCCAACATGGTGAAACCCT 90297
GT ACGGGGTTTTCACCATGTTGGTTAG
|||||||
TGTCCCAAAGTGGTACAACCGGTC

GAM2546 LOC200853 3' CTGGGAGACAGAGCGAAACCCC 90328 ACCA GG
GGGGTTTC TGTT TTAG
||||| ||| |||
CCCCAAAG ACAG GGTC
CGAG AG

GAM2546 LOC200904 3' CCAACGTGGTGAAACCCC 91777
GGGGTTTTCACCATGTTGG
|||||||
CCCCAAAGTGGTGCAACC

GAM2546 LOC200918 3' CTGGCCAACATGGTGAAACCCC 90367
GT ACGGGGTTTTCACCATGTTGGTTAG
|||||||
TGCCCCAAAGTGGTACAACCGGTC

GAM2546 LOC200940 3' CCAACATAGCGAAAACCCGT 90390 G ACC
ACGGG TTTC ATGTTGG
||||| |||
TGCCC AAAG TACAACC
A CGA

GAM2546 LOC201173 3' CTAACATGGTGAAACCCC 88682
GGGGTTTTCACCATGTTGG
|||||||
CCCCAAAGTGGTACAATC

GAM2546 LOC201182 5' CCAACATTGTGAAACCCC 91335 C
GGGGTTTTCAC ATGTTGG
||||||| |||
CCCCAAAGTG TACAACC
T

GAM2546 LOC201220 3' CTAACATGGTGAAACCCC 88717
GGGGTTTTCACCATGTTGG
|||||||
CCCCAAAGTGGTACAATC

GAM2546 LOC201252 3' CAACTTGGTAAAACCCCGT 89546 C T
ACGGGGTTT ACCA GTTG
||||||| ||| |||

		TGCCCCAAA TGGT CAAC	
		A T	
GAM2546	LOC201627 3'	CTGGCCAACATGGTGAAACCCC 90453	
	GT	ACGGGGTTTCACCATGTTGGT TAG	
		TGCCCCAAAGTGGTACAACCGGTC	
GAM2546	LOC201685 3'	CCAACCTGGTGAAACCCC 91839	T
		GGGGTTTCACCA GTTGG	
		CCCCAAAGTGGT CAACC	
		C	
GAM2546	LOC201810 3'	CTGACCAACATGGTGAAACCCC 90502	
	GT	ACGGGGTTTCACCATGTTGGT TAG	
		TGCCCCAAAGTGGTACAACCAGTC	
GAM2546	LOC201868 3'	CCAAGATGGTGAAACCCC 90517	G
		GGGGTTTCACCAT TTGG	
		CCCCAAAGTGGTA AACC	
		G	
GAM2546	LOC201868 5'	CTGACCAACATGGTGAAACCCC 90525	
		GGGGTTTCACCATGTTGGT TAG	
		CCCCAAAGTGGTACAACCAGTC	
GAM2546	LOC201895 3'	CTGGCCAACATGGTGAAACCCT 90544	
	GT	ACGGGGTTTCACCATGTTGGT TAG	
		TGTCCCCAAAGTGGTACAACCGGTC	
GAM2546	LOC201931 3'	CTAACACGGTGAAACCCTGT 90565	A
		ACGGGGTTTCACC TGTTGG	
		TGTCCCCAAAGTGG ACAATC	
		C	
GAM2546	LOC202020 3'	CTGGCCAACATAGTGAAACCCC 90599	C
	GT	ACGGGGTTTCAC ATGTTGGT TAG	
		TGCCCCAAAGTG TACAACCGGTC	
		A	
GAM2546	LOC202038 3'	CTAACACGGTGAAACCCC 90622	A
		GGGGTTTCACC TGTTGG	
		CCCCAAAGTGG ACAATC	
		C	
GAM2546	LOC202052 3'	CTGGCCAACACAGTGAAACCCC 91899	CA
		GGGGTTTCAC TGTTGGT TAG	

CCCCAAAGTG ACAACCGGTC
 AC
 GAM2546 LOC202134 5' CTGGCCAACATGGTGAAACCCC 91921
 GGGGTTTCACCATGTTGGTTAG
 |||||
 CCCCAAAGTGGTACAACCGGTC

GAM2546 LOC202781 3' CGACACGGTGAAACCCCGT 91969 A
 ACGGGGTTTCACC TGTTG
 |||||
 TGCCCCAAAGTGG ACAGC
 C

GAM2546 LOC202868 3' CTAACATGGTGAAACCCCGT 91999
 ACGGGGTTTCACCATGTTGG
 |||||
 TGCCCCAAAGTGGTACAATC

GAM2546 LOC202868 3' CTAACATGGTGAAACCCTGT 92000
 ACGGGGTTTCACCATGTTGG
 |||||
 TGTCCCCAAAGTGGTACAATC

GAM2546 LOC203025 3' CTGGCCAACATGGTGAAACCCC 90745
 GT ACGGGGTTTCACCATGTTGGTTAG
 |||||
 TGCCCCAAAGTGGTACAACCGGTC

GAM2546 LOC203083 3' CTGGCCAACATGGTGAAACCCC 92087
 GGGGTTTCACCATGTTGGTTAG
 |||||
 CCCCAAAGTGGTACAACCGGTC

GAM2546 LOC203246 3' GACCACGGTGAAACCCCGT 90831 ATGT
 ACGGGGTTTCACC TGTT
 |||||
 TGCCCCAAAGTGG ACCAG
 C__

GAM2546 LOC203276 3' CAACATATCAAAACCCCGT 92109 CACC
 ACGGGGTTT ATGTTG
 |||||
 TGCCCCAAA TACAAC
 ACTA

GAM2546 LOC203276 3' CTGGCCAACATGGTGAAACCCT 92122
 GT ACGGGGTTTCACCATGTTGGTTAG
 |||||
 TGTCCCCAAAGTGGTACAACCGGTC

GAM2546 LOC203289 3' CCAACGTGGTGAAACCCCGT 90865
 ACGGGGTTTCACCATGTTGG
 |||||

TGCCCCAAAGTGGTGCAACC

GAM2546 LOC203305 3' CAACATATCAAAACCCCGT 92162 CACC
ACGGGGTTT ATGTTG
||||||| |||||
TGCCCCAAA TACAAC
ACTA

GAM2546 LOC203305 3' CTGGCCAACATGGTGAAACCCT 92175
GT ACGGGGTTTCACCATGTTGGTTAG
|||||||
TGTCCCAAAGTGGTACAACCGGTC

GAM2546 LOC203378 3' AACATGGCGAAACCCCGT 92265 A
ACGGGGTTTC CCATGTT
||||||| |||||
TGCCCCAAAG GGTACAA
C

GAM2546 LOC203378 3' CCAACATGGCAAACCTCGT 92286 CA
ACGGGGTTT CCATGTTGG
||||||| |||||
TGCTCCAAA GGTACAACC
AC

GAM2546 LOC203397 3' CCAACATGGCGAAATCCCGT 90898 A
ACGGGGTTTC CCATGTTGG
||||||| |||||
TGCCCTAAAG GGTACAACC
C

GAM2546 LOC219376 3' CTGGCCAACATGGTGAAACCCT 95515
GT ACGGGGTTTCACCATGTTGGTTAG
|||||||
TGTCCCAAAGTGGTACAACCGGTC

GAM2546 LOC219540 3' CCAACATGGCGAAACCCC 95241 A
GGGGTTTC CCATGTTGG
||||||| |||||
CCCCAAAG GGTACAACC
C

GAM2546 LOC219627 3' CTGGCCAACATGGTGAAACCCT 93806
GT ACGGGGTTTCACCATGTTGGTTAG
|||||||
TGTCCCAAAGTGGTACAACCGGTC

GAM2546 LOC219649 3' CTGGCCAACATGGTGAAACCCC 94552
GGGGTTTCACCATGTTGGTTAG
|||||||
CCCCAAAGTGGTACAACCGGTC

GAM2546 LOC219667 3' CTATGCAACATCATGAAACCCC 92947 CC GT
GGGGTTTCA ATGTTG TAG
||||||| ||||| |||

	CCCCAAAGT TACAAC ATC		
	AC GT		
GAM2546 LOC219744 5'	CTAGCAACATGGCGCAACCCC 93003	TCA	G
	GGGGTT CCATGTTG TTAG		
	CCCCAA GGTACAAC GATC		
	CGC _		
GAM2546 LOC219919 3'	CCAATGTGGTGAAACCCC 94923		
	GGGGTTTCACCATGTTGG		
	CCCCAAAGTGGTGTAACC		
GAM2546 LOC220662 3'	CCAACGTGGTGAAACCCC 92812		
	GGGGTTTCACCATGTTGG		
	CCCCAAAGTGGTGCAACC		
GAM2546 LOC220662 3'	CTGACATGGTGAAACTCC 92815	TG	
	GGGGTTTCACCATGT G		
	CCTCAAAGTGGTACA C		
	GT		
GAM2546 LOC221042 3'	CTGGCCAACATGGTGAAACCCT 94799		
GT	ACGGGGTTTCACCATGTTGGTTAG		
	TGTCCCAAAGTGGTACAACCGGTC		
GAM2546 LOC221069 3'	CAACACGGTGAAACCCCGT 94816	A	
	ACGGGGTTTCACC TGTTG		
	TGCCCCAAAGTGG ACAAC		
	C		
GAM2546 LOC221271 3'	CTAACACAGTGAAACCCTGT 93512	CA	
	ACGGGGTTTCAC TGTTGG		
	TGTCCCAAAGTG ACAATC		
	AC		
GAM2546 LOC221271 3'	CTAACACGGTGAAACCCC 93513	A	
	GGGGTTTCACC TGTTGG		
	CCCCAAAGTGG ACAATC		
	C		
GAM2546 LOC221288 3'	GACCACGGTGAAACCCCGT 95259	ATGT	
	ACGGGGTTTCACC TGGTT		
	TGCCCCAAAGTGG ACCAG		
	C__		
GAM2546 LOC221410 3'	CTAACATGGTGAAACCCC 93694		
	GGGGTTTCACCATGTTGG		

CCCCAAAGTGGTACAATC

GAM2546 LOC221477 3' CCAACAGGGTGAAACCCC 93769 A
GGGGTTTCACC TGTTGG
||||||| |||||
CCCCAAAGTGG ACAACC
G

GAM2546 LOC221490 3' CCAATATGGTGAAACCCC 95301
GGGGTTTCACCATGTTGG
|||||||
CCCCAAAGTGGTATAACC

GAM2546 LOC221543 5' CTAACACGGTGAAACCTCGT 95372 A
ACGGGGTTTCACC TGTTGG
||||||| |||||
TGCTCCAAAGTGG ACAATC
C

GAM2546 LOC221543 3' CTGGCCAACATGGTGAAACCCC 95374
GGGGTTTCACCATGTTGGTTAG
|||||||
CCCCAAAGTGGTACAACCGGTC

GAM2546 LOC221543 3' CTGGCCAACATGGTGAAACCCC 95375
GGGGTTTCACCATGTTGGTTAG
|||||||
CCCCAAAGTGGTACAACCGGTC

GAM2546 LOC221550 3' CCAACATGGCAAAAACCC 93742 CA_
GGGTTT CCATGTTGG
||||| |||||
CCCAA GGTACAACC
AAC

GAM2546 LOC221943 5' CTGGCCAACATGGCGAAACCCC 95621 A
GGGGTTTC CCATGTTGGTTAG
||||| |||||
CCCCAAG GGTACAACCGGTC
C

GAM2546 LOC221954 5' CTGGCCAACATGGTGAAACCC 95646
GGGTTTCACCATGTTGGTTAG
|||||||
CCCAAAGTGGTACAACCGGTC

GAM2546 LOC222060 5' CAACATGGTGAAACCCCGT 95750
ACGGGGTTTCACCATGTTG
|||||||
TGCCCCAAAGTGGTACAAC

GAM2546 LOC222066 3' CCAAAGTGGTGAAACCCTGT 94315 G
ACGGGGTTTCACCAT TTGG
||||||| |||

TGTCCCAAAGTGGTG AACC		
A		
GAM2546 LOC222160 3'	CCAGCATGGCAAAACCCCGT 95778	CA
	ACGGGGTTT CCATGTTGG	
	TGCCCCAAA GGTACGACC	
AC		
GAM2546 LOC222160 5'	CTAACACGGTGAAACCCTGT 95784	A
	ACGGGGTTTCACC TGTTGG	
	TGTCCCAAAGTGG ACAATC	
C		
GAM2546 LOC222182 3'	CTGGCCAACATGGTGAAACCCC 95855	
GT	ACGGGGTTTCACCATGTTGGTTAG	
	TGCCCCAAAGTGGTACAACCGGTC	
GAM2546 LOC222256 3'	CTAGATGGCAAAACCCTGT 95910	CA G
	ACGGGGTTT CCAT TTGG	
	TGTCCCAA GGTA GATC	
AC _		
GAM2546 LOC222865 3'	CTAACACGGTGAAACCCCGT 94445	A
	ACGGGGTTTCACC TGTTGG	
	TGCCCCAAAGTGG ACAATC	
C		
GAM2546 LOC253532 3'	CTGGCCAACATGGTGAAACCCT 97734	
GT	ACGGGGTTTCACCATGTTGGTTAG	
	TGTCCCAAAGTGGTACAACCGGTC	
GAM2546 LOC253612 5'	CTGACCAACATGGTGAAACCCC 98548	
GT	ACGGGGTTTCACCATGTTGGTTAG	
	TGCCCCAAAGTGGTACAACCAGTC	
GAM2546 LOC253639 3'	CCAATATGGTGAAACCCCGT 97512	
	ACGGGGTTTCACCATGTTGG	
	TGCCCCAAAGTGGTATAACC	
GAM2546 LOC253778 5'	CTGGCCAACATGGTGAAACCCC 96526	
	GGGGTTTCACCATGTTGGTTAG	
	CCCCAAAGTGGTACAACCGGTC	
GAM2546 LOC253840 3'	CCAACATGGAGAAACCCCGT 97910	A
	ACGGGGTTTC CCATGTTGG	

		TGCCCCAAAG GGTACAACC	
		A	
GAM2546	LOC253927 3'	AACATGGTGAAACCTCGT 96723	
		ACGGGGTTTCACCATGTT	
		TGCTCCAAAGTGGTACAA	
GAM2546	LOC254045 3'	CTGGCCAACATGGCAAAACCCC 98268	CA
		GGGGTTT CCATGTTGGTTAG	
		CCCCAAA GGTACAACCGGTC	
		AC	
GAM2546	LOC254100 3'	CCAACATAGTGAAACCCC 98152	C
		GGGGTTTCAC ATGTTGG	
		CCCCAAAGTG TACAACC	
		A	
GAM2546	LOC254176 3'	CTGGCCAACATGGTGAAACCCC 99168	
		GGGGTTTCACCATGTTGGTTAG	
		CCCCAAAGTGGTACAACCGGTC	
GAM2546	LOC254243 3'	CAACATATCAAAACCCCGT 99248	CACC
		ACGGGGTTT ATGTTG	
		TGCCCCAAA TACAAC	
		ACTA	
GAM2546	LOC254243 3'	CTGGCCAACATGGTGAAACCCT 99261	
	GT	ACGGGGTTTCACCATGTTGGTTAG	
		TGTCCCAAAGTGGTACAACCGGTC	
GAM2546	LOC254249 5'	CAACATGGTGAAACCCTGT 97180	
		ACGGGGTTTCACCATGTTG	
		TGTCCCAAAGTGGTACAAC	
GAM2546	LOC254266 3'	CTAACACAGTGAAACCCCGT 99200	CA
		ACGGGGTTTCAC TGTTGG	
		TGCCCCAAAGTG ACAATC	
		AC	
GAM2546	LOC254351 3'	CAACATGGTGAAACCCGGT 96683	G
		AC GGGTTTCACCATGTTG	
		TG CCCAAAGTGGTACAAC	
		G	
GAM2546	LOC254531 5'	CTGACCAACATGGCAAAACCCC 96667	CA
		GGGGTTT CCATGTTGGTTAG	

	CCCCAAA GGTACAACCAGTC	
	AC	
GAM2546 LOC254808 3'	CTAACACGGTGAAACCCCGT 98806	A
	ACGGGGTTTCACC TGTTGG	
	TGCCCCAAAGTGG ACAATC	
	C	
GAM2546 LOC254875 3'	CTGGCCAACATGGTGAAACCCT 97779	
GT	ACGGGGTTTCACCATGTTGGTTAG	
	TGTCCCAAAGTGGTACAACCGGTC	
GAM2546 LOC255042 3'	CAACATGGAGAAACCCCGT 97034	A
	ACGGGGTTTC CCATGTTG	
	TGCCCCAAAG GGTACAAC	
	A	
GAM2546 LOC255042 3'	CAACATGGTGAAACCCTGT 97035	
	ACGGGGTTTCACCATGTTG	
	TGTCCCAAAGTGGTACAAC	
GAM2546 LOC255042 3'	CCAATACGATGAAACCCTGT 97040	CCA
	ACGGGGTTTCA TGTTGG	
	TGTCCCAAAGT ATAACC	
	AGC	
GAM2546 LOC255177 3'	GACCAACATGATGAAACCCCGT 98393	C
	ACGGGGTTTCA CATGTTGGTT	
	TGCCCCAAAGT GTACAACCAG	
	A	
GAM2546 LOC255185 3'	CTGTTTAACACGGGGGAAACCCC 96831	A A T
GT	ACGGGGTTTC CC TGTTGG TAG	
	TGCCCCAAAG GG ACAATT GTC	
	G C T	
GAM2546 LOC255196 3'	CCAACATGGTGAAACCCC 98951	
	GGGGTTTCACCATGTTGG	
	CCCCAAAGTGGTACAACC	
GAM2546 LOC255326 3'	CTAACACGTTGAAACCCCGT 98119	CCA
	ACGGGGTTTCA TGTTGG	
	TGCCCCAAAGT ACAATC	
	TGC	
GAM2546 LOC255671 3'	CCACATGGTGAAACCCTGT 99070	T
	ACGGGGTTTCACCATGT GG	

TGTCCCAAAGTGGTACA CC

GAM2546 LOC255937 3' CTGACCAACATGGTGAAACTCC 97680
GGGGTTTTCACCATGTTGGTTAG
|||||||
CCTCAAAGTGGTACAACCAGTC

GAM2546 LOC255971 3' CCAATATGGTGAAACCCCGT 98310
ACGGGGTTTTCACCATGTTGG
|||||||
TGCCCAAAGTGGTATAACC

GAM2546 LOC256207 3' CCAACATGGTGAAACCCCGT 96874
ACGGGGTTTTCACCATGTTGG
|||||||
TGCCCAAAGTGGTACAACC

GAM2546 LOC256248 5' AACCAACATAGAGCCCC 98029 CACC
GGGGTTT ATGTTGGTT
||||| |||||
CCCCGAG TACAACCA
A

GAM2546 LOC256267 3' CTGGCCAACATGGTGAAACCCC 98611
GGGGTTTTCACCATGTTGGTTAG
|||||||
CCCCAAAGTGGTACAACCGGTC

GAM2546 LOC256277 3' CTGGCCAACATGGTGAAACCCT 96349
GT ACGGGGTTTTCACCATGTTGGTTAG
|||||||
TGTCCCAAAGTGGTACAACCGGTC

GAM2546 LOC256515 3' CTGGCCAACATGGTGAAACCCC 98212
GGGGTTTTCACCATGTTGGTTAG
|||||||
CCCCAAAGTGGTACAACCGGTC

GAM2546 LOC256520 3' CTGGCCAACATGGTGAAACCCC 97666
GT ACGGGGTTTTCACCATGTTGGTTAG
|||||||
TGCCCAAAGTGGTACAACCGGTC

GAM2546 LOC256544 3' CCAACGTGGTGAAACCCCGT 97929
ACGGGGTTTTCACCATGTTGG
|||||||
TGCCCAAAGTGGTGCAACC

GAM2546 LOC256594 3' CCAATGTGGTGAAACCCC 98860
GGGGTTTTCACCATGTTGG
|||||||

CCCCAAAGTGGTGTAAACC

GAM2546 LOC256867 3' CTAATATTTCCGGCAAAATCCC 96513 CA ____
GGGGTTT CC ATGTTGG
||||| || |||||
CCCTAAA GG TATAATC
AC CCTT

GAM2546 LOC256980 3' CTAACGTGGTGAAACCCTGT 96927
ACGGGGTTTCACCATGTTGG
|||||||
TGTCCCAAAGTGGTGCAATC

GAM2546 LOC257180 3' CTGGCCAACATAGTGAAACCCT 97314 C
GT ACGGGGTTTCAC ATGTTGGTTAG
||||||| |||||
TGTCCCAAAGTG TACAACCGGTC
A

GAM2546 LOC257495 3' CCAACATGGCAAAAACCC 99569 CA_
GGGTTT CCATGTTGG
||||| |||||
CCCAA GGTACAACC
AAC

GAM2546 LOC257539 3' CTAACACGGTGAAACCCCGT 99549 A
ACGGGGTTTCACC TGTTGG
||||||| |||||
TGCCCCAAAGTGG ACAATC
C

GAM2546 LOC257576 3' CCAACATGGCAAAAACCC 99706 CA_
GGGTTT CCATGTTGG
||||| |||||
CCCAA GGTACAACC
AAC

GAM2546 LOC257578 3' CTAACACGGTGAAACCCCGT 99661 A
ACGGGGTTTCACC TGTTGG
||||||| |||||
TGCCCCAAAGTGG ACAATC
C

GAM2546 LOC257596 5' CTAACACGGTGAAACCTCGT 99775 A
ACGGGGTTTCACC TGTTGG
||||||| |||||
TGCTCCAAAGTGG ACAATC
C

GAM2546 LOC257596 3' CTGGCCAACATGGTGAAACCCC 99777
GGGGTTTCACCATGTTGGTTAG
|||||||
CCCCAAAGTGGTACAACCGGTC

GAM2546 LOC257596 3' CTGGCCAACATGGTGAAACCCC 99778
GGGGTTTCACCATGTTGGTTAG
|||||||

CCCCAAAGTGGTACAACCGGTC

GAM2546 LOC51122 3' CTAACATGGTGAAACCCC 66195
GGGGTTTTCACCATGTTGG
|||||||
CCCCAAAGTGGTACAATC

GAM2546 LOC51145 3' CTGGCCAACATGGTGAAACCCC 32924
GGGGTTTTCACCATGTTGGTTAG
|||||||
CCCCAAAGTGGTACAACCGGTC

GAM2546 LOC51279 3' CTAAGCAACATAGTGAAACCCC 33754 C G
GGGGTTTTCAC ATGTTG TTAG
||||||| |||||
CCCCAAAGTG TACAAC AATC
A G

GAM2546 LOC51279 3' CTGGCCAACATGGTGAAACCCC 33755
GGGGTTTTCACCATGTTGGTTAG
|||||||
CCCCAAAGTGGTACAACCGGTC

GAM2546 LOC51333 3' CTGGCCAACATGGTGAAACCCG 34052 G
GT AC GGGTTTTCACCATGTTGGTTAG
|| |||||
TG CCCAAAGTGGTACAACCGGTC
G

GAM2546 LOC55974 3' CTAACATGGTGAAACCCC 38745
GGGGTTTTCACCATGTTGG
|||||||
CCCCAAAGTGGTACAATC

GAM2546 LOC57118 3' CTGACCAACATGGTGAAACCCC 40222
GGGGTTTTCACCATGTTGGTTAG
|||||||
CCCCAAAGTGGTACAACCAGTC

GAM2546 LOC64167 3' CTAACACGGTGAGACCCCGT 42538 A
ACGGGGTTTTCACC TGTTGG
||||||| |||||
TGCCCCAGAGTGG ACAATC
C

GAM2546 LOC85479 5' CTAACACAGTGAAAGCCC 53565 G CA
GGG TTTCAC TGTTGG
||| ||||| |||||
CCC AAAGTG ACAATC
G AC

GAM2546 LOC89890 3' CTGGCCAACATGGTGAAACCCC 61206
GT ACGGGGTTTTCACCATGTTGGTTAG
|||||||

TGCCCCAAAGTGGTACAACCGGTC

GAM2546 LOC90038 3' CTGGCCAACATGGTGAAACCCT 61805
GT ACGGGGTTTCACCATGTTGGTTAG
|||||||
TGTCCCCAAAGTGGTACAACCGGTC

GAM2546 LOC90092 3' CTGGCCAACATAATGAAACCCC 62062 CC
GGGGTTTCA ATGTTGGTTAG
||||| |||||
CCCCAAAGT TACAACCGGTC
AA

GAM2546 LOC90321 3' CCAATATGGTGAAACACC 62932 G
GG GTTTCACCATGTTGG
|| |||||
CC CAAAGTGGTATAACC
A

GAM2546 LOC90509 3' CTAACACGGTGAAACCCCGT 63792 A
ACGGGGTTTCACC TGTTGG
||||||| |||||
TGCCCCAAAGTGG ACAATC
C

GAM2546 LOC90573 3' CCAACATGCAAAACCCCGT 63955 CAC
ACGGGGTTT CATGTTGG
||||||| |||||
TGCCCCAAA GTACAACC
AC_

GAM2546 LOC90591 3' CAACATAGTGAAACCCTGT 64151 C
ACGGGGTTTCAC ATGTTG
||||||| |||||
TGTCCCCAAAGTG TACAAC
A

GAM2546 LOC90591 3' CGACACGGTGAAACCCCGT 64164 A TG
ACGGGGTTTCACC TGT G
||||||| ||| |
TGCCCCAAAGTGG ACA C
C GT

GAM2546 LOC90591 3' CTAACATGGCAAAACCCC 64165 CA
GGGGTTT CCATGTTGG
||||| |||||
CCCCAAA GGTACAATC
AC

GAM2546 LOC90624 3' CCAATGTGGTGAAACCCC 64368
GGGGTTTCACCATGTTGG
|||||||
CCCCAAAGTGGTGTAACC

GAM2546 LOC90785 3' CCAACGTGGTGAAACCTCGT 64713
ACGGGGTTTCACCATGTTGG
|||||||

TGCTCCAAAGTGGTGCAACC

GAM2546 LOC90841 5' CTGGCCAACATGGTGAAACCCT 64867
GT ACGGGGTTTCACCATGTTGGTTAG
|||||||
TGCTCCAAAGTGGTACAACCGGTC

GAM2546 LOC90918 5' CTGACCAACATGGTGAAACCCC 65001
GGGGTTTCACCATGTTGGTTAG
|||||||
CCCCAAAGTGGTACAACCAGTC

GAM2546 LOC91035 3' CAACATGGAGAAACCCCGT 65294 A
ACGGGGTTTC CCATGTTG
|||||||
TGCCCCAAAG GGTACAAC
A

GAM2546 LOC91056 3' CCAGCATGGCGAAACCCTGT 96404 A
ACGGGGTTTC CCATGTTGG
|||||||
TGCTCCAAAG GGTACGACC
C

GAM2546 LOC91064 3' CTGGCCAACATGGTGAAACCCC 65385
GGGGTTTCACCATGTTGGTTAG
|||||||
CCCCAAAGTGGTACAACCGGTC

GAM2546 LOC91115 3' CTGGCCAACATAGTGAAACCCC 65564 C
GT ACGGGGTTTCAC ATGTTGGTTAG
|||||||
TGCCCCAAAGTG TACAACCGGTC
A

GAM2546 LOC91380 3' CTGGCCAACATGGCGAAACCCT 66447 A
GGGGTTTC CCATGTTGGTTAG
|||||||
TCCCAAAG GGTACAACCGGTC
C

GAM2546 LOC91547 3' CTAGCACGGCGAAACCCTGT 67000 A A
ACGGGGTTTC CC TGTTGG
|||||||
TGCTCCAAAG GG ACGATC
C C

GAM2546 LOC91574 3' CTGGCCAACATGGTGAAACCCC 67110
GT ACGGGGTTTCACCATGTTGGTTAG
|||||||
TGCCCCAAAGTGGTACAACCGGTC

GAM2546 LOC91660 3' CTAGCCAACATGGCAAAACCCC 67402 CA
GGGGTTT CCATGTTGGTTAG
|||||||

	CCCCAAA GGTACAACCGATC		
	AC		
GAM2546 LOC91750 3'	CCAATATGGTGAAACCCTGT 67650		
	ACGGGGTTTCACCATGTTGG		
	TGTCCCAAAGTGGTATAACC		
GAM2546 LOC91963 3'	CTAGGCAACATGGCAAAACCCC 68318	CA	G
	GGGGTTT CCATGTTG TTAG		
	CCCCAAA GGTACAAC GATC		
	AC G		
GAM2546 LOC91963 5'	CTGGCCAACATGACAAAACCCCT 68319	CAC	
G	CGGGGTTT CATGTTGGTTAG		
	GTCCCAA GTACAACCGGTC		
	ACA		
GAM2546 LOC92078 3'	CTGGCCAACATGGCGAAACCCT 68601	A	
	GGGGTTTC CCATGTTGGTTAG		
	TCCCAAAG GGTACAACCGGTC		
	C		
GAM2546 LOC92223 3'	CCAATATGATGAAACCCC 69048	C	
	GGGGTTTCA CATGTTGG		
	CCCCAAAGT GTATAACC		
	A		
GAM2546 LOC92228 3'	CCAACATGGTGAGACCCC 69071		
	GGGGTTTCACCATGTTGG		
	CCCAGAGTGGTACAACC		
GAM2546 LOC92267 3'	CCAATATGGTGAAACCCC 69167		
	GGGGTTTCACCATGTTGG		
	CCCCAAAGTGGTATAACC		
GAM2546 LOC92270 5'	CCAACATGGTGAAACCTCGT 69185		
	ACGGGGTTTCACCATGTTGG		
	TGCTCCAAAGTGGTACAACC		
GAM2546 LOC92283 3'	CTAACATGGTGAAACCCCGT 69304		
	ACGGGGTTTCACCATGTTGG		
	TGCCCCAAAGTGGTACAATC		
GAM2546 LOC92299 3'	CTGGCCAACATGGTGAAACCCC 69368		
GT	ACGGGGTTTCACCATGTTGGTTAG		

TGCCCCAAAGTGGTACAACCGGTC

GAM2546 LOC92360 3' CTGGCCAACATGGCGAAACCCC 69625 A
GGGGTTTC CCATGTTGGTTAG
||||| |||||||
CCCCAAAG GGTACAACCGGTC
C

GAM2546 LOC92405 3' CTGGCCAACATGGTGAAACCCC 69712
GT ACGGGGTTTCACCATGTTGGTTAG
|||||
TGCCCCAAAGTGGTACAACCGGTC

GAM2546 LOC92465 5' CTGGCCAACATGGTGAAACTCC 69949
GGGGTTTCACCATGTTGGTTAG
|||||
CCTCAAAGTGGTACAACCGGTC

GAM2546 LOC92466 3' CTGGCCAACATGGTGAAACCCC 69967
GGGGTTTCACCATGTTGGTTAG
|||||
CCCCAAAGTGGTACAACCGGTC

GAM2546 LOC92482 3' CTGGCCAACATGGTGAAACCCT 70020
GT ACGGGGTTTCACCATGTTGGTTAG
|||||
TGTCCCAAAGTGGTACAACCGGTC

GAM2546 LOC92573 5' CCAACGTGTTGAAACCCCGT 70372 C
ACGGGGTTTCA CATGTTGG
|||||
TGCCCCAAAGT GTGCAACC
T

GAM2546 LOC92573 3' CCAGCATGGTGAAACCCC 70373
GGGGTTTCACCATGTTGG
|||||
CCCCAAAGTGGTACGACC

GAM2546 LOC92661 5' CCAACATGGGAAAACCCC 70622 CA
GGGGTTT CCATGTTGG
|||||
CCCCAAA GGTACAACC
AG

GAM2546 LOC92771 3' CTGGCCAACATGGTGAAACCCC 54212
GGGGTTTCACCATGTTGGTTAG
|||||
CCCCAAAGTGGTACAACCGGTC

GAM2546 LOC93070 3' CTGGCCAACATGGTGAAACACC 71807 G
GT ACGG GTTTCACCATGTTGGTTAG
||| |||||||

		TGCC CAAAGTGGTACAACCGGTC			
		A			
GAM2546	LOC93132	5'	CCACATGGCAAAACCCCGT	71983	CA T
			ACGGGGTTT CCATGT GG		
			TGCCCCAAA GGTACA CC		
			AC _		
GAM2546	LOC93132	5'	CTGACCAACATGGTGAAACCCT	71986	
	GT		ACGGGGTTTTCACCATGTTGGTTAG		
			TGTCCCAAAGTGGTACAACCAGTC		
GAM2546	LOC96597	5'	CTGGCCAACATGGCGAAACCCC	67456	A
	GT		ACGGGGTTTC CCATGTTGGTTAG		
			TGCCCCAAAG GGTACAACCGGTC		
			C		
GAM2547	ABCA3	5'	CCATCGCCTTCCCTGCCT	8441	TA AG
			AGGCA GAAGGCGA TGG		
			TCCGT CTTCCGCT ACC		
			CC _		
GAM2547	ABR	3'	CCACCTCCTGCCCTCCATACCT	41997	C A A _ A
			AGG AT GA GGC GA GTGG		
			TCC TA CT CCG CT CACC		
			A C C TC C		
GAM2547	CLC	3'	CTACCACTTGGCCAGTGCC	26025	AGAA G
			GGCAT GGC AAGTGGTAG		
			CCGTG CCG TTCACCATC		
			A_ G		
GAM2547	DMPK	5'	TCCACCACTTTCTCCCCCAGC	16616	ATAGA_ C A
	CT		AGGC AGG GAAGTGGT GA		
			TCCG TCC TTTCACCA CT		
			ACCCCC _ C		
GAM2547	DPH2L2	5'	ACCACCCAAGCTGTGCCT	9113	AA_ CGAA
			AGGCATAG GG GTGGT		
			TCCGTGTC CC CACCA		
			GAA _		
GAM2547	GDF5	3'	ACCATTTCTCCTCACCT	6894	CATA A C
			AGG GA GG GAAGTGGT		
			TCC CT CC CTTTACCA		
			A_ _ T		
GAM2547	HADH2	3'	CTACCAGTCGCCCTCTGTGCCT	16896	A AG
			AGGCATAGA GGCGA TGGTAG		

TCCGTGTCT CCGCT ACCATC
 C G_
 GAM2547 IGF2 5' TCACGCCCGCCCTCTCGCCT 7037 AT A AA_
 AGGC AGA GGCG GTGG
 ||| ||| ||| |||
 TCCG TCT CCGC CACT
 C_ C CCG
 GAM2547 KRT16 3' CTACCACAGCCTCCTGCC 96888 TA A GAA
 GGCA G AGGC GTGGTAG
 ||| | ||| |||||
 CCGT C TCCG CACCATC
 _ C A_
 GAM2547 LCP1 3' CTACCCTGCCTCCCATGACT 11282 G AGA GA T
 AG CAT AGGC AG GG TAG
 || ||| ||| || |||||
 TC GTA TCCG TC CCATC
 A CCC _ _
 GAM2547 NRXN3 3' CACCACTTCCGCAGGCCT 58072 ATAGAAG _ A
 AGGC GCG AAGTGGT G
 ||| ||| ||||| |
 TCCG CGC TTCACCA C
 GA_ C C
 GAM2547 OSM 3' CTGAGCTGGCCTCCTATGCCT 40449 A GA GG
 AGGCATAG AGGC AGT TAG
 ||||| ||| ||| |||
 TCCGTATC TCCG TCG GTC
 C G_ A_
 GAM2547 SELL 3' ACCACTTCTTTTATAACT 7225 GC GGC
 AG ATAGAA GAAGTGGT
 || ||||| |||||
 TC TATTTT CTTACCA
 AA _
 GAM2547 TEAD2 3' TCTACCACCCTCACTCCATGAC 14585 _ A A GC A_
 CT AGG CAT GA G GA GTGGTAGA
 ||| ||| || | || |||||
 TCC GTA CT C CT CACCATCT
 A C _ A_ CC
 GAM2547 TM4SF6 3' CTAAGTCCACCTTCTATCC 13795 C C_ AG
 GG ATAGAAGG GA TGG
 || ||||| || |||
 CC TATCTTCC CT ATC
 _ AC GA
 GAM2547 ASML3B 3' TCCACCATTTCCTCCGCGCCT 27878 ATAGAA C_ A
 AGGC GG GAAGTGGT GA
 ||| || ||||| ||
 TCCG CC CTTTACCA CT
 CG_ TC C
 GAM2547 BRAP 5' TCGGCTCGCCTTCCAGCCT 23177 ATA AG
 AGGC GAAGGCGA TGG
 ||| ||||| |||

			TCCG CTTCCGCT GCT		
			AC_ CG		
GAM2547	CALN1	3'	CCACCACGTCTCTATGCC 49661	A	AA
			GGCATAGA GGCG GTGG		
			CCGTATCT CTGC CACC		
			_ AC		
GAM2547	CDH9	3'	CCAGTTCACCCTCTTTGCCT 33256	T	A C G
			AGGCA AGA GG GAA TGG		
			TCCGT TCT CC CTT ACC		
			T C A G		
GAM2547	CDKL2	5'	CCACCTGCCTCCCTGCCT 15470	TA	A AA
			AGGCA GA GGCG GTGG		
			TCCGT CT CCGT CACC		
			CC _ C_		
GAM2547	DDR2	3'	CTACCACTCACCCATGCCT 21636	AGAA	C A
			AGGCAT GG GA GTGGTAG		
			TCCGTA CC CT CACCATC		
			C_ A _		
GAM2547	DMWD	3'	TCCACCACTTTCTCCCCCAGC 61555	ATAGA_	C A
	CT		AGGC AGG GAAGTGGT GA		
			TCCG TCC TTTCACCA CT		
			ACCCCC _ C		
GAM2547	FLJ10482	3'	TCTACCACTTCCTGTGTGCCT 36651	GAA	C
			AGGCATA GG GAAGTGGTAGA		
			TCCGTGT TC CTTACCATCT		
			G_ _		
GAM2547	FLJ12294	5'	CCGTGCCCCCTCTATGCCT 47714	A_	AAG
			AGGCATAGA GGCG TGG		
			TCCGTATCT CCGT GCC		
			CCC _		
GAM2547	FLJ14547	3'	CCACTCATGCCCTTATGCCT 52495	AA	A_
			AGGCATAG GGCG AGTGG		
			TCCGTATT CCGT TCACC		
			C_ AC		
GAM2547	HTMP10	3'	TCTACCACCTTCCTCCTACCT 53760	CA	A C A
			AGG TAG AGG GA GTGGTAGA		
			TCC ATC TCC TT CACCATCT		
			_ C _ C		
GAM2547	KIAA1671	3'	CCACCCAGCCTTTTACACCT 66270	CA	GAA
			AGG TAGAAGGC GTGG		

TCC ATTTTCCG CACC
 AC ACC
 GAM2547 L3MBTL2 3' TCTACCACCACCACCATGCCT 90161 AGAA CGAA
 AGGCAT GG GTGGTAGA
 ||||| || |||||
 TCCGTA CC CACCATCT
 CCA_ AC_
 GAM2547 MGC10702 3' CCACTAGAGCCTTCCAGCCT 51990 ATA GA_
 AGGC GAAGGC AGTGG
 ||| ||||| |||||
 TCCG CTTCCG TCACC
 AC_ AGA
 GAM2547 MGC13053 3' CTTCCCGCCTTCTACCCT 52107 CA AAGT T
 AGG TAGAAGGCG GG AG
 ||| ||||| |||||
 TCC ATCTTCCGC CC TC
 C_ _ T
 GAM2547 MOST2 5' CTACGGTGCCTTCTTGCCT 40060 T AA
 AGGCA AGAAGGCG GTGG
 ||||| ||||| |||||
 TCCGT TCTTCCGT CATC
 _ GG
 GAM2547 PEG10 3' CCAGATTACACTCCTATGCCT 31200 A GC_ G_
 AGGCATAG AG GAA TGG
 ||||| || ||| |||
 TCCGTATC TC CTT ACC
 C ACA AG
 GAM2547 SERPINB7 3' TCTACCACCATGTGTCTCACC 15033 CAT AG AA
 GG AGA GCG GTGGTAGA
 || ||| ||| |||||
 CC TCT TGT CACCATCT
 AC_ G_ AC
 GAM2547 SIAT8C 5' TCACCATTTCCCCCTACTCC 32452 CA AA C A
 GG TAG GG GAAGTGGT GA
 || ||| ||||| |||||
 CC ATC CC CTTTACCA CT
 TC C_ _ C
 GAM2547 TOSO 3' CTATCACTTCCCATGCC 19568 AGAA C _
 GGCAT GG GAAGTGGT AG
 ||||| ||||| |||||
 CCGTA CC CTTCACTA TC
 _ _ C
 GAM2547 ZNF213 5' GCTGGCTCGCCTTCCCGCCT 65700 ATA AG
 AGGC GAAGGCGA TGGT
 ||||| ||||| |||||
 TCCG CTTCCGCT GTCG
 CC_ CG
 GAM2547 LOC123232 3' GCCTCACCTCCTTTGCCT 74657 T A C AGT
 AGGCA AG AGG GA GGT
 ||||| ||||| |||||

TCCGT TC TCC CT CCG
 T C A ____
 GAM2547 LOC125079 3' CTACCACAGCCTCCTGCC 74850 TA A GAA
 GGCA G AGGC GTGGTAG
 ||| | ||| |||||
 CCGT C TCCG CACCATC
 __ C A__
 GAM2547 LOC143098 5' CCAGTGTTCCTCCTATGCCT 76974 A AG_
 AGGCATAG AGGCGA TGG
 ||||| ||||| |||
 TCCGTATC TCCGTT ACC
 C GTG
 GAM2547 LOC145678 5' GCCTCTCCTCCTATGCCT 84435 A C AGT
 AGGCATAG AGG GA GGT
 ||||| ||| |||
 TCCGTATC TCC CT CCG
 C T ____
 GAM2547 LOC145945 3' TCTACCACTTCCTAGCACACCT 84572 CATAGAA C
 AGG GG GAAGTGGTAGA
 || || |||||
 TCC TC CTTCACCATCT
 ACACGA__
 GAM2547 LOC146728 5' TCTGTGGTTCCGCCCTGTGC 84775 AA A GG
 CT AGGCATAG GGCG AGT TAGA
 ||||| ||| ||| |||
 TCCGTGTC CCGC TTG GTCT
 CC C GT
 GAM2547 LOC147965 5' GCCACCCGCCTCCTGTGCCT 79301 A AA
 AGGCATAG AGGCG GTGGT
 ||||| ||||| |||||
 TCCGTGTC TCCGC CACCG
 C C_
 GAM2547 LOC158263 3' CCACCTTTGCCTTCCATCCT 82727 C A _
 AGG AT GAAGGCGAAG TGG
 ||| || ||||| |||
 TCC TA CTTCGGTTTC ACC
 _ C C
 GAM2547 LOC159199 5' TCTACCACCTTCGCCTCGCC 83068 ATA A _
 GGC GA GGCGAAG TGGTAGA
 ||| || ||||| |||||
 CCG CT CCGCTTC ACCATCT
 __ _ C
 GAM2547 LOC221042 5' CTTTGTCACTTCTACACCT 94800 CA _
 AGG TAGAAG GCGAAG
 ||| ||||| |||||
 TCC ATCTTC TGTTTC
 AC AC
 GAM2547 LOC90092 5' CCACACGCCCTCCTATGCCT 62057 AA__ AA
 AGGCATAG GGCG GTGG
 ||||| ||| |||

TCCGTATC CCGC CACC
 CTCCC A_
 GAM2547 LOC91689 3' CCACGCCCTTCTATACCT 53975 C CGAA
 AGG ATAGAAGG GTGG
 ||| ||||| |||
 TCC TATCTTCC CACC
 A CCG_
 GAM2548 ATP4A 3' CCAAGAGTCCCAGCCCCA 7372 CAGCCT _
 TGGGGCTG GGGC CTTGG
 ||||| ||| |||||
 ACCCCGAC CCTG GAACC
 _____ A
 GAM2548 FCER2 3' ACCCTCTCCAGATGCAGCCCCA 10599 GC CCTT
 TGGGGCTGCA CTGGG GGT
 ||||| |||| |||
 ACCCCGACGT GACCT CCA
 A_ CTC_
 GAM2548 FOXO1A 3' CCAATAACCCCAGCCCCA 10649 CAGCCT CC_
 TGGGGCTG GGG TTGG
 ||||| ||| |||||
 ACCCCGAC CCC AACC
 _____ AAT
 GAM2548 INPPL1 3' ACCAAGGCCCAGCTATGGCCCC 9602 GC C
 A TGGGGCT AGC TGGGCCTTGGT
 ||||| ||| |||||
 ACCCCGG TCG ACCCGGAACCA
 TA _
 GAM2548 LRP1 3' CCAAACCCCAGCCCCA 11358 CAGCCT CC
 TGGGGCTG GGG TTGG
 ||||| ||| |||||
 ACCCCGAC CCC AACC
 _____ A_
 GAM2548 PIM1 5' GCCACAGCCACAGCCCCA 92686 CA C _
 TGGGGCTG GC TG GGC
 ||||| || || |||
 ACCCCGAC CG AC CCG
 AC _ A
 GAM2548 PRX2 3' GTACCAGAGACTGCAGCCC 33308 C_ _
 GGGCTGCAG CTGG GC
 ||||| |||| ||
 CCGACGTC GACC TG
 AGA A_
 GAM2548 RET 3' GGCCAAGCCTCAGCCCCA 40549 C C G
 TGGGGCTG AG CT GGCC
 ||||| || || |||
 ACCCCGAC TC GA CCGG
 _ C A
 GAM2548 SLC5A2 3' CTTGGTACCATAAGCCACAGCC 13180 CA C_ _ CTTG
 TCA TGGGGCTG GC TGG GC G
 ||||| || || || |

ACTCCGAC CG ACC TG C
 AC AAT A__ GTTC
 GAM2548 ADAMTS10 5' ACCAAGGCCAGAGAGGGAGGC 48979 GCAGC__
 CC GGGCT CTGGGCCTTGGT
 ||||| |||||
 CCCGG GACCCGGAACCA
 AGGGAGA
 GAM2548 DC-TM4F2 3' CCGTGCCTAGCCACAACCCCA 48898 C CA C CT
 TGGGG TG GC TGGGC TGG
 ||||| || ||||| ||
 ACCCC AC CG ATCCG GCC
 A AC _ T_
 GAM2548 FBXO27 3' ACCAAAACCCCTCCGATCCAGCC 74994 CAGCCT_ CC
 CCA TGGGGCTG GGG TTGGT
 ||||| || |||||
 ACCCCGAC CCC AACCA
 CTAGCCT AA
 GAM2548 FLJ14249 3' GTACCAGAAGCCAGCCCCA 42644 CA _ _
 TGGGGCTG GC CTGG GC
 ||||| || ||||| ||
 ACCCCGAC CG GACC TG
 C_ AA A__
 GAM2548 GDF10 5' CCCTGTCAGCTGCAGCCCCA 18298 CT__
 TGGGGCTGCAGC GGG
 ||||| ||||| ||
 ACCCCGACGTCG CCC
 ACTGT
 GAM2548 KIAA0140 3' CTTGGTACCAGCAAGCCAGCC 28514 CA _ _ CTTG
 CCA TGGGGCTG GC CTGG GC G
 ||||| || ||||| || |
 ACCCCGAC CG GACC TG C
 C_ AAC A__ GTTC
 GAM2548 KIAA0444 3' CCTTTCCCCAGGCACAGCCCCA 62998 CA CCTT
 TGGGGCTG GCCTGGG GG
 ||||| ||||| ||
 ACCCCGAC CGGACCC CC
 A_ CTTT
 GAM2548 KIAA0450 5' GCCCAGGCCGCACCCCA 28357 C A
 TGGGG TGC GCCTGGGC
 ||||| ||||| |||||
 ACCCC ACG CGGACCCG
 _ C
 GAM2548 KIAA1077 3' AGCCCCAGGCTGCAGCCC 73285 C
 GGGCTGCAGCCTGGG CT
 ||||| ||||| ||
 CCCGACGTCGGACCC GA
 C
 GAM2548 MGC10986 3' GCCTTGGTACTCGCCAGGCTGC 48325 _ CTTG
 AGCCTCA TGGGGCTGCAGCCTGG GC GT
 ||||| ||||| || ||

	ACTCCGACGTCGGACC	TG	CG
	GCTCA__ GTTC		
GAM2548 MGC11352	5' CCGTGCCTAGCCACAACCCCA	65430	C CA C CT
	TGGGG TG GC TGGGC TGG		
	ACCCC AC CG ATCCG GCC		
	A AC _ T_		
GAM2548 PPP1R16B	5' CCATGAGGCCCCAGCCCCA	62035	CAGCCT _
	TGGGGCTG GGGCCT TGG		
	ACCCCGAC CCCGGA ACC		
	GT		
GAM2548 TM4SF11	3' CTTGGTACTCCAGACCTGCAGC	32587	C_ _ CTTG
	CCCA TGGGGCTGCAG CTGG GC G		
	ACCCCGACGTC GACC TG C		
	CA TCA__ GTTC		
GAM2548 LOC154834	5' GTACACCAGGCTCAGCCCCA	87496	C _
	TGGGGCTG AGCCTGG GC		
	ACCCCGAC TCGGACC TG		
	_ ACA__		
GAM2548 LOC200030	3' ACCAAGACCCATCATGCCCA	80124	TGCAGCC C
	TGGGGC TGGG CTTGGT		
	ACCCCG ACCC GAACCA		
	TACT__ A		
GAM2548 LOC200030	3' ACCAAGACCCATCATGCCCA	80125	TGCAGCC C
	TGGGGC TGGG CTTGGT		
	ACCCCG ACCC GAACCA		
	TACT__ A		
GAM2548 LOC200030	3' ACCAAGACCCATCATGCCCA	80126	TGCAGCC C
	TGGGGC TGGG CTTGGT		
	ACCCCG ACCC GAACCA		
	TACT__ A		
GAM2548 LOC200030	3' ACCAAGGCCACCATGCCCA	80127	TGCAGCC
	TGGGGC TGGGCCTTGGT		
	ACCCCG ACCCGGAACCA		
	TACC__		
GAM2548 LOC200030	3' ACCAAGGCCACCATGCCCA	80128	TGCAGCC
	TGGGGC TGGGCCTTGGT		
	ACCCCG ACCCGGAACCA		
	TACC__		
GAM2548 LOC221431	3' CCAAGACTCTGCAGCCC	93728	CCT GC
	GGGCTGCAG GG CTTGG		

CCGGACGTC TC GAACC
 ____ A_
 GAM2549 ELK4 3' ACCACCAAAGAACTCATCCATG 10513 CGG____ A
 TA TACATGGATGGG GG GGT
 ||||| ||||
 ATGTACCTACTC CC CCA
 AAGAAA A
 GAM2549 ICAM1 3' ACCTCCCCACCCACATACAT 72032 GA__ C
 ATG TGGG GGGGAGGT
 || ||| |||||
 TAC ACCC CCCCTCCA
 ATAC A
 GAM2549 MAN2A2 3' GCCACCTGACCTCCATGTA 21512 T G GA
 TACATGGA GG CGGG GGT
 ||||| || ||| |||
 ATGTACCT CC GTCC CCG
 _ A A_
 GAM2549 OGN 3' TACCTTCCCACCCATACA 26768 G C
 TG ATGGG GGGGAGGTA
 || ||| |||||
 AC TACCC CCCTTCCAT
 A A
 GAM2549 OGN 3' TACCTTCCCACCCATACA 53400 G C
 TG ATGGG GGGGAGGTA
 || ||| |||||
 AC TACCC CCCTTCCAT
 A A
 GAM2549 VDR 3' ACCTCCCCTATCCACCCA 6335 A C_
 TGG TGGG GGGGAGGT
 ||| ||| |||||
 ACC ACCT CCCCTCCA
 C AT
 GAM2549 C20orf177 3' GTTACCTCCCCATTTTCACATG 62839 _ TG GC
 CATG GA G GGGGAGGTAAC
 ||| || | |||||
 GTAC CT T CCCCTCCATTG
 A TT A_
 GAM2549 CHST3 3' TACCTCCTCTGACCCATCCA 16244 _ _
 TGGATGGG CGG GGAGGTA
 ||||| || |||||
 ACCTACCC GTC CCTCCAT
 A T
 GAM2549 DKFZP434E2135 5' ACCCCCTGTTTCCATCCAT 48683 _ A
 ATGGATGG GCGGGG GGT
 ||||| ||||| |||
 TACCTACC TGTCCC CCA
 TT _
 GAM2549 DKFZP434F1735 3' ACCTTGAGTCCATCCATG 32110 GGG
 CATGGATGGGC GAGGT
 ||||| |||||

GTACCTACCTG TTCCA
 AG_
 GAM2549 KIAA0494 3' GCCTTCCCCACCCACCCA 29403 A C _
 TGG TGGG GGGGA GGT
 ||| ||| ||||| |||
 ACC ACCC CCCCT CCG
 C A T
 GAM2549 MGC7036 3' ACCTCCCTGTGCCACACA 59613 GA _
 TG TGG GCGGGGAGGT
 || ||| ||||| |||||
 AC ACC TGTCCCTCCA
 AC G
 GAM2549 SLC26A6 3' GCTACCCAGGAGTCCCCTCCAT 43584 T CG____ A
 GTA TACATGGA GGG GGG GGT
 ||||| ||| ||| |||
 ATGTACCT CCC CCC TCG
 C TGAGGA A
 GAM2549 LOC124976 3' ACCCACCTCCCATCCATG 74839 C GA
 CATGGATGGG GGG GGT
 ||||| ||| |||
 GTACCTACCC TCC CCA
 _ AC
 GAM2549 LOC206480 5' ACCTCCCCATTACCCCCACGT 92405 A A_ C
 AC TGG TGGG GGGGAGGT
 || ||| ||| ||||| |||||
 TG ACC ACTT CCCCTCCA
 C CC A
 GAM2549 LOC256158 5' CTCCCCGCCCATCCACGTG 99493 A
 TAC TGGATGGGCGGGGAG
 ||| ||||| ||||| |||||
 GTG ACCTACCCGCCCCTC
 C
 GAM2549 LOC90917 5' TTGCCACCCCCCCACACA 64990 GA C A
 TG TGGG GGGG GGTA
 || ||| ||| ||||| |||||
 AC ACCC CCCC CCGTT
 AC _ A
 GAM2550 DDIT3 5' ATACATCACCACACCTGA 15832 A GAAC AA
 TCAG TG TGG GATGTAT
 ||| || ||| ||||| |||||
 AGTC AC ACC CTACATA
 C ____ A_
 GAM2550 HLCS 3' TCTTCCAGTCCCAGCTGA 6422 A A
 TCAG TGG ACTGGAAGA
 ||| ||| ||||| |||||
 AGTC ACC TGACCTTCT
 G C
 GAM2550 MMP14 3' GTCTGTCCAGCCCCATCTGA 18431 AA _
 TCAGATGG CTGGA AGAT
 ||||| ||||| |||||


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AGTCTACC GACCT TCTG
      CC  G
GAM2550 XT3   3' CATCTCATCTTCCAGCTTCACC 39904   A  A   T_
      TGA          TCAG TGGA CTGGAAGATG ATG
                |||| ||| ||||| |||
                AGTC ACTT GACCTTCTAC TAC
                C  C   TC
GAM2550 C20orf45 3' CATAcATTGGAActCCACCTGA 32642   A  ACTGGAA
                TCAG TGGA   GATGTATG
                |||| |||  |||||
                AGTC ACCT   TTACATAC
                C  CAAGG__
GAM2550 C21orf42 3' CATCTTCCCTATTCCATCT 55226   CT_
                AGATGGAA GGAAGATG
                ||||| |||||
                TCTACCTT CCTTCTAC
                ATC
GAM2550 KIAA0930 3' CATGGTCCAGCCCCATTTGA 71067   AA  AG
                TCAGATGG CTGGA ATG
                ||||| |||| |||
                AGTTTACC GACCT TAC
                CC  GG
GAM2550 P115   3' ACATCTTTTATTTAAATCCATC 14937   AC____
                TGA          TCAGATGGA   TGGAAAGATGT
                ||||| |||||
                AGTCTACCT ATTTTCTACA
                AAATTT
GAM2550 PRO0386 5' CAGATTCCAGTTCCACTGA 38301   A   GA
                TCAG TGGAActGGAA TG
                ||| ||||| ||| ||
                AGTC ACCTTGACCTT AC
                _   AG
GAM2550 SDCCAG3 3' GGTTTTCCAGTCCCATC 22804   A   TG
                GATGG ACTGGAAGA T
                |||| ||||| |
                CTACC TGACCTTTT G
                C   GT
GAM2550 LOC149111 3' ACGTCCCCAGCTCCCATCTGA 79930   AA_  AA
                TCAGATGG CTGG GATGT
                ||||| ||| ||||
                AGTCTACC GACC CTGCA
                CTC  C_
GAM2550 LOC199725 3' CATAcATCTTTGCCCATC 91412   AACTG
                GATGG  GAAGATGTATG
                ||||  |||||
                CTACC TTTCTACATAC
                CG____
GAM2550 LOC203232 5' CATTCCCCACCCCATCTGA 71917   AAC  AA
                TCAGATGG TGG GATG
                ||||| ||| |||

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		AGTCTACC ACC TTAC		
		CC_ CC		
GAM2550	LOC205418 5'	ACATCTTTTCATTTTCCACTGA 92364	A	C_
		TCAG TGGAA TGAAGATGT		
		AGTC ACCTT ACTTTCTACA		
		_ TT		
GAM2551	TRPC5 3'	AAATTCTACTGTCTTCCAAG 25922	ATTAT	
		CTTGGAAGA GAATTT		
		GAACCTTCT CTTAAA		
		GTCAT		
GAM2551	TRPV3 3'	AAATCCAAGATTCTTCCAGG 96812	A A	
		CTTGGAAGAATT TG ATTT		
		GGACCTTCTTAG AC TAAA		
		A C		
GAM2551	CDC14B 3'	AAATTTTTTTTTCTTCCAA 14768	TTAT	
		TTGGAAGAA GAATTT		
		AACCTTCTT TTTAAA		
		TTTT		
GAM2551	FLJ20171 3'	AAATTCTTAAGTTCTTCCAAGG 35171	_ T	
		CCTTGGAAGAA TTA GAATTT		
		GGAACCTTCTT AAT CTTAAA		
		C T		
GAM2551	KIAA0513 3'	AAATTCACCATATCCAAGGG 29000	AGAATTA	
		CCCTTGGA TGAATTT		
		GGAACCT ACTTAAA		
		ATACC_		
GAM2551	LOC257358 3'	AAATGCAGCATTCTCCAAGGG 98896	AG TA A	
	TA	TACCCTTGGA AAT TG ATTT		
		ATGGGAACCT TTA AC TAAA		
		CT CG G		
GAM2552	HMG1 3'	CATGTTGTTTTTTAGTAG 18302	TGTCC	
		TTACT AAAAACAACATG		
		GATGA TTTTGTGTGAC		
		T_		
GAM2552	NCOA6 5'	ATTGTGTGACCTTGGACAAATA 26829	C AAACA TG	
	A	TTA TTGTCCAA ACA AT		
		AAT AACAGGTT TGT TA		
		A CCAG_ GT		
GAM2552	PKD2 3'	CATGTTGTTACATGTAA 60716	T CCAA	
		TTAC TGT AACAACATG		

AATG ACA TTGTTGTAC
 T _____
 GAM2552 TSPY 3' ATCATGTTGTTCTTTTCGGAGTA 83000 TTG _ _
 A TTAC TCC AAA AACAACATGAT
 |||| ||| ||| |||||
 AATG AGG TTT TTGTTGTACTA
 _ C C
 GAM2552 FLJ12568 3' ATCATGTTAGTGAGCAGACAA 47139 CAAAA _
 TTGTC AC AACATGAT
 |||| || |||||
 AACAG TG TTGTACTA
 ACGAG A
 GAM2552 TNRC9 3' ATCACTTTGTTTTTAAACAAG 71798 CC CA
 CTTGT AAAAACA TGAT
 |||| ||||| |||
 GAACA TTTTGT ACTA
 AA TC
 GAM2552 LOC130355 5' GTTGCATCTCTGGACAAGTAA 75434 AAAA_
 TTACTTGTCCA CAAC
 ||||| |||
 AATGAACAGGT GTTG
 CTCTAC
 GAM2552 LOC145854 3' CATGTTGTTTTTTAGTAG 78006 TGTCC
 TTACT AAAAACAACATG
 |||| |||||
 GATGA TTTTGTGTAC
 T_____
 GAM2553 AIRE 3' TGGGAGCCTGAGGCATGAGAA 7247 C C
 TTC CATGCC CAGGCTCCTG
 || ||||| |||||
 AAG GTACGG GTCCGAGGGT
 A A
 GAM2553 BCAS1 3' CTCGGGAGCCCAACGCACGAGA 14711 CCA CCCA C
 A TTC TGC GGCTCCTG AG
 || || ||||| ||
 AAG ACG CCGAGGGC TC
 AGC CAAC _
 GAM2553 DAG1 3' CTGCAGGATGTAACATGG 16553 CCCCAG _
 CCATG GC TCCTGCAG
 |||| || |||||
 GGTAC TG AGGACGTC
 AA____ T
 GAM2553 GPRK7 3' CGGGAGCCTGAGGCAGGAGAA 58313 _ A C
 TTC CC TGCC CAGGCTCCTG
 || || ||| |||||
 AAG GG ACGG GTCCGAGGGC
 A _ A
 GAM2553 KIF1B 3' TGGGAGCCTGAGGCAGGAGAA 31273 _ A C
 TTC CC TGCC CAGGCTCCTG
 || || ||| |||||

		AAG GG ACGG GTCCGAGGGT	
		A _ A	
GAM2553 NCAM1	5'	CTGCAGGGGGGGGGGCACAGAA 7040	CCA AGG
		TTC TGCCCC CTCCTGCAG	
		AAG ACGGGG GGGGACGTC	
		AC_ GG_	
GAM2553 NOS1	3'	CTGCAGGGTCCCCAAGGATGG 7095	G CCA_ CT
		CCAT CC GG CCTGCAG	
		GGTA GG CC GGACGTC	
		_ AACC TG	
GAM2553 PDGFRB	3'	TGCCCCAGGGACATGGGAA 66584	_ CA CTCCT
		TTCCCATG CCC GG GCA	
		AAGGGTAC GGG CC CGT	
		A AC _____	
GAM2553 RAB31	3'	CTGCAGGGGGCGGGGCAGGAA 23440	CA AGG
		TTCC TGCCCC CTCCTGCAG	
		AAGG ACGGGG GGGGACGTC	
		_ CG_	
GAM2553 SCN4A	3'	CTGCGTTCCCAGACCATGGGAA 6200	CCCCA CTCC
		TTCCCATG GG TGCAG	
		AAGGGTAC CC GCGTC	
		CAGAC TT__	
GAM2553 WHSC1	3'	CTGCAATGACTGCAGGGGCTGGG 24667	T __ GCTCC
AA		TTCCCA GCCC CAG TGCAG	
		AAGGGT CGGG GTC ACGTC	
		_ AC AGTA_	
GAM2553 WHSC1	3'	CTGCAATGACTGCAGGGGCTGGG 24668	T __ GCTCC
AA		TTCCCA GCCC CAG TGCAG	
		AAGGGT CGGG GTC ACGTC	
		_ AC AGTA_	
GAM2553 WHSC1	3'	CTGCAATGACTGCAGGGGCTGGG 24669	T __ GCTCC
AA		TTCCCA GCCC CAG TGCAG	
		AAGGGT CGGG GTC ACGTC	
		_ AC AGTA_	
GAM2553 ZFP36L1	3'	CTGCAGGAAGGAAGGCTG 18201	T __ AGGC
		CA GCC CC TCCTGCAG	
		GT CGG GG AGGACGTC	
		_ AA A__	
GAM2553 C20orf64	5'	CAAGAGCCCTTCCTGCAGGGAA 54334	A CCCA__ C
		TTCCC TGC GGCTC TG	

			AAGGG ACG CCGAG AC	
			_ TCCTTC A	
GAM2553	DRIL2	3'	CTGCAGGGTGTGGGCAGAGAA 22350	CCA C G T
			TTC TGCCC A GC CCTGCAG	
			AAG ACGGG T TG GGACGTC	
			AG_ _ G _	
GAM2553	FEM-2	3'	CTGCAGGGCCAAGCCACAGGAA 28312	CAT_ CCCA T
			TTCC GC GGC CCTGCAG	
			AAGG CG CCG GGACGTC	
			ACAC AA_ _	
GAM2553	FLJ10737	3'	CTGCAGTCCAAGCTGAACATGG 37054	CCCCA C_
			GAA TTCCCATG GGCT CTGCAG	
			AAGGGTAC TCGA GACGTC	
			AAG_ ACCT	
GAM2553	FLJ10898	5'	CTGCCAAACCTGCAACATGGGA 60133	CCC CTCCT
			A TTCCCATG CAGG GCAG	
			AAGGGTAC GTCC CGTC	
			AAC AAAC_	
GAM2553	FLJ11618	3'	CTGCAGGGGGAAGAGCCGGGAA 42624	AT CCCAGG
			TTCCC GC CTCCTGCAG	
			AAGGG CG GGGGACGTC	
			C_ AGAAG_	
GAM2553	FLJ12287	5'	TGCCTCTGGGGCCTGGGAA 42564	T CTCCT
			TTCCCA GCCCCAGG GCA	
			AAGGGT CGGGGTCT CGT	
			C C_	
GAM2553	FLJ14129	3'	TGGGAGCCTGGGGCAGGAGAA 48814	_ A
			TTC CC TGCCCCAGGCTCCTG	
			AAG GG ACGGGGTCCGAGGGT	
			A _	
GAM2553	KIAA0187	3'	CTGCAGGAGGAGGAACAGAGAA 29250	CCA CC AGG
			TTC TG CC CTCCTGCAG	
			AAG AC GG GAGGACGTC	
			AG_ AA AG_	
GAM2553	KIAA0416	5'	GGAAAGCCTGGGACACAGAA 32093	CCA C _
			TTC TG CCCAGGC TCC	
			AAG AC GGGTCCG AGG	
			AC_ A AA	
GAM2553	KIAA1266	3'	CTGCAAGGGCGAGCATGGGA 66695	CCCAG C
			TCCCATGC GCTC TGCAG	

AGGGTACG CGGG ACGTC
 AG___ A
 GAM2553 KIAA1483 3' CTGCAGGGAAAAGGATATAGGA 70434 C C CAGG T
 A TTCC ATG CC C CCTGCAG
 |||| ||| || | |||||
 AAGG TAT GG G GGACGTC
 A A AAAA _
 GAM2553 KIAA1706 3' TGCAGTGAGAGCATGGGA 94372 CCCAGG _
 TCCCATGC CTC CTGCA
 ||||| ||| |||||
 AGGGTACG GAG GACGT
 A_____ T
 GAM2553 KIAA1715 3' CTCAGGAGCCTGAGGCAGGAGA 68684 _ A C C
 A TTC CC TGCC CAGGCTCCTG AG
 ||| || ||| ||||| ||| ||
 AAG GG ACGG GTCCGAGGAC TC
 A _ A _
 GAM2553 KIAA1981 3' CAGGAGCCAAGGTCACAGAA 89710 CCA C CA
 TTC TG CC GGCTCCTG
 ||| ||| |||||
 AAG AC GG CCGAGGAC
 AC_ T AA
 GAM2553 MCAM 3' CAGGAACCTGGGGGCCTGTGAA 22457 C T _ C
 TTC CA GCCCC AGG TCCTG
 ||| || ||||| ||| |||||
 AAG GT CGGGG TCC AGGAC
 T C G A
 GAM2553 MRPS24 3' CTGCAGAGAATGAAAACGTGGG 50130 CC_ GG C
 AA TTCCCATG CCA CTC TGCAG
 ||||| ||| ||| |||||
 AAGGGTGC GGT GAG ACGTC
 AAA AA _
 GAM2553 MSE55 3' TGCAGGACAGACATGGGAG 23916 CCCCAGGC
 TTCCCATG TCCTGCA
 ||||| |||||
 GAGGGTAC AGGACGT
 AGAC_____
 GAM2553 OS4 3' CTGCTTTGTGCTAAAAGCATGG 20388 CCCA TCCT_
 GAA TTCCCATGC GGC GCAG
 ||||| ||| |||
 AAGGGTACG TCG CGTC
 AAAA TGTTT
 GAM2553 PASK 5' CAGGGTCTCGCCTGGGGCATT 31405 CC ____
 GAA TTC ATGCCCCAGGC TCCTG
 ||| ||||| ||||| |||||
 AAG TACGGGGTCCG GGGAC
 AT CTCT
 GAM2553 PRO1163 3' CTGAATGAGCCTGGGGCA 38323 CTG
 TGCCCCAGGCTC CAG
 ||||| |||

ACGGGGTCCGAG GTC
 TAA
 GAM2553 THEA 3' CTCAGGAAGCTGAGGCACAAGA 66887 CCA C GC C
 A TTC TGCC CAG TCCTG AG
 ||| ||| ||| ||||| ||
 AAG ACGG GTC AGGAC TC
 AAC A GA _
 GAM2553 WFDC3 3' GCTGACCAGAGCATGGGAA 98702 CCCA C CT
 TTCCCATGC GG TC GC
 ||||| || || ||
 AAGGGTACG CC AG CG
 AGA_ _ T_
 GAM2553 LOC122726 5' CTGCAGGAAACACTGAGGCTTG 76103 T C GC_
 GGAA TTCCCA GCC CAG TCCTGCAG
 ||||| ||| ||| ||||| ||
 AAGGGT CGG GTC AGGACGTC
 T A ACAA
 GAM2553 LOC129303 3' CTGCAGGAATTGGGGGCTGGGA 75373 T AG C
 A TTCCCA GCCCC G TCCTGCAG
 ||||| |||| | ||||| ||
 AAGGGT CGGGG T AGGACGTC
 _ GT A
 GAM2553 LOC132617 5' CTGCAGATCGAGGCATGGGA 76415 CCA CTC
 TCCCATGCC GG CTGCAG
 ||||| || ||||| ||
 AGGGTACGG CT GACGTC
 AG_ A_
 GAM2553 LOC145945 5' AGGGCCTGGACCATAGAA 84563 CC CC T
 TTC ATG CCAGGC CCT
 ||| ||| ||||| |||
 AAG TAC GGTCCG GGA
 A_ CA _
 GAM2553 LOC146332 3' CAGGAGCCTGGGGCCTGTGGA 78353 _ T
 TCC CA GCCCCAGGCTCCTG
 ||| || ||||| ||||| ||
 AGG GT CGGGGTCCGAGGAC
 T C
 GAM2553 LOC146714 5' TGCAGGGCAGGCACAGGGA 84754 A_ CCAG T
 TCCC TGCC GC CCTGCA
 ||| ||| || ||||| ||
 AGGG ACGG CG GGACGT
 AC A_ _
 GAM2553 LOC147958 3' CTGCAGGGCAGGCAGCAGAA 88523 CCA CCAG T
 TTC TGCC GC CCTGCAG
 ||| ||| || ||||| ||
 AAG ACGG CG GGACGTC
 ACG A_ _
 GAM2553 LOC149501 3' CTGCAAGAGCCTGGCTGGGAA 75800 T CC C
 TTCCCA GCC AGGCTC TGCAG
 ||||| ||| ||||| ||||| ||

AAGGGT CGG TCCGAG ACGTC
 _ _ A
 GAM2553 LOC150397 3' CAGGAGCCTGAGTGAAGGA 80655 CA CC
 TCC TGC CAGGCTCCTG
 ||| ||| |||||
 AGG GTG GTCCGAGGAC
 AA A_
 GAM2553 LOC150397 3' GCAGGAGCCTGCAGGAGA 80664 _ A CCC
 TC CC TGC AGGCTCCTGC
 || ||| |||||
 AG GG ACG TCCGAGGACG
 A _ _
 GAM2553 LOC150517 5' CTGCAGGTAGGAGCACAGAA 80725 CCA C AGGCT
 TTC TGC CC CCTGCAG
 ||| ||| |||||
 AAG ACG GG GGACGTC
 AC_ A AT_
 GAM2553 LOC153688 3' TGGGAGGCTGGGGCATGAGAA 87341 C G
 TTC CATGCCCCAG CTCCTG
 ||| ||||| |||||
 AAG GTACGGGGTC GAGGGT
 A G
 GAM2553 LOC154849 3' CTGCAGGAGGTGGAAGATG 60941 GCC GG
 CAT CCA CTCCTGCAG
 ||| ||| |||||
 GTA GGT GAGGACGTC
 GAA G_
 GAM2553 LOC162137 3' GCAGGAGCTTCCCATAAAGAA 88480 CC_ CCCC
 TTC ATG AGGCTCCTGC
 ||| ||| |||||
 AAG TAC TTCGAGGACG
 AAA CC_
 GAM2553 LOC219654 3' CAGGAGCCCAGGGGATGGGAA 92925 G CA
 TTCCCAT CCC GGCTCCTG
 ||||| ||| |||||
 AAGGGTA GGG CCGAGGAC
 G AC
 GAM2553 LOC255042 3' CTCGGGAGCCTGAGGCAGGAGA 97042 _ A C C
 A TTC CC TGCC CAGGCTCCTG AG
 ||| ||| ||||| |||
 AAG GG ACGG GTCCGAGGGC TC
 A _ A _
 GAM2553 LOC257000 3' CTGCAGGACTCAGAGCATGG 98587 CCCA C
 CCATGC GG TCCTGCAG
 ||||| || |||||
 GGTACG TC AGGACGTC
 AGAC _
 GAM2553 LOC91750 3' TGGGGGCCTGAGGCACGAGAA 67659 CCA C
 TTC TGCC CAGGCTCCTG
 ||| ||| |||||

AAG ACGG GTCCGGGGGT
 AGC A
 GAM2554 ADAM19 3' TGGAACAGTCAGAGCAGGGA 53849 TAC AC_
 TCCCT CT ATTGTTCCA
 |||| || |||||
 AGGGA GA TGACAAGGT
 C_ GAC
 GAM2554 GPR85 3' TGGAGCAAATAGCCAAGGGA 39109 AC CA
 TCCCTT CTA TTGTTCCA
 |||| || |||||
 AGGGAA GAT AACGAGGT
 CC A_
 GAM2554 CCR5 3' ATAGTACAGGTAAGGTGA 6961 _ AC
 TC CCTTACCT ATTGT
 || ||||| ||||
 AG GGAATGGA TGATA
 T CA
 GAM2554 CLCA4 3' AACAAATGTAAGTAAAGGA 62747 C C
 TCC TTAC TACATTGTT
 || || |||||
 AGG AATG ATGTAACAA
 A A
 GAM2554 DKFZP586M1120 3' TGTTGGGCAGGCAGGTAAGGGG 49290 ACA T
 TCCCTTACCT TTGT CCAACA
 ||||| || |||||
 GGGGAATGGA GACG GGTTGT
 CG_ _
 GAM2554 FLJ00024 3' TGTTAGTCTCAAAGGTAAGG 64509 ACA TTCC_
 CCTTACCT TTG AACA
 ||||| || ||||
 GGAATGGA AAC TTGT
 _ TCTGA
 GAM2554 FLJ10713 3' GTTATTACAAGTAGGGGA 37004 CTACA TCC
 TCCCTTAC TTGT AAC
 ||||| || ||||
 AGGGGATG AACA TTG
 _ TTA
 GAM2554 FLJ20446 3' TGGAACAGCGAGCAAGGGA 35636 AC ACA
 TCCCTT CT TTGTTCCA
 |||| || |||||
 AGGGAA GA GACAAGGT
 C_ GC_
 GAM2554 KIAA0447 3' TGTTGGAAGAAGTAAACAAG 72136 ACC A G
 CTT TAC TT TTCCAACA
 || || || |||||
 GAA ATG AA AAGGTTGT
 CAA _ G
 GAM2554 PILR(BETA) 5' GGAGCAATTAGGCAAGGGA 26484 A C
 TCCCTT CCTA ATTGTTCC
 |||| || |||||

			AGGGAA GGAT TAACGAGG		
			C _		
GAM2554	SH120	3'	TGGA	ACTCTGGGGCAAGAGA 33393	C A A TT
			TC CTT CCT CA GTTCCA		
			AG GAA GGG GT CAAGGT		
			A C _ CT		
GAM2554	ZNF17	3'	TGTTGGAACACATGGTAAG 83279		TACAT
			CTTACC GTTCCAACA		
			GAATGG ACAAGGTTGT		
			TAC_		
GAM2554	LOC112840	3'	TGTTGGAAGATGTAGGTGAG 55615		G
			CTTACCTACATT TTCCAACA		
			GAGTGGATGTAG AAGGTTGT		
			-		
GAM2554	LOC132617	3'	TTGGAACAGTGAAAGCAAGAGA 76423		C ACCTA
			TC CTT CATTGTTCCAA		
			AG GAA GTGACAAGGTT		
			A CGAAA		
GAM2554	LOC143153	5'	GTGGACAGCAGGTAGGG 76983		ACA T A
			CCTTACCT TTGT CC AC		
			GGGATGGA GACA GG TG		
			C_ _ C		
GAM2554	LOC148809	3'	TGGAATTCAGGGAAGGGA 79767		A ACATT
			TCCCTT CCT GTTCCA		
			AGGGAA GGG TAAGGT		
			_ ACT_		
GAM2554	LOC149506	3'	GTTGAAGCTAGACGAGGGA 85646		AC CATT C
			TCCCTT CTA GTT CAAC		
			AGGGAG GAT CGA GTTG		
			CA _ _ A		
GAM2554	LOC151516	3'	GAACAGGCACAGGTGAGGGA 81065		ACA_
			TCCCTTACCT TTGTTC		
			AGGGAGTGGGA GACAAG		
			CACG		
GAM2554	LOC155060	3'	TGTTGGAGCAGGCAGGCAAAGG 87609		A_ ACA
			CCCTT CCT TTGTTCCAACA		
			GGGAA GGA GACGAGGTTGT		
			AC CG_		
GAM2554	LOC205418	5'	TGTTGGAGCTCAGGGAAGGGA 92377		A ACATT
			TCCCTT CCT GTTCCAACA		

		AGGGAA GGG CGAGGTTGT		
		_ ACT_		
GAM2554	LOC205713 5'	TTGGAACGAAACATAAGGGA 91082	CCTACA	
		TCCCTTA TTGTTCCAA		
		AGGGAAT AGCAAGGTT		
		ACAA_		
GAM2554	LOC254394 3'	TGAAATTTCTTAGGTAGGGA 97673	T CATT C	
		TCCCT ACCTA GTT CA		
		AGGGA TGGAT TAA GT		
		_ TCTT A		
GAM2554	LOC64182 5'	TTGGAGCGGATAGAAAGG 42557	AC CA	
		CCTT CTA TTGTTCCAA		
		GGAA GAT GGCGAGGTT		
		A_ A_		
GAM2555	FLJ22332 5'	GGAAAGAAAACATCACA 45637	G A	_____
		TGTG AT TAGTTTTT CC		
		ACAC TA ATCAAAAG GG		
		_ C AAA_		
GAM2556	AMACR 3'	TTGTATGCATGGAAACATGGA 69103	ATC G	
		TCCAT TCCATGCATG CGG		
		AGGTA AGGTACGTAT GTT		
		CAA _		
GAM2556	BCL2L11 3'	TCGCCCAGAGATATGGA 57615	CA CAT G	
		TCCATATCTC TG GGCG A		
		AGGTATAGAG AC CCGC T		
		_ _ G		
GAM2556	BCL2L11 3'	TCGCCCAGAGATATGGA 57616	CA CAT G	
		TCCATATCTC TG GGCG A		
		AGGTATAGAG AC CCGC T		
		_ _ G		
GAM2556	FGFR2 5'	CGTCCACATGGAGATATGGA 43763	CA _	
		TCCATATCTCCATG TGG CG		
		AGGTATAGAGGTAC ACC GC		
		_ T		
GAM2556	FGFR2 5'	CGTCCACATGGAGATATGGA 43767	CA _	
		TCCATATCTCCATG TGG CG		
		AGGTATAGAGGTAC ACC GC		
		_ T		
GAM2556	FGFR2 5'	CGTCCACATGGAGATATGGA 43771	CA _	
		TCCATATCTCCATG TGG CG		

			AGGTATAGAGGTAC ACC GC		
			— T		
GAM2556	FGFR2	5'	CGTCCACATGGAGATATGGA 5559	CA	_
			TCCATATCTCCATG TGG CG		
			AGGTATAGAGGTAC ACC GC		
			— T		
GAM2556	FGFR2	5'	CGTCCACATGGAGATATGGA 43633	CA	_
			TCCATATCTCCATG TGG CG		
			AGGTATAGAGGTAC ACC GC		
			— T		
GAM2556	FGFR2	5'	CGTCCACATGGAGATATGGA 43638	CA	_
			TCCATATCTCCATG TGG CG		
			AGGTATAGAGGTAC ACC GC		
			— T		
GAM2556	FGFR2	5'	CGTCCACATGGAGATATGGA 43642	CA	_
			TCCATATCTCCATG TGG CG		
			AGGTATAGAGGTAC ACC GC		
			— T		
GAM2556	FGFR2	5'	CGTCCACATGGAGATATGGA 43652	CA	_
			TCCATATCTCCATG TGG CG		
			AGGTATAGAGGTAC ACC GC		
			— T		
GAM2556	FGFR2	5'	CGTCCACATGGAGATATGGA 43665	CA	_
			TCCATATCTCCATG TGG CG		
			AGGTATAGAGGTAC ACC GC		
			— T		
GAM2556	FGFR2	5'	CGTCCACATGGAGATATGGA 43674	CA	_
			TCCATATCTCCATG TGG CG		
			AGGTATAGAGGTAC ACC GC		
			— T		
GAM2556	FGFR2	5'	CGTCCACATGGAGATATGGA 43678	CA	_
			TCCATATCTCCATG TGG CG		
			AGGTATAGAGGTAC ACC GC		
			— T		
GAM2556	MAP3K14	3'	ATCCGCCACGTGAAGAGA 15541	CA	A
			TCTC TGC TGGCGGAT		
			AGAG GTG ACCGCCTA		
			AA C		
GAM2556	KIAA0819	3'	CCCCAGCATCACAGGAGACATG 64330	A	_____ A C
	GA		TCCAT TCTCC ATGC TGG GG		

AGGTA AGAGG TACG ACC CC
 C ACAC _ _
 GAM2556 PORIMIN 3' CATACATGGAGTATGGA 54702 T C
 TCCATA CTCCATG ATG
 ||||| ||||| ||
 AGGTAT GAGGTAC TAC
 _ A
 GAM2556 RDC1 3' CCGGCACGGGATATGGA 72832 T A A
 TCCATATC CC TGC TGG
 ||||| || ||| ||
 AGGTATAG GG ACG GCC
 _ C _
 GAM2556 VEZATIN 3' ATCCGCCACAACAGACAATG 34656 A_ CCA CA
 CAT TCT TG TGGCGGAT
 ||| ||| || |||||
 GTA AGA AC ACCGCCTA
 AC CA_ _
 GAM2556 LOC147645 5' ATCCGCTGGTGGCAGAGACACG 79065 ATA CA AT_
 G CC TCTC TGC GGCGGAT
 || ||| ||| |||||
 GG AGAG ACG TCGCCTA
 CAC _ GTGG
 GAM2556 LOC199775 3' TTGCTGCATCAGAGATATG 89726 C_ TG
 CATATCTC ATGCA GCGG
 ||||| |||| |||
 GTATAGAG TACGT CGTT
 AC _
 GAM2556 LOC51279 3' CCGCTATTAGAGTATGGA 33752 T CATGC
 TCCATA CTC ATGGCGG
 ||||| ||| |||||
 AGGTAT GAG TATCGCC
 _ AT_
 GAM2557 FLJ21458 3' CCATAGTCATCTGCCCAGTCA 46278 CATC GA C
 TGA CTGGGT GA AC ATGG
 ||||| || || |||
 ACTGACCCG CT TG TACC
 T_ AC A
 GAM2557 LOC148089 3' CATGGTCCCACCCAGTTA 79325 CATCGA A
 TGA CTGGGT GA CCATG
 ||||| || |||||
 ATTGACCCA CT GGTAC
 CC_ _
 GAM2557 LOC255452 3' CCATGGTTCTAGACCC 99392 ATCG
 GGGTC AGAACCATGG
 |||| |||||
 CCCAG TCTTGGTACC
 A_
 GAM2558 ANK3 3' AAAGATTTTATCTGTAAAC 8561 C GG
 GTTTACAGA AAGA TTT
 ||||| ||| |||

		CAAATGTCT TTTT AAA	
		A AG	
GAM2558	CRYZ	3' AAACCTCTATTCTAAACT 10308	AC CA
		AGTTT AGA AGAGGTTT	
		TCAAA TCT TCTCCAAA	
		__ TA	
GAM2558	RRM2B	3' AAACCTCTTGTTTTAAAACT 68430	AC
		AGTTT AGACAAGAGGTTT	
		TCAAA TTTGTTCTCCAAA	
		AT	
GAM2558	SLC2A6	3' CTCCTATCTGCAAACGTGTG 34570	A CAA
		TACAGTTT CAGA GAG	
		GTGTCAAA GTCT CTC	
		C ATC	
GAM2558	TEM8	3' AAACCTCTATAAGACTGTA 50817	ACAGACA
		TACAGTTT AGAGGTTT	
		ATGTCAGA TCTTCAAA	
		ATA__	
GAM2558	UBL3	3' GAACAGTCTGCCTGTAAAC 24023	ACA G_
		GTTTACAG AGA GTTT	
		CAAATGTC TCT CAAG	
		CG_ GA	
GAM2558	DKFZp547I014	5' GACCATTTTGTGTTTGCAAAC 39943	A _
		AGTTT CAGACAAGA GGTT	
		TCAAA GTTTGTTTT CCAG	
		C A	
GAM2558	FLJ10971	3' AAACCTCTCACCTGAATTTTGT 37480	TTTA ACA
	G	TACAG CAG AGAGGTTT	
		GTGTT GTC TCTCCAAA	
		TTAA CAC	
GAM2558	HTEX4	5' GAAACATATCTGTAAACT 93724	CAAGAG
		AGTTTACAGA GTTTC	
		TCAAATGTCT CAAAG	
		ATA__	
GAM2558	KIAA0945	3' GAAACCTCTTGCCAGAACT 30902	ACAGA
		AGTTT CAAGAGGTTTC	
		TCAAG GTTCTCCAAAG	
		AC__	
GAM2558	KIAA1024	3' GACATTCTATCTGTAAAC 69617	CA _
		GTTTACAGA AGAG GTT	

		CAAATGTCT TCTT CAG	
		A_ A	
GAM2558 KIAA1163	3'	GAAACCTCCCGTGAAGACT 79648	A GACAA
		AGTTT CA GAGGTTTC	
		TCAGA GT CTCCAAAG	
		A GCC_	
GAM2558 KIAA1203	3'	AAATGTCAGTGTCTATAAACTG 72085	C A_ G
	TA	TACAGTTTA AGACA GA GTTT	
		ATGTCAAAT TCTGT CT TAAA	
		A GA G	
GAM2558 KIAA1718	3'	AAACCTTTTCGAAACTGTA 64970	ACAGACA
		TACAGTTT AGAGGTTT	
		ATGTCAAA TTTCCAAA	
		GC_	
GAM2558 KIAA1854	3'	GAAACCTCTTGACAAGACTGTA 72208	ACAGA
		TACAGTTT CAAGAGGTTTC	
		ATGTCAGA GTTCTCCAAAG	
		ACA_	
GAM2558 KIAA1962	3'	GAAACCCTGGGATGTAAACTTA 82800	C GACA A
		A AGTTTACA AG GGTTC	
		A TCAAATGT TC CCAAAG	
		T AGGG _	
GAM2558 KLHL8	3'	AAACCTTTTTGTAGACTGTA 63501	CAA
		TACAGTTTACAGA GAGGTTT	
		ATGTCAGATGTTT TTCCAAA	
		—	
GAM2558 MGC33182	5'	AAACCCTCGCAAACCTGTG 76091	ACA CAA A
		TACAGTTT GA G GGTTC	
		GTGTCAAA CT C CCAA	
		CG_ _ _	
GAM2558 PTPRU	3'	AATTTCCCCATCTGTAAACTGT 20317	CAA_
	A	TACAGTTTACAGA GAGGTT	
		ATGTCAAATGTCT CTTTAA	
		ACCC	
GAM2558 PTPRU	3'	AATTTCCCCATCTGTAAACTGT 20318	CAA_
	A	TACAGTTTACAGA GAGGTT	
		ATGTCAAATGTCT CTTTAA	
		ACCC	
GAM2558 RIT	3'	GAAGTGTTTATCTGTGAACTG 23583	CA GG
		CAGTTTACAGA AGA TTTC	

			GTCAAGTGTCT TTT GAAG		
			A_ GT		
GAM2558	LOC148438	3'	AAACCTCTTGCCTGAAGC 85308	A	A
			GTTT CAG CAAGAGGTTT		
			CGAA GTC GTTCTCCAAA		
			_ C		
GAM2558	LOC166713	5'	GAACCTCCCGTCTGTAACCTG 88612	T	AA
			CAG TTACAGAC GAGGTTT		
			GTC AATGTCTG CTCCAAG		
			C CC		
GAM2559	BRCA1	3'	GTTTGCCAGAAAACACCA 24573	AA	GC
			TGG TTTTCTGG CGAAT		
			ACC AAAAGACC GTTTG		
			AC _		
GAM2559	EYA4	3'	TATTTGGAATAAAAATTCCA 15886	C	GG
			TGGAATTTT TG CCGAATA		
			ACCTTAAAA AT GGTTTAT		
			_ AA		
GAM2559	MECP2	3'	ATTTGGCAGAAAATTACA 18385	G	GG
			TG AATTTTCT GCCGAAT		
			AC TTAAAAGA CGGTTTA		
			A _		
GAM2559	ZFH1B	3'	TTCGACTGAAAATTCCA 29608	T	GC
			TGGAATTTTC GG CGAA		
			ACCTTAAAAG TC GCTT		
			_ A_		
GAM2559	CENTB5	3'	TACTCGGCCCCAGAGCC 97234	AATT	A
			GG TTCTGGGCCGA TA		
			CC GAGACCCGGCT AT		
			_ C		
GAM2559	CG012	3'	TGGCTACCCAGAAAATTTCA 84171		
			TGGAATTTTCTGG GCCG		
			ACTTTAAAAGACC CGGT		
			CAT		
GAM2559	FLJ13057	3'	TCACCCAGAAAATCCA 97366	A	CC
			TGGA TTTTCTGGG GA		
			ACCT AAAAGACCC CT		
			_ A_		
GAM2559	HBXAP	3'	ATTTTTCCTAGAAAATCCA 33880	A	CC
			TGGA TTTTCTGGG GAAT		

		ACCT AAAAGATCC TTTA		
		C TT		
GAM2559 KIAA0997	3'	TCAACCCAAAAAGTTCCA 30889	C	CC
		TGGAATTTT TGGG GA		
		ACCTTGAAA ACCC CT		
		A AA		
GAM2559 KIAA1014	3'	GTATTCTCCATAAAATTCCA 65961	C	CC
		TGGAATTTT TGGG GAATAC		
		ACCTTAAAA ACCT CTTATG		
		T _		
GAM2559 MAGEH1	3'	GTATTCGTTTTAAATTCC 26771	CT	C
		GGAATTTT GGGC GAATAC		
		CCTTAAAA TTTG CTTATG		
		T_ _		
GAM2559 PSK	5'	TATTCGGGGTTCAGACCCCA 32882	AATTT	_
		TGG TCTGGGCC GAATA		
		ACC AGACTTGG CTTAT		
		CC_ GG		
GAM2559 SDF1	3'	TATTCCTAGAACTTCCA 92520	T	CC
		TGGAA TTTCTGGG GAATA		
		ACCTT AAAGATCC CTTAT		
		C _		
GAM2559 TAO1	5'	TATTCGGGGTTCAGACCCCA 17720	AATTT	_
		TGG TCTGGGCC GAATA		
		ACC AGACTTGG CTTAT		
		CC_ GG		
GAM2559 VMP	3'	GTACCCGGCCACCAGAAAACCC 55765	AA	_ AA
C		GG TTTTCTGG GCCG TAC		
		CC AAAAGACC CGGC ATG		
		CC AC CC		
GAM2559 LOC126295	3'	GTATAATGCTCCAGAAAATTC 74975	_	CGA
		GAATTTTCTGG GC ATAC		
		CTTAAAAGACC CG TATG		
		T TAA		
GAM2559 LOC146184	5'	ATTCAACCAGAAAATTTCA 84596	GCC	
		TGGAATTTTCTGG GAAT		
		ACTTTAAAAGACC CTTA		
		AA_		
GAM2559 LOC150407	3'	GTATTCCAAGAAAATTTCA 80643	GGGCC	
		TGGAATTTTCT GAATAC		

		ACTTTAAAAGA	CTTATG		
		AC__			
GAM2559	LOC154089	3'	TTGACTGAAAATTCCA	81948	T GC
			TGGAATTTTC	GG CGA	
			ACCTTAAAAG	TC GTT	
			_ A_		
GAM2559	LOC221479	3'	GTATGTACAGAAAATTC	93846	GG CGA
			GAATTTTCTG	C ATAC	
			CTTAAAAGAC	G TATG	
			AT__		
GAM2559	LOC91496	5'	TTTGGCAGAAAATGCCA	66813	A GG
			TGG ATTTTCT	GCCGAA	
			ACC TAAAAGA	CGGTTT	
			G__		
GAM2560	ERBB2IP	3'	CTCTTTGTAAATTTTAACTCA	38614	C__ ACC
			TGAGTTAGAAT	CAA AGAG	
			ACTCAATTTTA	GTT TCTC	
			AAT__		
GAM2560	PTHLH	3'	CTCTGGTTTCTACCAGCTCA	12544	__ TCCAA
			TGAGT TAGAA	ACCAGAG	
			ACTCG ATCTT	TGGTCTC	
			ACC__		
GAM2560	FLJ20151	3'	GGCCCTGGATTCTCACTCA	35146	T AA_
			TGAGT AGAATCCA	CC	
			ACTCA TCTTAGGT	GG	
			C CCC		
GAM2560	HEMK	3'	AGCTCTGGTCTGTGCAGACTCA	32949	AGAATC A
			TGAGTT CA	ACCAGAGCT	
			ACTCAG GT	TGGTCTCGA	
			ACGT__	C	
GAM2560	KIAA0800	3'	GCTCTGGCCTGTGACTCA	28805	GAATC AA
			TGAGTTA CA	CCAGAGC	
			ACTCAGT GT	GGTCTCG	
			__ CC		
GAM2560	MAPK8IP3	3'	AGCTCTGGTCCAGTCAAGCCA	54136	A A ATCCAA
			TG GTT GA	ACCAGAGCT	
			AC CGA CT	TGGTCTCGA	
			_ A GACC__		
GAM2560	RHOBTB2	3'	AGCCCTGGTTTCCTGTCACTCA	61594	TA ATCC A
			TGAGT GA	AAACCAG GCT	

		ACTCA CT TTTGGTC CGA		
		__ GTCC C		
GAM2560	SCYA21	5' GCTCTGGCCTCTTACTCA 12979	T	ATCCAAA
		TGAGT AGA CCAGAGC		
		ACTCA TCT GGTCTCG		
		T CC__		
GAM2560	SYNPO2	3' AGCTCTGGTCTGTCAATCTCA 72384	TTA ATC A	
		TGAG GA CA ACCAGAGCT		
		ACTC CT GT TGGTCTCGA		
		TAA __ C		
GAM2560	XP5	3' GCTCTGATTTCTGACTCA 83705	TCCAAAC	
		TGAGTTAGAA CAGAGC		
		ACTCAGTCTT GTCTCG		
		TA__		
GAM2560	LOC133926	3' TGATTTGAATTCTAATTCA 75635	C C	
		TGAGTTAGAAT CAAA CA		
		ACTTAATCTTA GTTT GT		
		A A		
GAM2560	LOC145719	5' AGCTCTGGCTTTTCTCTAACCC 84459	A	ATCCAAA
	G	TG GTTAGA CCAGAGCT		
		GC CAATCT GGTCTCGA		
		C CTTTTC_		
GAM2560	LOC145720	5' AGCTCTGGCTTTTCTCTAACCC 84445	A	ATCCAAA
	G	TG GTTAGA CCAGAGCT		
		GC CAATCT GGTCTCGA		
		C CTTTTC_		
GAM2560	LOC147669	5' CTGCTGGATTCAAACCCA 85182	A A	AAC
		TG GTT GAATCCA CAG		
		AC CAA CTTAGGT GTC		
		C A C_		
GAM2560	LOC150157	5' AGCTCTGGCTCATGGATCTCA 86022	TTAGA	AA__
		TGAG ATCCA CCAGAGCT		
		ACTC TAGGT GGTCTCGA		
		__ ACTC		
GAM2560	LOC170425	3' GCTCCTGGGCCCTAACTCA 76888	AA	AACCA
		TGAGTTAG TCCA GAGC		
		ACTCAATC GGGT CTCG		
		CC C_		
GAM2560	LOC196890	5' AGCTCTGGCTCATGGATCTCA 91224	TTAGA	AA__
		TGAG ATCCA CCAGAGCT		

			ACTC TAGGT GGTCTCGA		
			_____ ACTC		
GAM2560	LOC197114	5'	AGCTCTGGCTTTTCTCTAACCC	91264	A ATCCAAA
	G		TG GTTAGA CCAGAGCT		
			GC CAATCT GGTCTCGA		
			C CTTTTC_		
GAM2560	LOC91010	3'	AGCTCTGGTCTAGATGTATCTA	65222	___ CAA
			TAGA ATC ACCAGAGCT		
			ATCT TAG TGGTCTCGA		
			ATG ATC		
GAM2560	LOC96573	3'	AGCTCTGGTTTGAAAGTAGCCA	63871	A GAATC
			TG GTTA CAAACCAGAGCT		
			AC CGAT GTTTGGTCTCGA		
			_ GAAA_		
GAM2561	D12S2489E	5'	AGTGGATTACATATTCCAA	24760	___
			TTGGAATG AGTCCACT		
			AACCTTAT TTAGGTGA		
			ACA		
GAM2561	FRZB	3'	AGTGGACTTCCTATTA	9397	T ATG
			TAAT GGA AGTCCACT		
			ATTA CCT TCAGGTGA		
			T _____		
GAM2561	GAN	3'	AGTGAGTTCCTCCAGTTA	42118	AT TC
			TAATTGGA GAG CACT		
			ATTGACCT CTT GTGA		
			C_ GA		
GAM2561	HTLF	5'	AGTGAGGGTCTTCCAATTG	10974	T G _
			TAATTGGAA GA TC CACT		
			GTTAACCTT CT GG GTGA		
			_ G A		
GAM2561	KLRC2	5'	AGTGGATTACATATTCCAA	96170	___
			TTGGAATG AGTCCACT		
			AACCTTAT TTAGGTGA		
			ACA		
GAM2561	NOVA1	3'	AGTAGACTCATTTTTTTT	11816	TT C
			AA GGAATGAGTC ACT		
			TT TTTTACTCAG TGA		
			TT A		
GAM2561	NOVA1	3'	AGTAGACTCATTTTTTTT	22418	TT C
			AA GGAATGAGTC ACT		

		TT TTTTACTCAG TGA		
		TT A		
GAM2561	PTGER2	3' AGTGGACTCAGTGGGTTA	8172	GGAA
		TAATT TGAGTCCACT		
		ATTGG ACTCAGGTGA		
		GTG_		
GAM2561	C22orf19	3' AGTGGAAAAAGATTCCAATT	14817	GAG__
		AATTGGAAT TCCACT		
		TTAACCTTA AGGTGA		
		GAAAA		
GAM2561	FLJ10748	5' AGTGGACTCATCAATTG	37094	GA
		TAATTG ATGAGTCCACT		
		GTTAAC TACTCAGGTGA		
		—		
GAM2561	JDD1	3' AGTAGATCCTCTGATTCCAATT	63911	G ____ C
	A	TAATTGGAAT AG TC ACT		
		ATTAACCTTA TC AG TGA		
		G TCCT A		
GAM2561	KIAA0854	5' AGTGTTGGTGCCATTCCAATT	30777	A _____
		AATTGGAATG GT CCACT		
		TTAACCTTAC CG GGTGA		
		_ TGGTT		
GAM2561	NY-REN-41	3' AGTAGACCTAATCCAATTA	55560	A A C
		TAATTGGA TG GTC ACT		
		ATTAACCT AT CAG TGA		
		A C A		
GAM2561	WBSCR22	3' GACTCTGGATTCCAATTG	34468	_____
		TAATTGGAAT GAGTC		
		GTTAACCTTA CTCAG		
		GGT		
GAM2561	ZNF220	3' TGGACCTTTTCCAGTTA	23161	T _
		TAATTGGAA GAG TCCA		
		ATTGACCTT TTC AGGT		
		T C		
GAM2561	LOC166785	5' AGTGTTTTCTCCAGTTA	83549	AT TC
		TAATTGGA GAG CACT		
		ATTGACCT CTT GTGA		
		— TT		
GAM2562	IRS1	3' CCATAGATGGTTCTCAATTGTA	19874	C TGAAC
		TACA ATTGAGAACC ATGG		

		ATGT TAACTCTTGG	TACC	
		— TAGA_		
GAM2562	SERPINF1	3' CCTGTAAGGTTTCAATG	12038	A GA T
		CATTGAGA CCT ACA GG		
		GTAAC TTT GGA TGT CC		
		— A_ —		
GAM2562	HSA243396	3' CCATGTT CAGCAATGTCAATG	37844	GAAC_
		CATTGA CTGAACATGG		
		GTAAC T GACTTGTACC		
		GTAAC		
GAM2562	KIAA1387	3' CAGGAATTTTCAATATGTA	71444	C —
		TACA ATTGAGAA CCTG		
		ATGT TAACTTTT GGAC		
		A AA		
GAM2562	MGC16063	3' TTCAAATTC CAATGTGTA	54930	A CC
		TACACATTG GAA TGAA		
		ATGTGTAAC CTT ACTT		
		— AA		
GAM2562	SMCR8	3' CCATGCTCAGGTTTGACTATGT	59253	TGA_ A
		ACAT GAACCTGA CATGG		
		TGTA TTTGGA CT GTACC		
		TCAG C		
GAM2562	UPLC1	3' CCATGCTAGGCCCAATGT	35227	AGAA AA
		ACATTG CCTG CATGG		
		TGTAAC GGAT GTACC		
		CCC_ C_		
GAM2562	ZNF334	3' CCATAAGTCAACCCTCAATGT	36637	AACC AC_
		ACATTGAG TGA ATGG		
		TGTA ACTC ACT TACC		
		CCA_ GAA		
GAM2562	LOC145082	3' TATGGAATGCCCTTAATGTGTA	84196	AACCTGAA
		TACACATTGAG CATG		
		ATGTGTAATTC GTAT		
		CCGTAAG_		
GAM2562	LOC157723	3' CCAAGTAAGTTCTCAAATGT	82465	_ GA A
		ACATT GAGAACCT AC TGG		
		TGTAA CTCTTGGA TG ACC		
		A A_ A		
GAM2562	LOC219988	5' CCATGTT CGGCCCAATG	93262	AGAAC
		CATTG CTGAACATGG		

		GTAAC GGCTTGTACC CCCC_	
GAM2563	ATP6V0C	3' CCCCAGTAGTTGGTCTTGTA 88658	CTG _ A
		TACAAGATCA ACT CTG GG ATGTTCTGGT TGA GAC CC _ T C	
GAM2563	DLX4	3' GTCCCCAGAACCCTTGGTCTTG 10421	CTGAC A
		CAAGATCA TCTG GGAC GTTCTGGT AGAC CCTG TCCCA C	
GAM2563	MNT	3' TCCTCAGAGGCTGAGCCTGTA 40089	AGA CTGA
		TACA TCA CTCTGAGGA ATGT AGT GAGACTCCT CCG CG_	
GAM2563	TCF2 G	3' GTCCCCAGAACCAGCTGCAGAT 6617	AGAT _ AC A
		CA CA CTG TCTG GGAC GT GT GAC AGAC CCTG AGAC C CA C	
GAM2563	VNN1	3' TCCTCAGAGCAATTCTCTGTA 17423	_ TCAC A
		TACA AGA TG CTCTGAGGA ATGT TCT AC GAGACTCCT C TA_ _	
GAM2563	BMF	5' CCTCAGAGTCAAACCTTTGTG 54280	ATCAC
		TACAAG TGA CTCTGAGG GTGTTT ACTGAGACTCC CAA_	
GAM2563	DDX33	3' GTCCTCAGTGCGTGACCCTGT 39786	AGA T ACT
		ACA TCAC G CTGAGGAC TGT AGTG C GACTCCTG CCC _ GT_	
GAM2563	FLJ20364	3' CCTCAGAGCCATGTATTTG 35528	AT C A
		CAAG CA TG CTCTGAGG GTTT GT AC GAGACTCC AT _ C	
GAM2563	HMGH4	3' TCCTTTCCCCAGTGATTTGTA 22034	A ACTCT
		TACA GATCACTG GAGGA ATGT TTAGTGAC TTCCT _ CCCT_	
GAM2563	KIAA0449	3' TCCCCAGCACTCATGATCTTG 34639	C CT_ A
		CAAGATCA TGA CTG GGA 	

		GTTCTAGT ACT GAC CCT	
		_ CAC C	
GAM2563 KIAA1061	3'	GTCCTCAGAGTGCATTTCTG 71723	A TCAC _
		CA GA TG ACTCTGAGGAC	
		GT CT AC TGAGACTCCTG	
		C TT_ G	
GAM2563 KIAA1535	3'	GTCCTCAGCTCAAGAATCCTGT 80214	A CAC CT
A		TACA GAT TGA CTGAGGAC	
		ATGT CTA ACT GACTCCTG	
		C AGA C_	
GAM2563 LCHN	3'	TCCTCAGAGTATGTCTTG 87478	CACTG
		CAAGAT ACTCTGAGGA	
		GTTCTG TGAGACTCCT	
		TA_	
GAM2563 MAGEH1	3'	TCATAATCTATGATCTTGTA 26772	CT CTC
		TACAAGATCA GA TGA	
		ATGTTCTAGT CT ACT	
		AT AAT	
GAM2563 LOC154789	5'	TCCTCAGAGCTCTCCTGTG 82034	A TCACT _
		TACA GA GA CTCTGAGGA	
		GTGT CT CT GAGACTCCT	
		C _ _ C	
GAM2563 LOC197201	3'	TCCTCAGAAGGTATTTGTA 89289	ATC GAC
		TACAAG ACT TCTGAGGA	
		ATGTTT TGG AGACTCCT	
		A_ A_	
GAM2563 LOC255193	3'	CCTCAGAGTCAGGCCTGTA 97103	AGATCA
		TACA CTGACTCTGAGG	
		ATGT GACTGAGACTCC	
		CCG_	
GAM2563 LOC96597	5'	TCCCCAGAATTCTCTTGT 67468	TCACT C_ A
		ACAAGA GA TCTG GGA	
		TGTTCT CT AGAC CCT	
		_ TA C	
GAM2564 ABCB4	5'	GCAGAGACTGAAGAACTGT 38761	GACCA _
		GCAGTTTCT TC CTGC	
		TGTCAAAGA AG GACG	
		AGTC_ A	
GAM2564 ALX3	3'	GGCAGGGAGACACTGC 22425	T GACCA
		GCAGT TCT TCCTGCC	

			CGTCA AGA GGGACGG		
			C _____		
GAM2564	CYP46	3'	GGCAGGACGAGACTCCTC 22864	C	TGACCA
			GAG AGTTTC TCCTGCC		
			CTC TCAGAG AGGACGG		
			C C_____		
GAM2564	NCOR2	3'	GCAGGATGACCACGCACCTC 21959	CA	TTC AC
			GAG GT TG CATCCTGC		
			CTC CG AC GTAGGACG		
			CA C__ CA		
GAM2564	NOX5	5'	AGGCAGGACGGTACTCCGCTG 44707	TTCTG	A
			CAGT ACC TCCTGCCT		
			GTCG TGG AGGACGGA		
			CCTCA C		
GAM2564	POLR2C	3'	AGGCAGGATAGGTCTTTACTG 12204	TTCT	_
			CAGT GACC ATCCTGCCT		
			GTCA CTGG TAGGACGGA		
			TTT_ A		
GAM2564	DKFZP564J047	3'	CAGTGTTCAGAACTGT 50444	CC	TC
			GCAGTTTCTGA A CTG		
			TGTCAAAGACT T GAC		
			T_ GT		
GAM2564	FLJ20085	3'	GCAGGGATTCCAGAAGCTGC 35008	ACCA	
			GCAGTTTCTG TCCTGC		
			CGTCGAAGAC GGGACG		
			CTTA		
GAM2564	KIAA0193	3'	GCAAGATGATACAGAAAGCTGC 29315	_ AC_	C
	TC		GAGCAGTTT CTG CATC TGC		
			CTCGTCGAA GAC GTAG ACG		
			A ATA A		
GAM2564	KIAA1969	3'	AGGCAGGATAATCACTTGAAC 79471	C__	CC
			GTTT TGA ATCCTGCCT		
			CAAG ACT TAGGACGGA		
			TTC AA		
GAM2564	KIAA1981	3'	AGGCAGGACGGCCCTGATGCTG 89709	T TGA_	A
			CAGT TC CC TCCTGCCT		
			GTCG AG GG AGGACGGA		
			T TCCC C		
GAM2564	MAC30	3'	GCAGGACCAGACCAGAACTGC 63354	ACCA__	
	T		AGCAGTTTCTG TCCTGC		

		TCGTCAAAGAC	AGGACG		
		CAGACC			
GAM2564	NTSR2	3' GCAAAATGACCAGCTGCTT	25635	TTT AC CC	
		GAGCAG CTG CAT TGC			
		TTCGTC GAC GTA ACG			
		___ CA AA			
GAM2564	RHOBTB2	3' GCAGGACGGGAGACAACCTGCTT	61603	_ GA A	
		GAGCAGTT TCT CC TCCTGC			
		TTCGTCAA AGA GG AGGACG			
		C G_ C			
GAM2564	LOC125434	3' AGGCAGGACTTCAGAAAAACCC	74869	CAG_ CCA	
	TC	GAG TTTCTGA TCCTGCCT			
		CTC AAAGACT AGGACGGA			
		CCAA TC_			
GAM2564	LOC126282	3' AGGCAGGATAATCACTTGAAC	74942	C__ CC	
		GTTT TGA ATCCTGCCT			
		CAAG ACT TAGGACGGA			
		TTC AA			
GAM2564	LOC147650	5' GCAGGATAGCGACTGGTC	79019	G T GACC	
		GA CAGTT CT ATCCTGC			
		CT GTCAG GA TAGGACG			
		G C ____			
GAM2564	LOC152283	3' AGGTGGCCAGAAACCGTCC	86863	AG A A T	
		G C GTTTCTG CCA CCT			
		C G CAAAGAC GGT GGA			
		CT C C _			
GAM2564	LOC155006	3' AGGCAAATGACTCAAAACTGCT	82159	C C_ CC	
	C	GAGCAGTTT TGA CAT TGCCT			
		CTCGTCAAA ACT GTA ACGGA			
		_ CA A_			
GAM2564	LOC155036	5' AGACAAGATGGTCAGATTTGTT	87610	TT C C	
		AGCAG TCTGACCATC TG CT			
		TTGTT AGACTGGTAG AC GA			
		T_ A A			
GAM2564	LOC219627	3' AGGCAGGGCTGAAAACCTGC	93797	CTGAC _	
		GCAGTTT CA TCCTGCCT			
		CGTCAAA GT GGGACGGA			
		A__ C			
GAM2564	LOC257464	5' AGGTGGTAGAAAACCTGCTC	91239	A T	
		GAGCAGTTTCTG CCA CCT			

CTCGTCAAAGAT GGT GGA

GAM2564 LOC91445 3' AGGCAGAAAGAGAGAAACTGT 61163 GACCATC
GCAGTTTCT CTGCCT
||||||| |||||
TGTCAAAGA GACGGA
GAGAAA_
GAM2565 SCAMP1 3' GCTAAATAAATATTCTCC 18013 T C
GGA AATATT ATTTAGC
||| ||||| |||||
CCT TTATAA TAAATCG
C A
GAM2565 SCAMP1 3' GCTAAATAAATATTCTCC 54501 T C
GGA AATATT ATTTAGC
||| ||||| |||||
CCT TTATAA TAAATCG
C A
GAM2565 NX-17 3' TGAATATCAGCCCCTAATA 40706 ATA_
TATTAGGG ATATTCA
||||||| |||||
ATAATCCC TATAAGT
CGAC
GAM2565 LOC161589 3' GCTAAATGAATATTATCCCTAA 83159
TA TATTAGGGATAATATTCATTTAGC
|||||||
ATAATCCCTATTATAAGTAAATCG
GAM2566 SCAMP1 3' GCTAAATAAATATTCTCC 54500 T C
GGA AATATT ATTTAGC
||| ||||| |||||
CCT TTATAA TAAATCG
C A
GAM2566 SCAMP1 3' GCTAAATAAATATTCTCC 54501 T C
GGA AATATT ATTTAGC
||| ||||| |||||
CCT TTATAA TAAATCG
C A
GAM2566 NX-17 3' TGAATATCAGCCCCTAATA 40706 ATA_
TATTAGGG ATATTCA
||||||| |||||
ATAATCCC TATAAGT
CGAC
GAM2566 LOC161589 3' GCTAAATGAATATTATCCCTAA 83159
TA TATTAGGGATAATATTCATTTAGC
|||||||
ATAATCCCTATTATAAGTAAATCG
GAM2567 ABH 3' CCCAGACAAGCCAAAAACAGAG 60461 C AA _ _
A TC TTGTTTTT CT GT TGGG
|| ||||| || |||||

		AG GACAAAAA GA CA ACCC	
		A CC A G	
GAM2567 ACE2	3'	CTGAAGTTGAAAACAAGGATA 41728	G TG
		TATCCTTGTTTTTA ACT T G	
		ATAGGAACAAAAGTTGA A C	
		_ GT	
GAM2567 APOB48R	3'	CCCCATCTTTTAAAAACAA 38584	CTGT
		TTGTTTTTAA TGGGG	
		AACAAAAATT ACCCC	
		TTCT	
GAM2567 COL10A1	3'	CCTGCTATGTAAAAACAA 6683	_ TT
		TTGTTTTTAACT TG GGG	
		AACAAAAATTG AT TCC	
		T CG	
GAM2567 GRIA1	3'	CCCTTCAGTGCCAAAAACAA 7710	A__ TT
		TTGTTTTT ACTG GGG	
		AACAAAAA TGAC CCC	
		CCG TT	
GAM2567 PRKCSH	3'	CCCCAACAGCCTCCAAAGATG 12293	C TTTTAA
		TATC TTG CTGTTGGGG	
		GTAG AAC GACAACCCC	
		A CTCC__	
GAM2567 RFPL1	3'	CCCCACTGCAAAAAAACAA 41050	AAC __
		TTGTTTTT TGT TGGGG	
		AACAAAAA ACG ACCCC	
		A__ TC	
GAM2567 TCFL4	3'	CCAACCAAAAACAAGG 64208	AACT
		CCTTGTTTTT GTTGG	
		GGAACAAAAA CAACC	
		C__	
GAM2567 TRAM	3'	CCCATTTTTAAAAACAA 27452	CTGT
		TTGTTTTTAA TGGGG	
		AACAAAAATT ACCCC	
		TT__	
GAM2567 ARHGEF16	5'	CCCGGCCAAAAACAAG 27820	AACT
		CTTGTTTTT GTTGGG	
		GAACAAAAA CGGCCC	
		C__	
GAM2567 ATP6V1B2	3'	CCCTGTAATTA AAAACAAAGA 9884	C C TT
		TC TTGTTTTTAA TG GGG	

			AG AACAAAAATT AT CCC		
			A A GT		
GAM2567	CNOT4	3'	CTAAAACTAAAAACAAGGA 26166	ACTG	
			TCCTTGTTTTTA TTGG		
			AGGAACAAAAAT AATC		
			CAA_		
GAM2567	FLJ23511	3'	CCCTGATTTTCACAAACAAGGAT 50937	TTAACT TG	
	A		TATCCTTGTTT GT GGG		
			ATAGGAACAAA TA CCC		
			CACTT_ GT		
GAM2567	HTEX4	5'	CCGTAGTTAAAAACAA 99563	TTG	
			TTGTTTTTAACTG GG		
			AACAAAAATTGAT CC		
			G_		
GAM2567	HTEX4	5'	CCGTAGTTAAAAACAA 99719	TTG	
			TTGTTTTTAACTG GG		
			AACAAAAATTGAT CC		
			G_		
GAM2567	HTEX4	5'	CCGTAGTTAAAAACAA 93722	TTG	
			TTGTTTTTAACTG GG		
			AACAAAAATTGAT CC		
			G_		
GAM2567	KIAA0152	3'	CCCAGCTGACTGAAAACAAGGA 28969	ACT_	
			TCCTTGTTTTTA GTTGGG		
			AGGAACAAAAGT CGACCC		
			CAGT		
GAM2567	KIAA0416	3'	CCAGCATCAAAAAGCAAAGATA 32089	C AAC	
			TATC TTGTTTTT TGTTGG		
			ATAG AACGAAAA ACGACC		
			A ACT		
GAM2567	KIAA1211	3'	CTAGCTAAAAGCAAG 69469	ACT	
			CTTGTTTTTA GTTGG		
			GAACGAAAAT CGATC		
			—		
GAM2567	PEG10	5'	CCCCAACAACAACAACAA 31201	T AAC	
			TTGTT TT TGTTGGGG		
			AACAA AA ACAACCCC		
			C CA_		
GAM2567	PFDN1	3'	CAAATTATGTTAAAAACAAGGA 12046	TG_	
			TCCTTGTTTTTAAC TTG		

			AGGAACAAAAATTG AAC	
			TATTA	
GAM2567	STATI2	3'	CCTTTAAAGCTAAAGACAAG 15269	A GTT_
			CTTGTTTTTA CT GGG	
			GAACAGAAAT GA TCC	
			C AATT	
GAM2567	STATI2	3'	CCTTTAAAGCTAAAGACAAG 96190	A GTT_
			CTTGTTTTTA CT GGG	
			GAACAGAAAT GA TCC	
			C AATT	
GAM2567	LOC152345	3'	CCCCAACAGTTAGAGACAAGCA 81445	C
	TA		TAT CTTGTTTTTAACTGTTGGGG	
			ATA GAACAGAGATTGACAACCCC	
			C	
GAM2567	LOC157695	3'	CCCCTCACGTAAAAACAAG 87810	AC TT
			CTTGTTTTTA TG GGGG	
			GAACAAAAAT AC CCCC	
			GC T_	
GAM2567	LOC161378	5'	CCCTCTCAGAAAACAAG 83148	TAA TT
			CTTGTTTT CTG GGGG	
			GAACAAAA GAC TCCC	
			___ TC	
GAM2567	LOC220567	3'	CCCCATCTTTTAAAAACAA 92433	CTGT
			TTGTTTTTAA TGGGG	
			AACAAAAATT ACCCC	
			TTCT	
GAM2568	ADAM20	5'	GACAGATGGCTCCATAATGAC 15102	C AACA A
			GTCA TTA AGCCATCT TC	
			CAGT AAT TCGGTAGA AG	
			_ ACC_ C	
GAM2568	CAV3	3'	AGATCATGTTTAAGTGAC 54026	AGCC
			GTCACTTAAACA ATCT	
			CAGTGAATTTGT TAGA	
			AC__	
GAM2568	DRD5	3'	ATGGCTTGTTTCAGTCAC 7682	C TA
			GT ACT AACAAGCCAT	
			CA TGA TTGTTTCGGTA	
			C C_	
GAM2568	EGFL6	3'	GATAGACTTTTGCCTAAGTGGC 31939	AA CCA
			GTCACTTA CAAG TCTATC	

			CGGTGAAT GTTT AGATAG		
			CC TC_		
GAM2568	IFNB1	3'	AGATGCTGTTTAAAGTGAC 10981	A C	
			GTCACCTAAACA GC ATCT		
			CAGTGAATTTGT CG TAGA		
			- -		
GAM2568	NOVA1	3'	GATATGCTTGTTTAAATGA 11818	C C_	
			TCA TTAACAAGC ATC		
			AGT AATTTGTTTCG TAG		
			A TA		
GAM2568	C20orf38	3'	ATAGATGGCTTAAAGT 37628	AAAC	
			ACTT AAGCCATCTAT		
			TGAA TTCGGTAGATA		
			A_		
GAM2568	C8orf4	3'	AGATGGCTGGAGATGAC 39691	_ AAA A	
			GTCA CTT CA GCCATCT		
			CAGT GAG GT CGGTAGA		
			A _ _		
GAM2568	CNNM4	3'	GGATAGATAGCCTGTCTGACTG 39871	C A A C	
	A		TCA TTA ACA GC ATCTATCC		
			AGT AGT TGT CG TAGATAGG		
			C C C A		
GAM2568	DKFZp762E1312	5'	GGACAGATGGCTCCGTGCAAG 37904	AA A_ A	
			CTT AC AGCCATCT TCC		
			GAA TG TCGGTAGA AGG		
			CG CC C		
GAM2568	MSC	3'	GACAGGGTTTTAAGTGAC 76841	CAA AT A	
			GTCACCTAAA GCC CT TC		
			CAGTGAATTT TGG GA AG		
			_ _ C		
GAM2568	PRO1430	3'	AGATGGCTGGAGATGAC 38355	_ AAA A	
			GTCA CTT CA GCCATCT		
			CAGT GAG GT CGGTAGA		
			A _ _		
GAM2568	LOC148183	5'	GGTGACTCACTTGAGTGAC 85266	ACA C	
			GTCACCTAA AG CATC		
			CAGTGAGTT TC GTGG		
			CAC A		
GAM2568	LOC151904	5'	ATGGCCTTGCCTGAGTGAC 81201	AA _	
			GTCACCTA CAAG CCAT		

		CAGTGAGT GTTC GGTA	
		CC C	
GAM2568	LOC204285 3'	GATAGATGCTTCAGGTGAC 91019	AAAC C
		GTCACCTT AAGC ATCTATC	
		CAGTGGA TTCG TAGATAG	
		C__ _	
GAM2568	LOC256586 3'	ATGGTTGCTGTTTAAGTGAT 96617	__
		GTCACCTTAAACA AGCCAT	
		TAGTGAATTTGT TTGGTA	
		CG	
GAM2568	LOC93259 5'	AGATGGCTTGTCCAAGCGGC 72280	A AA
		GTC CTT ACAAGCCATCT	
		CGG GAA TGTTCCGGTAGA	
		C CC	
GAM2569	MTMR2 3'	AAATTAAGCTTTCTACTCCAAG 32907	T A A
	TA	TACTTGG GTA AGA CTTAATTT	
		ATGAACC CAT TTT GAATTAAA	
		T C C	
GAM2569	CD84-H1 3'	AAATTAAGTGACCACCAA 54222	TAAAGA
		TTGGTG ACTTAATTT	
		AACCAC TGAATTAAA	
		CAG__	
GAM2569	KIAA0326 3'	GGGTTCTCCCCACACCAGG 64968	AA__
		CTTGGTGT AGAACTT	
		GGACCACA TCTTGGG	
		CCCC	
GAM2569	KIAA0447 3'	AAATTATATTTCTTTTATACCA 72101	_ CT_
	A	TTGGTGTAAG AA TAATTT	
		AACCATATTTTCTT ATTTAA	
		C TAT	
GAM2569	MGC32104 3'	AAATTAAGTGTACACCAA 59058	A AAC
		TTGGTGTA AG TTAATTT	
		AACCACAT TC AATTAAA	
		G __	
GAM2569	LOC161753 3'	AAATTATTTTCTACACCAA 83171	A CT
		TTGGTGTA AGAA TAATTT	
		AACCACAT TTTT ATTTAA	
		C T_	
GAM2570	AHR 3'	AAACCAAATTTTAATTTTGTGCT 9671	__ C_
	TTT	AAAAGCAAAA TAAA TTGGTTT	

TTTTCGTTTT ATTT AACCAAA
 TA TA
 GAM2570 DXS1283E 3' AAACCATAACAGTTTGCTTTCC 71385 A ATAAACT
 A AAAGCAAA TGGTTT
 | ||||| |||||
 C TTTTCGTTT ACCAAA
 C GACAAT_
 GAM2570 FRK 3' TAAACCAAGTTATTTTTCTTTT 10718 C A
 T AAAAAG AAAATAA CTTGGTTTA
 ||||| ||||| |||||
 TTTTTC TTTTATT GAACCAAAT
 T _
 GAM2570 ITGB1 3' TAAATCTGTTATTTTGCT 11053 ACTT
 AGCAAAATAA GGTTTA
 ||||| |||||
 TCGTTTTATT CTAAAT
 GT_
 GAM2570 MLLT2 3' TAAACCAAGTCCATTTTG 21032 AA
 CAAAAT ACTTGGTTTA
 ||||| |||||
 GTTTTA TGAACCAAAT
 CC
 GAM2570 PCDHB12 3' TAAACCAGTAATCTTGCTTTT 38933 AATAA T
 AAAAGCAA ACT GGTTTA
 ||||| || |||||
 TTTTCGTT TGA CCAAAT
 CTAA_ _
 GAM2570 RALBP1 3' ATAAACCAAAAATCGTCTTTTCT 23269 AT _ _ _
 TTGCTTTT AAAAAGCAAA AA AC TTGGTTTA T
 ||||| || || ||||| |
 TTTTTCGTTT TT TG AACCAAAT A
 CT C CTAA _
 GAM2570 SLC25A12 3' ACTGGCTTAGTTTTGCTTTCC 14919 A A C TG
 A AAAGCAAAAT AA T GT
 | ||||| || | ||
 C TTTTCGTTTG TT G CA
 C A C GT
 GAM2570 SLC6A5 5' AAACCAAGGGCACCTTGCTTT 16139 AATAAA
 AAAGCAA CTTGGTTT
 ||||| |||||
 TTTCGTT GAACCAA
 CCACGG
 GAM2570 SORCS1 3' AGGTTTGCTTTGCTTTT 54676 A
 AAAAAGCAAA TAACTT
 ||||| |||||
 TTTTTCGTTT GTTTGGA
 C
 GAM2570 SPG4 3' TAAGTTTATTTTCTTTT 30811 C
 AAAAAG AAAATAAACTTG
 ||||| |||||

TTTTTC TTTTATTTGAAT

GAM2570 SULT1C1 3' TAAACCAAGTGAGGTGTTCTTT 8323 C A AA_
T AAAAG AA AT ACTTGGTTTA

||||| || || |||||
TTTTTC TT TG TGAACCAAAT
_ G GAG

GAM2570 TRPC5 3' AACCTTTTTGCTTTGCTTTT 25923 A CTT
AAAAGCAAA TAAA GGTT

||||||| ||| |||
TTTTTCGTTT GTTT CCAA
C TT_

GAM2570 AP1GBP1 3' TAAACTGATGTTCTGCTTTTT 24354 A AAC TG
AAAAAGCA AATA T GTTTA

||||||| ||| | |||||
TTTTTCGT TTGT A CAAAT
C _ GT

GAM2570 AP1GBP1 3' TAAACTGATGTTCTGCTTTTT 55441 A AAC TG
AAAAAGCA AATA T GTTTA

||||||| ||| | |||||
TTTTTCGT TTGT A CAAAT
C _ GT

GAM2570 C1orf24 3' TGAGTTTGTTTTGCTTTT 54798
AAAAGCAAAATAAACTTG

|||||||
TTTTTCGTTTTGTTTGAGT

GAM2570 C5orf6 3' AGAATTGGTTCATTTTGCTTT 33946 A TGG
AAAGCAAAAT AACT TTT

||||||| ||| |||
TTTCGTTTTA TTGG AGA
C TTA

GAM2570 DKFZp761O17121 3' AACTATGGTTTCTTTGCTTTTT 51129 AT _
AAAAAGCAAA AACT TGGTT

||||||| |||| |||||
TTTTTCGTTT TTTGG ATCAA
C_ T

GAM2570 ERP70 3' AAATCATGTTGATTTTGCTCTT 96144 A A T
T AAA AGCAAAAT AAC TGGTTT

||| ||||| ||| |||||
TTT TCGTTTTA TTG ACTAAA
C G T

GAM2570 FLJ11017 3' TAAACTGTTTACCTTGCTTTT 37546 AA TT
AAAAGCAA TAAAC GGTTTA

||||||| |||| |||||
TTTTCGTT ATTTG TCAAAT
CC _

GAM2570 FLJ11783 3' TAAATGTGAGTTGATTTTGCTT 46550 A _
TTT AAAAAGCAAAAT AACTTG GTTTA

||||||| ||||| |||||

TTTTTCGTTTTA TTGAGT TAAAT
 G G
 GAM2570 FLJ20297 3' AAACCAAGCCTTTGTTTT 35368 ATAAA
 AAAGCAAA CTTGGTTT
 ||||| |||||
 TTTTGTTT GAACCAAA
 CC__
 GAM2570 FLJ20297 3' AAACCAAGCCTTTGTTTT 36075 ATAAA
 AAAGCAAA CTTGGTTT
 ||||| |||||
 TTTTGTTT GAACCAAA
 CC__
 GAM2570 FLJ22215 3' AAACCAAGTCAATTTTCT 98634 C AA
 AG AAAAT ACTTGGTTT
 || |||| |||||
 TC TTTTA TGAACCAAA
 _ AC
 GAM2570 FLJ22693 3' AGTTGAGTCCAGTTTTGCTTTT 43048 AA_ GG
 T AAAAAGCAAAAT ACTT TT
 ||||| ||||| |||||
 TTTTTCGTTTTG TGAG GA
 ACC TT
 GAM2570 FLJ33069 3' TAAACCAAGTTTTTAATCTT 58969 CAAAAT
 AAG AAACCTTGGTTTA
 || |||||
 TTC TTTGAACCAAAT
 TAATT_
 GAM2570 HELO1 3' AAGTCAATTTTGCTTTTCC 41794 A AA
 A AAAGCAAAAT ACTT
 | ||||| |||||
 C TTTTCGTTTTA TGAA
 C AC
 GAM2570 KIAA0976 3' TCAAACCAAGTCTAGGCTAGCT 30556 AAAA_ A A__C
 TT AAAGC TA ACTTGGTTT A
 |||| || ||||| |
 TTTTCG AT TGAACCAAA T
 ATCGG C C__A
 GAM2570 KIAA1430 3' TAAACCAAGGCTTTATTTTCT 81650 C _
 AG AAAATAAA CTTGGTTTA
 || ||||| |||||
 TC TTTTATTT GAACCAAAT
 _ CG
 GAM2570 KIAA1492 3' ACTGAGTGCTATTTTGCTCTTT 65124 A A_ TG
 AAA AGCAAAATA ACT GT
 || ||||| ||||| |||||
 TTT TCGTTTTAT TGA CA
 C CG GT
 GAM2570 MAP3K3 3' AAGTGTTATTTTGTTTTT 11535 _
 AAAAGCAAAATAA ACTT
 ||||| ||||| |||||

		TTTTTGTTTTATT TGAA	
		G	
GAM2570	MGC4251	3' AGCTGCTGTTTATTTATGCTTT 51465	_ TT_
		TT	
		AAAAAGCA AAATAAAC GGTT	
		TTTTTCGT TTTATTTG TCGA	
		A TCG	
GAM2570	MRF2	5' AAACCAAGAATTTTGT 77026 AAA	
		GCAAAAT CTTGGTTT	
		TGTTTGA GAACCAAA	
		A_	
GAM2570	NUDT12	3' AAACCAAGATTCTCTGCTTTT 49528 AAATAAA	
		AAAAGCA CTTGGTTT	
		TTTTCGT GAACCAAA	
		CTCTTA_	
GAM2570	PCDH10	3' AAGTTGGCTCTATTTTGCTTT 40821	_____
		AAAGCAAAATA AACTT	
		TTTCGTTTTAT TTGAA	
		CTCGG	
GAM2570	PRO1600	5' CATGTTTCTTTTGCTTTT 26875	T T
		AAAAGCAAAA AAAC TG	
		TTTCGTTTTT TTTG AC	
		C T	
GAM2570	PTBP2	3' AGTTTAATTTTGCTTTTT 41329	_
		AAAAAGCAAAAT AACT	
		TTTTTCGTTTTA TTTGA	
		A	
GAM2570	SNRPD1	3' ACTTTTGTTTCTTTTGCTTTTT 23662	T TT_
		AAAAAGCAAAA AAAC GGT	
		TTTTTCGTTTT TTTG TCA	
		C TTT	
GAM2570	TRIP-Br2	3' AATTGTTTTTATTTTGTTTTT 29257	CT
		AAAAAGCAAAATAAA TGGTT	
		TTTTTTGTTTTATTT GTTAA	
		TT	
GAM2570	LOC144305	3' CAATTTTATTTTGCTTTTT 83968	C
		AAAAAGCAAAATAAA TTG	
		TTTTTCGTTTTATTT AAC	
		T	
GAM2570	LOC144438	3' CAAGTTTATTTTGCTTTTT 77324	_ _
		AAAAG CAAAATAAA CTTG	

		TTTTC GTTTTATTT GAAC		
		T T		
GAM2570	LOC145790 3'	AACATGTTTATTTTGTTT 77952	TTG	
		AAGCAAATAAAC GTT		
		TTTGTTTATTTG CAA		
		TA_		
GAM2570	LOC150776 3'	AAACCAAGCCTTTGTTTT 63920	ATAAA	
		AAAGCAA CTTGGTTT		
		TTTTGTT GAACCAA		
		CC__		
GAM2570	LOC221830 3'	GCTATTTTATTTTGCTTTTT 94103	CT	
		AAAAAGCAAAATAAA TGGT		
		TTTTTCGTTTTATTT ATCG		
		T_		
GAM2570	LOC222242 3'	CATGTATTTTGCTTTTT 95952	AACT	
		AAAAAGCAAAATA TG		
		TTTTTCGTTTTAT AC		
		GT__		
GAM2570	LOC253250 3'	CTGGGTTCTTCTGCTTTTT 96358	A TA TG	
		AAAAAGCA AA AACT G		
		TTTTTCGT TT TTGG C		
		C CC GT		
GAM2570	LOC55885 3'	GGCTTTGTTTTGCTTTTT 38443	_	
		AAAAAGCAAAATAAA CT		
		TTTTTCGTTTTGTTT GG		
		C		
GAM2570	LOC92573 5'	AAACCGTGTTTGCTTTGCTTTT 70363	A T	
		AAAAGCAA TAAAC TGGTTT		
		TTTTCGTTT GTTTG GCCAAA		
		C T		
GAM2571	CYFIP2 5'	GACCTGCTTGAAGAGCTTC 73966	_ TGAC	
		GAAGC CTT CAAGCAGGTC		
		CTTCG GAA GTTCGTCCAG		
		A ____		
GAM2571	FUT6 3'	GACCTGCTCCAGAGACCTTC 5637	C_ ACCA	
		GAAG CTTTG AGCAGGTC		
		CTTC GAGAC TCGTCCAG		
		CA CC__		
GAM2571	GPM6A 3'	GTGTGGTCAGAGGCCCTA 19175	AA A	
		TAG GCCTTGACCA GC		

ATC CGGAGACTGGT TG
 CC G
 GAM2571 NR5A2 3' CTGTGAATCAAAGGCTTC 15117 CCAA
 GAAGCCTTTGA GCAG
 ||||| |||
 CTTCGGAAACT TGTC
 AAG_
 GAM2571 PAH 3' GACCTGCTTCATTCAAGCTTC 6063 CT CC_
 GAAGC TTGA AAGCAGGTC
 |||| ||| |||||
 CTTCG AACT TCGTCCAG
 _ TAC
 GAM2571 TXNRD1 3' GACCTGCTCAGCAGTTTCTTCT 13921 CCT ACCA
 AGAAG TTG AGCAGGTC
 |||| ||| |||||
 TCTTC GAC TCGTCCAG
 TTT GAC_
 GAM2571 BAG5 3' ACCTGCTCGGAATTAAGGCTT 18032 _ A
 C GAAGCCTTTGA CC AGCAGGT
 ||||| || |||||
 CTTCGGAAATT GG TCGTCCA
 AA C
 GAM2571 C20orf188 3' ACCCAGGCAAAGGCTTCTG 32218 A AAGCA
 TAGAAGCCTTTG CC GGT
 ||||| || |||
 GTCTTCGGAAAC GG CCA
 _ AC_
 GAM2571 EHM2 3' ACCTGCTTTCTGAGGCTTCTG 39415 T CC
 TAGAAGCCTT GA AAGCAGGT
 ||||| || |||||
 GTCTTCGGAG CT TTCGTCCA
 T _
 GAM2571 FLJ12700 3' GACCTGCTCCAGGCAAGGCCCT 46656 AA T A A_
 A TAG GCCTT G CC AGCAGGTC
 || |||| | || |||||
 ATC CGGAA C GG TCGTCCAG
 C_ _ _ ACC
 GAM2571 FLJ20203 3' GTCTCTGGCCAAGGCTTC 35238 T A A C GT
 GAAGCCTT G CCA G AG C
 ||||| | || | || |
 CTTCGGAA C GGT C TC G
 _ C _ _ TG
 GAM2571 MGC32104 3' ACCTGTTGTCTCTGCCCAAAGG 59062 A AC ____
 CTCCTA TAG AGCCTTTG CA AGCAGGT
 || ||||| || |||||
 ATC TCGGAAAC GT TTGTCCA
 C CC CTCTG
 GAM2571 MGC5566 3' GACCTGCTCATGTCAGCTTCT 44124 CTT CA_
 AGAAGC TGAC AGCAGGTC
 |||| ||| |||||

		TCTTCG ACTG TCGTCCAG	
		___ TAC	
GAM2571	SYNCOILIN 3'	GACCTGCTTAAAAAGATTCTA 48629	GC GACC
		TAGAA CTTT AAGCAGGTC	
		ATCTT GAAA TTCGTCCAG	
		A_ AA_	
GAM2571	UNG2 3'	ACCTGCTTGGTCAGCTGC 41253 CT	
		GC TTGACCAAGCAGGT	
		CG GACTGGTTCGTCCA	
		TC	
GAM2571	LOC115110 3'	GACCTGCTCTGAGAGGCTTC 72177	GAC _
		GAAGCCTTT CA AGCAGGTC	
		CTTCGGAGA GT TCGTCCAG	
		___ C	
GAM2571	LOC157653 5'	ATCTGCAGTTAAAGGCT 82440	CAA
		AGCCTTTGAC GCAGGT	
		TCGGAAATTG CGTCTA	
		A_	
GAM2571	LOC163911 5'	ACCTGTCACTCAAAGGCCCT 88419	AA CCAA
		AG GCCTTTGA GCAGGT	
		TC CGGAAACT TGTCCA	
		CC CAC_	
GAM2571	LOC222662 5'	GACCTGCTTCTAGGCCTC 94413	A TT CCA
		GA GCCT GA AGCAGGTC	
		CT CGGA CT TCGTCCAG	
		C T_ _	
GAM2572	ABP1 5'	GCAGAGCGAACTGGGAGCAGAG 63799	CCGC C
		CTCTGTTCTT CGCTC GC	
		GAGACGAGGG GCGAG CG	
		TCAA A	
GAM2572	AHCY 3'	GGCAACTGAGAAAGAACAGAG 7304	__ _
		CTCTGTTCTT C C GCC	
		GAGACAAGAA G G CGG	
		A A TCAA	
GAM2572	BSN 3'	GGCAGAGGCAAGAGCAGAG 14387	CC G _
		CTCTGTTCTT GCC CT CC	
		GAGACGAGAA CGG GA GG	
		_ A C	
GAM2572	CSE1L 5'	GCGGAGCGGCGGCAGGAGC 62513	_
		GTTCTT CCGCCGCTCCGC	

			CGAGGA GGCGGCGAGGCG	
			C	
GAM2572 EHD4	3'	AGTGGCAAAAAATAGAG	58362	C CC
		CTCTGTT TT GCCGCT		
		GAGATAA AA CGGTGA		
		A AA		
GAM2572 EIF2C1	3'	AGCCCAGCTGAAGAACAGA	25181	C C__
		TCTGTTCTTC GC GCT		
		AGACAAGAAG CG CGA		
		T ACC		
GAM2572 KCNK4	3'	GCGAGCAGCAGAGCAGG	33986	TCC C C
		TCTGTTCT GC GCTC GC		
		GGACGAGA CG CGAG CG		
		__ A A		
GAM2572 MYO1D	3'	GCGGAACAGCCCATCCAGCAGA	72249	CTTCC_ CGC
GT		ACTCTGTT GC TCCGC		
		TGAGACGA CG AGGCG		
		CCTACC ACA		
GAM2572 NUP62	3'	GGCAAAGCAGCACAGTGTGAAT	25650	TTCC__ C CC
AGA		TCTGTTC GC GCT GCC		
		AGATAAG CG CGA CGG		
		TGTGACA A AA		
GAM2572 RABIF	3'	GGCATGTGCAGAAAAACAGAGT	12728	C C C TCC
		ACTCTGTT TTC GC GC GCC		
		TGAGACAA AAG CG TG CGG		
		A A _ TA_		
GAM2572 RAX	3'	GCAGGGGAGGCGGAAAAATAGA	26466	C G _
GT		ACTCTGTT TTCCGCC CTCC GC		
		TGAGATAA AAGGCGG GGGG CG		
		A A A		
GAM2572 RBM10	3'	GGCAGGGAAGGACAGAGT	20247	__
		ACTCTGTTCTTCC GCC		
		TGAGACAGGAAGG CGG		
		GA		
GAM2572 RGS16	3'	GGCAGGGCCCAGGAGAACAAAG	12869	C T GCC C
T		ACT TGTTCT CC GCTC GCC		
		TGA ACAAGA GG CGGG CGG		
		A _ ACC A		
GAM2572 ROM1	3'	GGAACAGCAAAGAACAGAGT	6165	CC CGC
		ACTCTGTTCTT GC TCC		

			TGAGACAAGAA CG AGG		
			A_ ACA		
GAM2572	SLC21A2	3'	GCAAAGCAAGTGATGAAGCAGA 20084	_ TTC	C_ CC
	GT		ACTCTGTT C CGC GCT GC		
			TGAGACGAG G GTG CGA CG		
			A TA_ AA AA		
GAM2572	SMARCA5	5'	AGCCCCGCGGAAGAGCAGA 14588	C__	
			TCTGTTCTTCCGC GCT		
			AGACGAGAAGGCG CGA		
			CCC		
GAM2572	SYNGR1	3'	GGCAGAGCGGCAAGGACAGGG 17507	CC	C
			CTCTGTTCTT GCCGCTC GCC		
			GGGACAGGAA CGGCGAG CGG		
			_ A		
GAM2572	TRAM	5'	AGCAGCTGGGAAGAGCAGA 27451	_ C	
			TCTGTTCTTCC GC GCT		
			AGACGAGAAGG CG CGA		
			GT A		
GAM2572	VAT1	3'	AGCAGGGAAGTACAGAGT 22088	T	GCC
			ACTCTGT CTTCC GCT		
			TGAGACA GAAGG CGA		
			T GA_		
GAM2572	CBX1	3'	AGCAATGGAAAAGAACAGA 23308	_	CC
			TCTGTTCT TCCG GCT		
			AGACAAGA AGGT CGA		
			AA AA		
GAM2572	CDC14A	5'	GGCGGAGCAGCAGCTGCAGCAG 53967	_	TCTTCC C
			CT CTGT GC GCTCCGCC		
			GA GACG CG CGAGGCGG		
			C TCGA_ A		
GAM2572	CDC14A	5'	GGCGGAGCAGCAGCTGCAGCAG 14785	_	TCTTCC C
			CT CTGT GC GCTCCGCC		
			GA GACG CG CGAGGCGG		
			C TCGA_ A		
GAM2572	DKFZp547l224	5'	GATGGGGAAAAAACAGAG 39956	C_	G C
			CTCTGTT TTCC CCG TC		
			GAGACAA AAGG GGT AG		
			AA _ _		
GAM2572	ECE2	3'	GCAGGGAAAAAGGAAGAACAGAG 28732	GCCG	C
	T		ACTCTGTTCTTCC CTC GC		

		TGAGACAAGAAGG GGG CG	
		AAAA A	
GAM2572	FLJ10648 3'	CGAAGCAAACCAAGAACAGAG 36890	CCGCC C
		CTCTGTTCTT GCT CG	
		GAGACAAGAA CGA GC	
		C AAA A	
GAM2572	GRIN3A 3'	GCGGAGCAAGTGCCAAGCAGA 56783	CTTC C_
		TCTGTT CGC GCTCCGC	
		AGACGA GTG CGAGGCG	
		ACC_ AA	
GAM2572	INE1 3'	GCAGGTGTTAGACGAAAGAACA 14757	C CC_ T _
	GA	TCTGTTCTT CG GC CC GC	
		AGACAAGAA GC TG GG CG	
		A AGAT T A	
GAM2572	KIAA0410 3'	GCAGAGCTTAAGAATAGA 29426	CCGCC C
		TCTGTTCTT GCTC GC	
		AGATAAGAA CGAG CG	
		TT_ A	
GAM2572	KIAA0964 5'	GCGGAACGGCAGAGCGGG 30448	TCC C
		TCTGTTCT GCCG TCCGC	
		GGGCGAGA CGGC AGGCG	
		_ A	
GAM2572	KIAA1218 5'	AGCAGCACAAAAGAAACAGAGT 95958	_ CC_ C
		ACTCTGTT CTT GC GCT	
		TGAGACAA GAA CG CGA	
		A AACA A	
GAM2572	KIAA1322 3'	GGCAGCCGAGAAGAACAGA 73112	_ CC _
		TCTGTTCTTC CG GCT CC	
		AGACAAGAAG GC CGA GG	
		A _ C	
GAM2572	KIAA1391 3'	AGTGGAGAAAAACAGAGT 67851	C CG
		ACTCTGTT TTC CCGCT	
		TGAGACAA AAG GGTGA	
		A A_	
GAM2572	MGC13251 3'	AGCAGCCATAGAAAGGACAGA 52134	_ C_ C
		TCTGTTCTT C GC GCT	
		AGACAGGAA G CG CGA	
		A ATAC A	
GAM2572	MYH7B 3'	GGCGGAGCAGCAGGCCAACA 71058	CTT _ C
		TGTT CC GC GCTCCGCC	

			ACAA GG CG CGAGGCGG		
			CC_ A A		
GAM2572	NCOA2	3'	GGCAAGGAGAAGAGCAAAGT 22572	C	CG GCT
			ACT TGTTCCTTC CC CC		
			TGA ACGAGAAG GG GG		
			A A_ AAC		
GAM2572	PTRF	3'	GGCAGTGGGGAAGACAGAG 64242	T G _	
			CTCTGT CTTCC CCGCT CC		
			GAGACA GAAGG GGTGA GG		
			_ _ C		
GAM2572	RHOBTB2	3'	AGCAGGAGGAAAAGCAGAGT 61593	C G _	
			ACTCTGTT TTCC CC GCT		
			TGAGACGA AAGG GG CGA		
			A A A		
GAM2572	TAGAP	3'	AGACTGCAAGGAACAGAGT 55099	CC CG_	
			ACTCTGTTCTT GC CT		
			TGAGACAAGGA CG GA		
			A_ TCA		
GAM2572	VELI1	3'	AGTGTAAGAAGAATAAAGT 17417	C CGC	
			ACT TGTTCCTTC CGCT		
			TGA ATAAGAAG GTGA		
			A AAT		
GAM2572	LOC145783	5'	GCGGAGCGACGGAGACACAG 77949	TC C	
			CTGT TTCCG CGCTCCGC		
			GACA GAGGC GCGAGGCG		
			CA A		
GAM2572	LOC150157	3'	AGCAAATGGAAGAAGAACAGA 86020	_ CC_	
			TCTGTTCT TCCG GCT		
			AGACAAGA AGGT CGA		
			AA AAA		
GAM2572	LOC151516	5'	GGCGGAGCTTCCAGAACAAAG 81068	C TCCGCC	
			CT TGTTCT GCTCCGCC		
			GA ACAAGA CGAGGCGG		
			A CCTT_		
GAM2572	LOC153769	3'	GGCGGAGCAGCATGAGAAAGA 81807	G CC C	
			TCT TTCTT GC GCTCCGCC		
			AGA AAGAG CG CGAGGCGG		
			_ TA A		
GAM2572	LOC161734	3'	GATGGGGAAAAAACAGAG 88467	C_ G C	
			CTCTGTT TTCC CCG TC		

		GAGACAA AAGG GGT AG	
		AA _ _	
GAM2572	LOC167026 5'	GGCGGAGCGGCGGGCGGA 88620	TCTT
		TCTGT CCGCCGCTCCGCC	
		AGGCG GGCGGCGAGGCGG	

GAM2572	LOC196890 3'	AGCAAATGAAAAAGAACAGA 91222	__ CC_
		TCTGTTCT TCCG GCT	
		AGACAAGA AGGT CGA	
		AA AAA	
GAM2572	LOC200731 5'	AGCACTGAAGAACAGAGT 91688	CGCC
		ACTCTGTTCTTC GCT	
		TGAGACAAGAAG CGA	
		TCA_	
GAM2572	LOC221504 5'	CGGAGCGGCGGGGCAGGAG 94020	GTTC
		CTCT TTCCGCCGCTCCG	
		GAGG GGGGCGGCGAGGC	
		AC_	
GAM2572	LOC221663 5'	GCAAGCCCAGAACAGAGT 95463	TCCGCC CC
		ACTCTGTTCT GCT GC	
		TGAGACAAGA CGA CG	
		CC____ AA	
GAM2572	LOC256310 3'	GGCAGAGCAGCGGGAGCAGGAG 98102	GTT C C
		CTCT CTTCCGC GCTC GCC	
		GAGG GAGGGCG CGAG CGG	
		AC_ A A	
GAM2572	LOC51762 3'	GGCCTAGCAAAAAGAACAGA 33708	CCGCC CC
		TCTGTTCTT GCT GCC	
		AGACAAGAA CGA CGG	
		AA____ TC	
GAM2572	LOC91266 5'	GGCTGAGGAAAAACAGAGT 66024	__ C
		ACTCTGT TCTTC GCC	
		TGAGACA AGGAG CGG	
		AAA T	
GAM2573	AQP7 5'	GACAGTCACGGAGGAACAAGAT 8605	A_
	CAA	TTGATCTT TCCTCCGTGACTGTC	
		AACTAGAA AGGAGGCACTGACAG	
		CA	
GAM2573	MMP14 5'	GACTAAGCAGAAGAAAGATCAA 18428	A C C GACT
		TTGATCTT TC TC GT GTC	

		AACTAGAA AG AG CG CAG	
		_ A A AAT_	
GAM2573 KIAA0433	5'	ACAGTCATCATAATATCAA 31498	C CCTCC
		TTGAT TTAT GTGACTGT	
		AACTA AATA TACTGACA	
		T C__	
GAM2573 KIAA1915	5'	GACAGTATTTTAAAAATAAGGT 73667	CCTCCGTG_
	CAA	TTGATCTTAT ACTGTC	
		AACTGGAATA TGACAG	
		AAAATTTTA	
GAM2573 MGC5370	3'	CAGTTGAAAAGATCAA 52193	A CTCCGT
		TTGATCTT TC GACTG	
		AACTAGAA AG TTGAC	
		A _____	
GAM2573 TREX1	5'	GACAGCTGGAGACAGAGATCAA 54382	ATC TGA
		TTGATCTT CTCCG CTGTC	
		AACTAGAG GAGGT GACAG	
		ACA C__	
GAM2573 TREX1	5'	GACAGCTGGAGACAGAGATCAA 54388	ATC TGA
		TTGATCTT CTCCG CTGTC	
		AACTAGAG GAGGT GACAG	
		ACA C__	
GAM2573 LOC127534	3'	ACAGCAGATAAGATCAA 75963	CTCCG A _
		TTGATCTTATC TG CTG T	
		AACTAGAATAG AC GAC A	
		_____ _ T	
GAM2573 LOC150480	5'	GACAGTCACGGAGGAAGAAGAT 61025	A_
	CAA	TTGATCTT TCCTCCGTGACTGTC	
		AACTAGAA AGGAGGCACTGACAG	
		GA	
GAM2573 LOC158279	5'	GACAGTCACAGAGGAACAAGAT 60330	A_ C
	CAA	TTGATCTT TCCTC GTGACTGTC	
		AACTAGAA AGGAG CACTGACAG	
		CA A	
GAM2573 LOC201522	3'	GACCTTCGGGAGAACGAGATCA 89637	ATC G CT
	A	TTGATCTT CTCC TGA GTC	
		AACTAGAG GAGG GCT CAG	
		CAA _ TC	
GAM2573 LOC220864	5'	GACAGTCACAGAGGAACAAGAT 92487	A_ C
	CAA	TTGATCTT TCCTC GTGACTGTC	

			AACTAGAA AGGAG CACTGACAG		
			CA A		
GAM2573	LOC254381	5'	GACAGTCACGACAGCAGACCAA 99328	A	TATCCTC
			TTG TCT CGTGA CTGTC		
			AAC AGA GCACTGACAG		
			C CGACA__		
GAM2574	CYP24	5'	CAGTGCAAGGAGGCACCAA 7595	CACA	
			TTGG TCCTTG CATTG		
			AACC AGGAACGTGAC		
			ACGG		
GAM2574	TEM7	3'	CAGGGCAAGGATGCCCAA 40250	CA	A
			TTGG CATCCTTGC TTG		
			AACC GTAGGAACG GAC		
			C_ G		
GAM2574	UMPK	3'	AATAACAAA CTGTGCCAA 25934	TCC	CA
			TTGGCACA TTG TTGTT		
			AACCGTGT AAC AATAA		
			CAA _		
GAM2574	AKL3L	3'	GGATACTAAGGATGTGCCAA 33269	CAT	
			TTGGCACATCCTTG TGTTC		
			AACCGTGTAGGAAT ATAGG		
			C_		
GAM2574	C3IP1	3'	AGAATAATCAAGGACAACCAA 41575	CACA	C
			TTGG TCCTTG ATTGTTCT		
			AACC AGGAAC TAATAAGA		
			AAC_ _		
GAM2574	CYYR1	3'	AGAACAGAACATGTGCCAA 54758	TCCT	CA
			TTGGCACA TG TTGTTCT		
			AACCGTGT AC GACAAGA		
			_ AA		
GAM2574	DKFZP434L0718	3'	GGAAGCAAGGATGCAACAA 50458	GCA	ATTG
			TTG CATCCTTGC TTCT		
			AAC GTAGGAACG AAGG		
			AAC _		
GAM2574	FLJ10504	3'	AGAACAATAAATATGTGCCA 36678	CC	GC
			TGGCACAT TT ATTGTTCT		
			ACCGTGTA AA TAACAAGA		
			T_ A_		
GAM2574	KIAA0459	3'	TAGAAGCTGCAAAGATGTGCCA 61659	C	TTG
			TGGCACATC TTGCA TTCTA		

			ACCGTGTAG AACGT AAGAT		
			A CG_		
GAM2574	KIAA0620	3'	AGCTGGGCAAGGATTCGCCAA 62808	AC	ATT
			TTGGC ATCCTTGC GTT		
			AACCG TAGGAACG CGA		
			CT GGT		
GAM2574	KIAA1102	3'	AGAAAGTGCAAGACATGCCAA 69580	CATC	G
			TTGGCA CTTGCATT TTCT		
			AACCGT GAACGTGA AAGA		
			ACA_ _		
GAM2574	PL6	3'	CAAGGCAAGGATTTGCCAA 23813	C	A
			TTGGCA ATCCTTGC TTG		
			AACCGT TAGGAACG AAC		
			T G		
GAM2574	ZNF323	3'	AACAGAGGATGATACCAA 48818	CA_	GCAT
			TTGG CATCCTT TGTT		
			AACC GTAGGAG ACAA		
			ATA _		
GAM2574	LOC144266	5'	AGAACAGCCCAGCTGTGCCAA 77264	TCC	CA
			TTGGCACA TTG TTGTTCT		
			AACCGTGT GAC GACAAGA		
			C_ CC		
GAM2574	LOC157860	5'	AACAGGGGATGTTCCAA 87875	C	TGCA
			TTGG ACATCCT TTGTT		
			AACC TGTAGGG GACAA		
			T _		
GAM2574	LOC90918	5'	AGAACAAATGCAAGGAAGTCA 64993	ACA	
			TGGC TCCTTGCATTGTTCT		
			ACTG AGGAACGTAACAAGA		
			A_		
GAM2575	GPD1	3'	TCATGCCACCACATTTG 60398	C	C
			TAAATG GGTGGCAT GA		
			GTTTAC CCACCGTA CT		
			A _		
GAM2575	IL5RA	5'	TCGCATGGCCACCGCATTT 6906	AT_	
			AAATGCGGTGGC CGA		
			TTTACGCCACCG GCT		
			GTAC		
GAM2575	MYO1C	3'	TGCCGATGCCAAATATTTG 61873	CGG	A
			TAAATG TGGCATCG CA		

			GTTTAT ACCGTAGC GT		
			AA_ C		
GAM2575	C6orf37	3'	TGTCACACTGCATTTA 68097	GCATC	
			TAAATGCGGTG GACA		
			ATTTACGTCAC CTGT		
			A____		
GAM2575	DNAJC6	3'	TTGCAGAACCACCGCATT 29498	CA GA	
			AATGCGGTGG TC CAA		
			TTACGCCACC AG GTT		
			A_ AC		
GAM2575	FLJ11210	3'	GTCGATGTGCATGCTTTTA 60319	T GTG	
			TAAA GCG GCATCGAC		
			ATTT CGT TGTAGCTG		
			T ACG		
GAM2575	FLJ12476	3'	TCGATCTTCTGCATTTA 43270	T C	
			TAAATGCGG GG ATCGA		
			ATTTACGTC TC TAGCT		
			T _		
GAM2575	KIAA1034	3'	TCGATGGCATCCGCATTTG 63134	_ G	
			TAAATGCGG TG CATCGA		
			GTTTACGCC AC GTAGCT		
			T G		
GAM2575	KIAA1987	3'	TCATGTAAGTGCATTTA 89391	G C	
			TAAATGCGGT GCAT GA		
			ATTTACGTCA TGTA CT		
			A _		
GAM2575	MGC16063	3'	TGTCCTGGCCACTGCATT 54929	ATC	
			AATGCGGTGGC GACA		
			TTACGTCACCG CTGT		
			GTC		
GAM2575	LOC147949	3'	TGTCAGATGTCCACATTGCA 79279	— — —	
			TGCG GTGG CATC GACA		
			ACGT CACC GTAG CTGT		
			TA T A		
GAM2575	LOC150577	3'	GTCCTCACCGCATTTG 86258	CATC	
			TAAATGCGGTGG GAC		
			GTTTACGCCACT CTG		
			C____		
GAM2575	LOC158219	3'	TGTGTGTCACCACATTT 82694	C CG	
			AAATG GGTGGCAT ACA		

		TTTAC CCACTGTG TGT		
		A _		
GAM2575	LOC202020	3' TGTCTCACCACATTTA	90605	C CATC
		TAAATG GGTGG GACA		
		ATTTAC CCACT CTGT		
		A _		
GAM2575	LOC90826	5' TGTCGATGCAGGTTTATTTG	64788	CGGTG
		TAAATG GCATCGACA		
		GTTTAT CGTAGCTGT		
		TTGGA		
GAM2575	LOC93587	3' TTGTCTTTACCTGCATTTA	73042	_ CATC
		TAAATGC GGTGG GACAA		
		ATTTACG CCATT CTGTT		
		T T _		
GAM2576	CPD	3' GCTTCCTCCCTTGAAA	8951	T A
		TTTCAAGGGA GGAA GT		
		AAAGTTCCCT CCTT CG		
		- -		
GAM2576	D1S155E	5' ACTTTCATCCTTTGAAA	24101	G
		TTTCAAGGGATG AAAGT		
		AAAGTTTCCTAC TTTCA		
		-		
GAM2576	DLG5	3' GGTGACTTTGGCATTCTT	83820	G_
		AGGGATG AAAGTCACC		
		TTCTTAC TTTCAGTGG		
		GG		
GAM2576	FOX E1	3' ACTCTCCCCCTTTCCCTTGAGA	16776	T_ A
		TTTCAAGGGA GGA AGT		
		AGAGTTCCCT CCT TCA		
		TTCCC C		
GAM2576	GABRE	3' GGTGACTTCCTGGGGCCAAGAA	18287	AAG AT_ A
		TTC GG GGAA GTCACC		
		AAG CC CCTT CAGTGG		
		AA_ GGGGT _		
GAM2576	GABRE	3' GGTGACTTCCTGGGGCCAAGAA	42058	AAG AT_ A
		TTC GG GGAA GTCACC		
		AAG CC CCTT CAGTGG		
		AA_ GGGGT _		
GAM2576	GABRE	3' GGTGACTTCCTGGGGCCAAGAA	42062	AAG AT_ A
		TTC GG GGAA GTCACC		

			AAG CC CCTT CAGTGG		
			AA_ GGGGT _		
GAM2576	GABRE	3'	GGTGACTTCCTGGGGCCAAGAA 42074	AAG AT___	A
			TTC GG GGAA GTCACC		
			AAG CC CCTT CAGTGG		
			AA_ GGGGT _		
GAM2576	GALNT2	3'	TGGAAACCATCCTTGAAA 16821	G AAAG	
			TTTCAAGG ATGG TCA		
			AAAGTTCC TACC GGT		
			_ AAA_		
GAM2576	GRINL1A	3'	GGTGACTTTTCATGTGCTTGAAA 70065	GGATG	
			TTTCAAG GAAAGTCACC		
			AAAGTTC CTTTCAGTGG		
			GTGTA		
GAM2576	LUZP1	5'	GACAACTGCCTTTGAAA 54400	A AAA	
			TTTCAAGGG TGG GTC		
			AAAGTTTCC GTC CAG		
			_ AA_		
GAM2576	NT5C3	3'	GGTATCACCATCTCTTGAAA 33661	AAA C	
			TTTCAAGGGATGG GT ACC		
			AAAGTTCTCTACC TA TGG		
			AC_ _		
GAM2576	PITX2	3'	GGCAACTCCGCCCTTGAAA 6158	A AA_	
			TTTCAAGGG TGGG GTC		
			AAAGTTCCC GCCT CGG		
			_ CAA		
GAM2576	SMARCD1	3'	ATTTTCCCTCCCTTGAAA 13259	T	
			TTTCAAGGGA GGAAAGT		
			AAAGTTCCCT CCTTTTA		
			C		
GAM2576	SMARCD1	3'	ATTTTCCCTCCCTTGAAA 58185	T	
			TTTCAAGGGA GGAAAGT		
			AAAGTTCCCT CCTTTTA		
			C		
GAM2576	ZK1	3'	GTACAGTCATCCCTTGA 20575	AAA C	
			TCAAGGGATGG GT AC		
			AGTTCCCTACT CA TG		
			GA_ _		
GAM2576	AFAP	3'	GATGTCCATCCTTGAAA 41608	G AA	
			TTTCAAGG ATGGA GTC		

			AAAGTTCC TACCT TAG		
			— G—		
GAM2576 AKL3L	3'	TGACTTGTTTCCTTTGAAA	33272	TGGA	
		TTTCAAGGGA AAGTCA			
		AAAGTTTCCT TTCAGT			
		TTG—			
GAM2576 ATP10D	3'	GGCATTTCATTCCCTGAAA	73528	A AA	
		TTTCA GGGATGGA GTC			
		AAAGT CCTTACTT CGG			
		C A—			
GAM2576 EPB41L1	3'	TGACTCTCCTTTGAAA	71119	T GAA	
		TTTCAAGGGA G AGTCA			
		AAAGTTTCCT C TCAGT			
		— — —			
GAM2576 FHOD2	5'	GGTAACTTTTGACTTTGAAA	74263	GATG C	
		TTTCAAGG GAAAGT ACC			
		AAAGTTTC TTTTCA TGG			
		AG— A			
GAM2576 FLJ10008	3'	GGCAACCTGTCCCTTGAGA	36191	AAA	
		TTTCAAGGGATGG GTC			
		AGAGTTCCCTGTC CGG			
		CAA			
GAM2576 FLJ12847	3'	GGTGACTTTTCTGATGACTGAA	45078	A GG _	
		TTCA G AT GGAAAGTCACC			
		AAGT C TA TCTTTCAGTGG			
		_AG G			
GAM2576 FLJ20498	3'	TGACCCTCCACTCCTTGAAA	39283	GA AA	
		TTTCAAGG TGGA GTCA			
		AAAGTTCC ACCT CAGT			
		TC CC			
GAM2576 FLJ23323	3'	GATAACCCATTCTGAAA	45386	A AAA	
		TTTCA GGGATGG GTC			
		AAAGT CCTTACC TAG			
		— CAA			
GAM2576 FREQ	3'	GACATCTCCTCCCCTGAAA	27373	A T AA_	
		TTTCA GGGA GGA GTC			
		AAAGT CCCT CCT CAG			
		C _ CTA			
GAM2576 HSNV1	3'	GGTGGGTCAGCCCTTGAAA	34440	ATG AAG	
		TTTCAAGGG GA TCACC			

AAAGTTCCC CT GGTGG
 GA_ G__
 GAM2576 KIAA0285 3' ACTGGTTATCCTTTGAAA 29680 AA
 TTTCAAGGGATGG AGT
 ||||| ||
 AAAGTTTCCTATT TCA
 GG
 GAM2576 KIAA0731 3' GACCTTTCCATCCTTGAAA 67480 G _
 TTTCAAGG ATGGAAAG TC
 ||||| ||||| ||
 AAAGTTCC TACCTTTC AG
 _ C
 GAM2576 KIAA1046 3' GGTGACTTTTCTTTTTTTG 30662 T
 CAAGGGA GGAAAGTCACC
 ||||| ||||| ||
 GTTTTTT TCTTTCAGTGG
 _
 GAM2576 KIAA1160 3' GACACATCTCTTGAAA 40758 GAAA
 TTTCAAGGGATG GTC
 ||||| ||
 AAAGTTCTCTAC CAG
 A__
 GAM2576 KIAA1495 5' GGTTATTTGCACCCCTTGAAA 73567 A G GTC
 TTTCAAGGG TG AAA ACC
 ||||| || || ||
 AAAGTTCCC AC TTT TGG
 C G AT_
 GAM2576 KIAA1755 5' GGTACCCTCCATCCCTCGA 62018 A AA C
 TC AGGGATGGA GT ACC
 || ||||| || ||
 AG TCCCTACCT CA TGG
 C CC _
 GAM2576 NTT73 3' GTGACTTTTAACTTG 36495 GGA
 CAAG TGGAAAGTCAC
 ||| ||||| ||
 GTTC ATTTTTCAGTG
 A__
 GAM2576 P2RXL1 3' CGGTGACCCCCAGCCCAACCC 19560 A_____ AAA ____
 CTTGGAA TTTCAAGGG TGG GTCACC G
 ||||| || ||||| |
 AAGGTTCCC ACC CAGTGG C
 CAACCCG CCC ____
 GAM2576 PRO1600 5' GGCAACCCTATCTCTTGAGA 26878 AAA_
 TTTCAAGGGATGG GTC
 ||||| ||
 AGAGTTCTCTATC CGG
 CCAA
 GAM2576 SLC5A7 3' ACTTCAGTCACTCCCTTGAA 41802 _ A_
 TTCAAGGGA TGG AAGT
 ||||| || |||

		AAGTCCCT ACT TTCA		
		C GAC		
GAM2576	ZNF297B	3' GTGACTTTCTAAATATGAAA 82706	AGGGA	
		TTTCA TGGAAAGTCAC		
		AAAGT ATCTTTCAGTG		
		ATAA_		
GAM2576	ZNF297B	3' GTGACTTTCTAAATATGAAA 26671	AGGGA	
		TTTCA TGGAAAGTCAC		
		AAAGT ATCTTTCAGTG		
		ATAA_		
GAM2576	ZNF313	3' TGACTTTCCAGAAAGTGAGA 38566	AGGGA	
		TTTCA TGGAAAGTCA		
		AGAGT ACCTTTCAGT		
		GAAAG		
GAM2576	LOC121274	3' GACCCCATCCCTAGAAA 74497	A	AAA
		TTTC AGGGATGG GTC		
		AAAG TCCCTACC CAG		
		A C_		
GAM2576	LOC145231	3' GGCTTGTCATCCCTTGA 84253		_
		TCAAGGGATGGA AAGTC		
		AGTCCCTACCT TTCGG		
		G		
GAM2576	LOC146499	5' GGTGACTTTGAAGACTTGGAA 71368	GGATGG	
		TTTCAAG AAAGTCACC		
		AAGGTTT TTTTCAGTGG		
		AGAAG_		
GAM2576	LOC147176	5' GGTGACTTTGAAGACTTGGAA 61148	GGATGG	
		TTTCAAG AAAGTCACC		
		AAGGTTT TTTTCAGTGG		
		AGAAG_		
GAM2576	LOC149837	5' GGCTCCATCCTCTGAAA 85901	AG	AA
		TTTCA GGATGGA GTC		
		AAAGT CCTACCT CGG		
		CT _		
GAM2576	LOC152982	3' TGACTTTCATGTGCTTGAAA 81639	GGATG	
		TTTCAAG GAAAGTCA		
		AAAGTTT CTTTCAGT		
		GTGTA		
GAM2576	LOC160717	5' GGCCCCACCCTTGAAA 83130	A	AAA
		TTTCAAGGG TGG GTC		

	AAAGTTCCC ACC CGG	
	— C—	
GAM2576 LOC196424 3'	GGTGACTTTTATAAGCATGAAA 89057	AGGGATG
	TTTCA GAAAGTCACC	
	AAAGT TTTTCAGTGG	
	ACGAATA	
GAM2576 LOC222237 3'	TGACCTTTCCAGACCTTGAAA 95948	GA —
	TTTCAAGG TGGAAAG TCA	
	AAAGTTCC ACCTTTC AGT	
	AG C	
GAM2576 LOC253336 3'	GTAACCTTCTTCATCCCTTGAA 99181	— C
	TTCAAGGGATG GAAAGT AC	
	AAGTCCCTAC CTTTCA TG	
	TT A	
GAM2576 LOC253675 5'	ACTGACCACCCTTGAAA 98572	A AA
	TTTCAAGGG TGG AGT	
	AAAGTTCCC ACC TCA	
	— AG	
GAM2576 LOC256714 3'	TGACCTTTTCTTCTTTGAAA 98047	T —
	TTTCAAGGGA GGAAAG TCA	
	AAAGTTTCTT CTTTTC AGT	
	— C	
GAM2576 LOC90576 3'	GTACAGTCATCCCTTGA 64078	AAA C
	TCAAGGGATGG GT AC	
	AGTCCCTACT CA TG	
	GA_ _	
GAM2576 LOC96610 5'	GGTGACTTTGAAGACTTGGA 56055	GGATGG
	TTTCAAG AAAGTCACC	
	AAGGTTT TTTTCAGTGG	
	AGAAG_	
GAM2577 BBS4 3'	ATTTGCCCAAAGGGAATCCAGA 53447	G_ G_ A
ACA	TGTTCTGGA CT TTGG CAAAT	
	ACAAGACCT GG AACC GTTTA	
	AA GA C	
GAM2577 CENTD2 3'	CCAACAACTCCAGAACA 31539	C_
	TGTTCTGGAG TGTTGG	
	ACAAGACCTC ACAACC	
	AA	
GAM2577 HAMP 3'	TCCTGCTGCCCCAGAACA 41289	A T T
	TGTTCTGG GC GT GGA	

		ACAAGACC CG CG CCT		
		C T T		
GAM2577	ITGA11	3' TCTGCCGGCCCCCAGGACA 25213	A_	TT
		TGTTCTGG GCTG GGA		
		ACAGGACC CGGC TCT		
		CC CG		
GAM2577	KITLG	3' ATTTGCATGGCTCCAGAA 8023	TGGA	
		TTCTGGAGCTGT CAAAT		
		AAGACCTCGGTA GTTTA		
		C_		
GAM2577	MAPK4	5' CCTGGGCAGCTCCAGATCA 12300	T	_
		TG TCTGGAGCTGTT GG		
		AC AGACCTCGACGG CC		
		T GT		
GAM2577	MGAT2	3' ATTTGTCCAAACAGGACA 11557	GAGCTG	
		TGTTCTG TTGGACAAAT		
		ACAGGAC AACCTGTTTA		
		A_		
GAM2577	PSPHL	5' TTGTCATACAGCTCCAAACA 94499	C	TG
		TGTT TGGAGCTGT GACAA		
		ACAA ACCTCGACA CTGTT		
		_ TA		
GAM2577	TTC3	3' TATTTGTCCAACAACCTGTCAGA 13885	_	C
	ATA	TGTTCTGG AG TGTTGGACAAATA		
		ATAAGACT TC ACAACCTGTTTAT		
		G A		
GAM2577	FLJ14213	3' TGATAACAGCTCCAGAA 46218	GA	
		TTCTGGAGCTGTTG CA		
		AAGACCTCGACAAT GT		
		A_		
GAM2577	H2BFQ	3' TTTAAGAGAACTCCAGGACA 60079	_	G
		TGTTCTGGAG CT TTGGA		
		ACAGGACCTC GA AATTT		
		AA G		
GAM2577	LRG	3' TCCATCCATGCTTCCTAGAACA 54825	_ _ _	T_
		TGTTCT GGA GC TG TGGA		
		ACAAGA CCT CG AC ACCT		
		T T T CT		
GAM2577	NMT2	3' ATTTGTCCATGTAACAGAACA 17852	GA	TGT
		TGTTCTG GC TGACAAAT		

ACAAGAC TG ACCTGTTTA
 AA T__
 GAM2577 NYD-SP21 3' TATTTGTCCAATCTAGATTCAG 51863 G __
 AACA TGTTCTGGA CT GTTGGACAAATA
 ||||| || |||||
 ACAAGACTT GA TAACCTGTTTAT
 A TC
 GAM2577 PSPH 3' TTGTCGTACAGCTCCAAACA 17143 C TG
 TGTT TGGAGCTGT GACAA
 ||| ||||| ||||
 ACAA ACCTCGACA CTGTT
 _ TG
 GAM2577 LOC122258 3' CCACCAGCCTCCGGAACA 59820 _ T
 TGTTCTGGAG CTG TGG
 ||||| ||| |||
 ACAAGGCCTC GAC ACC
 C C
 GAM2577 LOC151826 3' ATTTGTCCAACCTAGCACA 81176 T AGCT
 TGT CTGG GTTGGACAAAT
 ||| ||| |||||
 ACA GATC CAACCTGTTTA
 C ____
 GAM2577 LOC169611 3' TCCAGTGGCAGCTCCAGAA 83663 ____
 TTCTGGAGCTGT TGGA
 ||||| |||
 AAGACCTCGACG ACCT
 GTG
 GAM2577 LOC196746 3' TCAGAGCAGCTCCAAGACA 88903 TC G_
 TGT TGGAGCTGTT GA
 ||| ||||| ||
 ACA ACCTCGACGA CT
 GA GA
 GAM2577 LOC204119 5' TGCCACAACCTCAGAACA 92343 G C T A
 TGTTCTG AG TGT GG CA
 ||||| || ||| ||
 ACAAGAC TC ACA CC GT
 _ A _ _
 GAM2577 LOC253142 5' TTGCTAGGATGCCCCAGAATA 99230 A TG_ A
 TGTTCTGG GC TTGG CAA
 ||||| || ||| |||
 ATAAGACC CG GATC GTT
 C TAG _
 GAM2578 AXL 5' TCCCTGGCCCCTTTAAGAAAG 41894 C GACC TT
 CT TCT GG GGCCAGGGA
 || ||| || |||||
 GA AGA CC CCGGTCCCT
 A ATTT ____
 GAM2578 CASP8AP2 5' CCCTGGGAAACCAGAGAG 25060 GACC GG
 CTCTCT GGTT CCAGGG
 ||||| ||| |||||

			GAGAGA CCAA GGTCCC	
			_____ AG	
GAM2578	CLTA	3'	CCCTGGCATTTCAGAGAGG 10216	CCGGTTG
			CCTCTCTGA GCCAGGG	
			GGAGAGACT CCGTCCC	
			TA_____	
GAM2578	EXO1	3'	CCCTGTCCCCAGTCAGAGA 56116	C TT C
			TCTCTGAC GG GG CAGGG	
			AGAGACTG CC CC GTCCC	
			A _ _ T	
GAM2578	GFAP	3'	CCCCCAGCTGTGGGTACAGAGA 10780	_ _ _ CCA
	GG		CCTCTCTG ACC GGTTGG GGG	
			GGAGAGAC TGG TCGACC CCC	
			A GTG _ _ _	
GAM2578	GSBS	3'	TCCCTGTTGCCAGTTAGAGAGG 92734	C TGGC
			CCTCTCTGAC GGT CAGGGA	
			GGAGAGATTG CCG GTCCCT	
			A TT _ _	
GAM2578	MUC4	5'	TCCCTGGCCCCTTCGGAGA 37884	CC TT
			TCTCTGA GG GGCCAGGGA	
			AGAGGCT CC CCGGTCCCT	
			T _ _ _	
GAM2578	NDRG1	3'	TCCCTGGCCTTGAGTAGA 60313	AC TT
			TCTG CGG GGCCAGGGA	
			AGAT GTT CCGGTCCCT	
			GA _ _	
GAM2578	OTOF	3'	TCCCTGGCTACATGGTCA 17832	GT
			TGACCG TGGCCAGGGA	
			ACTGGT ATCGGTCCCT	
			AC	
GAM2578	PPP2R5B	3'	CCCTGGCCTTGCCAGAGTGG 21796	T GACC T _
			CC CTCT GGT GGCCAGGG	
			GG GAGA CCG CCGTCCC	
			T _ _ _ TT	
GAM2578	PRX	3'	CCCAAGTCCCCCGTCAGAGAG 40891	C TT CA
			CTCTCTGAC GG GGC GGG	
			GAGAGACTG CC CTG CCC	
			C C _ AA	
GAM2578	TGIF	5'	CCCCGGCCGGCTGCCAGAAG 13742	C AC A
			CT TCTG CCGTTGGCC GGG	

			GA AGAC GTCGGCCGG CCC	
			— C— C	
GAM2578	USF2	3'	TCCCCAGCCCTTAGCACAGAGA 14017	ACCGGTT CA
	GG		CCTCTCTG GGC GGA	
			GGAGAGAC CCG CCCT	
			ACGATTC AC	
GAM2578	VDR	3'	CCCTGAAAACCCAGAGAGG 6341	ACC GGC
			CCTCTCTG GGTT CAGGG	
			GGAGAGAC CCAA GTCCC	
			— AA—	
GAM2578	CRA	5'	TCCCCGGATGGAGCCAGAGA 22939	GACC GG— A
			TCTCT GGTT CC GGA	
			AGAGA CCGA GG CCCT	
			— GGTA C	
GAM2578	ESAM	5'	CCCTGACTCCGTCGCGCCAGG 58045	A T— C—
	GAGG		CCTCTCTG CCGG TGG CAGGG	
			GGAGGGAC GGCC GCC GTCCC	
			C CT TCA	
GAM2578	FLJ12783	3'	TCCCTGTTCTCTACTCAGAGAG 49490	CC TT GC
	G		CCTCTCTGA GG G CAGGGA	
			GGAGAGACT CT C GTCCCT	
			CA C— TT	
GAM2578	FLJ20294	3'	CCCCAGCAGCCAGAGGGG 35348	GACC G CA
			CCTCTCT GGTTG C GGG	
			GGGGAGA CCGAC G CCC	
			— — AC	
GAM2578	FLJ22529	3'	TCCCTTTTGCCAGTCAGGGA 45955	C TTG C—
			TCTCTGAC GG GC AGGGA	
			AGGGACTG CC CG TCCCT	
			A — TTT	
GAM2578	HSN44A4A	3'	TCCCTGGCTTAACTCAGAAAG 31736	C CCG —
			CT TCTGA GTTG GCCAGGGA	
			GA AGACT CAAT CGGTCCCT	
			A — T	
GAM2578	KIAA0775	5'	CCCCAAGGCGGCAGAGAGG 28952	A G GGCCA
			CCTCTCTG CCG TT GGG	
			GGAGAGAC GGC GA CCC	
			— G AC—	
GAM2578	KIAA1075	3'	CCCTGGCCTGGACCCAGGAG 62384	T ACC —
			CTC CTG GGTT GGCCAGGG	

		GAG GAC CCAG CCGGTCCC	
		— ——— GT	
GAM2578 KIAA1102	3'	CCCTGGTCTGTGATCAGCAAG 69582	CT C GTT
		CT CTGA CG GGCCAGGG	
		GA GACT GT CTGGTCCC	
		AC A GT_	
GAM2578 KNSL6	3'	TCCCTGGCCCTCCCCAGAGA 23381	ACC TT
		TCTCTG GG GGCCAGGGA	
		AGAGAC CC CCGGTCCCT	
		C_ TC	
GAM2578 LIMK2	3'	CCCTGGCCTTTGGGCCAGGAGG 19922	T A_ TT
		CCTC CTG CCGG GGCCAGGG	
		GGAG GAC GGTT CCGGTCCC	
		_ CG T_	
GAM2578 LLGL2	3'	TCCCTGCCCAACCGGAGAGG 16951	CTGA C_
		CCTCT CCGGTTGG CAGGGA	
		GGAGA GGCCAACC GTCCCT	
		—— CC	
GAM2578 MFN2	3'	CCCTGGCCACTGCCAAGAGA 30224	GAC T
		TCTCT CCGT GGCCAGGG	
		AGAGA GTCA CCGGTCCC	
		ACC _	
GAM2578 MGC10731	5'	CCCCGGGAGAGTCAGAGGG 48843	CGG GG A
		CTCTCTGAC TT CC GGG	
		GGGAGACTG AG GG CCC	
		—— AG C	
GAM2578 MGC15438	5'	TCCCTGGGCAGGGCCAGAGGGG 52852	A GG G
		CCTCTCTG CC TTG CCAGGGA	
		GGGGAGAC GG GAC GGTCCCT	
		C _ G	
GAM2578 MGC4707	3'	CCCAAGACCAGCCAGAGGGG 44362	GACC CCA_
		CCTCTCT GGTTGG GGG	
		GGGGAGA CCGACC CCC	
		—— AGAA	
GAM2578 MGC4832	3'	CCCTGACCTTCTGGCCAGAGAG 59657	A TT C
		CTCTCTG CCGG GG CAGGG	
		GAGAGAC GGTC CC GTCCC	
		C TT A	
GAM2578 NFAT5	5'	CCCCAGCACAAATCAGAGAG 57766	CCGG _ CA
		CTCTCTGA TTG GC GGG	

		GAGAGACT AAC CG CCC	
		_____ A AC	
GAM2578	PIPPIN 3'	CCCTGGCCCCCTTGAGAGAGG 80507	GACC TT
		CCTCTCT GG GGCCAGGG	
		GGAGAGA CC CCGGTCCC	
		GTT_ C_	
GAM2578	SCAMP-4 3'	CCCCGGCCAGTCTGCCAAGAGG 55343	C AC _ A
		CCTCT TG CGG TTGGCC GGG	
		GGAGA AC GTC GACCGG CCC	
		_ C_ T C	
GAM2578	SKB1 3'	CCCTTGCCCATCAGAGAGG 21470	CCGGTT C
		CCTCTCTGA GGC AGGG	
		GGAGAGACT CCG TCCC	
		AC_____ T	
GAM2578	TIMM22 3'	TCCTGTGCCGCGCAGAGAGG 78914	TGACC _
		CCTCTC GGTTGGC CAGGG	
		GGAGAG CCGGCCG GTCCT	
		_____ T	
GAM2578	LOC116113 3'	CCCTGGTCTTGACCAGTAGAG 93833	_ A_ TT
	G	CCTCT CTG CCGG GGCCAGGG	
		GGAGA GAC GGTT CTGGTCCC	
		T CA _	
GAM2578	LOC126520 3'	CCCTGAGGGTCAGAGTGG 75024	T GGTTGGC
		CC CTCTGACC CAGGG	
		GG GAGACTGG GTCCC	
		T GA_____	
GAM2578	LOC144596 3'	TCCCCAGCCCTTAGCACAGAGA 77429	ACCGGTT CA
	GG	CCTCTCTG GGC GGGA	
		GGAGAGAC CCG CCCT	
		ACGATTC AC	
GAM2578	LOC147229 3'	CCCCCAACCCAAGTGTACAGAGA 78918	C_____ CCA
		TCTCTGAC GGTTGG GGG	
		AGAGACTG CCAACC CCC	
		TGAAC _	
GAM2578	LOC150372 3'	TCCCTGACCTGTGGTCAGA 80622	GTT C
		TCTGACCG GG CAGGGA	
		AGACTGGT CC GTCCCT	
		GT_ A	
GAM2578	LOC151438 5'	TCCCTGGCAGGGTGCAGA 86561	_ GGTTG
		TCTG ACC GCCAGGGA	

	AGAC TGG CGGTCCCT	
	G GA__	
GAM2578 LOC158318 3'	CCCCACCAACACCGTCCAGAGA 88102	AC __ CCA
GG	CCTCTCTG CGGT TGG GGG	
	GGAGAGAC GCCA ACC CCC	
	CT CA AC_	
GAM2578 LOC200314 3'	TCCCTGGCCATCTTCAGAGGGG 91603	CC T
	CCTCTCTGA GG TGGCCAGGGA	
	GGGGAGACT TC ACCGGTCCCT	
	__ T	
GAM2578 LOC200868 5'	TCCCTGGCCCTTCCTGAGAGG 92397	TGACC TT_
	CCTCTC GG GGCCAGGGA	
	GGAGAG CC CCGGTCCCT	
	T__ TTC	
GAM2578 LOC203378 5'	TCCCTGGCCCAGCAAACCAAGA 92304	C ACCG _
GG	CCTCT TG GTTGG CCAGGGA	
	GGAGA AC CGACC GGTCCCT	
	_ CAAA C	
GAM2578 LOC90019 3'	CCCTGCGGCCAGCCAGGGAGG 57525	GACC __
	CCTCTCT GGTTGGCC AGGG	
	GGAGGGA CCGACCGG TCCC	
	__ CG	
GAM2578 LOC91308 3'	CCCCGGCCTGTATTTTCAGAGA 66165	CCGGTT_ A
GG	CCTCTCTGA GGCC GGG	
	GGAGAGACT CCGG CCC	
	TTTATGT C	
GAM2578 LOC92558 3'	CCCTGGCCCAGGGTCAAAGGAG 70309	C_ GGTT
	CTCT TGACC GGCCAGGG	
	GAGG ACTGG CCGGTCCC	
	AA GAC_	
GAM2579 CYP8B1 3'	CATAAATATGAAGCAAGC 16532	C_
	GCTTGTTTCATAT GTG	
	CGAACGAAGTATA TAC	
	AA	
GAM2579 MRE11A 3'	TTAATGGCACTGAGAAACATGC 20006	T ATA _
	GC TGTTTC TC GTGCCATTAA	
	CG ACAAAG AG CACGGTAATT	
	T __ T	
GAM2579 CYorf15B 3'	AATGGATTAAGAAACAAGC 51795	A TCGTG
	GCTTGTTTC TA CCATT	

CGAACAAAG AT GGTA
A TA____

GAM2579 FLJ12765 3' GCAATATGAAACCAGC 46280 T CG
GCT GTTTCATAT TGC
||| ||||| |||
CGA CAAAGTATA ACG
C ____

GAM2579 HHGP 3' TTAATGATGTTATGAAACGAGC 39889 T GC
GCTTGTTTCATA CGT CATTAA
||||||| ||| |||||
CGAGCAAAGTAT GTA GTAATT
T ____

GAM2579 MIG2 3' ATGTGCACTAAACAAGC 72857 CATATC _
GCTTGTTT GTGC CAT
||||| ||| |||
CGAACAAA CACG GTA
T____ T

GAM2579 NEUGRIN 5' TGAAACGACAGAAACAAGC 34062 ATA GC
GCTTGTTTC TCGT CA
||||| ||| ||
CGAACAAAG AGCA GT
AC_ AA

GAM2579 PRO2831 5' TAATACATGGCATGAAAAAAGC 38198 G AT CC
GCTT TTTCAT CGTG ATTA
||| ||||| ||| |||||
CGAA AAAGTA GTAC TAAT
A CG A_

GAM2579 LOC90148 3' AATGGATGATAAAACAAGT 62338 CA G
GCTTGTTT TATCGT CCATT
||||| ||||| |||||
TGAACAAA ATAGTA GGTA

GAM2580 BCL7A 3' GTATCCTGGTGGTTCTTACATC 40990 GC TG _ G
GATG AAGAAC CT GGA AC
||| ||||| || ||| ||
CTAC TTCTTG GG CCT TG
A_ GT T A

GAM2580 DISC1 3' GTACCATGCTAAGCCCTTGCCA 38512 AA _ _ AG
T ATGGCAAG CT GC TGG AC
||||| || || ||| ||
TACCGTTC GA CG ACC TG
CC AT T A_

GAM2580 GPR61 5' CCAGCAGCTCTTGCCATT 79658 A
GATGGCAAGA CTGCTGG
||||||| |||||
TTACCGTTCT GACGACC
C

GAM2580 GRM4 3' GTGTCTCCTTTCTGGCTCTTGC 7753 T A CT_
CTC GA GGCAAGA CTG GGAGACAC
|| ||||| ||| |||||

CT CCGTTCT GGT CCTCTGTG
 _ C CTTT
 GAM2580 JPH3 3' GTGTCCCCAGCAGTGAGGGCC 40677 AAGA A
 GGC ACTGCTGG GACAC
 ||| ||||| |||||
 CCG TGACGACC CTGTG
 GGAG C
 GAM2580 KAL1 3' TGTCTCCAGATATTGCCA 5838 GAACTG
 TGGCAA CTGGAGACA
 ||||| |||||
 ACCGTT GACCTCTGT
 ATA__
 GAM2580 PRKR 5' CTTTAGCAGTTCTTCCATC 12346 C
 GATGG AAGAACTGCTGGAG
 ||||| |||||
 CTACC TTCTTGACGATTTTC
 _
 GAM2580 RARRES3 3' TGCCTCCAGCAGCCTGACCCTC 68865 T CA AA A
 GA GG AG CTGCTGGAG CA
 || || ||||| ||
 CT CC TC GACGACCTC GT
 C AG C_ C
 GAM2580 RNASE3 3' GTATCAGCAGTCCTCATCATC 12875 CA A AG
 GATGG AG ACTGCTGG AC
 |||| ||||| ||
 CTA CT TC TGACGACT TG
 AC C A_
 GAM2580 WHSC1L1 3' TGAGACACGCATACAGCCTTTG 35506 AA C_____ GAGA
 CCATC GATGGCAAG CTG TG CA
 ||||| || || ||
 CTACCGTTT GAC AC GT
 CC ATACG__C AGAG
 GAM2580 BZW1 3' GTGTCCTGGTTCTTACATC 28588 GC GCT G
 GATG AAGAACT GGA AC
 ||| ||||| ||| ||
 CTAC TTCTTGG CCT TG
 A_ T_ G
 GAM2580 C20orf150 3' GTGTCTCCCCTGGCCTCGCCTT 66015 T A AACT ____
 C GA GGC AG GCT GGAGACAC
 || ||| || |||||
 CT CCG TC CGG CCTCTGTG
 T C ____ TCC
 GAM2580 C20orf20 3' GTGTGACTCAGTTCTTTCCATC 37392 C CT AG
 GATGG AAGAACTG GG ACAC
 ||||| ||||| || |||
 CTACC TTCTTGAC TC TGTG
 T ____ AG
 GAM2580 CECR2 3' GTGTCCCTTCCTGATTTTGCCA 49439 ACTGCT_ A
 TGGCAAGA GG GACAC
 ||||| || |||||

ACCGTTTT CC CTGTG
 AGTCCTT _
 GAM2580 CNNM4 5' TCTCCAGCAATCTGATCTC 39875 T CA AC
 GA GG AGA TGCTGGAGA
 || || ||| |||||
 CT CT TCT ACGACCTCT
 _ AG A_
 GAM2580 FLJ13448 3' TGTCTCCAGCACTATGCATC 47887 G _ AAC
 GATG CA AG TGCTGGAGACA
 |||| ||| |||||
 CTAC GT TC ACGACCTCTGT
 _ A _
 GAM2580 FLJ20275 3' TCTCCAGCACTAATGTTTCCAT 35309 CAA _
 C GATGG GAAC TGCTGGAGA
 |||| ||| |||||
 CTACC TTTG ACGACCTCT
 _ TAATC
 GAM2580 FLJ21596 3' GTGTCTCTTTGTCCCTGCCTC 46123 T AGA TGCT
 GA GGCA AC GGAGACAC
 || ||| || |||||
 CT CCGT TG TCTCTGTG
 _ CCC TT_
 GAM2580 HSA250839 3' GTTTCAGCAGTCCTCACCA 37853 CA A G
 TGG AG ACTGCTG AGAC
 ||| || ||||| |||
 ACC TC TGACGAC TTTG
 AC C _
 GAM2580 HSU79275 3' GTGTCTCCAACAGCCCTCAGCC 66921 A_ AA C
 GGC AG CTG TGGAGACAC
 ||| || ||| |||||
 CCG TC GAC ACCTCTGTG
 AC CC A
 GAM2580 KCND1 5' GTGTCTCCAAGCCCCCACCATC 18349 CAAGAACT _
 GATGG GCT GGAGACAC
 |||| ||| |||||
 CTACC CGA CCTCTGTG
 ACCCC_ A
 GAM2580 KIAA0172 3' GTGCCTTAGACTCTTGCCAT 65599 ACTG G A
 ATGGCAAGA CTG AG CAC
 ||||||| ||| |||
 TACCGTTCT GAT TC GTG
 CA_ _ C
 GAM2580 KIAA0202 3' TGAGACACACGCCTGTGCTTTG 65009 A_ T_ _ GAGA
 CCATC GATGGCAAG AC GC TG CA
 ||||||| || || |||
 CTACCGTTT TG CG AC GT
 CG TC CA_ C AGAG
 GAM2580 KIAA0712 5' TGTCAATCCAGCAGCTCCCCCA 28867 CAA A _
 TGG GA CTGCTGGA GACA
 ||| || ||||| |||

ACC CT GACGACCT CTGT
 CCC C A
 GAM2580 LGALS8 3' GTGTTCTCAGTCCTTGCCAT 22451 AACT GA
 ATGGCAAG GCTG GACAC
 ||||| ||| ||||
 TACCGTTC TGAC TTGTG
 C__ TC
 GAM2580 MGC16279 5' GTGCCGGCCTCACAGGCCTTGC 52991 AA ____ AG
 CATC GATGGCAAG CT GCTGG AC
 ||||| || |||| ||
 CTACCGTTC GA CGGCC TG
 CG CACTC G_
 GAM2580 MGC16279 5' GTGCCGGCCTCACAGGCCTTGC 52992 AA ____ AG
 CATC GATGGCAAG CT GCTGG AC
 ||||| || |||| ||
 CTACCGTTC GA CGGCC TG
 CG CACTC G_
 GAM2580 MGC16703 5' GTCTCCAGCCCCCTGCCCTC 73496 T AGAACT
 GA GGCA GCTGGAGAC
 || ||| |||||
 CT CCGT CGACCTCTG
 C CCCC_
 GAM2580 moblak 3' TGTCTCCAGCAGCCCGGCCA 56413 AAGAA
 TGGC CTGCTGGAGACA
 ||| |||||
 ACCG GACGACCTCTGT
 GCCC_
 GAM2580 PRO0149 3' GTCCCCAGGCGTTGCCATC 26943 GAAC _ A
 GATGGCAA TGC TGG GAC
 ||||| ||| ||| |||
 CTACCGTT GCG ACC CTG
 ____ G C
 GAM2580 SLC38A1 5' CTCCACATCGCCTTTTGCCA 48423 ACT ____
 TGGCAAGA GC TGGAG
 ||||| || ||||
 ACCGTTTT CG ACCTC
 C__ CTAC
 GAM2580 LOC119582 5' GTCTCCAGCTTCACCATC 76024 CAA CT
 GATGG GAA GCTGGAGAC
 |||| ||| |||||
 CTACC CTT CGACCTCTG
 A__ _
 GAM2580 LOC145801 3' GTGTCTTCAAGCTCCTGCC 77967 A ACT _
 GGCA GA GCT GGAGACAC
 ||| || ||| |||||
 CCGT CT CGA CTTCTGTG
 C ____ A
 GAM2580 LOC145845 3' TGTCTCCATTCTGCCATC 84548 A CTGC
 GATGGCA GAA TGGAGACA
 ||||| ||| |||||

CTACCGT CTT ACCTCTGT
 C ____
 GAM2580 LOC145921 3' TGTCTCCAGCCAGCGCCA 76527 AAGAA _
 TGGC CTG CTGGAGACA
 ||| ||| |||||
 ACCG GAC GACCTCTGT
 C____ C
 GAM2580 LOC145990 3' GTGTCTCCAAGCAGCCAGCCAT 78058 AAGAA _
 C GATGGC CTGCT GGAGACAC
 ||||| ||||| |||||
 CTACCG GACGA CCTCTGTG
 ACC__ A
 GAM2580 LOC150568 5' TCTCCAGCATTCTTGCCA 86228 C
 TGGCAAGAA TGCTGGAGA
 ||||| |||||
 ACCGTTCTT ACGACCTCT
 -
 GAM2580 LOC151579 3' GTGTCCTGGTTCTTACATC 69988 GC GCT G
 GATG AAGAACT GGA AC
 ||| ||||| ||| ||
 CTAC TTCTTGG CCT TG
 A_ T_ G
 GAM2580 LOC152317 3' TGAGACACATGTTACATTCTTG 86839 CTGC_____ GAGA
 CCATC GATGGCAAGAA TG CA
 ||||| || ||
 CTACCGTTCTT AC GT
 ACATTGTA__C AGAG
 GAM2580 LOC157349 5' GTCTCCAGCAGCCCCTGCC 82347 AGAA
 GGCA CTGCTGGAGAC
 ||| |||||
 CCGT GACGACCTCTG
 CCCC
 GAM2580 LOC196483 5' GTGCCGGCCTCACAGGCCTTGC 61026 AA _____ AG
 CATC GATGGCAAG CT GCTGG AC
 ||||| || ||||| ||
 CTACCGTTC GA CGGCC TG
 CG CACTC G_
 GAM2580 LOC200269 3' GTGTCCTCCACATTCTTGCCA 90076 C C _
 TGGCAAGAA TG TGGAG ACAC
 ||||| || ||||| |||
 ACCGTTCTT AC ACCTC TGTG
 - - C
 GAM2580 LOC253502 3' GTGTCCCATGACTTTGCCATC 96223 AACTGC A
 GATGGCAAG TGG GACAC
 ||||| || |||||
 CTACCGTTT ACC CTGTG
 CAGT__ _
 GAM2580 LOC253566 3' TGTCTCCAGCCAGCGCCA 96635 AAGAA _
 TGGC CTG CTGGAGACA
 ||| ||| |||||

ACCG GAC GACCTCTGT
 C____ C
 GAM2580 LOC254428 3' GTGTCCCTGTGGTCTCCAGCCA 97198 AA _ TG T A
 TGGC GA AC C GG GACAC
 |||| || | || ||||
 ACCG CT TG G CC CTGTG
 AC C GT T _
 GAM2580 LOC257295 3' GTGTCTTCAAGCTCCTGCC 96649 A ACT _
 GGCA GA GCT GGAGACAC
 |||| | || |||||
 CCGT CT CGA CTTCTGTG
 C ____ A
 GAM2581 SCA1 3' GCCACGTTGCAGAAAGAGCCAG 6180 A_ ____ TA
 C GC GCTCTTTC GACGTG GC
 || ||||| |||| |
 CG CGAGAAAG TTGCAC CG
 AC ACG _
 GAM2581 SPARC 3' CATTTTCATGAAAAAGCTGCTT 13344 C _ C
 AAGCAGCT TTTC GA GTG
 ||||| || | ||
 TTCGTCTGA AAAG CT TAC
 A TA T
 GAM2581 BOP 5' TGCATATGTCGAAAGAGCTGGC 86231 _ A
 T AGC AGCTCTTTCGACGTGT GCA
 || ||||| ||||| ||
 TCG TCGAGAAAGCTGTATA CGT
 G _
 GAM2581 FLJ12586 3' TGCTAAGATGGAAAGGGCTGCT 45214 GA G_
 T AAGCAGCTCTTTC CGT TAGCA
 ||||| || ||||
 TTCGTCTGGGAAAG GTA ATCGT
 _ GA
 GAM2581 FLJ20139 3' TGCTACAGCTAAAGAGCTG 35123 CGACG
 CAGCTCTTT TGTAGCA
 ||||| |||||
 GTCGAGAAA ACATCGT
 TCG_
 GAM2581 FLJ20209 3' CACTTTGGGTAAGAGCTGCT 86706 _ C
 AGCAGCTCTT TCGA GTG
 ||||| || ||
 TCGTCGAGAA GGTT CAC
 TG T
 GAM2581 FLJ21839 3' GCTACACCAGGGCTGC 41836 TTCGAC
 GCAGCTCT GTGTAGC
 ||||| |||||
 CGTCGGGA CACATCG
 C____
 GAM2581 GOLGIN-67 3' CATCATCAAAGAGCTGCT 96655 C C_
 AGCAGCTCTTT GA GTG
 ||||| || ||

TCGTCGAGAAA CT TAC
_ AC
GAM2581 IRF7 3' GCTACACGGAGGAACTGCTGC 15737 TC GA
GCAGC TTTC CGTGTAGC
||||| ||| |||||
CGTCG AAGG GCACATCG
TC AG
GAM2581 KIAA0643 3' GCCACACAAGTCTTGGCTGCTT 45977 CTTTC _ A
AAGCAGCT GAC GTGT GC
||||| ||| ||| ||
TTCGTCGG CTG CACA CG
TT__ AA C
GAM2581 KIAA0855 3' CATCATCAAAGAGCTGCT 31106 C C_
AGCAGCTCTTT GA GTG
||||||| || |||
TCGTCGAGAAA CT TAC
_ AC
GAM2581 RNB6 3' ACACACCGCAGAGCTGTCC 33398 A TT AC
A GCAGCTCT CG GTGT
| ||||| || |||
C TGTCGAGA GC CACA
C C_ CA
GAM2581 LOC145988 3' CATCATCAAAGAGCTGCT 78062 C C_
AGCAGCTCTTT GA GTG
||||||| || |||
TCGTCGAGAAA CT TAC
_ AC
GAM2581 LOC154282 5' TGCCTGGGGTCTGAAGGAGCTGC 87414 GTGTA
TT AAGCAGCTCTTTCGAC GCA
||||||| |||
TTCGTCGAGGAAGCTG CGT
GGGTC
GAM2581 LOC202460 3' TGCTACATTAAAGAAGCCACT 90681 CA _ CGAC
AG GCT CTTT GTGTAGCA
|| ||| ||| |||||
TC CGA GAAA TACATCGT
AC A T__
GAM2581 LOC254936 3' CATCGTCAAAGAGCTGCT 96650 C _
AGCAGCTCTTT GACG TG
||||||| ||| ||
TCGTCGAGAAA CTGC AC
_ T
GAM2581 LOC56891 5' ACAATTCCGAAGAGCTGC 39686 C CG
GCAGCTCTTT GA TGT
||||||| || |||
CGTCGAGAAG CT ACA
C TA
GAM2582 AQP7 5' GACAGTCACGGAGGAACAAGAT 8605 A_
CAA TTGATCTT TCCTCCGTGACTGTC
||||| |||||

		AACTAGAA AGGAGGCACTGACAG	
		CA	
GAM2582	MMP14	5' GACTAAGCAGAAGAAAGATCAA 18428	A C C GACT
		TTGATCTT TC TC GT GTC	
		AACTAGAA AG AG CG CAG	
		_ A A AAT_	
GAM2582	KIAA0433	5' ACAGTCATCATAATATCAA 31498	C CCTCC
		TTGAT TTAT GTGACTGT	
		AACTA AATA TACTGACA	
		T C_	
GAM2582	KIAA1915	5' GACAGTATTTTAAAAATAAGGT 73667	CCTCCGTG_
	CAA	TTGATCTTAT ACTGTC	
		AACTGGAATA TGACAG	
		AAAATTTTA	
GAM2582	MGC5370	3' CAGTTGAAAAGATCAA 52193	A CTCCGT
		TTGATCTT TC GACTG	
		AACTAGAA AG TTGAC	
		A _	
GAM2582	TREX1	5' GACAGCTGGAGACAGAGATCAA 54382	ATC TGA
		TTGATCTT CTCCG CTGTC	
		AACTAGAG GAGGT GACAG	
		ACA C_	
GAM2582	TREX1	5' GACAGCTGGAGACAGAGATCAA 54388	ATC TGA
		TTGATCTT CTCCG CTGTC	
		AACTAGAG GAGGT GACAG	
		ACA C_	
GAM2582	LOC127534	3' ACAGCAGATAAGATCAA 75963	CTCCG A _
		TTGATCTTATC TG CTG T	
		AACTAGAATAG AC GAC A	
		_ _ T	
GAM2582	LOC150480	5' GACAGTCACGGAGGAAGAAGAT 61025	A_
	CAA	TTGATCTT TCCTCCGTGACTGTC	
		AACTAGAA AGGAGGCACTGACAG	
		GA	
GAM2582	LOC158279	5' GACAGTCACAGAGGAACAAGAT 60330	A_ C
	CAA	TTGATCTT TCCTC GTGACTGTC	
		AACTAGAA AGGAG CACTGACAG	
		CA A	
GAM2582	LOC201522	3' GACCTTCGGGAGAACGAGATCA 89637	ATC G CT
	A	TTGATCTT CTCC TGA GTC	

AACTAGAG GAGG GCT CAG
 CAA _ TC
 GAM2582 LOC220864 5' GACAGTCACAGAGGAACAAGAT 92487 A_ C
 CAA TTGATCTT TCCTC GTGACTGTC
 ||||| ||| |||||
 AACTAGAA AGGAG CACTGACAG
 CA A
 GAM2582 LOC254381 5' GACAGTCACGACAGCAGACCAA 99328 A TATCCTC
 TTG TCT CGT GACTGTC
 ||| ||| |||||
 AAC AGA GCACTGACAG
 C CGACA_
 GAM2583 DKFZp547I224 3' CCCCCACTGTCAACATT 39955 T CCAG C
 AATGTTGACG TGG GG G
 ||||| ||| ||
 TTACAACTGT ACC CC C
 C _ A
 GAM2583 MGC20253 3' ACACCCTGGAAGGTCAACAT 58672 G GG C
 ATGTTGAC TT CCAGGG GT
 ||||| || ||||| ||
 TACAACTG AA GGTCCC CA
 G _ A
 GAM2583 MGC5391 3' TGGCCAACATCCCACTG 52197 A T C
 CA TGT GA GTTGGCCA
 || ||| || |||||
 GT ACA CT CAACCGGT
 C C A
 GAM2583 LOC92912 3' GCAGCCAAGTCAACATCA 71407 A G CAGG
 C ATGTTGAC TTGGC GC
 | ||||| ||||| ||
 A TACAACTG AACCG CG
 C _ A_
 GAM2584 ARHGEF1 3' ACCCCCACCCCCAAGTGCCT 17479 A CA AAG AA
 AG CAC TGGGG GTG GGT
 || ||| |||| ||| |||
 TC GTG ACCCC CAC CCA
 C A_ _ CC
 GAM2584 BSN 3' CCTGCCACCATGGTGTCT 14382 _ A
 AGACACCATGG GG AGG
 ||||| || |||
 TCTGTGGTACC CC TCC
 A G
 GAM2584 CHD4 3' ACCCTCACCTTCCTTCTG 8874 TG A
 CA GGGAAGGTGA GGT
 || ||||| |||
 GT TCCTTCCACT CCA
 CT C
 GAM2584 CTNS 3' ACCTCCACCTTCTCAGATG 18216 G_ A
 CAT GGGAAGGTG AGGT
 || ||||| |||

			GTA CTCTTCCAC TCCA			
			GA C			
GAM2584 DTNB	3'	CCAGCGGTTCTCCCCATGGTGT 53678			_ G AA	
	T	GACACCATGGGGA AG TG GG				
		TTGTGGTACCCCT TT GC CC				
		C G GA				
GAM2584 GATA4	3'	CTTCTCCCCCAGGTGCCT 10772	A A	AAG T		
		AG CACC TGGGG G GAAG				
		TC GTGG ACCCC C CTTC				
		C _ _ _ T				
GAM2584 HNF4A	3'	ACCTTCACCTTCATCCATG 6605		_		
		CATGGG GAAGGTGAAGGT				
		GTACCT CTTCCACTTCCA				
		A				
GAM2584 ITGA3	3'	ACCCCTCCTCCCCCAGTGTC 19731	CA A	TGAA		
		GACAC TGGGG AGG GGT				
		CTGTG ACCCC TCC CCA				
		_ C TCCC				
GAM2584 ITGA3	3'	ACCCCTCCTCCCCCAGTGTC 11027	CA A	TGAA		
		GACAC TGGGG AGG GGT				
		CTGTG ACCCC TCC CCA				
		_ C TCCC				
GAM2584 ITPKB	3'	ACCCCTCTCCCCATGG 11060		_ TGAA		
		CCATGGGGA AGG GGT				
		GGTACCCCT TCC CCA				
		C _ _ _				
GAM2584 NKX3A	3'	TGCCTTCCCCAGGGTGTCT 21618	A			
		AGACACC TGGGGAAGGTG				
		TCTGTGG ACCCCTTCCGT				
		G				
GAM2584 Nrap	3'	ACCTCCACCCTCCTTGG 58320	T AA A			
		CCA GGGG GGTG AGGT				
		GGT CCTC CCAC TCCA				
		T _ C				
GAM2584 Nrap	3'	ACCTCCACCCTCCTTGG 43621	T AA A			
		CCA GGGG GGTG AGGT				
		GGT CCTC CCAC TCCA				
		T _ C				
GAM2584 SEPX1	3'	ACCCTCACCTTCTTTTCTGG 33376	T _ _ A			
		CCA GG GGAAGGTGA GGT				

GGT CC TCTTCCACT CCA
_ TTT C
GAM2584 SLC1A5 3' ACCTCCTGTCCCCATGGT 20065 _ TGA
ACCATGGGGA AGG AGGT
||||||| ||| |||
TGGTACCCCT TCC TCCA
G _
GAM2584 SLC1A5 3' ACCTCCTGTCCCCATGGT 79235 _ TGA
ACCATGGGGA AGG AGGT
||||||| ||| |||
TGGTACCCCT TCC TCCA
G _
GAM2584 TEM8 3' ACCTTCACCCCTGTG 50822 AAG
CATGGGG GTGAAGGT
||||| |||||
GTGTCCC CACTTCCA
_
GAM2584 TM6SF2 3' CCATCATCCCCCATGG 72815 AA A
CCATGGGG GGTGA GG
||||| ||| ||
GGTACCCC CTA CT CC
C_ A
GAM2584 AGPAT1 3' ACCTTCACCTTCCCTCCCAGTG 22168 CAT_
T ACAC GGGGAAGGTGAAGGT
||| |||||
TGTG TCCCTTCCACTTCCA
ACCC
GAM2584 AGPAT1 3' ACCTTCACCTTCCCTCCCAGTG 52198 CAT_
T ACAC GGGGAAGGTGAAGGT
||| |||||
TGTG TCCCTTCCACTTCCA
ACCC
GAM2584 AQP10 3' ACCTTCACCCCTCTCGGGGATGC 55391 A _ ATG A
CT AG CA CC GGGGAAGGTGAAGGT
|| || ||| |||||
TC GT GG CTCT CCACTTCCA
C A GG_ C
GAM2584 ARHF 3' ACCCTCCAGCTCATGGTGTCT 39257 _ A
AGACACCATGG GGA GGT
||||||| ||| |||
TCTGTGGTACT CCT CCA
CGA C
GAM2584 CDC91L1 3' CCCCCACCTTGTGGCTCT 55402 CA GGGG AA
AGA CCAT AAGGTG GG
||| ||| ||||| ||
TCT GGTG TTCCAC CC
C_ _ CC
GAM2584 DKFZp547J036 3' TTGCCTTCCCCCGGTGTC 51125 AT TG
GACACC GGGGAAGG A
||||| ||||| |

CTGTGG CCCCTTCC T
 C_ GT
 GAM2584 DKFZP586B1621 3' ACCCTCACCTTCCCCCGG 32036 AT A
 CC GGGGAAGGTGA GGT
 || ||||| |||
 GG CCCCTTCCACT CCA
 C_ C
 GAM2584 DKFZP727G051 3' ACCTCAGCTCCCACAGTGCCT 70000 A CA GA G A
 AG CAC TGGG AG TGA GGT
 || ||| ||| ||| |||
 TC GTG ACCC TC ACT CCA
 C AC _ G _
 GAM2584 FLJ14810 3' ACCCCCACCCCGTTTCCCTGGT 52695 T _ AA
 G CACCA GGGGAA GGTG GGT
 ||||| ||||| ||| |||
 GTGGT CCCTTT CCAC CCA
 _ GCC CC
 GAM2584 FLJ20374 5' ACCTTCACCTGCTATG 35547 GGA
 CATGG AGGTGAAGGT
 ||||| |||||
 GTATC TCACTTCCA
 G_
 GAM2584 FLJ22671 3' CCCCTTCCCCAGGCATC 46311 CA A TGAA
 GA CC TGGGGAAGG GG
 || || ||||| ||
 CT GG ACCCCTTCC CC
 AC _ C_
 GAM2584 HCA4 3' ACCTTCACCCCTGTG 78037 AA
 CATGGGG GGTGAAGGT
 ||||| |||||
 GTGTCCC CCACTTCCA
 _
 GAM2584 KIAA0217 3' CCTTTACCCCCAGCAGTATCT 67599 C CA_ AAG
 AGA AC TGGGG GTGAAGG
 ||| || ||||| |||||
 TCT TG ACCCC CATTTCC
 A ACG _
 GAM2584 KIAA0240 3' ACCTTCACCCCAGCCACATG 94032 G AA_
 CATG GG GGTGAAGGT
 |||| || |||||
 GTAC CC CCACTTCCA
 A GACC
 GAM2584 KIAA1077 3' ACCTTCACCAAGTTCTGAT 73284 G A_
 AT GGGG GGTGAAGGT
 || ||| |||||
 TA TCTT CCACTTCCA
 G GAA
 GAM2584 KIAA1854 3' CCCCCACCTCGCACTGTCT 72200 CCA G GA AA
 AGACA TG G AGGTG GG
 |||| ||| ||||| ||

TCTGT AC C TCCAC CC
 C__ G__ CC
 GAM2584 MGC2705 5' ACCAGCGTCCCCCATGGCTTCT 52079 CA AA GT AA
 AGA CCATGGGG G G GGT
 ||| ||||| | | |||
 TCT GGTACCCC C C CCA
 TC __ TG GA
 GAM2584 SIRPB1 3' ACCTTCACAAGACCATGATG 21352 C GGAAG
 CA CATGG GTGAAGGT
 || |||| |||||
 GT GTACC CACTTCCA
 A AGAA_
 GAM2584 TRIM4 3' ACCCTCAAGTAGTCCCTGGTGT 53404 T AAGG_ A
 CT AGACACCA GGGG TGA GGT
 ||||| ||| ||| |||
 TCTGTGGT CCCT ACT CCA
 _ GATGA C
 GAM2584 LOC123745 3' ACCTCTCTCCCCATGGTGTTT 76139 AG TGA
 AGACACCATGGGGA G AGGT
 ||||| ||||| | ||||
 TTTGTGGTACCCCT C TCCA
 CT __
 GAM2584 LOC147859 5' ACCTTCACCTCCATCGTG 88516 _ A
 CATGG GGA GGTGAAGGT
 |||| | |||||
 GTGCT CCT CCACTTCCA
 A _
 GAM2584 LOC149461 3' ACCTTCACCTCCCCAGTC 80198 ACCA A
 GAC TGGGGA GGTGAAGGT
 || |||| |||||
 CTG ACCCCT CCACTTCCA
 __ C
 GAM2584 LOC150166 5' CCGACGCTTTCCCCACGG 86036 A AA
 CC TGGGGAAGGTG GG
 || ||||| ||
 GG ACCCCTTTTCGC CC
 C AG
 GAM2584 LOC151162 5' ACCTTACCCCACTGACGTCT 86424 AC _ _
 AGAC CA TGGGG AAGGT
 ||| || |||| ||||
 TCTG GT ACCCC TTCCA
 CA C A
 GAM2584 LOC153792 3' ACCTATTTATCCTCTCCATGAT 61015 C A _
 GTCT AGACA CATGGGGA GGTGA AGGT
 |||| ||||| |||| ||||
 TCTGT GTACCTCT CTATT TCCA
 A C TA
 GAM2584 LOC201158 3' ACCTCCACCTTCTCTGCGTGT 61084 CAT A
 ACAC GGGGAAGGTG AGGT
 ||| ||||| ||||

TGTG TCTCTTCCAC TCCA
 CG_ C
 GAM2584 LOC201736 5' ACCTTCACCTACCAGG 90481 A GGA
 CC TGG AGGTGAAGGT
 || ||| |||||
 GG ACC TCCA CT TCCA
 _ A_

GAM2584 LOC203377 5' ACCTTACCCCACTGACGTCT 92253 AC _ _
 AGAC CA TGGGG AAGGT
 ||| || ||||| |||||
 TCTG GT ACCCC TTCCA
 CA C A

GAM2584 LOC203429 3' CCTGCCGCCCATGGTATCT 90930 C GAA GA
 AGA ACCATGGG GGT AGG
 ||| ||||| ||| |||
 TCT TGGTACCC CCG TCC
 A G_ _

GAM2584 LOC206480 5' ACCCCACGTGCTCCCCATGGCC 92404 CA AG_ AA
 TCT AGA CCATGGGGA GTG GGT
 ||| ||||| ||| |||
 TCT GGTACCCCT CAC CCA
 CC CGTG C_

GAM2584 LOC256158 5' CCTTCACCCTCACC GTCC 99492 C G A
 C ATGG GA GGTGAAGG
 | ||| || |||||
 C TGCC CT CCACTTCC
 C A C

GAM2584 LOC57115 3' GCCTTCCCCTGGTGTCT 40209 T
 AGACACCA GGGGAAGGT
 ||||| |||||
 TCTGTGGT CCCCTTCCG

GAM2584 LOC91049 5' CTTCTCCCCCAGGTGCCT 65372 A A AAG T
 AG CACC TGGGG G GAAG
 || ||| |||| | |||
 TC GTGG ACCCC C CTTC
 C _ _ T

GAM2585 ANPEP 3' GCTCCAGGGCCAGATGAGC 8565 _ AGGGG
 GCTCATTTG C GGAGC
 ||||| | |||||
 CGAGTAGAC G CCTCG
 C GGA_

GAM2585 CLU 3' GCTCCCCCAAGATGAGC 10213 GCA
 GCTCATTT GGGGGGAGC
 ||||| |||||
 CGAGTAGA CCCCCTCG
 A_

GAM2585 F13A1 3' CTCAGCCTTGCAAATAGC 92710 C GG
 GCT ATTTGCAGGG GAG
 ||| ||||| |||

			CGA TAAACGTTCC CTC		
			GA		
GAM2585	HRH2	3'	GCTCCCTTTTAAAAGGAGC 42510	A	GC
			GCTC TTT AGGGGGGAGC		
			CGAG AAA TTTTCCCTCG		
			G A_		
GAM2585	IFNGR2	3'	CTTGACTTTGGCAAATGAGC 19848	_	GG
			GCTCATTTGC AGGG GAG		
			CGAGTAAACG TTTC TTC		
			G AG		
GAM2585	PAK4	3'	TCCAGCCCCTGCAGCAAATGA 20829	___	___
			TCATT TGCAGGGG GGA		
			AGTAA ACGTCCCC CCT		
			ACG GA		
GAM2585	PIM2	3'	CCCAATCCTACAAAGGAGC 60651	A	C ___
			GCTC TTTG AGGG GGG		
			CGAG AAAC TCCT CCC		
			G A AA		
GAM2585	PKHD1	5'	TTTGCTGGGACACAAACGAGT 57721	A	CAGGGGGG
			GCTC TTTG AGCCAAA		
			TGAG AAAC TCGGTTT		
			C ACAGGG_		
GAM2585	PLAT	3'	CTCCTCAAAAGCAAATGAG 53395	AGG_	
			CTCATTTGC GGGGAG		
			GAGTAAACG CTCCTC		
			AAAA		
GAM2585	RAI2	3'	TTTGACTTTTCACAAATGAGT 41717	CAGG	GG C
			GCTCATTTG G GAG CAAA		
			TGAGTAAAC C TTC GTTT		
			A__ TT A		
GAM2585	TGFB3	3'	GGCTCCGGGCAAATGGC 13719	T	AGGGG
			GC CATTTGC GGAGCC		
			CG GTAAACG CCTCGG		
			_ GG__		
GAM2585	BTN2A2	3'	TCCAGCCTACAGATGAGC 23771	C	GG
			GCTCATTTG AGG GGA		
			CGAGTAGAC TCC CCT		
			A GA		
GAM2585	C20orf72	5'	TTCGACCGTTGCAAATAG 54609	C	G G_
			CT ATTTGCAG GG GAG		

			GA TAAACGTT CC CTT		
			— G AG		
GAM2585	C6orf37	3'	CTAACTCTTGACAAATGAGT 68092	—	GG
			GCTCATTTG CAGGGG AG		
			TGAGTAAAC GTTCTC TC		
			A AA		
GAM2585	DOC2A	3'	GCTAGTCCCTGCAAATATGC 14563	TC	GG
			GC ATTTGCAGGGG AGC		
			CG TAAACGTCCCT TCG		
			TA GA		
GAM2585	FADS1	3'	GCTCCATAAGCAAGTGAGC 26382		AGGGG
			GCTCATTTGC GGAGC		
			CGAGTGAACG CCTCG		
			AATA_		
GAM2585	FLJ20413	3'	CTCAATCCCTGCAAATGA 35595		G_
			TCATTTGCAGGGG GAG		
			AGTAAACGTCCCT CTC		
			AA		
GAM2585	HTATIP2	3'	CTTATGACCGTGCAAATGAGC 22167		G GG_
			GCTCATTTGCA GG GAG		
			CGAGTAAACGT CC TTC		
			G AGTA		
GAM2585	KIAA1423	3'	CCCAACCCACTAAATGAGC 62392		CA _
			GCTCATTTG GGG GGG		
			CGAGTAAAT CCC CCC		
			CA AA		
GAM2585	MFN1	3'	TTCAACTTGAAAATGAGC 54322	G	GG
			GCTCATTT CAGG GGA		
			CGAGTAAA GTTC CTT		
			A AA		
GAM2585	MGC15619	3'	GCCTTAATTGAAAATGAGC 51402	G	GG A
			GCTCATTT CAG GGG GC		
			CGAGTAAA GTT TTC CG		
			A AA _		
GAM2585	MGEA6	5'	GCTCCCCCGCAGCCGGC 21013	CAT	A
			GCT TTGC GGGGGGAGC		
			CGG GACG CCCCCCTCG		
			CC_ _		
GAM2585	NMT1	3'	GCTCCCCTTCTGAATCAGC 41147	C	TG _
			GCT ATT CAGG GGGGAGC		

CGA TAA GTCT CCCCTCG
C _ T
GAM2585 P114-RHO-GEF 3' CTCAGCCCCCGGGAAATGAGC 31669 GCA _
GCTCATTT GGGGG GAG
||||||| ||||| |||
CGAGTAAA CCCCC CTC
GGG GA
GAM2585 TRPV5 5' CTCAGCTCTGCAAAGAGC 39522 A GG
GCTC TTTGCAGGG GAG
||||| ||||| |||
CGAG AAACGTCTC CTC
_ GA
GAM2585 LOC126961 3' GGCTCCCCCGCGCGTGA 75121 T A
TCAT TGC GGGGGGAGCC
||||| ||||| |||
AGTG GCG CCCCCCTCGG
C _
GAM2585 LOC143915 3' CTCCCCTCGGGCAACAAGC 83906 CAT A_
GCT TTGC GGGGGGAG
||| ||| |||||
CGA AACG CTCCCCTC
AC_ GG
GAM2585 LOC145623 5' TTGGCAGCTCCAGCAAATGAGC 84398 AG GA
GCTCATTTGC GGGG GCCAA
||||||| ||| |||||
CGAGTAAACG CCTC CGGTT
A_ GA
GAM2585 LOC146268 3' CCCGGAATCTGCAAATGAGC 78335 _____
GCTCATTTGCAGG GGG
||||||| |||
CGAGTAAACGTCT CCC
AAGGG
GAM2585 LOC148887 3' GGCTCCCCCGCATGCGC 85405 T TT AG
GC CA TGC GGGGGGAGCC
||| ||| |||||
CG GT ACG CCCCCTCGG
C _ _
GAM2585 LOC207043 3' GCTCCCCCGGGTATCAGC 91078 CATT A_
GCT TGC GGGGGGAGC
||| ||| |||||
CGA ATG CCCCCCTCG
CT_ GG
GAM2585 LOC253786 5' TTAACTTTGTCAAATGAGC 98836 GG
GCTCATTTGCAGGGG AG
||||||| |||
CGAGTAAACGTTTTC TT
AA
GAM2585 LOC253974 3' TTTGGCTCCCCCTGCAAATGA 99286
GC GCTCATTTGCAGGGGGGAGCCAAA
|||||||

CGAGTAAACGTCCCCCTCGGTTT

GAM2585 LOC256905 3' TCCATGTCCCTGCAAATGA 98663 ____
TCATTTGCAGGGG GGA
||||||| |||
AGTAAACGTCCCT CCT
GTA

GAM2585 LOC257395 3' GGCTCCCCCGCGCGTGA 97149 T A
TCAT TGC GGGGGGAGCC
||| ||| |||||
AGTG GCG CCCCCCTCGG
C _

GAM2585 LOC90233 3' CCCAGGTCCTGCAAAGGAGC 57193 A ____
GCTC TTTGCAGGG GGG
||| ||||| |||
CGAG AAACGTCCT CCC
G GGA

GAM2586 FLJ21438 5' CAAAACGCTTCCCCCATCCCA 62190 GAGATTATC
TGGGA AAGCGTTTGT
||| |||||
ACCCT TTCGCAAAAC
ACCCCC__

GAM2586 FLJ32334 3' AAAACGCTATTCCTTCCCA 58605 A TTATCA
TGGGAG GA AGCGTTTT
||| || |||||
ACCCTT CT TCGCAAAA
C TA__

GAM2586 HHLA2 3' CAATGTACTTTGTAATCTCCCC 23953 A C CG T
CA TGGG GAGATTAT AAG T TTG
||| ||||| ||| |||
ACCC CTCTAATG TTC G AAC
C T ATT

GAM2587 ADAT1 3' CCAGCAAAGAATGAAGGC 24914 _ C
GTC CATTCTTTGC GG
|| ||||| ||
CGG GTAAGAAACG CC
AA A

GAM2587 M17S2 5' CCGGTAGCGGACGGTCCTT 20910 ATTCT
AAGGACCGTCC TTGCCGG
||| ||| |||||
TTCCTGGCAGG GATGGCC
C__

GAM2587 ST14 5' CCGGCAGGGACGACGCCT 42042 AC CAT
AGG CGTC TCTTTGCCGG
|| ||| |||||
TCC GCAG AGGGACGGCC
_ C_

GAM2587 HTGN29 5' GCCAACTGTGTGGCGGTCC 39885 _ TC T
GGACCGTC CAT TT GC
||| ||| || ||

CCTGGCGG GTG AA CG
 T TC C
 GAM2587 PMAIP1 3' GCAAGAATGGAAGACCCTT 41211 ACCG T
 AAGG TCCATTCTT GC
 ||| ||||| ||
 TTCC AGGTAAGAA CG
 CAGA _
 GAM2587 LOC144278 3' GCCAGCAAAGACTGCTCGATGG 77274 _ T C
 TCCT AGGACCGTC CA TCTTTGC GGC
 ||||| || ||||| |||
 TCCTGGTAG GT AGAAACG CCG
 CTC C A
 GAM2587 LOC147976 3' CCGGTGAATGAAGACCCT 79287 ACC CA _ TG
 AGG GTC TTC TT CCGG
 || || ||| || |||
 TCC CAG AAG AA GGCC
 _ _ T GT
 GAM2587 LOC254263 5' GCCGGCAGCGGACGCGCC 96367 AC ATTCT
 GG CGTCC TTGCCGGC
 || ||| |||||
 CC GCAGG GACGGCCG
 GC C_
 GAM2588 ADCY8 5' GCTCACAGCGCTGCGGCTCCT 8501 A AT CAA
 AGGA CC GGC CTGTGAGC
 ||| || || |||||
 TCCT GG TCG GACACTCG
 C CG C_
 GAM2588 CIT 5' GCTCACAGAGCTACAGCTCTCC 70304 ACCA_ CAA
 GGA TGGC CTGTGAGC
 || ||| |||||
 CCT ATCG GACACTCG
 CTCGAC A_
 GAM2588 FAAH 5' GCGGTCTCCGGCCATGGCCCC 44452 AA A_
 GG CCATGGCC ACTGT
 || ||||| |||
 CC GGTACCGG TGGCG
 CC CCTC
 GAM2588 GSTM3 5' GCTCACAGTTTCCCTAGTCCT 68638 ACCAT CC
 AGGA GG AACTGTGAGC
 ||| || |||||
 TCCT CC TTGACACTCG
 GAT_ CT
 GAM2588 HMX1 3' GCGGTGCGCCATGGCC 38947 AA A
 GG CCATGGCC ACTGT
 || ||||| |||
 CC GGTACCGG TGGCG
 _ C
 GAM2588 HSD11B2 3' GCTCCGTGAGCCTTGGTTCCT 5771 T CA T T
 AGGAACCA GGC AC G GAGC
 ||||| || || |||

TCCTTGGT CCG TG C CTCG
 T AG __
 GAM2588 HYAL1 5' CTCCAGTGGCCATGCTCC 24603 AC A T
 GGA CATGGCCA CTG GAG
 ||| ||||| ||| |||
 CCT GTACCGGT GAC CTC
 C_ _ _
 GAM2588 MAT1A 3' TGGTGGCCATGCTCCT 92507 AC A
 AGGA CATGGCCA CTG
 |||| ||||| |||
 TCCT GTACCGGT GGT
 C_ _
 GAM2588 NPTX2 3' GCTGGAGTGGCCATGTCCCTT 94085 AAC A G G
 AAGG CATGGCCA CT T AGC
 |||| ||||| ||| |||
 TTCC GTACCGGT GA G TCG
 CT_ _ G_
 GAM2588 RFX2 3' GCCCCACCAGACCATGGGTTCC 7158 _ CCAA _ A_
 TT AAGGAACC ATGG CTG TG GC
 ||||| |||| ||| |||
 TTCCTTGG TACC GAC AC CG
 G A__ C CC
 GAM2588 SMAP 5' GCCCCACAGAGCCATGGTCC 22932 A CAA A_
 GGA CCATGGC CTGTG GC
 ||| ||||| |||| |||
 CCT GGTACCG GACAC CG
 _ A__ CC
 GAM2588 SMURF1 3' GCTCACAGCCCTGAGCTCTTT 94049 AC_ T CAAC
 AAGGA CA GGC TGTGAGC
 |||| || ||| |||||
 TTTCT GT CCG ACACTCG
 CGA C ____
 GAM2588 SORCS2 3' CAGTGCCCATGGTTCCT 40798 CCA
 AGGAACCATGG ACTG
 ||||| ||||| |||||
 TCCTTGGTACC TGAC
 CG_
 GAM2588 DC-TM4F2 3' ACTGTTGGCCAGGGCTCCT 48895 A A T
 AGGA CC TGGCCAAC GT
 |||| || ||||| |||
 TCCT GG ACCGGTTG CA
 C G T
 GAM2588 DKFZp566H0824 5' GCTCACAAACCCCATAGTTGCC 34488 _ C CCAAC
 T AGG AAC ATGG TGTGAGC
 ||| ||| |||| |||||
 TCC TTG TACC ACACTCG
 G A CCAA_
 GAM2588 FLJ10292 3' GCCCACAGTTGTTGGTTGTTCC 36432 C GGC A
 T AGGAAC AT CAACTGTG GC
 ||||| || ||||| |||

			TCCTTG TG GTTGACAC CG		
			T GTT C		
GAM2588	FLJ20085	3'	GCTCATGGTGCCACAGCCCCT 35009	AACCA	CA
			AGG TGGC ACTGTGAGC		
			TCC ACCG TGGTACTCG		
			CCGAC _		
GAM2588	FLJ22690	3'	GCTCACAGCCGACCTGTGGCCT 45575	AA	CCAA_
			AGG CCATGG CTGTGAGC		
			TCC GGTGTC GACACTCG		
			_ CAGCC		
GAM2588	FLJ32449	3'	GCATTTGGCCATGGTTCCTT 59378		C
			AAGGAACCATGGCCAA TGT		
			TTCCTTGGTACCGGTT ACG		
			T		
GAM2588	HPIP	3'	GCTCACAGCTGCCTTGGCCCC 40425	AA T	CAA
			GG CCA GGC CTGTGAGC		
			CC GGT CCG GACACTCG		
			CC T TC_		
GAM2588	ILF3	3'	GCTCACAGTCGAAGTACAGCTC 16924	ACCA	CCA_
	C		GGA TGG ACTGTGAGC		
			CCT ATC TGACACTCG		
			CGAC AAGC		
GAM2588	KIAA1190	3'	GCTCACAGAGCACCCAGTTCC 71651	CAT	CCAA
	T		AGGAAC GG CTGTGAGC		
			TCCTTG CC GACACTCG		
			ACC ACGA		
GAM2588	MGC11266	3'	GCTCACAGTGGTCAGGGCCC 44488	AA A	A
			GG CC TGGCCA CTGTGAGC		
			CC GG ACTGGT GACACTCG		
			CG _ _		
GAM2588	MGC11352	5'	ACTGTTGGCCAGGGCTCCT 65424	A A	T
			AGGA CC TGGCCAAC GT		
			TCCT GG ACCGGTTG CA		
			C G T		
GAM2588	MGC5590	3'	CACAACTTTGGTTTCTT 44149	T	CCAAC
			AAGGAACCA GG TGTG		
			TTCTTTGGT TC ACAC		
			T A_		
GAM2588	MKP-7	3'	GCTTCTCTTGGCCATGGTCCC 67015	A	CTGT
			GG ACCATGGCCAA GAGC		

			CC TGGTACCGGTT	TTCG		
			C	CTC_		
GAM2588	MSP	3'	GCTCAGGCAGGCCATGGCC	50245	AA	AA G
			GG CCATGGCC	CT TGAGC		
			CC GGTACCGG	GG ACTCG		
			_	AC _		
GAM2588	PGR1	3'	CTCACAGTTGGAGTTCTCC	53905	A	CATGG
			A GGAAC	CCAACTGTGAG		
			C TCTTG	GGTTGACACTC		
			C	A_		
GAM2588	PTPRT	3'	GCTTCGTGTTGGCCAAGACTCC	56502	ACCA	TGT
	TT		AAGGA	TGGCCAAC GAGC		
			TTCCT	ACCGGTTG TTCG		
			CAGA	TGC		
GAM2588	TRF4-2	3'	CTCAAACAAGCCATGGTTCCTT	42611		CAACTG
			AAGGAACCATGGC	TGAG		
			TTCCTTGGTACCG	ACTC		
			AACAA_			
GAM2588	LOC122786	3'	GCCTTTGGCCATGATTCT	74622	C	CT
			GGAA CATGGCCAA	GT		
			TCTT GTACCGGT	CG		
			A	TC		
GAM2588	LOC138428	3'	TAGTGGCCATGGCTGCCT	75862	AA_	A
			AGG CCATGGCCA	CTG		
			TCC GGTACCGGT	GAT		
			GTC	_		
GAM2588	LOC145581	3'	GCTCCATTAGACCATGGTTC	77794	CCAAC	T
			GAACCATGG	TG GAGC		
			CTTGGTACC	AC CTCG		
			AGATT _			
GAM2588	LOC146268	5'	GCTCACAGTCGGCTTGCTGCCT	78342	AAC T	A
			AGG CA GGCC	ACTGTGAGC		
			TCC GT TCGG	TGACACTCG		
			GTC _	C		
GAM2588	LOC147299	3'	GCTGTGAGCCGCCATGGTCCC	78981	A	CAA GTG
			GG ACCATGGC	CT AGC		
			CC TGGTACCG	GA TCG		
			C	CC_ GTG		
GAM2588	LOC159199	3'	GCTCACAGCTGGCGGCCCT	83062	AA ATG	A
			AGG CC GCCA	CTGTGAGC		

TCC GG CGGT GACACTCG
 C_ _ C
 GAM2588 LOC200982 5' AGTTGGCCATGGCTCTTT 91807 A
 AAGGA CCATGGCCAACT
 ||||| |||||
 TTTCT GGTACCGGTTGA
 C
 GAM2588 LOC221495 5' CCACAGCTTGGTTCCT 95493 T CAAC A
 AGGAACCA GGC TGTG G
 ||||| || |||||
 TCCTTGGT TCG ACAC C
 _ _ C
 GAM2588 LOC253842 3' GCTCATAGAAGCCTGGTCCCT 99238 A T CAA
 AGG ACCA GGC CTGTGAGC
 || ||| || |||||
 TCC TGGT CCG GATACTCG
 C _ AA_
 GAM2588 LOC254778 3' GCCCTGTGTTGGCCAAGGTTCC 97831 A TGTGA
 GGAACC TGGCCAAC GC
 ||||| ||||| ||
 CCTTGG ACCGGTTG CG
 A TGTCC
 GAM2588 LOC255231 3' CTCACAGTTAGCCAGCTGACC 97119 AACCA C
 GG TGGC AACTGTGAG
 || ||| |||||
 CC ACCG TTGACACTC
 AGTCG A
 GAM2588 LOC257358 5' GCTCGTGAAGAGCATGGTTCCT 98900 G CAACTG
 T AAGGAACCATG C TGAGC
 ||||| || |||||
 TTCCTTGGTAC G GCTCG
 _AGAAGT
 GAM2588 LOC90190 3' CGCCCACAGAGCAATTGGCCAT 62422 AC _ A _
 GCCTCC GGA CATGGCCAA CTGTG GC G
 || ||||| ||||| ||
 CCT GTACCGGTT GACAC CG C
 CC AACGA C _
 GAM2588 LOC90495 3' GCTCACAGTCAACTGCTTTCTT 63737 CCAT CA_
 T AAGGAA GGC ACTGTGAGC
 ||||| || |||||
 TTTCTT TCG TGACACTCG
 _ TCAAC
 GAM2588 LOC90750 3' GCTCACAGCCCTGCCCTGCCCC 64630 AAC T CAA_
 C GG CA GGC CTGTGAGC
 || ||| |||||
 CC GT CCG GACACTCG
 CCC C TCCC
 GAM2589 HRH1 3' CTCAAACATGTTTAGAGTGGA 7819 A TGG
 TCCA TCTGA GCATGTTTGAG
 ||| ||||| |||||

AGGT AGATT TGTACAAACTC
 G ____
 GAM2589 TRIM37 3' CTCAAATTTGTCATCAG 31625 G T
 CTGATGG CA GTTTGAG
 ||||| || |||||
 GACTACT GT TAAACTC
 _ T
 GAM2589 HTMP10 3' CTCAAAAAGCCATCAGATCTG 53758 CA G ATG
 A TC ATCTGATGG C TTTGAG
 || ||||| | |||||
 AG TAGACTACC G AAACTC
 TC _ AAA
 GAM2589 PAK2 5' CTCAAATATCACCAAAGTAGA 67140 A__ GC
 TCTG TGG ATGTTTGAG
 ||| || |||||
 AGAT ACC TATAAACTC
 CAA AC
 GAM2589 SEMA6A 3' CTCGAGTACCCACCAGA 40818 A CA
 TCTG TGGG TGTTTGAG
 ||| ||| |||||
 AGAC ACCC ATGAGCTC
 C ____
 GAM2589 TTY7 3' TCAAACATGCAGGCTGGA 50019 AT GATGG
 TCCA CT GCATGTTTGA
 ||| || |||||
 AGGT GA CGTACAAACT
 CG ____
 GAM2589 LOC144766 3' CTCAAACATGAGAAGACTGGG 77481 A GATGGG
 TCCA TCT CATGTTTGAG
 ||| || |||||
 GGGT AGA GTACAAACTC
 C AGA__
 GAM2589 LOC201685 5' TAAACACCCATCAGATGGA 91845 A CA
 TCCA TCTGATGGG TGTTTG
 ||| ||||| |||||
 AGGT AGACTACCC ACAAAT
 _ _
 GAM2589 LOC221596 5' CTCAAACAAAACCTCAGATT 93623 TG GCA
 AATCTGA G TGTTTGAG
 ||||| | |||||
 TTAGACT C ACAAACCTC
 _ AAA
 GAM2589 LOC93622 3' CTCTGCAGACCATCAGAT 57729 GCA TT
 ATCTGATGG TGT GAG
 ||||| ||| |||
 TAGACTACC ACG CTC
 AG_ T_
 GAM2590 EDNRA 3' TTTTAGCCCATTTTCTA 64804 AA
 TAGAAGAATG CTAAGG
 ||||| |||||

		ATCTTTTAC GATTTT	
		CC	
GAM2590 HAP1	3'	TAGACACCTCTGATCCCCTTC 15479	AAT ACTA
		GAAG GA AGGTGTCTA	
		CTTC CT TCCACAGAT	
		CC_ AGTC	
GAM2590 MEP1B	3'	AGCCACCTCATTCTTCTA 20997	ACTAA T
		TAGAAGAATGA GGTG CT	
		ATCTTCTTACT CCAC GA	
		_____ C	
GAM2590 PRKWNK3	3'	CACCTCAATCCATTCTTCTG 62227	AACTA
		TAGAAGAATG AGGTG	
		GTCTTCTTAC TCCAC	
		CTAAC	
GAM2590 STAC	3'	ATTGGAGTCCATTCTTCT 13424	A AA
		AGAAGAATG ACT GGT	
		TCTTCTTAC TGA TTA	
		C GG	
GAM2590 UNC13	3'	TAGACACCTCTCCACTCCTC 22101	A A AACTA
		GA GA TG AGGTGTCTA	
		CT CT AC TCCACAGAT	
		C C CTC__	
GAM2590 C1orf29	3'	ATTCTCTAATTTATTCTTCTA 23337	C AG T
		TAGAAGAATGAA TA G GT	
		ATCTTCTTATTT AT C TA	
		A CT T	
GAM2590 FLJ13397	3'	AGAAGAGTTCATTTTCTA 46903	AAGGTG
		TAGAAGAATGAACT TCT	
		ATCTTTTACTTGA AGA	
		GA_____	
GAM2590 FLJ20668	3'	CAGTTTAATTCATTCTTTTA 35929	C G
		TAGAAGAATGAA TAAG TG	
		ATTTTCTTACTT ATTT AC	
		A G	
GAM2590 GS3955	3'	CACTTCAACTCATTTCTTCTA 41618	_ ACTA
		TAGAAGAA TGA AGGTG	
		ATCTTCTT ACT TTCAC	
		T CAAC	
GAM2590 KATII	3'	TAGACACCTTTTAAAGTGCCTC 33168	AGA GAACT
TA		TAGA AT AAGGTGTCTA	

	ATCT TG TTCCACAGAT	
	CCG AAATT	
GAM2590 KIAA1210	3' ACCTAGCTCATTTTTCTA 98059	A A
	TAGAAGAATGA CTA GGT	
	ATCTTTTACT GAT CCA	
	C _	
GAM2590 MGC20253	3' AGACACCTCTTTCCTTT 58674	AAT CTA
	GAAG GAA AGGTGTCT	
	TTTC CTT TCCACAGA	
	_ TC_	
GAM2590 MGC4737	5' AGACACCTGTCCTTCCTTCTA 49637	AAT CTA_
	TAGAAG GAA AGGTGTCT	
	ATCTTC CTT TCCACAGA	
	_ CCTG	
GAM2590 PRO0365	3' TAGACACCAACCCATTCTC 26995	A AACTAA
	GA GAATG GGTGTCTA	
	CT CTTAC CCACAGAT	
	_ CCAA_	
GAM2590 ZNF237	3' AGAAGGCTAATGTCATTCTTC 27267	ACTAA G_
	GAAGAATGA GGT TCT	
	CTTCTTACT TCG AGA	
	GTAA_ GA	
GAM2590 LOC118786	5' GGAGTCCAGATCATTCTTC 76010	A AA TG
	GAAGAATGA CT GG TCT	
	CTTCTTACT GA CC AGG	
	A _ TG	
GAM2590 LOC144193	3' CAAGTAGTTCATTTTCTA 77197	A AGG
	TAGAAGA TGA ACTA TG	
	ATCTTTT ACTTGAT AC	
	_ GA_	
GAM2590 LOC144473	5' AGAAGCAGTTCATTTTTC 83992	AAG G
	GAAGAATGAACT GT TCT	
	CTTTTACTTGA CG AGA	
	_ A	
GAM2590 LOC145241	5' TAGACACCTCCCAGTGTTCCACC 63527	AA AACTA
TA	TAG GAATG AGGTGTCTA	
	ATC CTTGT TCCACAGAT	
	CA GACCC	
GAM2590 LOC155004	3' AGACCCAGTTCATTCT 82154	AA T
	AGAATGAACT GG GTCT	

TCTTACTTGA CC CAGA

GAM2590 LOC202908 5' CACCCAGTTCATTTTCTA 90713 A AA
TAGAAGA TGA ACT GGTG
||||| ||||| ||||
ATCTTTT ACTTGA CCAC

— C—
GAM2590 LOC255480 3' AGACACCTTGCTCCCTCT 98283 AT AC
AGA GA TAAGGTGTCT
||| || |||||
TCT CT GTTCCACAGA

CC C—
GAM2590 LOC257486 3' ACCTAGCTCATTTTCTA 69760 A A
TAGAAGAATGA CTA GGT
||||||| ||| |||
ATCTTTT TACT GAT CCA

C —
GAM2590 LOC90381 3' AGACACCTCAGCAGTGCTCTA 63209 AGA GAA A
TAGA AT CT AGGTGTCT
|||| || |||||
ATCT TG GA TCCACAGA
CG_ AC_ C

GAM2591 ZNF239 5' GGTGAAGATGACAACTCAGCA 20242 C ACA
TGT GGG TCATCTTCACC
||| ||| |||||
ACG CTC AGTAGAAGTGG
A AAC

GAM2591 DKFZP564M182 3' GTAAAGATGATGTGGCA 78640 GGG C
TGTC ACATCATCTT AC
|||| ||||| ||
ACGG TGTAGTAGAA TG
— A

GAM2591 FLJ10716 3' GGTGAAGACATGCTACA 37020 CG A CA
TGT GG CAT TCTTCACC
||| ||| |||||
ACA TC GTA AGAAGTGG
— — C—

GAM2591 FLJ22031 3' GTAAAGATGGTGCCACATTA 47589 CG A C
TAATGT GG CATCATCTT AC
|||| || ||||| ||
ATTACA CC GTGGTAGAA TG
— — A

GAM2591 LMOD1 5' GTGAAGACCCCGACAT 25106 ACATCA
ATGTCGGG TCTTCAC
||||| |||||
TACAGCCC AGAAGTG
C—

GAM2591 LSR7 5' GTGAAGATGAGGATATTA 38282 GGGACA
TAATGTC TCATCTTCAC
||||| |||||

ATTATAG AGTAGAAGTG
 G____
 GAM2591 LOC158295 5' GTGAAGATGACCAACA 88061 C GACA
 TGT GG TCATCTTCAC
 ||| || |||||
 ACA CC AGTAGAAGTG
 A ____
 GAM2592 AADAC 3' TTTTCGGAGATTTTCCTTCTTA 8434 ATGT A
 TAAGAAG GGGTCTCC AAAA
 ||||| ||||| |||
 ATTCTTC TTTAGAGG TTTT
 CT__ C
 GAM2592 BAZ2A 3' TTGGCAGTGCCCCACATCCTCT 26518 A T__ _
 TA TAAGA GATGTGGG CT CCAA
 ||||| ||||| || |||
 ATTCT CTACACCC GA GGTT
 C CGT C
 GAM2592 CENPE 3' TGGAGATCCAGCATTCTTA 10171 AA _
 TAAG GATG TGGGTCTCCA
 ||| ||| |||||
 ATTC TTAC ACCTAGAGGT
 C_ G
 GAM2592 DDX20 3' TTTGGATATCCATCCTCCTC 24232 A T_ C
 GA GA GTGGGT TCCAAA
 || || ||||| |||||
 CT CT TACCTA AGGTTT
 C CC T
 GAM2592 DNAJB1 3' TGGAGAATTCTGTCTTCT 21568 T _
 AGAAGATG GGGT CTCCA
 ||||| ||| |||||
 TCTTCTGT CTTA GAGGT
 _ A
 GAM2592 FOSB 3' TTGGCCCCTCACATCCTCT 23061 A TCT
 AGA GATGTGGG CCAA
 ||| ||||| |||
 TCT CTACACTC GGTT
 C CCC
 GAM2592 GEMIN5 5' TGGCTTCACATTTTCT 90646 TCT
 AGAAGATGTGGG CCA
 ||||| ||| |||
 TCTTTTACACTT GGT
 C__
 GAM2592 PAG 3' TTTTAAAGACTCACCTTTTTA 38015 AT CC
 TAAGAAG GTGGGTCT AAAAA
 ||||| ||||| |||||
 ATTTTTC CACTCAGA TTTT
 _ AA
 GAM2592 RNPEP 3' TGGAGTTTATATCCCCT 65702 AA T
 AG GATGTGGG CTCCA
 || ||||| |||||

		TC CTATATTT GAGGT	
		CC _	
GAM2592 TRIM37	3'	TTTTTGAGTATGTATCTTCT 31629	GT GGT
		AGAAGAT G CTCCAAAAA	
		TCTTCTA T GAGGTTTTT	
		TG AT_	
GAM2592 ZNF175	3'	TTGAAGAAGAGAACATCTTCT 24086	GGG_ C
		AGAAGATGT TCT CAA	
		TCTTCTACA AGA GTT	
		AGAGA A	
GAM2592 AP1S3	3'	TTTTTAGAAATGGGCATCTTTT 75430	GG C C
TA		TAAGAAGATGT GT TC AAAAA	
		ATTTTCTACG TA AG TTTT	
		GG A A	
GAM2592 CAP350	3'	TTTTTGAAGACCATTTTCTTC 29710	TGTG C
		GAAGA GGTCT CAAAAA	
		CTTCT CCAGA GTTTTT	
		TTTA A	
GAM2592 CYP2C18	3'	TTGTCAATCCACATCTTC 7578	CTC
		GAAGATGTGGGT CAA	
		CTTCTACACCTA GTT	
		ACT	
GAM2592 FLJ12610	3'	GAGACCCACTTCTCTCTT 45857	_ T
		AAGA AGA GTGGGTCTC	
		TTCT TCT CACCCAGAG	
		C T	
GAM2592 FLJ13102	3'	TTTTGGAGACAGCATCTC 46538	A GG
		GA GATGT GTCTCCAAAA	
		CT CTACG CAGAGGTTTT	
		_ A_	
GAM2592 FLJ14100	3'	TTGGAACCTTACACCCTCTTG 47342	AGA C
		TAAGA TGTGGGT TCCAA	
		GTTCT ACATTCA AGGTT	
		CCC _	
GAM2592 FLJ21802	3'	TTTTTGGAATTTGGATCTTTCA 45330	A G GG C
		A GAAGAT T GT TCCAAAAA	
		A TTTCTA G TA AGGTTTTT	
		C G TT _	
GAM2592 GFRA4	3'	TGGAGACCCAGATCCCCT 42421	AA G
		AG GAT TGGGTCTCCA	

		TC CTA ACCCAGAGGT	
		CC G	
GAM2592	H-L(3)MBT 3'	GAGCCTACATCTTCTTG	31923 T
		TAAGAAGATGTGGG CTC	
		GTTCTTCTACATCC GAG	
GAM2592	HINT3 3'	TTTTTGAAGCATTGCATCTTTT	57551 TG GT C
	TA	TAAGAAGATG G CT CAAAAA	
		ATTTTCTAC T GA GTTTT	
		GT AC A	
GAM2592	KIAA0172 5'	TGGAGACCTCACTCCCTTT	65600 AT_ _
		GAAG GTG GGTCTCCA	
		TTTC CAC CCAGAGGT	
		CCT T	
GAM2592	KIAA0317 3'	TTGGAGACACCCTCTTT	29750 TGT _
		GAAGA GG GTCTCCAA	
		TTTCT CC CAGAGGTT	
		C_ A	
GAM2592	KIAA0355 3'	TTTTTGAAACCCTCTCCTC	28715 A TGT C
		GA GA GGGT TCCAAAAA	
		CT CT CCCA AGGTTTTT	
		C CT_ A	
GAM2592	KIAA0594 3'	TTTTGAAACCTGCTTTT	65524 T TG C
		AAGA G GGT TCCAAAA	
		TTTT C CCA AGGTTTT	
		_GT A	
GAM2592	KIAA1190 3'	TTTGAGCTGGCTCACATTTTC	71657 _
		GAAGATGTGGGT CTCCAAA	
		CTTTTACACTCG GAGGTTT	
		GTC	
GAM2592	KIAA1240 3'	TTTTGGAGACTCCTCTCTTA	67298 A TGT
		TAAGA GA GGGTCTCCAAAA	
		ATTCT CT CTCAGAGGTTTT	
		_ C_	
GAM2592	KIAA1553 3'	TTTTGAAACCGTATTTTC	93572 T _ C
		GA GTG GGT TCCAAAA	
		CT TAT CCA AGGTTTT	
		T G A	
GAM2592	KIAA1671 3'	TTTGAAATCTGTCTTCTT	66294 GT C
		AAGAAGAT GGGT TCCAAA	

			TTCTTCTG TCTA AGGTTT		
			— A		
GAM2592	MGC3020	5'	TGGGGCTCCACATCCTTC 44123	—	GT
			GAAG ATGTGG CTCCA		
			CTTC TACACC GGGGT		
			C TC		
GAM2592	MGC5528	3'	TTTTAGAAACCTAGTCTTCT 44276	G	C C
			AGAAGAT TGGGT TC AAAA		
			TCTTCTG ATCCA AG TTTT		
			— A A		
GAM2592	OPRL1	3'	TGGGGGTCCCCACATCCTC 8073	A	—
			GA GATGTGGG TCTCCA		
			CT CTACACCC GGGGGT		
			C CT		
GAM2592	ORMDL2	3'	TTTGGTGATTACATCTTT 27196	G	T
			GAAGATGTGG TC CCAA		
			TTTCTACATT AG GGTTT		
			— T		
GAM2592	PMVK	3'	TGGAGACCTCATTTTCT 96254	T	
			AGAAGATG GGGTCTCCA		
			TCTTTTAC TCCAGAGGT		
			—		
GAM2592	SENP7	3'	TTTTAGAGACCTATGATCCTC 40675	A	— C
			GA GAT GTGGGTCTC AAAA		
			CT CTA TATCCAGAG TTTT		
			C G A		
GAM2592	TED	3'	TTGGAGACTCCCATCCTCT 32277	A	T
			AGA GATG GGGTCTCCAA		
			TCT CTAC CTCAGAGGTT		
			C C		
GAM2592	TERA	3'	TTGGGGGCACATTTCTTA 41426	A	GGT
			TAAGA GATGTG CTCCAA		
			ATTCT TTACAC GGGGTT		
			— —		
GAM2592	LOC146315	3'	TTTTTAGAGACCCCGTGTCTGT 61560	—	TG — C
		C	GA AGA TGGG TCTC AAAAA		
			CT TCT GCCC AGAG TTTTT		
			G GT C A		
GAM2592	LOC153811	3'	TTTTTAGAGACAGAGCTTCT 81857	ATGTGG	C
			AGAAG GTCTC AAAAA		

	TCTTC CAGAG TTTT	
	GAGA__ A	
GAM2592 LOC158825 3'	TTGGAGCCAGCATCTTC 82881	G T
	GAAGATGT GG CTCAA	
	CTTCTACG CC GAGGTT	
	A _	
GAM2592 LOC159963 5'	TTTTGAAACATCTTCTT 83077	GGGTC
	AAGAAGATGT TCCAAA	
	TTCTTCTACA AGGTTTT	
	A_____	
GAM2592 LOC200314 3'	TGGCCCCTCATCTTCTTA 91606	T TCT
	TAAGAAGATG GGG CCA	
	ATTCTTCTAC CCC GGT	
	T C__	
GAM2592 LOC221178 3'	TTTGAGACCCAGCTGCCTTT 95181	AT__
	GAAG G TGGGTCTCCAAA	
	TTTC C ACCCAGAGGTTT	
	CGT G	
GAM2592 LOC221191 5'	TTTTCAGAGACCCAACCTCTCT 95223	A TG CA
	AGA GA TGGGTCTC AAAA	
	TCT CT ACCCAGAG TTTT	
	_ CA AC	
GAM2592 LOC221763 5'	TTTTCAGAGACCTGCTTTC 95440	AT TG CA
	GAAG G GGTCTC AAAA	
	CTTT C CCAGAG TTTT	
	_ GT AC	
GAM2592 LOC253716 5'	TTTTTGAGAGCACATTTTC 96340	GGT _
	GAAGATGTG CTC CAAAAA	
	CTTTTACAC GAG GTTTTT	
	_ A	
GAM2592 LOC256683 5'	TGGAGAAACAATCTTCTTG 98022	G GG
	TAAGAAGAT TG TCTCA	
	GTTCTTCTA AC AGAGGT	
	_ AA	
GAM2592 LOC91138 5'	TTTTTGGGGACACCTTCTTA 65659	ATGTGG
	TAAGAAG GTCTCCAAAAA	
	ATTCTTC CAGGGGTTTTT	
	CA_____	
GAM2592 LOC91464 5'	TGGAGACTGACCTCCTCTT 66713	A T G
	AAGA GA GT GGTCTCCA	

		TTCT CT CA TCAGAGGT	
		C C G	
GAM2593 ACP2	3'	AGCCTGAAGTCTTCGGCAA 9650	AAGG A
		TTGCTGAA TCA GGCT	
		AACGGCTT AGT CCGA	
		CTGA _	
GAM2593 COX15	3'	AGCCAGCTGGTCTTCAGCAA 55277	AA GT A__
		TTGCTGA AG CA GGCT	
		AACGACT TC GT CCGA	
		_ TG CGA	
GAM2593 ENPP3	3'	AGCCATTTGCTTTTCAGAAGT 18467	G GTCAA
		ACTT CTGAAAAG GGCT	
		TGAA GACTTTTC CCGA	
		_ GTTTA	
GAM2593 MAPK7	3'	AGCCCTGGACCCAGCAGGTG 12307	AAAA AA_
		CACTTGCTG GGTC GGCT	
		GTGGACGAC CCAG CCGA	
		_ GTC	
GAM2593 MAPK7	3'	AGCCCTGGACCCAGCAGGTG 58159	AAAA AA_
		CACTTGCTG GGTC GGCT	
		GTGGACGAC CCAG CCGA	
		_ GTC	
GAM2593 MAPK7	3'	AGCCCTGGACCCAGCAGGTG 58161	AAAA AA_
		CACTTGCTG GGTC GGCT	
		GTGGACGAC CCAG CCGA	
		_ GTC	
GAM2593 MAPK7	3'	AGCCCTGGACCCAGCAGGTG 58163	AAAA AA_
		CACTTGCTG GGTC GGCT	
		GTGGACGAC CCAG CCGA	
		_ GTC	
GAM2593 MUCDHL	3'	AGCCGATGCCCTCAGCAAG 88634	AAA CAA
		CTTGCTGA GGT GGCT	
		GAACGACT CCG CCGA	
		CC_ TAG	
GAM2593 MUCDHL	3'	AGCCGATGCCCTCAGCAAG 49200	AAA CAA
		CTTGCTGA GGT GGCT	
		GAACGACT CCG CCGA	
		CC_ TAG	
GAM2593 NDUFA6	3'	AGCCTCTTTTTGCCTGAGCAAG 11762	GAAA CA_____
TGG		CCACTTGCT AGGT AGGCT	

GGTGAACGA TCCG TCCGA
G__ TTTTC
GAM2593 NOS2A 3' CTTGACCTCCTAACAAGT 7118 C AAA
ACTTG TG AGGTCAAG
||||| || |||||
TGAAC AT TCCAGTTC
A CC_

GAM2593 PRIM2A 3' AGCCTTGACCTTCCCAGCTCAA 8140 __ AA
GT ACTT GCTG AAGGTCAAGGCT
|||| ||| |||||
TGAA CGAC TTCCAGTTCCGA
CT CC

GAM2593 SEL1L 3' AGCCTTAACACCAGCAGGTG 18597 AAAAG C
CACTTGCTG GT AAGGCT
||||| || |||||
GTGGACGAC CA TTCCGA
CA__ A

GAM2593 SLC4A4 3' CCTTGACCTCCAGACAG 14993 _ AAA
TTG CTG AGGTCAAGG
||| ||| |||||
GAC GAC TCCAGTTCC
A C_

GAM2593 THY1 3' AGCCGGACACTTCTCAGGAAAT 21894 C G A _ AA
GG CCA TT CTGA AAG GTC GGCT
||| || ||| ||| |||
GGT AA GACT TTC CAG CCGA
A G C A G_

GAM2593 TJP1 5' AGCCTTGACCTCCCCGGGCTCA 13760 __ AAA
AG CTTG CTG AGGTCAAGGCT
|||| ||| |||||
GAAC GGC TCCAGTTCCGA
TCG CCC

GAM2593 USP7 3' AGCCGAAGTCTTCAGCAAGAGG 14416 A AAGG AA
CC CTTGCTGAA TC GGCT
|| ||||| || |||
GG GAACGACTT AG CCGA
A CTGA _

GAM2593 WFS1 5' GCCGGCTCTTCAGCAG 21168 AA AA
TTGCTGAA GGTC GGC
||||| ||| |||
GACGACTT TCGG CCG
C_ _

GAM2593 ARHGAP4 3' GCCCTGTCCAGCAAGTG 9795 GAAAA T A
CACTTGCT GG CA GGC
||||| || |||
GTGAACGA CC GT CCG
__ T C

GAM2593 ARHGEF4 3' GCCCTGCCAGCAACCGG 53373 AC AAAA T A
CC TTGCTG GG CA GGC
|| ||||| || |||

GG AACGAC CC GT CCG
CC ____ C
GAM2593 DOCK3 3' GCCCTGTTCCAGCAAGTGG 67097 AAAA GT A
CCACTTGCTG G CA GGC
||||||| | ||||
GGTGAACGAC C GT CCG
____ TT C
GAM2593 FLJ10052 3' AGCCTCCTGCACCCTCAGCAAG 36246 A AAA _ _
GG CC CTTGCTGA GGT CA AGGCT
|| ||||| ||| || ||||
GG GAACGACT CCA GT TCCGA
_ C_ C CC
GAM2593 FLJ10607 3' AGCCTCTAAGTTTTTTCAAAAA 77622 C GC GG CA_
TGG CCA TT TGAAAA T AGGCT
||| || ||||| | ||||
GGT AA ACTTTT G TCCGA
A A_ TT AATC
GAM2593 FLJ11467 3' AGCCTTGACCTCCCGGGCTCAA 46972 _ AAA
G CTTG CTG AGGTCAAGGCT
||| ||| |||||
GAAC GGC TCCAGTTCCGA
TCG CC_
GAM2593 FLJ14009 5' AGCCCTGGGACGCCCCAGCAGG 45752 AAAAG AA_
TG CACTTGCTG GTC GGCT
||||||| ||| ||||
GTGGACGAC CAG CCGA
CCCG_ GGTC
GAM2593 FLJ23816 3' AGCCTTGACCCCCGACAGCGAG 58977 AAAA_
CTTGCTG GGTCAAGGCT
||||||| |||||
GAGCGAC CCAGTTCCGA
AGCCC
GAM2593 IMPACT 3' AGCCTTGACCTTCCAGC 38000 AA
GCTG AAGGTCAAGGCT
||| |||||
CGAC TTCCAGTTCCGA
C_
GAM2593 KIAA0182 3' AGCCACACCTTCAGCAGTG 72496 T AA CAA
CACT GCTGA AGGT GGCT
||| ||||| ||| ||||
GTGA CGACT TCCA CCGA
_ _ CAC
GAM2593 KIAA1854 3' AGCCTCCCTTGCCTCAGCAAG 72196 A_ TCA
CTTGCTGA AAGG AGGCT
||||||| ||| ||||
GAACGACT TTCC TCCGA
CCG C_
GAM2593 KIAA1878 3' AGCCTGGGCTTCAGCAATTG 93364 C AAA A
CA TTGCTGA GGTC AGGCT
|| ||||| ||| ||||

		GT AACGACT TCGG TCCGA		
		T _ G		
GAM2593	MGC13007	3' AGCTAGGTCTTTTCAGAAAGTGG 51276	G	GT AA
		CCACTT CTGAAAAG C GGCT		
		GGTGAA GACTTTTC G TCGA		
		_ TG A_		
GAM2593	PAK2	3' AGCCTTAGGTCTTTCAGCAA 67138	A GT _	
		TTGCTGAAA G C AAGGCT		
		AACGACTTT C G TTCCGA		
		_ TG A		
GAM2593	PP1628	5' AGCCCCAACCCCTGTCTCAGCA 48071	AA_ TCAA_	
	AG	CTTGCTGA AGG GGCT		
		GAACGACT TCC CCGA		
		CTG CCAACC		
GAM2593	PSIP2	3' TTTGGCACTTCTCAGCAAGT 53783	A _	
		ACTTGCTGA AAG GTCAAG		
		TGAACGACT TTC CGGTTT		
		C A		
GAM2593	SYT13	3' AGCCTTGACCTCACTTAGCA 95095	AA_	
		TGCTGA AGGTCAAGGCT		
		ACGATT TCCAGTTCCGA		
		CAC		
GAM2593	TBC1D1	3' CCGGCTTGCCAGCAAGT 65289	AAA AA	
		ACTTGCTG AGGTC GG		
		TGAACGAC TTCGG CC		
		CG_ _		
GAM2593	LOC112724	3' AGCCTTGTTTCTTCAGCAGTG 57299	T A GT	
		CACT GCTGAA AG CAAGGCT		
		GTGA CGACTT TT GTTCCGA		
		_ C TG		
GAM2593	LOC112868	5' AGCCTGGGCTTCCAGCAGGTGG 73265	AAA A	
		CCACTTGCTG AGGTC AGGCT		
		GGTGGACGAC TTCGG TCCGA		
		C_ G		
GAM2593	LOC126526	3' AGCCTCCCTGTCCCCCTCAACT 75036	C_ AAA T _	
	AAGTGG	CCACTTG TGA GG CA AGGCT		
		GGTGAAT ACT CC GT TCCGA		
		CA CCC T CCC		
GAM2593	LOC144866	5' ACCAATTTTCAGCAAATGG 84133	C _	
		CCA TTGCTGAAAA GGT		

	GGT AACGACTTTT CCA		
	A AA		
GAM2593 LOC145371 3'	AGCCTAGCCTTCAGCAA 77680	AA CA	
	TTGCTGA AGGT AGGCT		
	AACGACT TCCG TCCGA		
	__ A_		
GAM2593 LOC148343 5'	CCTTGACCTCTCTAGCACATG 79542	CT AAA	
	CA TGCTG AGGTCAAGG		
	GT ACGAT TCCAGTTCC		
	AC CTC		
GAM2593 LOC149773 3'	AGCCTCTCAGCCTCTCAGCAAG 80290	A AA CA__	
GG	CC CTTGCTGA AGGT AGGCT		
	GG GAACGACT TCCG TCCGA		
	_ C_ ACTC		
GAM2593 LOC152217 3'	GCCTTTCCTCTGCAAGTGG 92869	TGAAA TC	
	CCACTTGC AGG AAGGC		
	GGTGAACG TCC TTCCG		
	TC__ T_		
GAM2593 LOC152220 3'	AGCCTTAGGTCTTTCAGCAA 86757	A GT _	
	TTGCTGAAA G C AAGGCT		
	AACGACTTT C G TTCCGA		
	_TG A		
GAM2593 LOC158476 5'	TCTTGCTATTTTCAGTAAGTG 88207	A T	
	CACTTGCTGAAA GG CAAGG		
	GTGAATGACTTT TC GTTCT		
	A _		
GAM2593 LOC201705 5'	AGCCTGTGCCCCCAGCAGGT 91853	AAAA CA	
	ACTTGCTG GGT AGGCT		
	TGGACGAC CCG TCCGA		
	CC__ TG		
GAM2593 LOC220558 3'	AGCCTCCCCAGTTTCAGCAAG 92770	A_ TCA	
	CTTGCTGAAA GG AGGCT		
	GAACGACTTT CC TCCGA		
	GA CC_		
GAM2593 LOC221794 5'	AGGTTTCTCCTCAGCAAG 95529	AAA TC G	
	CTTGCTGA GG AAG CT		
	GAACGACT CC TTT GA		
	__ TC G		
GAM2593 LOC253912 3'	GCCTTGACCCAGCAGTGG 99208	T AAAA _	
	CCACT GCTG GGTC AAGGC		

GGTGA CGAC CCAG TTCCG
— ——— G
GAM2593 LOC91585 5' AGCCTTGACTCCAGCAAG 67159 AAAA
CTTGCTG GGTCAAGGCT
||||| |||||
GAACGAC TCAGTTCCGA
C—
GAM2593 LOC92465 5' AGCCTTGACCTCCTCCTGGGC 69938 — AA
GCT GA AGGTCAAGGCT
||| || |||||
CGG CT TCCAGTTCCGA
GTC CC
GAM2593 LOC92609 3' AGCCTTGACCTCCCGGCTCAAG 73205 — AAA
TG CACTT GCTG AGGTCAAGGCT
|||| ||| |||||
GTGAA CGGC TCCAGTTCCGA
CT CC_
GAM2594 ATP6IP1 3' GAAGGGACCTCCACGACA 8632 C C
TG CGTGGAGG CTCTTC
|| ||||| |||||
AC GCACCTCC GGGAAG
A A
GAM2594 CAPZA1 3' CACCTAAAGAGGCTATGCTAC 73023 A— CAA
GTGG GGCCTCTT GTG
|||| ||||| |||
CATC TCGGAGAA CAC
GTA ATC
GAM2594 LTBR 3' GCAAACCTGAGGCCTCCCGGCA 11372 T TTCAAG
TGCCG GGAGGCCTC TGC
|||| ||||| |||
ACGGC CCTCCGGAG ACG
— TCCAA_
GAM2594 PRKAG1 3' CACTTGAAAAAACTTTCAGC 12281 CG CCTC
GC TGGAGG TTCAAGTG
|| ||||| |||||
CG ACTTTC AAGTTCAC
— AAAA
GAM2594 ZNF278 3' CACTACATAGGCCTCCAAGGCA 50265 G CTTCA
TGCC TGGAGGCCT AGTG
|||| ||||| |||
ACGG ACCTCCGGA TCAC
A TACA_
GAM2594 ZNF278 3' CACTACATAGGCCTCCAAGGCA 50266 G CTTCA
TGCC TGGAGGCCT AGTG
|||| ||||| |||
ACGG ACCTCCGGA TCAC
A TACA_
GAM2594 C20orf150 3' CACTCTGGGCCTCCAGGACA 66006 — G CTTCA
TG CC TGGAGGCCT AGTG
|| || ||||| |||

AC GG ACCTCCGGG TCAC
 A _ TC____
 GAM2594 KIAA0841 5' CACTTGAAGAGGCTGAGG 71888 GTGGA
 CC GGCCTCTTCAAGTG
 || |||||
 GG TCGGAGAAGTTCAC
 AG____
 GAM2594 KIAA1643 3' CACCCAGACCTCCAGAGCA 65153 CG CC TCAA
 TGC TGGAGG TCT GTG
 ||| ||||| ||| |||
 ACG ACCTCC AGA CAC
 AG _ CC____
 GAM2594 KIAA1949 3' CACCTGCCCCCATGGCA 99692 A CCTCTT A
 TGCCGTGG GG CA GTG
 ||||| || |||
 ACGGTACC CC GT CAC
 _ CC____ C
 GAM2594 LOC115219 3' GCACTCAAGCCTTCCACGACA 73696 C _ CTCTTCA
 TG CGTGGA GGC AGTGC
 || ||||| ||| |||||
 AC GCACCT CCG TCACG
 A T AAC____
 GAM2594 LOC151178 5' CACCTCTGGCCAGTCCCCACGG 80953 A____ TCTTCAA
 CA TGCCGTGG GGCC GTG
 ||||| ||| |||
 ACGGCACC CCGG CAC
 CCTGA TCTC____
 GAM2594 LOC92170 3' GCACCTGAAGGGGTCCACAGC 68908 C AG A
 GC GTGG GCCTCTTCA GTGC
 || ||| ||||| |||||
 CG CACC TGGGGAAGT CACG
 A _ C
 GAM2595 FNTA 3' TCCATCAGAGCTGGTCTGCAC 10709 T GA
 GTGCAG ACCAGTTC GATGGA
 ||||| ||||| |||||
 CACGTC TGGTCGAG CTACCT
 _ A_
 GAM2595 TCTA 3' CCACTAATACTACTGCAC 42490 ACC TCG A
 GTGCAGT AGT AG TGG
 ||||| ||| |||
 CACGTCA TCA TC ACC
 _ TAA _
 GAM2595 DKFZp761D081 3' CCATCCTTCCCTGGTACTGCA 34696 TTCGA
 TGCAGTACCAG GATGG
 ||||| |||||
 ACGTCATGGTC CTACC
 CTTC_
 GAM2595 FLJ14084 3' TCTTGAACATAATCCTGCAC 41597 TACC
 GTGCAG AGTTCGAGA
 ||||| |||||

CACGTC TCAAGTTCT
CTAA
GAM2595 GOLGA1 3' CCATTGAAGTGGTCCCACACG 10848 CAGT GA
CGTG ACCAGTTC GATGG
|||| |||||| ||||
GCAC TGGTCAAG TTACC
ACCC _
GAM2595 KLF12 3' CCACTCCACCACACTGCACG 33277 ACCA TC A
CGTGCAGT GT GAG TGG
|||||| || ||||
GCACGTCA CA CTC ACC
CAC_ C_ _
GAM2595 MGC12966 3' TCCATCCTGTCTGCAACGCTGC 52088 AC__ TT A
ACG CGTGCAGT CAG CG GATGGA
|||||| || ||||||
GCACGTCTG GTC GT CTACCT
CAAC T_ C
GAM2595 LOC149465 5' CCATCTCGCCGCACGCACG 80192 A ACCA T_
CGTGC GT GT CGAGATGG
|||| || || ||||||
GCACG CA CG GCTCTACC
_ _ _ CC
GAM2595 LOC219672 5' TTTGAACTGATACTGACG 92977 G C
CGT CAGTA CAGTTCGAG
|| |||| ||||||
GCA GTCAT GTCAAGTTT
_ A
GAM2595 LOC90786 5' CCATCTTTGGCATGCACG 64730 GTA GTTC
CGTGCA CCA GAGATGG
|||| || ||||||
GCACGT GGT TTCTACC
AC_ _
GAM2595 LOC91585 3' TCCATTTCAATACTGCCG 67160 T ACCA C
CG GCAGT GTT GAGATGGA
|| |||| || ||||||
GC CGTCA TAA CTTTACCT
_ _ _
GAM2596 PFKFB3 3' CTTGACCTGGGAAGACGCCT 83751 T TGA _
AG CGTCTTC CC GGTCAAG
|| |||||| || ||||||
TC GCAGAAG GG CCAGTTC
C _ T
GAM2596 DKFZP434C1715 3' GCCCAGAAGCGACTTA 87352 T ACC
TAAGTCG CTTCTG GGT
|||||| |||| ||
ATTCAGC GAAGAC CCG
_ _ _
GAM2596 MGC11102 5' ACCAGTGTGGGACGACTT 51298 CTG C
AAGTCGTCTT AC GGT
|||||| || ||

			TTCAGCAGGG TG CCA		
			TG_ A		
GAM2596	MS4A6E	3'	TGTCCTCAAAGACGACT 58361	C CC T	
			AGTCGTCTT TGA GG CA		
			TCAGCAGAA ACT CC GT		
			_ _ T		
GAM2597	B3GALT2	3'	CAGCAGGTGTACACATGC 15030	AT TG	
			GCAT TGTAC GCCTGCTG		
			CGTA ACATG TGGACGAC		
			C_ _		
GAM2597	FBN1	3'	CAGCATGTGCAATATGC 65037	TGGCC	
			GCATATTGTAC TGCTG		
			CGTATAACGTG ACGAC		
			T_		
GAM2597	GRLF1	3'	CAGCAGGCCAGCTGCAGTG 79256	_	
			TATTGTA CTGGCCTGCTG		
			GTGACGT GACCGGACGAC		
			C		
GAM2597	MAPRE1	3'	GCAGCAGGCAGGTGATCATGCT 25591	ATTG G	
	G		CAGCAT TACT GCCTGCTGC		
			GTCGTA GTGG CGGACGACG		
			CTA_ A		
GAM2597	SMURF1	3'	CAGCAGGCCAATGTTCCCTATGT 94044	TTGT _	
			GCATA AC TGGCCTGCTG		
			TGTAT TG ACCGGACGAC		
			CCT_ TA		
GAM2597	UQCRC1	5'	GCCAGGCCAGCACAATAGACTG 14015	CA A _	
			CAG TATTGT CTGGCCTG C		
			GTC ATAACA GACCGGAC G		
			AG C C		
GAM2597	DKFZP434P211	5'	CAGCAAGCCAGTGCTGTGTG 28026	T C	
			CATAT GTA CTGGC TGCTG		
			GTGTG CGTGACCG ACGAC		
			T A		
GAM2597	KIAA0063	3'	GCAGCGGTACAGCATGCTG 30259	A GC	
			CAGCAT TTGTA CTG CTGC		
			GTCGTA GACATGGC GACG		
			C _		
GAM2597	KIAA0795	3'	CAGCAAGCCAGGTATGGTG 47228	G TGTA C	
			CA CATAT CTGGC TGCTG		

	GT GTATG GACCG ACGAC	
	G ____ A	
GAM2597 KIAA1817 3'	GCAGCAGGCCACATTGCCGTGC 68781	ATT C__
	GCAT GTA TGGCCTGCTGC	
	CGTG CGT ACCGGACGACG	
	C__ TAC	
GAM2597 MGC14156 3'	GCAACTAGAGTCAATATGCTG 52959	TA_ CC
	CAGCATATTG CTGG TGC	
	GTCGTATAAC GATC ACG	
	TGA A_	
GAM2597 MYH7B 3'	GCAGCAGGCCAACACCAACCTG 71057	CATAT AC
	CAG TGT TGGCCTGCTGC	
	GTC ACA ACCGGACGACG	
	CAACC _	
GAM2597 NEK1 3'	CAGCTTCAATCACAATATGC 97561	AC_ CCT
	GCATATTGT TGG GCTG	
	CGTATAACA ACT CGAC	
	CTA T__	
GAM2597 LOC146455 5'	GCAACAGGCCAGCAGCCAAAAT 78461	A TA__ C
G	CAT TTG CTGGCCTG TGC	
	GTA AAC GACCGGAC ACG	
	A CGAC A	
GAM2597 LOC150174 5'	CAGCAAGCCAGTGCTGC 80433	TATT C
	GCA GTACTGGC TGCTG	
	CGT CGTGACCG ACGAC	
	____ A	
GAM2597 LOC150213 5'	CAGCAAGCCAGTGCTGTGTG 75352	T C
	CATAT GTACTGGC TGCTG	
	GTGTG CGTGACCG ACGAC	
	T A	
GAM2597 LOC150271 5'	CAGCAAGCTCTGAAGATATGCT 86134	GTACT C
G	CAGCATATT GGC TGCTG	
	GTCGTATAG TCG ACGAC	
	AAGTC A	
GAM2597 LOC160646 3'	CAGCAGGCAGAAATGCTG 83108	ATTGTA G
	CAGCAT CTG CCTGCTG	
	GTCGTA GAC GGACGAC	
	AA____ _	
GAM2597 LOC164714 5'	AGCAGGCAAGATGCTG 88579	ATTGTA G
	CAGCAT CT GCCTGCT	

GTCGTA GA CGGACGA
 _____ A
 GAM2597 LOC256809 3' CAGTGTGGAGTCAATATGCT 98130 T GG _
 AGCATATTG ACT CC TGCTG
 ||||| ||| || |||||
 TCGTATAAC TGA GG GTGAC
 _ _ T
 GAM2598 EIF2B1 3' TCCAGAAATACAAGTTAGATA 60392 C GCCACCCC
 TATCTAGC TGTG GGA
 ||||| ||| |||
 ATAGATTG ACAT CCT
 A AAAGA____
 GAM2598 ENO1 3' TCCGGGGTGGCCACAGGCTAGA 9280
 T ATCTAGCCTGTGGCCACCCCGGA
 |||||
 TAGATCGGACACCGGTGGGGCCT

 GAM2598 PON1 3' CCAGTTCACAGGCCAGA 6535 A CC CCC
 TCT GCCTGTGG AC GG
 ||| ||||| || ||
 AGA CGGACACT TG CC
 C _ A_
 GAM2598 RGS3 5' TGGCGGTGGCCGGCTAGA 57057 TGT _
 TCTAGCC GGCCACC CCG
 ||||| ||||| |||
 AGATCGG CCGGTGG GGT
 _ C
 GAM2598 SHANK2 3' TCCAAGGTGGCCAAGCAGATG 25532 A CTG CC
 TATCT GC TGGCCACC GGA
 ||||| || ||||| |||
 GTAGA CG ACCGGTGG CCT
 _ A_ AA
 GAM2598 FLJ20186 3' TCCAGTGTGGTGGCCACTAGC 35204 CT C____
 GC GTGGCCACC C GGA
 || ||||| || |||
 CG CACCGGTGG G CCT
 AT T TGA
 GAM2598 FRAT1 3' CCGGGGTGGCCACAGCGCCAG 19689 A _
 CT GC CTGTGGCCACCCCGG
 || || |||||
 GA CG GACACCGGTGGGGCC
 C C
 GAM2598 KIAA1987 3' TCCAGGACTCTGAAACCACAGG 89392 C__ C__ C
 C GCCTGTGG CA CC GGA
 ||||| || |||
 CGGACACC GT GG CCT
 AAA CTCA A
 GAM2598 MAP2K3 3' CCAGGGTGGCCACACCTCTA 59684 CC_ C
 TAG TGTGGCCACCC GG
 ||| ||||| ||

ATC ACACCGGTGGG CC
 TCC A
 GAM2598 MAP2K3 3' CCAGGGTGGCCACACCTCTA 12322 CC_ C
 TAG TGTGGCCACCC GG
 ||| ||||| ||
 ATC ACACCGGTGGG CC
 TCC A
 GAM2598 LOC200170 3' TCCGGGGTGGCCACAGGCAAGA 89997 A
 T ATCT GCCTGTGGCCACCCCGGA
 ||| ||||| |||||
 TAGA CGGACACCGGTGGGGCCT
 A
 GAM2598 LOC256072 3' TCCGGGGTGGCCACAGGCTAGA 96159
 T ATCTAGCCTGTGGCCACCCCGGA
 ||||| ||||| |||||
 TAGATCGGACACCGGTGGGGCCT

 GAM2598 LOC256520 3' CCGAAGTACCCAGCTGGATA 97665 C T CC CC
 TATCTAGC TG GG AC CGG
 ||||| || || || ||
 ATAGGTCTG AC CC TG GCC
 _ _ A_ AA
 GAM2599 BCAT1 3' AGAAAACAAAGAGGCATACT 66782 C AAT
 AG ATGCCTCTT TTTTCT
 || ||||| |||||
 TC TACGGAGAA AAAAGA
 A AC_
 GAM2599 ETF1 3' AGAAAAATTAAATTGCTGC 17587 T CTC
 GCA GC TTAATTTTCT
 ||| || ||||| |||||
 CGT CG AATTAAAAAGA
 _ TTA
 GAM2599 EXTL2 5' AGAAGGATAGATGCACGCTA 9325 A C TA
 TAGC TGC TCT ATTTTCT
 ||| ||| ||| |||||
 ATCG ACG AGA TAGGAAGA
 C T _
 GAM2599 FOXE1 3' AGAAAAATTAAGTTAGGGCA 16777 _
 TGCCT CTTAATTTTCT
 |||| ||||| |||||
 ACGGG GAATTAAAAAGA
 ATT
 GAM2599 FZD3 3' AGAAAAATGCTGGAACATGCT 34257 CC TA_
 AGCATG TCT ATTTTCT
 ||||| || |||||
 TCGTAC AGG TAAAAAGA
 A_ TCG
 GAM2599 RRM2B 3' AAAAATTAAGAGTGTGTT 68429 C
 AGCATGC TCTTAATTTT
 ||||| ||||| |||||

TTGTGTG AGAATTAAAA

GAM2599 ZNF132 3' AGAAAAATTACCTCCATGCT 14286 CCTCT
AGCATG TAATTTTCT
||||| |||||||
TCGTAC ATTA AAAAGA
CTCC_

GAM2599 BAP29 3' AGAAAAATATAAGCATGTTA 61331 CTCTTA
TAGCATGC ATTTTCT
||||| |||||||
ATTGTACG TAAAAAGA
AATA_

GAM2599 FAM8A1 3' AGAAAAATCTGGCATACTG 33197 C TCTTA
TAG ATGCC ATTTTCT
||| ||| |||||||
GTC TACGG TAAAAAGA
A TC_

GAM2599 FLJ10648 3' AGAAAAATTAGGTTCCATGC 36888 CCT
GCATG CTTAATTTTCT
||||| |||||||
CGTAC GGATTAAAAAGA
CTT

GAM2599 FLJ10970 3' AGAAAAATCAAGATAGGCCTG 37476 T _ A
CA GCC TCTT ATTTTCT
|| ||| ||| |||||||
GT CGG AGAA TAAAAAGA
C AT C

GAM2599 FLJ14735 3' AAAAACTGATGAGGCATGC 52663 _ A
GCATGCCTC TTA TTTT
||||||| ||| |||||
CGTACGGAG AGT AAAAA
T C

GAM2599 KIAA0830 3' AGAAAAATAGCGGAGGCA 70266 TA_
TGCCTCT ATTTTCT
||||| |||||||
ACGGAGG TAAAAAGA
CGA

GAM2599 KIAA0907 3' AGAAAAATTAAGCTGGGCA 30862 _
TGCCT CTTAATTTTCT
||||| |||||||
ACGGG GAATTAAAAAGA
TC

GAM2599 KIAA1348 3' AGAAACTTTGAGCCATGCTA 69116 CCT TT
TAGCATG CTAA TTTCT
||||| ||| |||||
ATCGTAC GAGTT AAAGA
C_ TC

GAM2599 RNF2 3' AGAAAAATTAAATTGGTAGT 24256 A TC_
GC TGCC TTAATTTTCT
|| ||| |||||||

		TG ATGG AATTAAAAAGA		
		— TTA		
GAM2599	LOC143146 3'	AGAAAATGGCCGAGGCATGCTA	60763	TTAAT
		TAGCATGCCTC TTTTCT		
		ATCGTACGGAG AAAAGA		
		CCGGT		
GAM2599	LOC146059 3'	AGAAAAGTCCAGAGATGC	78082	GC TA
		GCAT CTCT ATTTTTCT		
		CGTA GAGA TGAAAAGA		
		— CC		
GAM2599	LOC151391 3'	AGAAAGATCAAAGCATGC	86511	CTC A
		GCATGC TT ATTTTTCT		
		CGTACG AA TAGAAAGA		
		A_ C		
GAM2599	LOC157507 5'	AAAGAAGAGGAGGCAACTA	82374	CA AA
		TAG TGCCTCTT TTTT		
		ATC ACGGAGGA AGAAA		
		A_ GA		
GAM2599	LOC158434 3'	AAAAATTACAAGGCATGC	88156	CT
		GCATGCCT TAATTTT		
		CGTACGGA ATTA AAAA		
		AC		
GAM2599	LOC220020 5'	AGAAAACAGGTGAAGGCATGC	95043	_ TTAAT
		GCATGCCT C TTTTCT		
		CGTACGGA G AAAAGA		
		A TGGAC		
GAM2599	LOC221979 3'	AGAGTGCAGAAGGCATGC	94216	_ TA
		GCATGCCT CT ATTTT		
		CGTACGGA GA TGAGA		
		A CG		
GAM2599	LOC92078 3'	AGAAATCCGAAGAGGCAGCTA	68588	A AATT
		TAGC TGCCTCTT TTTCT		
		ATCG ACGGAGAA AAAGA		
		— GCCT		
GAM2599	LOC92080 5'	AGAAAAATCAAGACCATGTTA	68617	CC A
		TAGCATG TCTT ATTTTTCT		
		ATTGTAC AGAA TAAAAAGA		
		C_ C		
GAM2600	ABCC11 5'	TCTGCATGGCCCCAATATGC	53687	CACC _
		GCA GGGGCTATG AGA		

CGT CCCC GG TAC TCT
 ATAA G
 GAM2600 ABL1 3' GCTTCTCGGGGTCCAGTGC 24608 ACCG A
 GCAC GGGCT TGAGAAGC
 ||| ||| |||||
 CGTG CCTGG GCTCTTCG
 A__ G
 GAM2600 ABL1 3' GCTTCTCGGGGTCCAGTGC 18955 ACCG A
 GCAC GGGCT TGAGAAGC
 ||| ||| |||||
 CGTG CCTGG GCTCTTCG
 A__ G
 GAM2600 ACVR1B 3' GCGGGGAGTGCCCCGGTGCGC 40107 A T GAGAA
 GC CACCGGGGC AT GC
 || ||||| || ||
 CG GTGGCCCCG TG CG
 C _ AGGGG
 GAM2600 ADAM19 3' CTCCTAGCCCCGAGGTGC 53839 AC T
 GCAC CGGGGCTA GAG
 ||| ||||| ||
 CGTG GCCCCGAT CTC
 GA C
 GAM2600 AGL 5' GCCTCGGCGCTGCCCGGTCGC 7198 AC TA A_ A
 GC ACCGGGGC TG GA GC
 || ||||| || ||
 CG TGGCCCCG GC CT CG
 C_ TC GG C
 GAM2600 CD7 3' GCTTCTCAGTGGACAATGATGC 21543 _ CCGGGG _
 GCA CA CTA TGAGAAGC
 ||| || ||| |||||
 CGT GT GGT ACTCTTCG
 A AACA__ G
 GAM2600 CDKN2C 5' GCTTCTCGGGGGCCCCGCCGC 8847 ACAC G A
 GC CGGG CT TGAGAAGC
 || ||| || |||||
 CG GCCC GG GCTCTTCG
 CC__ G G
 GAM2600 CST2 3' GCTTCTCATAGCCCTGGT 8998
 ACCGGGGCTATGAGAAGC
 ||||| |||||
 TGGTCCCGATACTCTTCG
 GAM2600 CST3 3' GCTTCTCATAGCCCCGGTGTGC 5437
 GCACACCGGGGCTATGAGAAGC
 ||||| ||||| |||||
 CGTGTGGCCCCGATACTCTTCG
 GAM2600 EPHA8 3' GCCCCTCACTCTAGTGTGT 40435 CG CTA AA
 GCACAC GGG TGAG GC
 ||||| || ||| ||

			TGTGTG CTC ACTC CG		
			AT ____ CC		
GAM2600	FGFR1	3'	GCTCCCCATACCCCGGTGTGC 43888	C	AGA
			GCACACCGGGG TATG AGC		
			CGTGTGGCCCC ATAC TCG		
			____ CCC		
GAM2600	GFAP	3'	GCTTCTTAACCCAGTAAGC 10782	AC C	CTA
			GC AC GGGG TGAGAAGC		
			CG TG CCCC ATTCTTCG		
			AA A A__		
GAM2600	HADHA	3'	GCTTCTCACCACGGTGT 5735	G	CTA
			ACACCG GG TGAGAAGC		
			TGTGGC CC ACTCTTCG		
			A ____		
GAM2600	HPCAL1	5'	CTCCTCCCGGCTCGGCGC 10967	ACA	AT A
			GC CCGGGGCT GAG AG		
			CG GGCTCCGG CTC TC		
			C__ CC C		
GAM2600	ICAM1	3'	CTTCTCATTGGCCAACCTGC 72038	CACCGG	_
			GCA GGCTA TGAGAAG		
			CGT CCGGT ACTCTTC		
			CCAA__ T		
GAM2600	ILF1	5'	CTCAGCTCCGGTGCGC 16920	A	AT
			GC CACCGGGGCT GAG		
			CG GTGGCCTCGA CTC		
			C ____		
GAM2600	IRTA2	3'	GCTTCTCACACTTTCATGTGC 49232	CC GG	CTA
			GCACA G G TGAGAAGC		
			CGTGT C T ACTCTTCG		
			A_ TT CAC		
GAM2600	JUP	3'	GCTTCCCCAAGCACGGTGTGC 11109	GG A A_	
			GCACACCG GCT TG GAAGC		
			CGTGTGGC CGA AC CTTCG		
			A_ _ CC		
GAM2600	JUP	3'	GCTTCTCTCTCCAGGGTGC 11110	A _	CTAT
			GCAC CC GGGG GAGAAGC		
			CGTG GG CCTC CTCTTCG		
			_ A T__		
GAM2600	LZTS1	3'	GCTGTCCCAGCCCCGGCAAGC 41035	ACA	AT GA
			GC CCGGGGCT GA AGC		

CG GGCCCCGA CT TCG
 AAC CC G_
 GAM2600 MASP1 3' CTTCTTACCCCAGTGGC 58213 A C CTA
 GC CAC GGGG TGAGAAG
 || ||| ||| |||||
 CG GTG CCCC ATTCTTC
 _ A _
 GAM2600 NLGN2 5' CTCGTGGCCCGGCGTGC 89533 A G
 GCAC CCGGG CTATGAG
 ||| |||| |||||
 CGTG GGCCC GGTGCTC
 C _
 GAM2600 STX1A 3' GCTTCTCATGGGAAATGTGC 17211 CCGGGG
 GCACA CTATGAGAAGC
 |||| |||||
 CGTGT GGTACTCTTCG
 AAAG_
 GAM2600 SYK 3' CTTCTCTGGGTCCCGGGGTGC 13498 A AT
 GCAC CCGGGGCT GAGAAG
 ||| ||||| |||||
 CGTG GGCCCTGG CTCTTC
 G GT
 GAM2600 SYNGR1 3' TCCCCATGTCCTGGTGCGC 17513 A T A_
 GC CACCGGGGC ATG GA
 || ||||| ||| ||
 CG GTGGTCCTG TAC CT
 C _ CC
 GAM2600 TNFRSF1B 3' TTCCTCCGGTGTGC 8405 CTA
 GCACACCGGGG TGAG
 ||||| |||||
 CGTGTGGCCTC ACTT
 _
 GAM2600 TPS1 3' CTCCGGAGGGGCCCTGGTGTGC 61103 _ AT_
 GCACACC GGGGCT GAG
 ||||| ||||| |||
 CGTGTGG CCCC GG CTC
 T GAGGC
 GAM2600 UBE3A 3' CTTCTCATCCACTGTGC 56439 CCG GCT
 GCACA GG ATGAGAAG
 |||| || |||||
 CGTGT CC TACTCTTC
 CA_ _
 GAM2600 UBE3A 3' CTTCTCATCCACTGTGC 56442 CCG GCT
 GCACA GG ATGAGAAG
 |||| || |||||
 CGTGT CC TACTCTTC
 CA_ _
 GAM2600 UBE3A 5' GCCCCTCAGCCCCCGGTGTG 56443 CTA AA
 CACACCGGGG TGAG GC
 ||||| |||| ||

			GTGTGGCCCC	ACTC	CG			
			CCG	CC				
GAM2600	UBE3A	3'	CTTCTCATCCACTGTGC	6625	CCG	GCT		
			GCACA	GG	ATGAGAAG			
			CGTGT	CC	TACTCTTC			
			CA_	___				
GAM2600	USP13	5'	CTCGGCTCCGGTGCGC	15453	A	AT		
			GC	CACCGGGGCT	GAG			
			CG	GTGGCCTCGG	CTC			
			C	___				
GAM2600	ZFP103	5'	GCCCCTCGGGCCCCGGCCTGC	20228	CA	A	AA	
			GCA	CCGGGGCT	TGAG	GC		
			CGT	GGCCCCGG	GCTC	CG		
			CC	_	CC			
GAM2600	ZNF216	5'	CTTCCCGAGCTCCGGCGT	21172	A	A	A	
			AC	CCGGGGCT	TG	GAAG		
			TG	GGCCTCGA	GC	CTTC		
			C	_	C			
GAM2600	ADMR	5'	GCTCCCCATAGCCTGGACCTGC	24388	CA_	G	AGA	
			GCA	CCGGG	CTATG	AGC		
			CGT	GGTCC	GATAC	TCG		
			CCA	_	CCC			
GAM2600	ALS2CR3	3'	GCTTCTCATCAGATGACGTGGC	31183	A	CGGGG	_	
			GC	CAC	CT	ATGAGAAGC		
			CG	GTG	GA	TACTCTTCG		
			_	CAGTA	C			
GAM2600	AP1M2	3'	GCTTCCTTACAGCCCCGGATGC	19724	CA	A	_	
			GCA	CCGGGGCT	TGAG	AAGC		
			CGT	GGCCCCGA	ATTC	TTCG		
			A_	C	C			
GAM2600	ATF3	3'	GCTTGATGAGCCCCGGTGTGT	15734		ATGAG		
			GCACACCGGGGCT	AAGC				
			TGTGTGGCCCCGA	TTCG				
			GTAG_					
GAM2600	C2orf7	3'	CTTCTCATCAGGGTTGC	51272	C	GG	GCT	
			GCA	ACC	G	ATGAGAAG		
			CGT	TGG	C	TACTCTTC		
			_	GA	___			
GAM2600	CAM-KIIN	5'	GCTCCTCAGCCCCGGATGC	53835	CA	AT	A	
			GCA	CCGGGGCT	GAG	AGC		

CGT GGCCCCGA CTC TCG
 A _ _ C
 GAM2600 CHRFAM7A 3' CTCCTACATTGCCTGGTGTGC 96719 GT _ A
 GCACACCGGG C ATG AG AG
 ||||| ||||
 CGTGTGGTCC G TAC TC TC
 _ T A C
 GAM2600 DCOHM 3' GCTTCTCATCCCAGGATGC 50531 CA G CT
 GCA CC GGG ATGAGAAGC
 ||| |||||
 CGT GG CCC TACTCTTCG
 A _ A _
 GAM2600 DKFZP434I116 5' CTCACCCTGGTGTGC 31935 CTA
 GCACACCGGGG TGAG
 ||||| ||||
 CGTGTGGTCCC ACTC

 GAM2600 FBXO9 5' GCTTCTCAGGGCGGCTTGC 54256 CA GGG A
 GCA CC GCT TGAGAAGC
 ||| || |||||
 CGT GG CGG ACTCTTCG
 TC _ G
 GAM2600 FLJ20320 5' CTTCTCCAGCTGCCCCAGTGGC 35424 A C TAT_
 GC CAC GGGGC GAGAAG
 || ||||| |||||
 CG GTG CCCC G CTCTTC
 _ A TCGAC
 GAM2600 FLJ22215 3' CTCTGGCCCCGGAGTGC 98639 A T
 GCAC CCGGGGCTA GAG
 ||||| ||||| ||||
 CGTG GGCCCCGGT CTC
 A _
 GAM2600 GDAP2 3' GCTTCTTGGTTCCCAGGATGC 35125 CA G CTA
 GCA CC GGG TGAGAAGC
 ||| ||||| |||||
 CGT GG CCC GTTCTTCG
 A _ A TTG
 GAM2600 GTF3C1 3' CTCGGCAGACCCCACTGTGC 9507 CC _ A_
 GCACA GGGG CT TGAG
 ||||| ||||| ||||
 CGTGT CCCC GA GCTC
 CA A CG
 GAM2600 HSJ001348 5' GCTCCAAAGACCCCGACAGGC 62857 ACAC _ A A A
 GC CGGGG CT TG GA GC
 || ||||| ||||| ||||
 CG GCCC GA AC CT CG
 GACA A A _ _
 GAM2600 KIAA0354 3' GCTTCCAGCTGCCCAGTGGC 30193 A CG TA_ A
 GC CAC GGGC TG GAAGC
 || ||||| ||||| |||||

CG GTG CCCG AC CTTCG
 _ A_ TCG _
 GAM2600 KIAA0759 3' GCTCCCCACAGACCTGGTGT 67888 G A AGA
 ACACCGGG CT TG AGC
 ||||| || || ||
 TGTGGTCC GA AC TCG
 A C CCC
 GAM2600 KIAA0775 5' GCTGCCACAGCCCCGGTGCGC 28956 A A AGA
 GC CACCGGGGCT TG AGC
 || ||||| || ||
 CG GTGGCCCCGA AC TCG
 C C CG_
 GAM2600 KIAA0945 3' TCTCACAGTCATGGGTGTG 30906 GG_ A
 CACACC GGCT TGAGA
 |||| ||| ||||
 GTGTGG CTGA ACTCT
 GTA C
 GAM2600 KIAA1115 5' GCCTCCCAGGTACCCAGTGTG 30694 C CTA_ A A
 CACAC GGGG TG GA GC
 |||| ||| || ||
 GTGTG CCCC AC CT CG
 A ATGG C C
 GAM2600 KIAA1750 3' GCCTCCCATAGCCTCTTGC 68810 CACC A A
 GCA GGGGCTATG GA GC
 || ||||| || ||
 CGT CTCCGATAC CT CG
 T_ C C
 GAM2600 KIAA1918 3' CTTCTCCCTCCGGTGGC 73538 A CTAT
 GC CACCGGGG GAGAAG
 || ||||| ||||
 CG GTGGCCTC CTCTTC
 _ C_
 GAM2600 KIAA1952 5' GCCTCCGTGGTCCGATGTGC 73547 C G A A
 GCACA CGGG CTATG GA GC
 |||| ||| |||| || ||
 CGTGT GCCT GGTGC CT CG
 A _ _ C
 GAM2600 LSM1 5' GCTTCCGGCAGGCCCGGCGGC 27841 ACA A_ A
 GC CCGGGGCT TG GAAGC
 || ||||| || ||||
 CG GGCCCCGG GC CTTCG
 GC_ ACG _
 GAM2600 MAGE-E1 3' GCCCCTCGGCCCGGATGGC 48676 A C CTA AA
 GC CA CGGGG TGAG GC
 || || |||| ||| ||
 CG GT GCCCC GCTC CG
 _ A CG_ CC
 GAM2600 MGC26914 5' GCTTCTCCAGTGGCCCCGGTGG 59330 A _
 C GC CACCGGGGCTAT GAGAAGC
 || ||||| |||||

CG GTGGCCCCGGTG CTCTTCG
 — AC
 GAM2600 MGC3178 3' CTCTGGCCCTGGTGTGC 48717 T
 GCACACCGGGGCTA GAG
 |||||
 CGTGTGGTCCCGGT CTC

—
 GAM2600 NFASC 3' CTCAGCCCCGGGTGC 70857 A ATGA
 GCAC CCGGGGCT GAAG
 ||| ||||| |||
 CGTG GGCCCCGA CTC

— —
 GAM2600 NPD009 5' GCCTCTTCATCTCCCGGTG 96749 CT _ A
 CACCGGGG ATGA GA GC
 ||||| ||| ||
 GTGGCCCT TACT CT CG
 C_ T C

GAM2600 PIF1 5' GCTCCTCTAGCCCAGTGTGT 61677 CG T A
 GCACAC GGGCTA GAG AGC
 ||||| ||||| ||| |||
 TGTGTG CCGGAT CTC TCG
 A_ _ C

GAM2600 PPIL3 5' CTTCTTGTCCCAAGTGC 56476 ACC TAT
 GCAC GGGGC GAGAAG
 ||| |||| |||||
 CGTG CCCTG TTCTTC
 A_ _

GAM2600 PRO2405 5' GCTTCTCAACGTTCAAGTGC 38418 ACCG TA
 GCAC GGGC TGAGAAGC
 ||| ||| |||||
 CGTG CTTG ACTCTTCG
 A_ CA

GAM2600 RALGPS1A 3' GCTTTTTACACCCCAAGTGC 28333 ACC CTA
 GCAC GGGG TGAGAAGC
 ||| ||| |||||
 CGTG CCCC ATTTTTCG
 AA_ AC_

GAM2600 RCD-8 3' GCTCCGTTATGGCCCAGGTGCG 27521 A G GA_
 C GC CACC GGGCTATGA AGC
 || ||| ||||| |||
 CG GTGG CCGGTATT TCG
 C A GCC

GAM2600 SCLY 3' GCTCCTCTGGCCTCAGTGC 33670 ACC T A
 GCAC GGGGCTA GAG AGC
 ||| ||||| ||| |||
 CGTG CTCCGGT CTC TCG
 A_ _ C

GAM2600 SIMRP7 3' GCTTCTCATGCAAGCCACG 93978 G _
 CG GGCT ATGAGAAGC
 || ||| |||||

GC CCGA TACTCTTCG
 A ACG
 GAM2600 TA-PP2C 5' CTCTGGCTCCGGTGCGC 58405 A T
 GC CACCGGGGCTA GAG
 || ||||| ||
 CG GTGGCCTCGGT CTC
 C _
 GAM2600 TSPAN-5 5' GCTCCGGCGGCCTCGGCGC 20369 ACA A_ A A
 GC CCGGGGCT TG GA GC
 || ||||| || ||
 CG GGCTCCGG GC CT CG
 C_ CG _ _
 GAM2600 LOC112476 3' GCTTTTCAACCCCAGTCCGC 59787 AC C CTA
 GC AC GGGG TGAGAAGC
 || || ||| |||||
 CG TG CCCC ACTTTTCG
 CC A A_
 GAM2600 LOC121536 5' CTCGTTGAGCCCCGGCGC 74525 ACA _
 GC CCGGGGCT ATGAG
 || ||||| ||||
 CG GGCCCCGA TGCTC
 C_ GT
 GAM2600 LOC139496 5' CGCTTCCCAGCTGGCACCCCGG 76360 _ _ A _
 TGTG CACACCGGG GCTA TG GAAGC G
 ||||| ||| || ||| |
 GTGTGGCCC CGGT AC CTTCG C
 CA CG C _
 GAM2600 LOC142937 5' GCTTCTCAAGCTCAAATGC 57446 CACCG A
 GCA GGGCT TGAGAAGC
 || |||| |||||
 CGT CTCGA ACTCTTCG
 AAA_ _
 GAM2600 LOC143666 5' GCTCCTCCCTAGCCCCGCGC 83884 ACAC T_ A
 GC CGGGGCTA GAG AGC
 || ||||| || |||
 CG GCCCCGAT CTC TCG
 C_ CC C
 GAM2600 LOC145623 5' CTTCTCATCCACTGTGC 84392 CCG GCT
 GCACA GG ATGAGAAG
 |||| || |||||
 CGTGT CC TACTCTTC
 CA_ _
 GAM2600 LOC148089 3' CTCCTCAGCCCCGGCAGC 79331 ACA AT A
 GC CCGGGGCT GAG AG
 || ||||| || ||
 CG GGCCCCGA CTC TC
 AC_ _ C
 GAM2600 LOC148181 5' GCTCCTCCTGCCTCCCAGTGGC 79436 A C_ TAT A
 GC CAC GGGGC GAG AGC
 || ||| |||| ||| |||

	CG GTG CTCCG CTC TCG	
	_ ACC TC_ C	
GAM2600 LOC149276 3'	GCTTCCCATACCAGGAGC 85537	ACA GG C A
	GC CC GG TATG GAAGC	
	CG GG CC ATAC CTTCG	
	A__ A_ _ C	
GAM2600 LOC149373 3'	CTTCTCACTCTCGATGTG 80093	C CTA
	CACA CGGGG TGAGAAG	
	GTGT GCTCT ACTCTTC	
	A C__	
GAM2600 LOC149386 5'	CTTCTCATGGTTCATGC 85557	CACCG
	GCA GGGCTATGAGAAG	
	CGT CTTGGTACTCTTC	
	A__	
GAM2600 LOC149721 3'	CTTCTCATCTGCTGTGC 80317	C GGCT
	GCACA CGG ATGAGAAG	
	CGTGT GTC TACTCTTC	
	C _	
GAM2600 LOC150291 3'	CTTCCCATTCCAGTGTG 86131	C GCT A
	CACAC GGG ATG GAAG	
	GTGTG CCT TAC CTTC	
	A _ C	
GAM2600 LOC151300 3'	GCTTCTCACAGAAGGGTCTGC 86495	C GGGG A
	GCA ACC CT TGAGAAGC	
	CGT TGG GA ACTCTTCG	
	C GAA_ C	
GAM2600 LOC152018 3'	CTTCTCATAAACTGCATGC 86727	CAC GGC
	GCA CGG TATGAGAAG	
	CGT GTC ATACTCTTC	
	AC_ AA_	
GAM2600 LOC154990 5'	GCTCCTCCTGCCTCCCAGTGGC 82152	A C__ TAT A
	GC CAC GGGGC GAG AGC	
	CG GTG CTCCG CTC TCG	
	_ ACC TC_ C	
GAM2600 LOC155006 3'	CTCCTCATCCTGGTGT 82167	GCT A
	ACACCGGG ATGAG AG	
	TGTGGTCC TACTC TC	
	_ C	
GAM2600 LOC196812 3'	GCTTCTCACAGTTTTATGT 91126	CC A
	ACA GGGGCT TGAGAAGC	

TGT TTTTGA ACTCTTCG
 A_ C
 GAM2600 LOC202908 3' GCTCCTCCTGCCTCCCAGTGGC 90729 A C__ TAT A
 GC CAC GGGGC GAG AGC
 || ||| |||| ||| |||
 CG GTG CTCCG CTC TCG
 _ ACC TC_ C
 GAM2600 LOC203668 5' GCTCCTGCGTCCCCCGGTGTG 90983 CT _ A
 CACACCGGGG ATG AG AGC
 ||||| ||| ||| |||
 GTGTGGCCCC TGC TC TCG
 C_ G C
 GAM2600 LOC222057 3' GCTCCTCCTGCCTCCCAGTGGC 94357 A C__ TAT A
 GC CAC GGGGC GAG AGC
 || ||| |||| ||| |||
 CG GTG CTCCG CTC TCG
 _ ACC TC_ C
 GAM2600 LOC223009 5' GCCTCTCTAGTCCCAACTGC 96034 CACC T A
 GCA GGGGCTA GAGA GC
 ||| ||||| ||| |||
 CGT CCCTGAT CTCT CG
 CAA_ _ C
 GAM2600 LOC253258 5' GCTCCTCCCTAGCCCCGCGC 98230 ACAC T_ A
 GC CGGGGCTA GAG AGC
 || ||||| ||| |||
 CG GCCCGAT CTC TCG
 C__ CC C
 GAM2600 LOC253263 5' CATGAAACCCTGGTGTGC 98815 C__
 GCACACCGGGG TATG
 ||||| |||
 CGTGTGGTCCC GTAC
 AAA
 GAM2600 LOC255792 5' GCCCCTCGGATGCCCAAGTGTG 98470 CG TA_ AA
 CACAC GGGC TGAG GC
 |||| ||| ||| |||
 GTGTG CCCG GCTC CG
 A_ TAG CC
 GAM2600 LOC255975 5' GCCTCTCTAGTCCCAACTGC 97586 CACC T A
 GCA GGGGCTA GAGA GC
 ||| ||||| ||| |||
 CGT CCCTGAT CTCT CG
 CAA_ _ C
 GAM2600 LOC255975 3' GCTCCTCCTGCCTCCCAGTGGC 97587 A C__ TAT A
 GC CAC GGGGC GAG AGC
 || ||| |||| ||| |||
 CG GTG CTCCG CTC TCG
 _ ACC TC_ C
 GAM2600 LOC256158 5' GCTCCCAGAGGTCCCCAGGATG 99499 CA _ _ A_ A A
 C GCA CC GGGG CT TG GA GC
 ||| ||||| || ||| |||

CGT GG CCCC GG AC CT CG
 A_ A T AG C _
 GAM2600 LOC256451 3' GCTCCTGCTGCGGCCCGGGCG 97804 ACA ATG__ A
 C GC CCGGGGCT AG AGC
 || ||||| ||||
 CG GGCCCCGG TC TCG
 CG_ CGTCG C
 GAM2600 LOC256878 3' GCTCCTCCTGCCTCCCAGTGGC 98690 A C__ TAT A
 GC CAC GGGGC GAG AGC
 || || |||| ||||
 CG GTG CTCCG CTC TCG
 _ ACC TC_ C
 GAM2601 PPARGC1 3' TTTGGTAACCGAACTGGTGCTT 26086 G CTACAT
 AAGC ACCAG TTACCAA
 ||| |||| |||||
 TTCG TGGTC AATGGTTT
 _ AAGCC_
 GAM2601 RAB27A 3' TGAACATAGCTGGTGCTT 17151 G CA
 AAGC ACCAGCTA TTTA
 ||| ||||| |||
 TTCG TGGTCGAT AAGT
 _ AC
 GAM2601 C1orf22 3' GTAAATATTCCAGCCGGTCGTT 48042 A AC__
 T AAGCGACC GCT ATTTAC
 ||||| || ||||
 TTTGCTGG CGA TAAATG
 C CCTTA
 GAM2601 DKFZP566K1924 5' TTGGCATAGTGGTCGCTT 74201 G CATTTA
 AAGCGACCA CTA CCAA
 ||||| || |||
 TTCGCTGGT GAT GGTT
 _ AC__
 GAM2601 DKFZP586D0623 3' GTAAATGTGACTCGCT 72429 CCA C
 AGCGA G TACATTTAC
 |||| | |||||
 TCGCT C GTGTAAATG
 __ A
 GAM2601 DRG1 3' TGGTAGGCTGGTCAGCT 15974 _ ACATT
 AGC GACCAGCT TACCA
 || ||||| ||||
 TCG CTGGTCGG ATGGT
 A ____
 GAM2601 FLJ32861 5' GTATGATGTAGCCAATTGCT 59382 CCA _
 AGCGA GCTACATT TAC
 |||| ||||| |||
 TCGTT CGATGTAG ATG
 AAC T
 GAM2601 KIAA0016 3' GTAAATGTTTGGTTCCTT 29309 C CT
 AAG GACCAG ACATTTAC
 || ||||| |||||

				TTC TTGGTT TGTAATG			
				C _			
GAM2601	KIAA1674	3'	TTTGGTAAATGTAGACTGTGC	69352	AC	_	
			GCG CAG CTACATTTACCAA				
			CGT GTC GATGTAAATGGTTT				
			_ A				
GAM2601	MRVI1	5'	TGAGGCCAGCTGGTCGGCT	56099	_		ACA
			AGC GACCAGCT TTTA				
			TCG CTGGTCGA GAGT				
			G CCG				
GAM2601	LOC157681	5'	TTTGTTTCTGAAGCTGGTCCTT	82459	C		A TTT
			AAG GACCAGCT CA ACCAAA				
			TTC CTGGTCGA GT TGGTTT				
			_ A CT_				
GAM2601	LOC200197	3'	TTGGACAGGATGTAGCTGGTCA	90023	C		A_
	CT		AG GACCAGCTACATTT CCAA				
			TC CTGGTCGATGTAGG GGTT				
			A ACA				
GAM2601	LOC222936	5'	TGGTAAATTTTGCAGTTGCT	96027		CA	TAC
			AGCGAC GC ATTTACCA				
			TCGTTG CG TAAATGGT				
			A_ TTT				
GAM2601	LOC91064	5'	TTGGGGGTGTAGCTGGCGC	65393	A		A
			GCG CCAGCTACATTT CCAA				
			CGC GGTGATGTGGG GGTT				
			_ _				
GAM2601	LOC92196	3'	TTGGTAAATTAAGCAGCTT	68977		GACCA	AC
			AAGC GCT ATTTACCAA				
			TTCG CGA TAAATGGTT				
			A_ AT				
GAM2602	SCAMP1	3'	GCTAAATAAATATTCTCC	54500	T		C
			GGA AATATT ATTTAGC				
			CCT TTATAA TAAATCG				
			C A				
GAM2602	SCAMP1	3'	GCTAAATAAATATTCTCC	54501	T		C
			GGA AATATT ATTTAGC				
			CCT TTATAA TAAATCG				
			C A				
GAM2602	NX-17	3'	TGAATATCAGCCCCTAATA	40706		ATA_	
			TATTAGGG ATATTCA				

			ATAATCCC	TATAAGT		
			CGAC			
GAM2602	LOC161589	3'	GCTAAATGAATATTATCCCTAA	83159		
		TA	TATTAGGGATAATATTCATTTAGC			
			ATAATCCCTATTATAAGTAAATCG			
GAM2603	KLRC1	3'	GACACTTCAATAAAGCTA	11210	ACTG	CG
			TAGCTTTA	TGA	GGT	GTC
			ATCGAAAT	ACT	TCACAG	
			A			
GAM2603	SLC16A2	3'	GCACCACAGTTAAATCTA	22525	C	GACG
			TAG	TTTAACTGT	GGTGT	
			ATC	AAATTGACA	CCACG	
			T			
GAM2603	LGALS8	3'	ACACTTATAGCCAGTTAAAGC	22447		_GAC
			GCTTTAACTG	T	GGGTGT	
			CGAAATTGAC	G	TTCACA	
			C	ATA		
GAM2604	CDH12	3'	CTTATCATTTAAAGTGGTGTA	15777	CCCAA	GA
			TACACCACT	GAA	ATAAG	
			ATGTGGTGA	TTT	TATTC	
			AA		AC	
GAM2604	GOCAP1	3'	ATTGTTCTTGGGAGCAGTGTA	43007	CA	G
			TACAC	CTCCCAAGAA	AAT	
			ATGTG	GAGGGTTCTT	TTA	
			AC		G	
GAM2604	DKFZp434N2435	5'	CTTATTACTGTGGGGTGGT	98090	T	AGAAG
			ACCAC	CCCA	AATAAG	
			TGGTG	GGGT	TTATTC	
				GTCA		
GAM2604	DKFZP564I122	3'	CTTATTCTTCTCCCTCATGTGT	63877	CACTCCCA	
		A	TACAC	AGAAGAATAAG		
			ATGTG	TCTTCTTATTC		
			TACTCCC			
GAM2604	FLJ21791	3'	CTTATTTGCAGAAAGTGGTGTA	62126	CCCAAGAA	
			TACACCACT	GAATAAG		
			ATGTGGTGA	TTTATTC		
			AGACG			
GAM2604	HMP19	3'	CTTATTCTTTGTTAGGAAAATG	88860	CCAC	CAA
		TA	TACA	TCC	GAAGAATAAG	

		ATGT AGG TTTCTTATTC	
		AAA_ ATTG	
GAM2604 KIAA1579	3'	TACTCTTAGTGGTGTA 37154	CCCAAG A
		TACACCACT AAGA TA	
		ATGTGGTGGA TTCT AT	
		_____ C	
GAM2604 KIAA1719	3'	TCTGTCTTGGGAGTGGTGTA 68742	_
		TACACCACTCCCAAGA AGA	
		ATGTGGTGAGGGTTCT TCT	
		G	
GAM2604 KIAA1853	3'	TTTTTCTTGGAAGCAGTG 69929	CA C
		CAC CT CCAAGAAGAA	
		GTG GA GGTTCCTTTT	
		AC A	
GAM2604 KIAA1877	3'	CTTATTCTTCTGCCATGAGT 66748	CCA__
		ACTC AGAAGAATAAG	
		TGAG TCTTCTTATTC	
		TACCG	
GAM2604 KIAA1906	3'	CTTATTCTTCTTGACTTTTGG 73571	CTCC_
		CCA CAAGAAGAATAAG	
		GGT GTTCTTCTTATTC	
		TTTCA	
GAM2604 OSBPL11	3'	CTTAATTTCCCAAGAGTGGTG 43206	CCAA AA
		CACCACTC GAAG TAAG	
		GTGGTGAG CTTT ATTC	
		AACC A_	
GAM2604 YME1L1	3'	TCATTCTTGATGTGGTGTA 58438	TCC _
		TACACCAC CAAGAA GA	
		ATGTGGTG GTTCTT CT	
		TA_ A	
GAM2604 YME1L1	3'	TCATTCTTGATGTGGTGTA 27323	TCC _
		TACACCAC CAAGAA GA	
		ATGTGGTG GTTCTT CT	
		TA_ A	
GAM2604 ZNF262	3'	CTTATTTTGTGGGAGT 18723	A
		ACTCCCAAG AGAATAAG	
		TGAGGGTTT TTTTATTC	
		G	
GAM2604 LOC91960	3'	TGTGGCTTGGAACGTGGTGTA 68294	TC_ AAGA
		TACACCAC CCAAG ATA	

		ATGTGGTG GGTTC TGT		
		CAA GG__		
GAM2605	PROK1	3' CACCAACCTGCTGGCTTTAGAA 51567	TCAC G	AGC
		TTCT GG CAGCA TGGTG		
		AAGA TC GTCGT ACCAC		
		TT__ G CCA		
GAM2605	HSA404617	5' CACCAGCTCGCCCTTCTGAGAA 73089	CAC_	AGCA
		TTCTT GGGC AGCTGGTG		
		AAGAG CCCG TCGACCAC		
		TCTT C__		
GAM2605	KIAA0431	3' CACCAGCTTGGGCAACATAAGA 31546	CACGG	AG
	A	TTCTT GC CAAGCTGGTG		
		AAGAA CG GTTCGACCAC		
		TACAA G_		
GAM2605	PAK6	5' ACCAGCCTGCAGTGGAGAA 39806	GG	CAA
		TTCTTCAC GCAG GCTGGT		
		AAGAGGTG CGTC CGACCA		
		A_ _		
GAM2606	ADAMTS13	3' CCCCAAACGTGCATGGA 58151	G	CC A
		TC GTGTACGT TGG GG		
		AG TACGTGCA ACC CC		
		G AA _		
GAM2606	GPR84	3' CTCCAGGACCAAAGTG 40158	CGG	TAC
		CACT TG GTCCTGGAG		
		GTGA AC CAGGACCTC		
		A_ _		
GAM2606	PAX5	3' CCTCCAGGACCCCAGCAAGTG 34127	CG	GTAC
		CACT GT GTCCTGGAGG		
		GTGA CG CAGGACCTCC		
		A_ ACCC		
GAM2606	RBP3	3' CCTCTGGGACACACACCAAG 12795	C	AC TG
		CT GGTGT GTCC GAGG		
		GA CCACA CAGG CTCC		
		A CA GT		
GAM2606	TCF19	3' CCTCCAGGAAATTGCCAGTG 99578	C	TACG
		CACT GGTG TCCTGGAGG		
		GTGA CCGT AGGACCTCC		
		_ TAA_		
GAM2606	TCF19	3' CCTCCAGGAAATTGCCAGTG 99687	C	TACG
		CACT GGTG TCCTGGAGG		

			GTGA CCGT AGGACCTCC		
			_ TAA_		
GAM2606	TEM8	3'	CCTGGAGTTACGCACACTGAGT 36855	A ____	T
	G		CACTCGGTGT CG TCC GG		
			GTGAGTCACA GC AGG CC		
			C ATTG T		
GAM2606	UBASH3A	3'	CCTGCAGCATGTACACCGAGTG 39049	C	G
			CACTCGGTGTACGT CTG AGG		
			GTGAGCCACATGTA GAC TCC		
			C G		
GAM2606	CABP1	3'	CCTCCAGGACTGCCAAG 16256	C	TAC
			CT GGTG GTCCTGGAGG		
			GA CCGT CAGGACCTCC		
			A ____		
GAM2606	CABP1	3'	CCTCCAGGACTGCCAAG 49130	C	TAC
			CT GGTG GTCCTGGAGG		
			GA CCGT CAGGACCTCC		
			A ____		
GAM2606	DKFZp434A1010	3'	CCTCCAGGAGCCCCCAG 71854	C	T ACG
			CT GG GT TCCTGGAGG		
			GA CC CG AGGACCTCC		
			C C ____		
GAM2606	DOCK3	3'	CCTCCAGGGTAGAGATGCACCG 67092	C	CG ____
	AATG		CA TCGGTGTA TCCTGGAGG		
			GT AGCCACGT GGGACCTCC		
			A AGAGAT		
GAM2606	FLJ13782	3'	CCTCCAGGGTTCCCAGCAAGTG 46700	CG	GTACG_
			CACT GT TCCTGGAGG		
			GTGA CG GGGACCTCC		
			A_ ACCCTT		
GAM2606	FLJ21034	3'	CCTCCCTGCAACACCGAGTG 46864	AC	CCT
			CACTCGGTGT GT GGAGG		
			GTGAGCCACA CG CCTCC		
			A_ TC_		
GAM2606	KIAA0792	3'	CCTCCAGGGGGGCACCAAG 28765	C	ACG
			CT GGTGT TCCTGGAGG		
			GA CCACG GGGACCTCC		
			A G_		
GAM2606	KIAA1028	3'	CCTCCAGGACATAGCCAG 93589	C	GTAC
			CT GGT GTCCTGGAGG		

		GA CCG CAGGACCTCC	
		_ ATA_	
GAM2606	MGC9753	5' CCTCCAGGAAGGTCACAAAGTG 54187	CG T G_
		CACT GTG AC TCCTGGAGG	
		GTGA CAC TG AGGACCTCC	
		AA _ GA	
GAM2606	RARRES2	3' CCTCCAGGACCGCTGCGGGTG 12778	GT AC
		CACTCG GT GTCCTGGAGG	
		GTGGGC CG CAGGACCTCC	
		GT C_	
GAM2606	RDH-E2	3' CCTGGATACGCAGACCGAGTG 58070	_ AC T
		CACTCGGT GT GTCC GG	
		GTGAGCCA CG TAGG CC	
		GA CA T	
GAM2606	Spir-2	3' CCTCCAGGAGGCACCAG 71156	C ACG
		CT GGTGT TCCTGGAGG	
		GA CCACG AGGACCTCC	
		_ G_	
GAM2606	TRIM11	3' CTCCAGCCACCGGGTG 73190	TACGTC
		CACTCGGTG CTGGAG	
		GTGGGCCAC GACCTC	
		C_____	
GAM2606	ZNF340	5' CCTCCAGGACCTGCCCCTGTG 85711	T T C
		CAC CGG GTA GTCCTGGAGG	
		GTG GCC CGT CAGGACCTCC	
		T _ C	
GAM2606	LOC124411	3' CCCCAGAGGCCACACCGGG 74772	AC _ A
		CTCGGTGT GTC CTGG GG	
		GGGCCACA CGG GACC CC	
		CC A _	
GAM2606	LOC149076	3' CCTCCAGGAACCACCAAG 79877	C TACG
		CT GGTG TCCTGGAGG	
		GA CCAC AGGACCTCC	
		A CA_	
GAM2606	LOC165283	3' CCTCCAGGATGCACAGAGTG 88545	G AC
		CACTC GTGT GTCCTGGAGG	
		GTGAG CACG TAGGACCTCC	
		A _	
GAM2606	LOC166983	5' CTCCAGGAAGCCCAGTG 88618	C T ACG
		CACT GG GT TCCTGGAG	

GTGA CC CG AGGACCTC
 _ _ A_
 GAM2606 LOC197416 3' CCCCAGAGGCCACACCGGG 91322 AC _ A
 CTCGGTGT GTC CTGG GG
 ||||| ||| ||| ||
 GGGCCACA CGG GACC CC
 CC A _
 GAM2606 LOC200058 3' CCTCCAGGTCCACGGAGTG 89959 G TACGT
 CACTC GTG CCTGGAGG
 ||||| ||| |||||
 GTGAG CAC GGACCTCC
 G CT_
 GAM2606 LOC255652 3' CCTCCAGGACTGCCACAGAG 98530 G _ C
 CTC GTG TA GTCCTGGAGG
 ||| ||| || |||||
 GAG CAC GT CAGGACCTCC
 A C _
 GAM2606 LOC256581 5' CCTCCAGGAGGCACGGAATG 99432 C G ACG
 CA TC GTGT TCCTGGAGG
 || ||| ||| |||||
 GT AG CACG AGGACCTCC
 A G G_
 GAM2607 BMP1 3' GGTCATCACCTCCAGT 21523 C CCCC
 AC GGGAGGTGA TGACC
 || ||||| |||
 TG CCCTCCACT ACTGG
 A _
 GAM2607 BMP1 3' GGTCATCACCTCCAGT 21535 C CCCC
 AC GGGAGGTGA TGACC
 || ||||| |||
 TG CCCTCCACT ACTGG
 A _
 GAM2607 CRYAA 3' GGCCAGGTGCCTCCTG 6366 ACC A
 CGGGAGGTG CCTG CC
 ||||| ||| ||
 GTCCTCCGT GGAC GG
 _ C
 GAM2607 GALNT2 3' CTGGCCAGAGTCTGTCCTGGTG 16815 GGT CC A
 CACCGGA GAC CTG CCAG
 ||||| ||| ||| |||
 GTGGTCCT CTG GAC GGTC
 GT_ A_ C
 GAM2607 IL6 3' CTGGTCAGAAACCTGTCC 7007 _ GACCC
 GGG AGGT CTGACCAG
 ||| ||| |||||
 CCT TCCA GACTGGTC
 G AA_
 GAM2607 MYO1D 3' AGCTGGACCACCTCCCGCTG 72240 C AC _
 CA CGGGAGGTG CC CT
 || ||||| || ||

			GT GCCCTCCAC GG GA		
			C CA TC___		
GAM2607 OTX1	3'	GGCCAGAGCCTCCCGGCG	28056	A	GACCC A
		C CCGGGAGGT CTG CC			
		G GGCCCTCCG GAC GG			
		C A___ C			
GAM2607 PNUTL1	3'	CTGGGCGGTGAGCCACCTCCTG	12190		ACCC_ A
G		CCGGGAGGTG CTG CCAG			
		GGTCCTCCAC GGC GGTC			
		CGAGT G			
GAM2607 PTPN14	3'	CTGGAGGAGAGTCACCTCC	19428		C__ GA
		GGAGGTGAC CCT CCAG			
		CCTCCACTG GGA GGTC			
		AGA _			
GAM2607 RASD1	3'	CTGGCGTCTCCCCTCCCGG	32727		T CCCC A
		CCGGGAGG GA TG CCAG			
		GGCCCTCC CT GC GGTC			
		C CT__ _			
GAM2607 SFTPA2	3'	TGGTCAGGCTCTCCAGGTG	23631	G	TGACC
		CACC GGAGG CCTGACCA			
		GTGG CCTCT GGA CTGGT			
		A C___			
GAM2607 TAZ	5'	GTCAGGGGCCAGTGTCTCG	5485	G _ A	
		CGGGA G TG CCCCTGAC			
		GCTCT T AC GGGGACTG			
		G G C			
GAM2607 CST8	5'	CTGGTCAGGTCAGCTCCC	19713	G	CC
		GGGAG TGACC TGACCAG			
		CCCTC ACTGG ACTGGTC			
		G _			
GAM2607 DKFZp434J0226	3'	GTCACCGGCCACCTCCCAGG	72794	_	A CC
		CC GGGAGGTG CC TGAC			
		GG CCCTCCAC GG ACTG			
		A C CC			
GAM2607 FKSG28	3'	CTGGCCAGTAGGACCTCC	48908		GA C_ A
		GGAGGT CC CTG CCAG			
		CCTCCA GG GAC GGTC			
		_ AT C			
GAM2607 GAB3	3'	GTCAGGGGTCGTCCAAGTG	55522	CG	GG
		CAC GGA TGACCCCTGAC			

GTG CCT GCTGGGGACTG
 A_ _
 GAM2607 KIAA0415 3' TCGGGATCACTTCCCAGTG 94170 C CC
 CAC GGGAGGTGA CCTGA
 ||| ||||| ||||
 GTG CCCTTCACT GGGCT
 A A_
 GAM2607 KIAA0420 3' GTCAGGGGTCACCAACTTG 64093 A_
 CGGG GGTGACCCCTGAC
 ||| |||||
 GTTC CCACTGGGGACTG
 AA
 GAM2607 KIAA0495 5' CTGGCCTCGGTCACCTCCCGG 63265 CCTGA
 CCGGGAGGTGACC CCAG
 ||||| ||||
 GGCCCTCCACTGG GGTC
 CTCC_
 GAM2607 KIAA0616 3' GGTGTGTCACCTCCCG 47316 _ CCCT
 CGGGAGGTG AC GACC
 ||||| || ||||
 GCCCTCCAC TG TTGG
 C _
 GAM2607 KIAA0652 3' CGGGGGCAAAGTCACCTCCCAG 29122 C _
 TG CAC GGGAGGTGA CCCCTG
 ||| ||||| ||||
 GTG CCCTCCACT GGGGGC
 A GAAAC
 GAM2607 KIAA0876 3' CTGGCCAGGGGAAGCCCGG 65316 AGGTGA A
 CCGGG CCCCTG CCAG
 |||| ||||| ||||
 GGCCC GGGGAC GGTC
 GAA_ C
 GAM2607 KIAA1396 3' CTGACGGGGAGACACCTCCC 63669 AC_ AC
 GGGAGGTG CCCTG CAG
 ||||| |||| |||
 CCCTCCAC GGGGC GTC
 AGA A_
 GAM2607 KIAA1755 3' CTGGCCAGAGTGGCCCTG 62013 A G CC A
 CGGG GGT AC CTG CCAG
 ||| ||| || ||||
 GTCC CCG TG GAC GGTC
 _ G A_ C
 GAM2607 KIAA1958 3' CTGACCAGGTGTGACCTCCCGG 82782 G C AC
 T ACCGGGAGGT AC CCTG CAG
 ||||| || |||| |||
 TGGCCCTCCA TG GGAC GTC
 G T CA
 GAM2607 KIF13B 3' CTGACCAGCAGACTCACCTCCC 83714 CCC_ AC
 GGGAGGTGA CTG CAG
 ||||| || |||

			CCCTCCACT	GAC	GTC		
			CAGAC	CA			
GAM2607	KIF13B	3'	CTGACCAGCAGACTCACCTCCC	31561		CCC__	AC
			GGGAGGTGA	CTG	CAG		
			CCCTCCACT	GAC	GTC		
			CAGAC	CA			
GAM2607	KRT6	3'	GTCAGGAGCTCTCTCAGTG	83096	C	_	GACC
			CAC GGGAG GT	CCTGAC			
			GTG CTCTC CG	GGA	CTG		
			A	T	A__		
GAM2607	MGC5442	3'	TCGGGGGCCACCTCCCGG	49507	A	T	
			CCGGGAGGTG	CCCC	GA		
			GGCCCTCCAC	GGGG	CT		
			C	_			
GAM2607	MGC7036	3'	CTGGCAAACACCTCCCTGTG	59617	C		ACCCC A
			CAC GGGAGGTG	TG	CCAG		
			GTG CCCTCCAC	AC	GGTC		
			T	CAAA_ _			
GAM2607	NCOR1	5'	TTAGCCAGCTCCCGGTG	21957	G		ACCC
			CACCGGGAG TG	CTGA			
			GTGGCCCTC AC	GATT			
			G	C__			
GAM2607	PANX2	3'	GGCCAGCCTCCCGGTG	54519		TGACCC	A
			CACCGGGAGG	CTG	CC		
			GTGGCCCTCC	GAC	GG		
			_____	C			
GAM2607	PLSCR2	5'	TCAAATTCACCTCCCAGTG	40150	C		CCCC
			CAC GGGAGGTGA	TGA			
			GTG CCCTCCACT	ACT			
			A	TAA_			
GAM2607	SYNGR4	5'	TGGCTCCCACCTCCCAGTG	25865	C		ACCCCT _
			CAC GGGAGGTG	GA	CCA		
			GTG CCCTCCAC	CT	GGT		
			A	C_____	C		
GAM2607	LOC115399	3'	CTGGTCCCTTCACCTCCC	73814		CCCCT	
			GGGAGGTGA	GACCAG			
			CCCTCCACT	CTGGTC			
			TCC__				
GAM2607	LOC129450	5'	CGGGCAGCACCTCCCGGT	75380		ACC	
			ACCGGGAGGTG	CCTG			

		TGGCCCTCCAC GGGC		
		GAC		
GAM2607	LOC146332 3'	CTGGGGAGGGGGGTCACCTCC 78356	GA__	
		GGAGGTGACCCCT CCAG		
		CCTCCACTGGGGG GGTC		
		GAGG		
GAM2607	LOC147160 5'	CTGGCCAGAAATCCCCACTTCC 85076	ACCC__ A	
	C	GGGAGGTG CTG CCAG		
		CCCTTCAC GAC GGTC		
		CCCTAAA C		
GAM2607	LOC151009 3'	CTGGTCAACCTGCAACCTCCTG 86369	GACCCC_	
		CGGGAGGT TGACCAG		
		GTCCTCCA ACTGGTC		
		ACGTCCA		
GAM2607	LOC160646 3'	AGTGGTCACCTCCCCGTG 83105	C C	
		CAC GGGAGGTGACC CT		
		GTG CCCTCCACTGG GA		
		C T		
GAM2607	LOC257354 3'	GTCAGGGGTACCAACTTG 96795	A_	
		CGGG GGTGACCCCTGAC		
		GTTC CCACTGGGGACTG		
		AA		
GAM2607	LOC57406 5'	CTGGTCAGGAGTCAGCCAGCC 40716	GA _ C	
		GG GG TGAC CCTGACCAG		
		CC CC ACTG GGA CTGGTC		
		GA G A		
GAM2608	ALDH3B1 3'	TCCAACAGCAGCCAGGTGGTC 93161	G _	
		GA TAC GGCTGCTGTTGGA		
		CT GTG CCGACGACAACCT		
		G GA		
GAM2608	F2RL3 3'	CCACCACCGCACCTGCTA 15505	A A CTGC T	
		TGGCAG GT CGG TG TGG		
		ATCGTC CA GCC AC ACC		
		C C _ C		
GAM2608	MAT1A 3'	CCAACAGCTGGACCCTGACCA 92496	_ A ACGGCT	
		TGG CAG GT GCTGTTGG		
		ACC GTC CA CGACAACC		
		A C GGT__		
GAM2608	OPCML 3'	CCAACAACATCCTCTGCCA 11894	GTAC C C	
		TGGCAGA GG TG TGTTGG		

		ACCGTCT CC AC ACAACC	
		____ T A	
GAM2608	OPHN1 3'	CCCTCAAGCCAGACTCTGCCA 11907	AC GC TT
		TGGCAGAGT GGCT TG GG	
		ACCGTCTCA CCGA AC CC	
		GA _ TC	
GAM2608	FLJ12891 3'	CCAGAAGGTCATACTCTGCCA 46920	C GCTG
		TGGCAGAGTA GGCT TTGG	
		ACCGTCTCAT CTGG GACC	
		A AA_	
GAM2608	MGC3035 5'	CCAGAGGAGCCACACTCTGACA 44395	G AC G G
		TG CAGAGT GGCT CT TTGG	
		AC GTCTCA CCGA GA GACC	
		A CA G _	
GAM2608	LOC151273 5'	TCCAACAACAGCGACCTCTCCA 67576	C TA G C
		TGG AGAG CG CTG TGTTGGA	
		ACC TCTC GC GAC ACAACCT	
		_ CA _ A	
GAM2608	LOC159199 5'	TCCAGCAGGAGCCGTCTCCACC 83067	CA T G
	A	TGG GAG ACGGCT CTGTTGGA	
		ACC CTC TGCCGA GACGACCT	
		AC _ G	
GAM2608	LOC167994 5'	AGAAGCCATACCCTGCCA 83572	A C G
		TGGCAG GTA GGCT CT	
		ACCGTC CAT CCGA GA	
		C A A	
GAM2608	LOC254181 5'	CCAACAGATCCACTCCCCA 99440	CA AC CTG
		TGG GAGT GG CTGTTGG	
		ACC CTCA CC GACAACC	
		C_ _ TA_	
GAM2608	LOC51667 3'	CCCACGCTGCCATCTCTGCCA 32776	TAC T T T
		TGGCAGAG GGC GC GT GG	
		ACCGTCTC CCG CG CA CC	
		TA_ T _ C	
GAM2608	LOC58512 3'	CCATGGGGACCATCTCTGCCA 65281	TAC C GT
		TGGCAGAG GG TGCT TGG	
		ACCGTCTC CC ACGG ACC	
		TA_ _ GT	
GAM2608	LOC92840 3'	CCAACAGCAGCCCCTGCCA 57243	AGTAC
		TGGCAG GGCTGCTGTTGG	

ACCGTC CCGACGACAACC
 C____
 GAM2609 BRCA1 3' TAAGCCACCTAATTGTA 24574 T AAT AG
 TACAATT GGTG GG TG
 ||||| ||| || ||
 ATGTAA CCAC CC AT
 T ____ GA
 GAM2609 FCRH1 3' GTCAGTGTACCAAATT 54730 ATGG
 AATTTGGTGA AGTGAC
 ||||| |||||
 TTAAACCATT TCACTG
 G____
 GAM2609 LANCL1 3' GTCTTTTCACTAAATTGTA 21333 TGGAGT
 TACAATTTGGTGAA GAC
 ||||| ||||| |||
 ATGTAAATCACTT CTG
 TT____
 GAM2609 SP1 5' TCACTCCATGGATGAAAT 61920 G GA
 ATTT GT ATGGAGTGA
 ||| || |||||
 TAAA TA TACCTCACT
 G GG
 GAM2609 DKFZP566J091 3' GGTCACCCCATCTACTCCA 48864 T____ A
 TGG GAATGG GTGACC
 ||| ||||| |||||
 ACC CTTACC CACTGG
 TCAT C
 GAM2609 DKFZp761D0614 3' TCATTTATCACTAAATTG 88946 ATG
 CAATTTGGTGA GAGTGA
 ||||| |||||
 GTTAAATCACT TTTACT
 A____
 GAM2609 FLJ13397 3' GGTCATTTACTTACCAAATT 46905 ATG
 AATTTGGTGA GAGTGACC
 ||||| |||||
 TTAAACCATT TTTACTGG
 CA____
 GAM2609 GORASP2 3' CCACCTCACTAAACTGTA 32033 A A_
 TACA TTTGGTGA TGG
 ||| ||||| |||
 ATGT AAATCACT ACC
 C CC
 GAM2609 KIAA1573 3' ACATTATCCACCAAATTG 63361 A A
 CAATTTGGTGA ATGG GT
 ||||| ||| ||
 GTTAAACCAC TATT CA
 C A
 GAM2609 MGC1842 3' CACCCAGCCAAATTG 66250 GAA A
 CAATTTGGT TGG GTG
 ||||| ||| |||

GTAAACCG ACC CAC

GAM2609 LOC125058 3' GTCAACTCCACCAAAT 60548 GAAT _
ATTTGGT GGAGT GAC
||||| |||||
TAAACCA CCTCA CTG

____ A
GAM2609 LOC129039 3' CCACAACACCAGATTGTA 75367 AA_
TACAATTTGGTG TGG
||||||| ||
ATGTTAGACCAC ACC

AAC
GAM2610 ELF3 3' TGACCTTGACCTTGACCAA 16685 T GAT AAA
TTGGT CAAGG GG GTCA
||||| || |||
AACCA GTTCC TC CAGT

____ AGT ____
GAM2610 JAK2 3' TGACCTTCATTCTGAGACCAA 18318 CAA AA
TTGGTT GGGATGGA GTCA
||||| ||||| |||
AACCAG TCTTACTT CAGT

AG_ C_
GAM2610 SLC10A2 5' ACTCTCTGTCTTGACCAA 6590 CAA A
TTGGTT GGGATGGA AGT
||||| ||||| |||
AACCAG TTCTGTCT TCA

____ C
GAM2610 FLJ10803 3' GTGACTTTCAGTTAAAGCCAA 37205 CAAGG G
TTGGTT GAT GAAAGTCAC
||||| || |||||
AACCGA TTG CTTTCAGTG

AA__ A
GAM2610 KIAA1958 5' GTGACTTTGAACCCCAAACC 82788 CAA ATGG
GGTT GGG AAAGTCAC
||| || |||||
CCAA CCC TTTCAGTG

A__ CAAG
GAM2610 MARCKS 3' ACTTTCACCTGCCCCA 11411 TTCA A
TGG AGGG TGGAAAGT
||| ||| |||||
ACC TCCC ACCTTTCA

CG__ _
GAM2610 TUB 5' GTGGGACCATCCCTTAAACC 13898 C AAAG
GGTT AAGGGATGG TCAC
||| ||||| |||
CCAA TTCCCTACC GGTG

A AG__
GAM2610 LOC80298 3' ACTTTTACCTTGAACCA 48062 GATG
TGGTTCAAGG GAAAGT
||||||| |||||

			ACCAAGTTCC TTTTCA		
			A_		
GAM2611	GPD1	3'	TCATGCCACCACATTTG 60398	C	C
			TAAATG GGTGGCAT GA		
			GTTTAC CCACCGTA CT		
			A _		
GAM2611	IL5RA	5'	TCGCATGGCCACCGCATTT 6906	AT_	
			AAATGCGGTGGC CGA		
			TTTACGCCACCG GCT		
			GTAC		
GAM2611	MYO1C	3'	TGCCGATGCCAAATATTTG 61873	CGG	A
			TAAATG TGGCATCG CA		
			GTTTAT ACCGTAGC GT		
			AA_ C		
GAM2611	C6orf37	3'	TGTCACACTGCATTTA 68097	GCATC	
			TAAATGCGGTG GACA		
			ATTTACGTAC CTGT		
			A_		
GAM2611	DNAJC6	3'	TTGCAGAACCACCGCATT 29498	CA GA	
			AATGCGGTGG TC CAA		
			TTACGCCACC AG GTT		
			A_ AC		
GAM2611	FLJ11210	3'	GTCGATGTGCATGCTTTTA 60319	T GTG	
			TAAA GCG GCATCGAC		
			ATTT CGT TG TAGCTG		
			T ACG		
GAM2611	FLJ12476	3'	TCGATCTTCTGCATTTA 43270	T C	
			TAAATGCGG GG ATCGA		
			ATTTACGTC TC TAGCT		
			T _		
GAM2611	KIAA1034	3'	TCGATGGCATCCGCATTTG 63134	_ G	
			TAAATGCGG TG CATCGA		
			GTTTACGCC AC GTAGCT		
			T G		
GAM2611	KIAA1987	3'	TCATGTAAGTGCATTTA 89391	G C	
			TAAATGCGGT GCAT GA		
			ATTTACGTCA TGTA CT		
			A _		
GAM2611	MGC16063	3'	TGTCCTGGCCACTGCATT 54929	ATC	
			AATGCGGTGGC GACA		

		TTACGTCACCG CTGT		
		GTC		
GAM2611	LOC147949 3'	TGTCAGATGTCCACATTGCA	79279	— — —
		TGCG GTGG CATC GACA		
		ACGT CACC GTAG CTGT		
		TA T A		
GAM2611	LOC150577 3'	GTCCTCACCGCATTTG	86258	CATC
		TAAATGCGGTGG GAC		
		GTTTACGCCACT CTG		
		C_		
GAM2611	LOC158219 3'	TGTGTGTCACCACATT	82694	C CG
		AAATG GGTGGCAT ACA		
		TTTAC CCACTGTG TGT		
		A _		
GAM2611	LOC202020 3'	TGTCTCACACATTTA	90605	C CATC
		TAAATG GGTGG GACA		
		ATTTAC CCACT CTGT		
		A _		
GAM2611	LOC90826 5'	TGTCGATGCAGGTTTATTTG	64788	CGGTG
		TAAATG GCATCGACA		
		GTTTAT CGTAGCTGT		
		TTGGA		
GAM2611	LOC93587 3'	TTGTCTTTACCTGCATTTA	73042	_ CATC
		TAAATGC GGTGG GACAA		
		ATTTACG CCATT CTGTT		
		T T_		
GAM2612	CREBL2 3'	ACCCCTCACCTTTTTGTGATGA	8965	G TCC A
		TCATCA CAAGA GTGAGG GT		
		AGTAGT GTTTT CACTCC CA		
		_ TC_ C		
GAM2612	PTP4A2 3'	ACTCCTCAACCACTCTCCTAAT	14436	C CA TCCG_
	GA	TCAT AG AGA TGAGGAGT		
		AGTA TC TCT ACTCCTCA		
		A C_ CACCA		
GAM2612	PTP4A2 3'	ACTCCTCAACCACTCTCCTAAT	55369	C CA TCCG_
	GA	TCAT AG AGA TGAGGAGT		
		AGTA TC TCT ACTCCTCA		
		A C_ CACCA		
GAM2612	C12orf22 3'	ACTCCTACTTATCTTGCTCAT	48704	C CC G
		AT AGCAAGAT GT AGGAGT		

		TA TCGTTCTA CA TCCTCA	
		C TT _	
GAM2612	OAZIN	5' CCTTGGAACCTAGCTGATGA 32437	A A_ G
		TCATCAGC AG TCC TGAGG	
		AGTAGTCG TC AGG GTTCC	
		A CA _	
GAM2612	SHANK3	3' ACTCCTCACACTCAGCGATGA 66097	A AA TCC
		TCATC GC GA GTGAGGAGT	
		AGTAG CG CT CACTCCTCA	
		_ A_ CA_	
GAM2612	TOPBP1	3' ACTCCTCAGCTAGCTTGCTG 23820	ATCCG
		CAGCAAG TGAGGAGT	
		GTCGTTC ACTCCTCA	
		GATCG	
GAM2612	LOC221962	3' ACCCCTCACTGGATTGCTGA 94235	A _ A
		TCAGCA GATCC GTGAGG GT	
		AGTCGT TTAGG CACTCC CA	
		_ T C	
GAM2613	ALK	5' GAGCAGTGTAACGGCCTCCT 73772	ATCCAGCT C
		AGGAGGCC CAT GCTC	
		TCCTCCGG GTG CGAG	
		CAAAT__ A	
GAM2613	GRB10	3' AGCAGGCTGAATGGCCTC 19192	C CATC
		GAGGCCAT CAGCT GCT	
		CTCCGGTA GTCGG CGA	
		A A__	
GAM2613	NQO1	3' GACCGAGCTGGAAAACCTCCT 8048	CCA A_
		AGGAGG TCCAGCTC TC	
		TCCTCC AGGTCGAG AG	
		AAA CC	
GAM2613	OAS3	3' GAGAGCCAGAGGGCCTCCT 21652	A CA A
		AGGAGGCC TC GCTC TC	
		TCCTCCGG AG CGAG AG	
		G AC _	
GAM2613	PTPRF	5' GAGCCCTGGATGGCCCCT 56137	A _
		AGG GGCCATCCA GCTC	
		TCC CCGGTAGGT CGAG	
		_ CC	
GAM2613	PTPRF	5' GAGCCCTGGATGGCCCCT 12607	A _
		AGG GGCCATCCA GCTC	

		TCC CCGGTAGGT CGAG		
		— CC		
GAM2613	ACP33	5' AGCGAAGAGCGGCCTCCT 34036	ATCCA	A
		AGGAGGCC GCTC TCGCT		
		TCCTCCGG CGAG AGCGA		
		— A		
GAM2613	ERO1L	5' GAGCGTGCGGACTGGCCTCC 28160	— A	TCAT
		GGAGGCCA TCC GC CGCTC		
		CCTCCGGT AGG CG GCGAG		
		C — T—		
GAM2613	FLJ13441	3' AGTGGTGGACGACCTCCT 43909	CCA	CAG T
		AGGAGG TC C CATCGCT		
		TCCTCC AG G GTGGTGA		
		— CA—		
GAM2613	KIAA0240	3' AGCAAATGGAAATGGTCTCCT 94033	—	—
		AGGAGGCCA TCCA GCT		
		TCCTCTGGT AGGT CGA		
		AA AAA		
GAM2613	KIAA1040	3' AGCAAGTGGGTGGCCCCCT 72679	A	G CATC
		AGG GGCCATCCA CT GCT		
		TCC CCGGTGGGT GA CGA		
		C — A—		
GAM2613	KLHL6	3' TGGGGAGCTGGAGAGCCCCC 56178	A CA	AT
		GG GGC TCCAGCTC CG		
		CC CCG AGGTCGAG GT		
		C AG GG		
GAM2613	MAPK8IP3	3' GAGGGCTGGATACCCCCT 54141	A CC	A
		AGG GG ATCCAGCTC TC		
		TCC CC TAGGTCGGG AG		
		— CA —		
GAM2613	PDZD2	3' GAGCAAATGGAATGGTCTCCT 81723	—	—
		AGGAGGCCAT CCA GCTC		
		TCCTCTGGTA GGT CGAG		
		A AAA		
GAM2613	SLC6A13	3' GCTGAGCTGGAGGCCTCC 34002	A	TC
		GGAGGCC TCCAGCTCA GC		
		CCTCCGG AGGTCGAGT CG		
		— —		
GAM2613	LOC158438	5' GAGCTGTTGGCTGGAGGCCTCC 88169	A	C C
	T	AGGAGGCC TCCAGCT AT GCTC		

			TCCTCCGG AGGTCGG TG CGAG			
			— T T			
GAM2613	LOC200718	3'	AGCAATGAGCTGTTCTCT	91676	CCATC	C
			GGAGG CAGCTCAT GCT			
			TCTCT GTCGAGTA CGA			
			T— A			
GAM2613	LOC204579	5'	AGCAGCTACATGGCCTCC	91025	CC	CATC
			GGAGGCCAT AGCT GCT			
			CCTCCGGTA TCGA CGA			
			CA —			
GAM2614	DLEC1	3'	CATCTGGCCCTCCCTTG	24716	A	A C
			CAAGG AGGGC GG GTG			
			GTTCC TCCCG TC TAC			
			C G —			
GAM2614	DLEC1	3'	CATCTGGCCCTCCCTTG	24717	A	A C
			CAAGG AGGGC GG GTG			
			GTTCC TCCCG TC TAC			
			C G —			
GAM2614	PIP5K1A	3'	TATCCCACCCTGCCTTGATA	14520	A	CA C
			TATCAAGG AGGG GG GTG			
			ATAGTTCC TCCC CC TAT			
			G A_ C			
GAM2614	SOX11	3'	ACCCACCCCCCTTG GTA	13308	AA	CA C
			TATCAAGG GGG GG GT			
			ATGGTTCC CCC CC CA			
			CC A_ _			
GAM2614	CHL1	3'	TGTTACCTTTCCTCAATA	22768	CA	CA
			TAT AGGAAGGG GGCG			
			ATA TCCTTTCC TTGT			
			AC A_			
GAM2614	EPB41L1	3'	CATTCTGCCCTTCCCTGA	71104	A	C
			TCA GGAAGGGCAGG GTG			
			AGT CCTTCCCGTCT TAC			
			C _			
GAM2614	FLJ00060	3'	CATACCCCCTGCCCTCCTCTGA	61741	_	A CGTG
			TCA AGGA GGGCAGG ATG			
			AGT TCCT CCCGTCC TAC			
			C _ CCCA			
GAM2614	FLJ10898	5'	CACCACAGCCCTTTCTCAATA	60126	CA	AGGC
			TAT AGGAAGGGC GTG			

ATA TCTTTCCCG CAC
 AC ACAC
 GAM2614 FLJ22557 3' ATCATCCCATCCTTAATA 45581 C A CAGGC
 TAT AAGGA GGG GTGAT
 ||| ||||| ||| |||||
 ATA TTCCT CCC TACTA
 A A ____
 GAM2614 KIAA0574 3' CATCCCCTGCCCTCCCCTGA 69808 A A CGT
 TCA GG AGGGCAGG GATG
 ||| || ||||| |||
 AGT CC TCCCGTCC CTAC
 C C C__
 GAM2614 KIAA0632 3' CACCTCAGAAACCCTTCCTTGA 32071 CA__ C
 TCAAGGAAGGG GG GTG
 ||||| ||| |||
 AGTTCCTTCCC CT CAC
 AAAGA C
 GAM2614 KIAA1045 3' CATCACATGTCCTTCC 71599 GGC
 GGAAGGGCA GTGATG
 ||||| |||||
 CCTTCCTGT CACTAC
 A__
 GAM2614 KIAA1354 5' CAGTGACTGCCTTCCCTTGATA 61572 A G _
 TATCAAGG AGGGCAG CG TG
 ||||| ||||| || ||
 ATAGTTCC TTCCGTC GT AC
 C A G
 GAM2614 MGC20460 5' CACCGCCTCCTACCCTTCTT 54901 C__ _
 AGGAAGGG AGGCG TG
 ||||| ||||| ||
 TTCTTCCC TCCGC AC
 ATCC C
 GAM2614 LOC158476 3' CACGCCCGCCCCCCCCATTGA 88186 _ AA_ A
 TCAA GG GGGC GGC GTG
 ||| || ||| |||||
 AGTT CC CCG CCGCAC
 A CCC C
 GAM2614 LOC90459 3' CACACCCGCTAATTTTGT 63550 A_ A C
 CAAGGA GGGC GG GTG
 ||||| ||| || |||
 GTTTTT TCCG CC CAC
 AA C A
 GAM2615 DUOX1 5' TGCAGAGTGCTGGGCAA 34293 CTA
 TTGGCCCAGTAC TGCA
 ||||| ||||| |||
 AACCGGGTCGTG ACGT
 AG_
 GAM2615 FGF5 3' TGCATAAGTTGTATAGGCTAA 53671 CA C__
 TTGGCC GTAC TATGCA
 ||||| ||| |||||

		AATCGG TATG ATACGT	
		A_ TTGA	
GAM2615 FGF5	3'	TGCATAAGTTGTATAGGCTAA 53672	CA C__
		TTGGCC GTAC TATGCA	
		AATCGG TATG ATACGT	
		A_ TTGA	
GAM2615 NEURL	3'	TGGGTTCCCTGGGCCAAG 16138	T__
		CTTGGCCCAG ACCTA	
		GAACCGGGTC TGGGT	
		CCT	
GAM2615 P2RY6	3'	TGCATATCCAGCTGGGCCA 16002	ACC_
		TGGCCCAGT TATGCA	
		ACCGGGTCG ATACGT	
		ACCT	
GAM2615 PLXNA1	3'	TGGGAGCCACTGGGCCAGG 72774	A__
		CTTGGCCCAGT CCTA	
		GGACCGGGTCA GGGT	
		CCGA	
GAM2615 SLC2A3	3'	TGCACTCTAGCCTGGGCCA 23649	TAC __
		TGGCCCAG CTA TGCA	
		ACCGGGTC GAT ACGT	
		C__ CTC	
GAM2615 SLC9A1	3'	TGCAGGGGACTGGGCCA 70932	A A
		TGGCCCAGT CCT TGCA	
		ACCGGGTCA GGG ACGT	
		_ G	
GAM2615 SNX13	5'	GCGAGCGACCGGGCCGAG 31394	A AC A
		CTTGGCCC GT CT TGC	
		GAGCCGGG CA GA GCG	
		C GC _	
GAM2615 CDW92	3'	TGCATAAGTCCTAGTGGGTCAA 55432	G__ C
G		CTTGGCCCA T AC TATGCA	
		GAACTGGGT A TG ATACGT	
		G TCC A	
GAM2615 DKFZP434A043	3'	TGCACGTACATGGGCCAG 31824	_ CTA
		TTGGCCCA GTAC TGCA	
		GACCGGGT CATG ACGT	
		A C__	
GAM2615 FAM3A	3'	TGCCAGGACCGGGCCGAG 41733	A A AT
		CTTGGCCC GT CCT GCA	

	GAGCCGGG CA GGA CGT	
	C _ C_	
GAM2615 FLJ13902 3'	TGCACAAGGAGGCCCGGGCCAG 45384	A_ A_ A_
G	CTTGGCCC GT CCT TGCA	
	GGACCGGG CG GGA ACGT	
	CC GA AC	
GAM2615 KIAA0391 3'	TGCATTTCTCCTACTGGGCCA 28624	CCT__
	TGGCCAGTA ATGCA	
	ACCGGGTCAT TACGT	
	CCTCTT	
GAM2615 KIAA0630 3'	TGCATGGATCTGGGTCAAG 90953	TAC
	CTTGGCCCAG CTATGCA	
	GAACTGGGTC GGTACGT	
	TA_	
GAM2615 KIAA1924 3'	TGCACAGGGTGCCACGGGGCCA 74062	A__ A_
AG	CTTGGCCC GTACCT TGCA	
	GAACCGGG CGTGGG ACGT	
	GCAC AC	
GAM2615 MGC15396 3'	TGCATCACCTCTGGGCCAAG 54565	TACCT
	CTTGGCCCAG ATGCA	
	GAACCGGGTC TACGT	
	TCCAC	
GAM2615 PASK 5'	TGCAGGTGTCCTGGGCCAAG 31424	__ AT
	CTTGGCCCAG TACCT GCA	
	GAACCGGGTC GTGGA CGT	
	CT _	
GAM2615 PPP1R14A 5'	GCACAGCGCGGGGCCAGG 53829	A AC A
	CTTGGCCC GT CT TGC	
	GGACCGGG CG GA ACG	
	G C_ C	
GAM2615 RASGRP4 3'	TGCACAGGTGCTGGACAAG 54748	GC A
	CTTG CCAGTACCT TGCA	
	GAAC GGTTCGTGGA ACGT	
	A_ C	
GAM2615 TRIM16 5'	TGCACAGATCCTGGGCCAAG 22381	TAC A
	CTTGGCCCAG CT TGCA	
	GAACCGGGTC GA ACGT	
	CTA C	
GAM2615 WIT-1 5'	TGCAGCCTGCGGGGCCAAG 32400	A CCTA
	CTTGGCCC GTA TGCA	

	GAACCGGG CGT ACGT	
	G CCG_	
GAM2615 LOC126364 3'	TGCAGTCACTGGGCCAGG 76201	ACCTA
	CTTGGCCCAGT TGCA	
	GGACCGGGTCA ACGT	
	CTG_	
GAM2615 LOC132299 5'	CACAGACACTGGGTCAAG 75569	AC A
	CTTGGCCCAGT CT TG	
	GAACTGGGTCA GA AC	
	CA C	
GAM2615 LOC147645 3'	TGCACAGGGCGTTTTGGGCCAG 79073	TA__ A
	TTGGCCCAG CCT TGCA	
	GACCGGGTT GGA ACGT	
	TTGCG C	
GAM2615 LOC151996 5'	TGCATAGGCACAAGTGGGCCAG 86723	__ A
G	CTTGGCCCA GT CCTATGCA	
	GGACCGGGT CA GGATACGT	
	GAA C	
GAM2615 LOC200940 5'	TGCATGCCAGGTGGGCCGAG 90399	AGT __
	CTTGGCCC ACCT ATGCA	
	GAGCCGGG TGGA TACGT	
	__ CCG	
GAM2615 LOC205418 5'	TGCACGGGGGCTGGGCCA 92375	A TA
	TGGCCCAGT CC TGCA	
	ACCGGGTCG GG ACGT	
	_ GC	
GAM2615 LOC219653 3'	TGCACAGCCAGCTCAGCCAAG 92923	CC AC_ A
	CTTGGC AGT CT TGCA	
	GAACCG TCG GA ACGT	
	AC ACC C	
GAM2615 LOC51580 3'	CATAGGTGTGTTCCAGG 32429	CC G
	CTTGG CA TACCTATG	
	GGACC GT GTGGATAC	
	TT _	
GAM2615 LOC64182 3'	TGCCAGATACCGGGCTAAG 42556	A C AT
	CTTGGCCC GTA CT GCA	
	GAATCGGG CAT GA CGT	
	C A C_	
GAM2616 CDKN1A 5'	AGAGCCGAGCCAAGCGTGCC 55265	CGAA TC C
	GGCACGCT CT CGGC CT	

CCGTGCGA GA GCCG GA
 ACC_ _ A
 GAM2616 DKFZp761A052 5' GGCCGGAACAAGCGTAGC 73377 _ CGAAC
 GC ACGCT TTCCGGCC
 || |||| |||||
 CG TGC GA AAGGCCGG
 A AC_
 GAM2616 KIAA0415 3' GGCTCAGCCCGCGCTGCCA 94167 T AA TCC
 TGGCACGC CG CT GGCC
 ||||| || || |||
 ACCGTGCG GC GA TCGG
 _ CC C_
 GAM2616 PDE4DIP 5' AGAGCCGGAAGCCCGCTGACC 28402 _ C TCGAA C
 GG CA GC CTTCCGGC CT
 || || || ||||| ||
 CC GT CG GAAGGCCG GA
 A _ CCC_ A
 GAM2616 SCYB14 5' GGCCGGAAGGCGCGCC 18088 A TCGAA C
 GGC CGC CTTCCGGC C
 ||| ||| ||||| |
 CCG GCG GAAGGCCG G
 C _ _ A
 GAM2616 LOC144100 3' AGGGCCGAGCAGGAGCATGCT 77183 C GAAC
 A TGGCA GCTC TTCCGGCCCT
 |||| ||| |||||
 ATCGT CGAG GAGGCCGGGA
 A GAC_
 GAM2616 LOC145934 5' AGGGCCGAGAAGCGAGCGGCC 84558 A AAC
 A TGGC CGCTCG TTCCGGCCCT
 |||| |||| |||||
 ACCG GCGAGC GAGGCCGGGA
 _ GAA
 GAM2616 LOC148696 5' AGGGCCGAGAAGGCGCGTGCCA 85344 TCGAA _
 TGGCACGC CTTC CGGCCCT
 ||||| ||| |||||
 ACCGTGCG GAAG GCCGGGA
 CG_ A
 GAM2616 LOC253263 3' AGGGCCGCTCGTGAACAGCCA 98813 ACGCT_ ACTT
 TGGC CGA CCGGCCCT
 ||| ||| |||||
 ACCG GCT GGCCGGGA
 ACAAGT C_
 GAM2616 LOC254559 5' AGGGCGCGTGTTTCGGCGTGCC 98380 T TC _
 A TGGCACGC CGAACT CG GCCCT
 ||||| ||||| || |||||
 ACCGTGCG GCTTGG GC CGGGA
 _ T_ G
 GAM2616 LOC256444 5' AGGGCCGAGAAGCGAGCGGCC 98382 A AAC
 A TGGC CGCTCG TTCCGGCCCT
 |||| ||||| |||||

ACCG GCGAGC GAGGCCGGA
 _ GAA
 GAM2617 BIN3 3' GAGAGTAGGAAGAGCTGTGG 38576 TC T
 TCGC G CTCTTCCTACTCTC
 |||| | |||||
 GGTG C GAGAAGGATGAGAG
 T__
 GAM2617 COX7A2L 3' TAGGAAGATATGAAGATG 17532 GC C
 CATC TCGT TCTTCCTA
 |||| ||| |||||
 GTAG AGTA AGAAGGAT
 A_ T
 GAM2617 ESR2 5' AGAGCAGGCGGCGAGCGCTG 9323 T TCTT A
 CA CGCTCGTC CCT CTCT
 || ||||| ||| ||||
 GT GCGAGCGG GGA GAGA
 C C__ C
 GAM2617 PCTK3 3' GAGAGCAAGAAGAGACATGGC 73327 C_ CTA
 GCT GTCTCTTC CTCTC
 ||| ||||| ||||
 CGG CAGAGAAG GAGAG
 TA AAC
 GAM2617 SRC 3' AGAGCCTTTCCAAAGAGGAGCG 19448 G CTTCTTA__
 ATG CATCGCTC TCT CTCT
 ||||| ||| ||||
 GTAGCGAG AGA GAGA
 G AACCTTTCC
 GAM2617 STX8 5' AGAGCAGGAAGAGTCCGAGCGG 17944 T_ A
 TCGCTCG CTCTTCCT CTCT
 ||||| ||||| ||||
 GGCGAGC GAGAAGGA GAGA
 CT C
 GAM2617 BA108L7.2 5' AGAGCTTCAGAGAGCGATG 49063 G CTTCTTA
 CATCGCTC TCT CTCT
 ||||| ||| ||||
 GTAGCGAG AGA GAGA
 _ CTTCT__
 GAM2617 EVI5 3' GAGAGTAGAGGATACAAGTGAT 20210 C C C
 G CATCGCT GT TCTTC TACTCTC
 ||||| || |||| |||||
 GTAGTGA CA AGGAG ATGAGAG
 A T _
 GAM2617 FLJ21140 3' GAGAGTAGAAAGAAAAGGAGAG 45836 G GTC_ C
 A TC CTC TCTT CTA CTCTC
 || ||| ||| |||||
 AG GAG AGAA GATGAGAG
 A GAAA A
 GAM2617 FLJ22160 3' GAGTCAGGAAGAGACGGC 45032 T _
 GC CGTCTCTTCCT ACTC
 || ||||| ||||

CG GCAGAGAAGGA TGAG
 — C
 GAM2617 KCNS1 3' AGGCTAAGAGATGAGCGATG 11191 —
 CATCGCTCGTCTCTT CCT
 ||||| |||
 GTAGCGAGTAGAGAA GGA
 TC
 GAM2617 KIAA1952 5' GAGAGTAGAAGGCAAAGC 73545 C_ CTTC
 GCT GTCT CTACTCTC
 ||| ||| |||||
 CGA CGGA GATGAGAG
 AA A_—
 GAM2617 MGC10500 3' GAGAACAGAAGGGGGACGACG 49726 C C_ AC
 CG TCGTCTCTT CT TCTC
 || ||||| || |||||
 GC AGCAGGGGG GA AGAG
 — AA CA
 GAM2617 MGC12760 5' AGAGCAGGAAGAGGCGGTG 52153 T A
 CGC CGTCTCTTCCT CTCT
 ||| ||||| |||
 GTG GCGGAGAAGGA GAGA
 — C
 GAM2617 MGC2488 5' GAGAACAGAAAGAGAGGGTGG 44088 G C AC
 TCGCTC TCTCTT CT TCTC
 ||||| ||||| || |||||
 GGTGGG AGAGAA GA AGAG
 — A CA
 GAM2617 MT-ACT48 3' AGCAGAAAGAGAGAGTGG 25609 G C A
 TCGCTC TCTCTT CT CT
 ||||| ||||| || ||
 GGTGAG AGAGAA GA GA
 — A C
 GAM2617 PRO1496 3' GAGAAGTGGGAAAGAAGCAATG 38366 C CG C —
 CAT GCT TCT TTCCTACT CTC
 ||| ||| ||| ||||| |||
 GTA CGA AGA AAGGGTGA GAG
 A — — A
 GAM2617 RASAL2 5' GAGAGCAGGAAAGCGAGC 17910 T C A
 GCTCG CT TTCCT CTCTC
 ||||| || ||||| |||||
 CGAGC GA AAGGA GAGAG
 — — C
 GAM2617 STK22D 3' AGAGCAGGAAGAGCAGC 50141 C T A
 GCT G CTCTTCCT CTCT
 ||| | ||||| |||
 CGA C GAGAAGGA GAGA
 — — C
 GAM2617 SYT6 3' AGAGTAGGAAAAGACAAAGGGT 79515 — C
 G CGCTC GTCT TTCCTACTCT
 ||||| ||||| ||||| |||||

GTGGG CAGA AAGGATGAGA
 AAA A
 GAM2617 TUSP 5' GAGAAGGGAGACGAGC 40026 TT A
 GCTCGTCTC CCT CTC
 ||||| |||
 CGAGCAGAG GGA GAG
 _ A
 GAM2617 LOC151007 3' AGTAGAAGGAAGCGAT 80900 CG T C
 ATCGCT TC CTTC TACT
 |||| || ||| ||||
 TAGCGA AG GAAG ATGA
 _ _ _
 GAM2617 LOC151201 5' AGAGTAGGAAGAAGGT 86466 CGTC
 GCT TCTTCCTACTCT
 || |||||
 TGG AGAAGGATGAGA
 A_
 GAM2617 LOC203202 3' GAGAATAAAAAGAGACGA 66627 CC C
 TCGTCTCTT TA TCTC
 ||||| || |||
 AGCAGAGAA AT AGAG
 AA A
 GAM2617 LOC206426 5' GAGAACAGGAAGAGGCGGATG 91100 GCT AC
 CATC CGTCTCTTCCT TCTC
 ||| ||||| |||
 GTAG GCGGAGAAGGA AGAG
 _ CA
 GAM2617 LOC219855 3' GAGAGTAGAAAGAGGGGTTGGC 93141 CG C_
 GCT TCTCTT CTACTCTC
 || |||| |||||
 CGG GGGGAG GATGAGAG
 TT AAA
 GAM2617 LOC253263 3' GAGAATAGGAAGGAATTAAGC 98816 CG_ T C
 GCT TC CTTCCTA TCTC
 || || ||||| |||
 CGA AG GAAGGAT AGAG
 ATTA _ A
 GAM2618 ARHG 3' CTCAGGTTAGGGGCTCTCAG 77087 A _
 CT AGAGCCT TCTGAG
 || ||||| |||||
 GA TCTCGGG GGA CTC
 C GATT
 GAM2618 CXCR6 3' CTCAGAAGGCTCTTCTGACT 22673 _ C CTA
 AG CA GA AGAGCCTTCTGAG
 || || |||||
 TC GT CT TCTCGGAAGACTC
 A _ _
 GAM2618 H3FF 3' CAAAAGGCTCTTTTCAGAGC 14513 AC_ CT C
 GC GA AAGAGCCTT TG
 || || ||||| ||

		CG CT TTCTCGGAA AC	
		AGA T_ A	
GAM2618 JRK	3'	CTCAGAAGGCTCTATCTGCT 87824	C CTA
		AGCA GA AGAGCCTTCTGAG	
		TCGT CT TCTCGGAAGACTC	
		_ A_	
GAM2618 KCNJ10	3'	CTTAGAAGGCCTCAGCCATGCT 11155	CGA A A
T		AAGCA CT AG GCCTTCTGAG	
		TTCGT GA TC CGGAAGATTC	
		ACC C _	
GAM2618 MTMR3	3'	CAGAAGGCTTCCCTGGTGCT 41161	GACTAA
		AGCAC GAGCCTTCTG	
		TCGTG TTCGGAAGAC	
		GTCCC_	
GAM2618 POLR2G	3'	CAGAAGGCATCTGGTGCTT 12208	GACTA _
		AAGCAC AGA GCCTTCTG	
		TTCGTG TCT CGGAAGAC	
		G_ A	
GAM2618 SHMT2	3'	CAGAAGGCATCTGGTGCTT 19433	GACTA _
		AAGCAC AGA GCCTTCTG	
		TTCGTG TCT CGGAAGAC	
		G_ A	
GAM2618 USH3A	5'	CTCATTCCTGCCTCAGTTGTGC 54841	A A CTTC_
TT		AAGCACGACT AG GC TGAG	
		TTCGTGTTGA TC CG ACTC	
		C _ TCCTT	
GAM2618 CAMTA2	3'	CTCGTCCCTCCTGGTCGTGC 61885	A CCTTC
		GCACGACTA GAG TGAG	
		CGTGCTGGT CTC GCTC	
		C CCT_	
GAM2618 CCNG2	3'	CTCAGAAGAGTGAGTATGCT 16378	CG AAGA _
		AGCA ACT GC CTTCTGAG	
		TCGT TGA TG GAAGACTC	
		A_ G_ A	
GAM2618 DKFZP434A043	3'	CTCAGAAGACTCTTGTGTTTTG 31820	C _ C
TTT		AAGCA GAC TAAGAG CTTCTGAG	
		TTTGT TTG GTTCTC GAAGACTC	
		T T A	
GAM2618 HEAB	5'	CAGAAGGCCGAGCGGCTT 23359	A A AAGA
		AAGC CG CT GCCTTCTG	

TTCG GC GA CGGAAGAC
 _ _ GC_
 GAM2618 MAST205 5' CAGAAGGCTCGAAGGCGCCGC 31357 A_ A AA
 GC CG CT GAGCCTTCTG
 || || || |||||
 CG GC GA CTCGGAAGAC
 CC G AG
 GAM2618 TRIP-Br2 3' CAGAAGGCATCCATCATGTT 29260 C CTAA _
 AGCA GA GA GCCTTCTG
 |||| || || |||||
 TTGT CT CT CGGAAGAC
 A AC_ A
 GAM2618 LOC145547 3' GGGGGCCCTCAGTTGTGC 77783 A A
 GCACGACT AG GCCTTC
 ||||| || |||||
 CGTGTTGA TC CGGGGG
 C C
 GAM2618 LOC149668 3' CAGATGGGGCTCTCAGTGT 85694 GACTA _
 GCAC AGAGCCT TCTG
 ||| ||||| |||
 TGTG TCTCGGG AGAC
 AC_ GT
 GAM2618 LOC253070 5' CTCAGAAGCGTATCCGTGC 98787 ACTAA _ _
 GCACG GA GC CTTCTGAG
 |||| || || |||||
 CGTGC CT TG GAAGACTC
 _ _ A C
 GAM2618 LOC254835 5' CTCATAAGGCTCTTAGACGTGC 98709 A C
 TT AAGCACG CTAAGAGCCTT TGAG
 ||||| ||||| ||||| |||||
 TTCGTGC GATTCTCGGAA ACTC
 A T
 GAM2618 LOC255834 3' CAAAAGGCTCTTTTCAGAGC 96285 AC_ CT C
 GC GA AAGAGCCTT TG
 || || ||||| ||
 CG CT TTCTCGGAA AC
 AGA T_ A
 GAM2618 LOC257450 5' CTCAGAAGACTCTGAGAGGTG 91449 GA A C
 CAC CT AGAG CTTCTGAG
 ||| || |||| |||||
 GTG GA TCTC GAAGACTC
 GA G A
 GAM2618 LOC58492 5' CTCAGGTGTCCTGTCGTGCT 73135 TA AG CT
 AGCACGAC AG C TCTGAG
 ||||| || | |||||
 TCGTGCTG TC G GGA CTC
 _ CT T_
 GAM2618 LOC90643 3' CTCAGAAGTTTTTAATATGC 64437 CGAC GC
 GCA TAAGA CTTCTGAG
 ||| |||| |||||

		CGT ATTTT GAAGACTC		
		ATA_ _		
GAM2618	LOC91818	3' CTCAGAAAGTTTAAATATGC 67856	CGAC	GC
		GCA TAAGA CTTCTGAG		
		CGT ATTTT GAAGACTC		
		ATA_ _		
GAM2619	BAPX1	3' AGGCCACACTAGTTCATGGT 8644	AGC	CCA
		GCCATGAA GG TGGCCT		
		TGGTACTT TC ACCGGA		
		GA_ AC_		
GAM2619	C1QBP	3' GCCATAGTTTCATGGC 60857	AGCG	C
		GCCATGAA GC ATGGC		
		CGGTACTT TG TACCG		
		_ _ A		
GAM2619	CELL	3' AGGCCATGACCGCCTACTGG 10167	TGAAA	C
		CCA GCGG CATGGCCT		
		GGT CGCC GTACCGGA		
		CATC_ A		
GAM2619	DLG5	5' AGGCCATGCTCAGCTCCACGGC 83810	A AA	_ GC
		GCC TG AGC G CATGGCCT		
		CGG AC TCG C GTACCGGA		
		C C_ A TC		
GAM2619	RERE	3' AGGCCCTGACCTTCATGGTGT 25013	AGC	C T
		ACGCCATGAA GG CA GGCCT		
		TGTGGTACTT CC GT CCGGA		
		_ _ A C		
GAM2619	TBX3	3' CCACGGGGCCCGCCATGGCGT 33808	AAA	_ A_
		ACGCCATG GCGG CC TGG		
		TGCGGTAC CGCC GG ACC		
		_ _ C GC		
GAM2619	DKFZp586C1924	5' AGGCCACAGTGAAGTCCGGCGT 51086	AT AAG	G CA
		ACGCC GA CG C TGGCCT		
		TGCGG CT GT G ACCGGA		
		C_ CAA _ AC		
GAM2619	FLJ13055	5' GCCATAGGGCGCTTTCACAGGC 43017	A_	G _
		GCC TGAAAGCG CC ATGGC		
		CGG ACTTTCGC GG TACCG		
		AC G A		
GAM2619	FLJ20034	3' AGGCCATGGCCCCTCATGAAGT 34835	GC	AAGC
		AC CATGA GGCCATGGCCT		

		TG GTACT CCGGTACCGGA		
		AA CC__		
GAM2619	FLJ20085	5' AGGCCACGGCCATGGCCATGG 35001	AAAGC	A
		CCATG GGCC TGGCCT		
		GGTAC CCGG ACCGGA		
		CGGTA C		
GAM2619	KIAA0237	3' GCCAGTCCTCCCATGGTCA 29226 C	AA C	CA
		A GCCATG AG GGC TGGC		
		A TGGTAC TC CTG ACCG		
		C CC _ _		
GAM2619	KIAA0356	3' GCCCACCGCTTTCTCAGCGT 66773	CAT	CCAT
		ACGC GAAAGCGG GGC		
		TGCG CTTTCGCC CCG		
		ACT AC__		
GAM2619	KIAA1301	3' AGGTTTCCGCTTTTCATGG 66944	CCAT	
		CCATGAAAGCGG GGCCT		
		GGTACTTTCGCC TTGA		
		T__		
GAM2619	KIAA1399	3' AGGCCATGACCACCACTGAGGG 70789	ATGAA C C__	
	C	GCC AG GG CATGGCCT		
		CGG TC CC GTACCGGA		
		GAG__ A ACCA		
GAM2619	KIAA1462	3' CCATCTGTTTTTATAGC 93025 C	CC	
		GC ATGAAAGCGG ATGG		
		CG TATTTTGTGTC TACC		
		A _		
GAM2619	MGC23280	3' AGGCCAGGATGCTTGCCATGGC 59052	A_ G A	
		GCCATG AAGCG CC TGGCCT		
		CGGTAC TTCGT GG ACCGGA		
		CG A _		
GAM2619	PER3	3' GTCACCGCTTTCTATGGCGT 34174	_	CCA
		ACGCCAT GAAAGCGG TGGC		
		TGCGGTA CTTTCGCC ACTG		
		T _		
GAM2619	LOC114987	3' CCATGGCTCCTCCTCAGC 59792	CA A_ C	
		GC TGA AG GGCCATGG		
		CG ACT TC TCGGTACC		
		_ CC C		
GAM2619	LOC115219	3' AGGCCATGGAAGCCCATGG 73688	AAA GG	
		CCATG GC CCATGGCCT		

GGTAC CG GGTACCGGA
C__ AA
GAM2619 LOC132332 3' GCCATCGCTTTCATGC 76668 C GCC C
GC ATGAAAGCG ATGG C
|| ||||| |||
CG TACTTTCGC TACC G
_ _ A
GAM2619 LOC143392 3' CCATGGCCAAGCAGATGGC 83852 GAAA _
GCCAT GC GGCCATGG
|||| || |||||
CGGTA CG CCGGTACC
GA__ AA
GAM2619 LOC143920 5' GCCATGGCGCTTCTCAGGGC 77114 A _ G
GCC TGA AAGCG CCATGGC
||| || |||| |||||
CGG ACT TTCGC GGTACCG
G C _
GAM2619 LOC146657 5' GCCATGGCGCTTCCACGGC 61079 A A_ G
GCC TG AAGCG CCATGGC
||| || |||| |||||
CGG AC TTCGC GGTACCG
C CC _
GAM2619 LOC160418 5' AGACCATGACTGTGGTTTCAGT 83089 _ _ C C
GGCGT ACGCCA TGAAA GCGG CATGG CT
||||| |||| ||| ||||| ||
TGCGGT ACTTT TGTC GTACC GA
G GG A A
GAM2619 LOC201475 3' AGGCCACAGAATCTCTCTCATG 89617 A C CCA_
GC GCCATGA AG GG TGGCCT
||||| || || |||||
CGGTACT TC CT ACCGGA
C T AAGAC
GAM2619 LOC221876 3' AGGCCCTGAAGTGTTCATGGC 95540 AA C_ T
GCCATGA GCGG CA GGCCT
||||| |||| || |||||
CGGTACT TGTC GT CCGGA
_ AA C
GAM2619 LOC257206 5' AGGTGGCGGCCACTCCCATGGC 98892 AA C ATG
GCCATG AG GGCC GCCT
||||| || |||| ||||
CGGTAC TC CCGG TGGA
CC A CGG
GAM2619 LOC257319 3' GCCTGTTACTTTCATGACGT 97473 C CG CAT
ACG CATGAAAG GC GGC
||| ||||| || |||
TGC GTACTTTC TG CCG
A AT T_
GAM2619 LOC90522 3' GGCCACCGCCCCAGGGCGT 63855 A AAA CCA
ACGCC TG GCGG TGGCC
||||| || |||| |||||

			TGCGG AC CGCC ACCGG		
			G CC_ _		
GAM2620	ADAT1	3'	CAGGAGAATTGCTTGAACCCAG 24912	CA	
	GA		TCC GGTTC AAGCAATTCTCCTG		
			AGG CCAAGTTCGTTAAGAGGAC		
			AC		
GAM2620	AHR	3'	CAGGAGAATAGCCTGAACCTGG 9672	A A	
	GA		TCCCAGGTTCA GC ATTCTCCTG		
			AGGGTCCAAGT CG TAAGAGGAC		
			C A		
GAM2620	AICDA	3'	CAGGAGAATCGCTTGAACCCAG 40690	CA	A
	GA		TCC GGTTC AAGC ATTCTCCTG		
			AGG CCAAGTTCG TAAGAGGAC		
			AC C		
GAM2620	AIRE	3'	CATGAGAATCACTTGAACCTCGG 7245	AG	CA C
	GA		TCCC GTTCAAG ATTCTC TG		
			AGGG CAAGTTC TAAGAG AC		
			CT AC T		
GAM2620	AK1	3'	CAGGAGAATGGCGTGAACCCGG 6634	A	A A
	GA		TCCC GGTTC A GC ATTCTCCTG		
			AGGG CCAAGT CG TAAGAGGAC		
			C G G		
GAM2620	ALDH3B1	3'	CAGGAGAATCGCTTGAACCCGG 93152	A	A
	GA		TCCC GGTTC AAGC ATTCTCCTG		
			AGGG CCAAGTTCG TAAGAGGAC		
			C C		
GAM2620	ALPP	3'	CAGGATAATCGCTTGAACCCGG 69410	A	A C
	G		CCC GGTTC AAGC ATT TCCTG		
			GGG CCAAGTTCG TAA AGGAC		
			C C T		
GAM2620	ANKH	3'	CAGGAGAATTTGCTTGATCCTG 55065	T	—
	GGA		TCCCAGG TCAAGCAA TTCTCCTG		
			AGGGTCC AGTTCGTT AAGAGGAC		
			T T		
GAM2620	APM1	3'	GAAGGTAGCTTGAGCCTG 17782	A	TC
			CAGGTTCAAGC AT TC		
			GTCCGAGTTCG TG AG		
			A GA		
GAM2620	APOL1	3'	CAGGAGAATGGCGTGAACCTGG 14732	A	A
	GA		TCCCAGGTTCA GC ATTCTCCTG		

			AGGGTCCAAGT CG TAAGAGGAC		
			G G		
GAM2620	ATM	3'	CAGGAGAATCTCTTGAACCTGG 5292	CA	
	GA		TCCCAGGTTCAAG ATTCTCCTG		
			AGGGTCCAAGTTC TAAGAGGAC		
			TC		
GAM2620	ATP1A2	3'	CAGGAGAATTGCTTGAACCTGT 7359	C	
	GA		TC CAGGTTCAAGCAATTCTCCTG		
			AG GTCCAAGTTCGTTAAGAGGAC		
			T		
GAM2620	BACE2	3'	AGGAGAATCAGCCTGGGG 58098	CAAGCA	
			TCCCAGGTT ATTCTCCT		
			GGGGTCCGA TAAGAGGA		
			C_____		
GAM2620	BACE2	3'	AGGAGAATCAGCCTGGGG 58099	CAAGCA	
			TCCCAGGTT ATTCTCCT		
			GGGGTCCGA TAAGAGGA		
			C_____		
GAM2620	BHMT2	3'	CAGGAGAATCGCTTGAACCCAG 34729	CA	A
	GA		TCC GGTTCAGC ATTCTCCTG		
			AGG CCAAGTTCG TAAGAGGAC		
			AC C		
GAM2620	BPHL	3'	GGGAGAATTGCCTGAGCCCAGG 16335	CA	A
	A		TCC GGTTCAGCAATTCTCCT		
			AGG CCGAGT CGTTAAGAGGG		
			AC C		
GAM2620	BRCA1	3'	CAGGAGAATCACTTCAGCCCGG 24546	A	C CA
	GA		TCCC GGTT AAG ATTCTCCTG		
			AGGG CCGA TTC TAAGAGGAC		
			C C AC		
GAM2620	BRCA1	3'	CAGGAGAATCACTTCAGCCCGG 24547	A	C CA
	GA		TCCC GGTT AAG ATTCTCCTG		
			AGGG CCGA TTC TAAGAGGAC		
			C C AC		
GAM2620	BRCA1	3'	CAGGAGAATCACTTCAGCCCGG 24548	A	C CA
	GA		TCCC GGTT AAG ATTCTCCTG		
			AGGG CCGA TTC TAAGAGGAC		
			C C AC		
GAM2620	BRCA1	3'	CAGGAGAATCACTTCAGCCCGG 24549	A	C CA
	GA		TCCC GGTT AAG ATTCTCCTG		

			AGGG CCGA TTC TAAGAGGAC		
			C C AC		
GAM2620	BRCA1	5'	CAGGAGAATCGCTAGAACCCGG 24550	A	A A
	GA		TCCC GGTTC AGC ATTCTCCTG		
			AGGG CCAAG TCG TAAGAGGAC		
			C A C		
GAM2620	C1orf1	3'	GGGAGAATTACCTGAGCCCAGG 8680	CA	AGC
	A		TCC GGTTC AATTCTCCT		
			AGG CCGAGT TTAAGAGGG		
			AC CCA		
GAM2620	C5R1	3'	GGGAGAATTGCTCGAACCTTGG 9974	C	A
	A		TCC AGGTTC AGCAATTCTCCT		
			AGG TCCAAG TCGTTAAGAGGG		
			T C		
GAM2620	CA12	3'	GAATCGCTTGAACCCAGGA 8690	CA	A
			TCC GGTTC AAGC ATTC		
			AGG CCAAGTTCG TAAG		
			AC C		
GAM2620	CARKL	3'	CAGGAAAATCACTTGAACCTCGG 26100	AG	CA C
	GA		TCCC GTTCAAG ATT TCCTG		
			AGGG CAAGTTC TAA AGGAC		
			CT AC A		
GAM2620	CASP10	3'	CAGGAGAATCTCTTGAATCCAG 53200	CA	CA
	GA		TCC GGTTC AAG ATTCTCCTG		
			AGG CTAAGTTC TAAGAGGAC		
			AC TC		
GAM2620	CASP10	3'	CAGGAGAATCTCTTGAATCCAG 53201	CA	CA
	GA		TCC GGTTC AAG ATTCTCCTG		
			AGG CTAAGTTC TAAGAGGAC		
			AC TC		
GAM2620	CASP6	3'	CAGGAGAATCACTTGAACCCAG 8731	CA	CA
	GA		TCC GGTTC AAG ATTCTCCTG		
			AGG CCAAGTTC TAAGAGGAC		
			AC AC		
GAM2620	CD28	3'	CATGAGAATCGCTTGAACCTGG 21551	A	C
			CCAGGTTCAAGC ATTCTC TG		
			GGTCCAAGTTCG TAAGAG AC		
			C T		
GAM2620	CD68	3'	AGAACTGCTTGAACCCAGGA 60499	CA	A
			TCC GGTTC AAGCA TTCT		

			AGG CCAAGTTCGT AAGA		
			AC C		
GAM2620	CEACAM5	3'	CAGGAGAATCGCTTGAACCCGG 16420	A	A
	GA		TCCC GGTTCAAGC ATTCTCCTG		
			AGGG CCAAGTTCG TAAGAGGAC		
			C C		
GAM2620	COPA	3'	CATGAGAATCGCTTGAACCTAG 16477	C	A C
	GA		TCC AGGTTCAAGC ATTCTC TG		
			AGG TCCAAGTTCG TAAGAG AC		
			A C T		
GAM2620	CPM	3'	CAGGAGAATCGCTTGAACC 60404	A	
			GGTTCAAGC ATTCTCCTG		
			CCAAGTTCG TAAGAGGAC		
			C		
GAM2620	CPT2	3'	AGAATTGCTTGAACCCAGGA 5419	CA	
			TCC GGTTCAAGCAATTCT		
			AGG CCAAGTTCGTTAAGA		
			AC		
GAM2620	CRACC	3'	CATGAGAATCGCTTGAACCTGG 41309	A	C
	GA		TCCCAGGTTCAAGC ATTCTC TG		
			AGGGTCCAAGTTCG TAAGAG AC		
			C T		
GAM2620	CTMP	3'	CAGGAGAATTGCTTGAACCCAG 54947	CA	
	GA		TCC GGTTCAAGCAATTCTCCTG		
			AGG CCAAGTTCGTTAAGAGGAC		
			AC		
GAM2620	CTMP	3'	GAATTGCTTGAACCCAGGA 54950	CA	
			TCC GGTTCAAGCAATTC		
			AGG CCAAGTTCGTTAAG		
			AC		
GAM2620	CUBN	3'	CAGGAGAATTGCTTGAACCCAG 8418	CA	
	GA		TCC GGTTCAAGCAATTCTCCTG		
			AGG CCAAGTTCGTTAAGAGGAC		
			AC		
GAM2620	CYP3A4	3'	CAGGAGAATCACTTGAACCTGG 34363	CA	
	GA		TCCCAGGTTCAAG ATTCTCCTG		
			AGGGTCCAAGTTC TAAGAGGAC		
			AC		
GAM2620	CYP4F3	3'	CAGGAGAATCACTTGAAACC 7997	_	CA
			GGTT CAAG ATTCTCCTG		

			CCAA GTTC TAAGAGGAC		
			A AC		
GAM2620	CYP4F3	3'	CAGGAGAATCGCTTGAACCCAG 7998	CA	A
	GA		TCC GGTCAAGC ATTCTCCTG		
			AGG CCAAGTTCG TAAGAGGAC		
			AC C		
GAM2620	DAPP1	3'	CAGGAGAATTGCTTGAACCCGG 27680	A	
	GA		TCCC GGTCAAGCAATTCTCCTG		
			AGGG CCAAGTTCGTTAAGAGGAC		
			C		
GAM2620	DBT	3'	CAGGAGAATCGCTTGAACCTGG 10367	A	
	GA		TCCCAGGTTCAAGC ATTCTCCTG		
			AGGGTCCAAGTTCG TAAGAGGAC		
			C		
GAM2620	DBT	3'	CAGGAGAATTGCTTGAGCC 10368		
			GGTCAAGCAATTCTCCTG		
			CCGAGTTCGTTAAGAGGAC		
GAM2620	DCLRE1C	3'	CAGGAGAATCACTTGAACCTGG 42820	CA	
	GA		TCCCAGGTTCAAG ATTCTCCTG		
			AGGGTCCAAGTTC TAAGAGGAC		
			AC		
GAM2620	DDOST	3'	CAGGAGAAAGGCATGAATCCAG 19061	CA	A AA
	GA		TCC GGTCA GC TTCTCCTG		
			AGG CTAAGT CG AAGAGGAC		
			AC A GA		
GAM2620	DFFA	3'	CAGGAGAATGGCATGAACCTGG 16590	A	A
	GA		TCCCAGGTTCA GC ATTCTCCTG		
			AGGGTCCAAGT CG TAAGAGGAC		
			A G		
GAM2620	DGKI	5'	CAGGAGAATGGCGTGAACCCAG 17525	CA	A A
	GA		TCC GGTCA GC ATTCTCCTG		
			AGG CCAAGT CG TAAGAGGAC		
			AC G G		
GAM2620	DHFR	3'	CAGGACGACTTGAGCC 7644	CAAT	_
			GGTCAAG TC TCCTG		
			CCGAGTTC AG AGGAC		
			____ C		
GAM2620	DMC1	3'	CAGGAGAATTGCTTGAACCCAG 23941	CA	
	GA		TCC GGTCAAGCAATTCTCCTG		

			AGG CCAAGTTCGTTAAGAGGAC		
			AC		
GAM2620	DNASE2	3'	CAGGAGAATCGCTTGAACCTCGG 9099	AG	A
	GA		TCCC GTTCAAGC ATTCTCCTG		
			AGGG CAAGTTCG TAAGAGGAC		
			CT C		
GAM2620	DPYSL3	3'	CAGAAGAAATATGTTCAACCTG 9121	CA	A__ C
	GGA		TCCCAGGTT AGCA TTCT CTG		
			AGGGTCCAA TTGT AAGA GAC		
			C_ ATA A		
GAM2620	DSC1	3'	CAGGAGAATCGCTTGAATCCAG 44602	CA	A
	GA		TCC GGTTC AAGC ATTCTCCTG		
			AGG CTAAGTTCG TAAGAGGAC		
			AC C		
GAM2620	DSC1	3'	CAGGAGAATCGCTTGAATCCAG 44603	CA	A
	GA		TCC GGTTC AAGC ATTCTCCTG		
			AGG CTAAGTTCG TAAGAGGAC		
			AC C		
GAM2620	DVL3	3'	AGAATCGCTTGAATCCAGGA 16635	CA	A
			TCC GGTTC AAGC ATTCT		
			AGG CTAAGTTCG TAAGA		
			AC C		
GAM2620	EGFL4	3'	CAGAAGAATCGCTTGAACCCAG 62455	CA	A C
	GA		TCC GGTTC AAGC ATTCT CTG		
			AGG CCAAGTTCG TAAGA GAC		
			AC C A		
GAM2620	EGFL5	3'	CAGGAGAATCACTTGAACCTGG 87909	CA	
	GA		TCCCAGGTTCAAG ATTCTCCTG		
			AGGGTCCAAGTTC TAAGAGGAC		
			AC		
GAM2620	EIF5A2	3'	CATGAGAATTGCTTGAACCCGG 40204	A	C
	GA		TCCC GGTTC AAGCAATTCTC TG		
			AGGG CCAAGTTCGTTAAGAG AC		
			C T		
GAM2620	ENPP3	3'	CAGGAGACTCGCTTGAACCCGG 73330	A	AAT
	GA		TCCC GGTTC AAGC TCTCCTG		
			AGGG CCAAGTTCG AGAGGAC		
			C CTC		
GAM2620	F2RL3	3'	CAGAAGGATCGCTTGAACCTGG 15501	A	C
	GA		TCCCAGGTTCAAGC ATTCT CTG		

			AGGGTCCAAGTTCG TAGGA GAC		
			C A		
GAM2620 F2RL3	3'	CAGGAGAATCGCTTGAACCTGG 15502		A	
GA		TCCCAGGTTCAAGC ATTCTCCTG			
		AGGGTCCAAGTTCG TAAGAGGAC			
		C			
GAM2620 F2RL3	3'	GGAGGATTGCTTGAAGCCAGG 15521	A _		
		CC GGTT CAAGCAATTCTCC			
		GG CCGA GTTCGTTAGGAGG			
		A A			
GAM2620 FCAR	3'	CAGGAGAATCACTTGAACCCAG 10584	CA CA		
GA		TCC GGTTCAAG ATTCTCCTG			
		AGG CCAAGTTC TAAGAGGAC			
		AC AC			
GAM2620 FCAR	3'	CAGGAGAATCACTTGAACCCAG 56562	CA CA		
GA		TCC GGTTCAAG ATTCTCCTG			
		AGG CCAAGTTC TAAGAGGAC			
		AC AC			
GAM2620 FCMD	3'	CAGGAGAATCACTTGAACCCGG 23029	A CA		
GA		TCCC GGTTCAAG ATTCTCCTG			
		AGGG CCAAGTTC TAAGAGGAC			
		C AC			
GAM2620 FGF2	3'	CAGGAGGATCGCTTGAGCCCAG 10615	CA A		
GA		TCC GGTTCAAGC ATTCTCCTG			
		AGG CCGAGTTCG TAGGAGGAC			
		AC C			
GAM2620 FGFR2	3'	CAGGAGAGTCACTTGAACCGGG 5558	A CA		
GA		TCCC GGTTCAAG ATTCTCCTG			
		AGGG CCAAGTTC TGAGAGGAC			
		G AC			
GAM2620 FLRT2	5'	CAGGAGGACCACTCGAGCC 25993	A CAA		
		GGTTC AG TTCTCCTG			
		CCGAG TC AGGAGGAC			
		C ACC			
GAM2620 FUT6	3'	CAGGAGAATGGTGTGAACCTGT 5631	C A A		
GA		TC CAGGTTCA GC ATTCTCCTG			
		AG GTCCAAGT TG TAAGAGGAC			
		T G G			
GAM2620 GALNT7	3'	GAGAATCGCTTGAACCCAGGA 55089	CA A		
		TCC GGTTCAAGC ATTCTC			

			AGG CCAAGTTCG TAAGAG		
			AC C		
GAM2620	GAS7	3'	CAGTAGAATCGCTTGAACCTGG 20844	A	C
	GA		TCCCAGGTTCAAGC ATTCT CTG		
			AGGGTCCAAGTTCG TAAGA GAC		
			C T		
GAM2620	GP2	3'	CAGGAGAATTGCTCGAACTCAG 9481	A_	A
	GG		CCC GGTTT AGCAATTCTCCTG		
			GGG TCAAG TCGTTAAGAGGAC		
			AC C		
GAM2620	GP6	3'	CAGGAGGATCGCTTGAGCCCAG 33472	CA	A
	GA		TCC GGTTCAAGC ATTCTCCTG		
			AGG CCGAGTTCG TAGGAGGAC		
			AC C		
GAM2620	GPRK7	3'	CAGGAGAATTGCTTGAACCCAG 58310	CA	
	GA		TCC GGTTCAAGCAATTCTCCTG		
			AGG CCAAGTTCGTTAAGAGGAC		
			AC		
GAM2620	GRAF	3'	CAGGAGAATGGCATGAGCCCGG 31223	A	A A
	GA		TCCC GGTTCA GC ATTCTCCTG		
			AGGG CCGAGT CG TAAGAGGAC		
			C A G		
GAM2620	GRM6	3'	CAGGAGAATCGCTTGAACCTGG 7760		A
	GA		TCCCAGGTTCAAGC ATTCTCCTG		
			AGGGTCCAAGTTCG TAAGAGGAC		
			C		
GAM2620	GTF2F1	3'	GAGATTCACCTTGAACCTGGGA 10891		CAAT
			TCCCAGGTTCAAG TCTC		
			AGGGTCCAAGTTC AGAG		
			ACTT		
GAM2620	HCS	3'	AGAATCACTTGAACCTGGGA 38962		CA
			TCCCAGGTTCAAG ATTCT		
			AGGGTTCAAGTTC TAAGA		
			AC		
GAM2620	HFE	3'	CAGGAGAGAGTTGAACCT 58119		GCAA
			AGGTTCAA TTCTCCTG		
			TCCAAGTT GAGAGGAC		
			GA__		
GAM2620	HIP1	3'	CAGGAGAATCACCTGAACC 19250		AGCA
			GGTTCA ATTCTCCTG		

			CCAAGT TAAGAGGAC		
			CCAC		
GAM2620	HLA-E	3'	CAGGAGAATGGCGTCAACCCGG 92671	A	CAA A
	GA		TCCC GGTT GC ATTCTCCTG		
			AGGG CCAA CG TAAGAGGAC		
			C CTG G		
GAM2620	HRH1	3'	GAGAATCGCTTGAACCCGGGA 7821	A	A
			TCCC GGTTCAAGC ATTCTC		
			AGGG CCAAGTTCG TAAGAG		
			C C		
GAM2620	HSPA5	3'	CAGGAGAATCACTCGAACCCGG 19281	A	A CA
	GA		TCCC GGTTC AG ATTCTCCTG		
			AGGG CCAAG TC TAAGAGGAC		
			C C AC		
GAM2620	IAPP	3'	CAGGAGAATCGCTTGAACCCAG 6439	CA	A
	GA		TCC GGTTCAAGC ATTCTCCTG		
			AGG CCAAGTTCG TAAGAGGAC		
			AC C		
GAM2620	IFIT4	3'	AGGGGGCCCCAACCTGGGA 71488	CAA	AATT
			TCCCAGGTT GC CTCCT		
			AGGGTCCAA CG GGGGA		
			CCC ____		
GAM2620	IFIT4	3'	CAGGAGAATGGCGTGAACCTGG 71491	A	A
			CCAGGTTCA GC ATTCTCCTG		
			GGTCCAAGT CG TAAGAGGAC		
			G G		
GAM2620	IFNAR1	3'	CAGGAGAATCGCTTGAAAACAG 7137	CAGG	A
	GA		TCC TTCAAGC ATTCTCCTG		
			AGG AAGTTCG TAAGAGGAC		
			ACAA C		
GAM2620	IL10	3'	GAGAATTGCTTGAACCCAGGA 6925	CA	
			TCC GGTTCAAGCAATTCTC		
			AGG CCAAGTTCGTTAAGAG		
			AC		
GAM2620	IL13RA1	3'	CAGGTGAATTGTTTGAACCTGG 9567		T
	GA		TCCCAGGTTCAAGCAATTC CCTG		
			AGGGTCCAAGTTTGTTAAG GGAC		
			T		
GAM2620	IL17R	3'	CAGGAGAATTGCTTGAATCTGG 27550		
	GA		TCCCAGGTTCAAGCAATTCTCCTG		

GAM2620	IL18 GA	3'	CAGGAGAATCACTTGACCTCCG 9589	CA	T	CA
			TCC GGT CAAG ATTCTCCTG			
			AGG TCA GTTC TAAGAGGAC			
			CC C AC			
GAM2620	IL1R1 GA	3'	CAGGAGAATTGCTTGAACCGGG 7921	A		
			TCCC GGTTCAAGCAATTCTCCTG			
			AGGG CCAAGTTCGTTAAGAGGAC			
			G			
GAM2620	IL2RA GA	3'	CAGGAGGATTGCTTGAGCCCAG 6449	CA		
			TCC GGTTCAAGCAATTCTCCTG			
			AGG CCGAGTTCGTTAGGAGGAC			
			AC			
GAM2620	IPP	3'	AGGATCGCTTGAGCCCAGGA 20902	CA		A
			TCC GGTTCAAGC ATTCT			
			AGG CCGAGTTCG TAGGA			
			AC C			
GAM2620	IPP GA	3'	CAGGGGGATCGCTTGAGCCCAG 20904	CA		A
			TCC GGTTCAAGC ATTCTCCTG			
			AGG CCGAGTTCG TAGGGGGAC			
			AC C			
GAM2620	ITGAL A	3'	AGGAGAATTGCTTGAACCTGGG 11040			
			TCCCAGGTTCAAGCAATTCTCCT			
			AGGGTCCAAGTTCGTTAAGAGGA			
GAM2620	ITPR2	3'	AGAACTTTGAACCTAGGA 11078	C		CAA
			TCC AGGTTCAAG TTCT			
			AGG TCCAAGTTT AAGA			
			A C__			
GAM2620	KAI1 GA	3'	CAGGAGAATGGTGTGAACCCGG 11120	A		A A
			TCCC GGTTCA GC ATTCTCCTG			
			AGGG CCAAGT TG TAAGAGGAC			
			C G G			
GAM2620	KCNA7 GA	3'	CAGGAGAATGGCATGAACCTGG 49893			A A
			TCCCAGGTTCA GC ATTCTCCTG			
			AGGGTCCAAGT CG TAAGAGGAC			
			A G			
GAM2620	KCNJ5 GA	3'	CAGAAGAATGGCATGAACCTGG 7970			A A C
			TCCCAGGTTCA GC ATTCT CTG			

		AGGGTCCAAGT CG TAAGA GAC			
		A G A			
GAM2620	KIF1B	3' CAGGAGAACTGCTTGAACCCAG 31264	CA	A	
	GA	TCC GGTTC AAGCA TTCTCCTG			
		AGG CCAAGTTCGT AAGAGGAC			
		AC C			
GAM2620	KNSL1	3' GAGAATCACTTGAACCCAGGA 16946	CA	CA	
		TCC GGTTC AAG ATTCTC			
		AGG CCAAGTTC TAAGAG			
		AC AC			
GAM2620	LAMC2	3' CAGGAGAATCGCTTGAACCCAG 19906	CA	A	
	GA	TCC GGTTC AAGC ATTCTCCTG			
		AGG CCAAGTTCG TAAGAGGAC			
		AC C			
GAM2620	LAMP2	3' CAGGAGAATCACTTGAACCCGG 26568	A	CA	
	GA	TCCC GGTTC AAG ATTCTCCTG			
		AGGG CCAAGTTC TAAGAGGAC			
		C AC			
GAM2620	LDLR	3' CAGGAGAATGGTGTGAACCCGG 6728	A	A A	
	GA	TCCC GGTTC A GC ATTCTCCTG			
		AGGG CCAAGT TG TAAGAGGAC			
		C G G			
GAM2620	LDLR	3' CAGGAGGATCGCCTGAGCCCAG 6729	CA	A A	
	GA	TCC GGTTC A GC ATTCTCCTG			
		AGG CCGAGT CG TAGGAGGAC			
		AC C C			
GAM2620	LEP	3' CAGGAGAATCGCTTAAACCTGG 5857	C	A	
	GA	TCCCAGGTT AAGC ATTCTCCTG			
		AGGGTCCAA TTCG TAAGAGGAC			
		A C			
GAM2620	LILRB1	3' CAGGAGAATCGCTTGAACCAGG 22870	A	A	
	GA	TCCC GGTTC AAGC ATTCTCCTG			
		AGGG CCAAGTTCG TAAGAGGAC			
		A C			
GAM2620	LRRC2	3' CAGGAGAATCGCTTGAACCTGG 44739		A	
	GA	TCCCAGGTTCAAGC ATTCTCCTG			
		AGGGTCCAAGTTCG TAAGAGGAC			
		C			
GAM2620	LRRC2	3' CAGGAGAATTGCTTGAACCCAG 44740	CA		
	GA	TCC GGTTC AAGCAATTCTCCTG			

			AGG CCAAGTTCGTTAAGAGGAC		
			AC		
GAM2620	LRR2	3'	GGGAAAATCACTTGAGCCCAGG 44755	CA	CA C
	A		TCC GGTTC AAG ATT TCCT		
			AGG CCGAGTTC TAA AGGG		
			AC AC A		
GAM2620	LUZP1	3'	CAGGAGAATCACTTGAACCCAG 54398	CA	CA
	GA		TCC GGTTC AAG ATTCTCCTG		
			AGG CCAAGTTC TAAGAGGAC		
			AC AC		
GAM2620	MAFF	3'	CAGGAGGATCACTTAAGCC 25576	C CA	
			GGTT AAG ATTCTCCTG		
			CCGA TTC TAGGAGGAC		
			A AC		
GAM2620	MCM4	3'	CAGGAGAATCGCTTAAACCCAG 62575	CA C A	
	G		CC GGTT AAGC ATTCTCCTG		
			GG CCAA TTCG TAAGAGGAC		
			AC A C		
GAM2620	MMP19	3'	CAGGAGGATCACTTGAGCCCAG 11620	CA	CA
	GA		TCC GGTTC AAG ATTCTCCTG		
			AGG CCGAGTTC TAGGAGGAC		
			AC AC		
GAM2620	MMP19	3'	CAGGAGGATCACTTGAGCCCAG 11621	CA	CA
	GA		TCC GGTTC AAG ATTCTCCTG		
			AGG CCGAGTTC TAGGAGGAC		
			AC AC		
GAM2620	MOG	3'	CAGGAGAATCGCTTGAACCCAG 11669	CA	A
	GA		TCC GGTTC AAGC ATTCTCCTG		
			AGG CCAAGTTCG TAAGAGGAC		
			AC C		
GAM2620	MS4A1	3'	CAGGAGAATCGCTTGAACCTGG 5545		A
	GA		TCCCAGGTTCAAGC ATTCTCCTG		
			AGGGTCCAAGTTCG TAAGAGGAC		
			C		
GAM2620	MSH3	3'	CAGGAGAATCTCTTGAACCTGG 11689		CA
	GA		TCCCAGGTTCAAG ATTCTCCTG		
			AGGGTCCAAGTTC TAAGAGGAC		
			TC		
GAM2620	MTMR8	3'	CAGGAGAATGGTGTGAACCCGG 31907	A A A	
	GA		TCCC GGTTCA GC ATTCTCCTG		

			AGGG CCAAGT TG TAAGAGGAC		
			C G G		
GAM2620	MYO1C	3'	CAGGAGAATCACTTGAACCCGG 61856	A	CA
	GA		TCCC GGTTCAAG ATTCTCCTG		
			AGGG CCAAGTTC TAAGAGGAC		
			C AC		
GAM2620	NFKBIL2	3'	CAGGAGAATGGCGTGAACCCGG 26445	A	A A
	GA		TCCC GGTTCA GC ATTCTCCTG		
			AGGG CCAAGT CG TAAGAGGAC		
			C G G		
GAM2620	NPHP1	3'	GAATTGTTTGAACCTGGGA 63143		
			TCCCAGGTTCAAGCAATTC		
			AGGGTCCAAGTTTGTTAAG		
GAM2620	NPHS1	3'	CATGAGAATTGCTTGAACCCAG 17368	CA	C
	GA		TCC GGTTCAAGCAATTCTC TG		
			AGG CCAAGTTCGTTAAGAG AC		
			AC T		
GAM2620	Nrap	3'	CAGGAGAATCACTTGAGCTCAG 56307	CA	CA
	GA		TCC GGTTCAAG ATTCTCCTG		
			AGG TCGAGTTC TAAGAGGAC		
			AC AC		
GAM2620	NRAS	3'	CAGGAGAAAGATGAACTG 11844	G	AGCAA
			CAG TTCA TTCTCCTG		
			GTC AAGT AAGAGGAC		
			A AGA__		
GAM2620	NT5C2	3'	CAGGAGAATTGCTTGAACCCAG 25255	CA	
	GA		TCC GGTTCAAGCAATTCTCCTG		
			AGG CCAAGTTCGTTAAGAGGAC		
			AC		
GAM2620	NUP62	3'	CAGGAGAATCACTTGAACCCAG 25644	CA	CA
	GA		TCC GGTTCAAG ATTCTCCTG		
			AGG CCAAGTTC TAAGAGGAC		
			AC AC		
GAM2620	OPA3	3'	CAGGAGAATTGCTTGAACC 47841		
			GGTTCAAGCAATTCTCCTG		
			CCAAGTTCGTTAAGAGGAC		
GAM2620	OPA3	3'	CAGGAGAATTGCTTGAACCTTGG 47842		
	GA		TCCCAGGTTCAAGCAATTCTCCTG		

AGGGTTCAAGTTCGTTAAGAGGAC

GAM2620	OPTN	3'	CAGGAGAATTGCTTGAACCCAG 42051	CA	
	GA		TCC GGTTC AAGCAATTCTCCTG		
			AGG CCAAGTTCGTTAAGAGGAC		
			AC		
GAM2620	OXR1	3'	CAGGAGAATGGCCCAAACCTG 36311	CAA A	
			CAGGTT GC ATTCTCCTG		
			GTCCAA CG TAAGAGGAC		
			ACC G		
GAM2620	P2RX7	3'	AGAATCACTTGAACCCGGA 11924	A	CA
			TCCC GGTTC AAG ATTCT		
			AGGG CCAAGTTC TAAGA		
			C AC		
GAM2620	PA2G4	3'	CAGGAGAGTTGCTTGGACCCGG 71826	A	
	GA		TCCC GGTTC AAGCAATTCTCCTG		
			AGGG CCAGGTTGTTGAGAGGAC		
			C		
GAM2620	PACE4	3'	CAGGAGGATTGCTTGAGCCCAG 11947	CA	
	GA		TCC GGTTC AAGCAATTCTCCTG		
			AGG CCGAGTTCGTTAGGAGGAC		
			AC		
GAM2620	PAICS	3'	CATGAGAATTGCTTGAACCCGG 22257	A	C
	GA		TCCC GGTTC AAGCAATTCTC TG		
			AGGG CCAAGTTCGTTAAGAG AC		
			C T		
GAM2620	PCDH11X	3'	CAGGAGAATAGCGTGAACCCGG 28008	A	A A
	GA		TCCC GGTTC A GC ATTCTCCTG		
			AGGG CCAAGT CG TAAGAGGAC		
			C G A		
GAM2620	PCDH11Y	3'	CAGGAGAATGGCGTGAACCCGG 53157	A	A A
	GA		TCCC GGTTC A GC ATTCTCCTG		
			AGGG CCAAGT CG TAAGAGGAC		
			C G G		
GAM2620	PCDHA9	3'	GAGAATCGCTTGAGCCTGGGA 49844		A
			TCCCAGGTTCAAGC ATTCTC		
			AGGGTCCGAGTTCG TAAGAG		
			C		
GAM2620	PCDHB9	3'	CAGGAGAATCGCTTGAACCCAG 39440	CA	A
	GA		TCC GGTTC AAGC ATTCTCCTG		

			AGG CCAAGTTCG TAAGAGGAC		
			AC C		
GAM2620	PCSK1	3'	AGAAAAGGCAAAACCTGGGA 6512	CAA	AA_
			TCCCAGGTT GC TTCT		
			AGGGTCCAA CG AAGA		
			AA_ GAA		
GAM2620	PDE4C	3'	AGGGGATCGCTTGAGCCCAGGA 8096	CA	AAT
			TCC GGTTC AAGC TCTCT		
			AGG CCGAGTTCG AGGGGA		
			AC CT_		
GAM2620	PDE4C	3'	CAGGAGAATCACTTGAATTCAG 8100	CA	CA
	GA		TCC GGTTC AAG ATTCTCCTG		
			AGG TTAAGTTC TAAGAGGAC		
			AC AC		
GAM2620	PIK3CG	3'	CAGGAGGATTGCCTGAGCCCAG 12120	CA	A
	GA		TCC GGTTC A GCAATTCTCCTG		
			AGG CCGAGT CGTTAGGAGGAC		
			AC C		
GAM2620	PKD2	3'	CAGGCGAATCACTTGAGCCCAG 33614	CA	CA T
	GA		TCC GGTTC AAG ATTC CCTG		
			AGG CCGAGTTC TAAG GGAC		
			AC AC C		
GAM2620	PLA2G2D	3'	CAGGAGAATCACTTGGACCTGG 25709		CA
	GA		TCCCAGGTTCAAG ATTCTCCTG		
			AGGGTCCAGGTTC TAAGAGGAC		
			AC		
GAM2620	POLH	3'	CAGAAGAATTGCTTTAACCTTG 22475	C	C C
	GA		TCC AGGTT AAGCAATTCT CTG		
			AGG TCCAA TTCGTTAAGA GAC		
			T T A		
GAM2620	POLH	3'	CAGGAGAATCACTTGAACCCAG 22476	CA	CA
	GA		TCC GGTTC AAG ATTCTCCTG		
			AGG CCAAGTTC TAAGAGGAC		
			AC AC		
GAM2620	POLK	3'	CAGGAGAACTACTTGAACCTGG 33098		CAA
	GA		TCCCAGGTTCAAG TTCTCCTG		
			AGGGTCCAAGTTC AAGAGGAC		
			ATC		
GAM2620	PPP1R12B	3'	CAGGAGAATGGCGTGAACCCGG 50346	A	A A
	GA		TCCC GGTTC A GC ATTCTCCTG		

			AGGG CCAAGT CG TAAGAGGAC		
			C G G		
GAM2620 PRKY	3'	CAGAAAAGATTGCTTGAGCCTGG 12364		CTC	
GA		TCCCAGGTTCAAGCAATT CTG			
		AGGGTCCGAGTTCGTTAG GAC			
		AAA			
GAM2620 PRKY	3'	CAGGAGAATATGGAACCTCAGGA 12365	CA	AAGCA	
		TCC GGTTT ATTCTCCTG			
		AGG TCAAG TAAGAGGAC			
		AC GTA__			
GAM2620 PSMB2	3'	CAGGAGAATTGCTTGAGCCCGG 12462	A		
GA		TCCC GGTTCAAGCAATTCTCCTG			
		AGGG CCGAGTTCGTTAAGAGGAC			
		C			
GAM2620 PSMB2	3'	GAATCGGTCTGAACCCGGGA 12473	A	AA A_	
		TCCC GGTTT GC ATTCT			
		AGGG CCAAG TG TAAG			
		C C_ GC			
GAM2620 PSMB9	3'	CAGAAGAATCACTTGAGCCCAG 12496	CA	CA C	
GA		TCC GGTTCAAG ATTCT CTG			
		AGG CCGAGTTC TAAGA GAC			
		AC AC A			
GAM2620 PSMB9	3'	CAGGAGAATTGCTTGAACCCGG 12497	A		
GA		TCCC GGTTCAAGCAATTCTCCTG			
		AGGG CCAAGTTCGTTAAGAGGAC			
		C			
GAM2620 PSMD5	3'	GAGAATCGCTTGAGCCTGGGA 18558		A	
		TCCCAGGTTCAAGC ATTCTC			
		AGGGTCCGAGTTCG TAAGAG			
		C			
GAM2620 PTAFR	3'	CAGGAGAATCGCTTGAACCTGG 8163		A	
GA		TCCCAGGTTCAAGC ATTCTCCTG			
		AGGGTCCAAGTTCG TAAGAGGAC			
		C			
GAM2620 PTGIS	3'	AGAATTGCTTGAACCCAGGA 8187	CA		
		TCC GGTTCAAGCAATTCT			
		AGG CCAAGTTCGTTAAGA			
		AC			
GAM2620 RAB7L1	3'	CAGGAGAATCACTTGAACCTGG 15401		CA	
GA		TCCCAGGTTCAAG ATTCTCCTG			

			AGGGTCCAAGTTC TAAGAGGAC		
			AC		
GAM2620	RAD1	3'	CAGGAAAATTGCTTGAACCCGG 12640	A	C
	GA		TCCC GGTTCAAGCAATT TCCTG		
			AGGG CCAAGTTCGTAA AGGAC		
			C A		
GAM2620	RBBP5	3'	CAGGAGAATCACTTGAACGTGG 18577	G	CA
	GA		TCCCA GTTCAAG ATTCTCCTG		
			AGGGT CAAGTTC TAAGAGGAC		
			G AC		
GAM2620	RBBP9	3'	AGGATTGCTTGAGCCCAGGA 70681	CA	
			TCC GGTTCAAGCAATTCT		
			AGG CCGAGTTCGTTAGGA		
			AC		
GAM2620	RBL1	3'	AGAATTGCTTGAACCCAGGA 12781	CA	
			TCC GGTTCAAGCAATTCT		
			AGG CCAAGTTCGTAAAGA		
			AC		
GAM2620	RBM3	3'	CAGGAGAATCGCTTGAACCCGG 71006	A	A
	GA		TCCC GGTTCAAGC ATTCTCCTG		
			AGGG CCAAGTTCG TAAGAGGAC		
			C C		
GAM2620	RFC2	3'	AATCGCTTGAACCCAGGA 12832	CA	A
			TCC GGTTCAAGC ATT		
			AGG CCAAGTTCG TAA		
			AC C		
GAM2620	RFC2	3'	CAGGCGAAATCGCTTGAACCCA 12838	CA	AA_ T
	GGA		TCC GGTTCAAGC TTC CCTG		
			AGG CCAAGTTCG AAG GGAC		
			AC CTA C		
GAM2620	ROCK2	3'	CAGGAGAATCGCTTGAACCCAG 66615	CA	A
	GA		TCC GGTTCAAGC ATTCTCCTG		
			AGG CCAAGTTCG TAAGAGGAC		
			AC C		
GAM2620	RPN1	5'	CAGGAGAATTGCTTGAACCCGG 12905	A	
	GA		TCCC GGTTCAAGCAATTCTCCTG		
			AGGG CCAAGTTCGTAAAGAGGAC		
			C		
GAM2620	SIGLEC11	3'	GAGAATTGGTTGAACCCGGGA 54653	A	G
			TCCC GGTTCAA CAATTCTC		

			AGGG CCAAGTT GTTAAGAG		
			C G		
GAM2620	SLC14A1	3'	GATTGCTTGAACCCAGGA 32413	CA	
			TCC GGTTCAAGCAATT		
			AGG CCAAGTTCGTTAG		
			AC		
GAM2620	SLC17A5	3'	AGGAGAATCACTTGAACCTGGG 25826	CA	
	A		TCCCAGGTTCAAG ATTCTCCT		
			AGGGTCCAAGTTC TAAGAGGA		
			AC		
GAM2620	SLC25A15	3'	CAGGAGAATCGCTTGAACCCGG 27290	A	A
	GA		TCCC GGTTCAAGC ATTCTCCTG		
			AGGG CCAAGTTCG TAAGAGGAC		
			C C		
GAM2620	SLC26A4	3'	CAGGAGAATGGCGTGAACCCGG 6523	A	A A
	GA		TCCC GGTTCA GC ATTCTCCTG		
			AGGG CCAAGT CG TAAGAGGAC		
			C G G		
GAM2620	SLC28A2	3'	CAGGAGAATGGCGTGAATCCGG 16145	A	A A
	GA		TCCC GGTTCA GC ATTCTCCTG		
			AGGG CTAAGT CG TAAGAGGAC		
			C G G		
GAM2620	SLC31A1	3'	CAGGAGAATCACTTGAACCTAG 10274	C	CA
	GA		TCC AGGTTCAAG ATTCTCCTG		
			AGG TCCAAGTTC TAAGAGGAC		
			A AC		
GAM2620	SMG1	3'	CAGGAGAATGGCGTGAACCCAG 31344	CA	A A
	GA		TCC GGTTCA GC ATTCTCCTG		
			AGG CCAAGT CG TAAGAGGAC		
			AC G G		
GAM2620	SRGAP1	5'	CAGGAGAATCACTTGAACCCGG 72713	A	CA
	GA		TCCC GGTTCAAG ATTCTCCTG		
			AGGG CCAAGTTC TAAGAGGAC		
			C AC		
GAM2620	STAT3	3'	CAGGAGAATCGCTTGAACCTGA 13433	C	A
	GA		TC CAGGTTCAAGC ATTCTCCTG		
			AG GTCCAAGTTCG TAAGAGGAC		
			A C		
GAM2620	SUDD	3'	CAGGAGAATCGCTTGAACCCGG 15155	A	A
	GA		TCCC GGTTCAAGC ATTCTCCTG		

			AGGG CCAAGTTCG TAAGAGGAC		
			C C		
GAM2620	SUV39H2	3'	CAGGAGAATCACTTGAATTCAG 45454	CA	CA
	GA		TCC GGTTC AAG ATTCTCCTG		
			AGG TTAAGTTC TAAGAGGAC		
			AC AC		
GAM2620	SWAP70	3'	CAGGAGAATCACTTGAACGTGG 71863	G	CA
	GA		TCCCA GTTCAAG ATTCTCCTG		
			AGGGT CAAGTTC TAAGAGGAC		
			G AC		
GAM2620	TADA2L	3'	CAGGAGAATTGCTTGAACACAG 56764	CAG	
	GA		TCC GTTCAAGCAATTCTCCTG		
			AGG CAAGTTCGTTAAGAGGAC		
			ACA		
GAM2620	TBX6	3'	CAGGAGAATCTCTTGAACCCAG 55810	CA	CA
	GA		TCC GGTTC AAG ATTCTCCTG		
			AGG CCAAGTTC TAAGAGGAC		
			AC TC		
GAM2620	TCF7	3'	AGAACTTCTGCCTGAACCTGGG 13613	A	A__
	G		TCCCAGGTTCA GCA TTCT		
			GGGGTCCAAGT CGT AAGA		
			C CTTT		
GAM2620	TCF7	3'	GGAAGAATCACTTGAACCCGGG 13623	A	CA _
	A		TCCC GGTTC AAG ATTCT CC		
			AGGG CCAAGTTC TAAGA GG		
			C AC A		
GAM2620	TCTA	3'	CAGGAGATTTGCTTGAACCTGG 42489		T
	GA		TCCCAGGTTCAAGCAA TCTCCTG		
			AGGGTCCAAGTTCGTT AGAGGAC		
			T		
GAM2620	TEM7	3'	CAGGAGGATCACTTGAGCCCGG 40249	A	CA
	GA		TCCC GGTTC AAG ATTCTCCTG		
			AGGG CCGAGTTC TAGGAGGAC		
			C AC		
GAM2620	TEM7	3'	GAGAATCACTTGAACCTGGGA 40260		CA
			TCCCAGGTTCAAG ATTCTC		
			AGGGTCCAAGTTC TAAGAG		
			AC		
GAM2620	TNFRSF1B	3'	AATCGTTTGAACCCGGGA 8378	A	A
			TCCC GGTTC AAGC ATT		

			AGGG CCAAGTTTG TAA		
			C C		
GAM2620	TNFSF10	3'	CAGGAGAATCGTTTGAACCCGG 15089	A	A
	GA		TCCC GGTTCAAGC ATTCTCCTG		
			AGGG CCAAGTTTG TAAGAGGAC		
			C C		
GAM2620	TNFSF15	3'	CAGAAGAATTGCTTGAACCTGGG 18863	A	C
	GA		TCCC GGTTCAAGCAATTCT CTG		
			AGGG TCAAGTTCGTTAAGA GAC		
			G A		
GAM2620	TPM4	3'	CAGGAGGATCGCTTGAACCCAG 13830	CA	A
	GA		TCC GGTTCAAGC ATTCTCCTG		
			AGG CCAAGTTCG TAGGAGGAC		
			AC C		
GAM2620	TRIM14	3'	GAATCACTTGAACCCGGG 29512	A	CA
			CCC GGTTCAAG ATTC		
			GGG CCAAGTTC TAAG		
			C AC		
GAM2620	TRIM14	3'	GAGAGTTGCTTGAACCCAGGA 29513	CA	
			TCC GGTTCAAGCAATTCTC		
			AGG CCAAGTTCGTTGAGAG		
			AC		
GAM2620	TRIM9	5'	CAGGAGAATCGCTTGAACCTGG 31445		A
	GA		TCCCAGGTTCAAGC ATTCTCCTG		
			AGGGTCCAAGTTCG TAAGAGGAC		
			C		
GAM2620	TRPM8	3'	AGAATTGCTGGAACCTGGGA 44204		A
			TCCCAGGTTC AGCAATTCT		
			AGGGTCCAAG TCGTTAAGA		
			G		
GAM2620	TSNAX	3'	CAGGAGACTCGCTTGAACCTGG 21155		AAT
	GA		TCCCAGGTTCAAGC TCTCCTG		
			AGGGTCCAAGTTCG AGAGGAC		
			CTC		
GAM2620	UBE2G2	3'	CAGGAGAATCGCTTGAACCCGG 65482	A	A
	GA		TCCC GGTTCAAGC ATTCTCCTG		
			AGGG CCAAGTTCG TAAGAGGAC		
			C C		
GAM2620	UBE2G2	3'	CAGGAGAATGGCGTGAACCCAG 65483	CA	A A
	GA		TCC GGTTCA GC ATTCTCCTG		

			AGG CCAAGT CG TAAGAGGAC		
			AC G G		
GAM2620 UC28	3'	GGAGAATTGCTTGAACCCGG 41588	A		
		CC GGTTC AAGCAATTCTCC			
		GG CCAAGTTCGTTAAGAGG			
		C			
GAM2620 UPK1B	3'	CAGGAGAATCACTTGACCGGGA 23699	A T CA		
		TCCC GGT CAAG ATTCTCCTG			
		AGGG CCA GTTC TAAGAGGAC			
		- - AC			
GAM2620 USP14	3'	GGGAGAATTGCTTGAACCTGG 18935			
		CCAGGTTCAAGCAATTCTCCT			
		GGTCCAAGTTCGTTAAGAGGG			
GAM2620 VHL	3'	CAGGAGAATCACTTGACCCAG 6838	CA T CA		
GA		TCC GG TCAAG ATTCTCCTG			
		AGG CC AGTTC TAAGAGGAC			
		AC C AC			
GAM2620 VHL	3'	CAGGAGAATGGCATGAACCTGG 6839	A A		
		CCAGGTTCA GC ATTCTCCTG			
		GGTCCAAGT CG TAAGAGGAC			
		A G			
GAM2620 VHL	3'	CAGGCGAATCTCTTGAACCCGG 6840	A CA T		
GA		TCCC GGTTCAAG ATTC CCTG			
		AGGG CCAAGTTC TAAG GGAC			
		C TC C			
GAM2620 VPS41	3'	CAGGAGAATCACTTGACCCAG 27689	CA T CA		
GA		TCC GG TCAAG ATTCTCCTG			
		AGG CC AGTTC TAAGAGGAC			
		AC C AC			
GAM2620 WBSCR14	3'	CAGGAGGGCCTGATCCCAGGA 53093	CA T A AAT		
		TCC GG TCA GC TCTCCTG			
		AGG CC AGT CG GGAGGAC			
		AC T C ____			
GAM2620 WIG1	3'	CAGGAGAATGGCGTGAACCCGG 96097	A A A		
GA		TCCC GGTTCA GC ATTCTCCTG			
		AGGG CCAAGT CG TAAGAGGAC			
		C G G			
GAM2620 XRCC2	3'	CAGGAGAATTGCTGGAACCCAG 19494	CA A		
GA		TCC GGTTCA AGCAATTCTCCTG			

			AGG CCAAG TCGTTAAGAGGAC		
			AC G		
GAM2620	XT3	3'	AGAATCATTTGAACCTAGGA 39901	C	CA
			TCC AGGTTCAAG ATTCT		
			AGG TCCAAGTTT TAAGA		
			A AC		
GAM2620	ZNF14	3'	CAGGAGAATCACTTGAACCTGG 41056		CA
			CCAGGTTCAAG ATTCTCCTG		
			GGTCCAAGTTC TAAGAGGAC		
			AC		
GAM2620	ZNF36	3'	CAGGAGAATCACTTGAACCCAG 95577	CA	CA
	GA		TCC GGTTC AAG ATTCTCCTG		
			AGG CCAAGTTC TAAGAGGAC		
			AC AC		
GAM2620	ZNF74	3'	AGGGGATCACTTGAGCCCAGGA 14256	CA	CAAT
			TCC GGTTC AAG TCTCCT		
			AGG CCGAGTTC AGGGGA		
			AC ACT_		
GAM2620	ZNF91	3'	CAGGAGAATGGCGTGAACCCGG 14277	A	A A
	GA		TCCC GGTTC A GC ATTCTCCTG		
			AGGG CCAAGT CG TAAGAGGAC		
			C G G		
GAM2620	AF020591	3'	CAGGAGAATGGCGCGAACATGG 27907	G	AA A
	GA		TCCA GTTC GC ATTCTCCTG		
			AGGGT CAAG CG TAAGAGGAC		
			A CG G		
GAM2620	AF020591	3'	CAGGTGGATCACTTGAGCCCAG 27908	CA	CA T
	GA		TCC GGTTC AAG ATTC CCTG		
			AGG CCGAGTTC TAGG GGAC		
			AC AC T		
GAM2620	AGMAT	3'	CAGGAGAATCGCTTAAGCCCAG 45736	CA	C A
	GA		TCC GGT AAGC ATTCTCCTG		
			AGG CCGA TTCG TAAGAGGAC		
			AC A C		
GAM2620	AKAP11	3'	CAGGAGAATTGCTTGAACCTGG 58458		
	GA		TCCCAGGTTCAAGCAATTCTCCTG		
			AGGGTCCAAGTTCGTTAAGAGGAC		
GAM2620	AKR1B10	5'	CAGGAGAATTGCTTGAACCCAG 40077	CA	
	GA		TCC GGTTC AAGCAATTCTCCTG		

			AGG CCAAGTTCGTTAAGAGGAC		
			AC		
GAM2620	ALTE	3'	GAGAATCGCTTGAACCTGGGA 61002	A	
			TCCCAGGTTCAAGC ATTCTC		
			AGGGTCCAAGTTCG TAAGAG		
			C		
GAM2620	AP1GBP1	3'	CAGGAGAATTGCTTGAACCCAG 24342	CA	
	GA		TCC GGTTC AAGCAATTCTCCTG		
			AGG CCAAGTTCGTTAAGAGGAC		
			AC		
GAM2620	APOF	3'	CGGGAGAATCACCTGAGCCTGG 9691	AGCA	
	GA		TCCCAGGTTCA ATTCTCCTG		
			AGGGTCCGAGT TAAGAGGGC		
			CCAC		
GAM2620	APOF	3'	CGGGAGAATCACCTGAGCCTGG 9692	AGCA	
	GA		TCCCAGGTTCA ATTCTCCTG		
			AGGGTCCGAGT TAAGAGGGC		
			CCAC		
GAM2620	APXL2	3'	CAGGAGAATGGCGTGAACCTGG 75673	A A	
	GA		TCCCAGGTTCA GC ATTCTCCTG		
			AGGGTCCAAGT CG TAAGAGGAC		
			G G		
GAM2620	ARNTL2	3'	GATTGCTTGAACCTGGGA 39851		
			TCCCAGGTTCAAGCAATT		
			AGGGTCCAAGTTCGTTAG		
GAM2620	AS AHL	3'	GGAGAATTGCTTGAACCTGGGA 64318		
			TCCCAGGTTCAAGCAATTCTCC		
			AGGGTCCAAGTTCGTTAAGAGG		
GAM2620	ATP1B4	3'	CAGGAGGATCACTTGAGCCCAG 24838	CA CA	
	GA		TCC GGTTC AAG ATTCTCCTG		
			AGG CCGAGTTC TAGGAGGAC		
			AC AC		
GAM2620	BANP	3'	CAGGAGAATTGCTTAGATT CAG 66799	CA TC	
	GA		TCC GGT AAGCAATTCTCCTG		
			AGG TTA TTCGTTAAGAGGAC		
			AC GA		
GAM2620	BIRC1	3'	AGACTTGCTTGAACCCGGGA 16985	A T	
			TCCC GGTTC AAGCAA TCT		

			AGGG CCAAGTTCGTT AGA		
			C C		
GAM2620	BIRC3	3'	GAGAATTACTTGAGCCCAGGA 67776	CA	C
			TCC GGTTCAAG AATTCTC		
			AGG CCGAGTTC TTAAGAG		
			AC A		
GAM2620	BLOV1	3'	CAGGAGAATCACTTGAACCCGG 76792	A	CA
	GA		TCCC GGTTCAAG ATTCTCCTG		
			AGGG CCAAGTTC TAAGAGGAC		
			C AC		
GAM2620	BLOV1	3'	CATGAGAATCGCTTGAGCCTGG 76793	A	C
	GA		TCCCAGGTTCAAGC ATTCTC TG		
			AGGGTCCGAGTTCG TAAGAG AC		
			C T		
GAM2620	BTN3A2	3'	CAGGAGAATGGCATGAACCCGG 23873	A	A A
			CC GGTTCA GC ATTCTCCTG		
			GG CCAAGT CG TAAGAGGAC		
			C A G		
GAM2620	C12orf2	3'	CAGAAGGATTGTTTGAACCCGG 83681	A	C
	GA		TCCC GGTTCAAGCAATTCT CTG		
			AGGG CCAAGTTTGTTAGGA GAC		
			C A		
GAM2620	C13orf1	3'	CAGGAGAATGGCTTGAACCCGG 40358	A	A
	GA		TCCC GGTTCAAGC ATTCTCCTG		
			AGGG CCAAGTTCG TAAGAGGAC		
			C G		
GAM2620	C1orf33	3'	CAGGAGAATCACTTGAACCCGG 32980	A	CA
	GA		TCCC GGTTCAAG ATTCTCCTG		
			AGGG CCAAGTTC TAAGAGGAC		
			C AC		
GAM2620	C1orf34	3'	AGAATCGCTTGAACCTGGGA 61294	A	
			TCCCAGGTTCAAGC ATTCT		
			AGGGTCCAAGTTCG TAAGA		
			C		
GAM2620	C1QTNF2	3'	CGGGAGAATCGCTTGAACCCAG 49972	CA	A
	GA		TCC GGTTCAAGC ATTCTCCTG		
			AGG CCAAGTTCG TAAGAGGGC		
			AC C		
GAM2620	C20orf106	3'	CAGGAGAATCACTTGAACCCTG 55901	—	CA
	G		CCAGG TTCAAG ATTCTCCTG		

			GGTCC AAGTTC TAAGAGGAC		
			C AC		
GAM2620	C20orf106	3'	CAGAAGAATGGCTTGAACCCTG 55899	—	A C
	G		CCAGG TTCAAGC ATTCT CTG		
			GGTCC AAGTTCG TAAGA GAC		
			C G A		
GAM2620	C20orf12	3'	CAGGAAAATCGCTTGAACCCGG 36845	A	A C
	GA		TCCC GGTTCAAGC ATT TCCTG		
			AGGG CCAAGTTCG TAA AGGAC		
			C C A		
GAM2620	C20orf142	3'	CAGGAGAATCGCTTGAACCCAG 75276	CA	A
	GA		TCC GGTTCAAGC ATTCTCCTG		
			AGG CCAAGTTCG TAAGAGGAC		
			AC C		
GAM2620	C20orf175	3'	CAGGAGAATCACTCGGACCCGG 55922	A	A CA
	GA		TCCC GGTTTC AG ATTCTCCTG		
			AGGG CCAGG TC TAAGAGGAC		
			C C AC		
GAM2620	C20orf177	3'	GAGAATCTCTTGAACCCGGGA 62834	A	CA
			TCCC GGTTCAAG ATTCTC		
			AGGG CCAAGTTC TAAGAG		
			C TC		
GAM2620	C20orf29	3'	GAATCACTTGAACCTGGGA 37710	CA	
			TCCCAGGTTCAAG ATTC		
			AGGGTCCAAGTTC TAAG		
			AC		
GAM2620	C21orf108	3'	CAGGGGAATCGCTTGAACCTGG 90110	A	
	GA		TCCCAGGTTCAAGC ATTCTCCTG		
			AGGGTCCAAGTTCG TAAGGGGAC		
			C		
GAM2620	C22orf20	3'	CAGGAGAATCACTTGAACCCAG 48193	CA	CA
	GA		TCC GGTTCAAG ATTCTCCTG		
			AGG CCAAGTTC TAAGAGGAC		
			AC AC		
GAM2620	C6.1A	3'	CAGGAGGATCACTTGAGCCCAG 44529	CA	CA
	GA		TCC GGTTCAAG ATTCTCCTG		
			AGG CCGAGTTC TAGGAGGAC		
			AC AC		
GAM2620	C6orf29	3'	CAGGAGAATCGCTTGAACCCGG 52455	A	A
	GA		TCCC GGTTCAAGC ATTCTCCTG		

			AGGG CCAAGTTCG TAAGAGGAC		
			C C		
GAM2620	C6orf5	3'	CAGGAGAATCACTTGAACCCGG 31977	A	CA
	GA		TCCC GGTTCAAG ATTCTCCTG		
			AGGG CCAAGTTC TAAGAGGAC		
			C AC		
GAM2620	C8orf2	3'	CAGGAGAATTGCTTGAACCTCGG 24149	AG	
	GA		TCCC GTTCAAGCAATTCTCCTG		
			AGGG CAAGTTCGTTAAGAGGAC		
			CT		
GAM2620	CAMKK2	5'	GAGAACTGCTTGAACCTGGGA 22621		A
			TCCCAGGTTCAAGCA TTCTC		
			AGGGTCCAAGTTCGT AAGAG		
			C		
GAM2620	CCR6	3'	GAGAATCGCTTGAACCCAGGA 49402	CA	A
			TCC GGTTCAAGC ATTCTC		
			AGG CCAAGTTCG TAAGAG		
			AC C		
GAM2620	CDT1	3'	CAGGAGAATGGTGTGAACCCAG 78158	CA	A A
	GA		TCC GGTTCA GC ATTCTCCTG		
			AGG CCAAGT TG TAAGAGGAC		
			AC G G		
GAM2620	cerk	3'	CAGGAGAATCGCTTGAACC 43161	A	
			GGTTCAAGC ATTCTCCTG		
			CCAAGTTCG TAAGAGGAC		
			C		
GAM2620	CG012	3'	CAGGAGAATCACTTCAACCCAG 84149	CA	C CA
	GA		TCC GGTT AAG ATTCTCCTG		
			AGG CCAA TTC TAAGAGGAC		
			AC C AC		
GAM2620	CG012	5'	GAATCATTTGAACCCAGGA 84159	CA	CA
			TCC GGTTCAAG ATTC		
			AGG CCAAGTTT TAAG		
			AC AC		
GAM2620	CG012	5'	GAGTCGCTTAAACCCAGGA 84160	CA	C A
			TCC GGTT AAGC ATTC		
			AGG CCAA TTCG TGAG		
			AC A C		
GAM2620	CHRFAM7A	3'	CATGAGAATCTCTTGAACC 96714	CA	C
			GGTTCAAG ATTCTC TG		

		CCAAGTTC TAAGAG AC		
		TC T		
GAM2620	CLONE24922	3' CAGGAGAATTGCTTGAGCCCAG 32249	CA	
	GA	TCC GGTCAAGCAATTCTCCTG		
		AGG CCGAGTTCGTTAAGAGGAC		
		AC		
GAM2620	CNNM1	3' CAGGAGAATCGCTTGAACCTGG 40115	A	
	GA	TCCCAGGTTCAAGC ATTCTCCTG		
		AGGGTCCAAGTTTCG TAAGAGGAC		
		C		
GAM2620	COE2	3' CAGGAAAATCGCTTGAACCCAG 64907	CA	A C
	GA	TCC GGTCAAGC ATT TCCTG		
		AGG CCAAGTTTCG TAA AGGAC		
		AC C A		
GAM2620	CPR2	3' CAGGTGAATCACTTGAACCCGG 48829	A	CA T
	GA	TCCC GGTTC AAG ATTC CCTG		
		AGGG CCAAGTTC TAAG GGAC		
		C AC T		
GAM2620	CRTAM	3' GGAGAATCGCTTGAACCTGGGA 39473	A	
		TCCCAGGTTCAAGC ATTCTCC		
		AGGGTCCAAGTTTCG TAAGAGG		
		C		
GAM2620	CSAD	3' AGAATTGCTTGAACCCAGGG 32576	A_	
		CCC GGTTC AAGCAATTCT		
		GGG CCAAGTTCGTTAAGA		
		AC		
GAM2620	D21S2056E	3' CAGGAGAATTGCTTGAACCTGG 14862		
	GA	TCCCAGGTTCAAGCAATTCTCCTG		
		AGGGTCCAAGTTTCGTTAAGAGGAC		
GAM2620	DAPK2	3' CAGGGGAATTGCTTGAAGTCAG 27511	CA	
	GA	TCC GGTTC AAGCAATTCTCCTG		
		AGG TCAAGTTCGTTAAGGGGAC		
		AC		
GAM2620	DDX34	3' CAGGAGAATGGAGTGAACCCGG 28663	A	AGCA
	GA	TCCC GGTTC A ATTCTCCTG		
		AGGG CCAAGT TAAGAGGAC		
		C GAGG		
GAM2620	DEGS	3' GGGAGAATTGCTTGAACCCAGG 59268	CA	
	A	TCC GGTTC AAGCAATTCTCT		

			AGG CCAAGTTCGTTAAGAGGG			
			AC			
GAM2620	DEGS	3'	GGGAGAATTGCTTGAACCCAGG 59269	CA		
	A		TCC GGTTC AAGCAATTCTCCT			
			AGG CCAAGTTCGTTAAGAGGG			
			AC			
GAM2620	DIS3	3'	CAGGAGAATCGCTTGAACCTGG 30913		A	
	GA		TCCCAGGTTCAAGC ATTCTCCTG			
			AGGGTCCAAGTTTCG TAAGAGGAC			
			C			
GAM2620	DIS3	3'	CAGGAGAATCGCTTGAACCTGG 30914		A	
	GA		TCCCAGGTTCAAGC ATTCTCCTG			
			AGGGTCCAAGTTTCG TAAGAGGAC			
			C			
GAM2620	DJ122O8.2	3'	CAGGAGAATCACTTGAACCCAG 40392	CA		CA
	GA		TCC GGTTC AAG ATTCTCCTG			
			AGG CCAAGTTC TAAGAGGAC			
			AC AC			
GAM2620	dJ383J4.3	3'	CAGGAGAATCGTTTTAACC 67491	C	A	
			GGTT AAGC ATTCTCCTG			
			CCAA TTTG TAAGAGGAC			
			T C			
GAM2620	DKFZP434B168	3'	CAGGAGAATGGTGTGAACCTGG 31864		A	A
	GA		TCCCAGGTTCA GC ATTCTCCTG			
			AGGGTCCAAGT TG TAAGAGGAC			
			G G			
GAM2620	DKFZP434C1715	3'	CAGAAGGATCACTTGAGCCCAG 87351	CA		CA C
	GA		TCC GGTTC AAG ATTCT CTG			
			AGG CCGAGTTC TAGGA GAC			
			AC AC A			
GAM2620	DKFZp434E0519	3'	CAGGAGAATTGCTTGAACCTGG 50986			
	GA		TCCCAGGTTCAAGCAATTCTCCTG			
			AGGGTCCAAGTTTCGTTAAGAGGAC			
GAM2620	DKFZp434E169	3'	CAGGAGAATGGTGTGAACCCGG 51073	A		A A
	GA		TCCC GGTTC A GC ATTCTCCTG			
			AGGG CCAAGT TG TAAGAGGAC			
			C G G			
GAM2620	DKFZp434E2220	5'	CAGGAGAATCCCTTGAACCTGG 34708			CA
	GA		TCCCAGGTTCAAG ATTCTCCTG			

		AGGGTCCAAGTTC TAAGAGGAC			
		CC			
GAM2620	DKFZP434F1735 3'	AGAAGAATCACTTGAGCCCAGG 32111	CA	CA	C
	A	TCC GGTTC AAG ATTCT CT			
		AGG CCGAGTTC TAAGA GA			
		AC AC A			
GAM2620	DKFZp434G171 3'	CAGGAGAATTGCTTCAATCTGG 80238	C		
		CCAGGTT AAGCAATTCTCCTG			
		GGTCTAA TTCGTTAAGAGGAC			
		C			
GAM2620	DKFZp434G171 3'	CAGGAGCATTGCTTGAACCCGG 80239	A	T	
	GA	TCCC GGTTCAAGCAAT CTCCTG			
		AGGG CCAAGTTCGTTA GAGGAC			
		C C			
GAM2620	DKFZP434I1735 3'	CAGGAAAATCGCTTGAACCTGG 89167	A	C	
		CCAGGTTCAAGC ATT TCCTG			
		GGTCCAAGTTCG TAA AGGAC			
		C A			
GAM2620	DKFZP434K1421 3'	AGAAGATCACTTGAGCCTAGGA 50463	C	CAAT	C
		TCC AGGTTCAAG TCT CT			
		AGG TCCGAGTTC AGA GA			
		A ACT_ A			
GAM2620	DKFZP434N1511 3'	CAGGAGAATGCTGTGAACCCTG 93053	_	_	A
	G	CCAGG TTCA AGCA TTCTCCTG			
		GGTCC AAGT TCGT AAGAGGAC			
		C G _			
GAM2620	DKFZp547C176 3'	CAGGAGAATCGCTTGAACCCGG 67798	A	A	
	GA	TCCC GGTTCAAGC ATTCTCCTG			
		AGGG CCAAGTTCG TAAGAGGAC			
		C C			
GAM2620	DKFZp547G183 3'	CAGGAGAATCACTTGAACCTGG 38640	CA		
	GA	TCCCAGGTTCAAG ATTCTCCTG			
		AGGGTCCAAGTTC TAAGAGGAC			
		AC			
GAM2620	DKFZP564B1023 3'	CAGGAGAATTGCTTGAACCTCGG 49363	AG		
	GA	TCCC GTTCAAGCAATTCTCCTG			
		AGGG CAAGTTCGTTAAGAGGAC			
		CT			
GAM2620	DKFZP564I052 3'	CAGGAGAATTGCTTGAACCCAG 67281	CA		
	GA	TCC GGTTCAAGCAATTCTCCTG			

		AGG CCAAGTTCGTTAAGAGGAC		
		AC		
GAM2620	DKFZp564K142 3'	GAGAATCACTTGAAGCTCAGGA 50433	CA	CA
		TCC GGTTCAAG ATTCTC		
		AGG TCAAGTTC TAAGAG		
		AC AC		
GAM2620	DKFZP564M182 3'	CAGGAGAATCACTTTAACCCGG 78621	A	C CA
	GA	TCCC GGTT AAG ATTCTCCTG		
		AGGG CCAA TTC TAAGAGGAC		
		C T AC		
GAM2620	DKFZP564M182 3'	CAGGAGAATTGCTTGAACCTGG 78622		
	GA	TCCCAGGTTCAAGCAATTCTCCTG		
		AGGGTCCAAGTTCGTTAAGAGGAC		
GAM2620	DKFZP564M182 3'	GATTGCTTGAACCCAGGA 78632	CA	
		TCC GGTTCAAGCAATT		
		AGG CCAAGTTCGTTAG		
		AC		
GAM2620	DKFZP564M182 3'	GATTGCTTGAACCCGGGA 78633	A	
		TCCC GGTTCAAGCAATT		
		AGGG CCAAGTTCGTTAG		
		C		
GAM2620	DKFZp566H0824 5'	CAGGAGAATGGCGTGAACCCGG 34479	A	A A
	GA	TCCC GGTTCA GC ATTCTCCTG		
		AGGG CCAAGT CG TAAGAGGAC		
		C G G		
GAM2620	DKFZP566J2046 3'	CAGGAGAATCAATTGAACCCGG 49135	A	GCA
	GA	TCCC GGTTCAA ATTCTCCTG		
		AGGG CCAAGTT TAAGAGGAC		
		C AAC		
GAM2620	DKFZP586C1324 3'	CAGAAGAATCGCTTGAACCTGG 70355	A	C
		CCAGGTTCAAGC ATTCT CTG		
		GGTCCAAGTTCG TAAGA GAC		
		C A		
GAM2620	DKFZP586D2223 3'	CAGGAGAATCGCTTGAACCTGG 38286		A
	GA	TCCCAGGTTCAAGC ATTCTCCTG		
		AGGGTCCAAGTTCG TAAGAGGAC		
		C		
GAM2620	DKFZP586D2223 3'	GGGAGAATTGCTCAAGCCCAGG 38294	CA	CA
	A	TCC GGTT AGCAATTCTCCT		

		AGG CCGA TCGTTAAGAGGG		
		AC AC		
GAM2620	DKFZp727G131	3' CAGGAGAATCTCTTAAACCAGG 59693	CA	C CA
	A	TCC GGTT AAG ATTCTCCTG		
		AGG CCAA TTC TAAGAGGAC		
		A_ A TC		
GAM2620	DKFZP761G1913	3' TAGGAGTTGCTTGAACCTGGGA 49698		TT
		TCCCAGGTTCAAGCAA CTCCTG		
		AGGGTCCAAGTTCGTT GAGGAT		
		—		
GAM2620	DPYSL4	3' GAGAAGGGCTGAACCTGGGG 22227	A	AA
		TCCCAGGTTCA GC TTCTC		
		GGGGTCCAAGT CG AAGAG		
		_ GG		
GAM2620	DRF1	3' CAGAAGAATCACTTGAACCTGA 47741	C	CA C
	GA	TC CAGGTTCAAG ATTCT CTG		
		AG GTCCAAGTTC TAAGA GAC		
		A AC A		
GAM2620	DRF1	3' CAGGAGAATCACTTGAACCCAG 47742	CA	CA
	GA	TCC GGTTCAAG ATTCTCCTG		
		AGG CCAAGTTC TAAGAGGAC		
		AC AC		
GAM2620	DSCR6	3' CAGGAGAATGGCTGGAACCCGG 39059	A	A A
	GA	TCCC GGTTT AGC ATTCTCCTG		
		AGGG CCAAG TCG TAAGAGGAC		
		C G G		
GAM2620	ERAP140	3' CAGGAGAATTGCTTGAATCCGG 75702	A	
	GA	TCCC GGTTCAAGCAATTCTCCTG		
		AGGG CTAAGTTCGTTAAGAGGAC		
		C		
GAM2620	FADS1	3' CAGGAGAATCGCTTGAACCGGG 26376	A	A
	GA	TCCC GGTTCAAGC ATTCTCCTG		
		AGGG CCAAGTTCG TAAGAGGAC		
		G C		
GAM2620	FBXO27	3' CAGGAGAATTGCTTGAGCCCGG 75008	A	
	GA	TCCC GGTTCAAGCAATTCTCCTG		
		AGGG CCGAGTTCGTTAAGAGGAC		
		C		
GAM2620	FBXO9	3' CAGGAGAATAGCTTAAGCCCAG 25654	CA	C A
	GA	TCC GGTT AAGC ATTCTCCTG		

			AGG CCGA TTCG TAAGAGGAC		
			AC A A		
GAM2620	FBXO9	3'	CAGGAGAATTGCCTGAGCCTGG 54242	A	
	GA		TCCCAGGTTCA GCAATTCTCCTG		
			AGGGTCCGAGT CGTTAAGAGGAC		
			C		
GAM2620	FKBP14	3'	AGAATCACTTGAACCCGG 36059	A	CA
			CC GGTTC AAG ATTCT		
			GG CCAAGTTC TAAGA		
			C AC		
GAM2620	FKBP14	3'	CAGGAGATTTGCTTGAACCCGG 36065	A	T
	GA		TCCC GGTTC AAGCAA TCTCCTG		
			AGGG CCAAGTTCGTT AGAGGAC		
			C T		
GAM2620	FKSG17	3'	CAGGAGAATCACTTGAATC 50153	CA	
			GGTTC AAG ATTCTCCTG		
			CTAAGTTC TAAGAGGAC		
			AC		
GAM2620	FLJ00060	3'	CAGGAGAATGGCGTGAACCCAG 61740	CA	A A
	GA		TCC GGTTC A GC ATTCTCCTG		
			AGG CCAAGT CG TAAGAGGAC		
			AC G G		
GAM2620	FLJ10008	3'	CAGGAGAATGGCGTGAACCTGG 36182	A	A
	GA		TCCCAGGTTCA GC ATTCTCCTG		
			AGGGTCCAAGT CG TAAGAGGAC		
			G G		
GAM2620	FLJ10043	3'	GAGACTTGCTTGAACCCAGGA 36234	CA	T
			TCC GGTTC AAGCAA TCTC		
			AGG CCAAGTTCGTT AGAG		
			AC C		
GAM2620	FLJ10058	3'	CAGGAGAATCGCTTGAACCCAG 36261	CA	A
	GA		TCC GGTTC AAGC ATTCTCCTG		
			AGG CCAAGTTCG TAAGAGGAC		
			AC C		
GAM2620	FLJ10244	3'	CAGGAGAATCACTTGAACACAG 36399	CAG	CA
	GA		TCC GTTCAAG ATTCTCCTG		
			AGG CAAGTTC TAAGAGGAC		
			ACA AC		
GAM2620	FLJ10314	3'	GAATCATTTGAACCCGGGA 36489	A	CA
			TCCC GGTTC AAG ATTCTCCTG		

			AGGG CCAAGTTT TAAG		
			C AC		
GAM2620	FLJ10439	5'	CAGAAGAATCGCTTGAACCCGG 36597	A	A C
		GA	TCCC GGTTCAAGC ATTCT CTG		
			AGGG CCAAGTTCG TAAGA GAC		
			C C A		
GAM2620	FLJ10460	3'	AGAATAATCGCTTGAACCCAGG 36608	CA	A__
		A	TCC GGTTCAAGC ATTCT		
			AGG CCAAGTTCG TAAGA		
			AC CTAA		
GAM2620	FLJ10520	3'	CAGGAGAATTGCTTGAACCCTG 36700		_
		GG	CCCAGG TTCAAGCAATTCTCCTG		
			GGGTCC AAGTTCGTTAAGAGGAC		
			C		
GAM2620	FLJ10547	3'	CAGGAGAATCGCTTGAACCCAG 36774	CA	A
		GA	TCC GGTTCAAGC ATTCTCCTG		
			AGG CCAAGTTCG TAAGAGGAC		
			AC C		
GAM2620	FLJ10607	3'	GAGAATCGCTTGAACCCGGGA 77635	A	A
			TCCC GGTTCAAGC ATTCTC		
			AGGG CCAAGTTCG TAAGAG		
			C C		
GAM2620	FLJ10613	3'	CAGGAGAATCGCCTGAACCTGG 39336	A	A
		GA	TCCCAGGTTCA GC ATTCTCCTG		
			AGGGTCCAAGT CG TAAGAGGAC		
			C C		
GAM2620	FLJ10613	3'	CAGGAGAATCGCCTGAACCTGG 39337	A	A
		GA	TCCCAGGTTCA GC ATTCTCCTG		
			AGGGTCCAAGT CG TAAGAGGAC		
			C C		
GAM2620	FLJ10650	3'	AGAATTGCTTGAACCCAGGA 36897	CA	
			TCC GGTTCAAGCAATTCT		
			AGG CCAAGTTCGTTAAGA		
			AC		
GAM2620	FLJ10704	3'	CAGGAGATTCGCTTGAATCAG 36977	CA	AAT
		GA	TCC GGTTCAAGC TCTCCTG		
			AGG TCAAGTTCG AGAGGAC		
			AC CTT		
GAM2620	FLJ10781	3'	GAATTGCTTGAATCCAGGA 37170	CA	
			TCC GGTTCAAGCAATTC		

			AGG CTAAGTTCGTTAAG		
			AC		
GAM2620	FLJ10803	3'	GAGAATTACTTGAACCCGGA 37203	A	C
			TCCC GGTTC AAG AATTCTC		
			AGGG CCAAGTTC TTAAGAG		
			C A		
GAM2620	FLJ10826	3'	CAGGAGAATTGGTTGAACCCAG 37245	CA	G
	GA		TCC GGTTC A CAATTCTCCTG		
			AGG CCAAGTT GTTAAGAGGAC		
			AC G		
GAM2620	FLJ10932	3'	CAGGAGAATCGTTTGAACCTGG 37426		A
	GA		TCCCAGGTTCAAGC ATTCTCCTG		
			AGGGTCCAAGTTTG TAAGAGGAC		
			C		
GAM2620	FLJ10936	3'	CAGGAGAATCGCTGGAACCTGG 37439	A	A
	GA		TCCCAGGTT C AGC ATTCTCCTG		
			AGGGTCCAAG TCG TAAGAGGAC		
			G C		
GAM2620	FLJ10989	3'	CAGGAGAATCACTTGAACCCTG 37499	—	CA
	G		CCAGG TTCAAG ATTCTCCTG		
			GGTCC AAGTTC TAAGAGGAC		
			C AC		
GAM2620	FLJ11036	3'	CAGGAGGACTGCTTGAGCCCAG 37553	CA	A
	GA		TCC GGTTC AAGCA TTCTCCTG		
			AGG CCGAGTTCGT AGGAGGAC		
			AC C		
GAM2620	FLJ11106	3'	CAGGAGAATGGTGTGAACCTGG 37621	A	A
	GA		TCCCAGGTTCA GC ATTCTCCTG		
			AGGGTCCAAGT TG TAAGAGGAC		
			G G		
GAM2620	FLJ11136	3'	CAGGAGAATCACTTGAACCTCGG 37665	AG	CA
	GG		TCCC GTTCAAG ATTCTCCTG		
			GGGG CAAGTTC TAAGAGGAC		
			CT AC		
GAM2620	FLJ11259	3'	CAGGAGGATTGCTTGAGCCTGG 37764		
	GA		TCCCAGGTTCAAGCAATTCTCCTG		
			AGGGTCCGAGTTCGTTAGGAGGAC		
GAM2620	FLJ11259	3'	GGGAGAATCACCTGAGCCCAGG 37770	CA	AGCA
	A		TCC GGTTC A ATTCTCCT		

			AGG CCGAGT TAAGAGGG		
			AC CCAC		
GAM2620	FLJ11301	3'	CAGGAGAATCACTTGAACCAGG 37803	A	CA
	GA		TCCC GGTTCAAG ATTCTCCTG		
			AGGG CCAAGTTC TAAGAGGAC		
			A AC		
GAM2620	FLJ11370	3'	CAGGAGAATCACTTGAACCTGG 46962		CA
	GA		TCCCAGGTTCAAG ATTCTCCTG		
			AGGGTCCAAGTTC TAAGAGGAC		
			AC		
GAM2620	FLJ11577	3'	CAGGAGAATCTCTTGAACCTGA 47955	C	CA
	GA		TC CAGGTTCAAG ATTCTCCTG		
			AG GTCCAAGTTC TAAGAGGAC		
			A TC		
GAM2620	FLJ11700	3'	CAGGAGAATTGCTTGAAACCCG 46558	A	—
	GG		CCC GGTT CAAGCAATTCTCCTG		
			GGG CCAA GTTCGTTAAGAGGAC		
			C A		
GAM2620	FLJ11715	3'	CAGGAGTATTGCTTGAGCCCGG 44976	A	T
			CC GGTTCAAGCAAT CTCCTG		
			GG CCGAGTTCGTTA GAGGAC		
			C T		
GAM2620	FLJ11722	3'	CGGGAGAATCCCTTGAACCTGG 47000		CA
	GA		TCCCAGGTTCAAG ATTCTCCTG		
			AGGGTCCAAGTTC TAAGAGGGC		
			CC		
GAM2620	FLJ11726	3'	CAGGAGAATTGTTTGAACCCTG 47017		—
	G		CCAGG TTCAAGCAATTCTCCTG		
			GGTCC AAGTTTGTTAAGAGGAC		
			C		
GAM2620	FLJ11827	3'	CAGGAGGATCACTTGAGCCCAG 47680	CA	CA
	GA		TCC GGTTCAAG ATTCTCCTG		
			AGG CCGAGTTC TAGGAGGAC		
			AC AC		
GAM2620	FLJ11996	3'	GAGAATTGCTTGACCCGGGA 47063	A	
			TCCC GGTTCAAGCAATTCTC		
			AGGG CCAGGTTTCGTTAAGAG		
			C		
GAM2620	FLJ12056	3'	CAGGAGAATTGCTTGAACCCAG 46819	CA	
	GA		TCC GGTTCAAGCAATTCTCCTG		

			AGG CCAAGTTCGTTAAGAGGAC		
			AC		
GAM2620	FLJ12078	3'	CAGGAGAATTGCTTGAACCTGG 47077		
	GA		TCCCAGGTTCAAGCAATTCTCCTG		
			AGGGTCCAAGTTCGTTAAGAGGAC		
GAM2620	FLJ12132	3'	CAGGAGCATCGCTTGAGCCCAG 47098	CA	A T
	GA		TCC GGTTC AAGC AT CTCCTG		
			AGG CCGAGTTCG TA GAGGAC		
			AC C C		
GAM2620	FLJ12190	3'	CAGGAGAATCTCTTGAACCCGG 47564	A	CA
	GA		TCCC GGTTC AAG ATTCTCCTG		
			AGGG CCAAGTTC TAAGAGGAC		
			C TC		
GAM2620	FLJ12294	3'	CAGGAGAATCGCTTGAATCCGG 47711	A	A
			CC GGTTC AAGC ATTCTCCTG		
			GG CTAAGTTCG TAAGAGGAC		
			C C		
GAM2620	FLJ12298	3'	AGGAGAATCACTTGAACCCAGG 50594	CA	CA
	A		TCC GGTTC AAG ATTCTCCT		
			AGG CCAAGTTC TAAGAGGA		
			AC AC		
GAM2620	FLJ12331	3'	AGAATCACTTGAACCCGGGA 47107	A	CA
			TCCC GGTTC AAG ATTCT		
			AGGG CCAAGTTC TAAGA		
			C AC		
GAM2620	FLJ12363	3'	CAGGAGAATCGCTTGAATATGA 50631	C G	A
	GA		TC CA GTTCAAGC ATTCTCCTG		
			AG GT TAAGTTCG TAAGAGGAC		
			A A C		
GAM2620	FLJ12448	3'	GGGAGAATCGCTTGAACCCAGG 43479	CA	A
	A		TCC GGTTC AAGC ATTCTCCT		
			AGG CCAAGTTCG TAAGAGGG		
			AC C		
GAM2620	FLJ12586	3'	CAGGAGAATTGCTTGAACCTGG 45208		
	GA		TCCCAGGTTCAAGCAATTCTCCTG		
			AGGGTCCAAGTTCGTTAAGAGGAC		
GAM2620	FLJ12606	3'	CAGGAGAATGGCATGAACCCGG 46063	A	A A
	GA		TCCC GGTTC A GC ATTCTCCTG		

			AGGG CCAAGT CG TAAGAGGAC		
			C A G		
GAM2620	FLJ12660	3'	CAGGAGAATCATTTCAACCCGG 47893	A C CA	
	GA		TCCC GGTT AAG ATTCTCCTG		
			AGGG CCAA TTT TAAGAGGAC		
			C C AC		
GAM2620	FLJ12666	3'	CAGTAGAATCACTTGAACCCTG 45066	_ CA C	
	G		CCAGG TTCAAG ATTCT CTG		
			GGTCC AAGTTC TAAGA GAC		
			C AC T		
GAM2620	FLJ12671	3'	CAGGAGAATCGCTTGAGCCCAG 49105	CA A	
	GA		TCC GGTTC AAGC ATTCTCCTG		
			AGG CCGAGTTCG TAAGAGGAC		
			AC C		
GAM2620	FLJ12921	3'	CAGGAGAATGGCATGAACCTGG 46395	A A	
			CCAGGTTCA GC ATTCTCCTG		
			GGTCCAAGT CG TAAGAGGAC		
			A G		
GAM2620	FLJ13117	3'	CAGGAGAATCGCTTGAACCCAG 43806	CA A	
	GA		TCC GGTTC AAGC ATTCTCCTG		
			AGG CCAAGTTCG TAAGAGGAC		
			AC C		
GAM2620	FLJ13162	3'	CAGGAGAATTGCTTGAACCCAG 47182	CA	
	GA		TCC GGTTC AAGCAATTCTCCTG		
			AGG CCAAGTTCGTTAAGAGGAC		
			AC		
GAM2620	FLJ13193	3'	CAGGAGAATCACCTGAACC 50711	AGCA	
			GGTTCA ATTCTCCTG		
			CCAAGT TAAGAGGAC		
			CCAC		
GAM2620	FLJ13193	3'	CAGGAGAATCACTTGAACCCAG 50712	CA CA	
	GA		TCC GGTTC AAG ATTCTCCTG		
			AGG CCAAGTTC TAAGAGGAC		
			AC AC		
GAM2620	FLJ13315	3'	CAGGATCACTTGAACCAAGGA 47197	CA CAATTC	
			TCC GGTTC AAG TCCTG		
			AGG CCAAGTTC AGGAC		
			AA ACT__		
GAM2620	FLJ13352	3'	GGGAGAATCGCTTGAGCCCAGG 45055	CA A	
	A		TCC GGTTC AAGC ATTCTCCT		

			AGG CCGAGTTCG TAAGAGGG		
			AC C		
GAM2620	FLJ13448	3'	AGAATCGCTTGAACCCGGGA 47878	A	A
			TCCC GGTTC AAGC ATTCT		
			AGGG CCAAGTTCG TAAGA		
			C C		
GAM2620	FLJ13456	3'	CAGGAGAATCGCTTGAACCTGG 66534		A
	GA		TCCCAGGTTCAAGC ATTCTCCTG		
			AGGGTCCAAGTTCG TAAGAGGAC		
			C		
GAM2620	FLJ13456	3'	CAGGAGGATTGCTTGAGCC 66535		
			GGTTC AAGCAATTCTCCTG		
			CCGAGTTCGTTAGGAGGAC		
GAM2620	FLJ13456	3'	GAGAATCACTTGAACCCAGGA 66546	CA	CA
			TCC GGTTC AAG ATTCTC		
			AGG CCAAGTTC TAAGAG		
			AC AC		
GAM2620	FLJ13611	3'	CAGGAGAATCACTTGAACCGGG 46865	A	CA
	GA		TCCC GGTTC AAG ATTCTCCTG		
			AGGG CCAAGTTC TAAGAGGAC		
			G AC		
GAM2620	FLJ13621	3'	CAGGAGAATGGCGTGAACCCGG 47219	A	A A
	GA		TCCC GGTTC A GC ATTCTCCTG		
			AGGG CCAAGT CG TAAGAGGAC		
			C G G		
GAM2620	FLJ13659	3'	CAGGAGAATTGCTTGAACCCGG 48028	A	
	GA		TCCC GGTTC AAGCAATTCTCCTG		
			AGGG CCAAGTTCGTTAAGAGGAC		
			C		
GAM2620	FLJ13769	3'	CAGGAGAATCACTTGAACCTGA 47246	C	CA
	GA		TC CAGGTTCAAG ATTCTCCTG		
			AG GTCCAAGTTC TAAGAGGAC		
			A AC		
GAM2620	FLJ13769	3'	CAGGAGAATTGCTTGAGCCTGG 47247		
	GA		TCCCAGGTTCAAGCAATTCTCCTG		
			AGGGTCCGAGTTCGTTAAGAGGAC		
GAM2620	FLJ13848	3'	CAGGAGACTCGCTTGAACCCAG 45817	CA	AAT
	GA		TCC GGTTC AAGC TCTCCTG		

			AGG CCAAGTTCG AGAGGAC		
			AC CTC		
GAM2620	FLJ13952	3'	CAGGAGAATCTCTTGAAGCCGG 46008	A _	CA
	GA		TCCC GGTT CAAG ATTCTCCTG		
			AGGG CCGA GTTC TAAGAGGAC		
			_ A TC		
GAM2620	FLJ14011	3'	CAGGAGAATCGCTTGAACCCAG 42314	CA	A
	GA		TCC GGTTCAAGC ATTCTCCTG		
			AGG CCAAGTTCG TAAGAGGAC		
			AC C		
GAM2620	FLJ14100	3'	CAGGAGAATGGTGTGAACCTGG 47330	A A	
	GA		TCCCAGGTTCA GC ATTCTCCTG		
			AGGGTCCAAGT TG TAAGAGGAC		
			G G		
GAM2620	FLJ14117	3'	AGAATTGCTTGAGCCTGGGA 43216		
			TCCCAGGTTCAAGCAATTCT		
			AGGGTCCGAGTTCGTTAAGA		
GAM2620	FLJ14129	3'	CAGGAGAATCACTTGAACCTGG 48805	CA	
	GA		TCCCAGGTTCAAG ATTCTCCTG		
			AGGGTCCAAGTTC TAAGAGGAC		
			AC		
GAM2620	FLJ14251	3'	CAGGAGAATCACTTGAGCCCAG 46475	CA	CA
	GA		TCC GGTTCAAG ATTCTCCTG		
			AGG CCGAGTTC TAAGAGGAC		
			AC AC		
GAM2620	FLJ14251	3'	CAGGCGAATTGCTTGAACCTGG 46476	T	
	GA		TCCCAGGTTCAAGCAATTC CCTG		
			AGGGTCCAAGTTCGTTAAG GGAC		
			C		
GAM2620	FLJ14280	3'	GGATCGCTTGAGCCCAGGA 46522	CA	A
			TCC GGTTCAAGC ATTC		
			AGG CCGAGTTCG TAGG		
			AC C		
GAM2620	FLJ14326	3'	CAGGAGAATCGTTTGAACACGG 50760	AG	A
	GA		TCCC GTTCAAGC ATTCTCCTG		
			AGGG CAAGTTTG TAAGAGGAC		
			CA C		
GAM2620	FLJ14326	3'	GACTTGCTTGAACCCGGGA 50771	A	T
			TCCC GGTTCAAGCAA TC		

			AGGG CCAAGTTCGTT AG		
			C C		
GAM2620	FLJ14327	3'	GAGAATTGCTTGAACCTGGGA 46680		
			TCCCAGGTTCAAGCAATTCTC		
			AGGGTCCAAGTTCGTTAAGAG		
GAM2620	FLJ14345	3'	CAGGAGAATCACTTGAACCTGG 45656	CA	
			GA TCCCAGGTTCAAG ATTCTCCTG		
			AGGGTCCAAGTTC TAAGAGGAC		
			AC		
GAM2620	FLJ14346	3'	CAGAAGAATGGCGTGAACCTGG 47359	A A C	
			GA TCCCAGGTTCA GC ATTCT CTG		
			AGGGTTCAAGT CG TAAGA GAC		
			G G A		
GAM2620	FLJ14397	3'	CAGGAGAATCGCTTGAACCTAG 52318	C A	
			GA TCC AGGTTCAAGC ATTCTCCTG		
			AGG TCCAAGTTCG TAAGAGGAC		
			A C		
GAM2620	FLJ14397	3'	CAGGAGAATGGTGTGAACCTGG 52319	A A	
			GA TCCCAGGTTCA GC ATTCTCCTG		
			AGGGTCCAAGT TG TAAGAGGAC		
			G G		
GAM2620	FLJ14399	3'	AGATCGCCTGAGCCTAGGA 52337	C A AAT	
			TCC AGGTTCA GC TCT		
			AGG TCCGAGT CG AGA		
			A C CT_		
GAM2620	FLJ14466	3'	CAGGAGAATCGCTTGAACCCAG 52423	CA A	
			GA TCC GGTTCAGC ATTCTCCTG		
			AGG CCAAGTTCG TAAGAGGAC		
			AC C		
GAM2620	FLJ14490	3'	CAGGAGAATGGCGTGAACCCAG 52439	CA A A	
			GA TCC GGTTCAGC ATTCTCCTG		
			AGG CCAAGT CG TAAGAGGAC		
			AC G G		
GAM2620	FLJ14621	3'	CAGGAAGAATCGCTTGAACCCG 52535	A A _	
			GGA TCCC GGTTCAGC ATTCT CCTG		
			AGGG CCAAGTTCG TAAGA GGAC		
			C C A		
GAM2620	FLJ14641	3'	CAGGAGAATCGCTTGAACCAGG 52553	A A	
			CC GGTTCAGC ATTCTCCTG		

			GG CCAAGTTCG TAAGAGGAC		
			A C		
GAM2620	FLJ20004	3'	CAGGAGAATCACTTGAACCCAG 34751	CA	CA
		GA	TCC GGTTC AAG ATTCTCCTG		
			AGG CCAAGTTC TAAGAGGAC		
			AC AC		
GAM2620	FLJ20004	3'	CAGGAGAATCGCTTGAACCTAGG 34752	A	A
		GA	TCCC GGTTC AAGC ATTCTCCTG		
			AGGG TCAAGTTCG TAAGAGGAC		
			A C		
GAM2620	FLJ20004	3'	CGGAGAATCACTTGAACCCAG 34757	CA	CA
		GA	TCC GGTTC AAG ATTCTCCTG		
			AGG CCAAGTTC TAAGAGGGC		
			AC AC		
GAM2620	FLJ20004	3'	CATGAGAATTGCTTGAACCTGG 97001		C
		GA	TCCCAGGTTCAAGCAATTCTC TG		
			AGGGTCCAAGTTCGTTAAGAG AC		
			T		
GAM2620	FLJ20006	3'	CAGGAAAATCGCTTGAACCTGG 34780	A	C
			CCAGGTTCAAGC ATT TCCTG		
			GGTCCAAGTTCG TAA AGGAC		
			C A		
GAM2620	FLJ20013	3'	GGGAGAATTGCTTGAACCTGGG 34799		
		A	TCCCAGGTTCAAGCAATTCTCCT		
			AGGGTCCAAGTTCGTTAAGAGGG		
GAM2620	FLJ20019	3'	AGAAAAGTGAAGTGAGCCTGGGA 34812	AG	A__
			TCCCAGGTTCA CA TTCT		
			AGGGTCCGAGT GT AAGA		
			GA CAA		
GAM2620	FLJ20045	3'	GGAGAATCGCTTGAACCCAGGA 34888	CA	A
			TCC GGTTC AAGC ATTCTCC		
			AGG CCAAGTTCG TAAGAGG		
			AC C		
GAM2620	FLJ20055	3'	GAGAATCACTTGAACCCAGGA 34910	CA	CA
			TCC GGTTC AAG ATTCTC		
			AGG CCAAGTTC TAAGAG		
			AC AC		
GAM2620	FLJ20059	3'	CAGGAGAATTGCTTGAACCCGG 34924	A	
		GA	TCCC GGTTC AAGCAATTCTCCTG		

AGGG CCAAGTTCGTTAAGAGGAC
 C
 GAM2620 FLJ20069 3' CAGGAGAATTGCTTGACCCAGG 34948 CA T
 A TCC GGT CAAGCAATTCTCCTG
 ||| ||| |||||||||
 AGG CCA GTTCGTTAAGAGGAC
 AC _
 GAM2620 FLJ20071 3' CAGGAGAATCGCTTGAACCCAG 34959 CA A
 GA TCC GGTTC AAGC ATTCTCCTG
 ||| ||||||| |||||||
 AGG CCAAGTTCG TAAGAGGAC
 AC C
 GAM2620 FLJ20170 3' CAGGATGATTGCTTAAGCCCAG 35163 CA C C
 GA TCC GGT AAGCAATT TCCTG
 ||| ||| ||||||| |||
 AGG CCGA TTCGTTAG AGGAC
 AC A T
 GAM2620 FLJ20211 3' CAGGAGAATTGCCTGAACCTGG 35258 A
 GA TCCCAGGTTCA GCAATTCTCCTG
 ||||||| |||||||
 AGGGTCCAAGT CGTTAAGAGGAC
 C
 GAM2620 FLJ20280 3' CAGGAGAATCACTTGAACCCAG 35326 CA CA
 GA TCC GGTTC AAG ATTCTCCTG
 ||| ||||||| |||||||
 AGG CCAAGTTC TAAGAGGAC
 AC AC
 GAM2620 FLJ20306 3' CAGGAGGATTGCTTGAGCCCAG 35386 CA
 GA TCC GGTTC AAGCAATTCTCCTG
 ||| ||||||||| |||
 AGG CCGAGTTCGTTAGGAGGAC
 AC
 GAM2620 FLJ20306 3' GAATCGCTTGAACCTGGGA 35393 A
 TCCCAGGTTCAAGC ATTC
 ||||||||| |||
 AGGGTCCAAGTTCG TAAG
 C
 GAM2620 FLJ20306 3' GGGAGAATCGCTTGAACCTGGG 35397 A
 A TCCCAGGTTCAAGC ATTCTCCT
 ||||||||| |||||||
 AGGGTCCAAGTTCG TAAGAGGG
 C
 GAM2620 FLJ20340 3' CAGGAGAATCGCTTGAACCCGG 35453 A A
 GA TCCC GGTTC AAGC ATTCTCCTG
 ||| ||||||| |||||||
 AGGG CCAAGTTCG TAAGAGGAC
 C C
 GAM2620 FLJ20413 3' CAGGAGAATGGCGTGAACCAGG 35591 A A A
 GA TCCC GGTTC A GC ATTCTCCTG
 ||| ||||| || |||||||

			AGGG CCAAGT CG TAAGAGGAC		
			A G G		
GAM2620	FLJ20456	3'	CAGAAGAATCGCTTGAGCCCGG 35662	A	A C
	GA		TCCC GGTTCAAGC ATTCT CTG		
			AGGG CCGAGTTCG TAAGA GAC		
			C C A		
GAM2620	FLJ20464	3'	CAGGAGAATCACTTGAACCCCGG 35689	A	CA
	GA		TCCC GGTTCAAG ATTCTCCTG		
			AGGG CCAAGTTC TAAGAGGAC		
			C AC		
GAM2620	FLJ20464	3'	CAGGAGAATCGCTTGAACCTGG 35690		A
	GA		TCCCAGGTTCAAGC ATTCTCCTG		
			AGGGTCCAAGTTCG TAAGAGGAC		
			C		
GAM2620	FLJ20546	3'	CAGGAGAATCATTTGAACTCAG 35807	CA	CA
	GA		TCC GGTTCAAG ATTCTCCTG		
			AGG TCAAGTTT TAAGAGGAC		
			AC AC		
GAM2620	FLJ20627	3'	CAGGAGAATCTCTTGAACCTTG 35908		CA
	GA		TCCCAGGTTCAAG ATTCTCCTG		
			AGGGTTCAAGTTC TAAGAGGAC		
			TC		
GAM2620	FLJ20666	5'	CAGGAGAATCACTTGATGGCTG 37658	GT_	CA
			CAG TCAAG ATTCTCCTG		
			GTC AGTTC TAAGAGGAC		
			GGT AC		
GAM2620	FLJ20686	3'	CAGGAGAATCGCTTGAACCTGAG 35952	CA	A
	G		CC GGTTCAAGC ATTCTCCTG		
			GG TCAAGTTCG TAAGAGGAC		
			AG C		
GAM2620	FLJ20694	3'	CAGGAGAATCACCTGAACCCAG 35973	CA	AGCA
	GA		TCC GGTTCA ATTCTCCTG		
			AGG CCAAGT TAAGAGGAC		
			AC CCAC		
GAM2620	FLJ20700	3'	CAGGAGAATGGCATGAACCCCGG 36000	A	A A
	G		CCC GGTTCA GC ATTCTCCTG		
			GGG CCAAGT CG TAAGAGGAC		
			C A G		
GAM2620	FLJ20783	3'	CAGGAGAATAGTGTGAACCCAG 36096	CA	A A
	GA		TCC GGTTCA GC ATTCTCCTG		

			AGG CCAAGT TG TAAGAGGAC		
			AC G A		
GAM2620	FLJ20802	3'	CAGGAGAATTGCTTGAACCTGG 36108		
			CCAGGTTCAAGCAATTCTCCTG		
			GGTCCAAGTTCGTTAAGAGGAC		
GAM2620	FLJ20825	3'	CAGGAGAATCGCTTGAACCCAG 36143	CA	A
			GA TCC GGTTC AAGC ATTCTCCTG		
			AGG CCAAGTTCG TAAGAGGAC		
			AC C		
GAM2620	FLJ20972	3'	CAGGAGAATCACTTGAACCCAG 47382	CA	CA
			GA TCC GGTTC AAG ATTCTCCTG		
			AGG CCAAGTTC TAAGAGGAC		
			AC AC		
GAM2620	FLJ21144	3'	GAATAGCTTGAACCTGAGA 43192	C	A
			TC CAGGTTCAAGC ATTC		
			AG GTCCAAGTTCG TAAG		
			A A		
GAM2620	FLJ21240	3'	CAGGAGAATTGCTTGAACCCAG 46260	CA	
			GA TCC GGTTC AAGCAATTCTCCTG		
			AGG CCAAGTTCGTTAAGAGGAC		
			AC		
GAM2620	FLJ21369	3'	GAGAATTGCTTGAACCCAGGA 46052	CA	
			TCC GGTTC AAGCAATTCTC		
			AGG CCAAGTTCGTTAAGAG		
			AC		
GAM2620	FLJ21551	3'	CAGGAGAATCGCTTGAACCCAG 46032	CA	A
			GA TCC GGTTC AAGC ATTCTCCTG		
			AGG CCAAGTTCG TAAGAGGAC		
			AC C		
GAM2620	FLJ21657	3'	AATGGCTTGAACCTGGGA 42791		A
			TCCCAGGTTCAAGC ATT		
			AGGGTCCAAGTTCG TAA		
			G		
GAM2620	FLJ21687	3'	GAGAATTGCTTGAATCCAGGA 46297	CA	
			TCC GGTTC AAGCAATTCTC		
			AGG CTAAGTTCGTTAAGAG		
			AC		
GAM2620	FLJ21777	5'	CAGAAGAACCCCTTGAACCCGG 50836	A	CAA C
			GA TCCC GGTTC AAG TTCT CTG		

		AGGG CCAAGTTC AAGA GAC		
		C CCC A		
GAM2620	FLJ21777 3'	GAGAATTGCTTGAACCCTGG 50843	—	
		CCAGG TTCAAGCAATTCTC		
		GGTCC AAGTTCGTTAAGAG		
		C		
GAM2620	FLJ22009 3'	CAGGAGGATCACTTGAGCCCAG 60916	CA	CA
	GA	TCC GGTTC AAG ATTCTCCTG		
		AGG CCGAGTTC TAGGAGGAC		
		AC AC		
GAM2620	FLJ22054 3'	GGAGAATCGCTTGAACCTGGGA 96050		A
		TCCCAGGTTCAAGC ATTCTCC		
		AGGGTCCAAGTTCG TAAGAGG		
		C		
GAM2620	FLJ22313 3'	CAGGAGAATTGCCTGAACCCAG 42577	CA	A
	GA	TCC GGTTC A GCAATTCTCCTG		
		AGG CCAAGT CGTTAAGAGGAC		
		AC C		
GAM2620	FLJ22389 3'	CAGGAAGATCACTTGAGCCCAG 46790	CA	CA TC
	GA	TCC GGTTC AAG AT TCCTG		
		AGG CCGAGTTC TA AGGAC		
		AC AC GA		
GAM2620	FLJ22474 3'	GAGAATCACTTGAACCTGGGA 45614		CA
		TCCCAGGTTCAAG ATTCTC		
		AGGGTCCAAGTTC TAAGAG		
		AC		
GAM2620	FLJ22692 3'	CAGGAGAATGGCGTGAACCCAG 47478	CA	A A
	GA	TCC GGTTC A GC ATTCTCCTG		
		AGG CCAAGT CG TAAGAGGAC		
		AC G G		
GAM2620	FLJ22814 3'	CAGGAGAATGACATGAACCCAG 46720	CA	AGCA
	GA	TCC GGTTC A ATTCTCCTG		
		AGG CCAAGT TAAGAGGAC		
		AC ACAG		
GAM2620	FLJ22965 3'	CAGGAGAATTGCTTGAACCTCGG 42294	AG	
	GA	TCCC GTTCAAGCAATTCTCCTG		
		AGGG CAAGTTCGTTAAGAGGAC		
		CT		
GAM2620	FLJ23022 3'	CAGGAGAATCGCTTGAACCCGG 47492	A	A
	GA	TCCC GGTTC AAGC ATTCTCCTG		

			AGGG CCAAGTTCG TAAGAGGAC		
			C C		
GAM2620	FLJ23040	3'	CAGGAAAATTGCTTGAACCTGG 47983		C
	GA		TCCCAGGTTCAAGCAATT TCCTG		
			AGGGTCCAAGTTCGTAA AGGAC		
			A		
GAM2620	FLJ23042	3'	CAGGAGAATCACTTGAACCCAG 47938	CA	CA
	GA		TCC GGTTC AAG ATTCTCCTG		
			AGG CCAAGTTC TAAGAGGAC		
			AC AC		
GAM2620	FLJ23042	3'	GAGGATCGCTTGAGCCCAGGA 47943	CA	A
			TCC GGTTC AAGC ATTCTC		
			AGG CCGAGTTCG TAGGAG		
			AC C		
GAM2620	FLJ23120	3'	CAGAGGAATTGCTTGAACCTGG 86325		TC
	GA		TCCCAGGTTCAAGCAATTC CTG		
			AGGGTCCAAGTTCGTAAAG GAC		
			GA		
GAM2620	FLJ23229	3'	GAATCGCTTGAACCTGGGA 47530		A
			TCCCAGGTTCAAGC ATTC		
			AGGGTCCAAGTTCG TAAG		
			C		
GAM2620	FLJ23235	3'	CAGGAGAATCACTTGAACCTGG 46877		CA
			CCAGGTTCAAG ATTCTCCTG		
			GGTCCAAGTTC TAAGAGGAC		
			AC		
GAM2620	FLJ23360	3'	CAGGAGAATCGCTTGAACCTGG 43824		A
	GA		TCCCAGGTTCAAGC ATTCTCCTG		
			AGGGTCCAAGTTCG TAAGAGGAC		
			C		
GAM2620	FLJ23447	3'	AGGAGAATCGCTTTAGGC 46129	G C A	
			G TT AAGC ATTCTCCT		
			C GA TTCG TAAGAGGA		
			G T C		
GAM2620	FLJ23447	3'	CAGGAGGATCGCTTGAGCC 46130		A
			GGTTC AAGC ATTCTCCTG		
			CCGAGTTCG TAGGAGGAC		
			C		
GAM2620	FLJ23476	3'	CGGGAGAACTGCTTGAGCCCAG 45313	CA	A
	GA		TCC GGTTC AAGCA TTCTCCTG		

			AGG CCGAGTTCGT AAGAGGGC		
			AC C		
GAM2620	FLJ23499	3'	CAGGAGAATTGCTTGAACCCAG 43128	CA	
	GA		TCC GGTCAAGCAATTCTCCTG		
			AGG CCAAGTTCGTTAAGAGGAC		
			AC		
GAM2620	FLJ23499	3'	CAGGGGAATCGCTTGAACCTGA 43129	C	A
	GA		TC CAGGTTCAAGC ATTCTCCTG		
			AG GTCCAAGTTCG TAAGGGGAC		
			A C		
GAM2620	FLJ23537	3'	CAGGAGAATCACTAGAACCGGG 88917	A	A CA
	A		TCCC GGTC AG ATTCTCCTG		
			AGGG CCAAG TC TAAGAGGAC		
			— A AC		
GAM2620	FLJ23556	3'	CAGAAGGATCACTTGAGCC 46433	CA	C
			GGTCAAG ATTCT CTG		
			CCGAGTTC TAGGA GAC		
			AC A		
GAM2620	FLJ23878	3'	CAGGAGAATGGCTTGAACCCGG 59368	A	A
			CC GGTCAAGC ATTCTCCTG		
			GG CCAAGTTCG TAAGAGGAC		
			C G		
GAM2620	FLJ25179	3'	CAGGAGGATTGCTTGAGCCCAG 59012	CA	
	GA		TCC GGTCAAGCAATTCTCCTG		
			AGG CCGAGTTCGTTAGGAGGAC		
			AC		
GAM2620	FLJ31168	3'	CAGGAGAATCGCTTGAGCCTGG 59178		A
	GA		TCCCAGGTTCAAGC ATTCTCCTG		
			AGGGTCCGAGTTCG TAAGAGGAC		
			C		
GAM2620	FLJ31455	3'	CAGGAGAATCACTTGAACCTCGG 59281	AG	CA
	GA		TCCC GTTCAAG ATTCTCCTG		
			AGGG CAAGTTC TAAGAGGAC		
			CT AC		
GAM2620	FLJ31455	3'	CAGGAGAATCGCCTGAACCCGG 59282	A	A A
	G		CCC GGTCA GC ATTCTCCTG		
			GGG CCAAGT CG TAAGAGGAC		
			C C C		
GAM2620	FLJ31737	3'	AGAATTGCTTAAACCCAGGA 59345	CA	C
			TCC GGTT AAGCAATTCT		

			AGG CCAA TTCGTTAAGA		
			AC A		
GAM2620	FLJ32915	5'	CAGGAGAGTCACTTGAACCCGG 59429	A	CA
	GA		TCCC GGTTCAAG ATTCTCCTG		
			AGGG CCAAGTTC TGAGAGGAC		
			C AC		
GAM2620	FRSB	3'	CAGGAAAATCTCTTGAACCAGG 20289	A	CA C
			CC GGTTCAAG ATT TCCTG		
			GG CCAAGTTC TAA AGGAC		
			A TC A		
GAM2620	FUSIP1	3'	GAGAATCGCTTGAACCTGGGA 55039		A
			TCCCAGGTTCAAGC ATTCTC		
			AGGGTCCAAGTTCG TAAGAG		
			C		
GAM2620	GALNT6	3'	CAGGAGAATCACTCGAACCCAG 24243	CA	A CA
	GA		TCC GGTTC AG ATTCTCCTG		
			AGG CCAAG TC TAAGAGGAC		
			AC C AC		
GAM2620	GCN2	3'	CAGGAAGACTGCTTGAAACCAG 63436	A	_ A TC
	G		CC GGTT CAAGCA T TCCTG		
			GG CCAA GTTCGT A AGGAC		
			A A C GA		
GAM2620	GLTP	3'	CAGGAGAATCGCTTGAACCCGG 33582	A	A
	GA		TCCC GGTTCAAGC ATTCTCCTG		
			AGGG CCAAGTTCG TAAGAGGAC		
			C C		
GAM2620	GP5	3'	CAGGAGAATCACTTGAACCCGG 16865	A	CA
	GA		TCCC GGTTCAAG ATTCTCCTG		
			AGGG CCAAGTTC TAAGAGGAC		
			C AC		
GAM2620	GSG2	3'	CAGGAGGATCGCTTGAGCC 50074		A
			GGTTCAAGC ATTCTCCTG		
			CCGAGTTCG TAGGAGGAC		
			C		
GAM2620	GTPBP5	3'	CAGGAGAATGGCGTGAACCTGG 65971		A A
	GA		TCCCAGGTTCA GC ATTCTCCTG		
			AGGGTCCAAGT CG TAAGAGGAC		
			G G		
GAM2620	GTSE1	3'	GGATTACTTGAGCCCAGGA 33564	CA	C
			TCC GGTTCAAG AATTC		

			AGG CCGAGTTC TTAGG		
			AC A		
GAM2620	HES2	3'	CAGGAGAATGGCATGAACCTGG 39371	A	A
	GA		TCCCAGGTTCA GC ATTCTCCTG		
			AGGGTCCAAGT CG TAAGAGGAC		
			A G		
GAM2620	HIC	3'	CAGGAGAATTGCTTGAACC 68044		
			GGTTCAAGCAATTCTCCTG		
			CCAAGTTCGTTAAGAGGAC		
GAM2620	HIG2	3'	GAATTGCTTGAACCCGGGG 26200	A	
			TCCC GGTTCAAGCAATTC		
			GGGG CCAAGTTCGTTAAG		
			C		
GAM2620	HRH4	3'	CAGGGGAATTGCTTGAACCCGG 41529	A	
	GA		TCCC GGTTCAAGCAATTCTCCTG		
			AGGG CCAAGTTCGTTAAGGGGAC		
			C		
GAM2620	HSA250303	3'	CAGGAGGATCGCTTGAACCCAG 38019	CA	A
	GA		TCC GGTTCAAGC ATTCTCCTG		
			AGG CCAAGTTCG TAGGAGGAC		
			AC C		
GAM2620	HSH2	3'	CGGGAGAATTGCTTGAACCCGG 52738	A	
	GA		TCCC GGTTCAAGCAATTCTCCTG		
			AGGG CCAAGTTCGTTAAGAGGGC		
			C		
GAM2620	HSPC043	3'	CAGGAGAATCGCTTGAACCTGG 68350		A
	GA		TCCCAGGTTCAAGC ATTCTCCTG		
			AGGGTCCAAGTTCG TAAGAGGAC		
			C		
GAM2620	ICAM4	3'	CAGGAGAATCGCTTGAGCCCAG 9538	CA	A
	GA		TCC GGTTCAAGC ATTCTCCTG		
			AGG CCGAGTTCG TAAGAGGAC		
			AC C		
GAM2620	ICAM4	3'	CAGGAGAATCGCTTGAGCCCAG 9539	CA	A
	GA		TCC GGTTCAAGC ATTCTCCTG		
			AGG CCGAGTTCG TAAGAGGAC		
			AC C		
GAM2620	IL-23R	3'	CAGGAGAATCACTTGAACCAGG 59130	CA	CA
	A		TCC GGTTCAAG ATTCTCCTG		

			AGG CCAAGTTC TAAGAGGAC		
			A_ AC		
GAM2620	IL10RB	3'	CAGGAGAATTGCATGAACCCGG 7125	A	A
	GA		TCCC GGTTCA GCAATTCTCCTG		
			AGGG CCAAGT CGTTAAGAGGAC		
			C A		
GAM2620	IMAGE:4907098	3'	CAGGAGAATCACTTGAACCTGG 57753		CA
	GA		TCCCAGGTTCAAG ATTCTCCTG		
			AGGGTCCAAGTTC TAAGAGGAC		
			AC		
GAM2620	KALI	3'	CAGGAGAATCGCTTGAACCCAG 54689	CA	A
	GA		TCC GGTTCAAGC ATTCTCCTG		
			AGG CCAAGTTCG TAAGAGGAC		
			AC C		
GAM2620	KBRAS2	3'	CAGGAGAATTGCTTGAACCTCAG 34620	CCA	
	A		TC GGTTCAAGCAATTCTCCTG		
			AG TCAAGTTCGTTAAGAGGAC		
			AC_		
GAM2620	KCNH6	3'	CAGGAGAATGGCATGAACCCGG 48570	A	A A
	GA		TCCC GGTTCA GC ATTCTCCTG		
			AGGG CCAAGT CG TAAGAGGAC		
			C A G		
GAM2620	KIAA0042	3'	CAGGAGGATCGCTTGAACCTGA 30234	C	A
	GA		TC CAGGTTCAAGC ATTCTCCTG		
			AG GTCCAAGTTCG TAGGAGGAC		
			A C		
GAM2620	KIAA0057	3'	CAGGAGAATCGCTTGAACCT 25404		A
			AGGTTCAAGC ATTCTCCTG		
			TCCAAGTTCG TAAGAGGAC		
			C		
GAM2620	KIAA0159	3'	CAGGAGAATCGCCTGAACC 30140	A	A
			GGTTCA GC ATTCTCCTG		
			CCAAGT CG TAAGAGGAC		
			C C		
GAM2620	KIAA0184	3'	CAGGAGAATGGTATGAACCAGG 65806	A	A A
	GA		TCCC GGTTCA GC ATTCTCCTG		
			AGGG CCAAGT TG TAAGAGGAC		
			A A G		
GAM2620	KIAA0226	3'	CAGGAGAATCGCTTGAACCTGG 64255		A
	GA		TCCCAGGTTCAAGC ATTCTCCTG		

			AGGGTCCAAGTTCG TAAGAGGAC		
			C		
GAM2620	KIAA0252	3'	CAGGAGAATCCCTTGAACCTGG 63451	CA	
	GA		TCCCAGGTTCAAG ATTCTCCTG		
			AGGGTCCAAGTTC TAAGAGGAC		
			CC		
GAM2620	KIAA0266	3'	CAGGAGAATTGCTTGAAACTGG 41638	G	
			CCAG TTCAAGCAATTCTCCTG		
			GGTC AAGTTCGTTAAGAGGAC		
			A		
GAM2620	KIAA0355	3'	CAGAAGAATCGCTTGAACCCGG 28701	A	A C
	GA		TCCC GGTTCAAGC ATTCT CTG		
			AGGG CCAAGTTCG TAAGA GAC		
			C C A		
GAM2620	KIAA0391	3'	GAATTGCTTGAAGCCAGG 28610	A	_
			CC GGTT CAAGCAATTC		
			GG CCGA GTTCGTTAAG		
			A A		
GAM2620	KIAA0408	3'	CAGGAGAATGGCATGAACCCGG 28796	A	A A
	GA		TCCC GGTTCA GC ATTCTCCTG		
			AGGG CCAAGT CG TAAGAGGAC		
			C A G		
GAM2620	KIAA0419	3'	CAGGCGAATTGCTTGAACCTGG 28858		T
	GA		TCCCAGGTTCAAGCAATTC CCTG		
			AGGGTCCAAGTTCGTTAAG GGAC		
			C		
GAM2620	KIAA0431	3'	CAGGACGATCACTTGAGCCCAG 31547	CA	CA C
	GA		TCC GGTTCAAG ATT TCCTG		
			AGG CCGAGTTC TAG AGGAC		
			AC AC C		
GAM2620	KIAA0441	3'	CAGGAGAATCACTTGAGCCCAG 29627	CA	CA
	GA		TCC GGTTCAAG ATTCTCCTG		
			AGG CCGAGTTC TAAGAGGAC		
			AC AC		
GAM2620	KIAA0445	5'	CAGGAGAATTGCTTGAACCTGG 28636		
	GA		TCCCAGGTTCAAGCAATTCTCCTG		
			AGGGTCCAAGTTCGTTAAGAGGAC		
GAM2620	KIAA0446	5'	CAGGAGAATGGCATGAACCCGG 69444	A	A A
	GA		TCCC GGTTCA GC ATTCTCCTG		

			AGGG CCAAGT CG TAAGAGGAC		
			C A G		
GAM2620	KIAA0447	3'	CAGGAGAATTGTTTGAACCCCG 72104	CA	
	GA		TCC GGTTC AAGCAATTCTCCTG		
			AGG CCAAGTTTGTTAAGAGGAC		
			CC		
GAM2620	KIAA0451	5'	CAGGAGGATCACTTGAGCCCAG 29765	CA	CA
	GA		TCC GGTTC AAG ATTCTCCTG		
			AGG CCGAGTTC TAGGAGGAC		
			AC AC		
GAM2620	KIAA0472	3'	AGGAGAATTGCTTGAACCCAGG 72333	CA	
	A		TCC GGTTC AAGCAATTCTCCT		
			AGG CCAAGTTCGTTAAGAGGA		
			AC		
GAM2620	KIAA0472	3'	CAGGAGAATCACTTGAACCCGG 72344	A	CA
	GA		TCCC GGTTC AAG ATTCTCCTG		
			AGGG CCAAGTTC TAAGAGGAC		
			C AC		
GAM2620	KIAA0472	3'	CAGGAGAATCGCTTGAACCTGG 72345		A
	GA		TCCCAGGTTCAAGC ATTCTCCTG		
			AGGGTCCAAGTTCG TAAGAGGAC		
			C		
GAM2620	KIAA0475	3'	CAGGAGAATCACTTGAATCCAG 30113	CA	CA
	GA		TCC GGTTC AAG ATTCTCCTG		
			AGG CTAAGTTC TAAGAGGAC		
			AC AC		
GAM2620	KIAA0547	3'	GAGAATCACTTGAACCAGGGA 29593	A	CA
			TCCC GGTTC AAG ATTCTC		
			AGGG CCAAGTTC TAAGAG		
			A AC		
GAM2620	KIAA0557	3'	GAGAATCACTTGAACCAGGGA 78562	A	CA
			TCCC GGTTC AAG ATTCTC		
			AGGG CCAAGTTC TAAGAG		
			A AC		
GAM2620	KIAA0563	3'	CAGGAGAATGGCATGAACCTGG 29873		A A
	GA		TCCCAGGTTCA GC ATTCTCCTG		
			AGGGTCCAAGT CG TAAGAGGAC		
			A G		
GAM2620	KIAA0565	3'	CAGGAAGATCACTTGAACCCAG 67433	CA	CA TC
	GA		TCC GGTTC AAG AT TCCTG		

		AGG CCAAGTTC TA AGGAC		
		AC AC GA		
GAM2620	KIAA0565	3' CAGGAGAATTGCTTGAACCTGG 67434		
	GA	TCCCAGGTTCAAGCAATTCTCCTG		
		AGGGTCCAAGTTCGTTAAGAGGAC		
GAM2620	KIAA0596	3' CAGGAGAATCGCTTGAACCCTG 63484	_	A
	G	CCAGG TTCAAGC ATTCTCCTG		
		GGTCC AAGTTCG TAAGAGGAC		
		C C		
GAM2620	KIAA0628	3' CAGGAGAATTGCTTGAGCCTGG 29527		
	GA	TCCCAGGTTCAAGCAATTCTCCTG		
		AGGGTCCGAGTTCGTTAAGAGGAC		
GAM2620	KIAA0635	3' CAGGAGAATTGCTTGAACCCGG 28412	A	
	GA	TCCC GGTTCAAGCAATTCTCCTG		
		AGGG CCAAGTTCGTTAAGAGGAC		
		C		
GAM2620	KIAA0643	3' CAGGAGAATCACTTGAGACCAG 45973	A _	CA
	G	CC GGT TCAAG ATTCTCCTG		
		GG CCA AGTTC TAAGAGGAC		
		A G AC		
GAM2620	KIAA0752	3' CAGGAGAATCACTTGAACCGAG 67632	CA	CA
	G	CC GGTTCAAG ATTCTCCTG		
		GG CCAAGTTC TAAGAGGAC		
		AG AC		
GAM2620	KIAA0794	3' CAGGGGAATGGCTTGAACCTGG 81227		A
	GA	TCCCAGGTTCAAGC ATTCTCCTG		
		AGGGTCCAAGTTCG TAAGGGGAC		
		G		
GAM2620	KIAA0795	3' GGGAGAATTGCTTAAACCGGGG 47230	A	C
	A	TCCC GGTT AAGCAATTCTCCT		
		AGGG CCAA TTCGTTAAGAGGG		
		G A		
GAM2620	KIAA0798	3' GGAGAATCACTTGAACCTGGGA 28449		CA
		TCCCAGGTTCAAG ATTCTCC		
		AGGGTCCAAGTTC TAAGAGG		
		AC		
GAM2620	KIAA0825	3' CAGGAGAATCACTTGAACCCGG 61682	A	CA
	GA	TCCC GGTTCAAG ATTCTCCTG		

			AGGG CCAAGTTC TAAGAGGAC		
			C AC		
GAM2620	KIAA0831	3'	GAATCGCTTGAACCGGGA 30636	A	A
			TCCC GGTTC AAGC ATTC		
			AGGG CCAAGTTCG TAAG		
			— C		
GAM2620	KIAA0872	3'	CAGGAGAATCACTTGAACC 30744		CA
			GGTTCAAG ATTCTCCTG		
			CCAAGTTC TAAGAGGAC		
			AC		
GAM2620	KIAA0872	3'	CAGGGGAATTGCTTGAACCCGG 30745	A	
			GA TCCC GGTTC AAGCAATTCTCCTG		
			AGGG CCAAGTTCGTTAAGGGGAC		
			C		
GAM2620	KIAA0884	3'	CAGGAAAATTACTTAAACCTGG 70751		C C C
			GA TCCCAGGTT AAG AATT TCCTG		
			AGGGTCCAA TTC TTAA AGGAC		
			A A A		
GAM2620	KIAA0889	3'	CAGGAGAATCACTTGAACC 31764		CA
			GGTTCAAG ATTCTCCTG		
			CCAAGTTC TAAGAGGAC		
			AC		
GAM2620	KIAA0889	3'	CAGGAGAATCGCGTGAACCCAG 31765	CA	A A
			GA TCC GGTTC A GC ATTCTCCTG		
			AGG CCAAGT CG TAAGAGGAC		
			AC G C		
GAM2620	KIAA0892	3'	CAGGAGGATCACTTGAGCCCAG 71567	CA	CA
			GA TCC GGTTC AAG ATTCTCCTG		
			AGG CCGAGTTC TAGGAGGAC		
			AC AC		
GAM2620	KIAA0894	3'	CAGGAGAATCGCTTGAATTCGG 30328	AG	A
			GA TCCC GTTCAAGC ATTCTCCTG		
			AGGG TAAGTTCG TAAGAGGAC		
			CT C		
GAM2620	KIAA0907	3'	CAGGAGAATCACTTGAACCTGG 30868		CA
			GA TCCCAGGTTCAAG ATTCTCCTG		
			AGGGTTCAAGTTC TAAGAGGAC		
			AC		
GAM2620	KIAA0907	3'	CAGGAGAATCGCTTCAACCTGG 30869		C A
			GA TCCCAGGTT AAGC ATTCTCCTG		

			AGGGTCCAA TTCG TAAGAGGAC		
			C C		
GAM2620	KIAA0930	3'	AGGAGAATCACTTGAACCT 71062	CA	
			AGGTTCAAG ATTCTCCT		
			TCCAAGTTC TAAGAGGA		
			AC		
GAM2620	KIAA0953	3'	CAGGAGGACTGCTTGAGCCCAG 67323	CA	A
			GA TCC GGTTC AAGCA TTCTCCTG		
			AGG CCGAGTTCGT AGGAGGAC		
			AC C		
GAM2620	KIAA0953	3'	GGGAGAATCACCTGAGCCTGGG 67328	AGCA	
			A TCCCAGGTTCA ATTCTCCT		
			AGGGTCCGAGT TAAGAGGG		
			CCAC		
GAM2620	KIAA0961	3'	CAGGAGAATCACTTGGGCCCGG 30394	A	CA
			GA TCCC GGTTC AAG ATTCTCCTG		
			AGGG CCGGGTTC TAAGAGGAC		
			C AC		
GAM2620	KIAA0981	3'	CAGGAGAATTGTTTGAACCTGG 62084		
			GA TCCCAGGTTCAAGCAATTCTCCTG		
			AGGGTCCAAGTTTGTTAAGAGGAC		
GAM2620	KIAA1001	3'	AGAATCGCTTGAGCCTGGGA 30998	A	
			TCCCAGGTTCAAGC ATTCT		
			AGGGTCCGAGTTCG TAAGA		
			C		
GAM2620	KIAA1001	3'	CAGGAGAGAATCGCTTGAACCG 31003	A	AA__
			GGGA TCCC GGTTC AAGC TTCTCCTG		
			AGGG CCAAGTTCG GAGAGGAC		
			G CTA		
GAM2620	KIAA1056	3'	CAGGAGAATTGCTTGAACCTGG 30311		
			CCAGGTTCAAGCAATTCTCCTG		
			GGTCCAAGTTCGTTAAGAGGAC		
GAM2620	KIAA1130	3'	CAGGAGAATCGCTTGAACCCGG 63079	A	A
			GA TCCC GGTTC AAGC ATTCTCCTG		
			AGGG CCAAGTTCG TAAGAGGAC		
			C C		
GAM2620	KIAA1143	3'	GAATTGCTTGAAGCCAGG 69241	A	_
			CC GGTTC AAGCAATTC		

			GG CCGA GTTCGTTAAG		
			A A		
GAM2620	KIAA1160	3'	CAGGAGAATCACTTGAACC 40753	CA	
			GGTTCAAG ATTCTCCTG		
			CCAAGTTC TAAGAGGAC		
			AC		
GAM2620	KIAA1164	3'	CAGGAGAATCGCTTGAACCCAG 70036	CA	A
			GA TCC GGTTC AAGC ATTCTCCTG		
			AGG CCAAGTTCG TAAGAGGAC		
			AC C		
GAM2620	KIAA1164	3'	CAGGAGAATTGCTTGAACCCGG 70037	A	
			CC GGTTC AAGCAATTCTCCTG		
			GG CCAAGTTCGTTAAGAGGAC		
			C		
GAM2620	KIAA1191	3'	CAGGAGAATCGCCTGAACCCAG 40332	CA	A A
			GA TCC GGTTC A GC ATTCTCCTG		
			AGG CCAAGT CG TAAGAGGAC		
			AC C C		
GAM2620	KIAA1202	3'	CAGGAGAATTGCTTGAACCTGG 72486		
			CCAGGTTCAAGCAATTCTCCTG		
			GGTCCAAGTTCGTTAAGAGGAC		
GAM2620	KIAA1228	3'	CAGGAGAATTGCTTGAACCCAG 65670	CA	
			GA TCC GGTTC AAGCAATTCTCCTG		
			AGG CCAAGTTCGTTAAGAGGAC		
			AC		
GAM2620	KIAA1244	3'	CAGGAGAATCGCTCGAACCCAG 72442	CA	A A
			GA TCC GGTTC AGC ATTCTCCTG		
			AGG CCAAG TCG TAAGAGGAC		
			AC C C		
GAM2620	KIAA1257	3'	CAGGAGAATGGCGTGAACCCAG 63395	CA	A A
			GA TCC GGTTC A GC ATTCTCCTG		
			AGG CCAAGT CG TAAGAGGAC		
			AC G G		
GAM2620	KIAA1277	3'	CAGAAGAATCGCTTGAACCTGGG 65073	A	A C
			GA TCCC GGTTC AAGC ATTCT CTG		
			AGGG TCAAGTTCG TAAGA GAC		
			G C A		
GAM2620	KIAA1328	3'	CAGGAGAATCACTTGAACCCGG 62318	A	CA
			GA TCCC GGTTC AAG ATTCTCCTG		

			AGGG CCAAGTTC TAAGAGGAC		
			C AC		
GAM2620	KIAA1348	3'	CAGGAAAATCACTTGAACCCGG 69120	A	CA C
	GA		TCCC GGTTCAAG ATT TCCTG		
			AGGG CCAAGTTC TAA AGGAC		
			C AC A		
GAM2620	KIAA1364	3'	CAGGAGAATCACTTGAACCTGG 64344		CA
	GA		TCCCAGGTTCAAG ATTCTCCTG		
			AGGGTCCAAGTTC TAAGAGGAC		
			AC		
GAM2620	KIAA1364	3'	CATGAGAATTGCTTGAACCTGG 64345		C
	GA		TCCCAGGTTCAAGCAATTCTC TG		
			AGGGTCCAAGTTCGTTAAGAG AC		
			T		
GAM2620	KIAA1377	3'	CAGGAGGATTACTTCAACCTGG 67755	C C	
	GA		TCCCAGGTT AAG AATTCTCCTG		
			AGGGTCCAA TTC TTAGGAGGAC		
			C A		
GAM2620	KIAA1456	3'	CAGAAGGATCACTTGAACCCAG 67538	CA	CA C
	GA		TCC GGTTCAAG ATTCT CTG		
			AGG CCAAGTTC TAGGA GAC		
			AC AC A		
GAM2620	KIAA1456	3'	CAGGAGAATCGCTTGAACCTGG 67539		A
	GA		TCCCAGGTTCAAGC ATTCTCCTG		
			AGGGTCCAAGTTCG TAAGAGGAC		
			C		
GAM2620	KIAA1473	3'	CAGGAGAATCACTTGAACCCGG 71205	A	CA
	GA		TCCC GGTTCAAG ATTCTCCTG		
			AGGG CCAAGTTC TAAGAGGAC		
			C AC		
GAM2620	KIAA1486	3'	CAGGAGAATGTGGTGAACCTGG 67971		A_ A
	GA		TCCCAGGTTCA GCA TTCTCCTG		
			AGGGTCCAAGT TGT AAGAGGAC		
			GG _		
GAM2620	KIAA1508	3'	GATAATTGCTTGAACCTGGGA 62551		C
			TCCCAGGTTCAAGCAATT TC		
			AGGGTTCAGTTCGTTAA AG		
			T		
GAM2620	KIAA1559	3'	CAGGAGAATCACTTGAATCCAG 73450	CA	CA
	GA		TCC GGTTCAAG ATTCTCCTG		

			AGG CTAAGTTC TAAGAGGAC		
			AC AC		
GAM2620	KIAA1586	5'	CATGAGAATTGCTTGAACCCGG 93935	A	C
	GA		TCCC GGTTCAAGCAATTCTC TG		
			AGGG CCAAGTTCGTTAAGAG AC		
			C T		
GAM2620	KIAA1594	3'	GAGAATCACTTGAACCCAGGA 72553	CA	CA
			TCC GGTTCAAG ATTCTC		
			AGG CCAAGTTC TAAGAG		
			AC AC		
GAM2620	KIAA1614	3'	CAGGAGAATTGCTTGAACCCGG 70663	A	
	GA		TCCC GGTTCAAGCAATTCTCCTG		
			AGGG CCAAGTTCGTTAAGAGGAC		
			C		
GAM2620	KIAA1630	3'	GAGAATCGCTTGAATCTGGGA 38654		A
			TCCCAGGTTCAAGC ATTCTC		
			AGGGTCTAAGTTCG TAAGAG		
			C		
GAM2620	KIAA1641	3'	GGGAGAATCACTTGAACCCGGG 81020	A	CA
	A		TCCC GGTTCAAG ATTCTCCT		
			AGGG CCAAGTTC TAAGAGGG		
			C AC		
GAM2620	KIAA1649	3'	CAGGAGAATCACTTGAACCCGG 67515	A	CA
	GA		TCCC GGTTCAAG ATTCTCCTG		
			AGGG CCAAGTTC TAAGAGGAC		
			C AC		
GAM2620	KIAA1649	5'	CAGGAGAACTGCTTGAGCCTAG 51221	C	A
	GA		TCC AGGTTCAAGCA TTCTCCTG		
			AGG TCCGAGTTCGT AAGAGGAC		
			A C		
GAM2620	KIAA1656	5'	CAGGAGAATCACTTGAACCCAG 66361	CA	CA
	GA		TCC GGTTCAAG ATTCTCCTG		
			AGG CCAAGTTC TAAGAGGAC		
			AC AC		
GAM2620	KIAA1674	3'	AGAACTCAAATCTGGGA 69327	CA	CAA
			TCCCAGGTT AG TTCT		
			AGGGTCTAA TC AAGA		
			AC ____		
GAM2620	KIAA1715	3'	CAGGAGAATTGCTTGAACACGG 68683	AG	
	GA		TCCC GTTCAAGCAATTCTCCTG		

			AGGG CAAGTTCGTTAAGAGGAC		
			CA		
GAM2620	KIAA1724	3'	CAGGAGAATCACTTGAACCTGG 67609	CA	
	GA		TCCCAGGTTCAAG ATTCTCCTG		
			AGGGTCCAAGTTC TAAGAGGAC		
			AC		
GAM2620	KIAA1724	3'	CAGGTGGATTGCTTGAGCCCAG 67610	CA	T
	GA		TCC GGTTC AAGCAATTC CCTG		
			AGG CCGAGTTCGTTAGG GGAC		
			AC T		
GAM2620	KIAA1735	3'	CAGGAAGACTGCTTGAGCCCAG 89000	CA	A TC
	GA		TCC GGTTC AAGCA T TCCTG		
			AGG CCGAGTTCGT A AGGAC		
			AC C GA		
GAM2620	KIAA1751	3'	GAGAATTGCTTGAACCCGGA 72157	A	
			TCCC GGTTC AAGCAATTCTC		
			AGGG CCAAGTTCGTTAAGAG		
			C		
GAM2620	KIAA1829	3'	CAGGAGAATCACTTGAACCTGG 62634	CA	
	GA		TCCCAGGTTCAAG ATTCTCCTG		
			AGGGTCCAAGTTC TAAGAGGAC		
			AC		
GAM2620	KIAA1841	3'	AGAATTGTTTGAACCCGGG 80844	A	
			CCC GGTTC AAGCAATTCT		
			GGG CCAAGTTTGTTAAGA		
			C		
GAM2620	KIAA1870	3'	AGATCGCTTGAGCCCAGGA 50576	CA	AAT
			TCC GGTTC AAGC TCT		
			AGG CCGAGTTCG AGA		
			AC CT_		
GAM2620	KIAA1871	3'	CAGGAGAATCACTTGAACCTGG 61897	CA	
	GA		TCCCAGGTTCAAG ATTCTCCTG		
			AGGGTCCAAGTTC TAAGAGGAC		
			AC		
GAM2620	KIAA1872	3'	CAGGAGAACTGCTTGAACCCAG 63603	CA	A
	GA		TCC GGTTC AAGCA TTCTCCTG		
			AGG CCAAGTTCGT AAGAGGAC		
			AC C		
GAM2620	KIAA1941	3'	CAGGAGAATCACTTGAACCTGG 75336	CA	
	GA		TCCCAGGTTCAAG ATTCTCCTG		

		AGGGTCCAAGTTC TAAGAGGAC		
		AC		
GAM2620	KIAA1948	5' CAGGAGAATCGCTTGAACCCAG 83297	CA	A
	GA	TCC GGTTC AAGC ATTCTCCTG		
		AGG CCAAGTTCG TAAGAGGAC		
		AC C		
GAM2620	KIAA1948	3' CAGGAGAATGGCTTGAACCCGG 83298	A	A
	GA	TCCC GGTTC AAGC ATTCTCCTG		
		AGGG CCAAGTTCG TAAGAGGAC		
		C G		
GAM2620	KIAA1951	3' CAGGAGAATGGCGTGAACCCGG 74149	A	A A
	GA	TCCC GGTTC A GC ATTCTCCTG		
		AGGG CCAAGT CG TAAGAGGAC		
		C G G		
GAM2620	KIAA1954	3' CAGATAGACTGCTTGAACCCAG 78222	CA	AT C_
	GA	TCC GGTTC AAGCA TCT CTG		
		AGG CCAAGTTCGT AGA GAC		
		AC C_ TA		
GAM2620	KIAA1958	3' CAGGAGAATTGCTTGAACCTGG 82780		
	GA	TCCCAGGTTCAAGCAATTCTCCTG		
		AGGGTCCAAGTTCGTTAAGAGGAC		
GAM2620	KIAA1969	3' CAGGATAATCACTTGAACCTGG 79475	CA	C
	GA	TCCCAGGTTCAAG ATT TCCTG		
		AGGGTCCAAGTTC TAA AGGAC		
		AC T		
GAM2620	KIAA1979	3' CAGGGGAATCTCTTGAACCCAG 89649	CA	CA
	GA	TCC GGTTC AAG ATTCTCCTG		
		AGG CCAAGTTC TAAGGGGAC		
		AC TC		
GAM2620	KLHL8	3' CAGGAGAATTGCTTGAACCCAG 63507	CA	
	GA	TCC GGTTC AAGCAATTCTCCTG		
		AGG CCAAGTTCGTTAAGAGGAC		
		AC		
GAM2620	KR18	3' CAGGAGAATTGCTTGAGTCCAG 53884	CA	GT
	GA	TCC G TCAAGCAATTCTCCTG		
		AGG C AGTTCGTTAAGAGGAC		
		AC TG		
GAM2620	KR18	3' CAGGAGAGTGCTTGAACCCAGG 53885	CA	A
	A	TCC GGTTC AAGCA TTCTCCTG		

			AGG CCAAGTTCGT GAGAGGAC		
			AC _		
GAM2620	KREMEN	3'	AGAATTGCTTGAACCTGGGA 50225		
			TCCCAGGTTCAAGCAATTCT		
			AGGGTCCAAGTTCGTTAAGA		
GAM2620	LANO	3'	GAGAATGCCTGAACCCGGGA 47972	A	A
			TCCC GGTTCA GCAATTCTC		
			AGGG CCAAGT CGTTAAGAG		
			C C		
GAM2620	LAP1B	3'	CAGGAGAATTGCTTGAACCCGG 65188	A	
	GA		TCCC GGTTCAAGCAATTCTCCTG		
			AGGG CCAAGTTCGTTAAGAGGAC		
			C		
GAM2620	LIAS	3'	CAGGAGAATCACTTGAACCTGG 71164		CA
	GA		TCCCAGGTTCAAG ATTCTCCTG		
			AGGGTCCAAGTTC TAAGAGGAC		
			AC		
GAM2620	LIAS	3'	GAATCACTTGAACCTGGGA 71165		CA
			TCCCAGGTTCAAG ATTC		
			AGGGTCCAAGTTC TAAG		
			AC		
GAM2620	LIM	3'	CAGGAAAATTCTTGAACCCAGG 22320	CA	C C
	A		TCC GGTTCAAG AATT TCCTG		
			AGG CCAAGTTC TTAA AGGAC		
			AC _ A		
GAM2620	LIM	3'	GAATCACTTGAACCCGGGA 22326	A	CA
			TCCC GGTTCAAG ATTC		
			AGGG CCAAGTTC TAAG		
			C AC		
GAM2620	LIM	3'	GAGAATCACTTGAACCCGGGA 22327	A	CA
			TCCC GGTTCAAG ATTCTC		
			AGGG CCAAGTTC TAAGAG		
			C AC		
GAM2620	LRG	3'	CAGGAGAATGGCGTGAACCTTG 54815		A A
	GA		TCCCAGGTTCA GC ATTCTCCTG		
			AGGGTTCAAGT CG TAAGAGGAC		
			G G		
GAM2620	LRRFIP1	3'	CAGGAGAATCGCTTGAACCTGC 17609	C	A
	GA		TC CAGGTTCAAGC ATTCTCCTG		

			AG GTCCAAGTTCG TAAGAGGAC		
			C C		
GAM2620	LSR68	3'	CAGGAGAATTCTTTTAACC 38552	C C	
			GGTT AAG AATTCTCCTG		
			CCAA TTT TTAAGAGGAC		
			T C		
GAM2620	MACF1	3'	CAGGAGAATAGCTTGAACCTGG 53426		A
			CCAGGTTCAAGC ATTCTCCTG		
			GGTCCAAGTTCG TAAGAGGAC		
			A		
GAM2620	MADHIP	5'	AGAAGCTTACAACCTGGGA 17814	C_	AA
			TCCCAGGTT AAGC TTCT		
			AGGGTCCAA TTCG AAGA		
			CA _		
GAM2620	MAWBP	3'	CAGGAGGATCACTTGAACCTAG 42379	C	CA
	GA		TCC AGGTTCAAG ATTCTCCTG		
			AGG TCCAAGTTC TAGGAGGAC		
			A AC		
GAM2620	MAWBP	3'	GGAGAATCGCTTGAACCCAGGA 42386	CA	A
			TCC GGTTCAAGC ATTCTCC		
			AGG CCAAGTTCG TAAGAGG		
			AC C		
GAM2620	MCAM	3'	CAGGAGAATGGTATGAATCCAG 22458	CA	A A
	GA		TCC GGTTCA GC ATTCTCCTG		
			AGG CTAAGT TG TAAGAGGAC		
			AC A G		
GAM2620	MESDC2	3'	CAGGAGAATGGCTTGAACCCGG 72910	A	A
	GA		TCCC GGTTCAAGC ATTCTCCTG		
			AGGG CCAAGTTCG TAAGAGGAC		
			C G		
GAM2620	METL	3'	AGAATTCAGACTTGAACCT 37839	C_	
			AGGTTCAAG AATTCT		
			TCCAAGTTC TTAAGA		
			AGAC		
GAM2620	MGC10200	3'	CAGGAGAATTGCTTGAACCTGG 59637		
	GA		TCCCAGGTTCAAGCAATTCTCCTG		
			AGGGTCCAAGTTCGTTAAGAGGAC		
GAM2620	MGC10765	3'	GAGAATCACTTGAACCCGGGA 44562	A	CA
			TCCC GGTTCAAG ATTCTC		

			AGGG CCAAGTTC TAAGAG		
			C AC		
GAM2620	MGC10771	3'	CAGGAGAATTGCTTGAATCCAG 44712	CA	
		GA	TCC GGTTC AAGCAATTCTCCTG		
			AGG CTAAGTTCGTTAAGAGGAC		
			AC		
GAM2620	MGC10814	3'	CAGGAGAATTGCTTGAACCCGG 52015	A	
		GA	TCCC GGTTC AAGCAATTCTCCTG		
			AGGG CCAAGTTCGTTAAGAGGAC		
			C		
GAM2620	MGC10814	5'	GGGAGAATCGCTTGAACCCGGG 52020	A	A
		A	TCCC GGTTC AAGC ATTCTCCT		
			AGGG CCAAGTTCG TAAGAGGG		
			C C		
GAM2620	MGC10999	3'	GAGAATCGCTTGAACCTCAGA 51195	CCA	A
			TC GGTTC AAGC ATTCTC		
			AG TCAAGTTCG TAAGAG		
			AC_ C		
GAM2620	MGC11386	3'	AGGAGAATTGCTTGAACCTGGG 53055		
		A	TCCCAGGTTCAAGCAATTCTCCT		
			AGGGTCCAAGTTCGTTAAGAGGA		
GAM2620	MGC13017	3'	CAGAAGAACTGCTTGAACCTGG 55571	A	C
		GA	TCCCAGGTTCAAGCA TTCT CTG		
			AGGGTCCAAGTTCGT AAGA GAC		
			C A		
GAM2620	MGC13053	3'	CAGGGGAATCACTTGAACCCGG 52102	A	CA
		GG	TCCC GGTTC AAG ATTCTCCTG		
			GGGG CCAAGTTC TAAGGGGAC		
			C AC		
GAM2620	MGC13198	5'	CAGGAGAATTGCTTGAACCTGG 52069		
		GA	TCCCAGGTTCAAGCAATTCTCCTG		
			AGGGTCCAAGTTCGTTAAGAGGAC		
GAM2620	MGC14126	3'	CAGGAGATTCGCTTGAACCTGG 52937	AAT	
		GA	TCCCAGGTTCAAGC TCTCCTG		
			AGGGTCCAAGTTCG AGAGGAC		
			CTT		
GAM2620	MGC14141	3'	CAGATGGCTGCTGCCCAACCT 53040	CA__	AT TC
		GGGA	TCCCAGGTT AGCA TC CTG		

			AGGGTCCAA	TCGT GG GAC		
			CCCCG	C_ TA		
GAM2620	MGC14407	3'	CAGGAGACTCTCTTGAACCCAG	52971	CA	CAAT
	GA		TCC GGTTC AAG	TCTCCTG		
			AGG CCAAGTTC	AGAGGAC		
			AC	TCTC		
GAM2620	MGC14436	3'	CAGGAGAATGGCGTGAGCCCGG	52923	A	A A
	GA		TCCC GGTTC A GC	ATTCTCCTG		
			AGGG CCGAGT CG	TAAGAGGAC		
			C	G G		
GAM2620	MGC14799	3'	CAGGAGAATCGCTTGAACCTGG	51325		A
	GA		TCCCAGGTTCAAGC	ATTCTCCTG		
			AGGGTCCAAGTTCG	TAAGAGGAC		
			C			
GAM2620	MGC15397	3'	CAGGAGAATTGCTTGAACCAAG	55552	CA	
	G		CC GGTTC AAGCAATTCTCCTG			
			GG CCAAGTTCGTTAAGAGGAC			
			AA			
GAM2620	MGC16037	3'	CAGGAGAATCGCTTGAACCCCGG	52891	A	A
	GA		TCCC GGTTC AAGC	ATTCTCCTG		
			AGGG CCAAGTTCG	TAAGAGGAC		
			C	C		
GAM2620	MGC16142	3'	CATGAGAATTACTTGAACCCAG	52262	CA	C C
	GA		TCC GGTTC AAG AATTCTC	TG		
			AGG CCAAGTTC	TTAAGAG AC		
			AC	A T		
GAM2620	MGC16175	3'	CAGGAGAATGACATGAACCTGG	52275		AGCA
	GA		TCCCAGGTTCA	ATTCTCCTG		
			AGGGTCCAAGT	TAAGAGGAC		
			ACAG			
GAM2620	MGC16385	3'	CAGGAGAATTGCTTGAACCTGG	59534		
	GA		TCCCAGGTTCAAGCAATTCTCCTG			
			AGGGTCCAAGTTCGTTAAGAGGAC			
GAM2620	MGC16703	3'	CAGGAGGATGGCGTGAACCCCGG	73489	A	A A
	GA		TCCC GGTTC A GC	ATTCTCCTG		
			AGGG CCAAGT CG	TAGGAGGAC		
			C	G G		
GAM2620	MGC23244	3'	AGCCTGGCTTGAACCTGGGA	58825		AATT
			TCCCAGGTTCAAGC	CT		

			AGGGTCCAAGTTCG	GA			
			GTCC				
GAM2620	MGC2562	3'	CAGGAGAATAGCATGAACCCGG	51431	A	A	A
			CC GGTTC	GC ATTCTCCTG			
			GG CCAAGT	CG TAAGAGGAC			
			C	A A			
GAM2620	MGC2663	3'	AGTGAATCACTTGAACCCAGGA	44329	CA	CA	TC
			TCC GGTTC	AAG ATTCTCCTG			
			AGG CCAAGTTC	TAAG GA			
			AC	AC T_			
GAM2620	MGC26641	3'	GAAAATCGCTGGAACCTGGGA	59322	A	A	C
			TCCCAGGTTTC	AGC ATTCTCCTG			
			AGGGTCCAAG	TCG TAA AG			
			G	C A			
GAM2620	MGC2731	3'	CAGGAGAATCTCTTGAAACCGG	44161	A	_	CA
	GA		TCCC GGTTC	CAAG ATTCTCCTG			
			AGGG CCAA	GTTC TAAGAGGAC			
			_	A TC			
GAM2620	MGC29891	3'	CAGGAGAATCGCTTGAACCCGG	58851	A	A	
	GA		TCCC GGTTC	AAGC ATTCTCCTG			
			AGGG CCAAGTTCG	TAAGAGGAC			
			C	C			
GAM2620	MGC29891	3'	CAGGAGAATTGCTTGAACCTGG	58852			
	GA		TCCCAGGTTCAAGCAATTCTCCTG				
			AGGGTCCAAGTTCGTTAAGAGGAC				
GAM2620	MGC29937	3'	CAGGAGAATCACTTGAACCTGG	58727		CA	
	GG		TCCCAGGTTCAAG	ATTCTCCTG			
			GGGGTCCAAGTTC	TAAGAGGAC			
			AC				
GAM2620	MGC3169	3'	CAGGAGAATCACATGAATCCAG	44183	CA	AGCA	
	GA		TCC GGTTC	ATTCTCCTG			
			AGG CTAAGT	TAAGAGGAC			
			AC	ACAC			
GAM2620	MGC3207	3'	CAGGAGAATGGCGTGAACTGG	63234	G	A	A
	GA		TCCCAG	TTCA GC ATTCTCCTG			
			AGGGTC	AAGT CG TAAGAGGAC			
			A	G G			
GAM2620	MGC3329	3'	CAGGAGACTCGCTTGAACCTGG	44241		AAT	
	GA		TCCCAGGTTCAAGC	TCTCCTG			

			AGGGTCCAAGTTCG AGAGGAC		
			CTC		
GAM2620	MGC4248	3'	CAGGAGAATCACTTGAACCTGG 51310	CA	
	GA		TCCCAGGTTCAAG ATTCTCCTG		
			AGGGTCCAAGTTC TAAGAGGAC		
			AC		
GAM2620	MGC4562	3'	CAGGAGAATTGCCTGAACCCAG 56736	CA	A
	GA		TCC GGTTC A GCAATTCTCCTG		
			AGG CCAAGT CGTTAAGAGGAC		
			AC C		
GAM2620	MGC4663	3'	CAGGAGAATGGCGTGAACCCGG 44784	A	A A
	GA		TCCC GGTTC A GC ATTCTCCTG		
			AGGG CCAAGT CG TAAGAGGAC		
			C G G		
GAM2620	MGC4771	3'	CAGGAGAATCGCTTGAATCCGG 52001	A	A
	GA		TCCC GGTTC AAGC ATTCTCCTG		
			AGGG CTAAGTTCG TAAGAGGAC		
			C C		
GAM2620	MGC4840	3'	AGAATTGCCTGAACCCAGGA 72015	CA	A
			TCC GGTTC A GCAATTCT		
			AGG CCAAGT CGTTAAGA		
			AC C		
GAM2620	MGC5384	3'	CAGGAGAATGGCATGAACCTGT 49088	C	A A
	GA		TC CAGGTTCA GC ATTCTCCTG		
			AG GTCCAAGT CG TAAGAGGAC		
			T A G		
GAM2620	MGC5457	3'	CAGGAGAATGGCTTGAACC 51937	A	
			GGTTCAAGC ATTCTCCTG		
			CCAAGTTCG TAAGAGGAC		
			G		
GAM2620	MOST2	5'	CAGGAGAATCACTTGTACCTGG 40058	T	CA
	GA		TCCCAGGT CAAG ATTCTCCTG		
			AGGGTCCA GTTC TAAGAGGAC		
			T AC		
GAM2620	MRPL56	3'	CAGGAGAATCGCTTGAACCCAG 52753	CA	A
	GA		TCC GGTTC AAGC ATTCTCCTG		
			AGG CCAAGTTCG TAAGAGGAC		
			AC C		
GAM2620	MRPS10	3'	CAGGAGAATCGCGTGAACCCGG 36815	A	A A
	G		CCC GGTTC A GC ATTCTCCTG		

			GGG CCAAGT CG TAAGAGGAC		
			C G C		
GAM2620	My015	3'	CAGGAGAATCGCTTGAACC 67230	A	
			GGTTCAAGC ATTCTCCTG		
			CCAAGTTCG TAAGAGGAC		
			C		
GAM2620	N4BP2	3'	CAGGAGAACCGCTTAAACCTGG 36935	C	AA
	GA		TCCCAGGTT AAGC TTCTCCTG		
			AGGGTCCAA TTCG AAGAGGAC		
			A CC		
GAM2620	NMNAT	3'	CAGGAGAATCACTTGACCCAG 43281	CA	T CA
	G		CC GG TCAAG ATTCTCCTG		
			GG CC AGTTC TAAGAGGAC		
			AC C AC		
GAM2620	NMNAT	3'	CAGGAGAATCGCTTGAACCCGG 43282	A	A
	GA		TCCC GGTTCAAGC ATTCTCCTG		
			AGGG CCAAGTTCG TAAGAGGAC		
			C C		
GAM2620	NMNAT	3'	CAGGAGAATCGCTTGAACCTGG 43283		A
	GA		TCCCAGGTTCAAGC ATTCTCCTG		
			AGGGTCCAAGTTCG TAAGAGGAC		
			C		
GAM2620	NMT2	3'	CAGGAGAATCGCTTGAACCTGA 17855	C	A
	GA		TC CAGGTTCAAGC ATTCTCCTG		
			AG GTCCAAGTTCG TAAGAGGAC		
			A C		
GAM2620	Nup43	3'	CAGGAGAATTGCTCAAACCCGG 45344	A	CA
	GA		TCCC GGTT AGCAATTCTCCTG		
			AGGG CCAA TCGTTAAGAGGAC		
			C AC		
GAM2620	OBTP	3'	AGGAGAACCGACCTG GGG 34662		CAAGCAA
			TCCCAGGTT TTCTCCT		
			GGGGTCCAG AAGAGGA		
			CC_____		
GAM2620	PAFAH2	3'	CAGAAGAATCACTTGAACCTAG 6498	C	CA C
	GA		TCC AGGTTCAAG ATTCT CTG		
			AGG TCCAAGTTC TAAGA GAC		
			A AC A		
GAM2620	PB1	3'	CAGGAGAATCGCTTGAACCCAG 36871	CA	A
	GA		TCC GGTTCAAGC ATTCTCCTG		

			AGG CCAAGTTCG TAAGAGGAC		
			AC C		
GAM2620	PB1	3'	CAGGAGAATGGCGTGAACCTGG 36872	A A	
	GA		TCCCAGGTTCA GC ATTCTCCTG		
			AGGGTCCAAGT CG TAAGAGGAC		
			G G		
GAM2620	phorbolin-1	3'	CAGGAGAGTAGCGTGAACCCGG 90206	A A A	
	GA		TCCC GGTTCA GC ATTCTCCTG		
			AGGG CCAAGT CG TGAGAGGAC		
			C G A		
GAM2620	PIP3-E	3'	CAGGAGAAATTGAATCCT 67347 _ GCAA		
			AGG TTCAA TTCTCCTG		
			TCC AAGTT AAGAGGAC		
			T A__		
GAM2620	PIWIL2	3'	CAGGAGAATCGCTTGAACCCGG 36541	A A	
	GA		TCCC GGTTCAAGC ATTCTCCTG		
			AGGG CCAAGTTCG TAAGAGGAC		
			C C		
GAM2620	POFUT1	3'	CAGGAGAATGGCTTGAACCTGG 70973	A	
	GA		TCCCAGGTTCAAGC ATTCTCCTG		
			AGGGTCCAAGTTCG TAAGAGGAC		
			G		
GAM2620	POLYDOM	3'	CAGGAGAATCGCTTGAACCCAG 44686	CA A	
	GA		TCC GGTTCAAGC ATTCTCCTG		
			AGG CCAAGTTCG TAAGAGGAC		
			AC C		
GAM2620	PPP1R3B	3'	CAGGAGAATCACTTGAACCCAG 45132	CA CA	
	GA		TCC GGTTCAAG ATTCTCCTG		
			AGG CCAAGTTC TAAGAGGAC		
			AC AC		
GAM2620	PPP1R3B	3'	CAGGAGAATGGCGGGAACCTGG 45133	AA A	
	GA		TCCCAGGTTC GC ATTCTCCTG		
			AGGGTCCAAG CG TAAGAGGAC		
			GG G		
GAM2620	PRIC285	3'	CAGGAGAATCGCTTGAAGTCCAG 62111	A T_ A	
	G		CC GG TCAAGC ATTCTCCTG		
			GG CC AGTTCG TAAGAGGAC		
			A TC C		
GAM2620	PRO0255	3'	CAGGAGAATCGCTTGAGCCTGG 26966	A	
	GA		TCCCAGGTTCAAGC ATTCTCCTG		

			AGGGTCCGAGTTCG TAAGAGGAC		
			C		
GAM2620	PRO0478	3'	AGAATTGCTTGAACCAGGGA 27015	A	
			TCCC GGTTC AAGCAATTCT		
			AGGG CCAAGTTCGTTAAGA		
			A		
GAM2620	PRO0478	5'	CAGGAGAATCGCTTGAGCCCAG 27026	CA	A
	GA		TCC GGTTC AAGC ATTCTCCTG		
			AGG CCGAGTTCG TAAGAGGAC		
			AC C		
GAM2620	PRO0478	3'	CAGGAGAATGATGTGAACCCGG 27027	A	AGCA
	GA		TCCC GGTTC A ATTCTCCTG		
			AGGG CCAAGT TAAGAGGAC		
			C GTAG		
GAM2620	PRO0618	3'	CAGGAGAATCGCTTGAAACCCGG 27048	A	A
	GA		TCCC GGTTC AAGC ATTCTCCTG		
			AGGG CCAAGTTCG TAAGAGGAC		
			C C		
GAM2620	PRO1048	3'	CAGGAGAATGGTGTGAACCCGG 38104	A	A A
	GA		TCCC GGTTC A GC ATTCTCCTG		
			AGGG CCAAGT TG TAAGAGGAC		
			C G G		
GAM2620	PRO1777	3'	CAGGAGGCTCACTTGAGCCCAG 38372	CA	CAAT
	GA		TCC GGTTC AAG TCTCCTG		
			AGG CCGAGTTC GGAGGAC		
			AC ACTC		
GAM2620	PRO2015	3'	CAGGAGAATCGCTTGAAACCCGG 38158	A	A
	GA		TCCC GGTTC AAGC ATTCTCCTG		
			AGGG CCAAGTTCG TAAGAGGAC		
			C C		
GAM2620	PRO2198	5'	CAGGAGAATCACATCAACCTGG 38406		CAAGCA
	GA		TCCCAGGTT ATTCTCCTG		
			AGGGTCCAA TAAGAGGAC		
			CTACAC		
GAM2620	PRO2730	3'	CAGGAGAATTGCTTGAAACCCAG 48180	CA	
	GA		TCC GGTTC AAGCAATTCTCCTG		
			AGG CCAAGTTCGTTAAGAGGAC		
			AC		
GAM2620	PRO2859	3'	CAGGAGAATCACTTGAAGTCAG 38208	CA	CA
	GA		TCC GGTTC AAG ATTCTCCTG		

			AGG TCAAGTTC TAAGAGGAC		
			AC AC		
GAM2620	PRO2893	3'	CAGGGGAATTGCTTGAACCCGG 38430	A	
	GA		TCCC GGTTCAAGCAATTCTCCTG		
			AGGG CCAAGTTCGTTAAGGGGAC		
			C		
GAM2620	PRO2964	3'	CAGGAGAATGGCGTGAACCCGG 38254	A	A A
	GA		TCCC GGTTCA GC ATTCTCCTG		
			AGGG CCAAGT CG TAAGAGGAC		
			C G G		
GAM2620	PSR	3'	CAGGAGAATCACTTGAACCCAG 65778	CA	CA
	GA		TCC GGTTCAAG ATTCTCCTG		
			AGG CCAAGTTC TAAGAGGAC		
			AC AC		
GAM2620	PTK6	3'	GAGGGCCTGGACCTGGGA 21078	A	AAT
			TCCCAGGTTCA GC TCTC		
			AGGGTCCAGGT CG GGAG		
			C		
GAM2620	PTRF	3'	GGGAGAATTGCTTGAACCTGGG 64243		
	A		TCCCAGGTTCAAGCAATTCTCCT		
			AGGGTCCAAGTTCGTTAAGAGGG		
GAM2620	RAB4B	5'	CAGGAGAATTGCTTGAACCTGG 32901		
	GA		TCCCAGGTTCAAGCAATTCTCCTG		
			AGGGTCCAAGTTCGTTAAGAGGAC		
GAM2620	Rabip4R	3'	CAGGAGAATCGCTTGAACCCGG 36275	A	A
	GA		TCCC GGTTCAAGC ATTCTCCTG		
			AGGG CCAAGTTCG TAAGAGGAC		
			C C		
GAM2620	RAD51	3'	GGGAGAATCACTTAAGCCTGG 12747	C	CA
			CCAGGTT AAG ATTCTCCT		
			GGTCCGA TTC TAAGAGGG		
			A AC		
GAM2620	RFX4	3'	GGGAGAATTGCTTGAGCCCAGG 12856	CA	
	A		TCC GGTTCAAGCAATTCTCCT		
			AGG CCGAGTTCGTTAAGAGGG		
			AC		
GAM2620	RHOBTB3	3'	CAGGAAAATCGCTTGAACCTGG 30424	A	C
	GA		TCCCAGGTTCAAGC ATT TCCTG		

		AGGGTCCAAGTTCG TAA AGGAC			
		C A			
GAM2620	RNO2	5'	CGGGAGAATCGCTTGAACCCGG 53933	A	A
	GA		TCCC GGTTCAAGC ATTCTCCTG		
		AGGG CCAAGTTCG TAAGAGGGC			
		C C			
GAM2620	RoXaN	3'	CAGGAGAATCACTTGAACCCAG 47278	CA	CA
	GA		TCC GGTTCAAG ATTCTCCTG		
		AGG CCAAGTTC TAAGAGGAC			
		AC AC			
GAM2620	RoXaN	3'	CAGGAGAATGGCATGAACCCAG 47279	CA	A A
	GA		TCC GGTTCA GC ATTCTCCTG		
		AGG CCAAGT CG TAAGAGGAC			
		AC A G			
GAM2620	Rpo1-2	3'	GATTGCTTGAACCCAGGA 39222	CA	
			TCC GGTTCAAGCAATT		
		AGG CCAAGTTCGTTAG			
		AC			
GAM2620	RRP4	3'	GGGAGAATCACTTGAACCTGGG 27359		CA
	A		TCCCAGGTTCAAG ATTCTCCT		
		AGGGTCCAAGTTC TAAGAGGG			
		AC			
GAM2620	SAMHD1	3'	CAGGAGAATCGCTTGAATCCGG 61978	A	A
	GA		TCCC GGTTCAAGC ATTCTCCTG		
		AGGG CTAAGTTCG TAAGAGGAC			
		C C			
GAM2620	SAMHD1	3'	CAGGAGGATTGCTCGAACCTGG 61979		A
	GA		TCCCAGGTTT AGCAATTCTCCTG		
		AGGGTCCAAG TCGTTAGGAGGAC			
		C			
GAM2620	SC65	3'	CAGGAGAATCGCTTGAACCTGG 22291		A
	GA		TCCCAGGTTCAAGC ATTCTCCTG		
		AGGGTCCAAGTTCG TAAGAGGAC			
		C			
GAM2620	SC65	3'	CAGGAGAATCGCCTGAACCCAG 22290	CA	A A
	GA		TCC GGTTCA GC ATTCTCCTG		
		AGG CCAAGT CG TAAGAGGAC			
		AC C C			
GAM2620	SCAND2	3'	CAGGAGAATCACTTGAGCCCAG 54417	CA	CA
	GA		TCC GGTTCAAG ATTCTCCTG		

			AGG CCGAGTTC TAAGAGGAC		
			AC AC		
GAM2620	SCIN	3'	CAGGAAAATTGCTTGAACCCAG 53600	CA	C
	GA		TCC GGTTC AAGCAATT TCCTG		
			AGG CCAAGTTCGTTAA AGGAC		
			AC A		
GAM2620	SCN12A	3'	CAGGAGAATCGCTTAAACCTGG 27079	C A	
	GA		TCCCAGGTT AAGC ATTCTCCTG		
			AGGGTCCAA TTCG TAAGAGGAC		
			A C		
GAM2620	SCYA5	3'	CAGGAAAATTGTTTGAACCCAG 12963	CA	C
	GA		TCC GGTTC AAGCAATT TCCTG		
			AGG CCAAGTTTGTAA AGGAC		
			AC A		
GAM2620	SCYA5	3'	CAGGAGAATGGCGTGAACCCGG 12964	A A A	
	GA		TCCC GGTTC A GC ATTCTCCTG		
			AGGG CCAAGT CG TAAGAGGAC		
			C G G		
GAM2620	SEMA3E	3'	CAGGAGAATGGCGTGAACCCGG 25804	A A A	
	GA		TCCC GGTTC A GC ATTCTCCTG		
			AGGG CCAAGT CG TAAGAGGAC		
			C G G		
GAM2620	SGKL	3'	CAGGAGAATCGCTTGAACCCGG 26055	A A	
	GA		TCCC GGTTC AAGC ATTCTCCTG		
			AGGG CCAAGTTCG TAAGAGGAC		
			C C		
GAM2620	SLC7A11	3'	CAGGAGAATTGCTTGAACCCGG 27529	A	
	GA		TCCC GGTTC AAGCAATTCTCCTG		
			AGGG CCAAGTTCGTTAAGAGGAC		
			C		
GAM2620	SMA3	3'	CAGGAAGAATTGCTTGAACCTG 23258		—
	GGA		TCCCAGGTTCAAGCAATTCT CCTG		
			AGGGTCCAAGTTCGTTAAGA GGAC		
			A		
GAM2620	SMAP-5	3'	CAGGAGAAAAGTGTGAACCCAG 48657	CA A AA	
	GA		TCC GGTTC A GC TTCTCCTG		
			AGG CCAAGT TG AAGAGGAC		
			AC G AA		
GAM2620	SPRY4	3'	CAGAAGAATCACTTGAACCCGG 49000	A CA C	
	GA		TCCC GGTTC AAG ATTCT CTG		

			AGGG CCAAGTTC TAAGA GAC		
			C AC A		
GAM2620	SPRY4	3'	CAGGAGAATCTCGAACCCAGGA 49002	CA	A CA
			TCC GGTTT AG ATTCTCCTG		
			AGG CCAAG TC TAAGAGGAC		
			AC C _		
GAM2620	SPTLC2	3'	CAGGAGAATCGCTTGAACCCAG 17982	CA	A
	GA		TCC GGTTCAAGC ATTCTCCTG		
			AGG CCAAGTTCG TAAGAGGAC		
			AC C		
GAM2620	SPTLC2	3'	GGGAGAATCACTTGAGCCTGGG 17998		CA
	A		TCCCAGGTTCAAG ATTCTCCT		
			AGGGTCCGAGTTC TAAGAGGG		
			AC		
GAM2620	SS18L1	3'	CAGGAGAATGGCTTGAACCCAG 65950	CA	A
	GA		TCC GGTTCAAGC ATTCTCCTG		
			AGG CCAAGTTCG TAAGAGGAC		
			AC G		
GAM2620	SSR3	3'	CAGGAGAACTGCCTGAACCCAG 24030	CA	A A
	GA		TCC GGTTCA GCA TTCTCCTG		
			AGG CCAAGT CGT AAGAGGAC		
			AC C C		
GAM2620	TA-LRRP	3'	CAGGGGAATTGCTTGAACCAGG 31710		A
	GA		TCCC GGTTCAAGCAATTCTCCTG		
			AGGG CCAAGTTCGTTAAGGGGAC		
			A		
GAM2620	TADA3L	3'	CAGGAGAATCAGTTGAACCTGG 22036		GCA
	GA		TCCCAGGTTCAA ATTCTCCTG		
			AGGGTCCAAGTT TAAGAGGAC		
			GAC		
GAM2620	THEA	3'	CAGGAGAATTGGTTGAACCCAG 66880	CA	G
	GA		TCC GGTTCAA CAATTCTCCTG		
			AGG CCAAGTT GTTAAGAGGAC		
			AC G		
GAM2620	TIP47	3'	GAGAATCTCTTGAACCTGAGA 20602	C	CA
			TC CAGGTTCAAG ATTCTC		
			AG GTCCAAGTTC TAAGAG		
			A TC		
GAM2620	TMG4	3'	CAGGAGAATTGCTCGAACCTGG 44212		A
	GA		TCCCAGGTTT AGCAATTCTCCTG		

			AGGGTCCAAG TCGTTAAGAGGAC		
			C		
GAM2620	TRIAD3	3'	CAGGAGAATCACTTGAACCTGG 96132	CA	
	GA		TCCCAGGTTCAAG ATTCTCCTG		
			AGGGTCCAAGTTC TAAGAGGAC		
			AC		
GAM2620	TRIM5	3'	AGAAAACTGCTTGGATCCTGGG 53461	—	A__
			CCCAGG TTCAAGCA TTCT		
			GGGTCC AGGTTCGT AAGA		
			T CAA		
GAM2620	VIT1	5'	CAGGAGAATTGCTTGAACCCGG 38602	A	
			CC GGTTC AAGCAATTCTCCTG		
			GG CCAAGTTCGTTAAGAGGAC		
			C		
GAM2620	VPS4B	3'	CGGGAGAATCACTTGAACCTGG 18021	CA	
	GA		TCCCAGGTTCAAG ATTCTCCTG		
			AGGGTCCAAGTTC TAAGAGGGC		
			AC		
GAM2620	WBSCR21	3'	CAGGAGAATCACTTGAACCCTG 49298	—	CA
	G		CCAGG TTCAAG ATTCTCCTG		
			GGTCC AAGTTC TAAGAGGAC		
			C AC		
GAM2620	WBSCR23	3'	AGGAGAATCCCTTGAACCCGGG 47414	A	CA
	A		TCCC GGTTC AAG ATTCTCCT		
			AGGG CCAAGTTC TAAGAGGA		
			C CC		
GAM2620	WBSCR23	3'	CAGAAGAATCGCTTGAACCCTG 47426	—	A C
	G		CCAGG TTCAAGC ATTCT CTG		
			GGTCC AAGTTCG TAAGA GAC		
			C C A		
GAM2620	WSB1	3'	CAGGAGAATTGCTTGAACCCAG 56967	CA	
	GA		TCC GGTTC AAGCAATTCTCCTG		
			AGG CCAAGTTCGTTAAGAGGAC		
			AC		
GAM2620	WSB1	3'	CAGGAGAATTGCTTGAACCCAG 56968	CA	
	GA		TCC GGTTC AAGCAATTCTCCTG		
			AGG CCAAGTTCGTTAAGAGGAC		
			AC		
GAM2620	YME1L1	3'	CAGGAGAATTGCTTGAGCCTGG 58428		
	GA		TCCCAGGTTCAAGCAATTCTCCTG		

AGGGTCCGAGTTCGTTAAGAGGAC

GAM2620 YME1L1 3' GAGAATTGCTTGAACCCAGGA 58433 CA
TCC GGTTCAAGCAATTCTC
||| |||||
AGG CCAAGTTCGTTAAGAG
AC

GAM2620 ZAK 3' CAGGAGAATCACTTGAACCCGG 34100 A CA
GA TCCC GGTTCAAG ATTCTCCTG
||| ||||| |||||
AGGG CCAAGTTC TAAGAGGAC
C AC

GAM2620 ZFD25 3' CAGGAGAATTGCTCAAACCTGG 33108 CA
GA TCCCAGGTT AGCAATTCTCCTG
||||| |||||
AGGGTCCAA TCGTTAAGAGGAC
AC

GAM2620 ZFP106 3' CAGGAGAATCACTTGAACCCTG 42718 _ CA
G CCAGG TTCAAG ATTCTCCTG
||||| |||||
GGTCC AAGTTC TAAGAGGAC
C AC

GAM2620 ZFP106 3' CAGGAGAATCGCTTGAACCCGG 42719 A A
GA TCCC GGTTCAAGC ATTCTCCTG
||| ||||| |||||
AGGG CCAAGTTCG TAAGAGGAC
C C

GAM2620 ZIM3 3' CAGGAGAATTGCTTGAACCTGG 54636
GA TCCCAGGTTCAAGCAATTCTCCTG
|||||
AGGGTCCAAGTTCGTTAAGAGGAC

GAM2620 ZNF197 3' CAGGAGAGTCGCTTGAACCTGG 23753 A
GA TCCCAGGTTCAAGC ATTCTCCTG
|||||
AGGGTCCAAGTTCG TGAGAGGAC
C

GAM2620 ZNF271 3' CATGAGAATCACTTGAACCTGG 96960 CA C
GA TCCCAGGTTCAAG ATTCTC TG
||||| |||||
AGGGTCCAAGTTC TAAGAG AC
AC T

GAM2620 ZNF297B 3' CAGGAGAATCACTTGAACCTGG 26650 CA
GA TCCCAGGTTCAAG ATTCTCCTG
|||||
AGGGTCCAAGTTC TAAGAGGAC
AC

GAM2620 ZNF297B 5' CAGGAGAATCGCTCGAAACC 26651 _ A A
GGTT C AGC ATTCTCCTG
||| | |||

			CCAA G TCG TAAGAGGAC		
			A C C		
GAM2620	ZNF317	3'	AGAATCCACGGAACCTTGGA 72471	AAGCA	
			TCCCAGGTTC ATTCT		
			AGGGTTCAAG TAAGA		
			GCACC		
GAM2620	ZNF333	3'	CAGGAGAATTCTTTGAACCCAG 51588	CA	C
			TCC GGTTC AAG AATTCTCCTG		
			AGG CCAAGTTT TTAAGAGGAC		
			AC C		
GAM2620	ZNF33A	3'	CAGAAGAATCACTTGAACCTGG 92992	CA	C
			TCCCAGGTTC AAG ATTCT CTG		
			AGGGTCCAAGTTC TAAGA GAC		
			AC A		
GAM2620	ZNF347	3'	CAGGAGAATCACTTGAACCCAG 51821	CA	CA
			TCC GGTTC AAG ATTCTCCTG		
			AGG CCAAGTTC TAAGAGGAC		
			AC AC		
GAM2620	LOC112687	3'	CAGGAGAATTGCTTGAACCCAG 73224	CA	
			TCC GGTTC AAGCAATTCTCCTG		
			AGG CCAAGTTCGTTAAGAGGAC		
			AC		
GAM2620	LOC113523	3'	CAGGAGAATAGCTTGAACCTGT 73416	C	A
			TC CAGGTTC AAGC ATTCTCCTG		
			AG GTCCAAGTTCG TAAGAGGAC		
			T A		
GAM2620	LOC114987	3'	CGGGAGAATCGCTTGAACCCAG 59796	CA	A
			TCC GGTTC AAGC ATTCTCCTG		
			AGG CCAAGTTCG TAAGAGGGC		
			AC C		
GAM2620	LOC115129	3'	CAGGAGAATCACTTGAACCCAG 73609	CA	CA
			TCC GGTTC AAG ATTCTCCTG		
			AGG CCAAGTTC TAAGAGGAC		
			AC AC		
GAM2620	LOC115129	5'	CAGGAGAATCATCTGAACCCAG 73610	CA	AGCA
			TCC GGTTC A ATTCTCCTG		
			AGG CCAAGT TAAGAGGAC		
			AC CTAC		
GAM2620	LOC115129	5'	CAGGAGATTTGCTTGAACCTGG 73611		T
			TCCCAGGTTC AAGCAA TCTCCTG		

		AGGGTCCAAGTTCGTT AGAGGAC			
		T			
GAM2620	LOC115129 3'	GATTGCTTGAGCCCAGGA 73619	CA		
		TCC GGTTCAAGCAATT			
		AGG CCGAGTTCGTTAG			
		AC			
GAM2620	LOC115196 3'	CAGGAGAATGGTGTGAACCCGG 73652	A	A	A
	GA	TCCC GGTTCA GC ATTCTCCTG			
		AGGG CCAAGT TG TAAGAGGAC			
		C G G			
GAM2620	LOC115273 3'	CAGGAGAATTGCTTGAACCTGG 73749			
	GA	TCCCAGGTTCAAGCAATTCTCCTG			
		AGGGTCCAAGTTCGTTAAGAGGAC			
GAM2620	LOC115761 3'	CAGGAGAATCGCTTGAGCC 93396	A		
		GGTTCAAGC ATTCTCCTG			
		CCGAGTTCG TAAGAGGAC			
		C			
GAM2620	LOC116143 3'	CAGGAGAATCACTTGAACCCAG 74179	CA	CA	
	GA	TCC GGTTCAAG ATTCTCCTG			
		AGG CCAAGTTC TAAGAGGAC			
		AC AC			
GAM2620	LOC116143 3'	CAGGAGAATGGCGTGAACCCGG 74180	A	A	A
	GA	TCCC GGTTCA GC ATTCTCCTG			
		AGGG CCAAGT CG TAAGAGGAC			
		C G G			
GAM2620	LOC116228 3'	CAGGAGAATCACTTGAACCCGA 74226	CA_	CA	
	GG	CC GGTTCAAG ATTCTCCTG			
		GG CCAAGTTC TAAGAGGAC			
		AGC AC			
GAM2620	LOC116236 3'	CAGGAGAATGGCGTGAACCCGG 74240	A	A	A
	GA	TCCC GGTTCA GC ATTCTCCTG			
		AGGG CCAAGT CG TAAGAGGAC			
		C G G			
GAM2620	LOC116349 3'	CAGGAGAATGGCGTGAACCCGG 74272	A	A	A
	GA	TCCC GGTTCA GC ATTCTCCTG			
		AGGG CCAAGT CG TAAGAGGAC			
		C G G			
GAM2620	LOC119504 5'	CAGGAGAATCGCTTAAATCCGG 74442	A	C	A
	GA	TCCC GGTT AAGC ATTCTCCTG			

		AGGG CTAA TTCG TAAGAGGAC		
		C A C		
GAM2620	LOC120526 3'	AGAATCACTTGAACCCAGGA 74462	CA	CA
		TCC GGTTCAAG ATTCT		
		AGG CCAAGTTC TAAGA		
		AC AC		
GAM2620	LOC122704 3'	CAGGAGAATCGCTTAAACTCGG 74602	AG	C A
	GA	TCCC GTT AAGC ATTCTCCTG		
		AGGG CAA TTCG TAAGAGGAC		
		CT A C		
GAM2620	LOC122970 3'	GATTGCTTGAGCCCGGGA 74642	A	
		TCCC GGTTCAAGCAATT		
		AGGG CCGAGTTCGTTAG		
		C		
GAM2620	LOC126282 3'	CAGGAAGATTGCTTGAACCTCAG 74946	CCA	TC
	A	TC GGTTCAAGCAAT TCCTG		
		AG TCAAGTTCGTTA AGGAC		
		AC_ GA		
GAM2620	LOC126282 3'	CAGGAGAATCGCTTGAACCTGG 74947		A
	GA	TCCCAGGTTCAAGC ATTCTCCTG		
		AGGGTCCAAGTTCG TAAGAGGAC		
		C		
GAM2620	LOC126282 3'	CAGGATAATCACTTGAACCAGG 74949	A	CA C
		CC GGTTCAAG ATT TCCTG		
		GG CCAAGTTC TAA AGGAC		
		A AC T		
GAM2620	LOC126669 3'	GAGAATCACTTGAGCCCAGGA 75934	CA	CA
		TCC GGTTCAAG ATTCTC		
		AGG CCGAGTTC TAAGAG		
		AC AC		
GAM2620	LOC127262 3'	CAGGAGGATCGCTTGAGCCCAG 76594	CA	A
	GA	TCC GGTTCAAGC ATTCTCCTG		
		AGG CCGAGTTCG TAGGAGGAC		
		AC C		
GAM2620	LOC127428 3'	GAATCGCTTGAACCTGGGA 75159		A
		TCCCAGGTTCAAGC ATTC		
		AGGGTCCAAGTTCG TAAG		
		C		
GAM2620	LOC130026 3'	CAGGAGAATGGCGTGAACCCGG 57434	A	A A
	GA	TCCC GGTTCA GC ATTCTCCTG		

		AGGG CCAAGT CG TAAGAGGAC		
		C G G		
GAM2620	LOC130162 3'	CAGGAGGATCGCTTGAGCCCAG 75418	CA	A
	GA	TCC GGTTC AAGC ATTCTCCTG		
		AGG CCGAGTTCG TAGGAGGAC		
		AC C		
GAM2620	LOC130535 3'	AATGGCTTGAACCCGGGA 76633	A	A
		TCCC GGTTC AAGC ATT		
		AGGG CCAAGTTCG TAA		
		C G		
GAM2620	LOC130535 3'	AGGAGAATCGCTTGAACCCAGG 76639	CA	A
	A	TCC GGTTC AAGC ATTCTCCT		
		AGG CCAAGTTCG TAAGAGGA		
		AC C		
GAM2620	LOC130535 3'	CAGGAGGATTGCCTGAGCCCAG 76646	CA	A
	GA	TCC GGTTC A GCAATTCTCCTG		
		AGG CCGAGT CGTTAGGAGGAC		
		AC C		
GAM2620	LOC130589 3'	CAGGAGAATCGCTTGAACCTGG 57929		A
	GA	TCCCAGGTTCAAGC ATTCTCCTG		
		AGGGTCCAAGTTCG TAAGAGGAC		
		C		
GAM2620	LOC132625 3'	CAGGAGGATAGCTTGAGCCCAG 76437	CA	A
	GA	TCC GGTTC AAGC ATTCTCCTG		
		AGG CCGAGTTCG TAGGAGGAC		
		AC A		
GAM2620	LOC133926 3'	CAGGAGAATGGCGTGAACCCAG 75629	CA	A A
	GA	TCC GGTTC A GC ATTCTCCTG		
		AGG CCAAGT CG TAAGAGGAC		
		AC G G		
GAM2620	LOC134265 3'	CAGGAGGACCGCTTGAGCCCAG 75656	CA	AA
	GA	TCC GGTTC AAGC TTCTCCTG		
		AGG CCGAGTTCG AGGAGGAC		
		AC CC		
GAM2620	LOC135154 3'	CAGGAGAATGGCTTAAACCCAG 75724	CA	C A
	GA	TCC GGT T AAGC ATTCTCCTG		
		AGG CCAA TTCG TAAGAGGAC		
		AC A G		
GAM2620	LOC137362 3'	CAGGAGAATCGCTTGAACCTGG 75782		A
	GA	TCCCAGGTTCAAGC ATTCTCCTG		

		AGGGTCCAAGTTCG TAAGAGGAC			
		C			
GAM2620	LOC138389 3'	CAGAAGAATGGCTTGAACCCTG 76727	—	A	C
	G	CCAGG TTCAAGC ATTCT CTG			
		GGTCC AAGTTCG TAAGA GAC			
		C G A			
GAM2620	LOC138428 3'	CAGGAGAATCACTTGAACCTGG 75855		CA	
	GA	TCCCAGGTTCAAG ATTCTCCTG			
		AGGGTCCAAGTTC TAAGAGGAC			
		AC			
GAM2620	LOC139422 3'	CAGGAGAATGGCGTAAACCCGG 76343	A	CAA	A
	GA	TCCC GGTT GC ATTCTCCTG			
		AGGG CCAA CG TAAGAGGAC			
		C ATG G			
GAM2620	LOC139770 3'	CAGAAGAATAGCTTGAGCCCAG 75903	CA	A	C
	GA	TCC GGTTCAAGC ATTCT CTG			
		AGG CCGAGTTCG TAAGA GAC			
		AC A A			
GAM2620	LOC142779 3'	CAGGAGAATCGCTTGAACCAGG 76903	A	A	
	GA	TCCC GGTTCAAGC ATTCTCCTG			
		AGGG CCAAGTTCG TAAGAGGAC			
		A C			
GAM2620	LOC143196 3'	CAGGAGAATAGCTTGAACCAGG 83801	A	A	
	GA	TCCC GGTTCAAGC ATTCTCCTG			
		AGGG CCAAGTTCG TAAGAGGAC			
		A A			
GAM2620	LOC143310 3'	CAGGAGAATGGCGAGAACCCGG 77037	A	AA	A
	GA	TCCC GGTT GC ATTCTCCTG			
		AGGG CCAAG CG TAAGAGGAC			
		C AG G			
GAM2620	LOC143465 3'	CATGAGAATTGCTTGAACCCAG 83869	CA		C
	GA	TCC GGTTCAAGCAATTCTC TG			
		AGG CCAAGTTCGTTAAGAG AC			
		AC T			
GAM2620	LOC143888 3'	CAGGAGAATCACTTGAACCTGG 77168		CA	
	GA	TCCCAGGTTCAAG ATTCTCCTG			
		AGGGTCCAAGTTC TAAGAGGAC			
		AC			
GAM2620	LOC143943 3'	CAGGAGAATGGCGTGAACCTGG 83916	A	A	
	GA	TCCCAGGTTCA GC ATTCTCCTG			

		AGGGTCCAAGT CG TAAGAGGAC		
		G G		
GAM2620	LOC144289 3'	CAGGAGAATCATTTGAACCCGG 83953	A	CA
	GA	TCCC GGTTCAAG ATTCTCCTG		
		AGGG CCAAGTTT TAAGAGGAC		
		C AC		
GAM2620	LOC144465 3'	CAGGAGAATCACTTGAACCTGG 77343		CA
	GA	TCCCAGGTTCAAG ATTCTCCTG		
		AGGGTCCAAGTTC TAAGAGGAC		
		AC		
GAM2620	LOC144465 3'	CAGGAGAATCACTTGAACCTGG 77344		CA
	GA	TCCCAGGTTCAAG ATTCTCCTG		
		AGGGTCCAAGTTC TAAGAGGAC		
		AC		
GAM2620	LOC144481 3'	CAGGAAGATGGCTTGAGCCCAG 84013	CA	A TC
	GA	TCC GGTTCAAGC AT TCCTG		
		AGG CCGAGTTCG TA AGGAC		
		AC G GA		
GAM2620	LOC144481 3'	CAGGAGAATCACTTGAACCCAG 84014	CA	CA
	GA	TCC GGTTCAAG ATTCTCCTG		
		AGG CCAAGTTC TAAGAGGAC		
		AC AC		
GAM2620	LOC144524 3'	CAGGAGAACTGCTTGAACCCAG 84050	CA	A
	GA	TCC GGTTCAAGCA TTCTCCTG		
		AGG CCAAGTTCGT AAGAGGAC		
		AC C		
GAM2620	LOC144524 3'	GAACTGCTTGAACCCAGGA 84055	CA	A
		TCC GGTTCAAGCA TTC		
		AGG CCAAGTTCGT AAG		
		AC C		
GAM2620	LOC144563 3'	GAGAATCACTTGAGCCCAGGA 77397	CA	CA
		TCC GGTTCAAG ATTCTC		
		AGG CCGAGTTC TAAGAG		
		AC AC		
GAM2620	LOC144817 3'	CAGGAGAATCCCTTGAACCCAG 77509	CA	CA
	GA	TCC GGTTCAAG ATTCTCCTG		
		AGG CCAAGTTC TAAGAGGAC		
		AC CC		
GAM2620	LOC144845 3'	CAGGAAAATCACTTGAACCCGG 57455	A	CA C
	GA	TCCC GGTTCAAG ATT TCCTG		

		AGGG CCAAGTTC TAA AGGAC		
		C AC A		
GAM2620	LOC145082 3'	CAGAAAGGATTGCTTGGACCCAG 84182	CA	C
	GA	TCC GGTTC AAGCAATTCT CTG		
		AGG CCAGGTTCTGTTAGGA GAC		
		AC A		
GAM2620	LOC145216 3'	CAGGAGAATCACTTGAACCCGG 84218	A	CA
		CC GGTTC AAG ATTCTCCTG		
		GG CCAAGTTC TAAGAGGAC		
		C AC		
GAM2620	LOC145231 3'	CAGGAGAATTGCTTGAACCCGG 84244	A	
	GA	TCCC GGTTC AAGCAATTCTCCTG		
		AGGG CCAAGTTCGTTAAGAGGAC		
		C		
GAM2620	LOC145231 3'	CAGGCGAATTACTTCAACCTGG 84245	C C T	
	GA	TCCCAGGTT AAG AATTC CCTG		
		AGGGTCCAA TTC TTAAG GGAC		
		C A C		
GAM2620	LOC145299 3'	CAGGAGAATGGCGTGAACCCGG 84273	A	A A
	GA	TCCC GGTTC A GC ATTCTCCTG		
		AGGG CCAAGT CG TAAGAGGAC		
		C G G		
GAM2620	LOC145333 3'	CAGGAGAATGGCGTGAACCTGG 84292	A A	
	GA	TCCCAGGTTCA GC ATTCTCCTG		
		AGGGTCCAAGT CG TAAGAGGAC		
		G G		
GAM2620	LOC145387 3'	CAGGAGAATTGCTTGAACCTGG 84331		
	GA	TCCCAGGTTCAAGCAATTCTCCTG		
		AGGGTCCAAGTTCGTTAAGAGGAC		
GAM2620	LOC145438 3'	CAGGAGAATGGCGTGAACCCGG 84310	A	A A
	GA	TCCC GGTTC A GC ATTCTCCTG		
		AGGG CCAAGT CG TAAGAGGAC		
		C G G		
GAM2620	LOC145453 3'	GAGAATCGCTTGAACCTGGGA 77662	A	
		TCCCAGGTTCAAGC ATTCTC		
		AGGGTCCAAGTTCG TAAGAG		
		C		
GAM2620	LOC145482 3'	GAATCATTTGAACCTGGGA 77743	CA	
		TCCCAGGTTCAAG ATTC		

		AGGGTCCAAGTTT TAAG		
		AC		
GAM2620	LOC145483 3'	CAGGAGAATCACTTGAACC 77753	CA	
		GGTTCAAG ATTCTCCTG		
		CCAAGTTC TAAGAGGAC		
		AC		
GAM2620	LOC145608 5'	CAGGAGAACGGCGTGAACCCGG 84378	A	A AA
	GA	TCCC GGTTCA GC TTCTCCTG		
		AGGG CCAAGT CG AAGAGGAC		
		C G GC		
GAM2620	LOC145609 3'	CAGGAGAACGGCGTGAACCCGG 84363	A	A AA
	GA	TCCC GGTTCA GC TTCTCCTG		
		AGGG CCAAGT CG AAGAGGAC		
		C G GC		
GAM2620	LOC145662 3'	AGAATCACTTGAACCAGG 77832	A	CA
		CC GGTTCAAG ATTCT		
		GG CCAAGTTC TAAGA		
		A AC		
GAM2620	LOC145663 3'	CAGGAGAATGGCGTGAACCCGG 84418	A	A A
	GA	TCCC GGTTCA GC ATTCTCCTG		
		AGGG CCAAGT CG TAAGAGGAC		
		C G G		
GAM2620	LOC145757 3'	CAGGAGAATCGCTGGAACCCAG 77920	CA	A A
	GA	TCC GGTTCA AGC ATTCTCCTG		
		AGG CCAAG TCG TAAGAGGAC		
		AC G C		
GAM2620	LOC145820 3'	CAGGAGAATGGGGAGAACCCGG 77974	A	AAGCA
	GA	TCCC GGTTCA ATTCTCCTG		
		AGGG CCAAG TAAGAGGAC		
		C AGGGG		
GAM2620	LOC146059 3'	CAGGAGACCTGCTTGAACCTGG 78085		AT
		CCAGGTTCAAGCA TCTCCTG		
		GGTCCAAGTTCGT AGAGGAC		
		CC		
GAM2620	LOC146159 3'	CAGGAGGATCACTTGAACCCAG 78172	CA	CA
	GA	TCC GGTTCAAG ATTCTCCTG		
		AGG CCAAGTTC TAGGAGGAC		
		AC AC		
GAM2620	LOC146229 3'	GAGAATTGCTTGAACCCGG 78280	A	
		CC GGTTCAAGCAATTCTC		

		GG CCAAGTTCGTTAAGAG		
		C		
GAM2620	LOC146512 3'	GAGGATCACTTGAGCCCAGGA 78500	CA	CA
		TCC GGTTCAAG ATTCTC		
		AGG CCGAGTTC TAGGAG		
		AC AC		
GAM2620	LOC146540 3'	GAGGATCACTTGAGCCTGGGA 78527		CA
		TCCCAGGTTCAAG ATTCTC		
		AGGGTCCGAGTTC TAGGAG		
		AC		
GAM2620	LOC146713 3'	CAGGAGAATCACTTGAACCCGG 84724	A	CA
	GA	TCCC GGTTCAAG ATTCTCCTG		
		AGGG CCAAGTTC TAAGAGGAC		
		C AC		
GAM2620	LOC146713 3'	GAGAATCACTTGAACCCGGGA 84730	A	CA
		TCCC GGTTCAAG ATTCTC		
		AGGG CCAAGTTC TAAGAG		
		C AC		
GAM2620	LOC146723 3'	CAGGAGAATCGCCTGAACCTGG 78675	A	A
	GA	TCCCAGGTTCA GC ATTCTCCTG		
		AGGGTCCAAGT CG TAAGAGGAC		
		C C		
GAM2620	LOC146728 3'	CAGGAGGATCGCTTGAGCCCAG 84762	CA	A
	GA	TCC GGTTCAAGC ATTCTCCTG		
		AGG CCGAGTTTC TAGGAGGAC		
		AC C		
GAM2620	LOC146728 5'	GAGAATCATTTGAACCTGGGA 84766		CA
		TCCCAGGTTCAAG ATTCTC		
		AGGGTCCAAGTTT TAAGAG		
		AC		
GAM2620	LOC146756 3'	CAGGAGAATGGTGTGAACCCGG 84796	A	A A
	GA	TCCC GGTTCA GC ATTCTCCTG		
		AGGG CCAAGT TG TAAGAGGAC		
		C G G		
GAM2620	LOC146780 5'	GAGGATCGCTTGAGCCCAGGA 84820	CA	A
		TCC GGTTCAAGC ATTCTC		
		AGG CCGAGTTTC TAGGAG		
		AC C		
GAM2620	LOC146895 3'	CAGGAGAATTGCTTGAACCTGG 84863		
	GA	TCCCAGGTTCAAGCAATTCTCCTG		

AGGGTCCAAGTTCGTTAAGAGGAC

GAM2620	LOC146923	3'	CAGGAGAATGGCGTGAACCCAG	78797	CA	A A
	GA		TCC GGTTC	GC ATTCTCCTG		
			AGG CCAAGT	CG TAAGAGGAC		
			AC	G G		
GAM2620	LOC147057	3'	CAGGAGAATCGCTTGAACCCAG	84975	CA	A
	GA		TCC GGTTC	AAGC ATTCTCCTG		
			AGG CCAAGTTCG	TAAGAGGAC		
			AC	C		
GAM2620	LOC147071	3'	CAGGAGAATGGCATGAACCTGG	73355		A A
	GA		TCCCAGGTTCA	GC ATTCTCCTG		
			AGGGTCCAAGT	CG TAAGAGGAC		
			A	G		
GAM2620	LOC147080	3'	AGAATTGCTTGAACCCGGGA	85022	A	
			TCCC GGTTC	AAGCAATTCT		
			AGGG CCAAGTTCGTTAAGA			
			C			
GAM2620	LOC147180	5'	CAGGAGAATCGCTTGAATCCAG	85096	CA	A
	GA		TCC GGTTC	AAGC ATTCTCCTG		
			AGG CTAAGTTCG	TAAGAGGAC		
			AC	C		
GAM2620	LOC147599	3'	CAGAAGTATTGCTTGAACCCAG	85160	CA	T C
	GA		TCC GGTTC	AAGCAAT CT CTG		
			AGG CCAAGTTCGTTA	GA GAC		
			AC	T A		
GAM2620	LOC147649	3'	CAGGAGAATGGCGTGAACCCGG	79055	A	A A
	GA		TCCC GGTTC	GC ATTCTCCTG		
			AGGG CCAAGT	CG TAAGAGGAC		
			C	G G		
GAM2620	LOC147664	3'	CAGGAGAATCGCTTGAACCCGG	79044	A	A
	GA		TCCC GGTTC	AAGC ATTCTCCTG		
			AGGG CCAAGTTCG	TAAGAGGAC		
			C	C		
GAM2620	LOC147700	3'	CAGGAGAATGGCTTGAACCCAG	59878	CA	A
	GA		TCC GGTTC	AAGC ATTCTCCTG		
			AGG CCAAGTTCG	TAAGAGGAC		
			AC	G		
GAM2620	LOC147727	5'	CAGGAGAATTGTTTGACCTGG	79131	T	
			CCAGGT CAAGCAATTCTCCTG			

GGTCCA GTTTGTTAAGAGGAC

GAM2620 LOC147727 5' CAGGAGGATCGCTTGAACCCAG 79132 CA A
GA TCC GGTCAAGC ATTCTCCTG

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AGG CCAAGTTCG TAGGAGGAC
AC C

GAM2620 LOC147727 5' GAATCACTTGAACCTGGGA 79136 CA
TCCCAGGTTCAAG ATTCTCCTG

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AGGGTCCAAGTTC TAAG
AC

GAM2620 LOC147837 3' CAGGATAATCACTTGAATCCGG 79203 A CA C
GA TCCC GGTTCAAG ATT TCCTG

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AGGG CTAAGTTC TAA AGGAC
C AC T

GAM2620 LOC147990 3' AGAATCACTTGAACCTCGGGA 85209 AG CA
TCCC GTTCAAG ATTCTCCTG

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AGGG CAAGTTC TAAGA
CT AC

GAM2620 LOC148137 3' GAGAATTGCTTGAACCTCAGA 59098 CCA
TC GGTTCAAGCAATTCTC

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AG TCAAGTTCGTTAAGAG
AC_

GAM2620 LOC148147 3' CAGGAGAATGGCGTGAACCTGG 79392 A A
GA TCCCAGGTTCA GC ATTCTCCTG

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AGGGTCCAAGT CG TAAGAGGAC
G G

GAM2620 LOC148166 3' CGGGAGAATCGCTTGAACCTGG 79413 A
GA TCCCAGGTTCAAGC ATTCTCCTG

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AGGGTCCAAGTTCG TAAGAGGGC
C

GAM2620 LOC148198 3' CAGGAGAATCACTTGAACCCAG 71220 CA CA
GA TCC GGTCAAG ATTCTCCTG

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AGG CCAAGTTC TAAGAGGAC
AC AC

GAM2620 LOC148206 3' CAGGAGAATCATTTGAACCTGG 79461 CA
GA TCCCAGGTTCAAG ATTCTCCTG

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AGGGTCCAAGTTT TAAGAGGAC
AC

GAM2620 LOC148254 3' CAGGAGAAGTGCTTGAACCTAG 79500 C A
GA TCC AGGTTCAAGCA TTCTCCTG

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		AGG TCCAAGTTCGT AAGAGGAC		
		A G		
GAM2620	LOC148397 3'	CAGGAGAATCACTTGAACCCGG 79562	A	CA
	GA	TCCC GGTTCAAG ATTCTCCTG		
		AGGG CCAAGTTC TAAGAGGAC		
		C AC		
GAM2620	LOC148534 3'	CAGGAGAATCGCTTGAACC 79632	A	
		GGTTCAAGC ATTCTCCTG		
		CCAAGTTCG TAAGAGGAC		
		C		
GAM2620	LOC148734 3'	CAGGAGAATGGCGTGAACCCGG 79709	A	A A
	GA	TCCC GGTTCA GC ATTCTCCTG		
		AGGG CCAAGT CG TAAGAGGAC		
		C G G		
GAM2620	LOC148758 5'	CAGGAGAATTGCTTGAACCCGG 79720	A	
	GA	TCCC GGTTCAAGCAATTCTCCTG		
		AGGG CCAAGTTCGTTAAGAGGAC		
		C		
GAM2620	LOC148809 5'	CAGGAGAATTGCTTGAACCCAG 79748	CA	
	GA	TCC GGTTCAAGCAATTCTCCTG		
		AGG CCAAGTTCGTTAAGAGGAC		
		AC		
GAM2620	LOC148918 5'	CAGGAGAATTGCTTGAACC 79820		
		GGTTCAAGCAATTCTCCTG		
		CCAAGTTCGTTAAGAGGAC		
GAM2620	LOC149113 5'	CAGGAGAATTGCTTGAACCCGG 79903	A	
	GA	TCCC GGTTCAAGCAATTCTCCTG		
		AGGG CCAAGTTCGTTAAGAGGAC		
		C		
GAM2620	LOC149175 3'	CAGGAGAATGGCGTGAACCCGG 79950	A	A A
	GA	TCCC GGTTCA GC ATTCTCCTG		
		AGGG CCAAGT CG TAAGAGGAC		
		C G G		
GAM2620	LOC149194 5'	CGGGAGAATCACTTGAACCCGG 79983	A	CA
	GA	TCCC GGTTCAAG ATTCTCCTG		
		AGGG CCAAGTTC TAAGAGGGC		
		C AC		
GAM2620	LOC149271 3'	CAGGAGAATCACTTGAACCCAG 79999	CA	CA
	GA	TCC GGTTCAAG ATTCTCCTG		

		AGG CCAAGTTC TAAGAGGAC		
		AC AC		
GAM2620	LOC149319 3'	CAGGAGAATCGCTAGAACCTGG 80068	A	A
	GG	TCCCAGGTTC AGC ATTCTCCTG		
		GGGGTCCAAG TCG TAAGAGGAC		
		A C		
GAM2620	LOC149460 3'	CAGGAGAATCGCTTGAACCTCG 85607	AG	A
	GA	TCCC GTTCAAGC ATTCTCCTG		
		AGGG CAAGTTCG TAAGAGGAC		
		CT C		
GAM2620	LOC149464 3'	CAGGAGAATCACTTGAACCAGG 85587	A	CA
	GA	TCCC GGTTCAAG ATTCTCCTG		
		AGGG CCAAGTTC TAAGAGGAC		
		A AC		
GAM2620	LOC149579 5'	CAGGAGAATTGCTTGAACCTGG 71690		
	GA	TCCCAGGTTCAAGCAATTCTCCTG		
		AGGGTCCAAGTTCGTTAAGAGGAC		
GAM2620	LOC149628 3'	CAGGGGAATTGCTTGAACCAGG 80278	A	
	GA	TCCC GGTTCAAGCAATTCTCCTG		
		AGGG CCAAGTTCGTTAAGGGGAC		
		A		
GAM2620	LOC149705 3'	CAGGAGAATCACTTAAACCCAG 85774	CA	C CA
	G	CC GGTT AAG ATTCTCCTG		
		GG CCAA TTC TAAGAGGAC		
		AC A AC		
GAM2620	LOC149705 3'	CAGGAGAATCGCTTGAACCTGG 85775		A
	GA	TCCCAGGTTCAAGC ATTCTCCTG		
		AGGGTCCAAGTTCG TAAGAGGAC		
		C		
GAM2620	LOC149711 5'	GAGGATCACTTGAGCCCAGGA 85853	CA	CA
		TCC GGTTCAAG ATTCTC		
		AGG CCGAGTTC TAGGAG		
		AC AC		
GAM2620	LOC150095 3'	CAGGAGAATGGAGTGAACCCGG 85992	A	AGCA
	GA	TCCC GGTTCA ATTCTCCTG		
		AGGG CCAAGT TAAGAGGAC		
		C GAGG		
GAM2620	LOC150139 3'	CGGGAGAATCGCTTGAGCCCAG 80411	CA	A
	GA	TCC GGTTCAAGC ATTCTCCTG		

		AGG CCGAGTTCG TAAGAGGGC		
		AC C		
GAM2620	LOC150142 5'	CAGGAGGATCGCTTGAGCCCAG 80403	CA	A
	GA	TCC GGTTC AAGC ATTCTCCTG		
		AGG CCGAGTTCG TAGGAGGAC		
		AC C		
GAM2620	LOC150185 3'	CAGGAGAATTGCTTGAACCCAG 86065	CA	
	GA	TCC GGTTC AAGCAATTCTCCTG		
		AGG CCAAGTTCGTTAAGAGGAC		
		AC		
GAM2620	LOC150225 3'	CAGGTGGATTGCTTGAACCCAG 86185	CA	T
	GA	TCC GGTTC AAGCAATTC CCTG		
		AGG CCAAGTTCGTTAGG GGAC		
		AC T		
GAM2620	LOC150225 3'	GAGAATCGCTTGAACCCGGGA 86192	A	A
		TCCC GGTTC AAGC ATTCTC		
		AGGG CCAAGTTCG TAAGAG		
		C C		
GAM2620	LOC150245 3'	AGGATCGCTTGAGCCCAGGA 86107	CA	A
		TCC GGTTC AAGC ATTCT		
		AGG CCGAGTTCG TAGGA		
		AC C		
GAM2620	LOC150299 3'	CAGGAGAATCGCTGGAACCCAG 86162	CA	A A
	GA	TCC GGTTC AGC ATTCTCCTG		
		AGG CCAAG TCG TAAGAGGAC		
		AC G C		
GAM2620	LOC150319 3'	CAGGAGAACCGCTTGAACCCGG 80465	A	AA
	GA	TCCC GGTTC AAGC TTCTCCTG		
		AGGG CCAAGTTCG AAGAGGAC		
		C CC		
GAM2620	LOC150319 3'	GAACCGCTTGAACCCGGGA 80472	A	AA
		TCCC GGTTC AAGC TTC		
		AGGG CCAAGTTCG AAG		
		C CC		
GAM2620	LOC150358 3'	CAGGAGAATCGCTTGAACCTGG 86090		A
	GA	TCCCAGGTTCAAGC ATTCTCCTG		
		AGGGTCCAAGTTCG TAAGAGGAC		
		C		
GAM2620	LOC150372 3'	CAGGAGAATCTCTTGAACCTGG 80607		CA
	GA	TCCCAGGTTCAAG ATTCTCCTG		

		AGGGTCCAAGTTC TAAGAGGAC		
		TC		
GAM2620	LOC150481 3'	CGGGAGAACTGCTTGAACCTGG 80698	A	
	GA	TCCCAGGTTCAAGCA TTCTCCTG		
		AGGGTCCAAGTTCGT AAGAGGGC		
		C		
GAM2620	LOC150622 3'	CAGGAGAATCGCTTGAACCCAG 80756	CA	A
	GA	TCC GGTTC AAGC ATTCTCCTG		
		AGG CCAAGTTCG TAAGAGGAC		
		AC C		
GAM2620	LOC150630 3'	CAGGAGAATCGCTTGAACC 86294	A	
		GGTTC AAGC ATTCTCCTG		
		CCAAGTTCG TAAGAGGAC		
		C		
GAM2620	LOC150630 5'	CAGGAGGACTGCTTGAGCCCAG 86295	CA	A
	GA	TCC GGTTC AAGCA TTCTCCTG		
		AGG CCGAGTTCGT AGGAGGAC		
		AC C		
GAM2620	LOC150889 3'	GGGAGAATTTCTTGAACCCGGG 80815	A	C
	A	TCCC GGTTC AAG AATTCTCCT		
		AGGG CCAAGTTC TTAAGAGGG		
		C T		
GAM2620	LOC151196 3'	CAGGAGAATCACTTGAACCCAG 86450	CA	CA
	G	CC GGTTC AAG ATTCTCCTG		
		GG CCAAGTTC TAAGAGGAC		
		AC AC		
GAM2620	LOC151248 3'	CAGGAGAATGGCGTGAACCCGG 80988	A	A A
	GA	TCCC GGTTC A GC ATTCTCCTG		
		AGGG CCAAGT CG TAAGAGGAC		
		C G G		
GAM2620	LOC151248 3'	GAGAATCGCTTGAACCCAGGA 80994	CA	A
		TCC GGTTC AAGC ATTCTC		
		AGG CCAAGTTCG TAAGAG		
		AC C		
GAM2620	LOC151429 3'	CAGGAGAACCGCTGGAACCCGG 86525	A	A AA
	GA	TCCC GGTTC AGC TTCTCCTG		
		AGGG CCAAG TCG AAGAGGAC		
		C G CC		
GAM2620	LOC151429 3'	CAGGAGAATGGCGTGAACCCGG 86526	A	A A
	GA	TCCC GGTTC A GC ATTCTCCTG		

		AGGG CCAAGT CG TAAGAGGAC		
		C G G		
GAM2620	LOC151446 3'	AGAATCACTTGAACCCAGGA 86566	CA	CA
		TCC GGTTC AAG ATTCT		
		AGG CCAAGTTC TAAGA		
		AC AC		
GAM2620	LOC151446 3'	GAATCACTTGAACCCAGGA 86571	CA	CA
		TCC GGTTC AAG ATTCT		
		AGG CCAAGTTC TAAG		
		AC AC		
GAM2620	LOC151556 3'	CAGGAGAATCGCTTGAATCTGG 81077		A
	GA	TCCCAGGTTCAAGC ATTCTCCTG		
		AGGGTCTAAGTTCTG TAAGAGGAC		
		C		
GAM2620	LOC151602 3'	GAGAATTGCTTGAACCCGGGA 81112	A	
		TCCC GGTTC AAGCAATTCTC		
		AGGG CCAAGTTCGTTAAGAG		
		C		
GAM2620	LOC151632 3'	CAGGAGAATCACTTGAGCCCAG 86641	CA	CA
	GA	TCC GGTTC AAG ATTCTCCTG		
		AGG CCGAGTTC TAAGAGGAC		
		AC AC		
GAM2620	LOC151720 3'	CAGGAGAATGGCATGAACCCAG 81148	CA	A A
	GA	TCC GGTTC A GC ATTCTCCTG		
		AGG CCAAGT CG TAAGAGGAC		
		AC A G		
GAM2620	LOC151904 3'	AGAATCATTTGAACCCGGGA 81199	A	CA
		TCCC GGTTC AAG ATTCT		
		AGGG CCAAGTTT TAAGA		
		C AC		
GAM2620	LOC152002 3'	CAGGAGAACTGTCGGGACCAGG 81265	CA	AA A
	A	TCC GGTTC GCA TTCTCCTG		
		AGG CCAGG TGT AAGAGGAC		
		A_ GC C		
GAM2620	LOC152106 3'	CAGGAGGATCGCTTGAACCCAG 70591	CA	A
	GA	TCC GGTTC AAGC ATTCTCCTG		
		AGG CCAAGTTCTG TAGGAGGAC		
		AC C		
GAM2620	LOC152271 3'	CAGGAGAATCACTTGAGCCCAG 81354	CA	CA
	GA	TCC GGTTC AAG ATTCTCCTG		

		AGG CCGAGTTC TAAGAGGAC		
		AC AC		
GAM2620	LOC152271 5'	CAGGAGAATCCCTTGAACCTGG 81355	CA	
	GA	TCCCAGGTTCAAG ATTCTCCTG		
		AGGGTCCAAGTTC TAAGAGGAC		
		CC		
GAM2620	LOC152283 3'	CAGGAGAATTGCTTGAACCTGG 86868		
	GA	TCCCAGGTTCAAGCAATTCTCCTG		
		AGGGTCCAAGTTCGTTAAGAGGAC		
GAM2620	LOC152426 3'	CAGGAGAATGGTGTGAACCTGG 86891	A A	
	GA	TCCCAGGTTCA GC ATTCTCCTG		
		AGGGTTCAAGT TG TAAGAGGAC		
		G G		
GAM2620	LOC152441 3'	CAGGAGGATCGCCTGAGCCCAG 86916	CA A A	
	GA	TCC GGTTC A GC ATTCTCCTG		
		AGG CCGAGT CG TAGGAGGAC		
		AC C C		
GAM2620	LOC152445 3'	CAGGAGAATCGCTTGAACCCGG 86938	A A	
	GA	TCCC GGTTC AAGC ATTCTCCTG		
		AGGG CCAAGTTCG TAAGAGGAC		
		C C		
GAM2620	LOC152445 3'	CAGGAGACTCGCTTGAACCTGG 86939	AAT	
	GA	TCCCAGGTTCAAGC TCTCCTG		
		AGGGTCCAAGTTCG AGAGGAC		
		CTC		
GAM2620	LOC152453 3'	CAGGAGAATTGCTTGAACCCAG 81466	CA	
	GA	TCC GGTTC AAGCAATTCTCCTG		
		AGG CCAAGTTCGTTAAGAGGAC		
		AC		
GAM2620	LOC152627 3'	AGAATTGCTTGAACCTGGGA 81500		
		TCCCAGGTTCAAGCAATTCT		
		AGGGTCCAAGTTCGTTAAGA		
GAM2620	LOC152627 5'	CAGGAGAATTGCTGGAACGTGG 81506	G A	
		CCA GTTC AGCAATTCTCCTG		
		GGT CAAG TCGTTAAGAGGAC		
		G G		
GAM2620	LOC152804 3'	CAGGAGAATCACTTGAACCTCAG 87072	CA CA	
	GA	TCC GGTTC AAG ATTCTCCTG		

		AGG TCAAGTTC TAAGAGGAC		
		AC AC		
GAM2620	LOC152804 3'	CAGGAGAATGGCTTGAACCTGG 87073	A	
	GA	TCCCAGGTTCAAGC ATTCTCCTG		
		AGGGTCCAAGTTCG TAAGAGGAC		
		G		
GAM2620	LOC152860 3'	CAGGAGAATCCCTTGAACCTGA 81575	C	CA
	GA	TC CAGGTTCAAG ATTCTCCTG		
		AG GTCCAAGTTC TAAGAGGAC		
		A CC		
GAM2620	LOC153077 3'	CAGGAGAATGGCATGAACCTGG 87114	A A	
	GA	TCCCAGGTTCA GC ATTCTCCTG		
		AGGGTCCAAGT CG TAAGAGGAC		
		A G		
GAM2620	LOC153077 3'	GATTGCTTGAACCCAGGA 87128	CA	
		TCC GGTTCAAGCAATT		
		AGG CCAAGTTCGTTAG		
		AC		
GAM2620	LOC153146 3'	CAGGAGAATCCCTTGAACCTGG 87145	CA	
	GA	TCCCAGGTTCAAG ATTCTCCTG		
		AGGGTCCAAGTTC TAAGAGGAC		
		CC		
GAM2620	LOC153260 3'	CAGGAGAAATGCTTGAACCCAG 81669	CA	A
	GA	TCC GGTTCAAGCA TTCTCCTG		
		AGG CCAAGTTCGT AAGAGGAC		
		AC A		
GAM2620	LOC153579 3'	CAGGAGAAGGGCGTGAACCCGG 81766	A	A AA
	GA	TCCC GGTTCA GC TTCTCCTG		
		AGGG CCAAGT CG AAGAGGAC		
		C G GG		
GAM2620	LOC153642 3'	CAGGAGGATCGCTTGAACCCGG 81783	A	A
	GA	TCCC GGTTCAAGC ATTCTCCTG		
		AGGG CCAAGTTCG TAGGAGGAC		
		C C		
GAM2620	LOC153688 3'	CATGAGAATTGCTTTAACCCGG 87302	A C	C
		CC GGTT AAGCAATTCTC TG		
		GG CCAA TTCGTTAAGAG AC		
		C T T		
GAM2620	LOC153727 3'	CAGGAGAAGAATCCCTTGAACC 87360	_	CAA__
	TAGGG	CCC AGGTTCAAG TTCTCCTG		

		GGG TCCAAGTTC	AAGAGGAC		
		A	CCTAAG		
GAM2620	LOC154089 3'	CAGGTGGATCGCTTGAGCCCAG	81940	CA	A T
	GA	TCC GGTTC AAGC ATTC CCTG			
		AGG CCGAGTTCG TAGG GGAC			
		AC	C T		
GAM2620	LOC154403 5'	CAGGAGAATTGCTTGAACCCGG	81969	A	
	GA	TCCC GGTTCAAGCAATTCTCCTG			
		AGGG CCAAGTTCGTTAAGAGGAC			
		C			
GAM2620	LOC154739 5'	CAGGAGAATCACTTGAACC	87432	CA	
		GGTTCAAG ATTCTCCTG			
		CCAAGTTC TAAGAGGAC			
		AC			
GAM2620	LOC154791 3'	CAGGAGAATCGCTTGAACCCGG	82050	A	A
	GA	TCCC GGTTCAAGC ATTCTCCTG			
		AGGG CCAAGTTCG TAAGAGGAC			
		C	C		
GAM2620	LOC154877 3'	CAGGAGAATCACTTGAACCCGG	87534	A	CA
	GA	TCCC GGTTCAAG ATTCTCCTG			
		AGGG CCAAGTTC TAAGAGGAC			
		C	AC		
GAM2620	LOC154881 3'	CAGGAGGATCACTTGAGCCCAG	82069	CA	CA
	GA	TCC GGTTC AAG ATTCTCCTG			
		AGG CCGAGTTC TAGGAGGAC			
		AC	AC		
GAM2620	LOC154992 5'	CAGGAGAATTGCTTGAACCCGG	82131	A	
	GA	TCCC GGTTCAAGCAATTCTCCTG			
		AGGG CCAAGTTCGTTAAGAGGAC			
		C			
GAM2620	LOC155006 3'	CAGGAGAATCTCTTGAACCTCG	82166	C	CA
	GA	TCC AGGTTCAAG ATTCTCCTG			
		AGG TCCAAGTTC TAAGAGGAC			
		C	TC		
GAM2620	LOC155054 3'	CAGGAGGATCGCTTGAGCCCAG	82201	CA	A
	GA	TCC GGTTC AAGC ATTCTCCTG			
		AGG CCGAGTTCG TAGGAGGAC			
		AC	C		
GAM2620	LOC155072 3'	CAGGAGAATGGCGTGAACCCGG	87657	A	A A
	GA	TCCC GGTTCA GC ATTCTCCTG			

		AGGG CCAAGT CG TAAGAGGAC		
		C G G		
GAM2620	LOC155072 3'	CAGGAGCATGGCGTGAACCTGG 87658	A A T	
	GA	TCCCAGGTTCA GC AT CTCCTG		
		AGGGTCCAAGT CG TA GAGGAC		
		G G C		
GAM2620	LOC155376 3'	CAGGAGAATAACTGGAATCCGG 82243	A A CA	
	GA	TCCC GGTTT AG ATTCTCCTG		
		AGGG CTAAG TC TAAGAGGAC		
		C G AA		
GAM2620	LOC155376 3'	CAGGAGAATCACTTGAGCCTGG 82244	CA	
	GA	TCCCAGGTTCAAG ATTCTCCTG		
		AGGGTCCGAGTTC TAAGAGGAC		
		AC		
GAM2620	LOC157247 5'	GGGAGAATCACTTGAGCCCAGG 82301	CA CA	
	A	TCC GGTTCAAG ATTCTCCT		
		AGG CCGAGTTC TAAGAGGG		
		AC AC		
GAM2620	LOC157657 3'	CAGGAAAATTTATTGAACCTGG 82433	GC C	
	GA	TCCCAGGTTCAA AATT TCCTG		
		AGGGTCCAAGTT TTAA AGGAC		
		AT A		
GAM2620	LOC157660 3'	CAGGAGAATCGCTTGAACCTGG 87801	A	
	GA	TCCCAGGTTCAAGC ATTCTCCTG		
		AGGGTCCAAGTTCG TAAGAGGAC		
		C		
GAM2620	LOC157983 3'	CAGGGGAATCACTTGAACCCGG 82537	A CA	
	GA	TCCC GGTTCAAG ATTCTCCTG		
		AGGG CCAAGTTC TAAGGGGAC		
		C AC		
GAM2620	LOC158088 3'	CAGGAGAAGGGCGTGAACCCGG 87971	A A AA	
	GA	TCCC GGTTCA GC TTCTCCTG		
		AGGG CCAAGT CG AAGAGGAC		
		C G GG		
GAM2620	LOC158187 3'	CAGGAGAATAGCTGGAACCCGG 87989	A A A	
	GA	TCCC GGTTT AGC ATTCTCCTG		
		AGGG CCAAG TCG TAAGAGGAC		
		C G A		
GAM2620	LOC158191 3'	CGGGAGAAGTCTTGAACCTGG 82670	A	
	GA	TCCCAGGTTCAAGCA TTCTCCTG		

		AGGGTCCAAGTTCGT AAGAGGGC			
		C			
GAM2620	LOC158292 5'	CAGAAGAATCACTTGAACCCAG 88042	CA	CA	C
	GA	TCC GGTTC AAG ATTCT CTG			
		AGG CCAAGTTC TAAGA GAC			
		AC AC A			
GAM2620	LOC158292 5'	CAGGAGAATGATGGGAACCCGG 88043	A	AAGCA	
	GA	TCCC GGTTC ATTCTCCTG			
		AGGG CCAAG TAAGAGGAC			
		C GGTAG			
GAM2620	LOC158677 5'	AGACTCACTTGAACCAGGGA 88243	A	CAAT	
		TCCC GGTTC AAG TCT			
		AGGG CCAAGTTC AGA			
		A ACTC			
GAM2620	LOC158819 5'	AGAATCGCTTGAACCAGG 88266	A	A	
		CC GGTTC AAGC ATTCT			
		GG CCAAGTTCG TAAGA			
		A C			
GAM2620	LOC158819 3'	GAGAATTGCTTGAACCCAGGA 88277	CA		
		TCC GGTTC AAGCAATTCTC			
		AGG CCAAGTTCGTTAAGAG			
		AC			
GAM2620	LOC158972 3'	AGGAGAATCGCTTGAGCC 88314	A		
		GGTTC AAGC ATTCTCCT			
		CCGAGTTCG TAAGAGGA			
		C			
GAM2620	LOC158987 3'	GGGAGAATTGCTTGAACCCAGG 88328	CA		
	A	TCC GGTTC AAGCAATTCTCCT			
		AGG CCAAGTTCGTTAAGAGGG			
		AC			
GAM2620	LOC159036 3'	CAGGAGAATCGCTTGAACC 88345	A		
		GGTTC AAGC ATTCTCCTG			
		CCAAGTTCG TAAGAGGAC			
		C			
GAM2620	LOC159053 3'	CAGGAGAATCACTTGAACCCGG 88366	A	CA	
	GA	TCCC GGTTC AAG ATTCTCCTG			
		AGGG CCAAGTTC TAAGAGGAC			
		C AC			
GAM2620	LOC159053 3'	CAGGAGAATGGCGTGAACCTGG 88367	A	A	
	GA	TCCCAGGTTCA GC ATTCTCCTG			

		AGGGTCCAAGT CG TAAGAGGAC		
		G G		
GAM2620	LOC159110 3'	CAGGTGAATCGCTTGAACCCAG 82985	CA	A T
	GA	TCC GGTTC AAGC ATTC CCTG		
		AGG CCAAGTTCG TAAG GGAC		
		AC C T		
GAM2620	LOC159116 3'	CAGGTGAATCGCTTGAACCCAG 82968	CA	A T
	GA	TCC GGTTC AAGC ATTC CCTG		
		AGG CCAAGTTCG TAAG GGAC		
		AC C T		
GAM2620	LOC161823 3'	GATTGCTTGATCCTAGGA 83175	C T	
		TCC AGG TCAAGCAATT		
		AGG TCC AGTTCGTTAG		
		A T		
GAM2620	LOC166979 5'	AGACTGACTTAGACCTGGGA 83557	TC _ AT	
		TCCCAGGT AAG CA TCT		
		AGGGTCCA TTC GT AGA		
		GA A C_		
GAM2620	LOC170395 3'	CAGGAGAATCACTTGAACCCGG 76865	A	CA
		CC GGTTC AAG ATTCTCCTG		
		GG CCAAGTTC TAAGAGGAC		
		C AC		
GAM2620	LOC196027 3'	AGGGGATCACTTGAACCCAGGA 88937	CA	CAAT
		TCC GGTTC AAG TCTCCT		
		AGG CCAAGTTC AGGGGA		
		AC ACT_		
GAM2620	LOC196047 5'	GAGAATCGCTTGAACCTGGGA 91153		A
		TCCCAGGTTCAAGC ATTCTC		
		AGGGTCCAAGTTCG TAAGAG		
		C		
GAM2620	LOC196529 3'	CAGGAGAATCTCTTGAACC 89125	CA	
		GGTTC AAG ATTCTCCTG		
		CCAAGTTC TAAGAGGAC		
		TC		
GAM2620	LOC196540 3'	CAGGAGAATCACTTGAGCCCCG 91197	A_	CA
	GG	CCC GGTTC AAG ATTCTCCTG		
		GGG CCGAGTTC TAAGAGGAC		
		CC AC		
GAM2620	LOC196761 3'	CAGGAGAATCACTTGAACCCAG 91117	CA	CA
	GA	TCC GGTTC AAG ATTCTCCTG		

		AGG CCAAGTTC TAAGAGGAC		
		AC AC		
GAM2620	LOC197132 3'	CAGGAGAATCGCTTGAACCCAG 89228	CA	A
	GA	TCC GGTTC AAGC ATTCTCCTG		
		AGG CCAAGTTCG TAAGAGGAC		
		AC C		
GAM2620	LOC197196 3'	CAGGAGAATCACTTGAACC 91299	CA	
		GGTTC AAG ATTCTCCTG		
		CCAAGTTC TAAGAGGAC		
		AC		
GAM2620	LOC197201 3'	CAGGCCGATTGCTTGAGCCCAG 89268	CA	CT
	GA	TCC GGTTC AAGCAATT CCTG		
		AGG CCGAGTTCGTTAG GGAC		
		AC CC		
GAM2620	LOC197201 3'	GAATTGCTTGAACCAGGGA 89274	A	
		TCCC GGTTC AAGCAATTC		
		AGGG CCAAGTTCGTTAAG		
		A		
GAM2620	LOC197319 3'	CAGGAGAATTGCTTGAAGATGG 89315	GG	
	GA	TCCCA TTCAAGCAATTCTCCTG		
		AGGGT AAGTTCGTTAAGAGGAC		
		AG		
GAM2620	LOC197408 5'	GGGAGAATCACTTGAGCC 91319	CA	
		GGTTC AAG ATTCTCCT		
		CCGAGTTC TAAGAGGG		
		AC		
GAM2620	LOC199676 3'	GAGAATCACTTGAACCCAGGA 91360	CA	CA
		TCC GGTTC AAG ATTCTC		
		AGG CCAAGTTC TAAGAG		
		AC AC		
GAM2620	LOC199733 3'	CAGGAGGATGGCTTGAGCCCAG 91436	CA	A
	GA	TCC GGTTC AAGC ATTCTCCTG		
		AGG CCGAGTTCG TAGGAGGAC		
		AC G		
GAM2620	LOC199858 3'	CAGGAGAATGGCATGAACCCGG 89794	A	A A
	GA	TCCC GGTTC A GC ATTCTCCTG		
		AGGG CCAAGT CG TAAGAGGAC		
		C A G		
GAM2620	LOC200251 5'	CAGGAGAATTGCTTGAACC 90059		
		GGTTC AAGCAATTCTCCTG		

CCAAGTTCGTTAAGAGGAC

GAM2620	LOC200251	3'	CAGGAGAATTGCTTGAACCAGG	90060	CA	
	A		TCC GGTTC AAGCAATTCTCCTG			
			AGG CCAAGTTCGTTAAGAGGAC			
			A_			
GAM2620	LOC200316	3'	GGGAGAATCGCTTGAGCC	90186	A	
			GGTTC AAGC ATTCTCCT			
			CCGAGTTCG TAAGAGGG			
			C			
GAM2620	LOC200317	3'	GAGAATTGCTTGGACTCAGGA	90224	CA	
			TCC GGTTC AAGCAATTCTC			
			AGG TCAGGTTCGTTAAGAG			
			AC			
GAM2620	LOC200728	3'	CAGGAGAATGGTGTGAACCCAG	91681	CA	A A
	GA		TCC GGTTC A GC ATTCTCCTG			
			AGG CCAAGT TG TAAGAGGAC			
			AC G G			
GAM2620	LOC200731	3'	CAGGAGAATCCCTTGAACCTGG	91693	CA	
	GA		TCCCAGGTTCAAG ATTCTCCTG			
			AGGGTCCAAGTTC TAAGAGGAC			
			CC			
GAM2620	LOC200904	3'	CAGGAGAAACACCTGAGCCCAG	91775	CA	AGCAA
	GA		TCC GGTTC A TTCTCCTG			
			AGG CCGAGT AAGAGGAC			
			AC CCACA			
GAM2620	LOC200904	5'	CAGGAGAATCCCTTGAACCTGG	91776	CA	
	GA		TCCCAGGTTCAAG ATTCTCCTG			
			AGGGTCCAAGTTC TAAGAGGAC			
			CC			
GAM2620	LOC200918	3'	CAGGAGAATCACTTGAACCTAG	90365	C	CA
	GA		TCC AGGTTCAAG ATTCTCCTG			
			AGG TCCAAGTTC TAAGAGGAC			
			A AC			
GAM2620	LOC200940	3'	CAGGAGAATCACTAGAACCTGG	90388	A	CA
	GA		TCCCAGGTTCA AG ATTCTCCTG			
			AGGGTCCAAG TC TAAGAGGAC			
			A AC			
GAM2620	LOC201173	3'	CAGGAGAATGGCGTGAACCTGG	88675	A	A
	GA		TCCCAGGTTCA GC ATTCTCCTG			

		AGGGTCCAAGT CG TAAGAGGAC		
		G G		
GAM2620	LOC201182 5'	CAGGAGAATTGCTTGAACCTCAG 91334	CCA	
	A	TC GGTTCAAGCAATTCTCCTG		
		AG TCAAGTTCGTTAAGAGGAC		
		AC_		
GAM2620	LOC201220 3'	CAGGAGAATGGCGTGAACCTGG 88710	A A	
	GA	TCCCAGGTTCA GC ATTCTCCTG		
		AGGGTCCAAGT CG TAAGAGGAC		
		G G		
GAM2620	LOC201252 3'	CATGAGAATCACTTGAACCTGG 89548	CA C	
	GA	TCCCAGGTTCAAG ATTCTC TG		
		AGGGTCCAAGTTC TAAGAG AC		
		AC T		
GAM2620	LOC201564 3'	CAGGAGAATTGCTTGAACCCGG 81273	A	
	GA	TCCC GGTTCAAGCAATTCTCCTG		
		AGGG CCAAGTTCGTTAAGAGGAC		
		C		
GAM2620	LOC201627 3'	GAATCACTTGAACCTGGGA 90454	CA	
		TCCCAGGTTCAAG ATTC		
		AGGGTCCAAGTTC TAAG		
		AC		
GAM2620	LOC201685 3'	AGTATTACTTGAGCCCAGGA 91837	CA C T	
		TCC GGTTCAAG AAT CT		
		AGG CCGAGTTC TTA GA		
		AC A T		
GAM2620	LOC201685 3'	CAGGAGAATGGCTCGAACCCGG 91838	A A A	
		CC GGTTCAAGC ATTCTCCTG		
		GG CCAAG TCG TAAGAGGAC		
		C C G		
GAM2620	LOC201868 5'	CAGGAGAATTGCTTGAACCCGG 90516	A	
	GA	TCCC GGTTCAAGCAATTCTCCTG		
		AGGG CCAAGTTCGTTAAGAGGAC		
		C		
GAM2620	LOC201895 3'	CAGGAGAATTGCTTGAACCCGG 90542	A	
	GA	TCCC GGTTCAAGCAATTCTCCTG		
		AGGG CCAAGTTCGTTAAGAGGAC		
		C		
GAM2620	LOC201911 3'	CAGGAAAATAGCTTGAACCCGG 91861	A A C	
	GA	TCCC GGTTCAAGC ATT TCCTG		

		AGGG CCAAGTTCG TAA AGGAC		
		C A A		
GAM2620	LOC201931 3'	CAGGAGAATGGTGTGGACCCAG 90562	CA	A A
	GA	TCC GGTTC A GC ATTCTCCTG		
		AGG CCAGGT TG TAAGAGGAC		
		AC G G		
GAM2620	LOC202020 3'	CAGGAGAATGGCTTGAATCCGG 90596	A	A
	GA	TCCC GGTTC AAGC ATTCTCCTG		
		AGGG CTAAGTTCG TAAGAGGAC		
		C G		
GAM2620	LOC202781 3'	CAGGAGGATTGCTTGAGCCCAG 91968	CA	
	GA	TCC GGTTC AAGCAATTCTCCTG		
		AGG CCGAGTTCGTTAGGAGGAC		
		AC		
GAM2620	LOC202868 3'	CAGGAGAATGGCATGAACCCGG 91992	A	A A
	GA	TCCC GGTTC A GC ATTCTCCTG		
		AGGG CCAAGT CG TAAGAGGAC		
		C A G		
GAM2620	LOC202868 3'	CAGGAGAATGGCATGAACCCGG 91993	A	A A
	GA	TCCC GGTTC A GC ATTCTCCTG		
		AGGG CCAAGT CG TAAGAGGAC		
		C A G		
GAM2620	LOC203025 3'	CAGGAGAATCGCTTGAACCTGG 90744		A
	GA	TCCCAGGTTCAAGC ATTCTCCTG		
		AGGGTCCAAGTTCG TAAGAGGAC		
		C		
GAM2620	LOC203083 5'	CAGGAGAATATCTTGAACCTGG 92083		CA
	GA	TCCCAGGTTCAAG ATTCTCCTG		
		AGGGTCCAAGTTC TAAGAGGAC		
		TA		
GAM2620	LOC203083 3'	CAGGAGAATCACTTGAGCCCAG 92084	CA	CA
	GA	TCC GGTTC AAG ATTCTCCTG		
		AGG CCGAGTTC TAAGAGGAC		
		AC AC		
GAM2620	LOC203246 3'	CAGGAGAATGGCGTGAACCCGG 90828	A	A A
		CC GGTTC A GC ATTCTCCTG		
		GG CCAAGT CG TAAGAGGAC		
		C G G		
GAM2620	LOC203276 3'	CAGGAGAATCACTTGAACCCAG 92112	CA	CA
	GA	TCC GGTTC AAG ATTCTCCTG		

		AGG CCAAGTTC TAAGAGGAC		
		AC AC		
GAM2620	LOC203276 3'	GAATCACTTGAACCCAGGA 92124	CA	CA
		TCC GGTTCAAG ATTC		
		AGG CCAAGTTC TAAG		
		AC AC		
GAM2620	LOC203289 3'	CAGGGGAATCACTTGAACCCGG 90864	A	CA
	GA	TCCC GGTTCAAG ATTCTCCTG		
		AGGG CCAAGTTC TAAGGGGAC		
		C AC		
GAM2620	LOC203305 3'	CAGGAGAATCACTTGAACCCAG 92165	CA	CA
	GA	TCC GGTTCAAG ATTCTCCTG		
		AGG CCAAGTTC TAAGAGGAC		
		AC AC		
GAM2620	LOC203305 3'	GAATCACTTGAACCCAGGA 92177	CA	CA
		TCC GGTTCAAG ATTC		
		AGG CCAAGTTC TAAG		
		AC AC		
GAM2620	LOC203350 3'	CAGGAAGATCACTTGAGCCAG 92231	CA	CA TC
	GA	TCC GGTTCAAG AT TCCTG		
		AGG CCGAGTTC TA AGGAC		
		AC AC GA		
GAM2620	LOC203378 3'	CAGGAGAATCACATGAACCTGG 92282		AGCA
		CCAGGTTCA ATTCTCCTG		
		GGTCCAAGT TAAGAGGAC		
		ACAC		
GAM2620	LOC203378 3'	CAGGAGAATTGCGTGAATCCAG 92283	CA	A
	GA	TCC GGTTCA GCAATTCTCCTG		
		AGG CTAAGT CGTTAAGAGGAC		
		AC G		
GAM2620	LOC219347 3'	CAGGAGAATGGCCTGAACCCGG 94575	A	A A
	GA	TCCC GGTTCA GC ATTCTCCTG		
		AGGG CCAAGT CG TAAGAGGAC		
		C C G		
GAM2620	LOC219406 3'	AGGAGAATCGCTTGAACC 95202	A	
		GGTTCAAGC ATTCTCCT		
		CCAAGTTCG TAAGAGGA		
		C		
GAM2620	LOC219540 3'	GAGAATTGCTTGAACCTGGGA 95242		
		TCCCAGGTTCAAGCAATTCTC		

AGGGTCCAAGTTCGTTAAGAG

GAM2620	LOC219627 3'	CAGGAAAATCGCTTGAACCCAG 93802	CA	A	C
	GA	TCC GGTTC AAGC ATT TCCTG			
		AGG CCAAGTTCG TAA AGGAC			
		AC C A			
GAM2620	LOC219627 3'	CAGGAGAATCGCTTGAACCTGG 93803		A	
	GA	TCCCAGGTTCAAGC ATTCTCCTG			
		AGGGTCCAAGTTCG TAAGAGGAC			
		C			
GAM2620	LOC219649 3'	CAGGAGAATGGTGTGAACCCGG 94546	A	A	A
	G	CCC GGTTC A GC ATTCTCCTG			
		GGG CCAAGT TG TAAGAGGAC			
		C G G			
GAM2620	LOC219649 3'	CAGGAGAATTGCTTGAACCCAG 94547	CA		
	GA	TCC GGTTC AAGCAATTCTCCTG			
		AGG CCAAGTTCGTTAAGAGGAC			
		AC			
GAM2620	LOC219672 5'	CAGAAGAATCGTTTGAACCCGG 92965	A	A	C
	GA	TCCC GGTTC AAGC ATTCT CTG			
		AGGG CCAAGTTTG TAAGA GAC			
		C C A			
GAM2620	LOC219722 5'	CAGAAGAATCACTTGAACCTGG 94676		CA	C
	GA	TCCCAGGTTCAAG ATTCT CTG			
		AGGGTCCAAGTTC TAAGA GAC			
		AC A			
GAM2620	LOC219919 3'	CAGGAGAATCACTTGAGCCCAG 94921	CA		CA
	GA	TCC GGTTC AAG ATTCTCCTG			
		AGG CCGAGTTC TAAGAGGAC			
		AC AC			
GAM2620	LOC219919 5'	CAGGAGAATCCCTTGAACCTGG 94922		CA	
	GA	TCCCAGGTTCAAG ATTCTCCTG			
		AGGGTCCAAGTTC TAAGAGGAC			
		CC			
GAM2620	LOC220370 3'	CAGTAGAATCGCTTGAACC 94395	A		C
		GGTTC AAGC ATTCT CTG			
		CCAAGTTCG TAAGA GAC			
		C T			
GAM2620	LOC220506 3'	CAGGAGAATTGCTTGAACCCGG 74517	A		
	GA	TCCC GGTTC AAGCAATTCTCCTG			

		AGGG CCAAGTTCGTTAAGAGGAC		
		C		
GAM2620	LOC220662 3'	AATCACTTGAGCCTAGGA	92798	C CA
		TCC AGGTTCAAG ATT		
		AGG TCCGAGTTC TAA		
		A AC		
GAM2620	LOC220662 3'	CAGGAGAATCGCTTGAACCTGG	92809	A
	GA	TCCCAGGTTCAAGC ATTCTCCTG		
		AGGGTCCAAGTTCG TAAGAGGAC		
		C		
GAM2620	LOC220662 3'	CAGGAGAATTCCTTGAACCTGG	92810	C
	GA	TCCCAGGTTCAAG AATTCTCCTG		
		AGGGTCCAAGTTC TTAAGAGGAC		
		C		
GAM2620	LOC220906 3'	CAGGAAAATCGCTTGAACCCAG	93031	CA A C
	GA	TCC GGTTC AAGC ATT TCCTG		
		AGG CCAAGTTCG TAA AGGAC		
		AC C A		
GAM2620	LOC220906 3'	CAGGAGAATCGCTTGGACCTGG	93032	A
	GA	TCCCAGGTTCAAGC ATTCTCCTG		
		AGGGTCCAGGTTCG TAAGAGGAC		
		C		
GAM2620	LOC220992 3'	AGGATTGCTTAAGCCCAGGA	93107	CA C
		TCC GGTT AAGCAATTCT		
		AGG CCGA TTCGTTAGGA		
		AC A		
GAM2620	LOC221042 3'	CAGGAGAATCGCTTGAACCCGG	94796	A A
	GA	TCCC GGTTCAAGC ATTCTCCTG		
		AGGG CCAAGTTCG TAAGAGGAC		
		C C		
GAM2620	LOC221069 3'	CAGGAGAATTGATTGAACCCGG	94819	A G
	GA	TCCC GGTTCAA CAATTCTCCTG		
		AGGG CCAAGTT GTTAAGAGGAC		
		C A		
GAM2620	LOC221271 3'	CAGGAGAATGGCGTGAACCCAG	93501	CA A A
	GA	TCC GGTTCA GC ATTCTCCTG		
		AGG CCAAGT CG TAAGAGGAC		
		AC G G		
GAM2620	LOC221271 3'	CAGGAGAATGGCGTGAACCCGG	93502	A A A
	GA	TCCC GGTTCA GC ATTCTCCTG		

		AGGG CCAAGT CG TAAGAGGAC		
		C G G		
GAM2620	LOC221288 3'	CAGGAGAATGGCCTGAACCCGG 95256	A	A A
	GA	TCCC GGTTCA GC ATTCTCCTG		
		AGGG CCAAGT CG TAAGAGGAC		
		C C G		
GAM2620	LOC221410 3'	CAGAAGAATCGCTTGAACCTGG 93691	A	C
	GA	TCCCAGGTTCAAGC ATTCT CTG		
		AGGGTCCAAGTTCG TAAGA GAC		
		C A		
GAM2620	LOC221474 3'	CAGGAGAATCACTTGAATCCAG 93991	CA	CA
	GA	TCC GGTTCAAG ATTCTCCTG		
		AGG CTAAGTTC TAAGAGGAC		
		AC AC		
GAM2620	LOC221477 3'	CAGGAAAATTGCTTGAACCGGG 93768	A	C
	GA	TCCC GGTTCAAGCAATT TCCTG		
		AGGG CCAAGTTCGTAA AGGAC		
		G A		
GAM2620	LOC221490 3'	CAGGAGAATCGCTTGAACCCAG 95300	CA	A
	GA	TCC GGTTCAAGC ATTCTCCTG		
		AGG CCAAGTTCG TAAGAGGAC		
		AC C		
GAM2620	LOC221543 3'	CAGGAGAATTGCTTGAATCTGG 95367		
	GA	TCCCAGGTTCAAGCAATTCTCCTG		
		AGGGTCTAAGTTCGTAAAGAGGAC		
GAM2620	LOC221550 3'	GAATTGCTTGAACCTGGGA 93746		
		TCCCAGGTTCAAGCAATTC		
		AGGGTCCAAGTTCGTAAAG		
GAM2620	LOC221550 3'	GAGAATTGCTTGAACCTGGGA 93747		
		TCCCAGGTTCAAGCAATTCTC		
		AGGGTCCAAGTTCGTAAAGAG		
GAM2620	LOC221795 3'	CAGGAGAATCACTTGAGCCCAG 94071	CA	CA
	GA	TCC GGTTCAAG ATTCTCCTG		
		AGG CCGAGTTC TAAGAGGAC		
		AC AC		
GAM2620	LOC221943 5'	CAGGAGAATCGTTTGAACCCAG 95619	CA	A
	GA	TCC GGTTCAAGC ATTCTCCTG		

		AGG CCAAGTTTG TAAGAGGAC		
		AC C		
GAM2620	LOC221954 5'	CAGGAGAATCGCTTGAACCTGG 95642	A	
	GA	TCCCAGGTTCAAGC ATTCTCCTG		
		AGGGTCCAAGTTCG TAAGAGGAC		
		C		
GAM2620	LOC221954 5'	CAGGAGAATGGCTTGAGCCCAG 95643	CA	A
	GA	TCC GGTTC AAGC ATTCTCCTG		
		AGG CCGAGTTCG TAAGAGGAC		
		AC G		
GAM2620	LOC221962 3'	CGGGAAAATTGCTTGAACCTCAG 94240	CA	C
	GA	TCC GGTTC AAGCAATT TCCTG		
		AGG TCAAGTTCGTTAA AGGGC		
		AC A		
GAM2620	LOC222060 5'	GGGAGAATTGCTTGAACCCGGG 95756	A	
	A	TCCC GGTTC AAGCAATTCTCCT		
		AGGG CCAAGTTCGTTAAGAGGG		
		C		
GAM2620	LOC222066 3'	CAGGAAAATCACTTGAACCCAG 94314	CA	CA C
	GA	TCC GGTTC AAG ATT TCCTG		
		AGG CCAAGTTC TAA AGGAC		
		AC AC A		
GAM2620	LOC222160 3'	CAGCAGAATCGCTTGAACCTGG 95775	A	C
	GA	TCCCAGGTTCAAGC ATTCT CTG		
		AGGGTCCAAGTTCG TAAGA GAC		
		C C		
GAM2620	LOC222160 5'	CAGGAGAATCGCTTGAACCCAG 95776	CA	A
	GA	TCC GGTTC AAGC ATTCTCCTG		
		AGG CCAAGTTCG TAAGAGGAC		
		AC C		
GAM2620	LOC222182 3'	CAGGAGAATCACTTGAACCTGG 95853	CA	
		CCAGGTTCAAG ATTCTCCTG		
		GGTCCAAGTTC TAAGAGGAC		
		AC		
GAM2620	LOC222865 3'	CAGGAGAATGGTGCGAACCCGG 94440	A	AA A
	GA	TCCC GGTTC GC ATTCTCCTG		
		AGGG CCAAG TG TAAGAGGAC		
		C CG G		
GAM2620	LOC253003 3'	CAGGAGAATGGCGTGAACCCGG 98674	A	A A
	GA	TCCC GGTTC GC ATTCTCCTG		

		AGGG CCAAGT CG TAAGAGGAC		
		C G G		
GAM2620	LOC253532 3'	CAGGAGAATAACTGGAATCCGG 97732	A	A CA
	GA	TCCC GGTTT AG ATTCTCCTG		
		AGGG CTAAG TC TAAGAGGAC		
		C G AA		
GAM2620	LOC253532 3'	CAGGAGAATCACTTGAGCCTGG 97733		CA
	GA	TCCCAGGTTCAAG ATTCTCCTG		
		AGGGTCCGAGTTC TAAGAGGAC		
		AC		
GAM2620	LOC253664 3'	CAGGAGGGTTACTTGAGCCCAG 96461	CA	C
	GA	TCC GGTTCAAG AATTCTCCTG		
		AGG CCGAGTTC TTGGGAGGAC		
		AC A		
GAM2620	LOC253778 5'	CAGGAGAGTCACTTGAACCTCAG 96524	CA	CA
	GA	TCC GGTTCAAG ATTCTCCTG		
		AGG TCAAGTTC TGAGAGGAC		
		AC AC		
GAM2620	LOC253786 3'	CAGGAGAATCGCTTGAACCCAG 98831	CA	A
	GA	TCC GGTTCAAGC ATTCTCCTG		
		AGG CCAAGTTCG TAAGAGGAC		
		AC C		
GAM2620	LOC253906 3'	CAGAAGGATTGCTTGAGCCCAG 98297	CA	C
	GA	TCC GGTTCAAGCAATTCT CTG		
		AGG CCGAGTTCGTTAGGA GAC		
		AC A		
GAM2620	LOC254041 5'	CAGGAGAATCGCTTGAACCTGG 96553		A
	G	CCCAGGTTCAAGC ATTCTCCTG		
		GGGTCCAAGTTCG TAAGAGGAC		
		C		
GAM2620	LOC254045 3'	CAGGAAGATGGCTTGAGCCCAG 98263	CA	A TC
	GA	TCC GGTTCAAGC AT TCCTG		
		AGG CCGAGTTCG TA AGGAC		
		AC G GA		
GAM2620	LOC254045 3'	CAGGAGAATCACTTGAACCCAG 98264	CA	CA
	GA	TCC GGTTCAAG ATTCTCCTG		
		AGG CCAAGTTC TAAGAGGAC		
		AC AC		
GAM2620	LOC254050 3'	CAGGAGAGTCGCTTGAACCTGG 96561		A
		CCAGGTTCAAGC ATTCTCCTG		

		GGTCCAAGTTCG TGAGAGGAC		
		C		
GAM2620	LOC254100 3'	CAGGAGAATTGCTTGAACCGGG 98150	A	
	A	TCCC GGTTC AAGCAATTCTCCTG		
		AGGG CCAAGTTCGTTAAGAGGAC		
		—		
GAM2620	LOC254176 5'	CAGGAGAATATCTTGAACCTGG 99164	CA	
	GA	TCCCAGGTTCAAG ATTCTCCTG		
		AGGGTCCAAGTTC TAAGAGGAC		
		TA		
GAM2620	LOC254176 3'	CAGGAGAATCACTTGAGCCCAG 99165	CA	CA
	GA	TCC GGTTC AAG ATTCTCCTG		
		AGG CCGAGTTC TAAGAGGAC		
		AC AC		
GAM2620	LOC254243 3'	CAGGAGAATCACTTGAACCCAG 99251	CA	CA
	GA	TCC GGTTC AAG ATTCTCCTG		
		AGG CCAAGTTC TAAGAGGAC		
		AC AC		
GAM2620	LOC254243 3'	GAATCACTTGAACCCAGGA 99263	CA	CA
		TCC GGTTC AAG ATTC		
		AGG CCAAGTTC TAAG		
		AC AC		
GAM2620	LOC254266 3'	CAGGAGAATGGCGTGAACCCAG 99194	CA	A A
	GA	TCC GGTTC A GC ATTCTCCTG		
		AGG CCAAGT CG TAAGAGGAC		
		AC G G		
GAM2620	LOC254351 3'	AGATCGCTTGAGCCTAGGA 96680	C	AAT
		TCC AGGTTCAAGC TCT		
		AGG TCCGAGTTCG AGA		
		A CT_		
GAM2620	LOC254531 5'	CAGGAGAATTGCTTGAACCTGG 96665		
	GA	TCCCAGGTTCAAGCAATTCTCCTG		
		AGGGTCCAAGTTCGTTAAGAGGAC		
GAM2620	LOC254659 3'	CAGGAGAATCGCTTTAACTGGG 96819	GTTC	A
	A	TCCAG AAGC ATTCTCCTG		
		AGGGTC TTCG TAAGAGGAC		
		AAT_ C		
GAM2620	LOC254808 3'	CAGGAGAATGGCGTGAACCCGG 98803	A	A A
	GA	TCCC GGTTC A GC ATTCTCCTG		

		AGGG CCAAGT CG TAAGAGGAC		
		C G G		
GAM2620	LOC254875 3'	CAGGAGAATAACTGGAATCCGG 97776	A	A CA
	GA	TCCC GGTTT AG ATTCTCCTG		
		AGGG CTAAG TC TAAGAGGAC		
		C G AA		
GAM2620	LOC254875 3'	CAGGAGAATCACTTGAGCCTGG 97777		CA
	GA	TCCCAGGTTCAAG ATTCTCCTG		
		AGGGTCCGAGTTC TAAGAGGAC		
		AC		
GAM2620	LOC255030 5'	CAGGAGAATCACTTGAACCCAG 99082	CA	CA
	GA	TCC GGTTCAAG ATTCTCCTG		
		AGG CCAAGTTC TAAGAGGAC		
		AC AC		
GAM2620	LOC255031 3'	CAGGAGAATTACTTGAACCTGG 99031		C
	GA	TCCCAGGTTCAAG AATTCTCCTG		
		AGGGTTCAAGTTC TTAAGAGGAC		
		A		
GAM2620	LOC255042 3'	CAGGAGAATCACTTGAACCCGG 97037	A	CA
	GA	TCCC GGTTCAAG ATTCTCCTG		
		AGGG CCAAGTTC TAAGAGGAC		
		C AC		
GAM2620	LOC255042 3'	CAGGAGAATCGCTTGAATTCGG 97038	AG	A
	GA	TCCC GTTCAAGC ATTCTCCTG		
		AGGG TAAGTTCG TAAGAGGAC		
		CT C		
GAM2620	LOC255042 3'	GAATTGCTTGAACCCAGGA 97046	CA	
		TCC GGTTCAAGCAATTC		
		AGG CCAAGTTCGTTAAG		
		AC		
GAM2620	LOC255177 3'	CAGGAGAATCACTTAAACATGG 98389	G C	CA
	GA	TCCA GTT AAG ATTCTCCTG		
		AGGGT CAA TTC TAAGAGGAC		
		A A AC		
GAM2620	LOC255252 3'	CAGGAGAATCGCTTGAACCCAG 96706	CA	A
	GA	TCC GGTTCAAGC ATTCTCCTG		
		AGG CCAAGTTCG TAAGAGGAC		
		AC C		
GAM2620	LOC255326 3'	CAGGAGAATGGCATGAACCCAG 98117	CA	A A
	GA	TCC GGTTCA GC ATTCTCCTG		

		AGG CCAAGT CG TAAGAGGAC		
		AC A G		
GAM2620	LOC255328 3'	CAGGAGAATCACTTGAACGTGG 98334	G	CA
	GA	TCCCA GTTCAAG ATTCTCCTG		
		AGGGT CAAGTTC TAAGAGGAC		
		G AC		
GAM2620	LOC255671 3'	CAGGAGAATGGCGTGAACCCGG 99069	A	A A
	GA	TCCC GGTTCA GC ATTCTCCTG		
		AGGG CCAAGT CG TAAGAGGAC		
		C G G		
GAM2620	LOC255937 3'	CATGAGAATCACTTGAACCCAG 97677	CA	CA C
	GA	TCC GGTTCAAG ATTCTC TG		
		AGG CCAAGTTC TAAGAG AC		
		AC AC T		
GAM2620	LOC255971 3'	CAGGAGAATCGCTTGAACCCAG 98309	CA	A
	GA	TCC GGTTCAAGC ATTCTCCTG		
		AGG CCAAGTTCG TAAGAGGAC		
		AC C		
GAM2620	LOC256207 3'	CAGGAAGATCACTTGAACCCAG 96872	CA	CA TC
	GA	TCC GGTTCAAG AT TCCTG		
		AGG CCAAGTTC TA AGGAC		
		AC AC GA		
GAM2620	LOC256207 3'	CAGGAGAATCGCTTGAACCTGG 96873		A
	GA	TCCCAGGTTCAAGC ATTCTCCTG		
		AGGGTCCAAGTTCG TAAGAGGAC		
		C		
GAM2620	LOC256236 3'	CAGGAAGCCTCGAGCCTGGGA 96976	A	CAATTC
		TCCCAGGTTC AG TCCTG		
		AGGGTCCGAG TC AGGAC		
		C CGA__		
GAM2620	LOC256267 3'	CAGGAGAATCTCTTGAACCCGG 98607	A	CA
	GA	TCCC GGTTCAAG ATTCTCCTG		
		AGGG CCAAGTTC TAAGAGGAC		
		C TC		
GAM2620	LOC256337 3'	CAGGAGAAGCAAAACCTCGGA 96341	C	CAA AA
		TCC AGGTT GC TTCTCCTG		
		AGG TCCAA CG AAGAGGAC		
		C AA_ __		
GAM2620	LOC256515 3'	CAGGAGAATCACTTGAGCCCAG 98207	CA	CA
	GA	TCC GGTTCAAG ATTCTCCTG		

		AGG CCGAGTTC TAAGAGGAC		
		AC AC		
GAM2620	LOC256515 5'	CAGGAGAATCCCTTGAACCTGG 98208	CA	
	GA	TCCCAGGTTCAAG ATTCTCCTG		
		AGGGTCCAAGTTC TAAGAGGAC		
		CC		
GAM2620	LOC256520 3'	AGAATCGCTTGAACCCGGGA 97663	A	A
		TCCC GGTTC AAGC ATTCT		
		AGGG CCAAGTTCG TAAGA		
		C C		
GAM2620	LOC256544 3'	CAGGGGAATCACTTGAACCCGG 97928	A	CA
	GA	TCCC GGTTC AAG ATTCTCCTG		
		AGGG CCAAGTTC TAAGGGGAC		
		C AC		
GAM2620	LOC256594 3'	CAGGAGAATCACTTCAGCCCAG 98857	CA	C CA
	GA	TCC GGT AAG ATTCTCCTG		
		AGG CCGA TTC TAAGAGGAC		
		AC C AC		
GAM2620	LOC256594 5'	CAGGAGAATTGCTTGAACCTGG 98858		
	GA	TCCCAGGTTCAAGCAATTCTCCTG		
		AGGGTCCAAGTTCGTTAAGAGGAC		
GAM2620	LOC256658 3'	CAGGAGAATCGTTTGCACCTGG 99147	T	A
	GA	TCCCAGGT CAAGC ATTCTCCTG		
		AGGGTCCA GTTTG TAAGAGGAC		
		C C		
GAM2620	LOC257017 5'	CAGGAGGATCACTTGAGCCCAG 99218	CA	CA
	GA	TCC GGTTC AAG ATTCTCCTG		
		AGG CCGAGTTC TAGGAGGAC		
		AC AC		
GAM2620	LOC257115 3'	CAGGTGGATCGCTTGAGCCCAG 98290	CA	A T
	GA	TCC GGTTC AAGC ATTC CTG		
		AGG CCGAGTTCG TAGG GGAC		
		AC C T		
GAM2620	LOC257282 5'	CAGAAGTATTGCTTGAACCCAG 98133	CA	T C
	GA	TCC GGTTC AAGCAAT CT CTG		
		AGG CCAAGTTCGTTA GA GAC		
		AC T A		
GAM2620	LOC257495 3'	GAATTGCTTGAACCTGGGA 99573		
		TCCCAGGTTCAAGCAATTC		

AGGGTCCAAGTTCGTTAAG

GAM2620 LOC257495 3' GAGAATTGCTTGAACCTGGGA 99574
TCCCAGGTTCAAGCAATTCTC
|||||||
AGGGTCCAAGTTCGTTAAGAG

GAM2620 LOC257539 3' CAGGAGAATGGCGTCAACCCGG 99545 A CAA A
GA TCCC GGTT GC ATTCTCCTG
||| ||| || |||||
AGGG CCAA CG TAAGAGGAC
C CTG G

GAM2620 LOC257576 3' GAATTGCTTGAACCTGGGA 99710
TCCCAGGTTCAAGCAATTC
|||||||
AGGGTCCAAGTTCGTTAAG

GAM2620 LOC257576 3' GAGAATTGCTTGAACCTGGGA 99711
TCCCAGGTTCAAGCAATTCTC
|||||||
AGGGTCCAAGTTCGTTAAGAG

GAM2620 LOC257578 3' CAGGAGAATGGCGTCAACCCGG 99657 A CAA A
GA TCCC GGTT GC ATTCTCCTG
||| ||| || |||||
AGGG CCAA CG TAAGAGGAC
C CTG G

GAM2620 LOC257596 3' CAGGAGAATTGCTTGAATCTGG 99770
GA TCCCAGGTTCAAGCAATTCTCCTG
|||||||
AGGGTCTAAGTTCGTTAAGAGGAC

GAM2620 LOC51145 3' CAGGAGAATCACTTGTACCCAG 32920 CA T CA
GA TCC GGT CAAG ATTCTCCTG
|| ||| ||| |||||
AGG CCA GTTC TAAGAGGAC
AC T AC

GAM2620 LOC51212 3' CAGGAGAGTGGTGTGAACCCGG 33499 A A A
GA TCCC GGTTCA GC ATTCTCCTG
||| |||| || |||||
AGGG CCAAGT TG TGAGAGGAC
C G G

GAM2620 LOC51277 3' CAGGAGGATTGCTTAAGCCCAG 80840 CA C
GA TCC GGTT AAGCAATTCTCCTG
|| ||| |||||
AGG CCGA TTCGTTAGGAGGAC
AC A

GAM2620 LOC51279 3' CAGGAGAATCACTTGAACCTGG 33751 CA
GA TCCCAGGTTCAAG ATTCTCCTG
||||||| |||||

		AGGGTCCAAGTTC TAAGAGGAC		
		AC		
GAM2620	LOC51279 3'	GAGGATCGCTTGAGCCCAGGA 33757	CA	A
		TCC GGTTCAAGC ATTCTC		
		AGG CCGAGTTCG TAGGAG		
		AC C		
GAM2620	LOC51333 3'	CATGAGAATCACTTGAACCTGG 34050	CA	C
	GA	TCCCAGGTTCAAG ATTCTC TG		
		AGGGTCCAAGTTC TAAGAG AC		
		AC T		
GAM2620	LOC51336 3'	CAGGAGAATCACTTGAACCTGG 34068	CA	
	GA	TCCCAGGTTCAAG ATTCTCCTG		
		AGGGTCCAAGTTC TAAGAGGAC		
		AC		
GAM2620	LOC51759 3'	CAGGAGAATTGCTTGAACC 73169		
		GGTTCAAGCAATTCTCCTG		
		CCAAGTTCGTTAAGAGGAC		
GAM2620	LOC55974 3'	CAGGAGAATTGCTTGAACCCAG 38742	CA	
	GA	TCC GGTTCAAGCAATTCTCCTG		
		AGG CCAAGTTCGTTAAGAGGAC		
		AC		
GAM2620	LOC57118 3'	CAGGAGAATCACTTGAACCCAG 40217	CA	CA
	GA	TCC GGTTCAAG ATTCTCCTG		
		AGG CCAAGTTC TAAGAGGAC		
		AC AC		
GAM2620	LOC63929 3'	CATGAGAATTGCTTGAACCTGG 42280		C
	GA	TCCCAGGTTCAAGCAATTCTC TG		
		AGGGTCCAAGTTCGTTAAGAG AC		
		T		
GAM2620	LOC85479 5'	CAGGAGAAGGGCGTGAACCTGG 53562	A	AA
	GA	TCCCAGGTTCA GC TTCTCCTG		
		AGGGTCCAAGT CG AAGAGGAC		
		G GG		
GAM2620	LOC89890 3'	CAGGAGAATTGCTGAAACCCGG 61204	A	CA
	GA	TCCC GGTT AGCAATTCTCCTG		
		AGGG CCAA TCGTTAAGAGGAC		
		C AG		
GAM2620	LOC90038 3'	CAGGAGAATCACTTGAACCCAG 61794	CA	CA
	GA	TCC GGTTCAAG ATTCTCCTG		

			AGG CCAAGTTC TAAGAGGAC		
			AC AC		
GAM2620	LOC90038	3'	GAATCACTTGAACCCAGGA	61807	CA CA
			TCC GGTTC AAG ATTC		
			AGG CCAAGTTC TAAG		
			AC AC		
GAM2620	LOC90072	5'	CAGGAGAATCTCTTGAACCTGG	61954	CA
			CCAGGTTCAAG ATTCTCCTG		
			GGTCCAAGTTC TAAGAGGAC		
			TC		
GAM2620	LOC90072	3'	CAGGAGGATCGCTTGAGCCCAG	61955	CA A
			TCC GGTTC AAGC ATTCTCCTG		
			AGG CCGAGTTCG TAGGAGGAC		
			AC C		
GAM2620	LOC90092	3'	CAGAAGAATCGCTTGAACC	62056	A C
			GGTTC AAGC ATTCT CTG		
			CCAAGTTCG TAAGA GAC		
			C A		
GAM2620	LOC90141	3'	CAGGAGGATCACTTGAGCCTAG	62300	C CA
			TCC AGGTTCAAG ATTCTCCTG		
			AGG TCCGAGTTC TAGGAGGAC		
			A AC		
GAM2620	LOC90155	5'	CAGGAGAATCGCTTGAACCCGG	62363	A A
			TCCC GGTTC AAGC ATTCTCCTG		
			AGGG CCAAGTTCG TAAGAGGAC		
			C C		
GAM2620	LOC90233	3'	CAGGAGAATCGCTTGAACC	57191	A
			GGTTC AAGC ATTCTCCTG		
			CCAAGTTCG TAAGAGGAC		
			C		
GAM2620	LOC90321	3'	CAGGAGAATTGCTTGAATCCAG	62931	CA
			TCC GGTTC AAGCAATTCTCCTG		
			AGG CTAAGTTCGTTAAGAGGAC		
			AC		
GAM2620	LOC90321	3'	GAGGATTGCTCAAGCCCAGGA	62934	CA CA
			TCC GGTTC AGCAATTCTC		
			AGG CCGA TCGTTAGGAG		
			AC AC		
GAM2620	LOC90393	5'	CAGGAGAATGGCGTGAACCCGG	63305	A A A
			TCCC GGTTC A GC ATTCTCCTG		

			AGGG CCAAGT CG TAAGAGGAC		
			C G G		
GAM2620	LOC90591	3'	CAGGAGAATCACTTGAACCCAG 64153	CA	CA
	GA		TCC GGTTC AAG ATTCTCCTG		
			AGG CCAAGTTC TAAGAGGAC		
			AC AC		
GAM2620	LOC90591	3'	CAGGAGAATGGCGTGAATCCAG 64154	CA	A A
	GA		TCC GGTTC A GC ATTCTCCTG		
			AGG CTAAGT CG TAAGAGGAC		
			AC G G		
GAM2620	LOC90591	3'	CAGGAGAATTGCTTGAACCTGG 64155		
	GA		TCCCAGGTTCAAGCAATTCTCCTG		
			AGGGTCCAAGTTCGTTAAGAGGAC		
GAM2620	LOC90624	3'	CAGGAAAATCACTTGAACCCGG 64367	A	CA C
	GA		TCCC GGTTC AAG ATT TCCTG		
			AGGG CCAAGTTC TAA AGGAC		
			C AC A		
GAM2620	LOC90777	3'	CAGGAGGATCACTTGAACCCAG 64665	A_	CA
	GG		CCC GGTTC AAG ATTCTCCTG		
			GGG CCAAGTTC TAGGAGGAC		
			AC AC		
GAM2620	LOC90784	5'	CAGGAGAATCACTTGAACCGGG 64693	A	CA
	GA		TCCC GGTTC AAG ATTCTCCTG		
			AGGG CCAAGTTC TAAGAGGAC		
			G AC		
GAM2620	LOC90785	3'	CAGGAGAATCACTTGAACCTGG 64711		CA
	GA		TCCCAGGTTCAAG ATTCTCCTG		
			AGGGTCCAAGTTC TAAGAGGAC		
			AC		
GAM2620	LOC90841	5'	CAGGAGAATCGCTTGAACCTGG 64865		A
	GA		TCCCAGGTTCAAGC ATTCTCCTG		
			AGGGTCCAAGTTCG TAAGAGGAC		
			C		
GAM2620	LOC90979	3'	CAGGAGAATTGCTTGAACCCAG 65135	CA	
	GA		TCC GGTTC AAGCAATTCTCCTG		
			AGG CCAAGTTCGTTAAGAGGAC		
			AC		
GAM2620	LOC91035	3'	CAGGAGAATCACTAGAAGCCAG 65296	A _ A	CA
	G		CC GGT C AG ATTCTCCTG		

		GG CCGA G TC TAAGAGGAC		
		A A A AC		
GAM2620	LOC91056 3'	CAGGAGAATTACTTGAACCTGG 96403	C	
	GA	TCCCAGGTTCAAG AATTCTCCTG		
		AGGGTCCAAGTTC TTAAGAGGAC		
		A		
GAM2620	LOC91250 5'	CAGGAGAATCGCTTGAACCTGG 65911	A	
	GA	TCCCAGGTTCAAGC ATTCTCCTG		
		AGGGTCCAAGTTCG TAAGAGGAC		
		C		
GAM2620	LOC91286 3'	GCAGGAGAATCGCTTGAACCTG 66060	A	___
	GGA	TCCCAGGTTCAAGC ATTCTCCTG C		
		AGGGTCCAAGTTCG TAAGAGGAC G		
		C		___
GAM2620	LOC91351 3'	AGAAAATGTGCATTAGAACCTG 66295	___	A___
	GGA	TCCCAGGTTC AA GCA TTCT		
		AGGGTCCAAG TT CGT AAGA		
		A A GTAA		
GAM2620	LOC91380 3'	CAGGAGAATCACTTGAACCTGG 66439	CA	
	G	CCCAGGTTCAAG ATTCTCCTG		
		GGGTCCAAGTTC TAAGAGGAC		
		AC		
GAM2620	LOC91380 3'	CAGGAGAATTGCTTGAACCCGG 66440	A	
	GA	TCCC GGTTC AAGCAATTCTCCTG		
		AGGG CCAAGTTCGTTAAGAGGAC		
		C		
GAM2620	LOC91442 3'	CATGAGAATCACTTGAACCCGG 66642	A	CA C
	GA	TCCC GGTTC AAG ATTCTC TG		
		AGGG CCAAGTTC TAAGAG AC		
		C AC T		
GAM2620	LOC91565 3'	CAGGAGGATGACTTGAGCCCAG 67052	CA	CA
	GA	TCC GGTTC AAG ATTCTCCTG		
		AGG CCGAGTTC TAGGAGGAC		
		AC AG		
GAM2620	LOC91812 3'	CAGGAGAATTGCTTGAACCAGG 67815	CA	
	A	TCC GGTTC AAGCAATTCTCCTG		
		AGG CCAAGTTCGTTAAGAGGAC		
		A_		
GAM2620	LOC91813 3'	CAGGAGAATTGCTTGAACCAGG 67839	CA	
	A	TCC GGTTC AAGCAATTCTCCTG		

			AGG CCAAGTTCGTTAAGAGGAC		
			A_		
GAM2620	LOC91862	3'	CAGGAGAATCGCTTGAATCTGG 54571	A	
	GA		TCCCAGGTTCAAGC ATTCTCCTG		
			AGGGTCTAAGTTCG TAAGAGGAC		
			C		
GAM2620	LOC91963	5'	CATGAGAATTGCTTGAGCCTAG 68316	C	C
	GA		TCC AGGTTCAAGCAATTCTC TG		
			AGG TCCGAGTTCGTTAAGAG AC		
			A T		
GAM2620	LOC92078	3'	CAGGAAAATTGCTTGAACCTCAG 68592	CA	C
	GA		TCC GGTTC AAGCAATT TCCTG		
			AGG TCAAGTTCGTTAA AGGAC		
			AC A		
GAM2620	LOC92223	3'	CAGGAGAATCACTTGAACCTGG 69046	CA	
	GA		TCCCAGGTTCAAG ATTCTCCTG		
			AGGGTCCAAGTTC TAAGAGGAC		
			AC		
GAM2620	LOC92228	3'	CAGGAGAATCGCTTGAACCTGG 69070	A	
	GA		TCCCAGGTTCAAGC ATTCTCCTG		
			AGGGTCCAAGTTCG TAAGAGGAC		
			C		
GAM2620	LOC92231	3'	GGATCACCTGAGCCTGGGA 69091	AGCA	
			TCCCAGGTTCA ATTC		
			AGGGTCCGAGT TAGG		
			CCAC		
GAM2620	LOC92267	3'	CAGGAGAATCGCTTGAATATGG 69166	G	A
	GA		TCCA GTTCAAGC ATTCTCCTG		
			AGGGT TAAGTTCG TAAGAGGAC		
			A C		
GAM2620	LOC92270	5'	CAGGAGAATTGCTTGAACCTGG 69184		
	GA		TCCCAGGTTCAAGCAATTCTCCTG		
			AGGGTCCAAGTTCGTTAAGAGGAC		
GAM2620	LOC92299	3'	CAGGAGAATTGCTTGAACCCGG 69361	A	
	G		CCC GGTTC AAGCAATTCTCCTG		
			GGG CCAAGTTCGTTAAGAGGAC		
			C		
GAM2620	LOC92405	3'	AGGAGAATCGCTTGAACCCGGG 69709	A	A
	A		TCCC GGTTC AAGC ATTCTCCT		

AGGG CCAAGTTCG TAAGAGGA
 C C
 GAM2620 LOC92421 3' CAGGAGAATTGCTTGAGCCCAG 69724 CA
 GA TCC GGTTC AAGCAATTCTCCTG
 ||| |||||
 AGG CCGAGTTCGTTAAGAGGAC
 AC
 GAM2620 LOC92465 5' CAGGAAAATCACTTGAACCCCG 69944 CA CA C
 GA TCC GGTTC AAG ATT TCCTG
 ||| ||||| ||| |||||
 AGG CCAAGTTC TAA AGGAC
 CC AC A
 GAM2620 LOC92465 5' CAGGAGAAATCACTTGAACCCA 69945 A_ CAA_
 GGG CCC GGTTC AAG TTCTCCTG
 ||| ||||| |||||
 GGG CCAAGTTC AAGAGGAC
 AC ACTA
 GAM2620 LOC92466 3' CAGGAGAATCTCTTGAACCCGG 69963 A CA
 GA TCCC GGTTC AAG ATTCTCCTG
 ||||| ||||| |||||
 AGGG CCAAGTTC TAAGAGGAC
 C TC
 GAM2620 LOC92482 3' CAGGAGAATTGCTTGAATCCAG 70018 CA
 G CC GGTTC AAGCAATTCTCCTG
 || |||||
 GG CTAAGTTCGTTAAGAGGAC
 AC
 GAM2620 LOC92499 5' CAGGAGAATCGCTTGAACCTGG 70104 A
 G CCCAGGTTCAAGC ATTCTCCTG
 ||||| |||||
 GGGTCCAAGTTCG TAAGAGGAC
 C
 GAM2620 LOC92573 5' CAGGAGAATCGCTTTAATCTAG 70370 C C A
 GA TCC AGGTT AAGC ATTCTCCTG
 ||| |||| ||| |||||
 AGG TCTAA TTCG TAAGAGGAC
 A T C
 GAM2620 LOC92573 3' CAGGAGAATTGCTTGAACC 70371
 GGTTC AAGCAATTCTCCTG
 ||||| |||||
 CCAAGTTCGTTAAGAGGAC
 AA AA
 GAM2620 LOC92609 3' AGAAGCAAGAACTTGGGA 73203
 TCCCAGGTTG GC TTCT
 ||||| || |||
 AGGGTTCAAG CG AAGA
 AA _
 GAM2620 LOC92771 3' CAGGAGAATTGCTTGAACCCAG 54209 CA
 GA TCC GGTTC AAGCAATTCTCCTG
 ||| |||||

			AGG CCAAGTTCGTTAAGAGGAC		
			AC		
GAM2620	LOC93070	3'	CAGGAGAATCGCTGGAACCTGG 71803	A	A
		GA	TCCCAGGTTC AGC ATTCTCCTG		
			AGGGTCCAAG TCG TAAGAGGAC		
			G C		
GAM2620	LOC93132	5'	CAGGAGAATCACTTGAAGCTGG 71981	G	CA
		GA	TCCCAG TTCAAG ATTCTCCTG		
			AGGGTC AAGTTC TAAGAGGAC		
			G AC		
GAM2620	LOC93132	5'	CAGGAGAATTGCTTGAACCCGG 71982	A	
		GA	TCCC GGTTCAAGCAATTCTCCTG		
			AGGG CCAAGTTCGTTAAGAGGAC		
			C		
GAM2620	LOC96597	5'	GAATTGCTTGAACCCAGG 67460	CA	
			CC GGTTCAAGCAATTC		
			GG CCAAGTTCGTTAAG		
			AC		
GAM2621	GPC6	3'	CCATGCCACAAAACTTA 20331	C	C _
			TAAGT TT GTGG ATGG		
			ATTCA AA CACC TACC		
			A A G		
GAM2621	P2RY6	3'	CCAAACCATGCGGAGA 15995	GG	C
			TCTTCGT ATGG TTGG		
			AGAGGCG TACC AACC		
			_ A		
GAM2621	PPP1R12B	3'	CCAAGTTTAAGAAGACTTA 50380	GTGGAT	
			TAAGTCTTC GGCTTGG		
			ATTCAGAAG TTGAACC		
			AAT__		
GAM2621	KIAA0318	5'	CTCCAAGCCAAGCTGGAGA 69529	TGGA	
			TCTTCG TGGCTTGGAG		
			AGAGGT ACCGAACCTC		
			CGA_		
GAM2621	KIAA0737	3'	CTCCAAGCCAGTGAAGAGTTA 29807	G	TGGA
			TAA TCTTCG TGGCTTGGAG		
			ATT AGAAGT ACCGAACCTC		
			G G__		
GAM2621	KIAA0779	3'	CCAAACTGCCTGAAGACTTA 86907	T	A C
			TAAGTCTTCG GG TGG TTGG		

		ATTCAGAAGT CC GTC AACC	
		— — A	
GAM2621	KIAA1297	3' CCAAACCCCTCCACGAAGAC 72631	T C_
		GTCTTCGTGGA GG TTGG	
		CAGAAGCACCT CC AACC	
		C CA	
GAM2621	LYSAL1	3' CTCACAGCTCCACGAAGACT 18123	TG TG
		AGTCTTCGTGGA GCT GAG	
		TCAGAAGCACCT CGA CTC	
		— CA	
GAM2621	LOC146433	5' CCAAGCCACCGGCTCAGAC 78436	TC _ A
		GTCT GT GG TGGCTTGG	
		CAGA CG CC ACCGAACC	
		CT G _	
GAM2621	LOC150282	3' CCCCTTCCACGAAGAC 80540	T CTT
		GTCTTCGTGGA GG GG	
		CAGAAGCACCT CC CC	
		T _	
GAM2621	LOC154386	5' CCAACAGCCCATGAAGACTTA 81987	ATG _
		TAAGTCTTCGTGG GCT TGG	
		ATTCAGAAGTACC CGA ACC	
		— CA	
GAM2622	GRIN2B	3' AGAGAAATGAGCTGCACT 7728	G GGCG C
		AGTG AGCT GTTTC TCT	
		TCAC TCGA TAAAG AGA	
		G G _ _	
GAM2622	KIF5A	5' AGAAGAGTCCCAGCCCCAC 18372	A C GT CC
		GTGG GCTGG G TT TCT	
		CACC CGACC C AG AGA	
		C _ TG A_	
GAM2622	PDE5A	3' TGAAAGGATCAACAACATCCAC 8429	GC GCG _ C
	T	AGTGGA TG GTT TCCT TCA	
		TCACCT AC CAA AGGA AGT	
		_ AA_ CT A	
GAM2622	PDE5A	3' TGAAAGGATCAACAACATCCAC 54218	GC GCG _ C
	T	AGTGGA TG GTT TCCT TCA	
		TCACCT AC CAA AGGA AGT	
		_ AA_ CT A	
GAM2622	PDE5A	3' TGAAAGGATCAACAACATCCAC 54220	GC GCG _ C
	T	AGTGGA TG GTT TCCT TCA	

			TCACCT AC CAA AGGA AGT		
			__ AA_ CT A		
GAM2622	PDE5A	3'	TGAAAGGATCAACAACATCCAC 54221	GC GCG	__ C
	T		AGTGGA TG GTT TCCT TCA		
			TCACCT AC CAA AGGA AGT		
			__ AA_ CT A		
GAM2622	RNGTT	3'	GAAAAAAGTAAAGCTCCATT 15065	G_ GG_	
			AGTGGAGCT GC TTTC		
			TTACCTCGA TG AAAG		
			AA AAA		
GAM2622	SNX13	3'	TGAGAGAAAAGTCCCCCAT 31396	AGCT	C
			GTGG GCGGTTT CTCTCA		
			TACC CCGTCAAA GAGAGT		
			C__ A		
GAM2622	STK4	3'	GAGGGCCCCAGCTCCAC 21865	C TT	
			GTGGAGCTGG GGT CCTC		
			CACCTCGACC CCG GGAG		
			- -		
GAM2622	TP53	3'	AGGAAATCTCACCCCAT 6794	AGC	C
			GTGG TGG GGTTTCCT		
			TACC ACT CTAAAGGA		
			CC_ _		
GAM2622	ABLM	3'	AAGGAAACCTTCCCT 11319	T CTGGC	C
			AG GGAG GGTTTCCT T		
			TC CCTT CCAAAGGA A		
			- - - - - A		
GAM2622	ABLM	3'	AAGGAAACCTTCCCT 22975	T CTGGC	C
			AG GGAG GGTTTCCT T		
			TC CCTT CCAAAGGA A		
			- - - - - A		
GAM2622	APCL	3'	AGGAAACCCCAGCCCCAC 20811	A C	
			GTGG GCTGG GGTTTCCT		
			CACC CGACC CCAAAGGA		
			C _		
GAM2622	Apg4B	3'	TGAGAGGAGCGGCAGCCACACT 26186	GA G GT	
			AGTG GCTG CG TTCCTCTCA		
			TCAC CGAC GC GAGGAGAGT		
			AC G _		
GAM2622	DKFZP434C0826	5'	GGCCAACCTCCAGCTCCAC 85154	C T_	
			GTGGAGCTGG GGTT CC		

CACCTCGACC CCAA GG
T CC
GAM2622 FLJ10759 3' AGGAATTGTCAGCCCTAC 37119 A T
GTGG GCTGGCGGTT CCT
||||| ||||| |||
CATC CGACTGTAA GGA
C _
GAM2622 FLJ20413 5' TGAGAGACACCAGCCTCCACT 35597 _ CG TTC
AGTGGAG CTGG GT CTCTCA
||||| ||| || |||||
TCACCTC GACC CA GAGAGT
C A_ _
GAM2622 FLJ23017 3' AGAAAAAACTGCTCTAC 43415 TGGC CC
GTGGAGC GGTTT TCT
||||| ||||| |||
CATCTCG TCAAA AGA
_ AA
GAM2622 HSPC048 3' GAGAGGATCTACTCCACT 27117 C CGGTT
AGTGGAG TGG TCCTCTC
||||| ||| |||||
TCACCTC ATC AGGAGAG
_ T_ _
GAM2622 KIAA0596 3' GGCAACCGCGCCCCACT 63494 A T T
AGTGG GC GGCGGTT CC
||||| || ||||| ||
TCACC CG CCGCCAA GG
C _ C
GAM2622 MGC2742 3' AGAAGAGACACATGCTCCACT 43978 TGGCG C
AGTGGAGC GTTTC TCT
||||| ||||| |||
TCACCTCG CAGAG AGA
TACA_ A
GAM2622 MMP24 3' GAGGTACCACAGCTCCACT 22919 GC TT
AGTGGAGCTG GGT CCTC
||||| ||| |||||
TCACCTCGAC CCA GGAG
A_ T_
GAM2622 NBR2 3' GAAAAAGGTCAGCTCCAC 20618 GG_
GTGGAGCTGGC TTTC
||||| ||||| |||
CACCTCGACTG AAAG
GAA
GAM2622 SGKL 3' AGAAGAAACCGTATTTTTCCAT 26049 CTG_ C
GTGGAG GCGGTTTC TCT
||||| ||||| |||
TACCTT TGCCAAAG AGA
TTTA A
GAM2622 ZNF291 3' TGAAAGAAAAATGTAACTCCA 40850 C G C C
TGGAG TGGCG TTT CT TCA
||||| ||||| ||| |||

			ACCTC ATTGT AAA GA AGT		
			A A A A		
GAM2622	LOC164382	5'	GAGAGGAGCAGACCCAC 88558	AG	GCGGT
			GTGG CTG TTCCTCTC		
			CACC GAC GAGGAGAG		
			CA _____		
GAM2622	LOC206012	5'	AACTACACCAGCTCCACT 91088	C__	
			AGTGGAGCTGG GGTT		
			TCACCTCGACC TCAA		
			ACA		
GAM2622	LOC220595	5'	AGAAAAAACTGCTCCCT 92774	T	TGGC CC
			AG GGAGC GGTTT TCT		
			TC CCTCG TCAAA AGA		
			— _____ AA		
GAM2622	LOC222128	5'	GAAATTGACCCAGCTCCACT 94285	—	
			AGTGGAGCTGG CGGTTTC		
			TCACCTCGACC GTTAAAG		
			CA		
GAM2622	LOC222242	5'	GAAATTGACCCAGCTCCACT 95953	—	
			AGTGGAGCTGG CGGTTTC		
			TCACCTCGACC GTTAAAG		
			CA		
GAM2622	LOC254722	5'	GAAAGGACTCAGCTCCACT 99426	CGGTT	C
			AGTGGAGCTGG TCCT TC		
			TCACCTCGACT AGGA AG		
			C_____ A		
GAM2623	BSG	3'	CAGCCTCAAGTCACTCCCAAGC 9953	A	
	CC		GGGCTTGGGAGTGA GCTG		
			CCCGAACCTCACTGAACT CGAC		
			C		
GAM2623	BSG	3'	CAGCCTCAAGTCACTCCCAAGC 68404	A	
	CC		GGGCTTGGGAGTGA GCTG		
			CCCGAACCTCACTGAACT CGAC		
			C		
GAM2623	CHGA	3'	CAGCCTCCAGCCTGCCCAAGCC 8879	AGTGA	T A
	C		GGGCTTGGG CT GA GCTG		
			CCCGAACCC GA CT CGAC		
			GTCC_ C C		
GAM2623	COL6A2	3'	CAGCCCCAGGTCTCCCCAGGCC 10250	AGT	AA
	C		GGGCTTGGG GACTTG GCTG		

		CCCGGACCC CTGGAC CGAC	
		CT_ CC	
GAM2623 GALR1	5'	CAGCTCCGGGCTCCCGAACCC 9423	C TGA A
		GGG TTGGGAG CTTG AGCTG	
		CCC AGCCCTC GGGC TCGAC	
		A _ C	
GAM2623 MUCDHL	3'	CAGCCCCACGCACGACCCCAAG 49202	A_ ACT AA
		CCC GGGCTTGGG GTG TG GCTG	
		CCCGAACCC CAC AC CGAC	
		CAG GC_ CC	
GAM2623 OSM	3'	CAGCCCCAAGTTCCCCAGGCCC 40448	AGT AA
		GGGCTTGGG GACTTG GCTG	
		CCCGGACCC TTGAAC CGAC	
		C_ CC	
GAM2623 PEX14	3'	AGCCCCAGCCCCAGGCCC 64399	A GACT AA
		GGGCTTGGG GT TG GCT	
		CCCGGACCC CG AC CGA	
		_ _ _ CC	
GAM2623 PRX2	3'	AGCCTGGACTCCCGAGCCC 33307	GA TGAA
		GGGCTTGGGAGT CT GCT	
		CCCGAGCCCTCA GG CGA	
		_ TC_	
GAM2623 SLC7A8	3'	CAGCCTCTCCACCCCAAGCC 25299	A ACTT A
		GGCTTGGG GTG GA GCTG	
		CCGAACCC CAC CT CGAC	
		C CT_ C	
GAM2623 TMEPAI	3'	AGCCCCATTTCCCAAGCTC 39823	TGACT AA
		GGGCTTGGGAG TG GCT	
		CTCGAACCTT AC CGA	
		T_ _ CC	
GAM2623 ASB16	5'	CAGGTGCCACTGCCCAAACCC 55975	C _ _
		GGG TTGGG AGTG ACTTG	
		CCC AACCC TCAC TGGAC	
		A G CG	
GAM2623 ERG-1	5'	CAGCCCCAATTACCCAAAGCC 42098	G A C AA
		GGCTT GG GTGA TTG GCTG	
		CCGAA CC CATT AAC CGAC	
		A _ _ CC	
GAM2623 FHX	3'	CAGCTCCCTTCCACCAAGCCC 37920	GAGT CTT A
		GGGCTTGG GA GA GCTG	

CCCGAACC CT CT CGAC
 AC__ TCC _
 GAM2623 FLJ12505 5' AGCCCCAGCCCCAGGCC 45711 A GACT AA
 GGGCTTGGG GT TG GCT
 ||||| || || ||
 CCCGGACCC CG AC CGA
 _ ____ CC
 GAM2623 FLJ13055 3' CAGGTCATCCCAAACCC 43013 C G
 GGG TTGGGA TGACTTG
 || |||| |||||
 CCC AACCT ACTGGAC
 A _
 GAM2623 FLJ20464 5' AGCTTCTCCCCAAACC 35683 C AGT CTT
 GG TTGGG GA GAAGCT
 || |||| || |||||
 CC AACCC CT CTCGA
 A C__ _
 GAM2623 KIAA0125 5' CAGCAGGGACTCACCCCAAGC 29562 A C GAA
 CC GGGCTTGGG GTGA TT GCTG
 ||||| |||| || ||||
 CCCGAACCC CACT AG CGAC
 C C GGA
 GAM2623 KIAA0125 3' CAGCAGGGACCCACCCCAAGC 61124 A AC GAA
 CC GGGCTTGGG GTG TT GCTG
 ||||| |||| || ||||
 CCCGAACCC CAC AG CGAC
 C CC GGA
 GAM2623 KIAA0255 3' CAGGATCACTCCCCAGCCC 29130 T _
 GGGCT GGGAGTGA CTTG
 |||| ||||| ||||
 CCCGA CCCTCACT GGAC
 C A
 GAM2623 KIAA1260 3' CAAGTCACCCCAAATCC 60667 GC A
 GG TTGGG GTGACTTG
 || |||| |||||
 CC AACCC CACTGAAC
 TA C
 GAM2623 KIAA1404 3' CAGCTTCTGCAGGCTCCAAACC 62683 CTTG GACTT
 C GGG GGAGT GAAGCTG
 || |||| |||||
 CCC CCTCG CTCGAC
 AAA_ GACGT
 GAM2623 KIAA1533 5' AGCTCCTGCCCCCAAGCC 74139 A ACTT A
 GGCTTGGG GTG GA GCT
 ||||| || ||||
 CCGAACCC CGT CT CGA
 C C__ _
 GAM2623 KIAA1656 3' GCTTCAAACCTAACCC 66372 C AGTGAC
 GGG TTGGG TTGAAGC
 || |||| |||||

		CCC AATCC AACTTCG		
		— A —		
GAM2623	MCF2L	3' CAGCCTCACGGTTCAGCCC	61525	T GTG _ A
		GGGCT GGA ACT TGA GCTG		
		CCCGA CCCT TGG ACT CGAC		
		— _ C C		
GAM2623	MGC12928	5' CTTCAGAAACCCCAAGCCT	52905	A GAC
		GGGCTTGGG GT TTGAAG		
		TCCGAACCC CA GACTTC		
		— AA_		
GAM2623	MGC13053	5' CAGCCTCCATCCCCAAGCC	52101	A_ ACTT A
		GGCTTGGG GTG GA GCTG		
		CCGAACCC TAC CT CGAC		
		CC _ C		
GAM2623	MGC15631	5' CAGGAGACCCCCCAAGCCC	52225	A_ GA
		GGGCTTGGG GT CTTG		
		CCCGAACCC CA GGAC		
		CCC GA		
GAM2623	P2RX1	3' AGCCCCAGCTCCCAAGGCC	67749	G GACT AA
		GG CTTGGGAGT TG GCT		
		CC GAACCCTCG AC CGA		
		G _ CC		
GAM2623	PTPRT	3' AGCTTCAAATCACAGCC	56484	TGGGA C
		GGCT GTGA TTGAAGCT		
		CCGA CACT AACTTCGA		
		_ A		
GAM2623	LOC115123	3' TGAGCGACCCCAAGCCC	73595	A GA
		GGGCTTGGG GT CTTG		
		CCCGAACCC CA GAGT		
		C GC		
GAM2623	LOC123876	5' CAAGCGACTCCCAAGCCC	74714	GA
		GGGCTTGGGAGT CTTG		
		CCCGAACCCTCA GAAC		
		GC		
GAM2623	LOC163915	5' CAGCTTCAGACCCCAACCC	88422	CT A GAC
		GGG TGGG GT TTGAAGCTG		
		CCC ACCC CA GACTTCGAC		
		AC C _		
GAM2623	LOC257181	3' CAGCCCTCCAGCACCCCAAG	96228	A ACTT A_
	CCC	GGGCTTGGG GTG GA GCTG		

		CCCGAACCC CAC CT CGAC	
		_ GACC CCC	
GAM2623	LOC91759	5' CAGCCTCAGGATCTTCCAAGCC 67688	TGA A
	C	GGGCTTGGGAG CTTGA GCTG	
		CCCGAACCTTC GGA CT CGAC	
		TA_ C	
GAM2624	BSG	3' GGGCCACGGGTCTGTGTTCTGA 9957	A
		TCGAACACAGACCC TGGCCC	
		AGCTTGTGTCTGGG ACCGGG	
		C	
GAM2624	BSG	3' GGGCCACGGGTCTGTGTTCTGA 68407	A
		TCGAACACAGACCC TGGCCC	
		AGCTTGTGTCTGGG ACCGGG	
		C	
GAM2624	ELK4	5' GGCGCATCGTGTTCGA 10515	A CCCA _
		TCGAACAC GA TG GCC	
		AGCTTGTG CT AC CGG	
		_ _ _ G	
GAM2624	ELK4	5' GGCGCATCGTGTTCGA 41718	A CCCA _
		TCGAACAC GA TG GCC	
		AGCTTGTG CT AC CGG	
		_ _ _ G	
GAM2624	FOXD2	5' GGGCCCAATCTGTGTTGA 16791	G CCCAT
		TC AACACAGA GGCCC	
		AG TTGTGTCT CCGGG	
		_ AAC_	
GAM2624	GAB2	3' GGGCCATGCCTTGGTGTTC 25462	A CC
		GAACAC GA CATGGCCC	
		CTTGTG TT GTACCGGG	
		G CC	
GAM2624	GAB2	3' GGGCCATGCCTTGGTGTTC 55407	A CC
		GAACAC GA CATGGCCC	
		CTTGTG TT GTACCGGG	
		G CC	
GAM2624	HMOX1	3' GGGCCATGAAC TTTGTCCGG 10943	A C ACC
		TCG ACA AG CATGGCCC	
		GGC TGT TC GTACCGGG	
		C T AA_	
GAM2624	MAT1A	3' GGCCATGGACTCTGTCCTGA 92502	AAC C_
		TCG ACAGA CCATGGCC	

			AGT TGTCT GGTACCGG		
			CC_ CA		
GAM2624	MAX	3'	GCCATGGGTCTGTGCTGA 59705	AA	
			TCG CACAGACCCATGGC		
			AGT GTGTCTGGGTACCG		
			C_		
GAM2624	PMM2	3'	GGACCGGCTCTGTGTTT 72562	C AT _	
			GAACACAGA CC GG CC		
			CTTGTGTCT GG CC GG		
			C _ A		
GAM2624	SLC9A1	3'	GGGCCATGGGTCTCTCGG 70930	ACACA	
			TCGA GACCCATGGCCC		
			GGCT CTGGGTACCGGG		
			C _		
GAM2624	SPP1	3'	GGGTTATGTCTATGTTT 6969	C CC	
			GAACA AGAC ATGGCCC		
			CTTGT TCTG TATTGGG		
			A _		
GAM2624	TYK2	5'	GCCCGGGTCTGTGCTGA 60564	AA AT	
			TCG CACAGACCC GGC		
			AGT GTGTCTGGG CCG		
			C_ C_		
GAM2624	AK5	3'	GGTGCCAGTCTGTGTCCG 24931	A CCA _	
			CG ACACAGAC TGGC CC		
			GC TGTGTCTG ACCG GG		
			C _ T		
GAM2624	EPB41L1	3'	GGGCCTGGTCTGTGCTC 71112	A CAT	
			GA CACAGACC GGCCC		
			CT GTGTCTGG CCGGG		
			C T_		
GAM2624	FLJ12242	3'	GGGCCCTCCTGTGTTTGA 45503	ACCCAT	
			TCGAACACAG GGCCC		
			AGTTTGTGTC CCGGG		
			CTC_		
GAM2624	FLJ14326	3'	GGACCACTCTGTGTTGA 50777	G CCCA _	
			TC AACACAGA TGG CC		
			AG TTGTGTCT ACC GG		
			_ C_ A		
GAM2624	FLJ23471	3'	GGGCCATGGGCTTGGCCCGG 45635	AACA GA	
			TCG CA CCCATGGCCC		

			GGC GT GGGTACCGGG		
			CCG_ TC		
GAM2624	GPR	5'	GCCATGGGCGCTGTCGG	24292	ACA A_
			TCGA CAG CCCATGGC		
			GGCT GTC GGGTACCG		
			___ GC		
GAM2624	HAPIP	3'	GGGCCATGGGCTCACCCCTCGG	15467	ACAC_ A
			TCGA AG CCCATGGCCC		
			GGCT TC GGGTACCGGG		
			CCCAC _		
GAM2624	KCNJ9	3'	GCCAGTCTGTGTTTGA	18366	CCA
			TCGAACACAGAC TGGC		
			AGTTTGTGTCTG ACCG		

GAM2624	KIAA0089	3'	CTCTGGGTTTGTACTCGA	70506	AC T
			TCGA ACAGACCCA GG		
			AGCT TGTTTGGGT TC		
			CA C		
GAM2624	KIAA0285	3'	GGGCCATGGGGCCGGTTGGA	29688	G ACAGA
			TC AAC CCCATGGCCC		
			AG TTG GGGTACCGGG		
			G GCCG_		
GAM2624	KIAA0352	3'	GGCCATGGGTGTATGTTT	29826	CAG
			GAACA ACCCATGGCC		
			CTTGT TGGGTACCGG		
			ATG		
GAM2624	KIAA0773	3'	GGCTACAGGCTGTGTTT	28727	A CA
			GAACACAG CC TGGCC		
			CTTGTGTC GG ATCGG		
			_ AC		
GAM2624	KIAA0773	3'	GGGCTTCTGGGTCTGTGCCGA	28728	AA T_
			TCG CACAGACCCA GGCCC		
			AGC GTGTCTGGGT TCGGG		
			C_ CT		
GAM2624	KIAA1908	5'	GGCTGGGTCTGTGCCCG	73793	AA TG
			CG CACAGACCCA GCC		
			GC GTGTCTGGGT CGG		
			CC _		
GAM2624	MGC29891	3'	GGGCCACAATTTGCACTGTGTT	58867	ACC _
	C		GAACACAG CA TGGCCC		

CTTGTGTC GT ACCGGG
 AC_ TTAAC
 GAM2624 PEPP3 3' GGGCCATGGGCTGCTGCCAGA 30710 GAA _ A
 TC CA CAG CCCATGGCCC
 || ||| |||||
 AG GT GTC GGGTACCGGG
 ACC C _
 GAM2624 SLC37A1 3' GGGCCATGGCGCTGCTGTTC 39093 _ AC
 GAACA CAG CCATGGCCC
 ||||| ||| |||||
 CTTGT GTC GGTACCGGG
 C GC
 GAM2624 LOC146083 5' GGGCTGGTGTCTGTGTCAGA 84584 GA _ TG
 TC ACACAGAC CCA GCCC
 || ||||| ||| ||||
 AG TGTGTCTG GGT CGGG
 AC T _
 GAM2624 LOC146159 5' GGACCATGACAAGCATGTGTTC 78177 GACC____ _
 GG TCGAACACA CATGG CC
 ||||| ||| ||
 GGCTTGTGT GTACC GG
 ACGAACA A
 GAM2624 LOC201191 3' GGGCCATGGGAGGTTGGA 91346 G ACAGA
 TC AAC CCCATGGCCC
 || ||| |||||
 AG TTG GGGTACCGGG
 G GA____
 GAM2624 LOC222662 3' CCAGGTCTGTGTCTGA 94410 A CA
 TCG ACACAGACC TGG
 ||| ||||| |||
 AGT TGTGTCTGG ACC
 C _
 GAM2625 CDH12 3' CTTATCATTTAAAGTGGTGTA 15777 CCCAA GA
 TACACCACT GAA ATAAG
 ||||| ||| ||||
 ATGTGGTGA TTT TATTC
 AA____ AC
 GAM2625 GOCAP1 3' ATTGTTCTTGGGAGCAGTGTA 43007 CA G
 TACAC CTCCCAAGAA AAT
 |||| ||||| |||
 ATGTG GAGGGTTCTT TTA
 AC G
 GAM2625 DKFZp434N2435 5' CTTATTACTGTGGGGTGGT 98090 T AGAAG
 ACCAC CCCA AATAAG
 |||| ||| ||||
 TGGTG GGGT TTATTC
 _ GTCA_
 GAM2625 DKFZP564I122 3' CTTATTCTTCTCCCTCATGTGT 63877 CACTCCCA
 A TACAC AGAAGAATAAG
 |||| |||||

		ATGTG	TCTTCTTATTC		
		TACTCCC_			
GAM2625	FLJ21791	3'	CTTATTTGCAGAAAGTGGTGTA	62126	CCCAAGAA
			TACACCACT	GAATAAG	
			ATGTGGTGA	TTTATTC	
			AGACG__		
GAM2625	HMP19	3'	CTTATTCTTTGTTAGGAAAATG	88860	CCAC CAA_
	TA		TACA TCC	GAAGAATAAG	
			ATGT AGG	TTTCTTATTC	
			AAA_	ATTG	
GAM2625	KIAA1719	3'	TCTGTCTTGGGAGTGGTGTA	68742	_
			TACACCACTCCCAAGA	AGA	
			ATGTGGTGAGGGTTCT	TCT	
			G		
GAM2625	KIAA1853	3'	TTTTTCTTGGAAGCAGTG	69929	CA C
			CAC CT	CCAAGAAGAA	
			GTG GA	GGTTCTTTTT	
			AC A		
GAM2625	KIAA1877	3'	CTTATTCTTCTGCCATGAGT	66748	CCA_
			ACTC	AGAAGAATAAG	
			TGAG	TCTTCTTATTC	
			TACCG		
GAM2625	KIAA1906	3'	CTTATTCTTCTTGACTTTTGG	73571	CTCC_
			CCA	CAAGAAGAATAAG	
			GGT	GTTCTTCTTATTC	
			TTTCA		
GAM2625	OSBPL11	3'	CTTAATTTCCCAAGAGTGGTG	43206	CCAA AA
			CACCACTC	GAAG TAAG	
			GTGGTGAG	CTTT ATTC	
			AACC	A_	
GAM2625	YME1L1	3'	TCATTCTTGATGTGGTGTA	58438	TCC _
			TACACCAC	CAAGAA GA	
			ATGTGGTG	GTTCTT CT	
			TA_	A	
GAM2625	ZNF262	3'	CTTATTTTGTGTTGGGAGT	18723	A
			ACTCCCAAG	AGAATAAG	
			TGAGGGTTT	TTTTATTC	
			G		
GAM2625	LOC91960	3'	TGTGGCTTGGAACGTGGTGTA	68294	TC_ AAGA
			TACACCAC	CCAAG ATA	

			ATGTGGTG GGTTC TGT		
			CAA GG__		
GAM2626	FLRT1	3'	CCCACGCAGCTCTCCCGCCACT 60365	ACCA__	CG__
			GGCCA TGGCCAGT AGAGT GTGGG		
			ACCGGTCA TCTCG CACCC		
			CCGCCC ACG		
GAM2626	MYF6	3'	CCCACCGACCCTTCCTGGCC 11735	TACC	A
			GGCCAG AAG GTCGGTGGG		
			CCGGTC TTC CAGCCACCC		
			C__ C		
GAM2626	NFIC	3'	CCTGCCGACTCCCAGCCCGGCC 20012	A_ ACCAA	TG
	A		TGGCC GT GAGTCGG GG		
			ACCGG CG CTCAGCC CC		
			CC ACC__ GT		
GAM2626	PPY	3'	CCCTCTGCACCCTTGCTCTGG 12254	TA A _ T	
	CCA		TGGCCAG CCAAG GT CGG GGG		
			ACCGGTC GGTTC CA GTC CCC		
			TC C C T		
GAM2626	PTPN7	3'	CCAGGTCTTCAACACTGGCCA 12593	ACC_ G GG	
			TGGCCAGT AAGA TC TGG		
			ACCGGTCA TTCT GG ACC		
			CAAC _ _		
GAM2626	PTPN7	3'	CCAGGTCTTCAACACTGGCCA 55459	ACC_ G GG	
			TGGCCAGT AAGA TC TGG		
			ACCGGTCA TTCT GG ACC		
			CAAC _ _		
GAM2626	PTPN7	3'	CCAGGTCTTCAACACTGGCCA 55466	ACC_ G GG	
			TGGCCAGT AAGA TC TGG		
			ACCGGTCA TTCT GG ACC		
			CAAC _ _		
GAM2626	ARTN	3'	GACTCTGGCACTGGCCA 15613	A A	
			TGGCCAGT CCA GAGTC		
			ACCGGTCA GGT CTCAG		
			C _		
GAM2626	ARTN	3'	GACTCTGGCACTGGCCA 55109	A A	
			TGGCCAGT CCA GAGTC		
			ACCGGTCA GGT CTCAG		
			C _		
GAM2626	ARTN	3'	GACTCTGGCACTGGCCA 55117	A A	
			TGGCCAGT CCA GAGTC		

ACCGGTCA GGT CTCAG
 C _
 GAM2626 ARTN 3' GACTCTGGCACTGGCCA 55137 A A
 TGGCCAGT CCA GAGTC
 ||||| || ||||
 ACCGGTCA GGT CTCAG
 C _
 GAM2626 C1QTNF6 3' CCTGCCCTCAGTGA CTGGCCA 49991 ACCAA TC TG
 TGGCCAGT GAG GG GG
 ||||| || || ||
 ACCGGTCA CTC CC CC
 GTGA_ _ GT
 GAM2626 DKFZP434G1415 3' CTGATACCCTTGGTATAACCA 49269 CCA A_
 TGG GTACCAAG GTCGG
 || ||||| ||||
 ACC TATGGTTC TAGTC
 AA_ CCA
 GAM2626 DKFZP586F1524 3' CTGGCTCTTAGCACTGACC 32106 C ACC
 GG CAGT AAGAGTCGG
 || |||| |||||
 CC GTCA TTCTCGGTC
 A CGA
 GAM2626 DKFZp761B1514 3' CCCACCGACCCGCCACCTGCCA 51139 C TACCAAGA
 TGGC AG GTCGGTGGG
 ||| || |||||
 ACCG TC CAGCCACCC
 _ CACCGCC_
 GAM2626 KIAA0843 5' CCTCTGGCTCCCGACACTGGCC 30798 ACCAA T
 GGCCAGT GAGTCGG GG
 ||||| ||||| ||
 CCGGTCA CTCGGTC CC
 CAGCC T
 GAM2626 KIAA1755 3' CCACCCTTCATACTGGCCA 62007 CC AGTC
 TGGCCAGTA AAG GGTGG
 ||||| || ||||
 ACCGGTCAT TTC CCACC
 AC _
 GAM2626 KREMEN 3' ACCCTCAGGACTGGCCA 50222 A AA TC
 TGGCCAGT CC GAG GGT
 ||||| || || ||
 ACCGGTCA GG CTC CCA
 _ A_ _
 GAM2626 N4BP3 3' CCCAGTCTGTCTTGGCACTGGC 66846 A GT _
 CA TGGCCAGT CCAAGA CGG TGGG
 ||||| ||||| || ||||
 ACCGGTCA GGTTCT GTC ACCC
 C _ TG
 GAM2626 PRO1843 5' CCCACTTCTTAGCTACTGGCCA 38141 CC_ GTC
 TGGCCAGTA AAGA GGTGGG
 ||||| || |||||

ACCGGTCAT TTCT TCACCC
 CGA ____
 GAM2626 STI2 3' CCCACCGACCCCGGGCTGGCTA 90406 A AAGA
 TGGCCAGT CC GTCGGTGGG
 ||||| || |||||
 ATCGGTCG GG CAGCCACCC
 _ CCC_
 GAM2626 LOC118611 5' CCCCCGGCTCTGGCCA 75995 GTACCAA T
 TGGCCA GAGTCGG GGG
 |||| | ||||| ||
 ACCGGT CTCGGCC CCC

 GAM2626 LOC149076 3' CCCAGTCTACCTCGGTGCTGGC 79874 A A C _
 CA TGGCCAGTACC AG GT GG TGGG
 ||||| || || ||||
 ACCGGTCGTGG TC CA CT ACCC
 C _ T G
 GAM2626 LOC256306 5' TGA CTCTTGATCTGGCCA 98521 TAC
 TGGCCAG CAAGAGTCG
 |||| | |||||
 ACCGGTC GTTCTCAGT
 TA_
 GAM2626 LOC90379 3' CCCACCGACTGATGACCGGC 63202 A AC AG
 GCC GT CA AGTCGGTGGG
 || | || |||||
 CGG CA GT TCAGCCACCC
 C _ AG
 GAM2627 CDH12 3' CTTATCATTTAAAGTGGTGTA 15777 CCCAA GA
 TACACCACT GAA ATAAG
 ||||| || ||||
 ATGTGGTGA TTT TATTC
 AA _ AC
 GAM2627 GOCAP1 3' ATTGTTCTTGGGAGCAGTGTA 43007 CA G
 TACAC CTCCCAAGAA AAT
 |||| ||||| ||
 ATGTG GAGGGTTCTT TTA
 AC G
 GAM2627 DKFZp434N2435 5' CTTATTACTGTGGGGTGGT 98090 T AGAAG
 ACCAC CCCA AATAAG
 |||| || ||||
 TGGTG GGGT TTATTC
 _ GTCA_
 GAM2627 DKFZP564I122 3' CTTATTCTTCTCCCTCATGTGT 63877 CACTCCCA
 A TACAC AGAAGAATAAG
 |||| | |||||
 ATGTG TCTTCTTATTC
 TACTCC_
 GAM2627 FLJ21791 3' CTTATTTGCAGAAAGTGGTGTA 62126 CCCAAGAA
 TACACCACT GAATAAG
 ||||| |||||

		ATGTGGTGA	TTTATTC	
		AGACG__		
GAM2627	HMP19	3' CTTATTCTTTGTTAGGAAAATG 88860	CCAC CAA_	
	TA	TACA TCC GAAGAATAAG		
		ATGT AGG TTTCTTATTC		
		AAA_ ATTG		
GAM2627	KIAA1719	3' TCTGTCTTGGGAGTGGTGTA 68742	_	
		TACACCACTCCCAAGA AGA		
		ATGTGGTGAGGGTTCT TCT		
		G		
GAM2627	KIAA1853	3' TTTTCTTGGAAGCAGTG 69929	CA C	
		CAC CT CCAAGAAGAA		
		GTG GA GGTTCCTTTT		
		AC A		
GAM2627	KIAA1877	3' CTTATTCTTCTGCCATGAGT 66748	CCA__	
		ACTC AGAAGAATAAG		
		TGAG TCTTCTTATTC		
		TACCG		
GAM2627	KIAA1906	3' CTTATTCTTCTTGACTTTTGG 73571	CTCC_	
		CCA CAAGAAGAATAAG		
		GGT GTTCTTCTTATTC		
		TTTCA		
GAM2627	OSBPL11	3' CTTAATTTCCCAAGAGTGGTG 43206	CCAA AA	
		CACCACTC GAAG TAAG		
		GTGGTGAG CTTT ATTC		
		AACC A_		
GAM2627	YME1L1	3' TCATTCTTGATGTGGTGTA 58438	TCC _	
		TACACCAC CAAGAA GA		
		ATGTGGTG GTTCTT CT		
		TA_ A		
GAM2627	ZNF262	3' CTTATTTTGTGTTGGGAGT 18723	A	
		ACTCCCAAG AGAATAAG		
		TGAGGGTTT TTTTATTC		
		G		
GAM2627	LOC91960	3' TGTGGCTTGGAACGTGGTGTA 68294	TC_ AAGA	
		TACACCAC CCAAG ATA		
		ATGTGGTG GGTTT TGT		
		CAA GG__		
GAM2628	APOB	3' TTGAACTTTCACATAGCACAGA 6356	TC CTAA	
		TCTGTGCT GTGAAG TCAA		

AGACACGA CACTTT AGTT
 TA CA__
 GAM2628 DKFZP727C091 3' TTGATTCTGTTCGCAAAGCACA 66795 C GCT
 GA TCTGTGCTT GTGAA AATCAA
 ||||| ||| |||||
 AGACACGAA CGCTT TTAGTT
 A GTC
 GAM2628 FLJ20055 3' AGCTTCATCAAAACAGA 34903 GC C
 TCTGT TT GTGAAGCT
 |||| |||||
 AGACA AA TACTTCGA
 A_ C
 GAM2628 FLJ30567 3' TAGTCTCATGAAGCACAGA 59479 AG
 TCTGTGCTTCGTGA CTA
 ||||| |||
 AGACACGAAGTACT GAT
 CT
 GAM2628 GLTP 3' TTGGAATTTACGACAGCACAG 33593 _ _
 A TCTGTGCT TCGTGAAG CTAA
 ||||| ||||| |||
 AGACACGA AGCACTTT GGTT
 C AA
 GAM2628 IPLA2(GAMMA) 3' AGCTTGCATAGCACAGA 61340 TC _
 TCTGTGCT GTG AAGCT
 ||||| ||| |||||
 AGACACGA TAC TTCGA
 _ G
 GAM2628 KIAA1016 3' GATTTTCCAGAAGCACA 93385 GT GCT
 TGTGCTTC GAA AATC
 ||||| ||| |||
 ACACGAAG CTT TTAG
 AC _
 GAM2628 KIAA1500 3' TGATCAGCCAGGCACAGA 64813 CGTGAA A
 TCTGTGCTT GCT ATCA
 ||||| ||| |||
 AGACACGGA CGA TAGT
 C_ C
 GAM2628 RAB6C 3' ATTAGCTTCACAAGCACA 50482 C
 TGTGCTT GTGAAGCTAAT
 ||||| |||||
 ACACGAA CACTTCGATTA
 _
 GAM2628 SLC5A6 5' TGATCTCAGGAAGCACA 41181 G A CTA
 TGTGCTTC TGA G ATCA
 ||||| ||| |||
 ACACGAAG ACT C TAGT
 G _
 GAM2628 TRAF2 3' AGCTCACGAAGACAGA 41234 G A
 TCTGT CTTCGTGA GCT
 ||||| ||||| |||

AGACA GAAGCACT CGA

GAM2628	LOC147645	3'	GGCCTACCAAGCACAGA	79071	C	AA
			TCTGTGCTT GTG GCT			
			AGACACGAA CAT CGG			
			C C_			
GAM2628	LOC256295	3'	TTGGCTTCCAGAAGCACAGA	98378	GT	
			TCTGTGCTTC GAAGCTAA			
			AGACACGAAG CTTCGGTT			
			AC			
GAM2629	CDH12	3'	CTTATCATTTAAAGTGGTGTA	15777	CCCAA	GA
			TACACCACT GAA ATAAG			
			ATGTGGTGA TTT TATTC			
			AA_ AC			
GAM2629	GOCAP1	3'	ATTGTTCTTGGGAGCAGTGTA	43007	CA	G
			TACAC CTCCCAAGAA AAT			
			ATGTG GAGGGTTCTT TTA			
			AC G			
GAM2629	DKFZp434N2435	5'	CTTATTACTGTGGGGTGGT	98090	T	AGAAG
			ACCAC CCCA AATAAG			
			TGGTG GGGT TTATTC			
			_ GTCA_			
GAM2629	DKFZP564I122	3'	CTTATTCTTCTCCCTCATGTGT	63877	CACTCCCA	
	A		TACAC AGAAGAATAAG			
			ATGTG TCTTCTTATTC			
			TACTCCC_			
GAM2629	FLJ21791	3'	CTTATTTGCAGAAAGTGGTGTA	62126	CCCAAGAA	
			TACACCACT GAATAAG			
			ATGTGGTGA TTTATTC			
			AGACG_			
GAM2629	HMP19	3'	CTTATTCTTTGTTAGGAAAATG	88860	CCAC	CAA_
	TA		TACA TCC GAAGAATAAG			
			ATGT AGG TTTCTTATTC			
			AAA_ ATTG			
GAM2629	KIAA1719	3'	TCTGTCTTGGGAGTGGTGTA	68742	_	
			TACACCACTCCCAAGA AGA			
			ATGTGGTGAGGGTTCT TCT			
			G			
GAM2629	KIAA1853	3'	TTTTTCTTGGAAGCAGTG	69929	CA	C
			CAC CT CCAAGAAGAA			

		GTG GA GGTTCCTTTT		
		AC A		
GAM2629	KIAA1877	3' CTTATTCTTCTGCCATGAGT 66748	CCA__	
		ACTC AGAAGAATAAG		
		TGAG TCTTCTTATTC		
		TACCG		
GAM2629	KIAA1906	3' CTTATTCTTCTTGACTTTTGG 73571	CTCC_	
		CCA CAAGAAGAATAAG		
		GGT GTTCTTCTTATTC		
		TTTCA		
GAM2629	OSBPL11	3' CTTAATTTCCCAAGAGTGGTG 43206	CCAA AA	
		CACCACTC GAAG TAAG		
		GTGGTGAG CTTT ATTC		
		AACC A_		
GAM2629	YME1L1	3' TCATTCTTGATGTGGTGTA 58438	TCC _	
		TACACCAC CAAGAA GA		
		ATGTGGTG GTTCTT CT		
		TA_ A		
GAM2629	ZNF262	3' CTTATTTTGTGTTGGGAGT 18723	A	
		ACTCCCAAG AGAATAAG		
		TGAGGGTTT TTTTATTC		
		G		
GAM2629	LOC91960	3' TGTGGCTTGGAACGTGGTGTA 68294	TC_ AAGA	
		TACACCAC CCAAG ATA		
		ATGTGGTG GGTC TGT		
		CAA GG__		
GAM2630	A1BG	3' GGCTGGTCTCCAACCTC 56293	C AG	
		GAG TGGAGACCA GCC		
		CTC ACCTCTGGT CGG		
		A _		
GAM2630	CA4	3' GCCTCTCTGTTGCCTCAGCTCT 7391	_A_ CA__	
		AGAGCTG G GAC AGGC		
		TCTCGAC C TTG TCCG		
		T CG TCTC		
GAM2630	CIAS1	5' CGGCCTTGCTAACTTTTC 18096	CTGG A	
		GAAGAG AG CCAAGGCCG		
		CTTTTC TC GGTTCGGC		
		AA__ _		
GAM2630	DVL1	3' GCCTGGCTGCTCCAGCTC 60058	A__ A	
		GAGCTGGAG CCA GGC		

			CTCGACCTC GGT CCG		
			GTC _		
GAM2630	RXRA	3'	GCCCTGACCTTCGGTTTTCCGA 12920	A	AC A
			TCG AGAGCTGGAG CA GGC		
			AGC TTTTGGCTTC GT CCG		
			C CA C		
GAM2630	TRIM9	5'	CGGCCTTGGCCTCCCAAAGT 31448	___	A
			GCT GGAG CCAAGGCCG		
			TGA CCTC GGTTCCGGC		
			AAC C		
GAM2630	BLCAP	3'	CGGCCTTGATCCCCTTGATAGA 22942	GAA_	CT A C
			TC GAG GG GA CAAGGCCG		
			AG TTC CC CT GTTCCGGC		
			ATAG _ _ A		
GAM2630	DBR1	3'	GGCTGGTCTCCAACCTC 33067	C	AG
			GAG TGGAGACCA GCC		
			CTC ACCTCTGGT CGG		
			A _		
GAM2630	HRD1	3'	GCCTTCCTCTCCAACCTCTC 70151	C	CC
			GAAGAG TGGAGA AAGGC		
			CTTCTC ACCTCT TTCCG		
			A CC		
GAM2630	HRIHFB2122	3'	CCCTGGTCCCCCTCTGTC 57617	_	CT A A
			GA AGAG GG GACCA GG		
			CT TCTC CC CTGGT CC		
			G C_ _ C		
GAM2630	KIAA1052	5'	CGGCCTTGACCTCCTGTGCTC 30940	T_	AC
			GAGC GGAG CAAGGCCG		
			CTCG CCTC GTTCCGGC		
			TGT CA		
GAM2630	RAB39	3'	GGCTGGTCTCCAACCTCTCG 77123	A C	AG
			CGA GAG TGGAGACCA GCC		
			GCT CTC ACCTCTGGT CGG		
			C A _		
GAM2630	SPINT1	5'	CGGCCGAGCCCCAGCTCTCCGA 63332	A	AGACCAA
			TCG AGAGCTGG GGCCG		
			AGC TCTCGACC CCGGC		
			C CCGAG_		
GAM2630	LOC116411	5'	CGGGCTGGTCTCCAGCTC 74299		A G
			GAGCTGGAGACCA G CCG		

		CTCGACCTCTGGT C GGC		
		_ G		
GAM2630	LOC124460 3'	GCCCTGTGTGCTCTCCAGCTC 76564	___	A
		GAGCTGGAGA C CA GGC		
		CTCGACCTCT G GT CCG		
		CGT T C		
GAM2630	LOC129880 3'	CGGGCTGGTCTCCAGCTC 75405		A G
		GAGCTGGAGACCA G CCG		
		CTCGACCTCTGGT C GGC		
		_ G		
GAM2630	LOC154562 3'	GCCTTGGTCCCTAAGCCTC 81997	_ _	A
		GAG CT GG GACCAAGGC		
		CTC GA CC CTGGTTCCG		
		C AT _		
GAM2630	LOC168451 5'	CGGCCCGGTCTCCAGGGGCCT 83585	___	AA
	C	GAG CTGGAGACC GGCCG		
		CTC GACCTCTGG CCGGC		
		CGGG CC		
GAM2630	LOC199958 3'	CCTTTACAGTTCCAGCTCCTCG 91491	A	ACC_
	G	TCGA GAGCTGGAG AAGG		
		GGCT CTCGACCTT TTCC		
		C GACAT		
GAM2630	LOC254100 3'	GGCTGGTCTCCAATC 98158	C	AG
		GAG TGGAGACCA GCC		
		CTC ACCTCTGGT CGG		
		A _		
GAM2631	ATRN 3'	ATCTTTTAAAGGCAGTAATGGA 58444	CG_	GG
		TCCATT GCT TTAAAAGAT		
		AGGTAA CGG AATTTTCTA		
		TGA A_		
GAM2631	CHC1 3'	ATCTTTTAACATTTTGAAT 8858		CTG
		ATTCGG GTTAAAAGAT		
		TAAGTT CAATTTTCTA		
		TTA		
GAM2631	GM2A 3'	ATCTGCCACAGCAGAATGGAG 68374	G	GTAAA
		CTCCATTG GCTG AGAT		
		GAGGTAAG CGAC TCTA		
		A ACCG_		
GAM2631	LDOC1 5'	TTGGCCGAGCCGAACCGAG 25549	CA	_
		CTC TTCGGCT GGTAA		

			GAG AAGCCGA CCGGTT		
			CC G		
GAM2631	NEDD4	3'	TCCTTTAACCAAACCTGAA 70546	C_	A
			TTCGG TGGTAAA GA		
			AAGTC ACCAATTT CT		
			AA C		
GAM2631	RCN1	3'	TTGGGAAGCCAAACGGAGT 60375	A C	GG
			ACTCC TT GGCT TTAA		
			TGAGG AA CCGA GGTT		
			C A AG		
GAM2631	FLJ11068	3'	CTTGGAACCAATGGAGT 37587	TCGGC	AA
			ACTCCAT TGGTT AAG		
			TGAGGTA ACCAA TTC		
			GG		
GAM2631	FLJ21596	3'	CTTTTAAAAACAAAATGGAGT 46115	CGGCTGG	
			ACTCCATT TTAAAAG		
			TGAGGTAA AATTTTC		
			AACAAA_		
GAM2631	G2	3'	CTTTTAAAAAGCGTATGGAGT 67241	TCG	GG
			ACTCCAT GCT TTAAAAG		
			TGAGGTA CGA AATTTTC		
			TG_ AA		
GAM2631	KIAA1198	3'	TTAACACTGAATGGAG 64073	CTG	
			CTCCATTCGG GTTAA		
			GAGGTAAGTC CAATT		
			A_		
GAM2631	LOC253003	3'	ATCTTTTAACATTTTGAAT 98673	CTG	
			ATTCGG GTTAAAAGAT		
			TAAGTT CAATTTTCTA		
			TTA		
GAM2632	CDH12	3'	CTTATCATTTAAAGTGGTGTA 15777	CCCAA	GA
			TACACCACT GAA ATAAG		
			ATGTGGTGA TTT TATTC		
			AA_ AC		
GAM2632	GOCAP1	3'	ATTGTTCTTGGGAGCAGTGTA 43007	CA	G
			TACAC CTCCCAAGAA AAT		
			ATGTG GAGGGTTCTT TTA		
			AC G		
GAM2632	DKFZp434N2435	5'	CTTATTACTGTGGGGTGGT 98090	T	AGAAG
			ACCAC CCCA AATAAG		

		TGGTG GGGT TTATTC	
		_ GTCA_	
GAM2632	DKFZP564I122	3' CTTATTCTTCTCCCTCATGTGT 63877	CACTCCCA
	A	TACAC AGAAGAATAAG	
		ATGTG TCTTCTTATTC	
		TACTCCC_	
GAM2632	FLJ21791	3' CTTATTTGCAGAAAGTGGTGTA 62126	CCCAAGAA
		TACACCACT GAATAAG	
		ATGTGGTGA TTTATTC	
		AGACG__	
GAM2632	HMP19	3' CTTATTCTTTGTTAGGAAAATG 88860	CCAC CAA_
	TA	TACA TCC GAAGAATAAG	
		ATGT AGG TTTCTTATTC	
		AAA_ ATTG	
GAM2632	KIAA1719	3' TCTGTCTTGGGAGTGGTGTA 68742	_
		TACACCACTCCCAAGA AGA	
		ATGTGGTGAGGGTTCT TCT	
		G	
GAM2632	KIAA1853	3' TTTTCTTGAAGCAGTG 69929	CA C
		CAC CT CCAAGAAGAA	
		GTG GA GGTTCTTTT	
		AC A	
GAM2632	KIAA1877	3' CTTATTCTTCTGCCATGAGT 66748	CCA_
		ACTC AGAAGAATAAG	
		TGAG TCTTCTTATTC	
		TACCG	
GAM2632	KIAA1906	3' CTTATTCTTCTTGACTTTTGG 73571	CTCC_
		CCA CAAGAAGAATAAG	
		GGT GTTCTTCTTATTC	
		TTTCA	
GAM2632	OSBPL11	3' CTTAATTTCCCAAGAGTGGTG 43206	CCAA AA
		CACCACTC GAAG TAAG	
		GTGGTGAG CTTT ATTC	
		AACC A_	
GAM2632	YME1L1	3' TCATTCTTGATGTGGTGTA 58438	TCC _
		TACACCAC CAAGAA GA	
		ATGTGGTG GTTCTT CT	
		TA_ A	
GAM2632	ZNF262	3' CTTATTTTGTGTTGGGAGT 18723	A
		ACTCCCAAG AGAATAAG	

			TGAGGGTTT TTTTATTC		
			G		
GAM2632	LOC91960	3'	TGTGGCTTGGAACGTGGTGTA 68294	TC_	AAGA
			TACACCAC CCAAG ATA		
			ATGTGGTG GGTTC TGT		
			CAA GG_		
GAM2633	ADCY8	5'	GCTCACAGCGCTGCGGCTCCT 8501	A AT	CAA
			AGGA CC GGC CTGTGAGC		
			TCCT GG TCG GACACTCG		
			C CG C_		
GAM2633	CIT	5'	GCTCACAGAGCTACAGCTCTCC 70304	ACCA_	CAA
			GGA TGGC CTGTGAGC		
			CCT ATCG GACACTCG		
			CTCGAC A_		
GAM2633	FAAH	5'	GCGGTCTCCGGCCATGGCCCC 97238	AA	A_
			GG CCATGGCC ACTGT		
			CC GGTACCGG TGGCG		
			CC CCTC		
GAM2633	GSTM3	5'	GCTCACAGTTTCCCTAGTCCT 68638	ACCAT	CC
			AGGA GG AACTGTGAGC		
			TCCT CC TTGACACTCG		
			GAT_ CT		
GAM2633	HSD11B2	3'	GCTCCGTGAGCCTTGTTTCCT 5771	T CA T T	
			AGGAACCA GGC AC G GAGC		
			TCCTTGGT CCG TG C CTCG		
			T AG _ _		
GAM2633	HYAL1	5'	CTCCAGTGGCCATGCTCC 53703	AC	A T
			GGA CATGGCCA CTG GAG		
			CCT GTACCGGT GAC CTC		
			C_ _ _		
GAM2633	NPTX2	3'	GCTGGAGTGGCCATGTCCCTT 94085	AAC	A G G
			AAGG CATGGCCA CT T AGC		
			TTCC GTACCGGT GA G TCG		
			CT_ _ G_		
GAM2633	RFX2	3'	GCCCCACCAGACCATGGGTTC 7158	_	CCAA _ A_
	TT		AAGGAACC ATGG CTG TG GC		
			TTCTTGG TACC GAC AC CG		
			G A_ C CC		
GAM2633	SMAP	5'	GCCCCACAGAGCCATGGTCC 22932	A	CAA A_
			GGA CCATGGC CTGTG GC		

			CCT GGTACCG GACAC CG		
			— A— CC		
GAM2633	SMURF1	3'	GCTCACAGCCCTGAGCTCTTT 94049	AC_ T	CAAC
			AAGGA CA GGC TGTGAGC		
			TTTCT GT CCG ACACTCG		
			CGA C —		
GAM2633	DC-TM4F2	3'	ACTGTTGGCCAGGGCTCCT 48895	A A	T
			AGGA CC TGGCCAAC GT		
			TCCT GG ACCGGTTG CA		
			C G T		
GAM2633	DKFZp566H0824	5'	GCTCACAAACCCCATAGTTGCC 34488	_ C	CCAAC
	T		AGG AAC ATGG TGTGAGC		
			TCC TTG TACC ACACTCG		
			G A CCAA_		
GAM2633	FLJ10292	3'	GCCCACAGTTGTTGGTTGTTCC 36432	C GGC	A
	T		AGGAAC AT CAACTGTG GC		
			TCCTTG TG GTTGACAC CG		
			T GTT C		
GAM2633	FLJ20085	3'	GCTCATGGTGCCACAGCCCCT 35009	AACCA	CA
			AGG TGGC ACTGTGAGC		
			TCC ACCG TGGTACTCG		
			CCGAC —		
GAM2633	FLJ22690	3'	GCTCACAGCCGACCTGTGGCCT 45575	AA	CCAA_
			AGG CCATGG CTGTGAGC		
			TCC GGTGTC GACACTCG		
			— CAGCC		
GAM2633	FLJ32449	3'	GCATTTGGCCATGGTTCCTT 59378	C	
			AAGGAACCATGGCCAA TGT		
			TTCCTTGGTACCGGTT ACG		
			T		
GAM2633	HPIP	3'	GCTCACAGCTGCCTTGGCCCC 40425	AA T	CAA
			GG CCA GGC CTGTGAGC		
			CC GGT CCG GACACTCG		
			CC T TC_		
GAM2633	ILF3	3'	GCTCACAGTCGAACTACAGCTC 25234	ACCA	CCA_
	C		GGA TGG ACTGTGAGC		
			CCT ATC TGACACTCG		
			CGAC AAGC		
GAM2633	KIAA1190	3'	GCTCACAGAGCACCCCAGTTCC 71651	CAT	CCAA
	T		AGGAAC GG CTGTGAGC		

			TCCTTG CC GACACTCG			
			ACC ACGA			
GAM2633	MGC11266	3'	GCTCACAGTGGTCAGGGCCC 44488	AA A	A	
			GG CC TGGCCA CTGTGAGC			
			CC GG ACTGGT GACACTCG			
			CG _ _			
GAM2633	MGC11352	5'	ACTGTTGGCCAGGGCTCCT 65424	A A	T	
			AGGA CC TGGCCAAC GT			
			TCCT GG ACCGGTTG CA			
			C G T			
GAM2633	MKP-7	3'	GCTTCTCTTGGCCATGGTCCC 67015	A	CTGT	
			GG ACCATGGCCAA GAGC			
			CC TGGTACCGTT TTCG			
			C CTC_			
GAM2633	MSP	3'	GCTCAGGCAGGCCATGGCC 50245	AA	AA G	
			GG CCATGGCC CT TGAGC			
			CC GGTACCGG GG ACTCG			
			_ AC _			
GAM2633	PGR1	3'	CTCACAGTTGGAGTTCTCC 53905	A	CATGG	
			A GGAAC CCAACTGTGAG			
			C TCTTG GGTGACACTC			
			C A_			
GAM2633	PTPRT	3'	GCTTCGTGTTGGCCAAGACTCC 56502	ACCA	TGT	
	TT		AAGGA TGGCCAAC GAGC			
			TTCCT ACCGGTTG TTCG			
			CAGA TGC			
GAM2633	TRF4-2	3'	CTCAAACAAGCCATGGTTCCTT 42611		CAACTG	
			AAGGAACCATGGC TGAG			
			TTCCTTGGTACCG ACTC			
			AACAA_			
GAM2633	LOC122786	3'	GCCTTTGGCCATGATTCT 74622	C	CT	
			GGAA CATGGCCAA GT			
			TCTT GTACCGGT CG			
			A TC			
GAM2633	LOC138428	3'	TAGTGGCCATGGCTGCCT 75862	AA_	A	
			AGG CCATGGCCA CTG			
			TCC GGTACCGGT GAT			
			GTC _			
GAM2633	LOC145581	3'	GCTCCATTAGACCATGGTTC 77794		CCAAC T	
			GAACCATGG TG GAGC			

CTTGGTACC AC CTCG
 AGATT _
 GAM2633 LOC146268 5' GCTCACAGTCGGCTTGCTGCCT 78342 AAC T A
 AGG CA GGCC ACTGTGAGC
 ||| || ||| |||||
 TCC GT TCGG TGACACTCG
 GTC _ C
 GAM2633 LOC147299 3' GCTGTGAGCCGCCATGGTCCC 78981 A CAA GTG
 GG ACCATGGC CT AGC
 || ||||| || |||
 CC TGGTACCG GA TCG
 C CC_ GTG
 GAM2633 LOC159199 3' GCTCACAGCTGGCGGCCCT 83062 AA ATG A
 AGG CC GCCA CTGTGAGC
 ||| || ||| |||||
 TCC GG CGGT GACACTCG
 C_ _ C
 GAM2633 LOC200982 5' AGTTGGCCATGGCTCTTT 91807 A
 AAGGA CCATGGCCAACT
 |||| |||||
 TTTCT GGTACCGGTTGA
 C
 GAM2633 LOC253842 3' GCTCATAGAAGCCTGGTCCCT 99238 A T CAA
 AGG ACCA GGC CTGTGAGC
 ||| ||| || |||||
 TCC TGGT CCG GATACTCG
 C _ AA_
 GAM2633 LOC254778 3' GCCCTGTGTTGGCCAAGGTTCC 97831 A TGTGA
 GGAACC TGGCCAAC GC
 ||||| ||||| ||
 CCTTGG ACCGGTTG CG
 A TGTCC
 GAM2633 LOC255231 3' CTCACAGTTAGCCAGCTGACC 97119 AACCA C
 GG TGGC AACTGTGAG
 || ||| |||||
 CC ACCG TTGACACTC
 AGTCG A
 GAM2633 LOC257358 5' GCTCGTGAAGAGCATGGTTCCT 98900 G CAACTG
 T AAGGAACCATG C TGAGC
 ||||| ||| |||||
 TTCCTTGGTAC G GCTCG
 _ AGAAGT
 GAM2633 LOC90190 3' CGCCCACAGAGCAATTGGCCAT 62422 AC _ A _
 GCCTCC GGA CATGGCCAA CTGTG GC G
 ||| ||||| ||| |||
 CCT GTACCGGTT GACAC CG C
 CC AACGA C _
 GAM2633 LOC90495 3' GCTCACAGTCAACTGCTTTCTT 63737 CCAT CA_
 T AAGGAA GGC ACTGTGAGC
 ||||| || |||||

TTTCTT TCG TGACACTCG
 _____ TCAAC
 GAM2633 LOC90750 3' GCTCACAGCCCTGCCCTGCCCC 64630 AAC T CAA_
 C GG CA GGC CTGTGAGC
 || ||| |||||
 CC GT CCG GACACTCG
 CCC C TCCC
 GAM2634 FLJ21438 5' CAAAACGCTTCCCCCATCCCA 62190 GAGATTATC
 TGGGA AAGCGTTTTG
 |||| |||||
 ACCCT TTCGCAAAAC
 ACCCCCC_
 GAM2634 FLJ32334 3' AAAACGCTATTCCTTCCCA 58605 A TTATCA
 TGGGAG GA AGCGTTTT
 |||| || |||||
 ACCCTT CT TCGCAAAA
 C TA____
 GAM2634 HHLA2 3' CAATGTACTTTGTAATCTCCCC 23953 A C CG T
 CA TGGG GAGATTAT AAG T TTG
 ||| ||||| || | |||
 ACCC CTCTAATG TTC G AAC
 C T AT T
 GAM2635 M17S2 5' CCGGTAGCGGACGGTCCTT 20910 A ATTCT
 AAGGACC TCC TTGCCGG
 ||||| || |||||
 TTCCTGG AGG GATGGCC
 C C____
 GAM2635 SCD 3' CCAAAACGAATGGTCTTT 18590 CCAT _ GCC
 AAGGACCAT TC TTT GG
 ||||| || ||| ||
 TTTCTGGTA AG AAA CC
 _____ C AT
 GAM2635 SLC35A1 3' CCGGGGAGAAGGATGACCC 22214 AC A G
 GG CATCC TTCTTT CCGG
 || |||| ||||| |||
 CC GTAGG AAGAGG GGCC
 CA _ _
 GAM2635 SYNGR1 3' CAAGGGCATGGGTGGTCC 17495 _
 GGACCATCCAT TCTTTG
 ||||| |||||
 CCTGGTGGGTA GGGAAC
 C
 GAM2635 VCX 5' GCTCCAAGAAGTGAATGGTCCT 69702 C CT CCG
 AGGACCAT CATT TTG GC
 ||||| ||| || ||
 TCCTGGTA GTGA AAC CG
 A AG CTA
 GAM2635 ARHGEF3 3' AAAGAATGAATGATTCTT 39455 C C
 AAGGA CAT CATTCTTT
 |||| ||| |||||

TTCTT GTA GTAAGAAA
 A A
 GAM2635 GROS1 3' CCAGAAGAGATGGTCCT 42552 CAT GCC
 AGGACCATC TCTTT GG
 ||||| ||| ||
 TCCTGGTAG AGAAG CC
 ____ AC
 GAM2635 KIAA1260 3' GCCACACAATGGATGGCTCT 60670 GA CTT CC
 AG CCATCCATT TG GGC
 || ||||| || |||
 TC GGTAGGTAA AC CCG
 TC C__ A_
 GAM2635 KIAA1467 3' GCCGGCAAAGCCAATATGACC 72070 AC CCATT
 GG CAT CTTTGCCGGC
 || ||| |||||
 CC GTA GAAACGGCCG
 A_ TAACC
 GAM2635 PMAIP1 3' GCAAGAATGGAAGACCCTT 41211 ACCA T
 AAGG TCCATTCTT GC
 ||| ||||| ||
 TTCC AGGTAAGAA CG
 CAGA _
 GAM2635 POPX1 3' GCCAATGCCTATGGGTGGCC 30475 A TCTTT C__
 GG CCATCCAT GC GGC
 || ||||| || |||
 CC GGTGGGTA CG CCG
 _ TC__ TAA
 GAM2635 LOC144278 3' GCCAGCAAAGACTGCTCGATGG 77274 ____ T C
 TCCT AGGACCATC CA TCTTTGC GGC
 ||||| || ||||| |||
 TCCTGGTAG GT AGAAACG CCG
 CTC C A
 GAM2635 LOC149842 3' GCGAGAATGGATAATCT 85884 CC T
 GGA ATCCATTCTT GC
 ||| ||||| ||
 TCT TAGGTAAGAG CG
 AA T
 GAM2635 LOC203286 5' CCTGTAAATAGATGGTCC 92143 CATTC C
 GGACCATC TTTGC GG
 ||||| ||| ||
 CCTGGTAG AAATG CC
 AT__ T
 GAM2635 LOC253142 5' GCCGGCAGGGAAACGGTCTCTT 99225 _ ATCCA
 AAG GACC TTCTTTGCCGGC
 ||| ||| |||||
 TTC CTGG AAGGGACGGCCG
 T CA__
 GAM2635 LOC84549 3' AAAGAATGGATGACACTT 51676 GAC
 AAG CATCCATTCTT
 ||| |||||

			TTC GTAGGTAAGAAA			
			ACA			
GAM2636	GRIK5	3'	ATGATCCCACCAGCC	10877	C	CGAG
			GGC TGGTGGG ATCAT			
			CCG ACCACCC TAGTA			
			— ———			
GAM2636	MEF2D	3'	TTGACAATCTCACCGCCCGCC	20991	CT	GC CA
			GGC GGTGG GAGAT TCAA			
			CCG CCGCC CTCTA AGTT			
			C_ A_ AC			
GAM2636	PCLO	3'	TGATAATCTGCCTCCACCAGCC	95890	C	_ G C
			GGC TGGTGG GC AGAT ATCA			
			CCG ACCACC CG TCTA TAGT			
			_ TC _ A			
GAM2636	PFKL	5'	TGACAAGCCCACCAGGCC	12061		GAGA
			GGCCTGGTGGGC TCA			
			CCGGACCACCCG AGT			
			AAC_			
GAM2636	PTMA	3'	ATGATCTCGGATGACCAAACC	12557	CC	_ GG
			GG TGGT G CGAGATCAT			
			CC ACCA T GCTCTAGTA			
			AA G AG			
GAM2636	SRM	3'	TGGCTCTCGCCACCAACC	13402	CC	_
			GG TGGTGGGCGAGA TCA			
			CC ACCACCCGCTCT GGT			
			A_ C			
GAM2636	FLJ10916	3'	TGATTTTGGCCCCCAAACC	37393	CC	T _
			GG TGG GGGC GAGATCA			
			CC ACC CCG TTTTAGT			
			AA _ G			
GAM2636	FLJ12750	3'	ATGTGTCTACCCACCGGCC	45439	T	C _
			GGCC GGTGGG GAGAT CAT			
			CCGG CCACCC CTCTG GTA			
			_ A T			
GAM2636	GFR	3'	GATATGCCACCAAGCC	25447	C	AG
			GGC TGGTGGGCG ATC			
			CCG ACCACCCGT TAG			
			A A_			
GAM2636	KIAA0436	3'	ATGATTGTTACCAAGC	60684	C	GA
			GC TGGTGGGC GATCAT			

		CG ACCACTTG TTAGTA		
		A _		
GAM2636	SCYA14	5' TGAAGCTCCCACCAGGCC 53108	CG	A_
		GGCCTGGTGGG AG TCA		
		CCGGACCACCC TC AGT		
		_ GA		
GAM2636	SCYA14	5' TGAAGCTCCCACCAGGCC 16053	CG	A_
		GGCCTGGTGGG AG TCA		
		CCGGACCACCC TC AGT		
		_ GA		
GAM2636	LOC122786	3' TGAGTCTCCCACCAGACCG 74623	C	C GA
		CGG CTGGTGGG GA TCA		
		GCC GACCACCC CT AGT		
		A T G_		
GAM2636	LOC145123	3' ATGATCTCGGATGACCAAACC 68135	CC	_ GG
		GG TGGT G CGAGATCAT		
		CC ACCA T GCTCTAGTA		
		AA G AG		
GAM2636	LOC150928	3' ATGATCTCCGATGACCAAACC 74580	CC	GGG _
		GG TGGT CG AGATCAT		
		CC ACCA GC TCTAGTA		
		AA GTA C		
GAM2636	LOC254182	5' TGATGTCCCCACCAGGCC 97751	C	C G
		GGC TGGTGGG GA ATCA		
		CCG ACCACCC CT TAGT		
		_ _ G		
GAM2636	LOC51337	3' TCGCCGCCACCAGGGCC 34088	_	A_
		GGCC TGGTGGGCG GA		
		CCGG ACCACCCGC CT		
		G CG		
GAM2637	GRM1	3' GCCACTAATATACATCCCTAAT 7739	A_	CATT
	A	TATTAGGGAT ATATT TGGC		
		ATAATCCCTA TATAA ACCG		
		CA TC_		
GAM2637	SLC20A2	5' CCAAATGAACTGTCCT 23117	ATA	
		GGGATA TTCATTTGG		
		TCCTGT AAGTAAACC		
		C_		
GAM2637	KIAA1579	3' CCTGACCCATCCCTAATA 37148	AATAT	TTT
		TATTAGGGAT TCA GG		

ATAATCCCTA AGT CC
 CCC__ __
 GAM2637 NX-17 3' TGAATATCAGCCCCTAATA 40705 ATA_
 TATTAGGG ATATTCA
 ||||| |||||
 ATAATCCC TATAAGT
 CGAC
 GAM2637 LOC114928 3' GCCAAATGAATATCAAACTGA 57391 GGATA
 TTAG ATATTCATTTGGC
 ||| |||||
 AGTC TATAAGTAAACCG
 AAAAC
 GAM2637 LOC161589 3' GCTAAATGAATATTATCCCTAA 83159
 TA TATTAGGGATAATATTCATTTGGC
 |||||
 ATAATCCCTATTATAAGTAAATCG

 GAM2638 AAT1 3' CTCCTGATTCAAAGACTGT 81332 GCT_ A
 ACAGTCTT TCAG GAAG
 ||||| |||
 TGTGAGAA AGTC CTTC
 ACTT _
 GAM2638 ADCY7 3' CTCCTGAAGCAAGCCCAGGA 8490 AACAT A
 TCC GCTTGCTTCAG GAAG
 || | |||||
 AGG C GAACGAAGTC CTTC
 ACC__ C
 GAM2638 CERD4 3' CTCCTGAATGGCCCTGCTGG 24878 A TCTT _
 CCA CAG GCT TCAGAGAAG
 ||| ||| |||||
 GGT GTC CGG AGTCTCTC
 C C__ TA
 GAM2638 CHRN4 3' TCTCTGAATGCCTTGGA 7451 CAGTCTT _
 TCCAA GC TTCAGAGA
 |||| || |||||
 AGGTT CG AAGTCTCT
 C__ T
 GAM2638 COMT 3' TCTCTGAACTGCAACTG 7476 C _
 CAGT TTGC TTCAGAGA
 ||| ||| |||||
 GTCA AACG AAGTCTCT
 C TC
 GAM2638 COMT 3' TCTCTGAACTGCAACTG 24599 C _
 CAGT TTGC TTCAGAGA
 ||| ||| |||||
 GTCA AACG AAGTCTCT
 C TC
 GAM2638 ELF3 3' CTCTCCCACAGAGTGCTGGA 16681 A G _ CTTC
 TCCA CA TCT TG AGAG
 ||| ||| |||

			AGGT GT AGA AC TCTC		
			C G C CC__		
GAM2638	IGF1	3'	TCTCTGAATCTTGGCTGCTGGA 7083	A	TTGC
			TCCA CAGTC TTCAGAGA		
			AGGT GTCGG AAGTCTCT		
			C TTCT		
GAM2638	MADD	5'	CTTCTCTGAGATAAACTGATG 14857	A	C C
			CA CAGT TTG TTCAGAGAAG		
			GT GTCA AAT GAGTCTCTTC		
			A _ A		
GAM2638	MADD	5'	CTTCTCTGAGATAAACTGATG 56208	A	C C
			CA CAGT TTG TTCAGAGAAG		
			GT GTCA AAT GAGTCTCTTC		
			A _ A		
GAM2638	MADD	5'	CTTCTCTGAGATAAACTGATG 56222	A	C C
			CA CAGT TTG TTCAGAGAAG		
			GT GTCA AAT GAGTCTCTTC		
			A _ A		
GAM2638	MADD	5'	CTTCTCTGAGATAAACTGATG 56226	A	C C
			CA CAGT TTG TTCAGAGAAG		
			GT GTCA AAT GAGTCTCTTC		
			A _ A		
GAM2638	MADD	5'	CTTCTCTGAGATAAACTGATG 56230	A	C C
			CA CAGT TTG TTCAGAGAAG		
			GT GTCA AAT GAGTCTCTTC		
			A _ A		
GAM2638	MADD	5'	CTTCTCTGAGATAAACTGATG 56234	A	C C
			CA CAGT TTG TTCAGAGAAG		
			GT GTCA AAT GAGTCTCTTC		
			A _ A		
GAM2638	MAPK3	3'	CTCTCCCGCCAGACTGTTAGA 73776	C	T TTC
			TC AACAGTCT GC AGAG		
			AG TTGTCAGA CG TCTC		
			A C CCC		
GAM2638	METTL1	3'	CTTCCCAGTTGAGACTGCTGGA 19331	A	_ TCA
			TCCA CAGTCTTG CT GAG		
			AGGT GTCAGAGT GA TTC		
			C T CCC		
GAM2638	METTL1	3'	CTTCCCAGTTGAGACTGCTGGA 43778	A	_ TCA
			TCCA CAGTCTTG CT GAG		

AGGT GTCAGAGT GA TTC
 C T CCC
 GAM2638 METTL1 3' CTTCCCAGTTGAGACTGCTGGA 43779 A _ TCA
 TCCA CAGTCTTG CT GAG
 |||| ||||| || |||
 AGGT GTCAGAGT GA TTC
 C T CCC
 GAM2638 SLC22A12 5' TCTCTGGGGAGATGCTGGA 58692 ACA TG
 TCCA GTCT CTTCAGAGA
 |||| ||| |||||
 AGGT TAGA GGGGTCTCT
 CG_ _
 GAM2638 TFAP2C 3' CTTCTCTGAAAGTGGTGCT 13684 C TG _
 AGT T CTT CAGAGAAG
 ||| | |||||
 TCG G GAA GTCTCTTC
 T GT A
 GAM2638 APOL5 3' TTCCCTGAAGAATACTG 48377 C G A
 CAGT TT CTTCAG GAA
 |||| || ||||| |||
 GTCA AA GAAGTC CTT
 T _ C
 GAM2638 CAMKK2 3' TTTTAGAGAAGACTGTTG 22634 G TC
 CAACAGTCTT CT AGAG
 ||||| || ||||
 GTTGTGAGAA GA TTTT
 _ GA
 GAM2638 CREB-H 3' CTTTTCTAAGACTGCCTG 51873 A_ GCTTC
 CA CAGTCTT AGAGAAG
 || ||||| |||||
 GT GTCAGAA TCTTTTC
 CC _
 GAM2638 DKFZp761N1114 3' CTTCCCTGGTTCAGACTGTTGG 79785 T CT A
 CCAACAGTCT G TCAG GAAG
 ||||| || |||||
 GGTTGTCAGA C GGTC CTTC
 _ TT C
 GAM2638 FLJ10774 3' TCTCTGGCTGGACTGTT 45419 T TT
 AACAGTCT GC CAGAGA
 ||||| || |||||
 TTGTCAGG CG GTCTCT
 T _
 GAM2638 FLJ23047 3' CTTCTCTGAAGTTATGT 44933 GTCTT
 ACA GCTTCAGAGAAG
 ||| |||||
 TGT TGAAGTCTCTTC
 AT_
 GAM2638 HA-1 5' CTCCCCGAAGCCTTTTCCTGTT 66156 TCTT_ A_
 GGG TCCAACAG GCTTC GAG
 ||||| ||||| |||

			GGGTTGTC	CGAAG	CTC		
			CTTTTC	CCC			
GAM2638	HYPK	5'	TCCCTGAAGCTTCTAGAACTGG	33517	ACAG	T__	A
	A		TCCA	TCT	GCTTCAG	GA	
			AGGT	AGA	CGAAGTC	CT	
			CA__	TCTT	C		
GAM2638	MGC2217	5'	CTGGTAAGAAGACTGTTAGA	44429	C	G__	
			TC	AACAGTCTT	CT	TCAG	
			AG	TTGTCAGAA	GA	GGTC	
			A	_	AT		
GAM2638	mPA-PLA1	3'	CTTCTCTAAAGTGCTGTTGGA	58358	CTT	C	
			TCCAACAGT	GCTT	AGAGAAG		
			AGGTTGTCG	TGAA	TCTCTTC		
			__	A			
GAM2638	PEG10	3'	TCTCTGAAACGGCTATGGA	31207	AC	TTGC	
			TCCA	AGTC	TTCAGAGA		
			AGGT	TCGG	AAGTCTCT		
			A_	CA__			
GAM2638	UBAP	3'	TTCCCCTGAGACTGGTGGGA	76843	A	TTGCT	A_
			TCCA	CAGTC	TCAG	GAA	
			AGGT	GTCAG	AGTC	CTT	
			G	__	CC		
GAM2638	URKL1	3'	TCCTGACCCAGGACTGTTG	35795	CT	A	
			CAACAGTCTTG	TCAG	GA		
			GTTGTCAGGAC	AGTC	CT		
			CC	_			
GAM2638	LOC132617	3'	CTCTGAAGCAGTGGA	76414	ACAGTC		
			TCCA	TTGCTTCAGAG			
			AGGT	GACGAAGTCTC			
			__				
GAM2638	LOC145748	3'	TCTGGGAAGCAAGACTGATG	84476	A	AG	
			CA	CAGTCTTGCTTC	AGA		
			GT	GTCAGAACGAAG	TCT		
			A	GG			
GAM2638	LOC147639	3'	CTCCCAAGACTGTGGA	79009	A	CTTCA	
			TCC	ACAGTCTTG	GAG		
			AGG	TGTCAGAAC	CTC		
			_	C__			
GAM2638	LOC169966	5'	CTTCAGAGTAAGACTGTT	83434	CA		
			AACAGTCTTGCTT	GAG			

		TTGTCAGAATGAG	TTC		
		AC			
GAM2638	LOC200035 5'	CTTCTCTGACTCCCAGCTGCTG	73636	A	CTTGCT
	GA	TCCA CAGT TCAGAGAAG			
		AGGT GTCG AGTCTCTTC			
		C ACCCTC			
GAM2638	LOC219513 5'	CTTCCCTGAAGCAGCCCGTTGG	95983	AGTC	A
	G	TCCAAC TTGCTTCAG GAAG			
		GGGTTG GACGAAGTC CTTC			
		CCC_ C			
GAM2638	LOC220895 3'	CTTCCCAGTTGAGACTGCTGGA	92492	A	_ TCA
		TCCA CAGTCTTG CT GAG			
		AGGT GTCAGAGT GA TTC			
		C T CCC			
GAM2638	LOC222256 3'	TTCTGATAAGCAAGACTGTT	95913	—	
		AACAGTCTTGCT TCAGAG			
		TTGTCAGAACGA AGTCTT			
		AT			
GAM2638	LOC222499 5'	TCTCTGAAACAAGGTGG	96015	ACAG	C
		CCA TCTTG TTCAGAGA			
		GGT GGAAC AAGTCTCT			
		— A			
GAM2638	LOC255995 5'	CTTCTCTGTGGTGA	98749	TT	T
		AGTC GCT CAGAGAAG			
		TCAG TGG GTCTCTTC			
		— T			
GAM2638	LOC90110 5'	TTCTCTGATGACTGTT	62184	TTGCT	
		AACAGTC TCAGAGAA			
		TTGTCAG AGTCTCTT			
		T—			
GAM2638	LOC90288 3'	TCTCTGAGAAGCAGACATTGGA	62802	CA	T —
		TCCAA GTCT GCT TCAGAGA			
		AGGTT CAGA CGA AGTCTCT			
		A_ _ AG			
GAM2638	LOC91948 5'	TCTCTGAATGAACTGTT	68247	C	C
		AACAGT TTG TTCAGAGA			
		TTGTCA AGT AAGTCTCT			
		— —			
GAM2638	LOC91960 3'	CTTCTCTGAGGGCAGCGCTG	68283	C	—
		CAGT TTGCT TCAGAGAAG			

GTCG GACGG AGTCTCTTC

C G